

# S1: Study protocol

## Specification for Herd immunity April, 2019

### Overview:

This study is a PhD project conducted by Ms. Hina Hakim, supervised by Dr. Holly O. Witteman, PhD, and co-supervised by Dr. Daniel Reinharz, professors, and researchers at the Faculty of Medicine at Laval University. The purpose of this study is to evaluate the effects of visualization conveying the concept of community immunity or herd immunity on risk perception (towards individual, family, community and vulnerable people in communities) (primary outcome) and on emotions, attitudes, knowledge, and behavioural intentions (secondary outcomes).

### People Involved:

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Witteman, H (Research supervisor)  
Parent, E (Designer and adviser on designing)  
Aziaka, D (Developer/Programmer)  
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### *Collaborating with:*

- The members of the National Institute of Public Health of Quebec (INSPQ) whose comments we have received as we planned this project are: Eve Dubé, Marc Dionne, Rodica Gilca, Manale Ouakki and Dominique Gagnon.
- The members of Public Health Ontario whose comments we have received as we planned this project are: Beate Sander and Bryna Warshawsky.

### *Co-investigators:*

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## INTRODUCTION

### Background and rationale

Herd immunity or community immunity exists when enough people in a given population are vaccinated. This provides an indirect protection to those who cannot get vaccinated due to a weak immune system as either they are too young, too old or immunocompromised (vulnerable people). Recent drop in vaccine uptake results in an outbreak of vaccine-preventable diseases which increases the risk of everyone to be in at high risk of being infected, especially vulnerable people. Research suggested that effective communication about herd immunity may increase vaccination intention ([Betsch et al. 2017](#)).

Visualization is a powerful communication mechanism that uses pre-attentive processing to communicate large amounts of information rapidly in understandable and compelling ways ([Healey and Enns 2012](#)). A systematic review demonstrates that there are some interventions available for conveying the concept of community immunity, and very few evaluate interventions for their effects

on vaccine intentions and uptake as well as their precursors, such as knowledge, attitudes, and none on emotions (Hakim et al. 2018).

The purpose of this study is to evaluate the effects of visualization conveying the concept of community immunity on risk perception (to individual, family, community and vulnerable people in communities) (primary outcome) and on emotions, attitudes, knowledge, and behavioural intentions (secondary outcomes).

## INTRODUCTION

### Contexte et justification

L'immunité collective existe quand suffisamment de personnes dans une population donnée sont vaccinées. Cela fournit une protection indirecte aux personnes qui ne peuvent pas se faire vacciner en raison de la faiblesse de leur système immunitaire, du fait qu'elles soient trop jeunes, trop âgées ou immunodéprimées (personnes vulnérables). La récente baisse des taux de vaccination a entraîné une épidémie des maladies pouvant être prévenues par la vaccination, ce qui augmente le risque pour chacun d'être infecté, en particulier les personnes vulnérables. Les recherches ont suggéré qu'une communication efficace sur l'immunité collective pourrait augmenter l'intention de vaccination (Betsch et al. 2017).

La visualisation est un mécanisme de communication puissant qui utilise un traitement pré-attentif pour communiquer rapidement de grandes quantités d'informations de manière compréhensible et convaincante (Healey et Enns 2012). Une revue systématique a montré que certaines interventions permettent de véhiculer le concept d'immunité collective et que très peu évaluent leurs effets sur les intentions liées à la vaccination ainsi que sur leurs précurseurs, telles que les connaissances, les attitudes, mais aucune ne portant sur les émotions (Hakim et al 2018).

Le but de cette étude est d'évaluer les effets de la visualisation transmettant le concept d'immunité collective sur la perception du risque (pour l'individu, la famille, la communauté et les personnes vulnérables dans les communautés) (résultat principal) et sur les émotions, les attitudes, les connaissances et les intentions comportementales (résultats secondaires).

### Objectives

To evaluate the effects of visualization conveying the concept of community immunity on risk perception (to individual, family, community and vulnerable people in communities) (primary outcome) and on emotions, attitudes, knowledge, and behavioural intentions (secondary outcomes). We hypothesize that the new visualization “Herdimm” (A visualization developed iteratively in our previous study) will help people understand the concept of community immunity better than the control condition or comparator:

- Control: No information about community immunity or herd immunity
- Intervention: Herdimm visualization

We will also conduct secondary analyses comparing the effects of visualization (Herdimm) versus five comparators:

- Measles: Guardian visualization (<https://www.theguardian.com/society/ng-interactive/2015/feb/05/-sp-watch-how-measles-outbreak-spreads-when-kids-get-vaccinated>)
- Measles: Visualization by theotheredmund: (<https://imgur.com/gallery/8M7q8#J7LANQ4>)
- Generic: Robert Koch Institut visualization (<http://rocs.hu-berlin.de/D3/herd/>)
- Generic: SBS News visualization: ([https://www.sbs.com.au/news/two-sydney-babies-too-young-to-be-vaccinated-infected-with-measles?fbclid=IwAR1Rns\\_ycauiZeTeY1HC22eJe8JE6dwcQG0A9fgq305WCskIHBT\\_AGzExLE](https://www.sbs.com.au/news/two-sydney-babies-too-young-to-be-vaccinated-infected-with-measles?fbclid=IwAR1Rns_ycauiZeTeY1HC22eJe8JE6dwcQG0A9fgq305WCskIHBT_AGzExLE))
- Influenza: Public Health Agency of Canada Flu: Don't Pass It On! (<https://www.canada.ca/en/public-health/services/video/the-flu-don-t-pass-it-on.html>)

## Objectifs

Évaluer les effets de la visualisation traduisant le concept d'immunité communautaire sur la perception du risque (pour l'individu, la famille, la communauté et les personnes vulnérables dans la communauté) (résultat principal) et sur les émotions, les attitudes, les Connaissances et les intentions comportementales (résultats secondaires).

Nous émettons l'hypothèse que la nouvelle visualisation « Herdimm » (visualisation développée de manière itérative dans notre précédente étude) aidera les gens à mieux comprendre le concept d'immunité collective que la condition de contrôle ou le comparateur :

- Contrôle : aucune éducation sur l'immunité de la communauté ou l'immunité collective
- Intervention : visualisation « Herdimm »

Nous effectuerons également des analyses secondaires comparant les effets de la visualisation (Herdimm) à ceux de six comparateurs :

- Rougeole : Visualisation de The Guardian (<https://www.theguardian.com/society/ng-interactive/2015/feb/05/-sp-watch-how-measles-outbreak-spreads-when-kids-get-vaccinated>)
- Rougeole : Visualisation par theotheredmund: (<https://imgur.com/gallery/8M7q8#J7LANQ4>)
- Générique : Visualisation de l'Institut Robert Koch (<http://rocs.hu-berlin.de/D3/herd/>)
- Générique : Visualisation de SBS (The Special Broadcasting Service) : ([https://www.sbs.com.au/news/two-sydney-babies-too-young-to-be-vaccinated-infected-with-measles?fbclid=IwAR1Rns\\_ycauiZeTeY1HC22eJe8JE6dwcQG0A9fgq305WCskIHBT\\_AGzExLE](https://www.sbs.com.au/news/two-sydney-babies-too-young-to-be-vaccinated-infected-with-measles?fbclid=IwAR1Rns_ycauiZeTeY1HC22eJe8JE6dwcQG0A9fgq305WCskIHBT_AGzExLE))
- Influenza : Agence de la santé publique du Canada Grippe: ne le transmettez pas! (<https://www.canada.ca/fr/sante-publique/services/video/la-grippe-n-en-passez-pas-les-maux.html>)

## METHODS: Study design, participants, interventions, and outcomes

### Study/Trial Design

A factor is a variable that is controlled and varied during the course of an experiment. In the clinical trial, treatment can be a factor i.e., treatment vs. control. Factorial clinical trials are experiments that test the effect of more than one treatment using a type of design that permits an assessment of potential interactions among the treatments. The randomized controlled trial is the robust research method for determining whether a cause and effect relation exists between an intervention and an outcome. By using randomized controlled trial one can generate high-quality evidence when evaluating the effectiveness of an intervention.

This study will be a multi-armed factorial randomized controlled trial. Factorial experiments allow for the estimation of main effects of multiple factors in a single experiment by combining experimental conditions ([Gallis et al. 2019](#)). Thus, such designs are useful options in health behaviour research to efficiently compare more than one intervention. In this study, our primary analysis will be no education about community immunity or herd immunity (control) versus our developed visualization (herdimm).

Each participant will be randomly allocated to focus on one of four possible vaccine-preventable diseases that is: measles, pertussis, flu (influenza), or a generic vaccine-preventable disease (hereby referred to as “generic”). All aspects of the study (visualization, questionnaire) will be focused on that one disease for that participant.

For secondary analyses, we will compare effects of disease-specific interventions (e.g., the measles version of the visualization) to the effects of disease-matched interventions (comparators)



drawn from existing visualizations available online. Specifically, we will compare our measles visualization to other measles visualizations, and so on. The comparators are:

- Measles: Guardian visualization (<https://www.theguardian.com/society/ng-interactive/2015/feb/05/-sp-watch-how-measles-outbreak-spreads-when-kids-get-vaccinated>)
- Measles: Gif by theotheredmund: (<https://imgur.com/gallery/8M7q8#J7LANQ4>)
- Generic: Robert Koch Institut visualization (<http://rocs.hu-berlin.de/D3/herd/>)
- Generic: SBS News visualization: ([https://www.sbs.com.au/news/two-sydney-babies-too-young-to-be-vaccinated-infected-with-measles?fbclid=IwAR1Rns\\_ycauiZeTeY1HC22eJe8JE6dwcQG0A9fgq305WCskIHBT\\_AGzExLE](https://www.sbs.com.au/news/two-sydney-babies-too-young-to-be-vaccinated-infected-with-measles?fbclid=IwAR1Rns_ycauiZeTeY1HC22eJe8JE6dwcQG0A9fgq305WCskIHBT_AGzExLE))
- Generic: NHS visualization (<https://www.nhs.uk/Video/Pages/Vaccinationanimation2.aspx>)
- Influenza: Public Health Agency of Canada Flu: Don't Pass It On! (<https://www.canada.ca/en/public-health/services/video/the-flu-don-t-pass-it-on.html>)

The primary and secondary outcomes of the study which are risk perception, emotion, knowledge, trust (in information provided), attitudes and a validated scale about vaccination (Betsch et al. 2018) will be assessed in an online questionnaire.

Because three online visualizations are available only in English whereas our study will be conducted in both English and French, we will use slightly different randomization patterns for English- and French-speaking participants.

## **MÉTHODES: Conception de l'étude, participants, interventions et résultats**

### **Conception de l'étude**

Un facteur est une variable contrôlée et variée au cours d'une expérience. Dans l'essai clinique, le traitement peut être un facteur, par exemple traitement versus contrôle. Les essais cliniques factoriels sont des expériences qui testent l'effet de plus d'un traitement en utilisant un type de conception permettant d'évaluer les interactions potentielles entre les traitements. L'essai contrôlé randomisé est la méthode de recherche robuste pour déterminer s'il existe une relation de cause à effet entre une intervention et un résultat. En utilisant des essais contrôlés randomisés, on peut générer des preuves de haute qualité lors de l'évaluation de l'efficacité d'une intervention.

Cette étude sera un essai contrôlé randomisé factoriel multi-bras. Les expériences factorielles permettent d'estimer les effets principaux de plusieurs facteurs dans une seule expérience en combinant des conditions expérimentales. Ainsi, de tels modèles sont des options utiles dans la recherche sur les comportements en matière de santé pour comparer efficacement plus d'une intervention. Dans cette étude, notre analyse principale portera sur l'absence d'éducation concernant l'immunité de la communauté ou l'immunité collective (contrôle) par rapport à notre visualisation développée (herdimm).

Chaque participant se verra attribuer au hasard une des quatre maladies pouvant être prévenues par un vaccin aux fins de l'étude : rougeole, coqueluche, grippe ou une maladie générique évitable par un vaccin (ci-après dénommée « générique »). Tous les aspects de l'étude (visualisation, questionnaire) seront centrés sur cette maladie pour ce participant.

Pour les analyses secondaires, nous comparerons les effets des interventions spécifiques à une maladie (par exemple, la version de la visualisation portant sur la rougeole) avec les effets des interventions appariées à la maladie (comparateurs) tirés des visualisations existantes disponibles en ligne. Plus précisément, nous comparerons notre visualisation de la rougeole à d'autres visualisations de la rougeole, et ainsi de suite. Les comparateurs sont :

- Rougeole : visualisation de The Guardian (<https://www.theguardian.com/society/ng-interactive/2015/feb/05/-sp-watch-how-measles-outbreak-spreads-when-kids-get-vaccinated>)
- Rougeole : Visualisation par theotheredmund: (<https://imgur.com/gallery/8M7q8#J7LANQ4>)
- Générique : Visualisation de l'Institut Robert Koch (<http://rocs.hu-berlin.de/D3/herd/>)
- Générique : Visualisation de SBS (The Special Broadcasting Service) : ([https://www.sbs.com.au/news/two-sydney-babies-too-young-to-be-vaccinated-infected-with-measles?fbclid=IwAR1Rns\\_ycauiZeTeY1HC22eJe8JE6dwcQG0A9fgq305WCskIHBT\\_AGzExLE](https://www.sbs.com.au/news/two-sydney-babies-too-young-to-be-vaccinated-infected-with-measles?fbclid=IwAR1Rns_ycauiZeTeY1HC22eJe8JE6dwcQG0A9fgq305WCskIHBT_AGzExLE))



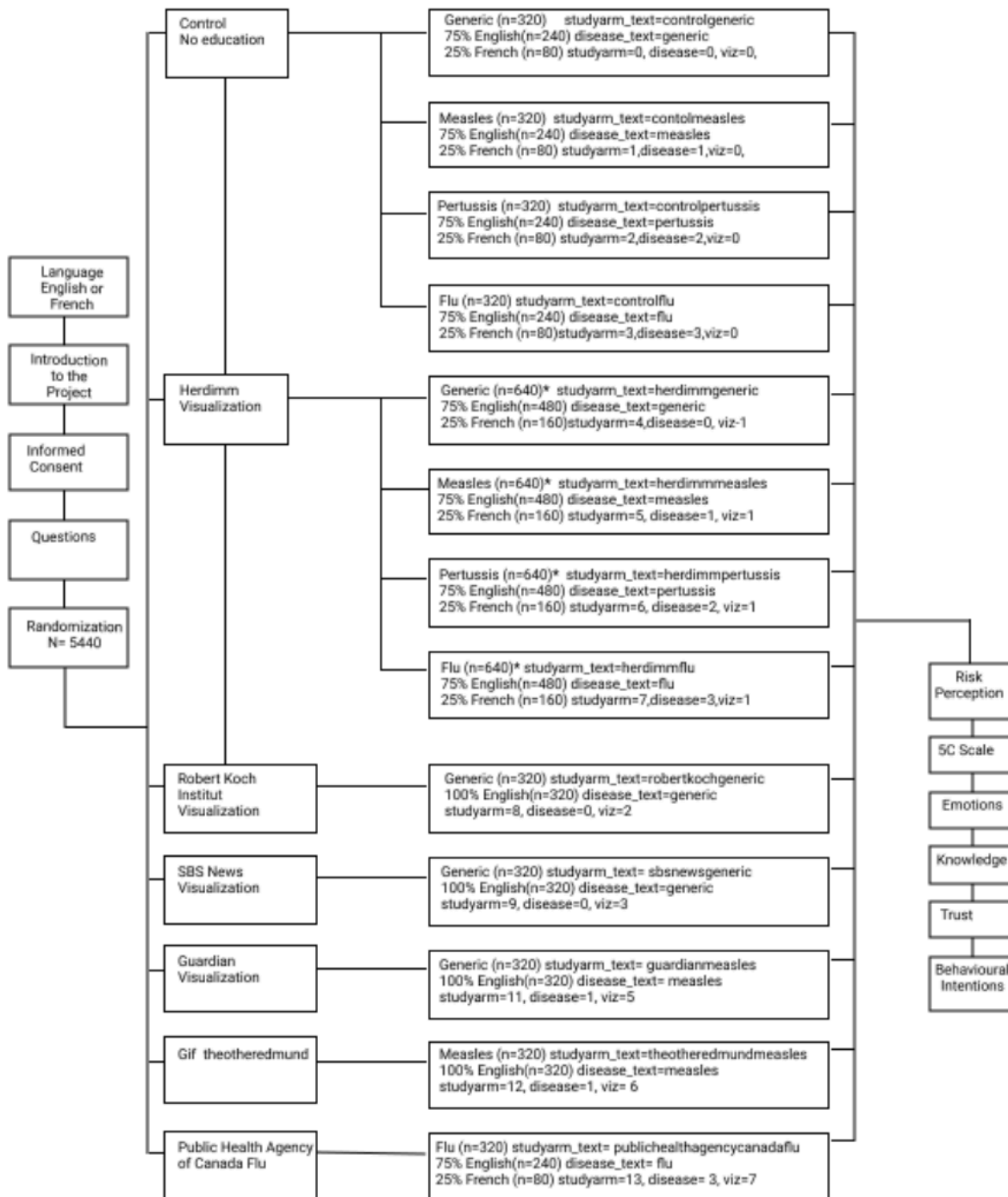
[measles?fbclid=IwAR1Rns\\_ycauiZeTeY1HC22eJe8JE6dwcQG0A9fgq305WCskIHBT\\_AGzExLE](https://www.youtube.com/watch?v=measles?fbclid=IwAR1Rns_ycauiZeTeY1HC22eJe8JE6dwcQG0A9fgq305WCskIHBT_AGzExLE))

- Générique: visualisation NHS (National Health Service)  
(<https://www.nhs.uk/Video/Pages/Vaccinationanimation2.aspx>)
- Influenza: Agence de la santé publique du Canada Grippe: ne le transmettez pas!  
(<https://www.canada.ca/fr/sante-publique/services/video/la-grippe-n-en-passez-pas-les-maux.html>)

Les résultats primaires et secondaires de l'étude (perception du risque, émotion, connaissances et une échelle validée concernant la vaccination (Betsch et al. 2018) seront évalués à l'aide d'un questionnaire en ligne.

Puisque trois visualisations en ligne sont disponibles uniquement en anglais alors que notre étude sera menée en anglais et en français, nous utiliserons des schémas de randomisation légèrement différents pour les participants anglophones et francophones.

Flow chart: Overall randomization



\* Sample size doubled for an embedded study of male versus female voice narration

### Study setting

- The online randomized controlled trial will be running in Qualtrics, an online survey software.

- Eligible participants will be adult members (18 years and over) of the general public in Canada (with a minimum of 25% of the sample with French as their preferred language compared to English).

### **Cadre de l'étude**

- L'essai contrôlé randomisé en ligne sera exécuté dans Qualtrics, un logiciel de sondage en ligne.
- Les participants admissibles seront des membres adultes (de 18 ans et plus) du grand public au Canada (au moins 25% de l'échantillon ayant le français comme langue préférée par rapport à l'anglais).

### **Eligibility criteria**

#### *Inclusion Criteria:*

- Members of the general population
- Be at least 18 years old
- To be able to provide free and informed consent and to be able to read and understand French or English
- Do not have vision problems not corrected
- To be able to use computer

#### *Exclusion Criteria:*

- Be under 18 years old
- Not being able to provide free and informed consent
- Have difficulty understanding and answering questions in French or English
- Have uncorrected vision problems

### **Critères d'éligibilité**

#### *Critères d'inclusion :*

- Membres de la population générale
- Avoir au moins 18 ans
- Être capable de donner son consentement libre et éclairé et savoir lire et comprendre le français ou l'anglais
- Ne pas avoir des problèmes de vision non corrigés
- Être en mesure d'utiliser un ordinateur

#### *Critères d'exclusion :*

- Avoir moins de 18 ans
- Être dans l'incapacité de donner un consentement libre et éclairé
- Avoir de la difficulté à comprendre et à répondre aux questions en français ou en anglais
- Avoir des problèmes de vision non corrigés

### **Interventions/ Interventions**

- Explained above (in section study design)
- Expliqué ci-dessus (dans la section conception de l'étude)



### **Incentive / Incitatif**

We will use paid panels that offer a small incentive (typically \$1-1.50) to members of panels to complete surveys.

Nous aurons recours à des panels rémunérés offrant un petit incitatif (généralement de 1 à 50 USD) aux membres des panels pour leur permettre de répondre aux sondages.

### **Outcomes / Résultats**

In this study we are evaluating the effects of visualization on risk perception (for the individual, family, community, and vulnerable people in communities) (1st outcome) and on emotions, attitudes, knowledge, and behavioural intentions (2nd outcome) with trust as a covariate.

Dans cette étude, nous évaluons les effets de la visualisation sur la perception du risque (pour l'individu, la famille, la communauté et les personnes vulnérables dans les communautés) (1<sup>er</sup> résultat) et sur les émotions, les attitudes, les Connaissances et les intentions comportementales (2<sup>e</sup> résultat) en utilisant la confiance comme covariable.

### **Participant timeline / Calendrier**

Following ethics approval from Laval University, we will collect data online from **December 2020 to February 2021**.

Suite à l'approbation éthique de l'Université Laval, nous collecterons les données en ligne du décembre 2020 au février 2021.

### **Sample size / Taille de l'échantillon**

To determine the sample size for this between-subjects design, we assumed a small effect size (Cohen's  $f=0.10$ ) and a statistical test power of 80% and 5% type 1 error, resulting in a required N of 320 participants for each arm with 75% of English and 25% of French speaking respondents which were sufficient to run our two-way analysis of variance. We estimated the sample size by using g power ([Universität Düsseldorf: gpower](#)) for continuous outcome.

Pour déterminer la taille de l'échantillon pour ce plan inter-sujets, nous avons supposé une petite taille d'effet ( $f=0,10$  de Cohen) et une puissance de test statistique de 80% et 5% d'erreur de type 1, ce qui a donné un N requis de 320 participants pour chaque bras avec 75% de répondants anglophones et 25% de répondants francophones qui étaient suffisants pour effectuer notre analyse de variance à deux voies. Nous avons estimé la taille de l'échantillon en utilisant la puissance ([Universität Düsseldorf: gpower](#)) pour un résultat continu.

### **Recruitment / Recrutement**

- The online randomized controlled trial will be run in Qualtrics, an online survey software.
- Eligible participants will be adult members of the general public in Canada (with a minimum of 25% of the sample with French as their preferred language compared to English).
- Participants will be recruited using established survey panels (subcontracted in Qualtrics).
- L'essai contrôlé randomisé en ligne sera exécuté dans Qualtrics, un logiciel de sondage en ligne.
- Les participants admissibles seront des membres adultes du grand public au Canada (au moins 25% de l'échantillon ayant le français comme langue préférée par rapport à l'anglais).
- Les participants seront recrutés sur des panels d'enquêtes établis (sous-traités dans Qualtrics)

## **METHODS: Assignment of interventions (for controlled trials)/MÉTHODES : Attribution des interventions (pour les essais contrôlés)**

### **Allocation/Allocation :**

#### **Sequence generation/Génération de séquences**

This study will be simple randomized (computer generated randomization) to eliminate selection bias, balancing both known and unknown prognostic factors, in the assignment of interventions.

Cette étude utilisera une randomisation simple (randomisation générée par ordinateur) pour éliminer le biais de sélection, en équilibrant les facteurs pronostiques connus et inconnus, dans l'attribution des interventions.

#### **Allocation concealment mechanism/Mécanisme de dissimulation des attributions**

This will be a single-blinded study because we cannot mask participants to the fact that they have been randomized to a visualization e.g., about measles. However, participants will not necessarily know the purpose of the study arm to which they are assigned, and investigators will be blinded to study arm during data analysis (investigators are not aware of whether the next eligible participant will be receiving treatment or control intervention).

Les participants et les investigateurs seront aveugles (à double insu) quant au processus d'attribution (les investigateurs ou les participants ne savent pas si le prochain participant éligible se verra attribué un traitement ou une intervention de contrôle).

### **Implementation/ Implémentation**

Qualtrics (computerized survey software) will use computerized randomization to automatically assign participants to interventions.

Qualtrics (logiciel d'enquête informatisé) utilisera la randomisation informatisée pour affecter automatiquement les participants aux interventions.

### **Blinding (masking)/ Aveuglement (masquage)**

This will be a single-blinded study because we cannot mask participants to the fact that they have been randomized to a visualization e.g., about measles. However, participants will not necessarily know the purpose of the study arm to which they are assigned, and investigators will be blinded to study arm during data analysis.

Ce sera une étude à simple insu car nous ne pouvons pas masquer aux participants le fait qu'ils ont été randomisés pour obtenir une visualisation p. ex., de la rougeole. Cependant, les participants ne connaîtront pas nécessairement le but du groupe d'étude auquel ils sont affectés et les investigateurs seront aveuglés pour étudier le groupe lors de l'analyse des données.

## **METHODS: Data collection, management, and analysis/MÉTHODES : collecte, traitement et analyse des données**

### **Data collection methods/Méthodes de collecte des données**

After seeking eligible participants' consent, participants will be randomized into different arms of the study and the effects of visualization on risk perception (for the individual, family, community, and vulnerable people in communities) (primary outcome) and on emotions, attitudes, knowledge, and behavioural intentions (secondary outcome) will be measured by questionnaire.

Après avoir recherché le consentement des participants éligibles, les participants seront randomisés dans différentes parties de l'étude et sur les effets de la visualisation sur la perception du risque (pour l'individu, la famille, la communauté et les personnes vulnérables dans les communautés) (résultat principal) et sur les émotions, les attitudes, les Connaissances et les intentions comportementales (résultat secondaire) seront mesurées par questionnaire.

### **Data management/Traitement des données**

All the information we collect will be confidential and used for research purposes only. In other words:

- Participant credentials will not be associated with the results of the study and no individual information will be presented in reports, publications or presentations.
- All data will be presented in aggregate form without individual identifiers.
- Data will be stored on Qualtrics servers located in Canada. When we work with data, the only people who will have access to our Qualtrics account will be the investigators and our team members who have complete and relevant ethics training. When the data is stored on our computers, each of our computers will be protected by a password. The data will be stored on a secure server, to which access is maintained and reserved for the members of the team (members of the team affiliated with Université Laval).

After the end of the study:

- Anonymized data (answers to questions in the survey including socio-demographic information) will be deposited in a public repository (Dataverse de l'Université Laval (Laval University)) which will allow data sharing with the scientific community. No information that would allow anyone to identify a person will be deposited in this public repository.
- Any other electronic data will be destroyed in June 2027.

Toutes les informations que nous recueillons seront confidentielles et utilisées uniquement à des fins de recherche. En d'autres termes:

- Les informations d'identification des participants ne seront pas associées aux résultats de l'étude et aucune information individuelle ne sera présentée dans des rapports, des publications ou des présentations.
- Toutes les données seront présentées sous forme agrégée, sans identificateurs individuels.
- Les données seront enregistrées sur les serveurs de Qualtrics situés au Canada. Lorsque nous travaillons avec des données, les seules personnes qui auront accès à notre compte Qualtrics seront les enquêteurs et les membres de notre équipe qui ont toute la formation éthique complète et pertinente. Lorsque les données seront stockées sur nos ordinateurs, chacun de nos ordinateurs sera protégé par un mot de passe. Les données seront stockées sur un serveur sécurisé, auquel l'accès est maintenu et réservé aux membres de l'équipe (membres de l'équipe affiliés à l'Université Laval).

Après la fin de l'étude :

- Les données anonymisées (réponses aux questions de l'enquête y inclus les informations sociodémographiques) seront déposées dans un dépôt public (Dataverse de l'Université Laval) qui permettra le partage des données avec la communauté scientifique. Aucune information qui permettrait d'identifier une personne ne sera déposée dans ce dépôt public.
- Toute autre donnée électronique sera détruite en juin 2027.



### Statistical methods/Méthodes statistiques

The type of comparison between intervention and control groups will be analyzed and reported as a superiority trial. The comparison will be done by using a linear regression for statistical analysis of continuous data.

Le type de comparaison entre le groupe d'intervention et le groupe de contrôle sera analysé et présenté comme un essai de supériorité. La comparaison sera effectuée en utilisant une régression linéaire pour l'analyse statistique des données continues.

Variables/ outcomes	Visualization (Herdimm)	Control 1(no visualization/ no education about community immunity)
Risk perception		
Emotions		
Attitudes		
Knowledge		
Behavioural intentions		
Trust		

Variables/ outcomes	Visualization (Herdimm)	Measles: Guardian visualization	Measles: theotheredmund visualization	Influenza: Public Health Agency of Canada Flu: Don't Pass It On!
Risk perception				
Emotions				
Attitudes				
knowledge				
Behavioural intentions				
Trust				

Variables/ outcomes	Visualization (Herdimm)	Generic: Robert Koch Institut visualization	Generic: SBS News visualization	Generic: NHS visualization
Risk perception				
Emotions				
Attitudes				
Knowledge				
Behavioural intentions				
Trust				

## **ETHICS AND DISSEMINATION/ÉTHIQUE ET DIFFUSION**

### **Research ethics approval/Approbation de l'éthique de la recherche**

This study is approved from the Laval University ethics committee (Approval No. 2017-137 Phase II A-6/ 10-09-2020).

Approbation de l'éthique de la recherche Cette étude est approuvée par le comité d'éthique de l'Université Laval (Approbation n° 2017-137 Phase II A-6/ 10-09-2020).

### **Consent/Consentement**

The free and informed consent will be sought before the start of the study. Participants will be able to withdraw from the study at anytime if they don't want to take part in the study. Participants who withdrew from the study in the middle and has not completed the study their data won't be analysed.

Le consentement libre et éclairé sera recherché avant le début de l'étude. Les participants pourront se retirer de l'étude à tout moment s'ils ne veulent pas participer à l'étude. Les participants qui se sont retirés de l'étude au milieu et qui n'ont pas terminé l'étude ne seront pas analysés.

### **Confidentiality/Confidentialité**

- Explained in the **data management** section above.
- Expliqué dans la section sur le **traitement des données** ci-dessus.

### **Declaration of interests/Déclaration d'intérêts**

- No competing interests.
- Pas de conflits d'intérêts.

### **Access to data/Accès aux données**

The data will be kept in the principal investigator's laboratory located on the campus of Laval University and only members of the research team will have access to data.

The data will be stored on Qualtrics Canadian servers, located in Canada and subject to Canadian data protection laws. When we work with data the only people who will have access to our Qualtrics account will be investigators and our team members who have all complete and relevant ethics training. When the data will be held on our computers each of our computers will be protected by the password. The data will be stored on a secure server, to which access is maintained and restricted to team members (team members affiliated at Laval university).

Les données seront conservées dans le laboratoire du chercheur principal situé sur le campus de l'Université Laval et seuls les membres de l'équipe de recherche auront accès aux données.

Les données seront stockées sur des serveurs canadiens de Qualtrics, situés au Canada. Lorsque nous travaillons avec des données, les seules personnes qui auront accès à notre compte Qualtrics seront les enquêteurs et les membres de notre équipe qui ont toute la formation éthique complète et pertinente. Lorsque les données seront stockées sur nos ordinateurs, chacun de nos ordinateurs sera protégé par un mot de passe. Les données seront stockées sur un serveur sécurisé, auquel l'accès est maintenu et réservé aux membres de l'équipe (membres de l'équipe affiliés à l'université Laval).

### **Dissemination policy/Politique de diffusion**

We intend to publish our results in a peer reviewed journal for healthcare professionals, the public, and other relevant groups to access.

Nous avons l'intention de publier nos résultats dans une revue évaluée par des pairs, à laquelle les professionnels de la santé, le public et d'autres groupes concernés pourront accéder.

### **Factors:**

<b><u>Factors:</u></b>	<b><u>Facteurs :</u></b>
Visualization (Herdimm)	Visualization (Herdimm)
Control 1(no visualization/ no education about community immunity)	Contrôle 1 (pas de visualisation / pas d'éducation sur l'immunité de la communauté)
Control 2 (Guardian visualization)	Contrôle 2 (visualization Guardian)
Control 3(Robert Koch Institut visualization)	Contrôle 3 (visualization Robert Koch Institut )
Control 4(theotheredmund visualization)	Contrôle 4 (visualization theotheredmund)
Control 5 (SBS news visualization)	Contrôle 5 (SBS news visualization)
Control 6 (NHS visualization)	Contrôle 6 (NHS visualization)
Control 7 (Flu: Public Health Agency of Canada Flu: Don't Pass It On!)	Contrôle 7 (Flu: Public Health Agency of Canada Flu: Don't Pass It On!)



## Measures

<u>Measures:</u>	<u>Mesures :</u>
Risk perception (primary outcome)	Perception du risque (résultat principal)
Emotions (secondary outcome)	Émotions (résultat secondaire)
Attitudes (secondary outcome)	Attitudes (résultat secondaire)
Knowledge (secondary outcome)	Connaissances (résultat secondaire)
Behavioural intentions (secondary outcome)	Intentions comportementales (résultat secondaire)
Trust (Covariates)	Confiance (covariables)

## Randomized variables:

<u>Randomized variables:</u>		<u>Valeurs randomisées :</u>
visualization	0= No education 1 = Herdimm 2 = Guardian visualization 3 = Robert Koch Institut visualization 4= theotheredmund visualization 5=SBS news visualization 6= NHS visualization 7= Flu: Public Health Agency of Canada	0= No education 1 = Herdimm 2 = visualization Guardian 3 = visualization Robert Koch Institut 4= visualization theotheredmund 5= SBS news visualization 6= NHS visualization 7= Flu: Public Health Agency of Canada

## References:

- Betsch, Cornelia, Robert Böhm, Lars Korn, and Cindy Holtmann. 2017. "On the Benefits of Explaining Herd Immunity in Vaccine Advocacy." *Nature Human Behaviour* 1 (3): s41562–017 – 0056.
- Betsch, Cornelia, Philipp Schmid, Dorothee Heinemeier, Lars Korn, Cindy Holtmann, and Robert Böhm. 2018. "Beyond Confidence: Development of a Measure Assessing the 5C Psychological Antecedents of Vaccination." *PloS One* 13 (12): e0208601.
- Gallis, John A., Gary G. Bennett, Dori M. Steinberg, Sandy Askew, and Elizabeth L. Turner. 2019. "Randomization Procedures for Multicomponent Behavioral Intervention Factorial

- Trials in the Multiphase Optimization Strategy Framework: Challenges and Recommendations.” *Translational Behavioral Medicine*. <https://doi.org/10.1093/tbm/iby131>.
- Hakim, Hina, Thierry Provencher, Christine T. Chambers, S. Michelle Driedger, Eve Dube, Teresa Gavaruzzi, Anik M. C. Giguere, et al. 2018. “Interventions to Help People Understand Community Immunity: A Systematic Review.” *Vaccine*, December. <https://doi.org/10.1016/j.vaccine.2018.11.016>.
- Healey, Christopher G., and James T. Enns. 2012. “Attention and Visual Memory in Visualization and Computer Graphics.” *IEEE Transactions on Visualization and Computer Graphics* 18 (7): 1170–88.
- “Universität Düsseldorf: Gpower.” n.d. Accessed July 28, 2020. <https://www.psychologie.hhu.de/arbeitsgruppen/allgemeine-psychologie-und-arbeitspsychologie/gpower.html>.

# S2: Study questionnaire

## contag\_phase3b

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### Start of Block: Introduction

#### Intro **Project Description**

### **Project Description**

#### **Introduction**

Thank you for participating in this study. This project is a collaboration with University Laval, Public Health Ontario (PHO) and The National Institute of Public Health of Quebec (INSPQ).

In this study, we will first give you some information to do with contagious diseases and then ask you to answer some questions.

The survey will take about 15 to 20 minutes. Your name will not be recorded anywhere in this survey. Researchers will not be able to associate your name with your answers. If you choose to leave the study, you can stop at any time. You may choose not to answer any questions you don't want to answer. If, for some reason, you cannot complete the survey, you may **restart** the survey at a later time by clicking on the survey link in your email invitation. You will have to **restart** the survey from the beginning.

If you become worried about your health while taking this survey, please talk to a healthcare provider.

#### **About the researchers**

This study is a PhD project conducted by Ms. Hina Hakim, PhD student, supervised by Holly O. Witteman, PhD, professor and researcher in the Faculty of Medicine at Laval University. Ms. Hakim is co-supervised by Dr. Daniel Reinharz, professor and researcher in the Faculty of Medicine at Laval University.

#### **Purpose of the study**

The purpose of this study is to evaluate the effects of information to do with contagious diseases on risk perception, knowledge, emotions, attitudes, beliefs, and behavioural intentions.

#### **What your participation entails**

Participating in this study will involve following:

- Answering survey questions.
- You may be asked to view or listen to information, which will require either the ability to read or hear.

- You may be asked to briefly visit another website in the middle the survey.

### **Risks and benefits**

The risks associated with participating in the study, specifically:

- Information and questions, we ask may make you feel uncomfortable or anxious. We suggest you to consult your healthcare professional, as the case may be;
- You may feel some discomfort having to focus on a computer screen.
- You may feel some fatigue from concentrating throughout the survey.

There is no personal benefit to participate in this study, however, the information we gather will help us to evaluate the effects of the information, which may help in improving the way health information is shared, and population health.

Your help means a lot to us. We thank you again for taking the time to complete this survey.

### **Confidentiality and data protection**

All information we collect will be confidential and used only for research purposes.

In other words:

- Participant credentials will not be associated with the results of the study and no individual information will be presented in reports, publications or presentations.
- All data will be presented in aggregate form without individual identifiers.
- Data will be stored on Qualtrics servers located in Canada. When we work with data, the only people who will have access to our Qualtrics account will be the investigators and our team members who have complete and relevant ethics training. When the data is stored on our computers, each of our computers will be protected by a password. The data will be stored on a secure server, to which access is maintained and reserved for the members of the team (members of the team affiliated with Université Laval).

After the end of the study:

- Anonymized data (answers to questions in the survey including socio-demographic information) will be deposited in a public repository (Dataverse de l'Université Laval (Laval University)) which will allow data sharing with the scientific community. No information that would allow anyone to identify a person will be deposited in this public repository.
- Any other electronic data will be destroyed in June 2027.

### **Contact people**

If you have any questions about the research study, or if you experience a problem as a result of participating in the study, please contact:



Holly Witteman  
Laval University  
Tel: (418) 656-2131 ext: 403981  
Email: holly.witteman@fmed.ulaval.ca

If you have concerns about your rights as a participant in this study or any complaints, you can communicate with the University Laval Ombudsman at:

Pavillon Alphonse-Desjardins  
2325, rue de l'Université, Local 3320  
Québec, QC G1V 0A6  
Tel: 418-656-3081  
Toll free: 1-866-323-2271  
Email: info@ombudsman.ulaval.ca

*This project has been approved by Laval University Research Ethics Board: Approval No. 2017-137 Phase II A-6/ 10-09-2020*

## **Description du projet**

### **Introduction**

Merci de participer à cette étude. Ce projet est réalisé en collaboration avec l'Université Laval, Santé publique Ontario (SPO) et l'Institut national de la santé publique du Québec (INSPQ).

Dans cette étude, nous vous donnerons d'abord quelques informations sur les maladies contagieuses et nous vous demanderons ensuite de répondre à quelques questions.

L'enquête durera environ 15 à 20 minutes. Votre nom ne sera enregistré nulle part dans cette enquête. Les chercheurs et les chercheuses ne pourront pas associer votre nom à vos réponses. Si vous choisissez de quitter l'étude, vous pouvez y mettre fin à tout moment. Vous pouvez choisir d'ignorer les questions auxquelles vous ne voulez pas répondre. Si, pour une raison quelconque, vous ne pouvez pas compléter le sondage, vous pourrez le recommencer ultérieurement en cliquant sur le lien du sondage dans votre invitation par courrier électronique. Vous devrez alors **recommencer** le sondage depuis le début.

Si vous ressentez de l'inquiétude pour votre santé en répondant à cette enquête, parlez-en à un.e professionnel.le de la santé.

### **À propos des chercheurs**

Cette étude est un projet de doctorat conduit par Mme Hina Hakim, candidate au doctorat en santé communautaire, supervisée par Mme Holly Witteman, Ph.D., professeure et chercheuse à la Faculté de médecine de l'Université Laval. Mme Hakim est co-dirigée par le Dr Daniel Reinharz, professeur et chercheur à la Faculté de médecine de l'Université Laval.

### **Aperçu de l'étude**

Le but de cette étude est d'évaluer l'effet de certaines informations relatives aux maladies contagieuses sur la perception du risque, la connaissance, les émotions, les attitudes, les croyances et les intentions comportementales.

### **Ce que votre participation implique**

Participer à cette étude impliquera de :

- Répondre aux questions du sondage
- Il se peut qu'on vous demande de lire ou d'écouter des informations, ce qui nécessiterait la capacité de voir ou d'entendre
- Il se peut que l'on vous demande de visiter brièvement un autre site web au milieu de l'enquête.

### **Risques et avantages**

Il existe certains risques associés à la participation à l'étude, notamment :

- Les informations et questions posées pourraient vous rendre mal à l'aise ou anxieux. Nous vous suggérons de consulter votre professionnel.le de la santé;
- Vous pouvez ressentir un certain inconfort à fixer un écran d'ordinateur.
- Vous pourriez ressentir de la fatigue due à la concentration demandée tout au long du sondage.

Il n'y a aucun avantage personnel à participer à cette étude. Toutefois, les données recueillies nous aideront à évaluer les effets des informations transmises, ce qui pourrait aider à améliorer le partage des informations sur la santé ainsi que la santé de la population.

Votre aide compte beaucoup pour nous. Nous vous remercions encore de prendre le temps de répondre à ce sondage.

### **Confidentialité et protection des données**

Toutes les informations que nous recueillons seront confidentielles et utilisées uniquement à des fins de recherche.

En d'autres termes:

- Les informations d'identification des participant.e.s ne seront pas associées aux résultats de l'étude et aucune information individuelle ne sera présentée dans des rapports, des publications ou des présentations.
- Toutes les données seront présentées sous forme agrégée, sans identificateurs individuels.
- Les données seront enregistrées sur les serveurs de Qualtrics situés au Canada. Lorsque nous travaillons avec des données, les seules personnes qui auront accès à notre compte Qualtrics seront les enquêteurs et les membres de notre équipe qui ont toute la formation éthique complète et pertinente. Lorsque les données seront stockées sur nos ordinateurs, chacun de nos ordinateurs sera protégé par un mot de passe. Les données seront stockées sur un serveur sécurisé, auquel l'accès est maintenu et réservé aux membres de l'équipe (membres de l'équipe affiliés à l'Université Laval).

Après la fin de l'étude :

- Les données anonymisées (réponses aux questions de l'enquête y inclus les informations sociodémographiques) seront déposées dans un dépôt public (Dataverse de l'Université Laval) qui permettra le partage des données avec la communauté scientifique. Aucune information qui permettrait d'identifier une personne ne sera déposée dans ce dépôt public.
- Toute autre donnée électronique sera détruite en juin 2027.

### Contact

Si vous avez des questions sur le projet de recherche, ou si vous rencontrez un problème en participant à l'étude, veuillez contacter:

Prof. Holly Witteman  
 Université Laval  
 Téléphone: (418) 656-2131 ext: 403981  
 Courriel: [holly.witteman@fmed.ulaval.ca](mailto:holly.witteman@fmed.ulaval.ca)

Si vous avez des plaintes ou des préoccupations au sujet de vos droits en tant que participant à cette étude, vous pouvez communiquer avec l'Ombudsman de l'Université Laval à:

Pavillon Alphonse-Desjardins  
 2325, rue de l'Université, Local 3320  
 Québec, QC G1V 0A6  
 Téléphone: 418-656-3081  
 Sans frais: 1-866-323-2271  
 Courriel: [info@ombudsman.ulaval.ca](mailto:info@ombudsman.ulaval.ca)

*« Ce projet a été approuvé par le Comité d'éthique de la recherche de l'Université Laval :  
 No d'approbation 2017-137 Phase II A-6/ 10-09-2020 »*

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### End of Block: Introduction

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### Start of Block: Consent for participation:



#### Consent

1. I have been informed about the nature and purpose of this study and the research procedures.
2. I was informed in English which is a language I understand fluently.
3. I understand that my participation in this study is voluntary and that I can withdraw at any time without penalty or consequences of any kind.
4. I understand that the information collected is confidential and will only be used for research purposes.
5. I have read the project description and informed consent form and I voluntarily agree to participate in this study.

☐ Yes I Consent (1)

☐ No I do not Consent (0)

#### Consent

1. J'ai été informé.e de la nature et du but de cette étude et des procédures de recherche.
2. J'ai été informé.e en français, une langue que je comprends et parle couramment.
3. Je comprends que ma participation à cette étude est volontaire et que je peux me retirer à tout moment sans pénalité ni conséquence d'aucune sorte.



4. Je comprends que les informations recueillies sont confidentielles et ne seront utilisées qu'à des fins de recherche.
5. J'ai lu la description du projet et le formulaire de consentement éclairé et j'accepte volontairement de participer à cette étude.

☐ Oui, je consens (1)

☐ Non, je n'y consens pas (0)

*Skip To: End of Survey If I have been informed about the nature and purpose of this study and the research procedures. I wa... = No I do not Consent*

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yearofbirth In what year were you born?

▼ Prefer not to answer (888) ... 2010 (2010)

yearofbirth Quelle est votre année de naissance?

▼ Je préfère ne pas répondre (888) ... 2010 (2010)



bornincanada Were you born in Canada? (Check one only.)

- ☐ Prefer not to answer (888)
- ☐ Yes (1)
- ☐ No - What year did you arrive in Canada? (0)

bornincanada Êtes-vous né(e) au Canada? (Cochez une seule réponse)

- ☐ Je préfère ne pas répondre (888)
- ☐ Oui (1)
- ☐ Non - en quelle année êtes-vous arrivé(e) au Canada? (0)

Display This Question:

If If False



hp Were you born outside North America? (Check one only.)

- ☐ Prefer not to answer (888)
- ☐ Yes (1)
- ☐ No - What year did you arrive in North America? (0)
- 

hp Êtes-vous né(e) hors de l'Amérique du Nord? (Cochez une seule réponse)

- ☐ Je préfère ne pas répondre (888)
- ☐ Oui (1)
- ☐ Non - en quelle année êtes-vous arrivé(e) au Canada? (0)
- 



language What language would you feel most comfortable speaking in with your healthcare provider? (doctor, nurse, dentist, pharmacist)? (Check all that apply.)

- ☐ Prefer not to answer (888)
- ☐ ☐ English (1)
- ☐ ☐ French (2)
- ☐ ☐ Other, please specify: (3)
-

language Dans quelle(s) langue(s) êtes-vous à l'aise pour parler avec un.e professionnel.le de la santé (médecin, infirmière, dentiste, pharmacien)? (Cochez tout ce qui s'applique)

☐ Je préfère ne pas répondre (888)

☐ Anglais (1)

☐ Français (2)

☐ Autre, précisez : (3)

---





ethnicity Which of the following best describes your racial or ethnic group(s)? (Check all that apply.)

- ☐ Prefer not to answer (888)
- ☐ Asian - East (e.g., Chinese, Japanese, Korean) (1)
- ☐ Asian - Central (e.g., Kazakhstani, Uzbekistani) (2)
- ☐ Asian - South (e.g., Indian, Pakistani, Sri Lankan) (3)
- ☐ Asian - South-East (e.g., Malaysian, Filipino, Vietnamese) (4)
- ☐ Black - African (e.g., Ghanaian, Kenyan, Somali) (13)
- ☐ Black - Caribbean (e.g., Barbadian, Jamaican) (14)
- ☐ Black - North American (e.g., Canadian, American) (15)
- ☐ First Nations (16)
- ☐ Indigenous or aboriginal person from outside of North America (e.g., Maori, Quechua) (5)
- ☐ Inuit (8)
- ☐ Latin American (e.g., Chilean, Mexican, Salvadorian) (9)
- ☐ Metis (Metis Nation in Canada) (10)
- ☐ Middle Eastern (e.g., Egyptian, Iranian, Lebanese) (12)
- ☐ North African (e.g., Moroccan, Tunisian) (11)
- ☐ White - European (e.g., English, Italian, Portuguese, Russian) (6)
- ☐ White - North American (e.g., Canadian, American) (7)

☐

Other, please specify: (17)

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ethnicity Laquelle ou lesquelles des catégories suivantes représente(nt) vos groupes raciaux ou ethniques? (Cochez tout ce qui s'applique.)

- ☐ Je préfère ne pas répondre (888)
- ☐ Asiatique de l'est (p.ex. : Chinois, Japonais, Coréen) (1)
- ☐ Asiatique du centre (p.ex. : Kazakh, Ouzbek) (2)
- ☐ Asiatique du sud (p.ex.: Indien, Pakistanais, Sri Lankais) (3)
- ☐ Asiatique du sud-est (p.ex.: Malaisien, Philippin, Vietnamien) (4)
- ☐ Noir Africain (p.ex. : Ghanéen, Kenyan, Somalien) (13)
- ☐ Noir Caribéen (p.ex. : Barbadien, Jamaïcain) (14)
- ☐ Noir Nord-américain (p.ex.: Canadien, États-Unien) (15)
- ☐ Premières Nations (16)
- ☐ Autochtone ou aborigène de hors de l'Amérique du Nord (p.ex.: Maori, Quechua) (5)
- ☐ Inuit (8)
- ☐ Latino-américain (p.ex. : Chilien, Mexicain, Salvadorien) (9)
- ☐ Métis (Nation métisse du Canada) (10)
- ☐ Moyen-oriental (p.ex. : Égyptien, Iranien, Libanais) (12)
- ☐ Maghrébin (p.ex. : Marocain, Tunisien) (11)
- ☐ Blanc Européen (p.ex.: Français, Anglais, Italien, Portugais, Russe) (6)

☐

Blanc Nord-Américain (p.ex.: Canadien, États-Unien) (7)

☐

Autre, précisez : (17)

---



disability Do you consider yourself to have a disability (e.g, physical disability, sensory disability (e.g., hearing or vision loss), chronic illness, learning disability, mental illness, developmental disability or other)? (Check one only.)

☐ ☐ Prefer not to answer (888)

☐ ☐ No disability (0)

☐ ☐ Yes, at least one disability (1)

disability Considérez-vous avoir une limitation ou un handicap (p.ex. : limitation ou déficience physique, limitation ou déficience sensorielle (p.ex. perte de vision ou d'audition), maladie chronique, trouble d'apprentissage, trouble de santé mentale, trouble du développement ou autre)? (Cochez une seule réponse.)

☐ Je préfère ne pas répondre (888)

☐ Non, aucune limitation ou handicap (0)

☐ Oui, au moins une limitation ou handicap (1)

---



techdisability Do you have a disability that limits your access to technology and computer based tools (p.ex. : computer, tablet, interactive terminal)? (Check one only.)

☐ ☐ Prefer not to answer (888)

☐ No (0)

☐ Yes (1)



techdisability Selon vous, avez-vous une limitation ou un handicap qui vous limite l'accès à certains outils technologiques ou informatiques (p.ex. : ordinateur, tablette, borne interactive)? (Cochez une seule réponse.)

- ☐ Je préfère ne pas répondre (888)
- ☐ Non (0)
- ☐ Oui (1)



sexatbirth What sex were you assigned at birth, meaning on your original birth certificate? (Check one only.)

- ☐ Prefer not to answer (888)
- ☐ Female (1)
- ☐ Male (2)

sexatbirth Quel sexe vous a-t-on assigné à la naissance, sur votre certificat de naissance original? (Cochez une seule réponse.)

- ☐ Je préfère ne pas répondre (888)
- ☐ Féminin (1)
- ☐ Masculin (2)



genderidentity Do you consider yourself: (Check one only.)

- ☐ Female (1)
- ☐ Male (2)
- ☐ Indigenous or other cultural gender minority identity (e.g., two-spirit) (3)
- ☐ Something else (e.g. non-binary, gender fluid) (4)
- ☐ Prefer not to answer (888)

genderidentity Vous considérez-vous comme : (Cochez une seule réponse.)

- ☐ Une femme (1)
- ☐ Un homme (2)
- ☐ Un(e) minorité de genre culturelle, autochtone ou autre (p.ex. : bispiritualité, « *two-spirit* ») (3)
- ☐ Autre (p.ex. : non-binaire, « *gender fluid* ») (4)
- ☐ Je préfère ne pas répondre (888)



income What was your total family income before taxes last year? (Check one only.)

- ☐ ☐ Prefer not to answer (888)
- ☐ ☐ 24 999 or less (1)
- ☐ ☐ 25 000 to 49 999 (2)
- ☐ ☐ 50 000 to 99 999 (3)
- ☐ ☐ 100 000 or more (4)
- ☐ ☐ Do not know (5)

income Quel était le revenu total (avant impôts) de votre ménage l'an dernier? (Cochez une seule réponse.)

- ☐ Je préfère ne pas répondre (888)
- ☐ 24 999 et moins (1)
- ☐ 25 000 à 49 999 (2)
- ☐ 50 000 à 99 999 (3)
- ☐ 100 000 ou plus (4)
- ☐ Je ne sais pas (5)



supportedbyincome How many people does this income support?

- ☐ Number of people: (1) \_\_\_\_\_
- ☐ Prefer not to answer (888)

supportedbyincome Combien de personnes ce revenu supporte-t-il?

- ☐ Nombre de personnes : (1) \_\_\_\_\_
- ☐ Je préfère ne pas répondre (888)



educationlevel What is the highest level of education you have completed? (Check one only.)

- ☐ ☐ Prefer not to answer (888)
- ☐ ☐ Elementary School (completed or not) (1)
- ☐ ☐ High School Diploma (2)
- ☐ ☐ Apprenticeship or trade certificate or diploma (3)
- ☐ ☐ College or polytechnical school certificate or diploma (4)
- ☐ ☐ University degree, bachelor level or below (5)
- ☐ ☐ University graduate degree (Master's level) (6)
- ☐ ☐ University graduate degree (Doctorate level) (7)
- ☐ ☐ Do not know (8)

educationlevel Quel est votre plus haut niveau de scolarité complété? (Cochez une seule réponse.)

- ☐ Je préfère ne pas répondre (888)
  - ☐ Études primaires (complétées ou non) (1)
  - ☐ Diplôme d'études secondaires (2)
  - ☐ Certificat ou diplôme d'apprentissage ou de métier (3)
  - ☐ Attestation ou diplôme d'études professionnelles (DES, ASP, DEP) (4)
  - ☐ Études universitaires de premier cycle (Certificat, Baccalauréat) ou moins (5)
  - ☐ Études universitaires de deuxième cycle (DESS, Maîtrise) (6)
  - ☐ Études universitaires de troisième cycle (Doctorat) (7)
  - ☐ Je ne sais pas (8)
-

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**End of Block: Standard Sociodemo Canada**

---

**Start of Block: Individualism and Collectivism Scale - Triandis1998 - EN/FR**

ih1 **Evaluate how well each of the following statements applies to you:**

I'd rather depend on myself rather than others.

- ☐ Never or definitely not =1 (1)
- ☐ 2 (2)
- ☐ 3 (3)
- ☐ 4 (4)
- ☐ 5 (5)
- ☐ 6 (6)
- ☐ 7 (7)
- ☐ 8 (8)
- ☐ Always or definitely yes = 9 (9)

ih1

**Évaluez à quel point chacun des énoncés suivants s'applique à vous :**

Je préfère dépendre de moi-même que des autres

- ☐ Jamais ou définitivement non = 1 (1)
  - ☐ 2 (2)
  - ☐ 3 (3)
  - ☐ 4 (4)
  - ☐ 5 (5)
  - ☐ 6 (6)
  - ☐ 7 (7)
  - ☐ 8 (8)
  - ☐ Toujours ou définitivement oui = 9 (9)
-

ih2 I rely on myself most of the time, I rarely rely on others.

- ☐ Never or definitely not = 1 (1)
- ☐ 2 (2)
- ☐ 3 (3)
- ☐ 4 (4)
- ☐ 5 (5)
- ☐ 6 (6)
- ☐ 7 (7)
- ☐ 8 (8)
- ☐ Always or definitely yes = 9 (9)

ih2 Je me fie à moi-même la plupart du temps, rarement aux autres.

- ☐ Jamais ou définitivement non = 1 (1)
  - ☐ 2 (2)
  - ☐ 3 (3)
  - ☐ 4 (4)
  - ☐ 5 (5)
  - ☐ 6 (6)
  - ☐ 7 (7)
  - ☐ 8 (8)
  - ☐ Toujours ou définitivement oui = 9 (9)
-



ih3 I often do "my own thing."

- ☐ Never or definitely not = 1 (1)
- ☐ 2 (2)
- ☐ 3 (3)
- ☐ 4 (4)
- ☐ 5 (5)
- ☐ 6 (6)
- ☐ 7 (7)
- ☐ 8 (8)
- ☐ Always or definitely yes = 9 (9)

ih3 Je fais souvent « ma propre affaire. »

- ☐ Jamais ou définitivement non = 1 (1)
  - ☐ 2 (2)
  - ☐ 3 (3)
  - ☐ 4 (4)
  - ☐ 5 (5)
  - ☐ 6 (6)
  - ☐ 7 (7)
  - ☐ 8 (8)
  - ☐ Toujours ou définitivement oui = 9 (9)
-

ih4 My personal identity, independent of others, is very important to me.

- ☐ Never or definitely not = 1 (1)
- ☐ 2 (2)
- ☐ 3 (3)
- ☐ 4 (4)
- ☐ 5 (5)
- ☐ 6 (6)
- ☐ 7 (7)
- ☐ 8 (8)
- ☐ Always or definitely yes = 9 (9)

ih4 Mon identité personnelle, indépendante des autres, est très importante pour moi.

- ☐ Jamais ou définitivement non = 1 (1)
  - ☐ 2 (2)
  - ☐ 3 (3)
  - ☐ 4 (4)
  - ☐ 5 (5)
  - ☐ 6 (6)
  - ☐ 7 (7)
  - ☐ 8 (8)
  - ☐ Toujours ou définitivement oui = 9 (9)
-

iv1 It is important that I do my job better than others.

- ☐ Never or definitely not = 1 (1)
- ☐ 2 (2)
- ☐ 3 (3)
- ☐ 4 (4)
- ☐ 5 (5)
- ☐ 6 (6)
- ☐ 7 (7)
- ☐ 8 (8)
- ☐ Always or definitely yes = 9 (9)

iv1 Il est important pour moi de faire mon travail mieux que les autres.

- ☐ Jamais ou définitivement non = 1 (1)
  - ☐ 2 (2)
  - ☐ 3 (3)
  - ☐ 4 (4)
  - ☐ 5 (5)
  - ☐ 6 (6)
  - ☐ 7 (7)
  - ☐ 8 (8)
  - ☐ Toujours ou définitivement oui = 9 (9)
-

iv2 Winning is everything.

- ☐ Never or definitely not = 1 (1)
- ☐ 2 (2)
- ☐ 3 (3)
- ☐ 4 (4)
- ☐ 5 (5)
- ☐ 6 (6)
- ☐ 7 (7)
- ☐ 8 (8)
- ☐ Always or definitely yes = 9 (9)

iv2 Gagner, c'est tout ce qui compte.

- ☐ Jamais ou définitivement non = 1 (1)
  - ☐ 2 (2)
  - ☐ 3 (3)
  - ☐ 4 (4)
  - ☐ 5 (5)
  - ☐ 6 (6)
  - ☐ 7 (7)
  - ☐ 8 (8)
  - ☐ Toujours ou définitivement oui = 9 (9)
-

iv3 Competition is the law of nature.

☐ Never or definitely not = 1 (1)

☐ 2 (2)

☐ 3 (3)

☐ 4 (4)

☐ 5 (5)

☐ 6 (6)

☐ 7 (7)

☐ 8 (8)

☐ Always or definitely yes = 9 (9)

iv3 La compétition est la loi de la nature.

☐ Jamais ou définitivement non = 1 (1)

☐ 2 (2)

☐ 3 (3)

☐ 4 (4)

☐ 5 (5)

☐ 6 (6)

☐ 7 (7)

☐ 8 (8)

☐ Toujours ou définitivement oui = 9 (9)

---

iv4 When another person does better than I do, I get tense and aroused.

- ☐ Never or definitely not = 1 (1)
- ☐ 2 (2)
- ☐ 3 (3)
- ☐ 4 (4)
- ☐ 5 (5)
- ☐ 6 (6)
- ☐ 7 (7)
- ☐ 8 (8)
- ☐ Always or definitely yes = 9 (9)

iv4 Quand une autre personne fait mieux que moi, je deviens tendu et agité.

- ☐ Jamais ou définitivement non = 1 (1)
  - ☐ 2 (2)
  - ☐ 3 (3)
  - ☐ 4 (4)
  - ☐ 5 (5)
  - ☐ 6 (6)
  - ☐ 7 (7)
  - ☐ 8 (8)
  - ☐ Toujours ou définitivement oui = 9 (9)
-

ch1 If a coworker gets a prize, I would feel proud.

- ☐ Never or definitely not = 1 (1)
- ☐ 2 (2)
- ☐ 3 (3)
- ☐ 4 (4)
- ☐ 5 (5)
- ☐ 6 (6)
- ☐ 7 (7)
- ☐ 8 (8)
- ☐ Always or definitely yes = 9 (9)

ch1 Si un collègue remportait un prix, je me sentrais fier.

- ☐ Jamais ou définitivement non = 1 (1)
  - ☐ 2 (2)
  - ☐ 3 (3)
  - ☐ 4 (4)
  - ☐ 5 (5)
  - ☐ 6 (6)
  - ☐ 7 (7)
  - ☐ 8 (8)
  - ☐ Toujours ou définitivement oui = 9 (9)
-



ch2 The well-being of my coworkers is important to me.

- ☐ Never or definitely not = 1 (1)
- ☐ 2 (2)
- ☐ 3 (3)
- ☐ 4 (4)
- ☐ 5 (5)
- ☐ 6 (6)
- ☐ 7 (7)
- ☐ 8 (8)
- ☐ Always or definitely yes = 9 (9)

ch2 Le bien-être de mes collègues est important pour moi.

- ☐ Jamais ou définitivement non = 1 (1)
  - ☐ 2 (2)
  - ☐ 3 (3)
  - ☐ 4 (4)
  - ☐ 5 (5)
  - ☐ 6 (6)
  - ☐ 7 (7)
  - ☐ 8 (8)
  - ☐ Toujours ou définitivement oui = 9 (9)
-

ch3 To me, pleasure is spending time with others.

- ☐ Never or definitely not = 1 (1)
- ☐ 2 (2)
- ☐ 3 (3)
- ☐ 4 (4)
- ☐ 5 (5)
- ☐ 6 (6)
- ☐ 7 (7)
- ☐ 8 (8)
- ☐ Always or definitely yes = 9 (9)

ch3 Pour moi, le plaisir c'est de passer du temps avec les autres.

- ☐ Jamais ou définitivement non = 1 (1)
  - ☐ 2 (2)
  - ☐ 3 (3)
  - ☐ 4 (4)
  - ☐ 5 (5)
  - ☐ 6 (6)
  - ☐ 7 (7)
  - ☐ 8 (8)
  - ☐ Toujours ou définitivement oui = 9 (9)
-

ch4 I feel good when I cooperate with others.

- ☐ Never or definitely not = 1 (1)
- ☐ 2 (2)
- ☐ 3 (3)
- ☐ 4 (4)
- ☐ 5 (5)
- ☐ 6 (6)
- ☐ 7 (7)
- ☐ 8 (8)
- ☐ Always or definitely yes = 9 (9)

ch4 Je me sens bien lorsque je coopère avec les autres.

- ☐ Jamais ou définitivement non = 1 (1)
  - ☐ 2 (2)
  - ☐ 3 (3)
  - ☐ 4 (4)
  - ☐ 5 (5)
  - ☐ 6 (6)
  - ☐ 7 (7)
  - ☐ 8 (8)
  - ☐ Toujours ou définitivement oui = 9 (9)
-

cv1 Parents and children must stay together as much as possible.

- ☐ Never or definitely not = 1 (1)
- ☐ 2 (2)
- ☐ 3 (3)
- ☐ 4 (4)
- ☐ 5 (5)
- ☐ 6 (6)
- ☐ 7 (7)
- ☐ 8 (8)
- ☐ Always or definitely yes = 9 (9)

cv1 Les parents et les enfants doivent rester ensemble autant que possible.

- ☐ Jamais ou définitivement non = 1 (1)
  - ☐ 2 (2)
  - ☐ 3 (3)
  - ☐ 4 (4)
  - ☐ 5 (5)
  - ☐ 6 (6)
  - ☐ 7 (7)
  - ☐ 8 (8)
  - ☐ Toujours ou définitivement oui = 9 (9)
-

cv2 It is my duty to take care of my family, even when I have to sacrifice what I want.

- ☐ Never or definitely not = 1 (1)
- ☐ 2 (2)
- ☐ 3 (3)
- ☐ 4 (4)
- ☐ 5 (5)
- ☐ 6 (6)
- ☐ 7 (7)
- ☐ 8 (8)
- ☐ Always or definitely yes = 9 (9)

cv2 C'est mon devoir de prendre soin de ma famille, même si je dois sacrifier mes propres désirs.

- ☐ Jamais ou définitivement non = 1 (1)
  - ☐ 2 (2)
  - ☐ 3 (3)
  - ☐ 4 (4)
  - ☐ 5 (5)
  - ☐ 6 (6)
  - ☐ 7 (7)
  - ☐ 8 (8)
  - ☐ Toujours ou définitivement oui = 9 (9)
-

cv3 Family members should stick together, no matter what sacrifices are required.

- ☐ Never or definitely not = 1 (1)
- ☐ 2 (2)
- ☐ 3 (3)
- ☐ 4 (4)
- ☐ 5 (5)
- ☐ 6 (6)
- ☐ 7 (7)
- ☐ 8 (8)
- ☐ Always or definitely yes = 9 (9)

cv3 Les membres d'une même famille devraient être solidaires peu importe les sacrifices requis.

- ☐ Jamais ou définitivement non = 1 (1)
  - ☐ 2 (2)
  - ☐ 3 (3)
  - ☐ 4 (4)
  - ☐ 5 (5)
  - ☐ 6 (6)
  - ☐ 7 (7)
  - ☐ 8 (8)
  - ☐ Toujours ou définitivement oui = 9 (9)
-

cv4 It is important to me that I respect the decisions made by my groups.

- ☐ Never or definitely not = 1 (1)
- ☐ 2 (2)
- ☐ 3 (3)
- ☐ 4 (4)
- ☐ 5 (5)
- ☐ 6 (6)
- ☐ 7 (7)
- ☐ 8 (8)
- ☐ Always or definitely yes = 9 (9)

cv4 Il est important pour moi de respecter les décisions prises par mes groupes.

- ☐ Jamais ou définitivement non = 1 (1)
  - ☐ 2 (2)
  - ☐ 3 (3)
  - ☐ 4 (4)
  - ☐ 5 (5)
  - ☐ 6 (6)
  - ☐ 7 (7)
  - ☐ 8 (8)
  - ☐ Toujours ou définitivement oui = 9 (9)
-



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#### End of Block: Individualism and Collectivism Scale - Triandis1998 - EN/FR

---

#### Start of Block: media

*Display This Question:*

*If viz = 0*

control Now we need your answers to some questions about contagious diseases.

control Nous avons maintenant également besoin de votre avis sur certaines questions concernant les maladies contagieuses.

---

*Display This Question:*

*If viz = 1*

*Or viz = 2*

robertkochgeneric Now you will visit another website with some information about contagious diseases.

When you are done, **please come back here to finish the survey.**

robertkochgeneric Vous allez maintenant visiter un autre site web contenant des informations sur les maladies contagieuses.

Lorsque vous aurez terminé, **revenez ici pour terminer ce sondage, s'il vous plaît.**

---

*Display This Question:*

*If viz = 1*

*And disease = 0*

*And voice = 1*

herdimmgenericmale [Please click here to go to the other website](#)

herdimmgenericmale [Veuillez cliquer ici pour accéder à l'autre site web](#)

*Display This Question:*

*If viz = 1*

*And disease = 0*

*And voice = 2*

herdimmgenericfemale [Please click here to go to the other website](#)

herdimmgenericfemale [Veuillez cliquer ici pour accéder à l'autre site web](#)

*Display This Question:*

*If viz = 1*

*And disease = 1*

*And voice = 1*

herdimmmeaslesmale [Please click here to go to the other website](#)

herdimmmeaslesmale [Veuillez cliquer ici pour accéder à l'autre site web](#)

*Display This Question:*

*If viz = 1*

*And disease = 1*

*And voice = 2*

herdimmmeaslesfemale [Please click here to go to the other website](#)

herdimmmeaslesfemale [Veuillez cliquer ici pour accéder à l'autre site web](#)

*Display This Question:*

*If viz = 1*

*And disease = 2*

*And voice = 1*

herdimpertussismale [Please click here to go to the other website](#)

herdimpertussismale [Veuillez cliquer ici pour accéder à l'autre site web](#)

---

*Display This Question:*

*If viz = 1*

*And disease = 2*

*And voice = 2*

herdimpertussisfema [Please click here to go to the other website](#)

herdimpertussisfema [Veuillez cliquer ici pour accéder à l'autre site web](#)

---

*Display This Question:*

*If viz = 1*

*And disease = 3*

*And voice = 1*

herdimmlumale [Please click here to go to the other website](#)

herdimmlumale [Veuillez cliquer ici pour accéder à l'autre site web](#)

---

*Display This Question:*

*If viz = 1*

*And disease = 3*

*And voice = 2*

herdimmlufemale [Please click here to go to the other website](#)

herdimmlufemale [Veuillez cliquer ici pour accéder à l'autre site web](#)

---

*Display This Question:*

*If Q\_Language = EN*

*And viz = 2*

robertkoch [Please click here to go to the other website](#)

robertkoch NA

---

*Display This Question:*

*If Q\_Language = EN*

*And viz = 3*

sbsnewsgeneric Now we ask you to please watch the video below with some information to do with contagious diseases and then continue the survey.

sbsnewsgeneric NA

---

*Display This Question:*

*If Q\_Language = EN*

*And viz = 5*

guardianmeasles

Now we ask you to please watch the video below with some information to do with contagious diseases and then continue the survey.

guardianmeasles NA

---

*Display This Question:*

*If Q\_Language = EN*

*And viz = 6*

theotheredmundmeasle Now we ask you to please watch the video below with some information to do with contagious diseases and then continue the survey.

theotherredmundmeasle NA

---

*Display This Question:*

*If viz = 7*

publichealthagencyca Now we ask you to please watch the video below with some information to do with contagious diseases and then continue the survey.

publichealthagencyca Nous vous demandons maintenant de visionner la vidéo ci-dessous, qui contient des informations sur les maladies contagieuses, puis de poursuivre le sondage.

---

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**End of Block: media**

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**Start of Block: Risk Perception**

riskpercep1 Imagine there are two groups of 100 people each. In one group, there is 1 UNvaccinated person surrounded by 99 vaccinated people. In the other group, there is 1 vaccinated person surrounded by 99 UNvaccinated people. Who is at higher risk of getting infected with [\\${e://Field/diseasedescEN}](#)?

The 1 UNvaccinated person surrounded by 99 vaccinated people is at higher risk.	They are both equally at risk.	The 1 vaccinated person surrounded by a group of 99 UNvaccinated people is at higher risk.
---	--------------------------------	--



riskpercep1 Imaginez deux groupes composés de 100 personnes dans chacun d'eux. Dans un des groupes, il y a 99 individus vaccinés et une personne NON vaccinée. Dans l'autre groupe, il y a 1 personne vaccinée et 99 NON vaccinées. Qui serait le plus à risque de contracter [\\${e://Field/diseasedescFR-CA}](#)?

La personne NON vaccinée dans un groupe de 99 personnes vaccinées est plus à risque.	Elles ont le même niveau de risque.	La personne vaccinée dans un groupe de 99 personnes NON vaccinées est plus à risque.
--	-------------------------------------	--



riskpercep2 A person's decision to be vaccinated or not against [\\${e://Field/diseasedescEN}](#) affects only them, individually.

- ☐ strongly disagree (1)
- ☐ moderately disagree (2)
- ☐ slightly disagree (3)
- ☐ neutral (4)
- ☐ slightly agree (5)
- ☐ moderately agree (6)
- ☐ strongly agree (7)

riskpercep2 La décision d'une personne de se faire vacciner ou non contre [\\${e://Field/diseasedescFR-CA}](#) ne touche que cette personne individuellement.

- ☐ fortement en désaccord (1)
- ☐ modérément en désaccord (2)
- ☐ légèrement en désaccord (3)
- ☐ neutre (4)
- ☐ légèrement en accord (5)
- ☐ modérément en accord (6)
- ☐ fortement en accord (7)





riskpercep3 People who are vaccinated against [\\${e://Field/diseasedescEN}](#) are less likely to pass it on to others.

- ☐ strongly disagree (1)
- ☐ moderately disagree (2)
- ☐ slightly disagree (3)
- ☐ neutral (4)
- ☐ slightly agree (5)
- ☐ moderately agree (6)
- ☐ strongly agree (7)

riskpercep3 Les personnes qui sont vaccinées contre [\\${e://Field/diseasedescFR-CA}](#) sont moins susceptibles de la transmettre.

- ☐ fortement en désaccord (1)
- ☐ modérément en désaccord (2)
- ☐ légèrement en désaccord (3)
- ☐ neutre (4)
- ☐ légèrement en accord (5)
- ☐ modérément en accord (6)
- ☐ fortement en accord (7)



riskpercep4 My decision to be vaccinated against [\\${e://Field/diseasedescEN}](#) has **no impact** on anyone else's chances of catching [\\${e://Field/diseasedescEN}](#).

- ☐ strongly disagree (1)
- ☐ moderately disagree (2)
- ☐ slightly disagree (3)
- ☐ neutral (4)
- ☐ slightly agree (5)
- ☐ moderately agree (6)
- ☐ strongly agree (7)

riskpercep4 Ma décision de me faire vacciner ou non contre [\\${e://Field/diseasedescFR-CA}](#) n'a **aucune incidence** sur les chances des autres de contracter [\\${e://Field/diseasedescFR-CA}](#).

- ☐ fortement en désaccord (1)
- ☐ modérément en désaccord (2)
- ☐ légèrement en désaccord (3)
- ☐ neutre (4)
- ☐ légèrement en accord (5)
- ☐ modérément en accord (6)
- ☐ fortement en accord (7)



riskpercep5 My decision NOT to be vaccinated against  $\{e://Field/diseasedescEN\}$  has **no impact** on anyone else's chances of catching  $\{e://Field/diseasedescEN\}$ .

- ☐ strongly disagree (1)
- ☐ moderately disagree (2)
- ☐ slightly disagree (3)
- ☐ neutral (4)
- ☐ slightly agree (5)
- ☐ moderately agree (6)
- ☐ strongly agree (7)

riskpercep5 Ma décision de ne PAS me faire vacciner contre  $\{e://Field/diseasedescFR-CA\}$  n'a **aucune incidence** sur les chances des autres de contracter  $\{e://Field/diseasedescFR-CA\}$ .

- ☐ fortement en désaccord (1)
- ☐ modérément en désaccord (2)
- ☐ légèrement en désaccord (3)
- ☐ neutre (4)
- ☐ légèrement en accord (5)
- ☐ modérément en accord (6)
- ☐ fortement en accord (7)



riskpercep6 If I get vaccinated against [\\${e://Field/diseasedescEN}](#), it lowers the risk of vulnerable people in my community (babies, young children, older people, cancer patients) getting sick.

- ☐ strongly disagree (1)
- ☐ moderately disagree (2)
- ☐ slightly disagree (3)
- ☐ neutral (4)
- ☐ slightly agree (5)
- ☐ moderately agree (6)
- ☐ strongly agree (7)

riskpercep6 Si je me fais vacciner contre [\\${e://Field/diseasedescFR-CA}](#), cela réduit le risque que des personnes vulnérables de ma communauté (bébés, jeunes enfants, personnes âgées, patients atteints de cancer) tombent malades.

- ☐ fortement en désaccord (1)
  - ☐ modérément en désaccord (2)
  - ☐ légèrement en désaccord (3)
  - ☐ neutre (4)
  - ☐ légèrement en accord (5)
  - ☐ modérément en accord (6)
  - ☐ fortement en accord (7)
-

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### End of Block: Risk Perception

---

### Start of Block: 5CScale



confidence1 I am completely confident that vaccines are safe.

- ☐ strongly disagree (1)
- ☐ moderately disagree (2)
- ☐ slightly disagree (3)
- ☐ neutral (4)
- ☐ slightly agree (5)
- ☐ moderately agree (6)
- ☐ strongly agree (7)

confidence1 Je suis complètement confiant que les vaccins sont sans danger.

- ☐ fortement en désaccord (1)
- ☐ modérément en désaccord (2)
- ☐ légèrement en désaccord (3)
- ☐ neutre (4)
- ☐ légèrement en accord (5)
- ☐ modérément en accord (6)
- ☐ fortement en accord (7)



confidence2 Vaccinations are effective.

- ☐ strongly disagree (1)
- ☐ moderately disagree (2)
- ☐ slightly disagree (3)
- ☐ neutral (4)
- ☐ slightly agree (5)
- ☐ moderately agree (6)
- ☐ strongly agree (7)

confidence2 Les vaccins sont efficaces.

- ☐ fortement en désaccord (1)
- ☐ modérément en désaccord (2)
- ☐ légèrement en désaccord (3)
- ☐ neutre (4)
- ☐ légèrement en accord (5)
- ☐ modérément en accord (6)
- ☐ fortement en accord (7)



confidence3 Regarding vaccines, I am confident that public authorities decide in the best interest of the community.

- ☐ strongly disagree (1)
- ☐ moderately disagree (2)
- ☐ slightly disagree (3)
- ☐ neutral (4)
- ☐ slightly agree (5)
- ☐ moderately agree (6)
- ☐ strongly agree (7)

confidence3 En ce qui concerne les vaccins, je suis convaincu que les autorités publiques décident dans le meilleur intérêt de la communauté.

- ☐ fortement en désaccord (1)
  - ☐ modérément en désaccord (2)
  - ☐ légèrement en désaccord (3)
  - ☐ neutre (4)
  - ☐ légèrement en accord (5)
  - ☐ modérément en accord (6)
  - ☐ fortement en accord (7)
- 



complacency1 Vaccination is unnecessary because vaccine-preventable diseases are not common anymore.

- ☐ strongly disagree (1)
- ☐ moderately disagree (2)
- ☐ slightly disagree (3)
- ☐ neutral (4)
- ☐ slightly agree (5)
- ☐ moderately agree (6)
- ☐ strongly agree (7)



complacency1 La vaccination est inutile car les maladies évitables par la vaccination ne sont plus courantes.

- ☐ fortement en désaccord (1)
  - ☐ modérément en désaccord (2)
  - ☐ légèrement en désaccord (3)
  - ☐ neutre (4)
  - ☐ légèrement en accord (5)
  - ☐ modérément en accord (6)
  - ☐ fortement en accord (7)
- 



complacency2 My immune system is so strong, it also protects me against diseases.

- ☐ strongly disagree (1)
- ☐ moderately disagree (2)
- ☐ slightly disagree (3)
- ☐ neutral (4)
- ☐ slightly agree (5)
- ☐ moderately agree (6)
- ☐ strongly agree (7)

complacency2 Mon système immunitaire est suffisamment fort pour me protéger des maladies.

- ☐ fortement en désaccord (1)
- ☐ modérément en désaccord (2)
- ☐ légèrement en désaccord (3)
- ☐ neutre (4)
- ☐ légèrement en accord (5)
- ☐ modérément en accord (6)
- ☐ fortement en accord (7)



complacency3 Vaccine-preventable diseases are not so severe that I should get vaccinated.

- ☐ strongly disagree (1)
- ☐ moderately disagree (2)
- ☐ slightly disagree (3)
- ☐ neutral (4)
- ☐ slightly agree (5)
- ☐ moderately agree (6)
- ☐ strongly agree (7)

complacency3 Les maladies évitables par la vaccination ne sont pas graves au point de devoir me faire vacciner.

- ☐ fortement en désaccord (1)
  - ☐ modérément en désaccord (2)
  - ☐ légèrement en désaccord (3)
  - ☐ neutre (4)
  - ☐ légèrement en accord (5)
  - ☐ modérément en accord (6)
  - ☐ fortement en accord (7)
- 



constraints1 Everyday stress prevents me from getting vaccinated.

- ☐ strongly disagree (1)
- ☐ moderately disagree (2)
- ☐ slightly disagree (3)
- ☐ neutral (4)
- ☐ slightly agree (5)
- ☐ moderately agree (6)
- ☐ strongly agree (7)

constraints1 Le stress quotidien m'empêche de me faire vacciner.

- ☐ fortement en désaccord (1)
- ☐ modérément en désaccord (2)
- ☐ légèrement en désaccord (3)
- ☐ neutre (4)
- ☐ légèrement en accord (5)
- ☐ modérément en accord (6)
- ☐ fortement en accord (7)



constraints2 For me, it is inconvenient to receive vaccinations.

- ☐ strongly disagree (1)
- ☐ moderately disagree (2)
- ☐ slightly disagree (3)
- ☐ neutral (4)
- ☐ slightly agree (5)
- ☐ moderately agree (6)
- ☐ strongly agree (7)

constraints2 Pour moi, il est peu pratique de recevoir des vaccins.

- ☐ fortement en désaccord (1)
- ☐ modérément en désaccord (2)
- ☐ légèrement en désaccord (3)
- ☐ neutre (4)
- ☐ légèrement en accord (5)
- ☐ modérément en accord (6)
- ☐ fortement en accord (7)



constraints3 Visiting the doctor's makes me feel uncomfortable; this keeps me from getting vaccinated.

- ☐ strongly disagree (1)
- ☐ moderately disagree (2)
- ☐ slightly disagree (3)
- ☐ neutral (4)
- ☐ slightly agree (5)
- ☐ moderately agree (6)
- ☐ strongly agree (7)

constraints3 Visiter le médecin me met mal à l'aise; cela m'empêche de me faire vacciner.

- ☐ fortement en désaccord (1)
- ☐ modérément en désaccord (2)
- ☐ légèrement en désaccord (3)
- ☐ neutre (4)
- ☐ légèrement en accord (5)
- ☐ modérément en accord (6)
- ☐ fortement en accord (7)



calculation1 When I think about getting vaccinated, I weigh benefits and risks to make the best decision possible.

- ☐ strongly disagree (1)
- ☐ moderately disagree (2)
- ☐ slightly disagree (3)
- ☐ neutral (4)
- ☐ slightly agree (5)
- ☐ moderately agree (6)
- ☐ strongly agree (7)

calculation1 Quand je pense à me faire vacciner, je mesure les avantages et les risques pour prendre la meilleure décision possible.

- ☐ fortement en désaccord (1)
  - ☐ modérément en désaccord (2)
  - ☐ légèrement en désaccord (3)
  - ☐ neutre (4)
  - ☐ légèrement en accord (5)
  - ☐ modérément en accord (6)
  - ☐ fortement en accord (7)
- 



calculation2 For each and every vaccination, I closely consider whether it is useful for me.

- ☐ strongly disagree (1)
- ☐ moderately disagree (2)
- ☐ slightly disagree (3)
- ☐ neutral (4)
- ☐ slightly agree (5)
- ☐ moderately agree (6)
- ☐ strongly agree (7)

calculation2 Pour chaque vaccin, j'évalue de près si cela m'est utile.

- ☐ fortement en désaccord (1)
- ☐ modérément en désaccord (2)
- ☐ légèrement en désaccord (3)
- ☐ neutre (4)
- ☐ légèrement en accord (5)
- ☐ modérément en accord (6)
- ☐ fortement en accord (7)



calculation3 It is important for me to fully understand the topic of vaccination, before I get vaccinated.

- ☐ strongly disagree (1)
- ☐ moderately disagree (2)
- ☐ slightly disagree (3)
- ☐ neutral (4)
- ☐ slightly agree (5)
- ☐ moderately agree (6)
- ☐ strongly agree (7)



calculat3 Il est important pour moi de bien comprendre tout ce qu'englobe la vaccination avant de me faire vacciner.

- ☐ fortement en désaccord (1)
  - ☐ modérément en désaccord (2)
  - ☐ légèrement en désaccord (3)
  - ☐ neutre (4)
  - ☐ légèrement en accord (5)
  - ☐ modérément en accord (6)
  - ☐ fortement en accord (7)
- 



collectiverespon1 When everyone else is vaccinated, I don't have to get vaccinated, too.

- ☐ strongly disagree (1)
- ☐ moderately disagree (2)
- ☐ slightly disagree (3)
- ☐ neutral (4)
- ☐ slightly agree (5)
- ☐ moderately agree (6)
- ☐ strongly agree (7)

collectiverespon1 Quand tous les autres sont vaccinés, je n'ai pas à me faire vacciner aussi.

- ☐ fortement en désaccord (1)
- ☐ modérément en désaccord (2)
- ☐ légèrement en désaccord (3)
- ☐ neutre (4)
- ☐ légèrement en accord (5)
- ☐ modérément en accord (6)
- ☐ fortement en accord (7)



collectiverespon2 I get vaccinated because I can also protect people with a weaker immune system.

- ☐ strongly disagree (1)
- ☐ moderately disagree (2)
- ☐ slightly disagree (3)
- ☐ neutral (4)
- ☐ slightly agree (5)
- ☐ moderately agree (6)
- ☐ strongly agree (7)

collectiverespon2 Je me fais vacciner parce que je peux aussi protéger les personnes dont le système immunitaire est plus faible.

- ☐ fortement en désaccord (1)
  - ☐ modérément en désaccord (2)
  - ☐ légèrement en désaccord (3)
  - ☐ neutre (4)
  - ☐ légèrement en accord (5)
  - ☐ modérément en accord (6)
  - ☐ fortement en accord (7)
- 



collectiverespon3 Vaccination is a collective action to prevent the spread of diseases.

- ☐ strongly disagree (1)
- ☐ moderately disagree (2)
- ☐ slightly disagree (3)
- ☐ neutral (4)
- ☐ slightly agree (5)
- ☐ moderately agree (6)
- ☐ strongly agree (7)

collectiverespon3 La vaccination est une action collective visant à prévenir la propagation des maladies

- ☐ fortement en désaccord (1)
  - ☐ modérément en désaccord (2)
  - ☐ légèrement en désaccord (3)
  - ☐ neutre (4)
  - ☐ légèrement en accord (5)
  - ☐ modérément en accord (6)
  - ☐ fortement en accord (7)
- 

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**End of Block: 5CScale**

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**Start of Block: Emotion**



emotion1 I am worried about getting \${e://Field/diseasedescEN}.

- ☐ strongly disagree (1)
- ☐ moderately disagree (2)
- ☐ slightly disagree (3)
- ☐ neutral (4)
- ☐ slightly agree (5)
- ☐ moderately agree (6)
- ☐ strongly agree (7)

emotion1 Je suis inquiet de contracter \${e://Field/diseasedescFR-CA}.

- ☐ fortement en désaccord (1)
- ☐ modérément en désaccord (2)
- ☐ légèrement en désaccord (3)
- ☐ neutre (4)
- ☐ légèrement en accord (5)
- ☐ modérément en accord (6)
- ☐ fortement en accord (7)



emotion2 I am worried about people in my life (family, friends) getting  
\${e://Field/diseasedescEN}.

- ☐ strongly disagree (1)
- ☐ moderately disagree (2)
- ☐ slightly disagree (3)
- ☐ neutral (4)
- ☐ slightly agree (5)
- ☐ moderately agree (6)
- ☐ strongly agree (7)

emotion2 Je suis inquiet que mon entourage (famille, amis) contracte  
\${e://Field/diseasedescFR-CA}.

- ☐ fortement en désaccord (1)
- ☐ modérément en désaccord (2)
- ☐ légèrement en désaccord (3)
- ☐ neutre (4)
- ☐ légèrement en accord (5)
- ☐ modérément en accord (6)
- ☐ fortement en accord (7)



emotion3 I am worried about vulnerable people in my community (babies, young children, older people, cancer patients) getting [\\${e://Field/diseasedescEN}](#).

- ☐ strongly disagree (1)
- ☐ moderately disagree (2)
- ☐ slightly disagree (3)
- ☐ neutral (4)
- ☐ slightly agree (5)
- ☐ moderately agree (6)
- ☐ strongly agree (7)

emotion3 Je suis inquiet que des gens vulnérables de ma communauté (bébés, jeunes enfants, personnes âgées, patients atteints du cancer) contractent [\\${e://Field/diseasedescFR-CA}](#).

- ☐ fortement en désaccord (1)
- ☐ modérément en désaccord (2)
- ☐ légèrement en désaccord (3)
- ☐ neutre (4)
- ☐ légèrement en accord (5)
- ☐ modérément en accord (6)
- ☐ fortement en accord (7)



emotion4 I would feel guilty if someone in my life (a family member, a friend) got the [\\${e://Field/diseasedescEN}](#) from me.

- ☐ strongly disagree (1)
- ☐ moderately disagree (2)
- ☐ slightly disagree (3)
- ☐ neutral (4)
- ☐ slightly agree (5)
- ☐ moderately agree (6)
- ☐ strongly agree (7)

emotion4 Je me sentirais coupable si je transmettais à quelqu'un de mon entourage (famille, amis) [\\${e://Field/diseasedescFR-CA}](#).

- ☐ fortement en désaccord (1)
- ☐ modérément en désaccord (2)
- ☐ légèrement en désaccord (3)
- ☐ neutre (4)
- ☐ légèrement en accord (5)
- ☐ modérément en accord (6)
- ☐ fortement en accord (7)





emotion5 I would feel guilty if a vulnerable person (a baby, a young child, an older person, a cancer patient) got [\\${e://Field/diseasedescEN}](#) from me.

- ☐ strongly disagree (1)
- ☐ moderately disagree (2)
- ☐ slightly disagree (3)
- ☐ neutral (4)
- ☐ slightly agree (5)
- ☐ moderately agree (6)
- ☐ strongly agree (7)

emotion5 Je me sentirais coupable si je transmettais à une personne vulnérable (un bébé, un jeune enfant, une personne âgée, un patient atteint du cancer) [\\${e://Field/diseasedescFR-CA}](#).

- ☐ fortement en désaccord (1)
  - ☐ modérément en désaccord (2)
  - ☐ légèrement en désaccord (3)
  - ☐ neutre (4)
  - ☐ légèrement en accord (5)
  - ☐ modérément en accord (6)
  - ☐ fortement en accord (7)
- 

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#### End of Block: Emotion

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#### Start of Block: Knowledge



know01 When a person gets vaccinated, it can help protect: (check one)

- ☐ The person (1)
- ☐ The people around them (2)
- ☐ Vulnerable people in their community (3)
- ☐ All of the above (4)

know01 Quand une personne est vaccinée, cela peut aider à protéger : (cochez une réponse)

- ☐ La personne elle-même (1)
- ☐ Les gens autour d'elle (2)
- ☐ Les personnes vulnérables dans sa communauté (3)
- ☐ Toutes ces réponses (4)



know02 Which people are considered more vulnerable to contagious diseases, either because they can catch them more easily, or the diseases can make them sicker? (check all that apply)

- ☐ People who are very old (1)
- ☐ People who are very young (babies, etc.) (2)
- ☐ People who are athletes (3)
- ☐ People who have cancer (4)
- ☐ People who are healthy adults (5)

know02 Quelles personnes peuvent être considérées comme étant plus vulnérables aux maladies contagieuses, soit parce qu'ils peuvent attraper les maladies plus facilement, et les maladies peuvent les rendre plus malades? (Cochez toutes les réponses qui s'appliquent)

- ☐ Les personnes très âgées (1)
- ☐ Les personnes très jeunes (bébés, etc.) (2)
- ☐ Les personnes qui sont des athlètes (3)
- ☐ Les personnes atteintes du cancer (4)
- ☐ Les adultes en bonne santé (5)



statement For the following statements, please indicate whether they are true, false, or you don't know:

	True (1)	False (0)	I don't know (77)
<p><a href="#">\${e://Field/diseasedescEN_CAP}</a> can spread from one person to another person. (know03)</p>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
<p>When you come into contact with someone who is infected with <a href="#">\${e://Field/diseasedescEN}</a>, there is a chance you could get the disease. (know04)</p>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
<p>The only way to get <a href="#">\${e://Field/diseasedescEN}</a> is to touch someone who has the disease. (know05)</p>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
<p><a href="#">\${e://Field/diseasedescEN_CAP}</a> always spread through groups of people at the same speed. (know07)</p>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
<p>Some vaccines provide less protection than others. (know08)</p>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
<p>Every vaccine provides full protection from a single dose (one needle/shot, one dose of drops in the mouth, or a one spray up the nose). (know10)</p>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
<p>Some vaccines only provide partial protection after one dose and require multiple doses to get protected. (know11)</p>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
<p>Some vaccines become less effective over time and need booster doses. (know12)</p>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
<p>Community protection (or herd immunity) means everyone in the community has been vaccinated. (know13)</p>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
<p>Unvaccinated people in a population can be protected from infections when enough people in their community are vaccinated. (know14)</p>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>

Every person in a community (100%) must be vaccinated to achieve community protection. (know15)

☐☐☐

The percentage of people (that is, how many members of a community) who must be vaccinated for the community to achieve community protection depends on the disease and the vaccine. (know16)

☐☐☐

An individual's decision to get vaccinated or not affects only that individual. (know17)

☐☐☐

statement Pour les énoncés suivants, veuillez indiquer s'ils sont vrais, faux ou si vous ne savez pas :

	Vrai (1)	Faux (0)	Je ne sais pas (77)
<p><a href="#">\${e://Field/diseasedescFR-CA_CAP}</a> peut se propager d'une personne à l'autre (know03)</p>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
<p>Lorsque vous entrez en contact avec une personne infectée par <a href="#">\${e://Field/diseasedescFR-CA}</a>, vous risquez de contracter cette maladie. (know04)</p>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
<p>La seule façon de contracter <a href="#">\${e://Field/diseasedescFR-CA}</a> est d'être en contact direct avec une personne infectée. (know05)</p>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
<p><a href="#">\${e://Field/diseasedescFR-CA_CAP}</a> se propage à travers une communauté à la même vitesse. (know07)</p>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
<p>Certains vaccins offrent moins de protection que d'autres. (know08)</p>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
<p>Chaque vaccin offre une protection complète avec une seule dose (une injection par aiguille, une dose de gouttes dans la bouche ou une seule pulvérisation dans le nez). (know10)</p>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
<p>Certains vaccins ne procurent qu'une protection partielle après une dose et nécessitent plusieurs doses pour être protégé. (know11)</p>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
<p>Certains vaccins deviennent moins efficaces avec le temps et nécessitent des doses de</p>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>

rappel. (know12)			
La protection communautaire (ou l'immunité collective) signifie que tout le monde dans la communauté a été vacciné. (know13)	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Les gens non-vaccinés d'une population peuvent être protégés des infections quand assez de gens de leur communauté sont vaccinés. (know14)	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
100% des membres d'une communauté doivent être vaccinés pour assurer la protection communautaire. (know15)	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Le pourcentage de personnes (c'est-à-dire combien de membres d'une communauté) qui doivent être vaccinées pour que la communauté puisse assurer la protection communautaire dépend de la maladie et du vaccin. (know16)	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
La décision d'un individu de se faire vacciner ou non affecte seulement cet individu. (know17)	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>

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t\_know Timing  
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### End of Block: Knowledge

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### Start of Block: Trust



trustinfo \${e://Field/trustq\_EN}

- ☐ not at all trustworthy (1)
- ☐ moderately untrustworthy (2)
- ☐ slightly untrustworthy (3)
- ☐ neutral (4)
- ☐ slightly trustworthy (5)
- ☐ moderately trustworthy (6)
- ☐ strongly trustworthy (7)

trustinfo \${e://Field/trustq\_FR-CA}

- ☐ pas du tout digne de confiance (1)
- ☐ modérément NON digne de confiance (2)
- ☐ légèrement NON digne de confiance (3)
- ☐ neutre (4)
- ☐ légèrement digne de confiance (5)
- ☐ moyennement digne de confiance (6)
- ☐ fortement digne de confiance (7)



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t\_trustinfo Timing

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t\_trustinfo Durée

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**End of Block: Trust**

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**Start of Block: Behavioural intentions**

*Display This Question:*

*If disease = 1*

*Or disease = 2*

*Or disease = 3*



immune To the best of your knowledge, are you already immune to [\\${e://Field/diseasedescEN}](#)?

☐ Yes (1)

☐ No (0)

☐ I don't know (77)

immune A votre connaissance, êtes-vous déjà immunisé contre [\\${e://Field/diseasedescFR-CA}](#)?

☐ Oui (1)

☐ Non (0)

☐ Je ne sais pas (77)

---

t\_immune Timing

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t\_immune Durée

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Page Break

Display This Question:

If To the best of your knowledge, are you already immune to \${e://Field/diseasedescEN}? = Yes  
Or If  
disease = 0

Q For the next question, imagine you were **not** already immune to \${e://Field/diseasedescEN}.

Q Imaginez que vous **n'étiez pas** déjà immunisé contre \${e://Field/diseasedescFR-CA}.

vaxintention If you were eligible to receive a free vaccine against \${e://Field/diseasedescEN},  
how likely would you be to get vaccinated?

Extremely unlikely, I would definitely NOT be vaccinated  
Extremely likely, I would definitely BE vaccinated

1 ( )



vaxintention Si vous étiez admissible à recevoir gratuitement un vaccin contre  
\${e://Field/diseasedescFR-CA}, quelle serait votre probabilité de recevoir le vaccin ?

Extrêmement improbable, je ne serais certainement PAS vacciné  
Extrêmement probable, je SERAIS certainement vacciné



t\_vaxintention Timing

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t\_vaxintention Durée  
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Page Break



c19vax Have you already received a COVID-19 vaccine (between Dec 2020 and now)?

- ☐ Yes (1)
- ☐ No (0)
- ☐ I don't know (77)

c19vax Avez-vous déjà reçu un vaccin contre la COVID-19 (entre décembre 2020 et maintenant) ?

- ☐ Oui (1)
- ☐ Non (0)
- ☐ Je ne sais pas (77)

---

t\_c19vax Timing  
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t\_c19vax Durée  
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Page Break

**Display This Question:**

*If Have you already received a COVID-19 vaccine (between Dec 2020 and now)? = No*

*Or Have you already received a COVID-19 vaccine (between Dec 2020 and now)? = I don't know*

c19vaxintention Assuming you will be eligible to get a COVID-19 vaccine this year, how likely are you to get the vaccine?

Extremely unlikely, I will definitely NOT get a COVID-19 vaccine      Extremely likely, I will definitely get a COVID-19 vaccine



c19vaxintention En supposant que vous soyez éligible pour recevoir un vaccin COVID-19 cette année, quelle est la probabilité que vous receviez le vaccin ?

Extrêmement improbable (c.-à-d. je ne me ferai certainement PAS vacciner contre la COVID-19)      Extrêmement probable, (c.-à-d. je me ferai certainement vacciner contre la COVID-19)



t\_c19vaxintention Timing

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t\_c19vaxintention Durée

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**End of Block: Behavioural intentions**



```

1  # S3: Study statistical analysis plan
2  # Project: herdimmm
3
4  # Description: code for analysing the results of Hina Hakim's final PhD study
5
6  # Script developed by: Hina Hakim Jul 2019 - Dec 2020 with the collaboration of
7  Anne-Sophie Julien
8  # (statistician) and Holly Witterman (PhD advisor). Reviewed externally by a statistician
9  # unaffiliated with the project in October 2020; report received 2020-10-30.
10
11 # Last run: 2021-09-20 with real data from 2021-07-05
12
13 ##### RESEARCH QUESTIONS #####
14
15 # This project uses the herdimmm intervention to convey the concept of community
16 immunity or herd
17 immunity. The herdimmm intervention is described in detail here: DOI: 10.2196/20113
18
19 # Research question 1 (primary): Across 4 vaccine-preventable diseases, does the herdimmm
20 intervention influence risk perception compared to a control?
21
22 # Research question 2 (secondary): Across 4 vaccine-preventable diseases, does the
23 herdimmm
24 intervention influence other outcomes (5C scale, emotions, trust, knowledge,
25 behavioural
26 intentions) compared to a control?
27
28 # Research question 3 (secondary): For any of the 4 diseases, do existing interventions
29 already
30 available online outperform the herdimmm intervention?
31
32 # Research question 4 (add-on, may be reported separately from Hina Hakim's thesis):
33 Are the effects
34 of the herdimmm intervention different when the narration uses a female or male voice?
35
36 ##### LOAD LIBRARIES #####
37
38 # Libraries are required to run different packages for running the code below.
39 library(psych) # describeBy
40 library(emmeans) # emmeans
41 library(moments) # kurtosis, skewness
42 library(car) # Anova
43 library(MASS) # Box-Cox
44 library(olsrr) # testing collinearity
45 library(readr) # read files
46 library(tidyverse)
47 library(dplyr)
48 library(ggplot2) # for plots
49 library(BlandAltmanLeh) # for Bland Altman test
50 library(ltm) # to determine Cronbach alpha
51 library(mice) # for multiple imputations
52 library(naniar)
53 library(R2HTML) #CHANGELOG ASJ: to output results 2021-08-06.
54 library(mitml) #CHANGELOG ASJ: add global test after multiple imputation 21-09-20.
55
56 sessionInfo() # for citing packages in paper
57
58 ##### IMPORT DATA #####
59
60 # Import CSV file of raw data, removing Qualtrics artifacts in rows 1-2 (unneeded
61 variable headers)
62 # and columns 1-16 (unneeded data automatically collected by default by Qualtrics.)
63
64 datRaw = (
65   read.csv(
66     "./contag_phase3b_July 5, 2021_08.19.csv",
67     header = T,
68     sep = ",",
69   )[-c(1, 2)]
70 ) #CHANGELOG Changed to new file name 2021-07-05

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63 # View(datRaw)
64
65 # Subset the data we need: people who started (Consent==1) and finished (Finished==1)
the study.
66 #CHANGELOG ASJ: Replace subset by gc = 1 equivalent to Consent + Finished + Quality,
21-08-06
67 dat<-subset(datRaw,gc==1)
68 # View(dat)
69
70 #CHANGELOG ASJ: save and print results 2021-09-03.
71 HTMLStart(outdir=".\\",
72           file = "Herdimm Descriptive210903",extension = "html",echo=TRUE, HTMLframe =
TRUE)
73
74
75 ##### CLEAN DATA #####
76
77 ##### + Risk Perception #####
78
79 # First change the columns (variables) from character to numeric form so that we can
work with them.
80
81 dat$riskpercep1_1 <- as.numeric(as.character(dat$riskpercep1_1))
82 dat$riskpercep2 <- as.numeric(as.character(dat$riskpercep2))
83 dat$riskpercep3 <- as.numeric(as.character(dat$riskpercep3))
84 dat$riskpercep4 <- as.numeric(as.character(dat$riskpercep4))
85 dat$riskpercep5 <- as.numeric(as.character(dat$riskpercep5))
86 dat$riskpercep6 <- as.numeric(as.character(dat$riskpercep6))
87
88 # Then recode reverse-coded items riskpercep2, riskpercep4, riskpercep5.
89
90 dat$riskpercep2rev <- 8-dat$riskpercep2
91 dat$riskpercep4rev <- 8-dat$riskpercep4
92 dat$riskpercep5rev <- 8-dat$riskpercep5
93
94 # To check if risk percep_1 measures the same construct as riskpercep_2-6, we rescale
riskpercep_1
95 # so that it is measured on the same scale as the other items.
96
97 dat$score_riskpercep1_1 <- dat$riskpercep1_1*6/100+1
98 summary(dat$score_riskpercep1_1)
99
100 # To calculate the mean of the six other risk perception items (that is: riskpercep_2,
riskpercep_3,
101 # riskpercep_4, riskpercep_5, riskpercep_6), first, we create a subset of the items we
need.
102
103 dat_riskpercep2_6 <-
104   subset(
105     dat,
106     select = c(
107       riskpercep2rev,
108       riskpercep3,
109       riskpercep4rev,
110       riskpercep5rev,
111       riskpercep6
112     )
113   )
114
115 # Sum all items (riskpercept_2 to riskpercep_6) for each participant.
116
117 risk_sumrows <-rowSums(dat_riskpercep2_6,na.rm=T)
118
119 # Count the number of missing items (no response in items riskpercept_2 to
riskpercep_6) for each
120 # participant.
121
122 risk_summissing <-
123   is.na(dat_riskpercep2_6$riskpercep2rev) +

```

```

124   is.na(dat_riskpercep2_6$riskpercep3) +
125   is.na(dat_riskpercep2_6$riskpercep4rev) +
126   is.na(dat_riskpercep2_6$riskpercep5rev) +
127   is.na(dat_riskpercep2_6$riskpercep6)
128
129   table(risk_summissing)
130   prop.table(table(risk_summissing))*100
131
132   # Calculate the mean value (mean risk perception) from riskpercep_2 to riskpercep_6 of
133   # all answered
134   # items.
135   dat$mean_riskperception2_6<-risk_sumrows/(5-risk_summissing)
136   summary(dat$mean_riskperception2_6)
137
138   # To see if the item risk percep_1 and risk percept_2 to 6 are all measuring the same
139   # thing, we need
140   # a Bland Altman plot. To create a Bland Altman plot, we need the difference between _1
141   # and the mean
142   # of _2 to _6. So, for that purpose, we will create 2 new variables then create the plot.
143   dat$diff_riskp1_6 <-dat$score_riskpercep1_1-dat$mean_riskperception2_6
144   summary(dat$diff_riskp1_6)
145   dat$mean_riskp1_6<- (dat$score_riskpercep1_1+dat$mean_riskperception2_6)/2
146   summary(dat$mean_riskp1_6)
147
148   plot(dat$score_riskpercep1_1,dat$mean_riskperception2_6)
149
150   # We are using two = 1.96 (two standard deviations) rather than two = 2.0. If there are
151   # data points
152   # outside these limits, this raises concerns that these two measures may not, in fact,
153   # measure the
154   # same construct.
155   bland.altman.plot(
156     dat$mean_riskperception2_6,
157     dat$score_riskpercep1_1,
158     two = 1.96,
159     mode = 1,
160     graph.sys = "base",
161     conf.int = 0,
162     silent = TRUE,
163     sunflower = FALSE,
164     geom_count = FALSE
165   )
166
167   # Then we formally test the hypothesis. If this test is statistically significant, it
168   # means the
169   # difference between the two new variables is not zero, which implies a lack of
170   # similarity between
171   # the two original measurement methods (i.e., riskpercep_1 and riskpercep_2 to _6.)
172   summary(lm(dat$mean_riskp1_6 ~ dat$diff_riskp1_6))
173
174   # If riskpercep_1 and riskpercep_2 to _6 are similar, we will combine them into a
175   # single measure if
176   # their combined Cronbach alpha is >=0.8 and will consider doing so if their combined
177   # Cronbach alpha
178   # can be raised to >=0.8 by removing inconsistent items. We will explore removing items
179   # because this
180   # measure is an ad hoc measure created specifically for this study.
181
182   # Create a subset for riskpercep_2 to_6 to determine Cronbach alpha more easily
183   dat_riskpercep2_6_alpha <-
184     subset(
185       dat,
186       select = c(

```

```

183     riskpercep2rev,
184     riskpercep3,
185     riskpercep4rev,
186     riskpercep5rev,
187     riskpercep6
188   )
189 )
190
191 # Cronbach alpha value for riskpercep_2-6
192
193 cronbach.alpha(
194   dat_riskpercep2_6_alpha,
195   standardized = FALSE,
196   CI = FALSE,
197   probs = c(0.025, 0.975),
198   B = 1000,
199   na.rm = TRUE
200 ) # CHANGELOG Change na.rm = FALSE to TRUE 2021-07-14
201
202 # Create a subset for riskpercep_1 to_6 to determine Cronbach alpha more easily
203
204 dat_riskpercep1_6_alpha <-
205   subset(
206     dat,
207     select = c(
208       score_riskpercep1_1,
209       riskpercep2rev,
210       riskpercep3,
211       riskpercep4rev,
212       riskpercep5rev,
213       riskpercep6
214     )
215   )
216
217 # Cronbach alpha value for riskpercep_1-6
218
219 cronbach.alpha(
220   dat_riskpercep1_6_alpha,
221   standardized = FALSE,
222   CI = FALSE,
223   probs = c(0.025, 0.975),
224   B = 1000,
225   na.rm = TRUE
226 ) # CHANGELOG Change na.rm = FALSE to TRUE 2021-07-14
227
228 # 1. If we can combine the measures (based on Bland Altman & Cronbach alpha) then we
229 # create a single
230 # measure using the same series of steps as above (subset, sum of all items, number of
231 # items, calculate mean). This is our preferred approach, so we are prioritizing this
232 # option in the
233 # pre-registered code.
234
235 # subset
236 dat_riskpercep <-
237   subset(
238     dat,
239     select = c(
240       score_riskpercep1_1,
241       riskpercep2rev,
242       riskpercep3,
243       riskpercep4rev,
244       riskpercep5rev,
245       riskpercep6
246     )
247   )
248
249 # sum of all items for each person
250 risk_sumrows <- rowSums(dat_riskpercep, na.rm=T)

```

```

249
250 # count of missing values
251 risk_summissing <-
252   is.na(dat_riskpercep$score_riskpercep1_1) +
253   is.na(dat_riskpercep$riskpercep2rev) +
254   is.na(dat_riskpercep$riskpercep3) +
255   is.na(dat_riskpercep$riskpercep4rev) +
256   is.na(dat_riskpercep$riskpercep5rev) +
257   is.na(dat_riskpercep$riskpercep6)
258
259 # mean
260 dat$mean_riskperception<-risk_sumrows/(6-risk_summissing)
261
262 # 2. If we cannot combine the measures, we will run the rest of the script once with
risk perception
263 # being the first item only, and then re-run the rest of the script with risk
perception being items
264 # 2 to 6. In that case, we will add a comment for which condition we are running the
ANOVA each
265 # time. For now, we have commented these out, as we hope not to have to use them.
266
267 # dat$mean_riskperception<-(dat$score_riskpercep1_1)
268
269 dat$mean_riskperception<-(dat$mean_riskperception2_6)
270
271 # CHANGELOG: As mentioned above that if risk perception item 1 and 2 to 6 are measuring
differently, we will use in our analysis ANOVA model separately
272 # CHANGELOG ASJ: Since riskperception 1 is asymmetric, no ANOVA will be run on it, so
the mean can be directly equal to 2-6, 2021-08-03
273
274 ##### + Betsch et al 5C measure #####
275
276 # Variables are coming in as data type character. Force them to be numeric so we can
work with them.
277
278 cols.num <- c(
279   "confidence1",
280   "confidence2",
281   "confidence3",
282   "complacency1",
283   "complacency2",
284   "complacency3",
285   "constraints1",
286   "constraints2",
287   "constraints3",
288   "calculation1",
289   "calculation2",
290   "calculation3",
291   "collectiverespon1",
292   "collectiverespon2",
293   "collectiverespon3"
294 )
295
296 dat[cols.num] <- sapply(dat[cols.num],as.numeric)
297
298 # Recode reverse-coded item collectiverespon1
299
300 dat$collectiverespon1rev <- 8-dat$collectiverespon1
301
302 # Calculate mean (subset, sum of all items, number of missing items, calculate mean).
303
304 dat_5c <-
305   subset(
306     dat,
307     select = c(
308       confidence1,
309       confidence2,
310       confidence3,
311       complacency1,

```

```

312     complacency2,
313     complacency3,
314     constraints1,
315     constraints2,
316     constraints3,
317     calculation1,
318     calculation2,
319     calculation3,
320     collectiverespon1rev,
321     collectiverespon2,
322     collectiverespon3
323   )
324 )
325
326 C5_sumrows <- rowSums(dat_5c, na.rm = T)
327
328 C5_summissing <-
329   is.na(dat_5c$confidence1) +
330   is.na(dat_5c$confidence2) +
331   is.na(dat_5c$confidence3) +
332   is.na(dat_5c$complacency1) +
333   is.na(dat_5c$complacency2) +
334   is.na(dat_5c$complacency3) +
335   is.na(dat_5c$constraints1) +
336   is.na(dat_5c$constraints2) +
337   is.na(dat_5c$constraints3) +
338   is.na(dat_5c$calculation1) +
339   is.na(dat_5c$calculation2) +
340   is.na(dat_5c$calculation3) +
341   is.na(dat_5c$collectiverespon1rev) +
342   is.na(dat_5c$collectiverespon2) +
343   is.na(dat_5c$collectiverespon3)
344
345 dat$mean_C5 <- C5_sumrows / (15 - C5_summissing)
346
347 # Determine Cronbach alpha of overall 5C scale.
348 #CHANGELOG ASJ: Overall consistency is low, while it's high for subscales. Analysis of
349 #subscales instead of total score, 2021-08-06
350 cronbach.alpha(dat_5c, standardized = FALSE, CI = FALSE,
351               probs = c(0.025, 0.975), B = 1000, na.rm = TRUE) # CHANGELOG Change na.rm
352               = FALSE to TRUE 2021-07-14
353
354 # Create subsets for each subscale .
355
356 dat_5c_confidence <-subset(dat,select=c(confidence1,confidence2,confidence3))
357 dat_5c_complacency<-subset(dat,select=c(complacency1,complacency2,complacency3))
358 dat_5c_constraints<-subset(dat,select=c(constraints1,constraints2,constraints3))
359 dat_5c_calculation<-subset(dat,select=c(calculation1,calculation2,calculation3))
360 dat_5c_collectiverespon<-subset(dat,select=c(collectiverespon1rev,collectiverespon2,colle
361 ctiverespon3))
362
363 # Determine Cronbach alpha values for each of 5C subscales.
364
365 # Confidence
366 cronbach.alpha(
367   dat_5c_confidence,
368   standardized = FALSE,
369   CI = FALSE,
370   probs = c(0.025, 0.975),
371   B = 1000,
372   na.rm = TRUE
373 ) # CHANGELOG Change na.rm = FALSE to TRUE 2021-07-14
374
375 # Complacency
376 cronbach.alpha(
377   dat_5c_complacency,
378   standardized = FALSE,
379   CI = FALSE,

```

```

378     probs = c(0.025, 0.975),
379     B = 1000,
380     na.rm = TRUE
381 ) # CHANGELOG Change na.rm = FALSE to TRUE 2021-07-14
382
383 # Constraints
384 cronbach.alpha(
385     dat_5c_constraints,
386     standardized = FALSE,
387     CI = FALSE,
388     probs = c(0.025, 0.975),
389     B = 1000,
390     na.rm = TRUE
391 ) # CHANGELOG Change na.rm = FALSE to TRUE 2021-07-14
392
393 # Calculation
394 cronbach.alpha(
395     dat_5c_calculation,
396     standardized = FALSE,
397     CI = FALSE,
398     probs = c(0.025, 0.975),
399     B = 1000,
400     na.rm = TRUE
401 ) # CHANGELOG Change na.rm = FALSE to TRUE 2021-07-14
402
403 # Collective responsibility
404 cronbach.alpha(
405     dat_5c_collectiverespon,
406     standardized = FALSE,
407     CI = FALSE,
408     probs = c(0.025, 0.975),
409     B = 1000,
410     na.rm = TRUE
411 ) # CHANGELOG Change na.rm = FALSE to TRUE 2021-07-14
412
413 #CHANGELOG ASJ: Calculate mean for each subscale because of low overall consistency,
414 2021-08-06.
415 C5conf_sumrows <- rowSums(dat_5c_confidence, na.rm = T)
416 C5comp_sumrows <- rowSums(dat_5c_complacency, na.rm = T)
417 C5cons_sumrows <- rowSums(dat_5c_constraints, na.rm = T)
418 C5calc_sumrows <- rowSums(dat_5c_calculation, na.rm = T)
419 C5coll_sumrows <- rowSums(dat_5c_collectiverespon, na.rm = T)
420
421 C5conf_summissing <- is.na(dat_5c$confidence1) + is.na(dat_5c$confidence2) +
422 is.na(dat_5c$confidence3)
423 C5comp_summissing <- is.na(dat_5c$complacency1) + is.na(dat_5c$complacency2) +
424 is.na(dat_5c$complacency3)
425 C5cons_summissing <- is.na(dat_5c$constraints1) + is.na(dat_5c$constraints2) +
426 is.na(dat_5c$constraints3)
427 C5calc_summissing <- is.na(dat_5c$calculation1) + is.na(dat_5c$calculation2) +
428 is.na(dat_5c$calculation3)
429 C5coll_summissing <- is.na(dat_5c$collectiverespon1rev) +
430 is.na(dat_5c$collectiverespon2) + is.na(dat_5c$collectiverespon3)
431
432
433 dat$mean_C5_conf <- C5conf_sumrows / (3 - C5conf_summissing)
434 dat$mean_C5_comp <- C5comp_sumrows / (3 - C5comp_summissing)
435 dat$mean_C5_cons <- C5cons_sumrows / (3 - C5cons_summissing)
436 dat$mean_C5_calc <- C5calc_sumrows / (3 - C5calc_summissing)
437 dat$mean_C5_coll <- C5coll_sumrows / (3 - C5coll_summissing)
438
439 #CHANGELOG ASJ: Dichotomize the five subscales because they are highly asymmetric,
440 21-09-03
441 hist(dat$mean_C5_conf)
442 hist(dat$mean_C5_comp)
443 hist(dat$mean_C5_cons)
444 hist(dat$mean_C5_calc)
445 hist(dat$mean_C5_coll)

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```

440 summary(dat$mean_C5_conf) #6
441 summary(dat$mean_C5_comp) #2.33
442 summary(dat$mean_C5_cons) #2
443 summary(dat$mean_C5_calc) #5.33
444 summary(dat$mean_C5_coll) #6.33
445
446 dat$mean_C5_conf2<-ifelse(dat$mean_C5_conf>=6,1,0)
447 dat$mean_C5_comp2<-ifelse(dat$mean_C5_comp<=2.34,1,0)
448 dat$mean_C5_cons2<-ifelse(dat$mean_C5_cons<=2,1,0)
449 dat$mean_C5_calc2<-ifelse(dat$mean_C5_calc>=5.33,1,0)
450 dat$mean_C5_coll2<-ifelse(dat$mean_C5_coll>=6.33,1,0)
451
452 table(dat$mean_C5_conf2,dat$mean_C5_conf)
453 table(dat$mean_C5_comp2,dat$mean_C5_comp)
454 table(dat$mean_C5_cons2,dat$mean_C5_cons)
455 table(dat$mean_C5_calc2,dat$mean_C5_calc)
456 table(dat$mean_C5_coll2,dat$mean_C5_coll)
457
458 table(dat$mean_C5_conf2)
459 table(dat$mean_C5_comp2)
460 table(dat$mean_C5_cons2)
461 table(dat$mean_C5_calc2)
462 table(dat$mean_C5_coll2)
463
464
465 ##### + Emotions #####
466
467 # Variables are coming in as data type character. Force them to be numeric so we can
work with them.
468
469 cols.num <- c("emotion1", "emotion2", "emotion3", "emotion4", "emotion5")
470 dat[cols.num] <- sapply(dat[cols.num],as.numeric)
471
472 # Calculate mean (subset, sum of all items, number of missing items, calculate mean).
473
474 dat_emotion <-
475   subset(dat, select = c(emotion1, emotion2, emotion3, emotion4, emotion5))
476
477 emotion_sumrows <- rowSums(dat_emotion, na.rm = T)
478
479 emotion_summissing <-
480   is.na(dat_emotion$emotion1) +
481   is.na(dat_emotion$emotion2) +
482   is.na(dat_emotion$emotion3) +
483   is.na(dat_emotion$emotion4) +
484   is.na(dat_emotion$emotion5)
485
486 dat$mean_emotion <- emotion_sumrows / (5 - emotion_summissing)
487
488 # Calculate Cronbach alpha for emotions questions.
489
490 cronbach.alpha(
491   dat_emotion,
492   standardized = FALSE,
493   CI = FALSE,
494   probs = c(0.025, 0.975),
495   B = 1000,
496   na.rm = TRUE
497 ) # CHANGELOG Change na.rm = FALSE to TRUE 2021-07-14
498
499 ##### + Knowledge #####
500
501 # Variables are coming in as data type character. Force them to be numeric so we can
work with them.
502 # The original knowledge scale included slightly repetitive items know06 and know09
that were
503 # removed to shorten the overall survey.
504
505 cols.num <-

```

```

506   c(
507     "know01",
508     "know02_1",
509     "know02_2",
510     "know02_3",
511     "know02_4",
512     "know02_5",
513     "know03",
514     "know04",
515     "know05",
516     "know07",
517     "know08",
518     "know10",
519     "know11",
520     "know12",
521     "know13",
522     "know14",
523     "know15",
524     "know16",
525     "know17"
526   )
527
528   dat[cols.num] <- lapply(dat[cols.num], as.numeric)
529
530   # Calculate the knowledge score. If the participant selected the correct response, they
531   # get 1 point
532   # for that item. Otherwise they get 0 for that item. know01 and know02 are multiple
533   # choice.
534   # know03-17 are true/false. For know01, we required a single correct choice. For
535   # know02, we require
536   # all correct options selected. For know03-17, we require the correct choice (true or
537   # false.)
538
539   dat$know01_score <- ifelse(dat$know01 == 4, 1, 0)
540   dat$know02_score <- ifelse(dat$know02_1 == 1 &
541     dat$know02_2 == 1 &
542     dat$know02_3 == 0 &
543     dat$know02_4 == 1 &
544     dat$know02_5 == 0, 1, 0)
545   dat$know03_score <- ifelse(dat$know03 == 1, 1, 0)
546   dat$know04_score <- ifelse(dat$know04 == 1, 1, 0)
547   dat$know05_score <- ifelse(dat$know05 == 1, 1, 0)
548   dat$know07_score <- ifelse(dat$know07 == 0, 1, 0)
549   dat$know08_score <- ifelse(dat$know08 == 1, 1, 0)
550   dat$know10_score <- ifelse(dat$know10 == 0, 1, 0)
551   dat$know11_score <- ifelse(dat$know11 == 1, 1, 0)
552   dat$know12_score <- ifelse(dat$know12 == 1, 1, 0)
553   dat$know13_score <- ifelse(dat$know13 == 0, 1, 0)
554   dat$know14_score <- ifelse(dat$know14 == 1, 1, 0)
555   dat$know15_score <- ifelse(dat$know15 == 0, 1, 0)
556   dat$know16_score <- ifelse(dat$know16 == 1, 1, 0)
557   dat$know17_score <- ifelse(dat$know17 == 0, 1, 0)
558
559   # Subset the items so we can easily calculate total score.
560
561   dat_know <-
562     subset(
563       dat,
564       select = c(
565         know01_score,
566         know02_score,
567         know03_score,
568         know04_score,
569         know05_score,
570         know07_score,
571         know08_score,
572         know10_score,
573         know11_score,
574         know12_score,

```



```

571         know13_score,
572         know14_score,
573         know15_score,
574         know16_score,
575         know17_score
576     )
577 )
578
579 # Calculate sum of correct answers out of 15 total.
580
581 dat$sum_knowledge <- rowSums(dat_know,na.rm=T)
582
583 # If we want to know the number of NA's in the data we can run the line below. This
584 # would allow us
585 # to distinguish between people who selected the wrong answer and people who indicated
586 # they didn't
587 # know. We will do this if knowledge scores are very low across all conditions (e.g.,
588 # mean scores
589 # less than about 5.) It is commented out for the preregistered code because we hope
590 # not to need it.
591
592 #CHANGELOG ASJ: the mean of sum_knowledge is 8.9, so no need for it, 2021-08-03
593 # dat$sum_knowledge <-rowSums(dat_know,na.rm=F)
594
595 ##### + Trust #####
596
597 # Variable is coming in as data type character. Force it to be numeric so we can
598 # work with it.
599
600 dat$trustinfo <- as.numeric(dat$trustinfo)
601
602 ##### + Behaviourial Intentions #####
603
604 # Variables are coming in as data type character. Force them to be numeric so we can
605 # work with them.
606
607 cols.num <-
608   c(
609     "immune",
610     "vaxintention_1",
611     "c19vax",
612     "c19vaxintention_1"
613   )
614
615 dat[cols.num] <- sapply(dat[cols.num], as.numeric)
616
617 ##### + Individualism and Collectivism Scale #####
618
619 # Variables are coming in as data type character. Force them to be numeric so we can
620 # work with them.
621
622 cols.num <-
623   c(
624     "ih1",
625     "ih2",
626     "ih3",
627     "ih4",
628     "iv1",
629     "iv2",
630     "iv3",
631     "iv4",
632     "ch1",
633     "ch2",
634     "ch3",
635     "ch4",
636     "cv1",
637     "cv2",
638     "cv3",
639     "cv4"

```

```

633 )
634
635 dat[cols.num] <- apply(dat[cols.num], as.numeric)
636
637 # This scale may have up to 4 dimensions, so we need to check for collinearity. To do
638 # this, we
639 # calculate mean scores for each participant for each of the 4 subscales, using the
640 # same method as
641 # above (subset, sum, count missing, calculate mean scores.) Then we enter these in a
642 # linear model
643 # on our primary outcome and check VIF for indications of multicollinearity. If all the
644 # VIF are
645 # below 10, it means there is no multicollinearity. If some of the VIF values are more
646 # than 10, it
647 # means that variables are correlated. If there is collinearity then we can not use the 4
648 # dimensions in the model. In that case, we can use either 2 dimensions or just one or
649 # 3 dimensions.
650 # If there is no collinearity then we can use the 4 dimensions.
651
652 dat_indivhorz <- subset(dat, select=c(ih1, ih2, ih3, ih4))
653 dat_indivvertical <- subset(dat, select=c(iv1, iv2, iv3, iv4))
654 dat_collhorz <- subset(dat, select=c(ch1, ch2, ch3, ch4))
655 dat_collvertical <- subset(dat, select=c(cv1, cv2, cv3, cv4))
656 dat_indiv_coll <-
657 subset(dat, select=c(ih1, ih2, ih3, ih4, iv1, iv2, iv3, iv4, ch1, ch2, ch3, ch4, cv1, cv2, cv3, cv4))
658
659 # Cronbach alpha for subscales (each dimension) of the scale.
660 # CHANGELOG Change below na.rm = FALSE to TRUE 2021-07-14
661
662 cronbach.alpha(dat_indivhorz, standardized = FALSE, CI = FALSE,
663               probs = c(0.025, 0.975), B = 1000, na.rm = TRUE)
664 cronbach.alpha(dat_indivvertical, standardized = FALSE, CI = FALSE,
665               probs = c(0.025, 0.975), B = 1000, na.rm = TRUE)
666 cronbach.alpha(dat_collhorz, standardized = FALSE, CI = FALSE,
667               probs = c(0.025, 0.975), B = 1000, na.rm = TRUE)
668 cronbach.alpha(dat_collvertical, standardized = FALSE, CI = FALSE,
669               probs = c(0.025, 0.975), B = 1000, na.rm = TRUE)
670 cronbach.alpha(dat_indiv_coll, standardized = FALSE, CI = FALSE,
671               probs = c(0.025, 0.975), B = 1000, na.rm = TRUE)
672
673 # Sum all items
674
675 indivhorz_sumrows <- rowSums(dat_indivhorz, na.rm=T)
676 indivvertical_sumrows <- rowSums(dat_indivvertical, na.rm=T)
677 collhorz_sumrows <- rowSums(dat_collhorz, na.rm=T)
678 collvertical_sumrows <- rowSums(dat_collvertical, na.rm=T)
679
680 # Count missing items
681
682 indivhorz_summissing <-
683   is.na(dat_indivhorz$ih1) + is.na(dat_indivhorz$ih2) + is.na(dat_indivhorz$ih3) +
684   is.na(dat_indivhorz$ih4)
685
686 indivvertical_summissing <-
687   is.na(dat_indivvertical$iv1) + is.na(dat_indivvertical$iv2) +
688   is.na(dat_indivvertical$iv3) +
689   is.na(dat_indivvertical$iv4)
690
691 collhorz_summissing <-
692   is.na(dat_collhorz$ch1) + is.na(dat_collhorz$ch2) + is.na(dat_collhorz$ch3) +
693   is.na(dat_collhorz$ch4)
694
695 collvertical_summissing <-
696   is.na(dat_collvertical$cv1) + is.na(dat_collvertical$cv2) +
697   is.na(dat_collvertical$cv3) +
698   is.na(dat_collvertical$cv4)
699
700 # Calculate mean scores

```

```

693 dat$mean_indivhorz <- indivhorz_sumrows/(4- indivhorz_summissing)
694 dat$mean_indivvertical <- indivvertical_sumrows/(4 -indivvertical_summissing)
695 dat$mean_collhorz <- collhorz_sumrows/(4 - collhorz_summissing)
696 dat$mean_collvertical <- collvertical_sumrows/(4 - collvertical_summissing)
697
698 # Test for collinearity
699 #CHANGELOG ASJ: no collineary, the 4 variables will be kept for analysis as covariates,
    2021-08-03
700
701 model <-
702   lm(
703     mean_riskperception ~ mean_indivhorz + mean_indivvertical + mean_collhorz +
        mean_collvertical ,
704     data = dat
705   )
706 vif(model)
707 ols_coll_diag(model)
708
709 ##### + Other data cleaning for demographics #####
710
711 # Force year of birth as numeric and calculate age accordingly.
712
713 dat$yearofbirth <- as.numeric(dat$yearofbirth)
714 dat$yearofbirth[dat$yearofbirth==888] <- NA
715 #CHANGELOG ASJ: year of the survey was postponed to 2021 instead of 2020, 2021-08-03
716 dat$age <- 2021 - dat$yearofbirth
717
718
719 dat$agecat <- as.numeric(dat$agecat)
720
721 # Recode multiple answers for language and ethnicity so that people are appropriately
    counted in
722 # each group. These questions are set up so that people "check all that apply." Each of
    the
723 # questions also includes a single option to indicate "I prefer not to answer." For
    each language
724 # and ethnicity, we want to count the number of participants who affirmatively checked it
725 # (indicating 'yes' for that option), those who did not check it but did check other
    options in the
726 # list (indicating 'no' for that option), and those who checked that they prefer not to
    answer
727 # (indicating 'prefer not to answer' for each option in the list). To do this, we use a
    2-step
728 # process in which we first recode the true 'no' values for each option as 0, meaning
    that all 'yes'
729 # answers are 1 and all 'no' answers are 0. Then we assign any 'prefer not to answer'
    to be 'NA'.
730
731 # Force variables to be numeric.
732
733 cols.num <-
734   c(
735     "bornincanada",
736     "language_1",
737     "language_2",
738     "language_3",
739     "language_888",
740     "ethnicity_1",
741     "ethnicity_2",
742     "ethnicity_3",
743     "ethnicity_4",
744     "ethnicity_5",
745     "ethnicity_6",
746     "ethnicity_7",
747     "ethnicity_8",
748     "ethnicity_9",
749     "ethnicity_10",
750     "ethnicity_11",
751     "ethnicity_12",

```

```

752     "ethnicity_13",
753     "ethnicity_14",
754     "ethnicity_15",
755     "ethnicity_16",
756     "ethnicity_17",
757     "ethnicity_888",
758     "disability",
759     "techdisability",
760     "sexatbirth",
761     "genderidentity",
762     "supportedbyincome",
763     "educationlevel",
764     "studyarm",
765     "viz",
766     "disease",
767     "immune",
768     "c19vax"
769   )
770
771   dat[cols.num] <- lapply(dat[cols.num], as.numeric)
772
773   # NB. language_1=English, language_2=French, language_3=Other
774
775   dat$language_1[is.na(dat$language_1)] <- 0
776   dat$language_2[is.na(dat$language_2)] <- 0
777   dat$language_3[is.na(dat$language_3)] <- 0
778
779   dat$language_1[dat$language_888==1&dat$language_1==0&dat$language_2==0&dat$language_3==0]
780     <- NA
781   dat$language_2[dat$language_888==1&dat$language_1==0&dat$language_2==0&dat$language_3==0]
782     <- NA
783   dat$language_3[dat$language_888==1&dat$language_1==0&dat$language_2==0&dat$language_3==0]
784     <- NA
785
786   # ethnicity_1=Asian - East (e.g., Chinese, Japanese, Korean)
787   dat$ethnicity_1[is.na(dat$ethnicity_1)] <- 0
788   # ethnicity_2=Asian - Central (e.g., Kazakhstani, Uzbekistani)
789   dat$ethnicity_2[is.na(dat$ethnicity_2)] <- 0
790   # ethnicity_3=Asian - South (e.g., Indian, Pakistani, Sri Lankan)
791   dat$ethnicity_3[is.na(dat$ethnicity_3)] <- 0
792   # ethnicity_4=Asian - South-East (e.g., Malaysian, Filipino, Vietnamese)
793   dat$ethnicity_4[is.na(dat$ethnicity_4)] <- 0
794   # ethnicity_5=Indigenous or aboriginal person from outside of North America (e.g.,
795   # Maori, Quechua)
796   dat$ethnicity_5[is.na(dat$ethnicity_5)] <- 0
797   # ethnicity_6=White / European (e.g., English, Italian, Portuguese, Russian)
798   dat$ethnicity_6[is.na(dat$ethnicity_6)] <- 0
799   # ethnicity_7=White / North American (e.g., Canadian, American)
800   dat$ethnicity_7[is.na(dat$ethnicity_7)] <- 0
801   # ethnicity_8=Inuit
802   dat$ethnicity_8[is.na(dat$ethnicity_8)] <- 0
803   # ethnicity_9=Latin American (e.g., Chilean, Mexican, Salvadorian)
804   dat$ethnicity_9[is.na(dat$ethnicity_9)] <- 0
805   # ethnicity_10=Metis (Metis Nation in Canada)
806   dat$ethnicity_10[is.na(dat$ethnicity_10)] <- 0
807   # ethnicity_11=North African (e.g., Moroccan, Tunisian)
808   dat$ethnicity_11[is.na(dat$ethnicity_11)] <- 0
809   # ethnicity_12=Middle Eastern (e.g., Egyptian, Iranian, Lebanese)
810   dat$ethnicity_12[is.na(dat$ethnicity_12)] <- 0
811   # ethnicity_13=Black - African (e.g., Ghanaian, Kenyan, Somali)
812   dat$ethnicity_13[is.na(dat$ethnicity_13)] <- 0
813   # ethnicity_14=Black - Caribbean (e.g., Barbadian, Jamaican)
814   dat$ethnicity_14[is.na(dat$ethnicity_14)] <- 0
815   # ethnicity_15=Black - North American (e.g., Canadian, American)
816   dat$ethnicity_15[is.na(dat$ethnicity_15)] <- 0
817   # ethnicity_16=First Nations
818   dat$ethnicity_16[is.na(dat$ethnicity_16)] <- 0
819   # ethnicity_17= Other
820   dat$ethnicity_17[is.na(dat$ethnicity_17)] <- 0

```

```

817
818 # Subset ethnicity values
819
820 dat_ethnicity <-
821   subset(
822     dat,
823     select = c(
824       ethnicity_1,
825       ethnicity_2,
826       ethnicity_3,
827       ethnicity_4,
828       ethnicity_5,
829       ethnicity_6,
830       ethnicity_7,
831       ethnicity_8,
832       ethnicity_9,
833       ethnicity_10,
834       ethnicity_11,
835       ethnicity_12,
836       ethnicity_13,
837       ethnicity_14,
838       ethnicity_15,
839       ethnicity_16,
840       ethnicity_17
841     )
842   )
843
844 # Sum of the 17 ethnicity categories checked
845
846 dat$sum_ethnicity <- rowSums(dat_ethnicity, na.rm=T)
847
848 # Assign NA when the participant selected prefer not to answer (_888) and no other
849 # option.
850
851 dat$ethnicity_1[dat$ethnicity_888==1 & dat$sum_ethnicity==0] <- NA
852 dat$ethnicity_2[dat$ethnicity_888==1 & dat$sum_ethnicity==0] <- NA
853 dat$ethnicity_3[dat$ethnicity_888==1 & dat$sum_ethnicity==0] <- NA
854 dat$ethnicity_4[dat$ethnicity_888==1 & dat$sum_ethnicity==0] <- NA
855 dat$ethnicity_5[dat$ethnicity_888==1 & dat$sum_ethnicity==0] <- NA
856 dat$ethnicity_6[dat$ethnicity_888==1 & dat$sum_ethnicity==0] <- NA
857 dat$ethnicity_7[dat$ethnicity_888==1 & dat$sum_ethnicity==0] <- NA
858 dat$ethnicity_8[dat$ethnicity_888==1 & dat$sum_ethnicity==0] <- NA
859 dat$ethnicity_9[dat$ethnicity_888==1 & dat$sum_ethnicity==0] <- NA
860 dat$ethnicity_10[dat$ethnicity_888==1 & dat$sum_ethnicity==0] <- NA
861 dat$ethnicity_11[dat$ethnicity_888==1 & dat$sum_ethnicity==0] <- NA
862 dat$ethnicity_12[dat$ethnicity_888==1 & dat$sum_ethnicity==0] <- NA
863 dat$ethnicity_13[dat$ethnicity_888==1 & dat$sum_ethnicity==0] <- NA
864 dat$ethnicity_14[dat$ethnicity_888==1 & dat$sum_ethnicity==0] <- NA
865 dat$ethnicity_15[dat$ethnicity_888==1 & dat$sum_ethnicity==0] <- NA
866 dat$ethnicity_16[dat$ethnicity_888==1 & dat$sum_ethnicity==0] <- NA
867 dat$ethnicity_17[dat$ethnicity_888==1 & dat$sum_ethnicity==0] <- NA
868
869 # Regrouping ethnicities for later covariate analyses. E.g., if participant checked one
870 # or more of
871 # Asian options, they get a 1 for Asian_group. If they checked no Asian options, they
872 # get a 0 for
873 # Asian_group.
874
875 dat$Asian_group <-
876   ifelse(
877     dat$ethnicity_1 == 1 |
878     dat$ethnicity_2 == 1 |
879     dat$ethnicity_3 == 1 |
880     dat$ethnicity_4 == 1,
881     1,
882     0
883   )
884
885 dat$Black_group <-

```

```

883     ifelse(
884       dat$ethnicity_13 == 1 |
885       dat$ethnicity_14 == 1 |
886       dat$ethnicity_15 == 1,
887       1,
888       0
889     )
890
891 dat$Indigenous_group <-
892   ifelse(
893     dat$ethnicity_16 == 1 |
894     dat$ethnicity_5 == 1 |
895     dat$ethnicity_8 == 1 |
896     dat$ethnicity_10 == 1,
897     1,
898     0
899   )
900
901 dat$MaghrebMiddleEast_group <-
902   ifelse(
903     dat$ethnicity_11 == 1 |
904     dat$ethnicity_12 == 1,
905     1,
906     0
907   )
908
909 dat$White_group <-
910   ifelse(
911     dat$ethnicity_6 == 1 |
912     dat$ethnicity_7 == 1,
913     1,
914     0
915   )
916
917 # CHANGELOG: We are creating a new variable for high and low edcation to be later used
918 # in 2 way and one way ANOVA analysis 2021-07-28
919 #CHANGELOG ASJ: We need to exclude the do not know and prefer not to answer from the
920 # falses, 2021-08-03
921 dat$edhi <- ifelse(dat$educationlevel == 4 |
922                   dat$educationlevel == 5 |
923                   dat$educationlevel == 6 |
924                   dat$educationlevel == 7, TRUE,
925                   ifelse(dat$educationlevel == 8 | dat$educationlevel == 888, NA, FALSE))
926 table(dat$educationlevel, dat$edhi)
927
928 # Now we assign NA for 'prefer not to answer' responses for the rest of the
929 # socidemographic items.
930 # We will report the count of 'prefer not to answer' responses in the paper, but for
931 # our statistical
932 # analyses, we group these with the other responses indicating a lack of affirmative
933 # response.
934
935 dat$bornincanada[dat$bornincanada==888] <- NA
936 dat$disability[dat$disability==888] <- NA
937 dat$techdisability[dat$techdisability==888] <- NA
938 dat$sexatbirth[dat$sexatbirth==888] <- NA
939 dat$genderidentity[dat$genderidentity==888] <- NA
940 dat$income[dat$income==888] <- NA
941 dat$income[dat$income==5] <- NA
942 dat$supportedbyincome[dat$supportedbyincome==888] <- NA
943 dat$educationlevel[dat$educationlevel==888] <- NA
944 dat$educationlevel[dat$educationlevel==8] <- NA
945
946 #CHANGELOG ASJ: i prefer not to answer also put to NA, 2021-08-03
947 dat$agecat[dat$agecat==888 | dat$agecat==1] <- NA
948
949 # Now we force all categorical variables as factors and add labels for ease of
950 # interpretation later.

```

```

946 dat$borninCanada <-
947   factor(dat$borninCanada,
948         levels = c(1, 0),
949         labels = c("Yes", "No"))
950
951 dat$language_1 <-
952   factor(dat$language_1,
953         levels = c(1, 0),
954         labels = c("Yes", "No"))
955
956 dat$language_2 <-
957   factor(dat$language_2,
958         levels = c(1, 0),
959         labels = c("Yes", "No"))
960
961 dat$language_3 <-
962   factor(dat$language_3,
963         levels = c(1, 0),
964         labels = c("Yes", "No"))
965
966 dat$ethnicity_1 <-
967   factor(dat$ethnicity_1,
968         levels = c(1, 0),
969         labels = c("Yes", "No"))
970
971 dat$ethnicity_2 <-
972   factor(dat$ethnicity_2,
973         levels = c(1, 0),
974         labels = c("Yes", "No"))
975
976 dat$ethnicity_3 <-
977   factor(dat$ethnicity_3,
978         levels = c(1, 0),
979         labels = c("Yes", "No"))
980
981 dat$ethnicity_4 <-
982   factor(dat$ethnicity_4,
983         levels = c(1, 0),
984         labels = c("Yes", "No"))
985
986 dat$ethnicity_5 <-
987   factor(dat$ethnicity_5,
988         levels = c(1, 0),
989         labels = c("Yes", "No"))
990
991 dat$ethnicity_6 <-
992   factor(dat$ethnicity_6,
993         levels = c(1, 0),
994         labels = c("Yes", "No"))
995
996 dat$ethnicity_7 <-
997   factor(dat$ethnicity_7,
998         levels = c(1, 0),
999         labels = c("Yes", "No"))
1000
1001 dat$ethnicity_8 <-
1002   factor(dat$ethnicity_8,
1003         levels = c(1, 0),
1004         labels = c("Yes", "No"))
1005
1006 dat$ethnicity_9 <-
1007   factor(dat$ethnicity_9,
1008         levels = c(1, 0),
1009         labels = c("Yes", "No"))
1010
1011 dat$ethnicity_10 <-
1012   factor(dat$ethnicity_10,
1013         levels = c(1, 0),
1014         labels = c("Yes", "No"))

```

```

1015
1016 dat$ethnicity_11 <-
1017     factor(dat$ethnicity_11,
1018           levels = c(1, 0),
1019           labels = c("Yes", "No"))
1020
1021 dat$ethnicity_12 <-
1022     factor(dat$ethnicity_12,
1023           levels = c(1, 0),
1024           labels = c("Yes", "No"))
1025
1026 dat$ethnicity_13 <-
1027     factor(dat$ethnicity_13,
1028           levels = c(1, 0),
1029           labels = c("Yes", "No"))
1030
1031 dat$ethnicity_14 <-
1032     factor(dat$ethnicity_14,
1033           levels = c(1, 0),
1034           labels = c("Yes", "No"))
1035
1036 dat$ethnicity_15 <-
1037     factor(dat$ethnicity_15,
1038           levels = c(1, 0),
1039           labels = c("Yes", "No"))
1040
1041 dat$ethnicity_16 <-
1042     factor(dat$ethnicity_16,
1043           levels = c(1, 0),
1044           labels = c("Yes", "No"))
1045
1046 dat$ethnicity_17 <-
1047     factor(dat$ethnicity_17,
1048           levels = c(1, 0),
1049           labels = c("Yes", "No"))
1050
1051 dat$Asian_group <-
1052     factor(dat$Asian_group,
1053           levels = c(1, 0),
1054           labels = c("Yes", "No"))
1055
1056 dat$MaghrebMiddleEast_group <-
1057     factor(dat$MaghrebMiddleEast_group,
1058           levels = c(1, 0),
1059           labels = c("Yes", "No"))
1060
1061 dat$Black_group <-
1062     factor(dat$Black_group,
1063           levels = c(1, 0),
1064           labels = c("Yes", "No"))
1065
1066 dat$White_group <-
1067     factor(dat$White_group,
1068           levels = c(1, 0),
1069           labels = c("Yes", "No"))
1070
1071 dat$Indigenous_group <-
1072     factor(dat$Indigenous_group,
1073           levels = c(1, 0),
1074           labels = c("Yes", "No"))
1075
1076 dat$disability <-
1077     factor(
1078         dat$disability,
1079         levels = c(0, 1),
1080         labels = c("No disability", "yes,at least one")
1081     )
1082
1083 dat$techdisability <-

```



```

1084     factor(dat$techdisability,
1085           levels = c(0, 1),
1086           labels = c("No", "Yes"))
1087
1088 dat$sexatbirth <-
1089     factor(dat$sexatbirth,
1090           levels = c(1, 2),
1091           labels = c("Female", "Male"))
1092
1093 dat$genderidentity <- factor(
1094     dat$genderidentity,
1095     levels = c(1, 2, 3, 4),
1096     labels = c(
1097         "Female",
1098         "Male",
1099         "Indigenous or other cultural gender minority identity",
1100         "Something else"
1101     )
1102 )
1103
1104 dat$income <-
1105     factor(
1106         dat$income,
1107         levels = c(1, 2, 3, 4),
1108         labels = c("24 999 or less", "25 000 to 49 999",
1109                   "50 000 to 99 999", "100 000 or more")
1110     )
1111
1112 dat$educationlevel <- factor(
1113     dat$educationlevel,
1114     levels = c(1, 2, 3, 4, 5, 6, 7),
1115     labels = c(
1116         "Some Elementary School",
1117         "High School Diploma",
1118         "Apprenticeship or trade certificate or diploma",
1119         "College or polytechnical school certificate or diploma",
1120         "University degree bachelor level or below",
1121         "University graduate degree Master level",
1122         "University graduate degree Doctorate level"
1123     )
1124 )
1125
1126 dat$agecat<-
1127     factor(
1128         dat$agecat,
1129         levels = c(2, 3, 4),
1130         labels = c("18-34 years", "35-49 years", "50 years and more")
1131     )
1132
1133 dat$UserLanguage <- as.factor(dat$UserLanguage)
1134
1135 dat$studyarm <-
1136     factor (
1137         dat$studyarm,
1138         levels = c(0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 11, 12, 13),
1139         labels = c(
1140             "controlgeneric",
1141             "controlmeasles",
1142             "controlpertussis",
1143             "controlflu",
1144             "herdimmgeneric",
1145             "herdimmmmeasles",
1146             "herdimmpertussis",
1147             "herdimmflu",
1148             "robertkochgeneric",
1149             "sbsnewsgeneric",
1150             "guardianmeasles",
1151             "theotheredmundmeasles",
1152             "publichealthagencycanadaflu"

```

```

1153     )
1154   )
1155
1156   dat$viz <- factor (
1157     dat$viz,
1158     levels = c(0, 1, 2, 3, 5, 6, 7),
1159     labels = c(
1160       "no visualization",
1161       "herdimm",
1162       "robertkoch",
1163       "sbsnews",
1164       "guardian",
1165       "theotherredmund",
1166       "publichealthagencycanada"
1167     )
1168   )
1169
1170   dat$disease <-
1171     factor (
1172       dat$disease,
1173       levels = c(0, 1, 2, 3),
1174       labels = c("Generic", "Measles", "Pertussis", "Flu")
1175     )
1176
1177
1178   #Keep I don't know categories as is, not as NA, to distinguish them, for these special
variables (COVID-19)
1179   dat$immune <-
1180     factor(
1181       dat$immune,
1182       levels = c(1, 0, 77),
1183       labels = c("Yes", "No", "I don't know")
1184     )
1185
1186   dat$cl9vax <-
1187     factor(
1188       dat$cl9vax,
1189       levels = c(1, 0, 77),
1190       labels = c("Yes", "No", "I don't know")
1191     )
1192
1193   #CHANGELOG ASJ: All variables related to children were removed from the final survey
and are deleted in the rest of the code (children, childimmune, childfluvax), 2021-08-06.
1194
1195
1196   #Make restrictions on the dataset for analysis of patients kept for analysis vs not
kept for analysis
1197   #CHANGELOG ASJ: Variables were different than planned, subset done differently because
of gc, 2021-08-06.
1198   datConsent<- subset(datRaw,Consent==1)
1199   datConsent$used<-ifelse(datConsent$gc==1 & datConsent$Finished ==1, 1,0) #used in our
analysis (n = 5516 vs others with consent (not finished, no quality))
1200   table(datConsent$used)
1201
1202
1203   # Note re: possibly recoding low-frequency data after collecting data
1204
1205   # If we observe low frequencies (below 5%) among socio demographic variables, we will
recode these
1206   # groups. This is because small subgroups are unlikely to work well in our planned
statistical
1207   # models.
1208
1209   # Descriptive statistics of all original variables will be examined. The following
steps will be
1210   # used if a category has frequency smaller than 5% of the total sample. We anticipate
this may be
1211   # necessary for gender identity and education level.
1212

```

```

1213 # For gender identity, we will remove smaller categories from inclusion in analytical
1214 # models since
1215 # they cannot be combined with other category. We still still report these statistics
1216 # in the
1217 # sociodemographic statistics of the same and will otherwise use these participants'
1218 # data as usual.
1219 # This means that if categories 3 and 4 have frequencies smaller than 5 % than we will
1220 # use this
1221 # code:
1222 #CHANGELOG ASJ: the variable is a factor, need to exclude with text instead of numbers,
1223 # 2021-08-03
1224 #CHANGELOG ASJ: this is removed from comments since <5% answered the two last categories
1225 dat$genderidentity[dat$genderidentity == "Something else" |
1226   dat$genderidentity == "Indigenous or other cultural gender
1227   minority identity"] <- NA
1228 dat$genderidentity <- droplevels(dat$genderidentity)
1229
1230 # For education level, we will regroup smaller categories with the closest bigger
1231 # categories with
1232 # which it makes sense to group them. If, for example, there are small frequencies for
1233 # 'some
1234 # elementary school' we will regroup it with high school diploma. Potential code would
1235 # be:
1236 # dat$educationlevel[dat$educationlevel== 1] <- 2; dat$educationlevel <-
1237 # factor(dat$educationlevel,levels = c(2,3,4,5,6,7), labels = c("Some Elementary School
1238 # or High
1239 # School Diploma", "Apprenticeship or trade certificate or diploma College or
1240 # polytechnical school
1241 # certificate or diploma", "University degree bachelor level or below","University
1242 # graduate degree
1243 # Master level", "University graduate degree Doctorate level", "Do not know"))
1244
1245 #CHANGELOG ASJ: Education was recoded as high vs low in edhi variable above, instead of
1246 # using this code, 2021-08-03.
1247
1248 # The rest won't change unless we need to. If we observe another category with
1249 # frequency below 5%,
1250 # we will follow similar procedures.
1251
1252 #CHANGELOG ASJ: Several covariates have categories with <5% (language_3,
1253 # MaghrebMiddleEast_group, Black_group, Indigenous_group, ethnicity_9, techdisability).
1254 # However, they are dichotomous variable, so it is not possible to combine categories.
1255 # They will simply be dropped from the models.
1256 #CHANGELOG ASJ: However, for techdisability, it will be combined with disability, we
1257 # don't want to loose that information. 2021-08-03.
1258 dat$disability_any <-ifelse(dat$disability == "yes,at least one" | dat$techdisability ==
1259 "Yes", 1, 0)
1260 dat$disability_any <-
1261   factor(
1262     dat$disability_any,
1263     levels = c(1, 0),
1264     labels = c("Yes", "No")
1265   )
1266
1267 #CHANGELOG ASJ: As mentioned later on in the preregistered code, we are recoding here
1268 # trust info because it is asymmetric, 2021-08-03
1269 dat$Htrustinfo <- ifelse(dat$Htrustinfo >= 5, 1, 0)
1270 dat$Htrustinfo <-
1271   factor(
1272     dat$Htrustinfo,
1273     levels = c(1, 0),
1274     labels = c("Yes", "No")
1275   )
1276
1277 #CHANGELOG ASJ: Because 1st variable of risk perception does not have enough variance
1278 # and is asymmetric, recode as dichotomic variable, 2021-08-03
1279 #CHANGELOG ASJ: Cutpoint = 80, keep people who correctly identified a high risk,

```

```

2021-08-06.
1261 hist(dat$riskpercep1_1)
1262 dat$RP1_dicho <- ifelse(dat$riskpercep1_1 >= 80, 1, 0)
1263 dat$RP1_dicho <-
1264   factor(
1265     dat$RP1_dicho,
1266     levels = c(1, 0),
1267     labels = c("High", "Low")
1268   )
1269 table(dat$RP1_dicho)
1270
1271 #CHANGELOG ASJ: Because vaxintention does not have enough variance and is asymmetric,
1272 #CHANGELOG ASJ: recode as dichotomic variable, 2021-08-06.
1273 hist(dat$vaxintention_1)
1274 summary(dat$vaxintention_1)
1275 dat$vaxintent<-ifelse(dat$vaxintention_1>=91,1,0)
1276
1277 dat$vaxintent <-
1278   factor(
1279     dat$vaxintent,
1280     levels = c(1, 0),
1281     labels = c("High", "Low")
1282   )
1283
1284 table(dat$vaxintent)
1285
1286 #CHANGELOG ASJ: Because c19vaxintention does not have enough variance and is asymmetric,
1287 #CHANGELOG ASJ: recode as dichotomic variable, 2021-08-06.
1288 hist(dat$c19vaxintention_1)
1289 summary(dat$c19vaxintention_1)
1290 dat$c19vaxintent<-ifelse(dat$c19vaxintention_1>=90,1,0)
1291
1292 dat$c19vaxintent <-
1293   factor(
1294     dat$c19vaxintent,
1295     levels = c(1, 0),
1296     labels = c("High", "Low")
1297   )
1298
1299 table(dat$c19vaxintent)
1300
1301 ##### + Subsets for primary and secondary analyses #####
1302
1303 # We create new subsets for primary and secondary analyses. The first subset (datMain)
1304 # is for our
1305 # primary research question. The other subsets are for the secondary question.
1306
1307 datMain <-
1308   subset(
1309     dat,
1310     dat$studyarm == "controlgeneric" |
1311     dat$studyarm == "controlmeasles" |
1312     dat$studyarm == "controlpertussis" |
1313     dat$studyarm == "controlflu" |
1314     dat$studyarm == "herdimmgeneric" |
1315     dat$studyarm == "herdimmmeasles" |
1316     dat$studyarm == "herdimpertussis" |
1317     dat$studyarm == "herdimmflu"
1318   )
1319
1320 don<-subset(datMain,select=c(studyarm,mean_riskperception, viz, disease,mean_indivhorz,
1321                             mean_indivvertical ,
1322                             mean_collhorz ,
1323                             mean_collvertical ,
1324                             bornincanada ,
1325                             language_1 ,
1326                             language_2 ,

```

```

1326         Asian_group ,
1327         White_group,
1328         disability_any ,
1329         genderidentity ,
1330         income ,
1331         edhi,
1332         age,
1333
1334         mean_riskperception2_6,RP1_dicho,vaxintent,mean_emotion,sum_k
1335         knowledge,Htrustinfo,
1336
1337         mean_C5_conf2,mean_C5_comp2,mean_C5_cons2,mean_C5_calc2,mean_
1338         C5_coll2)) # CHANGELOG ASJ updated restrictions
1339         #Added the code to determine the missing data
1340         # for variables later used in ANOVA analysis, only
1341         those with >5%, 2021-08-03
1342         #remove c19vaxintent, too many missing values
1343
1344
1345 datGeneric <-
1346   subset(
1347     dat,
1348     (
1349       dat$studyarm == "controlgeneric" |
1350       dat$studyarm == "herdimmgeneric" |
1351       dat$studyarm == "robertkochgeneric" |
1352       dat$studyarm == "sbsnewsgeneric"
1353     ) &
1354     UserLanguage == "EN"
1355   )
1356
1357 datMeasles <-
1358   subset(
1359     dat,
1360     dat$studyarm == "controlmeasles" |
1361     dat$studyarm == "herdimmmmeasles" |
1362     dat$studyarm == "guardianmeasles" |
1363     dat$studyarm == "theotherredmundmeasles"
1364   )
1365
1366 datFlu <-
1367   subset(
1368     dat,
1369     dat$studyarm == "controlflu" |
1370     dat$studyarm == "herdimmflu" |
1371     dat$studyarm == "publichealthagencycanadaflu"
1372   )
1373
1374 datMain$studyarm <- droplevels(datMain$studyarm)
1375 datGeneric$studyarm <- droplevels(datGeneric$studyarm)
1376 datMeasles$studyarm <- droplevels(datMeasles$studyarm)
1377 datFlu$studyarm <- droplevels(datFlu$studyarm)
1378
1379 #CHANGELOG ASJ, save r dataset for analysis, 2021-09-03
1380 write.csv(dat,file="./datMain.csv",row.names=T)
1381 write.csv(dat,file="./datGeneric.csv",row.names=T)
1382 write.csv(dat,file="./datMeasles.csv",row.names=T)
1383 write.csv(dat,file="./datFlu.csv",row.names=T)
1384
1385 save(dat,file="dat.RData")
1386 save(datMain,file="datMain.RData")
1387 save(datGeneric,file="datGeneric.RData")
1388 save(datMeasles,file="datMeasles.RData")
1389 save(datFlu,file="datFlu.RData")
1390 save(datConsent,file="datConsent.RData")
1391
1392 ##### DESCRIPTIVE STATISTICS #####

```

```

1390 # For each variable separately
1391
1392 ### Nominal variables - independent variables to which people were randomized
1393
1394 # frequencies - study arm
1395 table(dat$studyarm)
1396 # proportion of each study arm that is
1397 # 0 = controlgeneric
1398 # 1 = controlmeasles
1399 # 2 = controlpertussis
1400 # 3 = controlflu
1401 # 4 = herdimmgeneric
1402 # 5 = herdimmmmeasles
1403 # 6 = herdimmpertussis
1404 # 7 = herdimmflu
1405 # 8 = robertkochgeneric
1406 # 9 = sbsnewsgeneric
1407 # 10 = nhsgeneric (no longer included because has been taken down)
1408 # 11 = guardianmeasles
1409 # 12 = theotherredmundmeasles
1410 # 13 = publichealthagencycanadaflu
1411 prop.table(table(dat$studyarm)) * 100
1412
1413 # frequencies - Visualization
1414 table(dat$viz, exclude = NULL)
1415 # proportion of each visualization that is
1416 # 0 = no visualization
1417 # 1 = herdimm
1418 # 2 = robertkoch
1419 # 3 = sbsnews
1420 # 4 = nhs (no longer included because has been taken down)
1421 # 5 = guardian
1422 # 6 = theotherredmund
1423 # 7 = publichealthagencycanada
1424 prop.table(table(dat$viz, exclude = NULL)) * 100
1425
1426 # frequencies - Disease
1427 table(dat$disease, exclude = NULL)
1428 # proportion of each disease that is
1429 # 0 = Generic
1430 # 1 = Measles
1431 # 2 = Pertussis
1432 # 3 = Flu
1433 prop.table(table(dat$disease, exclude = NULL)) * 100
1434
1435 ### Nominal variables - in what language did the person complete the survey
1436
1437 # frequencies - User-language for survey
1438 table(dat$UserLanguage, exclude = NULL)
1439 # proportion of language that is
1440 # English (EN)
1441 # French (FR-CA)
1442 prop.table(table(dat$UserLanguage, exclude = NULL)) * 100
1443
1444 ### Nominal variables - Demographics # proportion of each demographic variable
1445 # CHANGELOG exclude = NULL added in code below to detemine NA's in the variable
1446 # 2021-05-10
1447
1447 # frequencies - place of birth (Canada or outside Canada)
1448 table(dat$bornincanada, exclude = NULL)
1449 prop.table(table(dat$bornincanada, exclude = NULL)) * 100
1450
1451 # frequencies - Language_English
1452 table(dat$language_1, exclude = NULL)
1453 prop.table(table(dat$language_1, exclude = NULL)) * 100
1454
1455 # frequencies - Language_French
1456 table(dat$language_2, exclude = NULL)
1457 prop.table(table(dat$language_2, exclude = NULL)) * 100

```

```

1458
1459 # frequencies - Language_Other
1460 table(dat$language_3,exclude = NULL)
1461 prop.table(table(dat$language_3,exclude = NULL)) * 100
1462
1463 # frequencies - Ethnicity_Asian - East (e.g., Chinese, Japanese, Korean)
1464 table(dat$ethnicity_1, exclude = NULL)
1465 prop.table(table(dat$ethnicity_1, exclude = NULL)) * 100
1466
1467 # frequencies - Ethnicity_Asian - Central (e.g., Kazakhstani, Uzbekistani)
1468 table(dat$ethnicity_2, exclude = NULL)
1469 prop.table(table(dat$ethnicity_2,exclude = NULL)) * 100
1470
1471 # frequencies - Ethnicity_Asian - South (e.g., Indian, Pakistani, Sri Lankan)
1472 table(dat$ethnicity_3,exclude = NULL)
1473 prop.table(table(dat$ethnicity_3, exclude = NULL)) * 100
1474
1475 # frequencies - Ethnicity_Asian - South-East (e.g., Malaysian, Filipino, Vietnamese)
1476 table(dat$ethnicity_4, exclude = NULL)
1477 prop.table(table(dat$ethnicity_4, exclude = NULL)) * 100
1478
1479 # frequencies - Ethnicity_Indigenous or aboriginal person from outside of North America
1480 # (e.g.,
1481 # Maori, Quechua)
1482 table(dat$ethnicity_5, exclude = NULL)
1483 prop.table(table(dat$ethnicity_5, exclude = NULL)) * 100
1484
1485 # frequencies - Ethnicity_White / European (e.g., English, Italian, Portuguese, Russian)
1486 table(dat$ethnicity_6, exclude = NULL)
1487 prop.table(table(dat$ethnicity_6, exclude = NULL)) * 100
1488
1489 # frequencies - Ethnicity_White / North American (e.g., Canadian, American)
1490 table(dat$ethnicity_7, exclude = NULL)
1491 prop.table(table(dat$ethnicity_7, exclude = NULL)) * 100
1492
1493 # frequencies - Ethnicity_Inuit
1494 table(dat$ethnicity_8,exclude = NULL)
1495 prop.table(table(dat$ethnicity_8,exclude = NULL)) * 100
1496
1497 # frequencies - Ethnicity_Latin American (e.g., Chilean, Mexican, Salvadorian)
1498 table(dat$ethnicity_9,exclude = NULL)
1499 prop.table(table(dat$ethnicity_9,exclude = NULL)) * 100
1500
1501 # frequencies - Ethnicity_Metis (Metis Nation in Canada)
1502 table(dat$ethnicity_10,exclude = NULL)
1503 prop.table(table(dat$ethnicity_10,exclude = NULL)) * 100
1504
1505 # frequencies - Ethnicity_North African (e.g., Moroccan, Tunisian)
1506 table(dat$ethnicity_11,exclude = NULL)
1507 prop.table(table(dat$ethnicity_11,exclude = NULL)) * 100
1508
1509 # frequencies - Ethnicity_Middle Eastern (e.g., Egyptian, Iranian, Lebanese)
1510 table(dat$ethnicity_12,exclude = NULL)
1511 prop.table(table(dat$ethnicity_12,exclude = NULL)) * 100
1512
1513 # frequencies - Ethnicity_Black - African (e.g., Ghanaian, Kenyan, Somali)
1514 table(dat$ethnicity_13,exclude = NULL)
1515 prop.table(table(dat$ethnicity_13,exclude = NULL)) * 100
1516
1517 # frequencies - Ethnicity_Black - Caribbean (e.g., Barbadian, Jamaican)
1518 table(dat$ethnicity_14,exclude = NULL)
1519 prop.table(table(dat$ethnicity_14,exclude = NULL)) * 100
1520
1521 # frequencies - Ethnicity_Black - North American (e.g., Canadian, American)
1522 table(dat$ethnicity_15,exclude = NULL)
1523 prop.table(table(dat$ethnicity_15,exclude = NULL)) * 100
1524
1525 # frequencies - Ethnicity_First Nations
1526 table(dat$ethnicity_16,exclude = NULL)

```

```

1526 prop.table(table(dat$ethnicity_16,exclude = NULL)) * 100
1527
1528 # frequencies - Ethnicity_Other
1529 table(dat$ethnicity_17,exclude = NULL)
1530 prop.table(table(dat$ethnicity_17,exclude = NULL)) * 100
1531
1532 # frequencies - Asian_group
1533 table(dat$Asian_group,exclude = NULL)
1534 prop.table(table(dat$Asian_group,exclude = NULL)) * 100
1535
1536 # frequencies - Black_group
1537 table(dat$Black_group, exclude = NULL)
1538 prop.table(table(dat$Black_group, exclude = NULL)) * 100
1539
1540 # frequencies - Indigenous_group
1541 table(dat$Indigenous_group,exclude = NULL)
1542 prop.table(table(dat$Indigenous_group, exclude = NULL)) * 100
1543
1544 # frequencies - MaghrebMiddleEast_group
1545 table(dat$MaghrebMiddleEast_group, exclude = NULL)
1546 prop.table(table(dat$MaghrebMiddleEast_group, exclude = NULL)) * 100
1547
1548 # frequencies - White_group
1549 table(dat$White_group, exclude = NULL)
1550 prop.table(table(dat$White_group, exclude = NULL)) * 100
1551
1552 # frequencies - disability
1553 table(dat$disability, exclude = NULL)
1554 prop.table(table(dat$disability,exclude = NULL )) * 100
1555
1556 # frequencies - tech disability
1557 table(dat$techdisability, exclude = NULL)
1558 prop.table(table(dat$techdisability, exclude = NULL)) * 100
1559
1560 #CHANGELOG ASJ: frequencies - any disability, 2021-08-03
1561 table(dat$disability_any, exclude = NULL)
1562 prop.table(table(dat$disability_any, exclude = NULL)) * 100
1563
1564 # frequencies - sex at birth
1565 table(dat$sexatbirth, exclude = NULL)
1566 prop.table(table(dat$sexatbirth, exclude = NULL)) * 100
1567
1568 # frequencies - gender identity
1569 table(dat$genderidentity, exclude = NULL)
1570 prop.table(table(dat$genderidentity, exclude = NULL)) * 100
1571
1572 # frequencies - income
1573 table(dat$income, exclude = NULL)
1574 prop.table(table(dat$income, exclude = NULL)) * 100
1575
1576 # frequencies - supportedbyincome
1577 table(dat$supportedbyincome, exclude = NULL)
1578 prop.table(table(dat$supportedbyincome, exclude = NULL)) * 100
1579
1580 # frequencies - education level
1581 table(dat$educationlevel, exclude = NULL)
1582 prop.table(table(dat$educationlevel, exclude = NULL)) * 100
1583
1584 #CHANGELOG ASJ: frequencies - education level high vs low, 2021-08-03
1585 table(dat$edhi, exclude = NULL)
1586 prop.table(table(dat$edhi, exclude = NULL)) * 100
1587
1588 # frequencies - age category
1589 table(dat$agecat,exclude = NULL)
1590 prop.table(table(dat$agecat, exclude = NULL)) * 100
1591
1592 # frequencies - already immune
1593 table(dat$immune, exclude = NULL)
1594 prop.table(table(dat$immune, exclude = NULL)) * 100

```



```

1595
1596 # frequencies - COVID-19 vax
1597 table(dat$cl9vax, exclude = NULL)
1598 prop.table(table(dat$cl9vax, exclude = NULL)) * 100
1599
1600
1601 ### Nominal variables - Other variables
1602 #CHANGELOG ASJ: Section added for new variables created, 2021-08-03
1603 table(dat$Htrustinfo)
1604 prop.table(table(dat$Htrustinfo)) * 100
1605
1606 table(dat$RP1_dicho)
1607 prop.table(table(dat$RP1_dicho)) * 100
1608
1609 table(dat$cl9vaxintent)
1610 prop.table(table(dat$cl9vaxintent)) * 100
1611
1612 table(dat$vaxintent)
1613 prop.table(table(dat$vaxintent)) * 100
1614
1615 #CHANGELOG ASJ: Add new variables 21-09-03
1616 table(dat$mean_C5_conf2)
1617 prop.table(table(dat$mean_C5_conf2)) * 100
1618
1619 table(dat$mean_C5_comp2)
1620 prop.table(table(dat$mean_C5_comp2)) * 100
1621
1622 table(dat$mean_C5_cons2)
1623 prop.table(table(dat$mean_C5_cons2)) * 100
1624
1625 table(dat$mean_C5_calc2)
1626 prop.table(table(dat$mean_C5_calc2)) * 100
1627
1628 table(dat$mean_C5_coll2)
1629 prop.table(table(dat$mean_C5_coll2)) * 100
1630
1631 ### Continuous variables - Demographics, scales, etc.
1632
1633 # Summary statistics for each continuous variable for all participants
1634 summary(dat$mean_riskperception) #CHANGELOG ASJ: this is equivalent to
riskperception2_6 2021-08-03
1635 summary(dat$score_riskpercep1_1) # CHANGELOG Added separate analysis for risk
perception item 1 2021-07-08
1636 summary(dat$mean_riskperception2_6) # CHANGELOG Added separate analysis for risk
perception item 2 to 6 2021-07-08
1637 summary(dat$mean_C5) #CHANGELOG Added separate analysis for 5 subscales, 2021-08-06
1638 summary(dat$mean_C5_conf)
1639 summary(dat$mean_C5_comp)
1640 summary(dat$mean_C5_cons)
1641 summary(dat$mean_C5_calc)
1642 summary(dat$mean_C5_coll)
1643 summary(dat$mean_emotion)
1644 summary(dat$sum_knowledge)
1645 summary(dat$trustinfo)
1646 summary(dat$vaxintention_1)
1647 summary(dat$age)
1648 summary(dat$cl9vaxintention_1)
1649 summary(dat$mean_indivhorz)
1650 summary(dat$mean_indivvertical)
1651 summary(dat$mean_collhorz)
1652 summary(dat$mean_collvertical)
1653
1654 ##### + Descriptive statistics per study arm #####
1655
1656 ### Continuous variables
1657
1658 # The describeBy function in the psych package returns the number of observations,
mean, median,
1659 # trimmed means, minimum, maximum, range, skew, kurtosis, and standard error of the

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```

mean for grouped
1660 # data.
1661
1662 describeBy(dat$mean_riskperception,dat$studyarm) #CHANGELOG ASJ: this is equivalent to
riskperception2_6 2021-08-03
1663 describeBy(dat$riskpercep1_1,dat$studyarm) # CHANGELOG Added separate analysis for risk
perception item 1 2021-07-08
1664 describeBy(dat$mean_riskperception2_6,dat$studyarm) # CHANGELOG Added separate analysis
for risk perception item 2 to 6 2021-07-08
1665 describeBy(dat$mean_C5,dat$studyarm) #CHANGELOG Added separate analysis for 5
subscales, 2021-08-06
1666 describeBy(dat$mean_C5_conf,dat$studyarm)
1667 describeBy(dat$mean_C5_comp,dat$studyarm)
1668 describeBy(dat$mean_C5_cons,dat$studyarm)
1669 describeBy(dat$mean_C5_calc,dat$studyarm)
1670 describeBy(dat$mean_C5_coll,dat$studyarm)
1671 describeBy(dat$mean_emotion,dat$studyarm)
1672 describeBy(dat$sum_knowledge,dat$studyarm)
1673 describeBy(dat$age,dat$studyarm)
1674 describeBy(dat$trustinfo,dat$studyarm)
1675 describeBy(dat$vaxintention_1,dat$studyarm)
1676 describeBy(dat$c19vaxintention_1,dat$studyarm)
1677 describeBy(dat$mean_indivhorz, dat$studyarm)
1678 describeBy(dat$mean_indivvertical, dat$studyarm)
1679 describeBy(dat$mean_collhorz, dat$studyarm)
1680 describeBy(dat$mean_collvertical, dat$studyarm)
1681
1682 ### Nominal variables - frequencies and proportion per arm
1683
1684 t1<-data.frame(dat$bornincanada,dat$studyarm)
1685 table(t1)
1686 prop.table(table(t1), 2) * 100
1687
1688 # Language_English
1689 t1<-data.frame(dat$language_1,dat$studyarm)
1690 table(t1)
1691 prop.table(table(t1), 2) * 100
1692
1693 # Language_French
1694 t1<-data.frame(dat$language_2,dat$studyarm)
1695 table(t1)
1696 prop.table(table(t1), 2) * 100
1697
1698 # Language_Other
1699 t1<-data.frame(dat$language_3,dat$studyarm)
1700 table(t1)
1701 prop.table(table(t1), 2) * 100
1702
1703 # Asian - East (e.g., Chinese, Japanese, Korean)
1704 t1<-data.frame(dat$ethnicity_1,dat$studyarm)
1705 table(t1)
1706 prop.table(table(t1), 2) * 100
1707
1708 # Asian - Central (e.g., Kazakhstani, Uzbekistani)
1709 t1<-data.frame(dat$ethnicity_2,dat$studyarm)
1710 table(t1)
1711 prop.table(table(t1), 2) * 100
1712
1713 # Asian - South (e.g., Indian, Pakistani, Sri Lankan)
1714 t1<-data.frame(dat$ethnicity_3,dat$studyarm)
1715 table(t1)
1716 prop.table(table(t1), 2) * 100
1717
1718 # Asian - South-East (e.g., Malaysian, Filipino, Vietnamese)
1719 t1<-data.frame(dat$ethnicity_4,dat$studyarm)
1720 table(t1)
1721 prop.table(table(t1), 2) * 100
1722
1723 # Indigenous or aboriginal person from outside of North America (e.g., Maori, Quechua)

```

```

1724 t1<-data.frame(dat$ethnicity_5,dat$studyarm)
1725 table(t1)
1726 prop.table(table(t1), 2) * 100
1727
1728 # White / European (e.g., English, Italian, Portuguese, Russian)
1729 t1<-data.frame(dat$ethnicity_6,dat$studyarm)
1730 table(t1)
1731 prop.table(table(t1), 2) * 100
1732
1733 # White / North American (e.g., Canadian, American)
1734 t1<-data.frame(dat$ethnicity_7,dat$studyarm)
1735 table(t1)
1736 prop.table(table(t1), 2) * 100
1737
1738 # Inuit
1739 t1<-data.frame(dat$ethnicity_8,dat$studyarm)
1740 table(t1)
1741 prop.table(table(t1), 2) * 100
1742
1743 # Latin American (e.g., Chilean, Mexican, Salvadorian)
1744 t1<-data.frame(dat$ethnicity_9,dat$studyarm)
1745 table(t1)
1746 prop.table(table(t1), 2) * 100
1747
1748 # Metis (Metis Nation in Canada)
1749 t1<-data.frame(dat$ethnicity_10,dat$studyarm)
1750 table(t1)
1751 prop.table(table(t1), 2) * 100
1752
1753 # North African (e.g., Moroccan, Tunisian)
1754 t1<-data.frame(dat$ethnicity_11,dat$studyarm)
1755 table(t1)
1756 prop.table(table(t1), 2) * 100
1757
1758 # Middle Eastern (e.g., Egyptian, Iranian, Lebanese)
1759 t1<-data.frame(dat$ethnicity_12,dat$studyarm)
1760 table(t1)
1761 prop.table(table(t1), 2) * 100
1762
1763 # Black - African (e.g., Ghanaian, Kenyan, Somali)
1764 t1<-data.frame(dat$ethnicity_13,dat$studyarm)
1765 table(t1)
1766 prop.table(table(t1), 2) * 100
1767
1768 # Black - Caribbean (e.g., Barbadian, Jamaican)
1769 t1<-data.frame(dat$ethnicity_14,dat$studyarm)
1770 table(t1)
1771 prop.table(table(t1), 2) * 100
1772
1773 # Black - North American (e.g., Canadian, American)
1774 t1<-data.frame(dat$ethnicity_15,dat$studyarm)
1775 table(t1)
1776 prop.table(table(t1), 2) * 100
1777
1778 # First Nations
1779 t1<-data.frame(dat$ethnicity_16,dat$studyarm)
1780 table(t1)
1781 prop.table(table(t1), 2) * 100
1782
1783 # Other
1784 t1<-data.frame(dat$ethnicity_17,dat$studyarm)
1785 table(t1)
1786 prop.table(table(t1), 2) * 100
1787
1788 # Asian_group
1789 t1<-data.frame(dat$Asian_group,dat$studyarm)
1790 table(t1)
1791 prop.table(table(t1), 2) * 100
1792

```

```
1793 # MaghrebMiddleEast_group
1794 t1<-data.frame(dat$MaghrebMiddleEast_group, dat$studyarm)
1795 table(t1)
1796 prop.table(table(t1), 2) * 100
1797
1798 # Black_group
1799 t1<-data.frame(dat$Black_group, dat$studyarm)
1800 table(t1)
1801 prop.table(table(t1), 2) * 100
1802
1803 # White_group
1804 t1<-data.frame(dat$White_group, dat$studyarm)
1805 table(t1)
1806 prop.table(table(t1), 2) * 100
1807
1808 # Indigenous_group
1809 t1<-data.frame(dat$Indigenous_group, dat$studyarm)
1810 table(t1)
1811 prop.table(table(t1), 2) * 100
1812
1813 # disability
1814 t1<-data.frame(dat$disability, dat$studyarm)
1815 table(t1)
1816 prop.table(table(t1), 2) * 100
1817
1818 # tech disability
1819 t1<-data.frame(dat$techdisability, dat$studyarm)
1820 table(t1)
1821 prop.table(table(t1), 2) * 100
1822
1823 #CHANGELOG ASJ: add any disability, 2021-08-03
1824 t1<-data.frame(dat$disability_any, dat$studyarm)
1825 table(t1)
1826 prop.table(table(t1), 2) * 100
1827
1828 # sex at birth
1829 t1<-data.frame(dat$sexatbirth, dat$studyarm)
1830 table(t1)
1831 prop.table(table(t1), 2) * 100
1832
1833 # gender identity
1834 t1<-data.frame(dat$genderidentity, dat$studyarm)
1835 table(t1)
1836 prop.table(table(t1), 2) * 100
1837
1838 # income
1839 t1<-data.frame(dat$income, dat$studyarm)
1840 table(t1)
1841 prop.table(table(t1), 2) * 100
1842
1843 # education level
1844 t1<-data.frame(dat$educationlevel, dat$studyarm)
1845 table(t1)
1846 prop.table(table(t1), 2) * 100
1847
1848 #CHANGELOG ASJ: add education level high/low, 2021-08-03
1849 t1<-data.frame(dat$edhi, dat$studyarm)
1850 table(t1)
1851 prop.table(table(t1), 2) * 100
1852
1853 # immune
1854 t1<-data.frame(dat$immune, dat$studyarm)
1855 table(t1)
1856 prop.table(table(t1), 2) * 100
1857
1858 # COVID-19 vax
1859 t1<-data.frame(dat$c19vax, dat$studyarm)
1860 table(t1)
1861 prop.table(table(t1), 2) * 100
```

```

1862
1863
1864 #CHANGELOG ASJ: add 4 new variables, 2021-08-06
1865 #Trust Info
1866 t1<-data.frame(dat$Htrustinfo,dat$studyarm)
1867 table(t1)
1868 prop.table(table(t1), 2) * 100
1869
1870 #Risk Perception 1
1871 t1<-data.frame(dat$RP1_dicho,dat$studyarm)
1872 table(t1)
1873 prop.table(table(t1), 2) * 100
1874
1875 #VaxIntention
1876 t1<-data.frame(dat$vaxintent,dat$studyarm)
1877 table(t1)
1878 prop.table(table(t1), 2) * 100
1879
1880 #Covid19 VaxIntention
1881 t1<-data.frame(dat$c19vaxintent,dat$studyarm)
1882 table(t1)
1883 prop.table(table(t1), 2) * 100
1884
1885 ##### + Graphics per arm #####
1886
1887 # Boxplots (NB. find nicer colours for publication/thesis)
1888
1889 par(mar=c(12,5,1,1)) #CHANGELOG ASJ: change margins to see the labels properly,
2021-08-03
1890
1891 # Risk perception
1892 # RECALL: Risk perception item 1 and item 2 to 6 are not measuring the same thing (item
1893 1 will be analysed as dichotomous variable)
1894 # Box plot of risk perception item 2 to 6 for overall data
1895 boxplot(
1896   dat$mean_riskperception2_6 ~ dat$studyarm,las=2,
1897   xlab = "",
1898   ylab = "Risk Perception2_6",
1899   main = "Boxplot",
1900   col = c(
1901     "white",
1902     "darksalmon",
1903     "darkolivegreen1",
1904     "lightcyan",
1905     "bisque3",
1906     "indianred4",
1907     "green4",
1908     "darkslateblue",
1909     "khaki",
1910     "gray75",
1911     "gray85",
1912     "firebrick3",
1913     "dodgerblue"
1914   )
1915 ) # CHANGELOG Added separate analysis for risk perception item 2 to 6 2021-07-08
1916
1917
1918 # Box plot of risk perception item 2 to 6 for subset Main data
1919 boxplot(
1920   datMain$mean_riskperception2_6 ~ datMain$studyarm,las=2,
1921   xlab = "",
1922   ylab = "Risk Perception2_6",
1923   main = "Boxplot",
1924   col = c(
1925     "white",
1926     "darksalmon",
1927     "darkolivegreen1",
1928     "lightcyan",

```

```

1929     "bisque3",
1930     "indianred4",
1931     "green4",
1932     "darkslateblue"
1933   )
1934 )
1935
1936 # Box plot of risk perception item 2 to 6 for subset Generic data
1937 boxplot(
1938   datGeneric$mean_riskperception2_6 ~ datGeneric$studyarm, las=2,
1939   xlab = "",
1940   ylab = "Risk Perception2_6",
1941   main = "Boxplot",
1942   col = c("white", "bisque3", "khaki", "gray75", "gray85")
1943 ) # CHANGELOG Added seperate analysis for risk perception item 2 to 6 2021-07-08
1944
1945
1946 par(mar=c(12,5,1,1)) #CHANGELOG ASJ: change margins to see the labels properly,
1947 2021-08-03
1948
1949 # Box plot of risk perceptiom item 2 to 6 for subset Measles data
1950 boxplot(
1951   datMeasles$mean_riskperception2_6 ~ datMeasles$studyarm, las=2,
1952   xlab = "",
1953   ylab = "Risk Perception2_6",
1954   main = "Boxplot",
1955   col = c("darksalmon", "indianred4", "firebrick3", "firebrick1")
1956 ) # CHANGELOG Added seperate analysis for risk perception item 2 to 6 2021-07-08
1957
1958
1959 # Box plot of risk perception item 2 to 6 for subset Flu data
1960 boxplot(
1961   datFlu$mean_riskperception2_6 ~ datFlu$studyarm, las=2,
1962   xlab = "",
1963   ylab = "Risk Perception2_6",
1964   main = "Boxplot",
1965   col = c("lightcyan", "darkslateblue", "dodgerblue")
1966 ) # CHANGELOG Added seperate analysis for risk perception item 2 to 6 2021-07-08
1967
1968 # Betsch et al C5
1969 #CHANGELOG ASJ: add boxplot for each subscales, 2021-08-06.
1970
1971
1972 boxplot(
1973   datMain$mean_C5_conf ~ datMain$studyarm, las=2,
1974   xlab = "",
1975   ylab = "C5 Confidence",
1976   main = "Boxplot",
1977   col = c(
1978     "white",
1979     "darksalmon",
1980     "darkolivegreen1",
1981     "lightcyan",
1982     "bisque3",
1983     "indianred4",
1984     "green4",
1985     "darkslateblue"
1986   )
1987 )
1988
1989 boxplot(
1990   datMain$mean_C5_comp ~ datMain$studyarm, las=2,
1991   xlab = "",
1992   ylab = "C5 complacency",
1993   main = "Boxplot",
1994   col = c(
1995     "white",
1996     "darksalmon",

```

```

1997     "darkolivegreen1",
1998     "lightcyan",
1999     "bisque3",
2000     "indianred4",
2001     "green4",
2002     "darkslateblue"
2003 )
2004 )
2005
2006 boxplot(
2007     datMain$mean_C5_cons ~ datMain$studyarm, las=2,
2008     xlab = "",
2009     ylab = "C5 constraints",
2010     main = "Boxplot",
2011     col = c(
2012         "white",
2013         "darksalmon",
2014         "darkolivegreen1",
2015         "lightcyan",
2016         "bisque3",
2017         "indianred4",
2018         "green4",
2019         "darkslateblue"
2020     )
2021 )
2022
2023 boxplot(
2024     datMain$mean_C5_calc ~ datMain$studyarm, las=2,
2025     xlab = "",
2026     ylab = "C5 calculation",
2027     main = "Boxplot",
2028     col = c(
2029         "white",
2030         "darksalmon",
2031         "darkolivegreen1",
2032         "lightcyan",
2033         "bisque3",
2034         "indianred4",
2035         "green4",
2036         "darkslateblue"
2037     )
2038 )
2039
2040 boxplot(
2041     datMain$mean_C5_coll ~ datMain$studyarm, las=2,
2042     xlab = "",
2043     ylab = "C5 Collective Respons.",
2044     main = "Boxplot",
2045     col = c(
2046         "white",
2047         "darksalmon",
2048         "darkolivegreen1",
2049         "lightcyan",
2050         "bisque3",
2051         "indianred4",
2052         "green4",
2053         "darkslateblue"
2054     )
2055 )
2056
2057
2058 boxplot(
2059     datGeneric$mean_C5_conf ~ datGeneric$studyarm, las=2,
2060     xlab = "",
2061     ylab = "C5 confidence",
2062     main = "Boxplot",
2063     col = c("white", "bisque3", "khaki", "gray75", "gray85")
2064 )
2065

```

```

2066 boxplot(
2067   datGeneric$mean_C5_comp ~ datGeneric$studyarm,las=2,
2068   xlab = "",
2069   ylab = "C5 complacency",
2070   main = "Boxplot",
2071   col = c("white", "bisque3", "khaki", "gray75", "gray85")
2072 )
2073
2074 boxplot(
2075   datGeneric$mean_C5_cons ~ datGeneric$studyarm,las=2,
2076   xlab = "",
2077   ylab = "C5 constraints",
2078   main = "Boxplot",
2079   col = c("white", "bisque3", "khaki", "gray75", "gray85")
2080 )
2081
2082 boxplot(
2083   datGeneric$mean_C5_calc ~ datGeneric$studyarm,las=2,
2084   xlab = "",
2085   ylab = "C5 calculation",
2086   main = "Boxplot",
2087   col = c("white", "bisque3", "khaki", "gray75", "gray85")
2088 )
2089
2090 boxplot(
2091   datGeneric$mean_C5_coll ~ datGeneric$studyarm,las=2,
2092   xlab = "",
2093   ylab = "C5 collective respons.",
2094   main = "Boxplot",
2095   col = c("white", "bisque3", "khaki", "gray75", "gray85")
2096 )
2097
2098
2099
2100 boxplot(
2101   datMeasles$mean_C5_conf ~ datMeasles$studyarm,las=2,
2102   xlab = "",
2103   ylab = "C5 confidence",
2104   main = "Boxplot",
2105   col = c("darksalmon", "indianred4", "firebrick3", "firebrick1")
2106 )
2107
2108 boxplot(
2109   datMeasles$mean_C5_comp ~ datMeasles$studyarm,las=2,
2110   xlab = "",
2111   ylab = "C5 complacency",
2112   main = "Boxplot",
2113   col = c("darksalmon", "indianred4", "firebrick3", "firebrick1")
2114 )
2115
2116 boxplot(
2117   datMeasles$mean_C5_cons ~ datMeasles$studyarm,las=2,
2118   xlab = "",
2119   ylab = "C5 constraints",
2120   main = "Boxplot",
2121   col = c("darksalmon", "indianred4", "firebrick3", "firebrick1")
2122 )
2123
2124 boxplot(
2125   datMeasles$mean_C5_calc ~ datMeasles$studyarm,las=2,
2126   xlab = "",
2127   ylab = "C5 calculation",
2128   main = "Boxplot",
2129   col = c("darksalmon", "indianred4", "firebrick3", "firebrick1")
2130 )
2131
2132 boxplot(
2133   datMeasles$mean_C5_coll ~ datMeasles$studyarm,las=2,
2134   xlab = "",

```



```

2135     ylab = "C5 collective respons.",
2136     main = "Boxplot",
2137     col = c("darksalmon", "indianred4", "firebrick3", "firebrick1")
2138 )
2139
2140
2141 boxplot(
2142     datFlu$mean_C5_conf ~ datFlu$studyarm, las=2,
2143     xlab = "",
2144     ylab = "C5 confidence",
2145     main = "Boxplot",
2146     col = c("lightcyan", "darkslateblue", "dodgerblue")
2147 )
2148
2149 boxplot(
2150     datFlu$mean_C5_comp ~ datFlu$studyarm, las=2,
2151     xlab = "",
2152     ylab = "C5 complacency",
2153     main = "Boxplot",
2154     col = c("lightcyan", "darkslateblue", "dodgerblue")
2155 )
2156
2157 boxplot(
2158     datFlu$mean_C5_cons ~ datFlu$studyarm, las=2,
2159     xlab = "",
2160     ylab = "C5 constraints",
2161     main = "Boxplot",
2162     col = c("lightcyan", "darkslateblue", "dodgerblue")
2163 )
2164
2165 boxplot(
2166     datFlu$mean_C5_calc ~ datFlu$studyarm, las=2,
2167     xlab = "",
2168     ylab = "C5 calculation",
2169     main = "Boxplot",
2170     col = c("lightcyan", "darkslateblue", "dodgerblue")
2171 )
2172
2173 boxplot(
2174     datFlu$mean_C5_coll ~ datFlu$studyarm, las=2,
2175     xlab = "",
2176     ylab = "C5 collective respons.",
2177     main = "Boxplot",
2178     col = c("lightcyan", "darkslateblue", "dodgerblue")
2179 )
2180
2181 # Emotion
2182
2183 boxplot(
2184     dat$mean_emotion ~ dat$studyarm, las=2,
2185     xlab = "",
2186     ylab = "emotion",
2187     main = "Boxplot",
2188     col = c(
2189         "white",
2190         "darksalmon",
2191         "darkolivegreen1",
2192         "lightcyan",
2193         "bisque3",
2194         "indianred4",
2195         "green4",
2196         "darkslateblue",
2197         "khaki",
2198         "gray75",
2199         "gray85",
2200         "firebrick3",
2201         "firebrick1",
2202         "dodgerblue"
2203     )

```

```

2204 )
2205
2206 boxplot(
2207   datMain$mean_emotion ~ datMain$studyarm, las=2,
2208   xlab = "",
2209   ylab = "emotion",
2210   main = "Boxplot",
2211   col = c(
2212     "white",
2213     "darksalmon",
2214     "darkolivegreen1",
2215     "lightcyan",
2216     "bisque3",
2217     "indianred4",
2218     "green4",
2219     "darkslateblue"
2220   )
2221 )
2222
2223 boxplot(
2224   datGeneric$mean_emotion ~ datGeneric$studyarm, las=2,
2225   xlab = "",
2226   ylab = "emotion",
2227   main = "Boxplot",
2228   col = c("white", "bisque3", "khaki", "gray75", "gray85")
2229 )
2230
2231 boxplot(
2232   datMeasles$mean_emotion ~ datMeasles$studyarm, las=2,
2233   xlab = "",
2234   ylab = "emotion",
2235   main = "Boxplot",
2236   col = c("darksalmon", "indianred4", "firebrick3", "firebrick1")
2237 )
2238
2239 boxplot(
2240   datFlu$mean_emotion ~ datFlu$studyarm, las=2,
2241   xlab = "",
2242   ylab = "emotion",
2243   main = "Boxplot",
2244   col = c("lightcyan", "darkslateblue", "dodgerblue")
2245 )
2246
2247 # Knowledge
2248
2249 boxplot(
2250   dat$sum_knowledge ~ dat$studyarm, las=2,
2251   xlab = "",
2252   ylab = "knowledge",
2253   main = "Boxplot",
2254   col = c(
2255     "white",
2256     "darksalmon",
2257     "darkolivegreen1",
2258     "lightcyan",
2259     "bisque3",
2260     "indianred4",
2261     "green4",
2262     "darkslateblue",
2263     "khaki",
2264     "gray75",
2265     "gray85",
2266     "firebrick3",
2267     "firebrick1",
2268     "dodgerblue"
2269   )
2270 )
2271
2272 boxplot(

```

```

2273   datMain$sum_knowledge ~ datMain$studyarm, las=2,
2274   xlab = "",
2275   ylab = "knowledge",
2276   main = "Boxplot",
2277   col = c(
2278     "white",
2279     "darksalmon",
2280     "darkolivegreen1",
2281     "lightcyan",
2282     "bisque3",
2283     "indianred4",
2284     "green4",
2285     "darkslateblue"
2286   )
2287 )
2288
2289 boxplot(
2290   datGeneric$sum_knowledge ~ datGeneric$studyarm, las=2,
2291   xlab = "",
2292   ylab = "knowledge",
2293   main = "Boxplot",
2294   col = c("white", "bisque3", "khaki", "gray75", "gray85")
2295 )
2296
2297 boxplot(
2298   datMeasles$sum_knowledge ~ datMeasles$studyarm, las=2,
2299   xlab = "",
2300   ylab = "knowledge",
2301   main = "Boxplot",
2302   col = c("darksalmon", "indianred4", "firebrick3", "firebrick1")
2303 )
2304
2305 boxplot(
2306   datFlu$sum_knowledge ~ datFlu$studyarm, las=2,
2307   xlab = "",
2308   ylab = "knowledge",
2309   main = "Boxplot",
2310   col = c("lightcyan", "darkslateblue", "dodgerblue")
2311 )
2312
2313
2314 #CHANGELOG ASJ: Boxplot removed for variables that will be analysed as dichotomous
variables (trust info & vax intention), 2021-08-06
2315
2316 ##### MISSING DATA EXPLORATION #####
2317
2318 # CHANGELOG The code added to determine percentage of the missing data 2021-07-08
2319
2320 don %>%
2321   naniar::vis_miss(.,
2322     sort_miss = TRUE,
2323     cluster = TRUE)
2324
2325 don %>%
2326   naniar::gg_miss_upset(., nsets = 6) # CHANGELOG Descriptive data of missing 2021-07-08
2327
2328 don %>%
2329   summarise(n_complete = sum(stats::complete.cases(.)),
2330     pct_complete = 100 * naniar::prop_complete_case(.),
2331     n_missing = sum(!stats::complete.cases(.)),
2332     pct_missing = 100 * naniar::prop_miss_case(.))
2333
2334 don %>%
2335   naniar::miss_case_table() # CHANGELOG Missing numbers
2336
2337 don %>%
2338   naniar::miss_var_summary() %>%
2339   dplyr::filter(n_miss > 0) # CHANGELOG nvar missing
2340
2341 don %>%

```

```

2341     naniar::miss_prop_summary() # CHANGELOG percentage of missing overall, % de var avec
    missing, % obs avec missingdon %>% #résumé des missing stat + plot avec VIM
2342
2343
2344 HTMLStop() #CHANGELOG ASJ: Stop output html 2021-08-06.
2345
2346
2347 #CHANGELOG ASJ Add descriptive statistic per visualization, 21-09-20.
2348 HTMLStart(outdir=".\\",
2349           file = "Herdimm Descriptive+ 210921",extension = "html",echo=TRUE, HTMLframe
           = TRUE)
2350
2351
2352 describeBy(dat$mean_riskperception2_6,dat$viz)
2353 describeBy(dat$mean_emotion,dat$viz)
2354 describeBy(dat$sum_knowledge,dat$viz)
2355 describeBy(dat$mean_C5_calc,dat$viz)
2356 describeBy(dat$mean_C5_conf,dat$viz)
2357 describeBy(dat$mean_C5_cons,dat$viz)
2358 describeBy(dat$mean_C5_comp,dat$viz)
2359 describeBy(dat$mean_C5_coll,dat$viz)
2360 describeBy(dat$trustinfo,dat$viz)
2361 describeBy(dat$vaxintention_1,dat$viz)
2362 describeBy(dat$c19vaxintention_1,dat$viz)
2363 describeBy(dat$riskpercep1_1,dat$viz)
2364
2365
2366 t1<-data.frame(dat$RP1_dicho,dat$viz)
2367 table(t1)
2368 prop.table(table(t1), 2) * 100
2369
2370 t1<-data.frame(dat$Htrustinfo,dat$viz)
2371 table(t1)
2372 prop.table(table(t1), 2) * 100
2373
2374 t1<-data.frame(dat$vaxintent,dat$viz)
2375 table(t1)
2376 prop.table(table(t1), 2) * 100
2377
2378 t1<-data.frame(dat$c19vaxintent,dat$viz)
2379 table(t1)
2380 prop.table(table(t1), 2) * 100
2381
2382 t1<-data.frame(dat$mean_C5_calc2,dat$viz)
2383 table(t1)
2384 prop.table(table(t1), 2) * 100
2385
2386 t1<-data.frame(dat$mean_C5_conf2,dat$viz)
2387 table(t1)
2388 prop.table(table(t1), 2) * 100
2389
2390 t1<-data.frame(dat$mean_C5_comp2,dat$viz)
2391 table(t1)
2392 prop.table(table(t1), 2) * 100
2393
2394 t1<-data.frame(dat$mean_C5_cons2,dat$viz)
2395 table(t1)
2396 prop.table(table(t1), 2) * 100
2397
2398 t1<-data.frame(dat$mean_C5_coll2,dat$viz)
2399 table(t1)
2400 prop.table(table(t1), 2) * 100
2401 HTMLStop()
2402
2403 ##### MULTIPLE IMPUTATION #####
2404
2405 # Create new data sets for imputed values to make analyses easier
2406
2407 #CHANGELOG ASJ: change list of variables for imputation according to above recoding,

```

2021-08-06

```
2408 datMain4Imputation <-
2409   subset(
2410     dat,
2411     dat$studyarm == "controlgeneric" |
2412     dat$studyarm == "controlmeasles" |
2413     dat$studyarm == "controlpertussis" |
2414     dat$studyarm == "controlflu" |
2415     dat$studyarm == "herdimmgeneric" |
2416     dat$studyarm == "herdimmmeasles" |
2417     dat$studyarm == "herdimmpertussis" |
2418     dat$studyarm == "herdimmmflu",
2419     select = c(
2420       viz,
2421       disease,
2422       mean_riskperception2_6,
2423       mean_C5_conf,
2424       mean_C5_comp,
2425       mean_C5_cons,
2426       mean_C5_calc,
2427       mean_C5_coll,
2428       mean_emotion,
2429       sum_knowledge,
2430       mean_indivhorz,
2431       mean_indivvertical,
2432       mean_collhorz,
2433       mean_collvertical,
2434       bornincanada,
2435       language_1,
2436       language_2,
2437       Asian_group,
2438       White_group,
2439       disability_any,
2440       genderidentity,
2441       income,
2442       edhi,
2443       age,
2444       Htrustinfo,
2445       RP1_dicho,
2446       vaxintent
2447     )
2448   )
2449
2450
2451 datGeneric4Imputation <-
2452   subset(
2453     dat,
2454     dat$studyarm == "controlgeneric" |
2455     dat$studyarm == "herdimmgeneric" |
2456     dat$studyarm == "robertkochgeneric" |
2457     dat$studyarm == "sbsnewsgeneric" & UserLanguage == "EN",
2458     select = c(
2459       studyarm,
2460       UserLanguage,
2461       mean_riskperception2_6,
2462       mean_C5_conf,
2463       mean_C5_comp,
2464       mean_C5_cons,
2465       mean_C5_calc,
2466       mean_C5_coll,
2467       mean_emotion,
2468       sum_knowledge,
2469       mean_indivhorz,
2470       mean_indivvertical,
2471       mean_collhorz,
2472       mean_collvertical,
2473       bornincanada,
2474       language_1,
2475       language_2,
```

```

2476     Asian_group,
2477     White_group,
2478     disability_any,
2479     genderidentity,
2480     income,
2481     edhi,
2482     age,
2483     Htrustinfo,
2484     RP1_dicho,
2485     vaxintent
2486   )
2487 )
2488
2489 datMeasles4Imputation <-
2490   subset(
2491     dat,
2492     dat$studyarm == "controlmeasles" |
2493     dat$studyarm == "herdimmmasles" |
2494     dat$studyarm == "guardianmeasles" |
2495     dat$studyarm == "theotheredmundmeasles",
2496     select = c(
2497       studyarm,
2498       UserLanguage,
2499       mean_riskperception2_6,
2500       mean_C5_conf,
2501       mean_C5_comp,
2502       mean_C5_cons,
2503       mean_C5_calc,
2504       mean_C5_coll,
2505       mean_emotion,
2506       sum_knowledge,
2507       mean_indivhorz,
2508       mean_indivvertical,
2509       mean_collhorz,
2510       mean_collvertical,
2511       bornincanada,
2512       language_1,
2513       language_2,
2514       Asian_group,
2515       White_group,
2516       disability_any,
2517       genderidentity,
2518       income,
2519       edhi,
2520       age,
2521       Htrustinfo,
2522       RP1_dicho,
2523       vaxintent
2524     )
2525   )
2526
2527 datFlu4Imputation <-
2528   subset(
2529     dat,
2530     dat$studyarm == "controlflu" |
2531     dat$studyarm == "herdimmmflu" |
2532     dat$studyarm == "publichealthagencycanadaflu",
2533     select = c(
2534       studyarm,
2535       UserLanguage,
2536       mean_riskperception2_6,
2537       mean_C5_conf,
2538       mean_C5_comp,
2539       mean_C5_cons,
2540       mean_C5_calc,
2541       mean_C5_coll,
2542       mean_emotion,
2543       sum_knowledge,
2544       mean_indivhorz,

```

```

2545     mean_indivvertical,
2546     mean_collhorz,
2547     mean_collvertical,
2548     bornincanada,
2549     language_1,
2550     language_2,
2551     Asian_group,
2552     White_group,
2553     disability_any,
2554     genderidentity,
2555     income,
2556     edhi,
2557     age,
2558     Htrustinfo,
2559     RP1_dicho,
2560     vaxintent
2561   )
2562 )
2563
2564 # Drop any unused levels to clean up the dataset
2565
2566 datMain4Imputation$viz <- droplevels(datMain4Imputation$viz)
2567
2568 datGeneric4Imputation$studyarm <- droplevels(datGeneric4Imputation$studyarm)
2569
2570 datMeasles4Imputation$studyarm <- droplevels(datMeasles4Imputation$studyarm)
2571
2572 datFlu4Imputation$studyarm <- droplevels(datFlu4Imputation$studyarm)
2573
2574 # Impute the missing values, using parameters:
2575 # m: Refers to 15 imputed data sets
2576 # maxit: Refers to number of iterations taken to impute missing values: 15
2577 #CHANGELOG ASJ: method removed from mice, use pmm, logreg or polyreg according to
    datatype, 21-09-20.
2578
2579 #CHANGELOG ASJ: Set the seed for reproducibility 2021-08-03
2580 seed_for_imp <- 20210920
2581
2582 datMainImputed <-
2583   mice(
2584     datMain4Imputation,
2585     m = 15,
2586     maxit = 15,
2587
2588     seed = seed_for_imp,
2589   )
2590 summary(datMainImputed)
2591
2592 #CHANGELOG ASJ: added to validate imputation. 2021-09-20.
2593 plot(datMainImputed, c("bornincanada", "language_1", "Asian_group", "White_group", "disability_
    _any",
2594
2595     "genderidentity", "income", "edhi", "age", "Htrustinfo", "RP1_dicho", "
2596     vaxintent"))
2597
2598 stripplot(datMainImputed, age)
2599 bwplot(datMainImputed, age)
2600 densityplot(datMainImputed, ~age)
2601 densityplot(datMainImputed, ~bornincanada)
2602 densityplot(datMainImputed, ~language_1)
2603 densityplot(datMainImputed, ~Asian_group)
2604 densityplot(datMainImputed, ~White_group)
2605 densityplot(datMainImputed, ~disability_any)
2606 densityplot(datMainImputed, ~genderidentity)
2607 densityplot(datMainImputed, ~income)
2608 densityplot(datMainImputed, ~edhi)
2609 densityplot(datMainImputed, ~Htrustinfo) #only one missing obs
2610 densityplot(datMainImputed, ~RP1_dicho)
2611 densityplot(datMainImputed, ~vaxintent)
2612 save(datMainImputed, file="datMainImputed.RData")

```

```

2610
2611
2612 datGenericImputed <-
2613   mice(
2614     datGeneric4Imputation,
2615     m = 15,
2616     maxit = 15,
2617     seed = seed_for_imp
2618   )
2619 summary(datGenericImputed)
2620
2621 #CHANGELOG ASJ: added to validate imputation. 2021-09-20.
2622 plot(datGenericImputed, c("borninacanada", "language_1", "Asian_group", "White_group", "disabil
ity_any",
2623
2624     "genderidentity", "income", "edhi", "age", "Htrustinfo", "RP1_dicho", "va
xintent"))
2624 stripplot(datGenericImputed, age)
2625 bwplot(datGenericImputed, age)
2626 densityplot(datGenericImputed, ~age)
2627 densityplot(datGenericImputed, ~borninacanada)
2628 densityplot(datGenericImputed, ~language_1)
2629 densityplot(datGenericImputed, ~Asian_group)
2630 densityplot(datGenericImputed, ~White_group)
2631 densityplot(datGenericImputed, ~disability_any)
2632 densityplot(datGenericImputed, ~genderidentity)
2633 densityplot(datGenericImputed, ~income)
2634 densityplot(datGenericImputed, ~edhi)
2635 densityplot(datGenericImputed, ~Htrustinfo) #only one missing obs
2636 densityplot(datGenericImputed, ~RP1_dicho)
2637 densityplot(datGenericImputed, ~vaxintent)
2638 save(datGenericImputed, file="datGenericImputed.RData")
2639
2640
2641
2642 datMeaslesImputed <-
2643   mice(
2644     datMeasles4Imputation,
2645     m = 15,
2646     maxit = 15,
2647     seed = seed_for_imp
2648   )
2649 summary(datMeaslesImputed)
2650
2651 #CHANGELOG ASJ: added to validate imputation. 2021-09-20.
2652 plot(datMeaslesImputed, c("borninacanada", "language_1", "Asian_group", "White_group", "disabil
ity_any",
2653
2654     "genderidentity", "income", "edhi", "age", "RP1_dicho", "vaxintent"))
2654 stripplot(datMeaslesImputed, age)
2655 bwplot(datMeaslesImputed, age)
2656 densityplot(datMeaslesImputed, ~age)
2657 densityplot(datMeaslesImputed, ~borninacanada)
2658 densityplot(datMeaslesImputed, ~language_1) #only 1 missing
2659 densityplot(datMeaslesImputed, ~Asian_group)
2660 densityplot(datMeaslesImputed, ~White_group)
2661 densityplot(datMeaslesImputed, ~disability_any)
2662 densityplot(datMeaslesImputed, ~genderidentity)
2663 densityplot(datMeaslesImputed, ~income)
2664 densityplot(datMeaslesImputed, ~edhi)
2665 densityplot(datMeaslesImputed, ~RP1_dicho)
2666 densityplot(datMeaslesImputed, ~vaxintent)
2667 save(datMeaslesImputed, file="datMeaslesImputed.RData")
2668
2669 datFluImputed <-
2670   mice(
2671     datFlu4Imputation,
2672     m = 15,
2673     maxit = 15,
2674     seed = seed_for_imp

```



```

2675 )
2676 summary(datFluImputed)
2677
2678 #CHANGELOG ASJ: added to validate imputation. 2021-09-20.
2679 plot(datFluImputed, c("borninacanada", "language_1", "Asian_group", "White_group", "disability_
any",
2680 "genderidentity", "income", "edhi", "age", "RP1_dicho", "vaxintent"))
2681 stripplot(datFluImputed, age)
2682 bwplot(datFluImputed, age)
2683 densityplot(datFluImputed, ~age)
2684 densityplot(datFluImputed, ~borninacanada)
2685 densityplot(datFluImputed, ~language_1) #only 1 missing
2686 densityplot(datFluImputed, ~Asian_group)
2687 densityplot(datFluImputed, ~White_group)
2688 densityplot(datFluImputed, ~disability_any)
2689 densityplot(datFluImputed, ~genderidentity)
2690 densityplot(datFluImputed, ~income)
2691 densityplot(datFluImputed, ~edhi)
2692 densityplot(datFluImputed, ~RP1_dicho)
2693 densityplot(datFluImputed, ~vaxintent)
2694 save(datFluImputed, file="datFluImputed.RData")
2695
2696
2697 ##### ANALYSES #####
2698
2699 ##### RESEARCH QUESTION 1 (PRIMARY): EFFECT OF HERDIMM ON RISK PERCEPTION #####
2700
2701 # + 2-way ANOVA (adjusted for covariates and with moderators) #####
2702
2703 # Recall: Research question 1 (primary): Across 4 vaccine-preventable diseases, does
the herdim
2704 # intervention influence risk perception compared to a control?
2705
2706 ##### + Model 1: Check for direct effects of factors without any covariates (Risk
perception1_1) #####
2707 # We have made a new variable with transformation. We want to know that when we look at
model 1 to model 3
2708 # what we get the significant results e.g., do we get significant results from
interaction for all, or between which diseases, or viz,
2709 # if it doesn't change then we use risk perception 2-6 without any transformation, and
we will be good with that
2710 # because yes, transformation makes residual better but it doesnt change the conclusion.
2711 # Note: if we do not see changes in the model 1-3 for datMain, we do not use transform
in imputation data,
2712 # if there is change then we use transformation variable in the imputation data.
2713
2714 #CHANGELOG. Analysis of RiskPerception2-6 only in anova model, 2021-08-04
2715 #CHANGELOG ASJ: After analysis of residuals, model also run with transformed variable
2716 #CHANGELOG ASJ: results are similar and residuals not that improved, keep original
variable
2717 hist(datMain$mean_riskperception2_6)
2718 datMain$mean_riskperception2_6trans<-datMain$mean_riskperception2_6 ** 2
2719 hist(datMain$mean_riskperception2_6trans)
2720 datMain$mean_riskperception2_6transinv<-log(8-datMain$mean_riskperception2_6)
2721 hist(datMain$mean_riskperception2_6transinv)
2722
2723 ##### + Model 1: Check for direct effects of factors without any covariates (for risk
perception 2 to 6) #####
2724
2725 options(contrasts=c("contr.sum", "contr.poly")) # CHANGELOG: The statement below is
added to calculate properly the type III sum of squares with lm 2021-07-27
2726
2727 mRP1_2_6 <- lm(mean_riskperception2_6 ~ viz * disease, data = datMain)
2728 Anova(mRP1_2_6, type="III")
2729 summary(mRP1_2_6)
2730
2731 # Model 2: Check for direct effects of factors with adjustment for other covariates
2732 #CHANGELOG ASJ: change list of covariates after recoding and deletion for <5%
categories, 2021-08-04

```

```

2733
2734 mRP2_2_6 <-
2735   lm(
2736     mean_riskperception2_6 ~ viz * disease +
2737     mean_indivhorz +
2738     mean_indivvertical +
2739     mean_collhorz +
2740     mean_collvertical +
2741     bornincanada +
2742     language_1 +
2743     language_2 +
2744     Asian_group +
2745     White_group +
2746     disability_any +
2747     genderidentity +
2748     income +
2749     edhi +
2750     age,
2751     data = datMain
2752   )
2753 Anova(mRP2_2_6, type = "III")
2754 summary(mRP2_2_6)
2755
2756 # Model 3: Check for moderating effects of individualism & collectivism with adjustment
2757 # for other
2758 # covariates
2759 mRP3_2_6 <-
2760   lm(
2761     mean_riskperception2_6 ~
2762     viz * disease * mean_indivhorz +
2763     viz * disease * mean_indivvertical +
2764     viz * disease * mean_collhorz +
2765     viz * disease * mean_collvertical +
2766     bornincanada +
2767     language_1 +
2768     language_2 +
2769     Asian_group +
2770     White_group +
2771     disability_any +
2772     genderidentity +
2773     income +
2774     edhi +
2775     age,
2776     data = datMain
2777   )
2778 Anova(mRP3_2_6, type = "III")
2779 summary(mRP3_2_6)
2780
2781 ##### + Adding interaction for high and low education with herdim vizsualization #####
2782 # CHANGELOG We have added 2 new models to check the interaction between
2783 # high and low education with herdim vizsualization 2021-07-22
2784
2785 ##### + Model 4: Check for interaction viz*edhi without any covariates (for risk
2786 perception 2 to 6) #####
2787
2788 mRP4_2_6 <- lm(mean_riskperception2_6 ~ viz * disease + viz * edhi, data = datMain)
2789 Anova(mRP4_2_6, type="III")
2790 summary(mRP4_2_6)
2791
2792 # Model 5: Check for interaction viz*edhi with covariates
2793
2794 mRP5_2_6 <-
2795   lm(
2796     mean_riskperception2_6 ~ viz * disease +
2797     viz * edhi +
2798     mean_indivhorz +
2799     mean_indivvertical +
2800     mean_collhorz +

```

```

2800     mean_collvertical +
2801     borninCanada +
2802     language_1 +
2803     language_2 +
2804     Asian_group +
2805     White_group +
2806     disability_any +
2807     genderidentity +
2808     income +
2809     age,
2810     data = datMain
2811 )
2812 Anova(mRP5_2_6, type = "III")
2813 summary(mRP5_2_6)
2814
2815
2816 ##### + Validating assumptions #####
2817
2818 # Check to see if the assumptions of the models are respected. If not, we will
2819 # transform the
2820 # outcome.
2821
2822 # First, create an assumption-checking function that we can run on each model for
2823 # efficiency.
2824
2825 checkassumptions <- function(modelname) {
2826   boxcox(modelname, lambda = seq(-2, 2, 0.1), plotit = T)
2827   # Extract the residuals from the model
2828   res <- studres(modelname)
2829   # Check their normality
2830   print(kurtosis(res) - 3)
2831   print(skewness(res))
2832   hist(res)
2833   qqnorm(res)
2834   qqline(res)
2835   print(ks.test(res, "pnorm", 0, 1))
2836   print(shapiro.test(res))
2837   # Homoscedasticity (homogeneity of variance)
2838   fitted <- fitted(modelname)
2839   plot(fitted, res)
2840   abline(h = c(-3, 0, 3))
2841 }
2842
2843 # Then run the function to check the assumptions for each model.
2844
2845 checkassumptions(mRP1_2_6)
2846 checkassumptions(mRP2_2_6)
2847 checkassumptions(mRP3_2_6)
2848 checkassumptions(mRP4_2_6) # CHANGELOG We have added check assumptions function for
2849 # Model 4, 5 and 6 2021-07-22
2850 checkassumptions(mRP5_2_6)
2851
2852
2853 ##### + Interpretation (Risk perception 2 to 6) #####
2854
2855 #CHANGELOG ASJ: only the appropriate section (with or without interaction) is kept for
2856 # each model, 2021-08-09
2857
2858 # Interpretation of model 1 in the case of an interaction
2859
2860 mRP1_2_6_vd <- emmeans(mRP1_2_6, ~viz|disease)
2861 mRP1_2_6_vd
2862 pairs(mRP1_2_6_vd) # Only do multiple comparisons if type 3 test is significant
2863 plot(mRP1_2_6_vd) # Explore options for less ugly plot for publication/thesis
2864
2865 mRP1_2_6_dv <- emmeans(mRP1_2_6, ~disease|viz)
2866 mRP1_2_6_dv
2867 pairs(mRP1_2_6_dv) # Only do multiple comparisons if type 3 test is significant
2868 plot(mRP1_2_6_dv)

```

```

2865
2866
2867 # Interpretation of model 2 in the case of an interaction
2868
2869 mRP2_2_6_vd <- emmeans(mRP2_2_6,~viz|disease)
2870 mRP2_2_6_vd
2871 pairs(mRP2_2_6_vd) # Only do multiple comparisons if type 3 test is significant
2872 plot(mRP2_2_6_vd) # Explore options for less ugly plot for publication/thesis
2873
2874 mRP2_2_6_dv <- emmeans(mRP2_2_6,~disease|viz)
2875 mRP2_2_6_dv
2876 pairs(mRP2_2_6_dv) # Only do multiple comparisons if type 3 test is significant
2877 plot(mRP2_2_6_dv)
2878
2879 # Interpretation of model 3 moderating effects
2880 #CHANGELOG ASJ: change the focus of the interpretation 2021-08-11.
2881
2882 emmip(mRP3_2_6, disease ~ mean_indivhorz, cov.reduce = range)
2883 emmip(mRP3_2_6, viz ~ mean_indivvertical, cov.reduce = range)
2884 emmip(mRP3_2_6, viz ~ mean_collhorz, cov.reduce = range)
2885
2886 emmeans(mRP3_2_6, ~ viz, at=list(mean_indivvertical=(2.5)))
2887 pairs(emmeans(mRP3_2_6, ~ viz, at=list(mean_indivvertical=(2.5))))
2888 emmeans(mRP3_2_6, ~ viz, at=list(mean_indivvertical=(5.0)))
2889 pairs(emmeans(mRP3_2_6, ~ viz, at=list(mean_indivvertical=(5.0))))
2890 emmeans(mRP3_2_6, ~ viz, at=list(mean_indivvertical=(7.5)))
2891 pairs(emmeans(mRP3_2_6, ~ viz, at=list(mean_indivvertical=(7.5))))
2892
2893 # Interpretation of model 4 in the case of an interaction viz*edhi
2894 # CHANGELOG We have added interpretation of model 4 2021-07-22
2895
2896 mRP4_2_6_ve <- emmeans(mRP4_2_6,~viz|edhi)
2897 mRP4_2_6_ve
2898 pairs(mRP4_2_6_ve) # Only do multiple comparisons if type 3 test is significant
2899 plot(mRP4_2_6_ve) # Explore options for less ugly plot for publication/thesis
2900
2901 mRP4_2_6_ev <- emmeans(mRP4_2_6,~edhi|viz)
2902 mRP4_2_6_ev
2903 pairs(mRP4_2_6_ev) # Only do multiple comparisons if type 3 test is significant
2904 plot(mRP4_2_6_ev)
2905
2906
2907 # Interpretation of model 5 in the case of an interaction viz*edhi
2908 #No interaction
2909
2910
2911 ##### + Analyses on imputed data #####
2912
2913 #CHANGELOG ASJ: No missing data for mean_riskperception2_6, no model with imputation
2914 performed, 21-09-20.
2915
2916 ##### RESEARCH QUESTION 2: EFFECT OF HERDIMM ON OTHER OUTCOMES #####
2917
2918 # Recall: Research question 2 (secondary): Across 4 vaccine-preventable diseases, does
2919 the herdimm
2920 # intervention influence other outcomes (5C scale, emotions, trust, knowledge,
2921 behavioural
2922 # intentions) compared to a control?
2923
2924 # The same analysis as above will be done for the secondary outcomes: mean_C5,
2925 mean_emotions,
2926 # sum_knowledge, and behavioural intentions. For trustinfo the same analysis will be
2927 done if the
2928 # distribution has enough variance (2-way ANOVA). However, if it's not the case the
2929 variable will be
2930 # dichotomised into 1 to 4 (low trust) and 5 to 7 (high trust) and we will run a
2931 logistic
2932 # regression.

```

```

2927
2928
2929 ##### +++ Emotions #####
2930
2931 options(contrasts=c("contr.sum", "contr.poly")) # CHANGELOG: The statement below is
added to calculate properly the type III sum of squares with lm 2021-07-27
2932
2933 ##### + Model 1: Check for direct effects of factors without any covariates (Emotions)
#####
2934 mEmotions_1 <- lm(mean_emotion ~ viz * disease, data = datMain)
2935 Anova(mEmotions_1, type="III")
2936 summary(mEmotions_1)
2937
2938 # Model 2: Check for direct effects of factors with adjustment for other covariates
2939
2940 mEmotions_2 <-
2941   lm(
2942     mean_emotion ~ viz * disease +
2943       mean_indivhorz +
2944       mean_indivvertical +
2945       mean_collhorz +
2946       mean_collvertical +
2947       borninCanada + #CHANGELOG ASJ: covariate list shortened 2021-08-04
2948       language_1 +
2949       language_2 +
2950       Asian_group +
2951       White_group +
2952       disability_any +
2953       genderidentity +
2954       income +
2955       edhi +
2956       age,
2957     data = datMain
2958   )
2959 Anova(mEmotions_2, type = "III")
2960 summary(mEmotions_2)
2961
2962 # Model 3: Check for moderating effects of individualism & collectivism with adjustment
for other
2963 # covariates
2964
2965 mEmotions_3 <-
2966   lm(
2967     mean_emotion ~
2968       viz * disease * mean_indivhorz +
2969       viz * disease * mean_indivvertical +
2970       viz * disease * mean_collhorz +
2971       viz * disease * mean_collvertical +
2972       borninCanada + #CHANGELOG ASJ: covariate list shortened 2021-08-04
2973       language_1 +
2974       language_2 +
2975       Asian_group +
2976       White_group +
2977       disability_any +
2978       genderidentity +
2979       income +
2980       edhi +
2981       age,
2982     data = datMain
2983   )
2984 Anova(mEmotions_3, type = "III")
2985 summary(mEmotions_3)
2986
2987 # + Adding interaction for high and low education with herdim vizualization
2988 # CHANGELOG We have added 2 new models to check the interaction between
2989 # high and low education with herdim vizualization 2021-07-26
2990
2991 ##### + Model 4: Check for interaction edhi*viz without any covariates (for Emotions) #####
2992

```

```

2993 mEmotions_4 <- lm(mean_emotion ~ viz * disease + viz * edhi, data = datMain)
2994 Anova(mEmotions_4, type="III")
2995 summary(mEmotions_4)
2996
2997 # Model 5: Check for interaction edhi*viz with covariates
2998
2999 mEmotions_5 <-
3000   lm(
3001     mean_emotion ~ viz * disease +
3002       viz * edhi +
3003       mean_indivhorz +
3004       mean_indivvertical +
3005       mean_collhorz +
3006       mean_collvertical +
3007       bornincanada + #CHANGELOG ASJ: covariate list shortened 2021-08-04
3008       language_1 +
3009       language_2 +
3010       Asian_group +
3011       White_group +
3012       disability_any +
3013       genderidentity +
3014       income +
3015       age,
3016     data = datMain
3017   )
3018 Anova(mEmotions_5, type = "III")
3019 summary(mEmotions_5)
3020
3021
3022 ##### + Validating assumptions #####
3023
3024 # Check to see if the assumptions of the models are respected. If not, we will
3025 # transform the
3026 # outcome.
3027
3027 checkassumptions(mEmotions_1)
3028 checkassumptions(mEmotions_2)
3029 checkassumptions(mEmotions_3)
3030 checkassumptions(mEmotions_4)
3031 checkassumptions(mEmotions_5)
3032
3033
3034 ##### + Interpretation (Emotions) #####
3035
3036 # Interpretation of model 1 in the case of no interaction
3037
3038 memory.size(max = TRUE)
3039
3040 mEmotions_1_v <- emmeans(mEmotions_1, ~viz)
3041 mEmotions_1_v
3042 plot(mEmotions_1_v)
3043
3044 mEmotions_1_d <- emmeans(mEmotions_1, ~ disease)
3045 mEmotions_1_d
3046 pairs(mEmotions_1_d) # Only do multiple comparisons if type 3 test is significant
3047 plot(mEmotions_1_d)
3048
3049
3050 # Interpretation of model 2 in the case of no interaction
3051
3052 mEmotions_2_v <- emmeans(mEmotions_2, ~viz)
3053 mEmotions_2_v
3054 plot(mEmotions_2_v)
3055
3056 mEmotions_2_d <- emmeans(mEmotions_2, ~ disease)
3057 mEmotions_2_d
3058 pairs(mEmotions_2_d) # Only do multiple comparisons if type 3 test is significant
3059 plot(mEmotions_2_d)
3060

```

```

3061
3062
3063 # Interpretation of model 3 in the case of an interaction with moderator
3064 emmip(mEmotions_3, viz*disease ~ mean_collhorz, cov.reduce = range)
3065
3066 # Interpretation of model 4 in the case of an interaction viz edhi
3067 # CHANGELOG We have added interpretation of model 4 2021-07-26
3068
3069 mEmotions_4_ve <- emmeans(mEmotions_4,~viz|edhi)
3070 mEmotions_4_ve
3071 pairs(mEmotions_4_ve) # Only do multiple comparisons if type 3 test is significant
3072 plot(mEmotions_4_ve)
3073
3074 mEmotions_4_ev <- emmeans(mEmotions_4,~edhi|viz)
3075 mEmotions_4_ev
3076 pairs(mEmotions_4_ev) # Only do multiple comparisons if type 3 test is significant
3077 plot(mEmotions_4_ev)
3078
3079 # Interpretation of model 5 in the case of an interaction viz edhi
3080 # CHANGELOG We have added interpretation of model 5 2021-07-26
3081
3082 mEmotions_5_ve <- emmeans(mEmotions_5,~viz|edhi)
3083 mEmotions_5_ve
3084 pairs(mEmotions_5_ve) # Only do multiple comparisons if type 3 test is significant
3085 plot(mEmotions_5_ve)
3086
3087 mEmotions_5_ev <- emmeans(mEmotions_5,~edhi|viz)
3088 mEmotions_5_ev
3089 pairs(mEmotions_5_ev) # Only do multiple comparisons if type 3 test is significant
3090 plot(mEmotions_5_ev)
3091
3092
3093 # Now we run the models on imputed data.
3094
3095 #CHANGELOG ASJ: No missing data for mean_emotion, no model with imputation performed,
3096 21-09-20.
3097
3098 ##### +++ Knowledge #####
3099 ##### + Model 1: Check for direct effects of factors without any covariates (Knowledge)
3100 #####
3101
3102 options(contrasts=c("contr.sum", "contr.poly")) # CHANGELOG: The statement below is
3103 added to calculate properly the type III sum of squares with lm 2021-07-27
3104
3105 mKnowledge_1 <- lm(sum_knowledge ~ viz * disease, data = datMain)
3106 Anova(mKnowledge_1,type="III")
3107 summary(mKnowledge_1)
3108
3109 # Model 2: Check for direct effects of factors with adjustment for other covariates
3110
3111 mKnowledge_2 <-
3112   lm(
3113     sum_knowledge ~ viz * disease +
3114     mean_indivhorz +
3115     mean_indivvertical +
3116     mean_collhorz +
3117     mean_collvertical +
3118     bornincanada + #CHANGELOG ASJ: covariate list shortened 2021-08-04
3119     language_1 +
3120     language_2 +
3121     Asian_group +
3122     White_group +
3123     disability_any +
3124     genderidentity +
3125     income +
3126     edhi +
3127     age,
3128     data = datMain

```

```

3127 )
3128 Anova(mKnowledge_2, type = "III")
3129 summary(mKnowledge_2)
3130
3131 # Model 3: Check for moderating effects of individualism & collectivism with adjustment
for other
3132 # covariates
3133
3134 mKnowledge_3 <-
3135   lm(
3136     sum_knowledge ~
3137       viz * disease * mean_indivhorz +
3138       viz * disease * mean_indivvertical +
3139       viz * disease * mean_collhorz +
3140       viz * disease * mean_collvertical +
3141       bornincanada + #CHANGELOG ASJ: covariate list shortened 2021-08-04
3142       language_1 +
3143       language_2 +
3144       Asian_group +
3145       White_group +
3146       disability_any +
3147       genderidentity +
3148       income +
3149       edhi +
3150       age,
3151     data = datMain
3152   )
3153 Anova(mKnowledge_3, type = "III")
3154 summary(mKnowledge_3)
3155
3156 # + Adding interaction for high and low education with herdim vizsualization
3157 # CHANGELOG We have added 2 new models to check the interaction between
3158 # high and low education with herdim vizsualization 2021-07-26
3159
3160 ##### + Model 4: Check for interaction viz*edhi without any covariates (for Knowledge)
#####
3161
3162 mKnowledge_4 <- lm(sum_knowledge ~ viz * disease + viz * edhi, data = datMain)
3163 Anova(mKnowledge_4, type="III")
3164 summary(mKnowledge_4)
3165
3166 # Model 5: Check for interaction disease*viz with covariates
3167
3168 mKnowledge_5 <-
3169   lm(
3170     sum_knowledge ~ viz * disease +
3171       viz * edhi +
3172       mean_indivhorz +
3173       mean_indivvertical +
3174       mean_collhorz +
3175       mean_collvertical +
3176       bornincanada + #CHANGELOG ASJ: covariate list shortened 2021-08-04
3177       language_1 +
3178       language_2 +
3179       Asian_group +
3180       White_group +
3181       disability_any +
3182       genderidentity +
3183       income +
3184       age,
3185     data = datMain
3186   )
3187 Anova(mKnowledge_5, type = "III")
3188 summary(mKnowledge_5)
3189
3190
3191 ##### + Validating assumptions #####
3192
3193 # Check to see if the assumptions of the models are respected. If not, we will

```



```

transform the
3194 # outcome.
3195
3196 checkassumptions(mKnowledge_1)
3197 checkassumptions(mKnowledge_2)
3198 checkassumptions(mKnowledge_3)
3199 checkassumptions(mKnowledge_4)
3200 checkassumptions(mKnowledge_5)
3201
3202 ##### + Interpretation (Knowledge) #####
3203
3204 # Interpretation of model 1 in the case of no interaction
3205
3206 memory.size(max = TRUE)
3207
3208 mKnowledge_1_v <- emmeans(mKnowledge_1,~viz)
3209 mKnowledge_1_v
3210 plot(mKnowledge_1_v)
3211
3212 mKnowledge_1_d <- emmeans(mKnowledge_1, ~ disease)
3213 mKnowledge_1_d
3214 pairs(mKnowledge_1_d) # Only do multiple comparisons if type 3 test is significant
3215 plot(mKnowledge_1_d)
3216
3217
3218 # Interpretation of model 2 in the case of an interaction
3219
3220 mKnowledge_2_vd <- emmeans(mKnowledge_2,~viz|disease)
3221 mKnowledge_2_vd
3222 pairs(mKnowledge_2_vd) # Only do multiple comparisons if type 3 test is significant
3223 plot(mKnowledge_2_vd)
3224
3225 mKnowledge_2_dv <- emmeans(mKnowledge_2,~disease|viz)
3226 mKnowledge_2_dv
3227 pairs(mKnowledge_2_dv) # Only do multiple comparisons if type 3 test is significant
3228 plot(mKnowledge_2_dv)
3229
3230 mKnowledge_3_d
3231 pairs(mKnowledge_3_d) # Only do multiple comparisons if type 3 test is significant
3232 plot(mKnowledge_3_d)
3233
3234 # Interpretation of model 3
3235 emmip(mKnowledge_3, viz ~ mean_indivvertical, cov.reduce = range)
3236
3237
3238 # Interpretation of model 4 in the case of an interaction viz edhi
3239 # CHANGELOG We have added interpretation of model 4 2021-07-26
3240
3241 mKnowledge_4_ve <- emmeans(mKnowledge_4,~viz|edhi)
3242 mKnowledge_4_ve
3243 pairs(mKnowledge_4_ve) # Only do multiple comparisons if type 3 test is significant
3244 plot(mKnowledge_4_ve)
3245
3246 mKnowledge_4_ev <- emmeans(mKnowledge_4,~edhi|viz)
3247 mKnowledge_4_ev
3248 pairs(mKnowledge_4_ev) # Only do multiple comparisons if type 3 test is significant
3249 plot(mKnowledge_4_ev)
3250
3251 # Interpretation of model 5 in case of an interaction viz*edhi
3252 # CHANGELOG We have added interpretation of model 5 2021-07-26
3253
3254 mKnowledge_5_ve <- emmeans(mKnowledge_5,~viz|edhi)
3255 mKnowledge_5_ve
3256 pairs(mKnowledge_5_ve) # Only do multiple comparisons if type 3 test is significant
3257 plot(mKnowledge_5_ve)
3258
3259 mKnowledge_5_ev <- emmeans(mKnowledge_5,~edhi|viz)
3260 mKnowledge_5_ev
3261 pairs(mKnowledge_5_ev) # Only do multiple comparisons if type 3 test is significant

```

```

3262 plot(mKnowledge_5_ev)
3263
3264 # Now we run the models on imputed data.
3265
3266
3267 #CHANGELOG ASJ: No missing data for sum_knowledge, no model with imputation performed,
3268 21-09-20.
3269
3270 #CHANGELOG ASJ: Add logistic regression models for dichotomous outcomes, 2021-08-05.
3271
3272
3273
3274 ##### +++ Logistic regression for RP1 #####
3275
3276 ##### + Model 1: Check for direct effects of factors without any covariates #####
3277
3278
3279
3280 options(contrasts=c("contr.sum", "contr.poly"))
3281 rlog_RP1_1 <- glm(relevel(RP1_dicho,ref="Low") ~ viz * disease, data =
3282 datMain,family=binomial("logit"))
3283 Anova(rlog_RP1_1,type="III")
3284 summary(rlog_RP1_1)
3285
3286 # Interpretation of model 1
3287 mRP1_v <- emmeans(rlog_RP1_1,~viz,type = "response") #proportions
3288 mRP1_v
3289 plot(mRP1_v)
3290 confint(pairs(mRP1_v,reverse = TRUE)) #Odds ratios
3291
3292 mRP1_d <- emmeans(rlog_RP1_1, ~ disease, type = "response") #proportions
3293 mRP1_d
3294 plot(mRP1_d)
3295 confint(pairs(mRP1_d,reverse = TRUE)) #Odds ratios
3296
3297 # Model 2: Check for direct effects of factors with adjustment for other covariates
3298
3299 rlog_RP1_2 <-
3300   glm(relevel(RP1_dicho,ref="Low") ~ viz * disease +
3301     mean_indivhorz +
3302     mean_indivvertical +
3303     mean_collhorz +
3304     mean_collvertical +
3305     bornincanada +
3306     language_1 +
3307     language_2 +
3308     Asian_group +
3309     White_group +
3310     disability_any +
3311     genderidentity +
3312     income +
3313     edhi +
3314     age,
3315     data = datMain,family=binomial("logit")
3316   )
3317 Anova(rlog_RP1_2, type = "III")
3318 summary(rlog_RP1_2)
3319
3320
3321 # Interpretation of model 2
3322 mRP1_2_v <- emmeans(rlog_RP1_2,~viz,type = "response")
3323 mRP1_2_v
3324 plot(mRP1_2_v)
3325 confint(pairs(mRP1_2_v,reverse = TRUE))
3326
3327 mRP1_2_d <- emmeans(rlog_RP1_2, ~ disease, type = "response")
3328 mRP1_2_d

```

```

3329 plot(mRP1_2_d)
3330 confint(pairs(mRP1_2_d,reverse = TRUE))
3331
3332
3333 # Model 3: Check for moderating effects of individualism & collectivism with adjustment
for other covariates
3334 rlog_RP1_3 <-
3335   glm(relevel(RP1_dicho,ref="Low") ~
3336     viz * disease * mean_indivhorz +
3337     viz * disease * mean_indivvertical +
3338     viz * disease * mean_collhorz +
3339     viz * disease * mean_collvertical +
3340     bornincanada +
3341     language_1 +
3342     language_2 +
3343     Asian_group +
3344     White_group +
3345     disability_any +
3346     genderidentity +
3347     income +
3348     edhi +
3349     age,
3350     data = datMain,family=binomial("logit")
3351   )
3352 Anova(rlog_RP1_3, type = "III")
3353 summary(rlog_RP1_3)
3354
3355 ## Interpretation of model 3 : no interaction with moderator to interpret
3356
3357 ##### + Model 4: Check for interaction viz*edhi without any covariates #####
3358
3359 rlog_RP1_4 <- glm(relevel(RP1_dicho,ref="Low") ~ viz * disease + viz * edhi, data =
datMain,family=binomial("logit"))
3360 Anova(rlog_RP1_4,type="III")
3361 summary(rlog_RP1_4)
3362
3363 # Interpretation of model 4
3364 mRP1_4_v <- emmeans(rlog_RP1_4,~viz|edhi,type = "response")
3365 mRP1_4_v
3366 confint(pairs(mRP1_4_v,reverse = TRUE))
3367 pairs(mRP1_4_v,reverse = TRUE,type = "response")
3368 plot(mRP1_4_v)
3369
3370 mRP1_4_e <- emmeans(rlog_RP1_4, ~ edhi|viz, type = "response")
3371 mRP1_4_e
3372 confint(pairs(mRP1_4_e,reverse = TRUE))
3373 pairs(mRP1_4_e,reverse = TRUE, type = "reponse")
3374 plot(mRP1_4_e)
3375
3376
3377 # Model 5: Check for interaction viz*edhi with adjustment for other covariates
3378
3379 rlog_RP1_5 <-
3380   glm(relevel(RP1_dicho,ref="Low") ~ viz * disease +
3381     viz * edhi +
3382     mean_indivhorz +
3383     mean_indivvertical +
3384     mean_collhorz +
3385     mean_collvertical +
3386     bornincanada +
3387     language_1 +
3388     language_2 +
3389     Asian_group +
3390     White_group +
3391     disability_any +
3392     genderidentity +
3393     income +
3394     age,
3395     data = datMain,family=binomial("logit")

```

```

3396   )
3397   Anova(rlog_RP1_5, type = "III")
3398   summary(rlog_RP1_5)
3399
3400   # Interpretation of model 5
3401   mRP1_5_v <- emmeans(rlog_RP1_5, ~viz|edhi, type = "response")
3402   mRP1_5_v
3403   confint(pairs(mRP1_5_v, reverse = TRUE))
3404   pairs(mRP1_5_v, reverse = TRUE, type = "response")
3405   plot(mRP1_5_v)
3406
3407   mRP1_5_e <- emmeans(rlog_RP1_5, ~ edhi|viz, type = "response")
3408   mRP1_5_e
3409   confint(pairs(mRP1_5_e, reverse = TRUE))
3410   pairs(mRP1_5_e, reverse = TRUE, type = "reponse")
3411   plot(mRP1_5_e)
3412
3413
3414   # Now we run the models on imputed data.
3415
3416   ##### + Imputed Model 1: Check for direct effects of factors without any covariates #####
3417
3418   imprlog_RP1_1 <-
3419     with(data = datMainImputed,
3420          exp = glm(relevel(RP1_dicho, ref="Low") ~ viz * disease, family =
3421                    binomial("logit")))
3422   combineimprlog_RP1_1 <- pool(imprlog_RP1_1)
3423   summary(combineimprlog_RP1_1)
3424
3425   ##### +++ Logistic regression for C19 vax intention #####
3426
3427   ##### + Model 1: Check for direct effects of factors without any covariates #####
3428
3429   options(contrasts=c("contr.sum", "contr.poly"))
3430   rlog_c19vi_1 <- glm(relevel(c19vaxintent, ref="Low") ~ viz * disease, data =
3431                     datMain, family=binomial("logit"))
3432   Anova(rlog_c19vi_1, type="III")
3433   summary(rlog_c19vi_1)
3434
3435   # Interpretation of model 1
3436   mc19vi_1_v <- emmeans(rlog_c19vi_1, ~viz, type = "response") #proportions
3437   mc19vi_1_v
3438   plot(mc19vi_1_v)
3439   confint(pairs(mc19vi_1_v, reverse = TRUE)) #Odds ratios
3440
3441   mc19vi_1_d <- emmeans(rlog_c19vi_1, ~ disease, type = "response") #proportions
3442   mc19vi_1_d
3443   plot(mc19vi_1_d)
3444   confint(pairs(mc19vi_1_d, reverse = TRUE)) #Odds ratios
3445
3446   # Model 2: Check for direct effects of factors with adjustment for other covariates
3447
3448   rlog_c19vi_2 <-
3449     glm(relevel(c19vaxintent, ref="Low") ~ viz * disease +
3450          mean_indivhorz +
3451          mean_indivvertical +
3452          mean_collhorz +
3453          mean_collvertical +
3454          bornincanada +
3455          language_1 +
3456          language_2 +
3457          Asian_group +
3458          White_group +
3459          disability_any +
3460          genderidentity +
3461          income +
3462          edhi +
3463          age,

```

```

3463     data = datMain,family=binomial("logit")
3464   )
3465   Anova(rlog_c19vi_2, type = "III")
3466   summary(rlog_c19vi_2)
3467
3468   # Interpretation of model 2
3469   mc19vi_2_v <- emmeans(rlog_c19vi_2,~viz,type = "response")
3470   mc19vi_2_v
3471   plot(mc19vi_2_v)
3472   confint(pairs(mc19vi_2_v,reverse = TRUE))
3473
3474   mc19vi_2_d <- emmeans(rlog_c19vi_2, ~ disease, type = "response")
3475   mc19vi_2_d
3476   plot(mc19vi_2_d)
3477   confint(pairs(mc19vi_2_d,reverse = TRUE))
3478
3479
3480
3481   # Model 3: Check for moderating effects of individualism & collectivism with adjustment
for other covariates
3482   rlog_c19vi_3 <-
3483     glm(relevel(c19vaxintent,ref="Low") ~
3484       viz * disease * mean_indivhorz +
3485       viz * disease * mean_indivvertical +
3486       viz * disease * mean_collhorz +
3487       viz * disease * mean_collvertical +
3488       bornincanada +
3489       language_1 +
3490       language_2 +
3491       Asian_group +
3492       White_group +
3493       disability_any +
3494       genderidentity +
3495       income +
3496       edhi +
3497       age,
3498     data = datMain,family=binomial("logit")
3499   )
3500   Anova(rlog_c19vi_3, type = "III")
3501   summary(rlog_c19vi_3)
3502
3503   # Interpretation of model 3
3504   emmip(rlog_c19vi_3, viz ~ mean_collvertical, cov.reduce = range, type = "response")
3505
3506   ##### + Model 4: Check for interaction viz*edhi without any covariates #####
3507
3508   rlog_c19vi_4 <- glm(relevel(c19vaxintent,ref="Low") ~ viz * disease + viz * edhi,
3509     data = datMain,family=binomial("logit"))
3510   Anova(rlog_c19vi_4,type="III")
3511   summary(rlog_c19vi_4)
3512
3513   # Interpretation of model 4 (no significant interaction viz edhi)
3514   mc19vi_4_v <- emmeans(rlog_c19vi_4,~viz|edhi,type = "response")
3515   mc19vi_4_v
3516   confint(pairs(mc19vi_4_v,reverse = TRUE))
3517   plot(mc19vi_4_v)
3518
3519   mc19vi_4_e <- emmeans(rlog_c19vi_4, ~ edhi|viz, type = "response")
3520   mc19vi_4_e
3521   confint(pairs(mc19vi_4_e,reverse = TRUE))
3522   plot(mc19vi_4_e)
3523
3524
3525   # Model 5: Check for interaction viz*edhi with adjustment for other covariates
3526
3527   rlog_c19vi_5 <-
3528     glm(relevel(c19vaxintent,ref="Low") ~ viz * disease +
3529       viz * edhi +

```

```

3530         mean_indivhorz +
3531         mean_indivvertical +
3532         mean_collhorz +
3533         mean_collvertical +
3534         bornincanada +
3535         language_1 +
3536         language_2 +
3537         Asian_group +
3538         White_group +
3539         disability_any +
3540         genderidentity +
3541         income +
3542         age,
3543         data = datMain,family=binomial("logit")
3544     )
3545     Anova(rlog_c19vi_5, type = "III")
3546     summary(rlog_c19vi_5)
3547
3548     # Interpretation of model 5
3549     mc19vi_5_v <- emmeans(rlog_c19vi_5,~viz|edhi,type = "response")
3550     mc19vi_5_v
3551     confint(pairs(mc19vi_5_v,reverse = TRUE))
3552     plot(mc19vi_5_v)
3553
3554     mc19vi_5_e <- emmeans(rlog_c19vi_5, ~ edhi|viz, type = "response")
3555     mc19vi_5_e
3556     confint(pairs(mc19vi_5_e,reverse = TRUE))
3557     plot(mc19vi_5_e)
3558
3559
3560     # Now we run the models on imputed data.
3561
3562     #CHANGELOG ASJ: No imputation for c19vaxintention, since 51% missing values, 21-09-20.
3563
3564
3565
3566     ##### +++ Logistic regression for vax intention #####
3567
3568     #In order for the pairs function to work properly, relelevel function must be removed
    from the model.
3569     datMain$vaxintentRel<-relelevel(datMain$vaxintent,ref="Low")
3570
3571     ##### + Model 1: Check for direct effects of factors without any covariates #####
3572
3573     options(contrasts=c("contr.sum", "contr.poly"))
3574     rlog_vi_1 <- glm(vaxintentRel ~ viz * disease, data = datMain,family=binomial("logit"))
3575     Anova(rlog_vi_1,type="III")
3576     summary(rlog_vi_1)
3577
3578     # Interpretation of model 1
3579     mvi_1_v <- emmeans(rlog_vi_1,~viz,type = "response") #proportions
3580     mvi_1_v
3581     plot(mvi_1_v)
3582     confint(pairs(mvi_1_v,reverse = TRUE)) #Odds ratios
3583
3584     mvi_1_d <- emmeans(rlog_vi_1, ~ disease, type = "response") #proportions
3585     mvi_1_d
3586     plot(mvi_1_d)
3587     pairs(mvi_1_d,reverse = TRUE,type = "response")
3588     confint(pairs(mvi_1_d,reverse = TRUE)) #Odds ratios
3589
3590     # Model 2: Check for direct effects of factors with adjustment for other covariates
3591
3592     rlog_vi_2 <-
3593         glm(vaxintentRel ~ viz * disease +
3594             mean_indivhorz +
3595             mean_indivvertical +
3596             mean_collhorz +
3597             mean_collvertical +

```

```

3598     bornincanada +
3599     language_1 +
3600     language_2 +
3601     Asian_group +
3602     White_group +
3603     disability_any +
3604     genderidentity +
3605     income +
3606     edhi +
3607     age,
3608     data = datMain, family=binomial("logit")
3609 )
3610 Anova(rlog_vi_2, type = "III")
3611 summary(rlog_vi_2)
3612
3613 # Interpretation of model 2
3614 mvi_2_v <- emmeans(rlog_vi_2, ~viz, type = "response")
3615 mvi_2_v
3616 plot(mvi_2_v)
3617 confint(pairs(mvi_2_v, reverse = TRUE))
3618
3619 mvi_2_d <- emmeans(rlog_vi_2, ~ disease, type = "response")
3620 mvi_2_d
3621 plot(mvi_2_d)
3622 confint(pairs(mvi_2_d, reverse = TRUE))
3623 pairs(mvi_2_d, reverse=TRUE, type="response")
3624
3625 # Model 3: Check for moderating effects of individualism & collectivism with adjustment
3626 # for other covariates
3627 rlog_vi_3 <-
3628   glm(vaxintentRel ~
3629     viz * disease * mean_indivhorz +
3630     viz * disease * mean_indivvertical +
3631     viz * disease * mean_collhorz +
3632     viz * disease * mean_collvertical +
3633     bornincanada +
3634     language_1 +
3635     language_2 +
3636     Asian_group +
3637     White_group +
3638     disability_any +
3639     genderidentity +
3640     income +
3641     edhi +
3642     age,
3643     data = datMain, family=binomial("logit")
3644   )
3645 Anova(rlog_vi_3, type = "III")
3646 summary(rlog_vi_3)
3647
3648 # Interpretation of model 3
3649 emmip(rlog_vi_3, disease ~ mean_indivvertical, cov.reduce = range, type = "response")
3650
3651 ##### + Model 4: Check for interaction viz*edhi without any covariates #####
3652
3653 rlog_vi_4 <- glm(vaxintentRel ~ viz * disease + viz * edhi, data =
3654   datMain, family=binomial("logit"))
3655 Anova(rlog_vi_4, type="III")
3656 summary(rlog_vi_4)
3657
3658 # Interpretation of model 4 (no significant interaction viz edhi)
3659 mvi_4_v <- emmeans(rlog_vi_4, ~viz|edhi, type = "response")
3660 mvi_4_v
3661 confint(pairs(mvi_4_v, reverse = TRUE))
3662 plot(mvi_4_v)
3663
3664 mvi_4_e <- emmeans(rlog_vi_4, ~ edhi|viz, type = "response")

```

```

3665 mvi_4_e
3666 confint(pairs(mvi_4_e,reverse = TRUE))
3667 plot(mvi_4_e)
3668
3669 # Model 5: Check for interaction viz*edhi with adjustment for other covariates
3670
3671
3672 rlog_vi_5 <-
3673   glm(vaxintentRel ~ viz * disease +
3674       viz * edhi +
3675       mean_indivhorz +
3676       mean_indivvertical +
3677       mean_collhorz +
3678       mean_collvertical +
3679       bornincanada +
3680       language_1 +
3681       language_2 +
3682       Asian_group +
3683       White_group +
3684       disability_any +
3685       genderidentity +
3686       income +
3687       age,
3688       data = datMain,family=binomial("logit")
3689   )
3690 Anova(rlog_vi_5, type = "III")
3691 summary(rlog_vi_5)
3692
3693 # Interpretation of model 5 ( no significant interaction)
3694 mvi_5_v <- emmeans(rlog_vi_5,~viz|edhi,type = "response")
3695 mvi_5_v
3696 confint(pairs(mvi_5_v,reverse = TRUE))
3697 plot(mvi_5_v)
3698
3699 mvi_5_e <- emmeans(rlog_vi_5, ~ edhi|viz, type = "response")
3700 mvi_5_e
3701 confint(pairs(mvi_5_e,reverse = TRUE))
3702 plot(mvi_5_e)
3703
3704
3705 # Now we run the models on imputed data.
3706
3707 ##### + Imputed Model 1: Check for direct effects of factors without any covariates #####
3708
3709 imprlog_vi_1 <-
3710   with(data = datMainImputed,
3711       exp = glm(relevel(vaxintent,ref="Low") ~ viz * disease,family =
3712           binomial("logit")))
3713 combineimprlog_vi_1 <- pool(imprlog_vi_1)
3714 summary(combineimprlog_vi_1)
3715
3716 ##### +++ Logistic regression for Trust info #####
3717
3718 datMain$Htrustinfo<-relevel(datMain$Htrustinfo,ref="No")
3719
3720 ##### + Model 1: Check for direct effects of factors without any covariates #####
3721
3722 options(contrasts=c("contr.sum", "contr.poly"))
3723 rlog_ti_1 <- glm(Htrustinfo ~ viz * disease, data = datMain,family=binomial("logit"))
3724 Anova(rlog_ti_1,type="III")
3725 summary(rlog_ti_1)
3726
3727 # Interpretation of model 1
3728 mti_1_v <- emmeans(rlog_ti_1,~viz|disease,type = "response") #proportions
3729 mti_1_v
3730 plot(mti_1_v)
3731 confint(pairs(mti_1_v,reverse = TRUE)) #Odds ratios
3732 pairs(mti_1_v,reverse=TRUE, type = "response")

```



```

3733
3734 mti_1_d <- emmeans(rlog_ti_1, ~ disease|viz, type = "response") #proportions
3735 mti_1_d
3736 plot(mti_1_d)
3737 pairs(mti_1_d,reverse = TRUE,type = "response")
3738 confint(pairs(mti_1_d,reverse = TRUE)) #Odds ratios
3739
3740 # Model 2: Check for direct effects of factors with adjustment for other covariates
3741
3742 rlog_ti_2 <-
3743   glm(Htrustinfo ~ viz * disease +
3744     mean_indivhorz +
3745     mean_indivvertical +
3746     mean_collhorz +
3747     mean_collvertical +
3748     bornincanada +
3749     language_1 +
3750     language_2 +
3751     Asian_group +
3752     White_group +
3753     disability_any +
3754     genderidentity +
3755     income +
3756     edhi +
3757     age,
3758     data = datMain,family=binomial("logit")
3759   )
3760 Anova(rlog_ti_2, type = "III")
3761 summary(rlog_ti_2)
3762
3763
3764 # Interpretation of model 2
3765 mti_2_v <- emmeans(rlog_ti_2,~viz|disease,type = "response")
3766 mti_2_v
3767 plot(mti_2_v)
3768 confint(pairs(mti_2_v,reverse = TRUE))
3769 pairs(mti_2_v,reverse=TRUE, type = "response")
3770
3771 mti_2_d <- emmeans(rlog_ti_2, ~ disease|viz, type = "response")
3772 mti_2_d
3773 plot(mti_2_d)
3774 confint(pairs(mti_2_d,reverse = TRUE))
3775 pairs(mti_2_d,reverse=TRUE,type="response")
3776
3777 # Model 3: Check for moderating effects of individualism & collectivism with adjustment
for other covariates
3778 rlog_ti_3 <-
3779   glm(Htrustinfo ~
3780     viz * disease * mean_indivhorz +
3781     viz * disease * mean_indivvertical +
3782     viz * disease * mean_collhorz +
3783     viz * disease * mean_collvertical +
3784     bornincanada +
3785     language_1 +
3786     language_2 +
3787     Asian_group +
3788     White_group +
3789     disability_any +
3790     genderidentity +
3791     income +
3792     edhi +
3793     age,
3794     data = datMain,family=binomial("logit")
3795   )
3796 Anova(rlog_ti_3, type = "III")
3797 summary(rlog_ti_3)
3798
3799 #No interaction with moderators
3800

```

```

3801
3802 ##### + Model 4: Check for interaction viz*edhi without any covariates #####
3803
3804 rlog_ti_4 <- glm(Htrustinfo ~ viz * disease + viz * edhi, data =
datMain,family=binomial("logit"))
3805 Anova(rlog_ti_4,type="III")
3806 summary(rlog_ti_4)
3807
3808 # Interpretation of model 4 (no significant interaction viz edhi)
3809 mti_4_v <- emmeans(rlog_ti_4,~viz|edhi,type = "response")
3810 mti_4_v
3811 confint(pairs(mti_4_v,reverse = TRUE))
3812 plot(mti_4_v)
3813
3814 mti_4_e <- emmeans(rlog_ti_4, ~ edhi|viz, type = "response")
3815 confint(pairs(mti_4_e,reverse = TRUE))
3816 plot(mti_4_e)
3817
3818
3819 # Model 5: Check for interaction viz*edhi with adjustment for other covariates
3820
3821 rlog_ti_5 <-
3822   glm(Htrustinfo ~ viz * disease +
3823     viz * edhi +
3824     mean_indivhorz +
3825     mean_indivvertical +
3826     mean_collhorz +
3827     mean_collvertical +
3828     bornincanada +
3829     language_1 +
3830     language_2 +
3831     Asian_group +
3832     White_group +
3833     disability_any +
3834     genderidentity +
3835     income +
3836     age,
3837     data = datMain,family=binomial("logit")
3838   )
3839 Anova(rlog_ti_5, type = "III")
3840 summary(rlog_ti_5)
3841
3842 # Interpretation of model 5 ( no significant interaction)
3843 mti_5_v <- emmeans(rlog_ti_5,~viz|edhi,type = "response")
3844 mti_5_v
3845 confint(pairs(mti_5_v,reverse = TRUE))
3846 plot(mti_5_v)
3847
3848 mti_5_e <- emmeans(rlog_ti_5, ~ edhi|viz, type = "response")
3849 mti_5_e
3850 confint(pairs(mti_5_e,reverse = TRUE))
3851 plot(mti_5_e)
3852
3853
3854 # Now we run the models on imputed data.
3855
3856 ##### + Imputed Model 1: Check for direct effects of factors without any covariates #####
3857
3858
3859 imprlog_ti_1 <-
3860   with(data = datMainImputed,
3861     exp = glm(relevel(Htrustinfo,ref="No") ~ viz * disease,family =
3862       binomial("logit")))
3863 combineimprlog_ti_1 <- pool(imprlog_ti_1)
3864 summary(combineimprlog_ti_1)
3865
3866 ##### +++ Logistic regression for Mean C5 Confidence #####
3867 datMain$mean_C5_conf2<-relevel(as.factor(datMain$mean_C5_conf2),ref="0")

```

```

3868
3869 ##### + Model 1: Check for direct effects of factors without any covariates #####
3870
3871 options(contrasts=c("contr.sum", "contr.poly"))
3872 rlog_c5conf_1 <- glm(mean_C5_conf2 ~ viz * disease, data =
3873   datMain,family=binomial("logit"))
3874 Anova(rlog_c5conf_1,type="III")
3875 summary(rlog_c5conf_1)
3876
3877 # Interpretation of model 1
3878 mc5conf_v <- emmeans(rlog_c5conf_1,~viz,type = "response") #proportions
3879 mc5conf_v
3880 plot(mc5conf_v)
3881 confint(pairs(mc5conf_v,reverse = TRUE)) #Odds ratios
3882
3883 mc5conf_d <- emmeans(rlog_c5conf_1, ~ disease, type = "response") #proportions
3884 mc5conf_d
3885 plot(mc5conf_d)
3886 confint(pairs(mc5conf_d,reverse = TRUE)) #Odds ratios
3887
3888 # Model 2: Check for direct effects of factors with adjustment for other covariates
3889
3890 rlog_c5conf_2 <-
3891   glm(mean_C5_conf2 ~ viz * disease +
3892     mean_indivhorz +
3893     mean_indivvertical +
3894     mean_collhorz +
3895     mean_collvertical +
3896     bornincanada +
3897     language_1 +
3898     language_2 +
3899     Asian_group +
3900     White_group +
3901     disability_any +
3902     genderidentity +
3903     income +
3904     edhi +
3905     age,
3906     data = datMain,family=binomial("logit")
3907   )
3908 Anova(rlog_c5conf_2, type = "III")
3909 summary(rlog_c5conf_2)
3910
3911 # Interpretation of model 2
3912 mc5conf_2_v <- emmeans(rlog_c5conf_2,~viz,type = "response")
3913 mc5conf_2_v
3914 plot(mc5conf_2_v)
3915 confint(pairs(mc5conf_2_v,reverse = TRUE))
3916
3917 mc5conf_2_d <- emmeans(rlog_c5conf_2, ~ disease, type = "response")
3918 mc5conf_2_d
3919 plot(mc5conf_2_d)
3920 confint(pairs(mc5conf_2_d,reverse = TRUE))
3921
3922
3923 # Model 3: Check for moderating effects of individualism & collectivism with adjustment
3924 for other covariates
3925 rlog_c5conf_3 <-
3926   glm(mean_C5_conf2 ~
3927     viz * disease * mean_indivhorz +
3928     viz * disease * mean_indivvertical +
3929     viz * disease * mean_collhorz +
3930     viz * disease * mean_collvertical +
3931     bornincanada +
3932     language_1 +
3933     language_2 +
3934     Asian_group +

```

```

3935         White_group +
3936         disability_any +
3937         genderidentity +
3938         income +
3939         edhi +
3940         age,
3941         data = datMain, family=binomial("logit")
3942     )
3943     Anova(rlog_c5conf_3, type = "III")
3944     summary(rlog_c5conf_3)
3945
3946     ## Interpretation of model 3
3947     emmip(rlog_c5conf_3, viz ~ mean_collvertical , cov.reduce = range, type = "response")
3948
3949
3950
3951     ##### + Model 4: Check for interaction viz*edhi without any covariates #####
3952
3953     rlog_c5conf_4 <- glm(mean_C5_conf2 ~ viz * disease + viz * edhi, data =
3954     datMain, family=binomial("logit"))
3955     Anova(rlog_c5conf_4, type="III")
3956     summary(rlog_c5conf_4)
3957
3958     # Interpretation of model 4
3959     mc5conf_4_v <- emmeans(rlog_c5conf_4, ~viz|edhi, type = "response")
3960     mc5conf_4_v
3961     confint(pairs(mc5conf_4_v, reverse = TRUE))
3962     pairs(mc5conf_4_v, reverse = TRUE, type = "response")
3963     plot(mc5conf_4_v)
3964
3965     mc5conf_4_e <- emmeans(rlog_c5conf_4, ~ edhi|viz, type = "response")
3966     mc5conf_4_e
3967     confint(pairs(mc5conf_4_e, reverse = TRUE))
3968     pairs(mc5conf_4_e, reverse = TRUE, type = "response")
3969     plot(mc5conf_4_e)
3970
3971     # Model 5: Check for interaction viz*edhi with adjustment for other covariates
3972
3973     rlog_c5conf_5 <-
3974     glm(mean_C5_conf2 ~ viz * disease +
3975         viz * edhi +
3976         mean_indivhorz +
3977         mean_indivvertical +
3978         mean_collhorz +
3979         mean_collvertical +
3980         bornincanada +
3981         language_1 +
3982         language_2 +
3983         Asian_group +
3984         White_group +
3985         disability_any +
3986         genderidentity +
3987         income +
3988         age,
3989         data = datMain, family=binomial("logit")
3990     )
3991     Anova(rlog_c5conf_5, type = "III")
3992     summary(rlog_c5conf_5)
3993
3994     # Interpretation of model 5
3995     mc5conf_5_v <- emmeans(rlog_c5conf_5, ~viz|edhi, type = "response")
3996     mc5conf_5_v
3997     confint(pairs(mc5conf_5_v, reverse = TRUE))
3998     pairs(mc5conf_5_v, reverse = TRUE, type = "response")
3999     plot(mc5conf_5_v)
4000
4001     mc5conf_5_e <- emmeans(rlog_c5conf_5, ~ edhi|viz, type = "response")
4002     mc5conf_5_e

```

```

4003 confint(pairs(mc5conf_5_e,reverse = TRUE))
4004 pairs(mc5conf_5_e,reverse = TRUE, type = "reponse")
4005 plot(mc5conf_5_e)
4006
4007
4008 # Now we run the models on imputed data.
4009 #CHANGELOG ASJ: No missing data for mean_C5_conf2, no model with imputation performed,
4010 21-09-20.
4011
4012 ##### +++ Logistic regression for Mean C5 Complacency #####
4013 datMain$mean_C5_comp2<-relevel(as.factor(datMain$mean_C5_comp2),ref="0")
4014
4015 ##### + Model 1: Check for direct effects of factors without any covariates #####
4016
4017 options(contrasts=c("contr.sum", "contr.poly"))
4018 rlog_c5comp_1 <- glm(mean_C5_comp2 ~ viz * disease, data =
4019 datMain,family=binomial("logit"))
4020 Anova(rlog_c5comp_1,type="III")
4021 summary(rlog_c5comp_1)
4022
4023 # Interpretation of model 1
4024 mc5comp_v <- emmeans(rlog_c5comp_1,~viz,type = "response") #proportions
4025 mc5comp_v
4026 plot(mc5comp_v)
4027 confint(pairs(mc5comp_v,reverse = TRUE)) #Odds ratios
4028
4029 mc5comp_d <- emmeans(rlog_c5comp_1, ~ disease, type = "response") #proportions
4030 mc5comp_d
4031 plot(mc5comp_d)
4032 confint(pairs(mc5comp_d,reverse = TRUE)) #Odds ratios
4033
4034 # Model 2: Check for direct effects of factors with adjustment for other covariates
4035
4036 rlog_c5comp_2 <-
4037   glm(mean_C5_comp2 ~ viz * disease +
4038     mean_indivhorz +
4039     mean_indivvertical +
4040     mean_collhorz +
4041     mean_collvertical +
4042     bornincanada +
4043     language_1 +
4044     language_2 +
4045     Asian_group +
4046     White_group +
4047     disability_any +
4048     genderidentity +
4049     income +
4050     edhi +
4051     age,
4052     data = datMain,family=binomial("logit")
4053   )
4054 Anova(rlog_c5comp_2, type = "III")
4055 summary(rlog_c5comp_2)
4056
4057 # Interpretation of model 2
4058 mc5comp_2_v <- emmeans(rlog_c5comp_2,~viz,type = "response")
4059 mc5comp_2_v
4060 plot(mc5comp_2_v)
4061 confint(pairs(mc5comp_2_v,reverse = TRUE))
4062
4063 mc5comp_2_d <- emmeans(rlog_c5comp_2, ~ disease, type = "response")
4064 mc5comp_2_d
4065 plot(mc5comp_2_d)
4066 confint(pairs(mc5comp_2_d,reverse = TRUE))
4067
4068
4069

```

```

4070 # Model 3: Check for moderating effects of individualism & collectivism with adjustment
4071 for other covariates
4072 rlog_c5comp_3 <-
4073   glm(mean_C5_comp2 ~
4074     viz * disease * mean_indivhorz +
4075     viz * disease * mean_indivvertical +
4076     viz * disease * mean_collhorz +
4077     viz * disease * mean_collvertical +
4078     bornincanada +
4079     language_1 +
4080     language_2 +
4081     Asian_group +
4082     White_group +
4083     disability_any +
4084     genderidentity +
4085     income +
4086     age,
4087     data = datMain, family=binomial("logit")
4088   )
4089 Anova(rlog_c5comp_3, type = "III")
4090 summary(rlog_c5comp_3)
4091
4092 ## Interpretation of model 3 : no moderating effect to interpret
4093
4094
4095
4096 ##### + Model 4: Check for interaction viz*edhi without any covariates #####
4097
4098 rlog_c5comp_4 <- glm(mean_C5_comp2 ~ viz * disease + viz * edhi, data =
4099   datMain, family=binomial("logit"))
4100 Anova(rlog_c5comp_4, type="III")
4101 summary(rlog_c5comp_4)
4102
4103 # Interpretation of model 4
4104 mc5comp_4_v <- emmeans(rlog_c5comp_4, ~viz|edhi, type = "response")
4105 mc5comp_4_v
4106 confint(pairs(mc5comp_4_v, reverse = TRUE))
4107 pairs(mc5comp_4_v, reverse = TRUE, type = "response")
4108 plot(mc5comp_4_v)
4109
4110 mc5comp_4_e <- emmeans(rlog_c5comp_4, ~ edhi|viz, type = "response")
4111 mc5comp_4_e
4112 confint(pairs(mc5comp_4_e, reverse = TRUE))
4113 pairs(mc5comp_4_e, reverse = TRUE, type = "reponse")
4114 plot(mc5comp_4_e)
4115
4116 # Model 5: Check for interaction viz*edhi with adjustment for other covariates
4117
4118 rlog_c5comp_5 <-
4119   glm(mean_C5_comp2 ~ viz * disease +
4120     viz * edhi +
4121     mean_indivhorz +
4122     mean_indivvertical +
4123     mean_collhorz +
4124     mean_collvertical +
4125     bornincanada +
4126     language_1 +
4127     language_2 +
4128     Asian_group +
4129     White_group +
4130     disability_any +
4131     genderidentity +
4132     income +
4133     age,
4134     data = datMain, family=binomial("logit")
4135   )
4136 Anova(rlog_c5comp_5, type = "III")

```

```

4137 summary(rlog_c5comp_5)
4138
4139 # Interpretation of model 5
4140 mc5comp_5_v <- emmeans(rlog_c5comp_5, ~viz|edhi, type = "response")
4141 mc5comp_5_v
4142 confint(pairs(mc5comp_5_v, reverse = TRUE))
4143 plot(mc5comp_5_v)
4144
4145 mc5comp_5_e <- emmeans(rlog_c5comp_5, ~ edhi|viz, type = "response")
4146 mc5comp_5_e
4147 confint(pairs(mc5comp_5_e, reverse = TRUE))
4148 plot(mc5comp_5_e)
4149
4150
4151 # Now we run the models on imputed data.
4152 #CHANGELOG ASJ: No missing data for mean_C5_comp2, no model with imputation performed,
4153 #21-09-20.
4154
4155
4156
4157 ##### +++ Logistic regression for Mean C5 Constraints #####
4158
4159 datMain$mean_C5_cons2<-relevel(as.factor(datMain$mean_C5_cons2),ref="0")
4160
4161 ##### + Model 1: Check for direct effects of factors without any covariates #####
4162
4163 options(contrasts=c("contr.sum", "contr.poly"))
4164 rlog_c5cons_1 <- glm(mean_C5_cons2 ~ viz * disease, data =
4165 datMain, family=binomial("logit"))
4166 Anova(rlog_c5cons_1, type="III")
4167 summary(rlog_c5cons_1)
4168
4169 # Interpretation of model 1
4170 mc5cons_v <- emmeans(rlog_c5cons_1, ~viz, type = "response") #proportions
4171 mc5cons_v
4172 plot(mc5cons_v)
4173 confint(pairs(mc5cons_v, reverse = TRUE)) #Odds ratios
4174
4175 mc5cons_d <- emmeans(rlog_c5cons_1, ~ disease, type = "response") #proportions
4176 mc5cons_d
4177 plot(mc5cons_d)
4178 confint(pairs(mc5cons_d, reverse = TRUE)) #Odds ratios
4179
4180 # Model 2: Check for direct effects of factors with adjustment for other covariates
4181
4182 rlog_c5cons_2 <-
4183   glm(mean_C5_cons2 ~ viz * disease +
4184     mean_indivhorz +
4185     mean_indivvertical +
4186     mean_collhorz +
4187     mean_collvertical +
4188     bornincanada +
4189     language_1 +
4190     language_2 +
4191     Asian_group +
4192     White_group +
4193     disability_any +
4194     genderidentity +
4195     income +
4196     edhi +
4197     age,
4198     data = datMain, family=binomial("logit")
4199   )
4200 Anova(rlog_c5cons_2, type = "III")
4201 summary(rlog_c5cons_2)
4202
4203

```

```

4204 # Interpretation of model 2
4205 mc5cons_2_v <- emmeans(rlog_c5cons_2, ~viz, type = "response")
4206 mc5cons_2_v
4207 plot(mc5cons_2_v)
4208 confint(pairs(mc5cons_2_v, reverse = TRUE))
4209
4210 mc5cons_2_d <- emmeans(rlog_c5cons_2, ~ disease, type = "response")
4211 mc5cons_2_d
4212 plot(mc5cons_2_d)
4213 confint(pairs(mc5cons_2_d, reverse = TRUE))
4214
4215
4216 # Model 3: Check for moderating effects of individualism & collectivism with adjustment
for other covariates
4217 rlog_c5cons_3 <-
4218   glm(mean_C5_cons2 ~
4219     viz * disease * mean_indivhorz +
4220     viz * disease * mean_indivvertical +
4221     viz * disease * mean_collhorz +
4222     viz * disease * mean_collvertical +
4223     bornincanada +
4224     language_1 +
4225     language_2 +
4226     Asian_group +
4227     White_group +
4228     disability_any +
4229     genderidentity +
4230     income +
4231     edhi +
4232     age,
4233     data = datMain, family=binomial("logit")
4234   )
4235 Anova(rlog_c5cons_3, type = "III")
4236 summary(rlog_c5cons_3)
4237
4238 ## Interpretation of model 3
4239 emmip(rlog_c5cons_3, viz ~ mean_indivvertical , cov.reduce = range, type = "response")
4240
4241
4242
4243 ##### + Model 4: Check for interaction viz*edhi without any covariates #####
4244
4245 rlog_c5cons_4 <- glm(mean_C5_cons2 ~ viz * disease + viz * edhi, data =
datMain, family=binomial("logit"))
4246 Anova(rlog_c5cons_4, type="III")
4247 summary(rlog_c5cons_4)
4248
4249 # Interpretation of model 4
4250 mc5cons_4_v <- emmeans(rlog_c5cons_4, ~viz|edhi, type = "response")
4251 mc5cons_4_v
4252 confint(pairs(mc5cons_4_v, reverse = TRUE))
4253 pairs(mc5cons_4_v, reverse = TRUE, type = "response")
4254 plot(mc5cons_4_v)
4255
4256 mc5cons_4_e <- emmeans(rlog_c5cons_4, ~ edhi|viz, type = "response")
4257 mc5cons_4_e
4258 confint(pairs(mc5cons_4_e, reverse = TRUE))
4259 pairs(mc5cons_4_e, reverse = TRUE, type = "response")
4260 plot(mc5cons_4_e)
4261
4262
4263 # Model 5: Check for interaction viz*edhi with adjustment for other covariates
4264
4265 rlog_c5cons_5 <-
4266   glm(mean_C5_cons2 ~ viz * disease +
4267     viz * edhi +
4268     mean_indivhorz +
4269     mean_indivvertical +
4270     mean_collhorz +

```



```

4271         mean_collvertical +
4272         borninacanada +
4273         language_1 +
4274         language_2 +
4275         Asian_group +
4276         White_group +
4277         disability_any +
4278         genderidentity +
4279         income +
4280         age,
4281         data = datMain, family=binomial("logit")
4282     )
4283     Anova(rlog_c5cons_5, type = "III")
4284     summary(rlog_c5cons_5)
4285
4286     # Interpretation of model 5
4287     mc5cons_5_v <- emmeans(rlog_c5cons_5, ~viz|edhi, type = "response")
4288     mc5cons_5_v
4289     confint(pairs(mc5cons_5_v, reverse = TRUE))
4290     pairs(mc5cons_5_v, reverse = TRUE, type = "response")
4291     plot(mc5cons_5_v)
4292
4293     mc5cons_5_e <- emmeans(rlog_c5cons_5, ~ edhi|viz, type = "response")
4294     mc5cons_5_e
4295     confint(pairs(mc5cons_5_e, reverse = TRUE))
4296     pairs(mc5cons_5_e, reverse = TRUE, type = "reponse")
4297     plot(mc5cons_5_e)
4298
4299
4300     # Now we run the models on imputed data.
4301     #CHANGELOG ASJ: No missing data for mean_C5_cons2, no model with imputation performed,
4302     #21-09-20.
4303
4304
4305     ##### +++ Logistic regression for Mean C5 Calculation #####
4306
4307     datMain$mean_C5_calc2<-relevel(as.factor(datMain$mean_C5_calc2),ref="0")
4308
4309     ##### + Model 1: Check for direct effects of factors without any covariates #####
4310
4311     options(contrasts=c("contr.sum", "contr.poly"))
4312     rlog_c5calc_1 <- glm(mean_C5_calc2 ~ viz * disease, data =
4313     datMain, family=binomial("logit"))
4314     Anova(rlog_c5calc_1, type="III")
4315     summary(rlog_c5calc_1)
4316
4317     # Interpretation of model 1
4318     mc5calc_v <- emmeans(rlog_c5calc_1, ~viz, type = "response") #proportions
4319     mc5calc_v
4320     plot(mc5calc_v)
4321     confint(pairs(mc5calc_v, reverse = TRUE)) #Odds ratios
4322
4323     mc5calc_d <- emmeans(rlog_c5calc_1, ~ disease, type = "response") #proportions
4324     mc5calc_d
4325     plot(mc5calc_d)
4326     confint(pairs(mc5calc_d, reverse = TRUE)) #Odds ratios
4327
4328     # Model 2: Check for direct effects of factors with adjustment for other covariates
4329
4330     rlog_c5calc_2 <-
4331         glm(mean_C5_calc2 ~ viz * disease +
4332             mean_indivhorz +
4333             mean_indivvertical +
4334             mean_collhorz +
4335             mean_collvertical +
4336             borninacanada +
4337             language_1 +

```

```

4338         language_2 +
4339         Asian_group +
4340         White_group +
4341         disability_any +
4342         genderidentity +
4343         income +
4344         edhi +
4345         age,
4346         data = datMain,family=binomial("logit")
4347     )
4348     Anova(rlog_c5calc_2, type = "III")
4349     summary(rlog_c5calc_2)
4350
4351
4352     # Interpretation of model 2
4353     mc5calc_2_v <- emmeans(rlog_c5calc_2,~viz,type = "response")
4354     mc5calc_2_v
4355     plot(mc5calc_2_v)
4356     confint(pairs(mc5calc_2_v,reverse = TRUE))
4357
4358     mc5calc_2_d <- emmeans(rlog_c5calc_2, ~ disease, type = "response")
4359     mc5calc_2_d
4360     plot(mc5calc_2_d)
4361     confint(pairs(mc5calc_2_d,reverse = TRUE))
4362
4363
4364     # Model 3: Check for moderating effects of individualism & collectivism with adjustment
4365     # for other covariates
4366     rlog_c5calc_3 <-
4367         glm(mean_C5_calc2 ~
4368             viz * disease * mean_indivhorz +
4369             viz * disease * mean_indivvertical +
4370             viz * disease * mean_collhorz +
4371             viz * disease * mean_collvertical +
4372             bornincanada +
4373             language_1 +
4374             language_2 +
4375             Asian_group +
4376             White_group +
4377             disability_any +
4378             genderidentity +
4379             income +
4380             edhi +
4381             age,
4382             data = datMain,family=binomial("logit")
4383         )
4384     Anova(rlog_c5calc_3, type = "III")
4385     summary(rlog_c5calc_3)
4386
4387     ## Interpretation of model 3 : no moderation effect to interpret
4388
4389
4390     ##### + Model 4: Check for interaction viz*edhi without any covariates #####
4391
4392     rlog_c5calc_4 <- glm(mean_C5_calc2 ~ viz * disease + viz * edhi, data =
4393         datMain,family=binomial("logit"))
4394     Anova(rlog_c5calc_4,type="III")
4395     summary(rlog_c5calc_4)
4396
4397     # Interpretation of model 4
4398     mc5calc_4_v <- emmeans(rlog_c5calc_4,~viz|edhi,type = "response")
4399     mc5calc_4_v
4400     confint(pairs(mc5calc_4_v,reverse = TRUE))
4401     plot(mc5calc_4_v)
4402
4403     mc5calc_4_e <- emmeans(rlog_c5calc_4, ~ edhi|viz, type = "response")
4404     mc5calc_4_e
4405     confint(pairs(mc5calc_4_e,reverse = TRUE))

```

```

4405 plot(mc5calc_4_e)
4406
4407
4408 # Model 5: Check for interaction viz*edhi with adjustment for other covariates
4409
4410 rlog_c5calc_5 <-
4411   glm(mean_C5_calc2 ~ viz * disease +
4412       viz * edhi +
4413       mean_indivhorz +
4414       mean_indivvertical +
4415       mean_collhorz +
4416       mean_collvertical +
4417       bornincanada +
4418       language_1 +
4419       language_2 +
4420       Asian_group +
4421       White_group +
4422       disability_any +
4423       genderidentity +
4424       income +
4425       age,
4426       data = datMain, family=binomial("logit")
4427   )
4428 Anova(rlog_c5calc_5, type = "III")
4429 summary(rlog_c5calc_5)
4430
4431 # Interpretation of model 5
4432 mc5calc_5_v <- emmeans(rlog_c5calc_5, ~viz|edhi, type = "response")
4433 mc5calc_5_v
4434 confint(pairs(mc5calc_5_v, reverse = TRUE))
4435 plot(mc5calc_5_v)
4436
4437 mc5calc_5_e <- emmeans(rlog_c5calc_5, ~ edhi|viz, type = "response")
4438 mc5calc_5_e
4439 confint(pairs(mc5calc_5_e, reverse = TRUE))
4440 plot(mc5calc_5_e)
4441
4442
4443 # Now we run the models on imputed data.
4444 #CHANGELOG ASJ: No missing data for mean_C5_calc2, no model with imputation performed,
4445 #21-09-20.
4446
4447
4448 ##### +++ Logistic regression for Mean C5 Collective Response #####
4449
4450 datMain$mean_C5_coll2<-relevel(as.factor(datMain$mean_C5_coll2),ref="0")
4451
4452 ##### + Model 1: Check for direct effects of factors without any covariates #####
4453
4454 options(contrasts=c("contr.sum", "contr.poly"))
4455 rlog_c5coll_1 <- glm(mean_C5_coll2 ~ viz * disease, data =
4456   datMain, family=binomial("logit"))
4457 Anova(rlog_c5coll_1, type="III")
4458 summary(rlog_c5coll_1)
4459
4460 # Interpretation of model 1
4461 mc5coll_v <- emmeans(rlog_c5coll_1, ~viz, type = "response") #proportions
4462 mc5coll_v
4463 plot(mc5coll_v)
4464 confint(pairs(mc5coll_v, reverse = TRUE)) #Odds ratios
4465
4466 mc5coll_d <- emmeans(rlog_c5coll_1, ~ disease, type = "response") #proportions
4467 mc5coll_d
4468 plot(mc5coll_d)
4469 confint(pairs(mc5coll_d, reverse = TRUE)) #Odds ratios
4470
4471 # Model 2: Check for direct effects of factors with adjustment for other covariates

```

```

4472
4473 rlog_c5coll_2 <-
4474   glm(mean_C5_coll2 ~ viz * disease +
4475       mean_indivhorz +
4476       mean_indivvertical +
4477       mean_collhorz +
4478       mean_collvertical +
4479       borninacanada +
4480       language_1 +
4481       language_2 +
4482       Asian_group +
4483       White_group +
4484       disability_any +
4485       genderidentity +
4486       income +
4487       edhi +
4488       age,
4489       data = datMain, family=binomial("logit")
4490   )
4491 Anova(rlog_c5coll_2, type = "III")
4492 summary(rlog_c5coll_2)
4493
4494
4495 # Interpretation of model 2
4496 mc5coll_2_v <- emmeans(rlog_c5coll_2, ~viz, type = "response")
4497 mc5coll_2_v
4498 plot(mc5coll_2_v)
4499 confint(pairs(mc5coll_2_v, reverse = TRUE))
4500
4501 mc5coll_2_d <- emmeans(rlog_c5coll_2, ~ disease, type = "response")
4502 mc5coll_2_d
4503 pairs(mc5coll_2_d, reverse = TRUE)
4504 plot(mc5coll_2_d)
4505 confint(pairs(mc5coll_2_d, reverse = TRUE))
4506
4507
4508 # Model 3: Check for moderating effects of individualism & collectivism with adjustment
4509 # for other covariates
4510 rlog_c5coll_3 <-
4511   glm(mean_C5_coll2 ~
4512       viz * disease * mean_indivhorz +
4513       viz * disease * mean_indivvertical +
4514       viz * disease * mean_collhorz +
4515       viz * disease * mean_collvertical +
4516       borninacanada +
4517       language_1 +
4518       language_2 +
4519       Asian_group +
4520       White_group +
4521       disability_any +
4522       genderidentity +
4523       income +
4524       edhi +
4525       age,
4526       data = datMain, family=binomial("logit")
4527   )
4528 Anova(rlog_c5coll_3, type = "III")
4529 summary(rlog_c5coll_3)
4530
4531 ## Interpretation of model 3
4532 emmnip(rlog_c5coll_3, viz ~ mean_indivvertical , cov.reduce = range, type = "response")
4533 emmnip(rlog_c5coll_3, viz ~ mean_collhorz , cov.reduce = range, type = "response")
4534
4535
4536 ##### + Model 4: Check for interaction viz*edhi without any covariates #####
4537
4538 rlog_c5coll_4 <- glm(mean_C5_coll2 ~ viz * disease + viz * edhi, data =
4539   datMain, family=binomial("logit"))

```

```

4539 Anova(rlog_c5coll_4,type="III")
4540 summary(rlog_c5coll_4)
4541
4542 # Interpretation of model 4
4543 mc5coll_4_v <- emmeans(rlog_c5coll_4,~viz|edhi,type = "response")
4544 mc5coll_4_v
4545 confint(pairs(mc5coll_4_v,reverse = TRUE))
4546 plot(mc5coll_4_v)
4547
4548 mc5coll_4_e <- emmeans(rlog_c5coll_4, ~ edhi|viz, type = "response")
4549 mc5coll_4_e
4550 confint(pairs(mc5coll_4_e,reverse = TRUE))
4551 plot(mc5coll_4_e)
4552
4553
4554 # Model 5: Check for interaction viz*edhi with adjustment for other covariates
4555
4556 rlog_c5coll_5 <-
4557   glm(mean_C5_coll2 ~ viz * disease +
4558       viz * edhi +
4559       mean_indivhorz +
4560       mean_indivvertical +
4561       mean_collhorz +
4562       mean_collvertical +
4563       bornincanada +
4564       language_1 +
4565       language_2 +
4566       Asian_group +
4567       White_group +
4568       disability_any +
4569       genderidentity +
4570       income +
4571       age,
4572       data = datMain,family=binomial("logit")
4573   )
4574 Anova(rlog_c5coll_5, type = "III")
4575 summary(rlog_c5coll_5)
4576
4577 # Interpretation of model 5
4578 mc5coll_5_v <- emmeans(rlog_c5coll_5,~viz|edhi,type = "response")
4579 mc5coll_5_v
4580 confint(pairs(mc5coll_5_v,reverse = TRUE))
4581 plot(mc5coll_5_v)
4582
4583 mc5coll_5_e <- emmeans(rlog_c5coll_5, ~ edhi|viz, type = "response")
4584 mc5coll_5_e
4585 confint(pairs(mc5coll_5_e,reverse = TRUE))
4586 plot(mc5coll_5_e)
4587
4588
4589 # Now we run the models on imputed data.
4590 #CHANGELOG ASJ: No missing data for mean_C5_coll2, no model with imputation performed,
4591 #21-09-20.
4592
4593
4594 ##### RESEARCH QUESTION 3: EXISTING INTERVENTIONS VS HERDIMM #####
4595
4596 # Recall: Research question 3 (secondary): For any of the 4 diseases, do existing
4597 # interventions
4598 # already available online outperform the herdimmm intervention?
4599
4600 # 1-way ANOVA (adjusted for covariates and with moderators)
4601
4602 # Here, we test to see if there is an existing intervention to convey the concept of
4603 # herd immunity
4604 # that outperforms our intervention. Because the existing interventions each only
4605 # represent one
4606 # disease whereas ours was built to explicitly represent to the epidemiology of

```

```

different infectious
4604 # diseases, we do this by comparing relevant study arms for one disease at a time.
These models are
4605 # therefore similar to our models for two-way analyses, but disease*viz collapses into
a single
4606 # variable (study arm).
4607
4608 ##### +++ ONE WAY ANOVA FOR RISK PERCEPTION 2-6 #####
4609 ##### + Generic #####
4610
4611 #CHANGELOG ASJ: Mean risk perception replaced by MRP2_6 in the rest of the section,
2021-08-05.
4612
4613 # Model 1: Check for direct effects of factors without any covariates
4614 options(contrasts=c("contr.sum", "contr.poly")) # CHANGELOG: Added to calculate
properly the type III sum of squares with lm 2021-07-27
4615 mG_RP1 <- lm(mean_riskperception2_6 ~ studyarm, data=datGeneric)
4616 Anova(mG_RP1,type="III")
4617 summary(mG_RP1)
4618
4619 # Model 2: Check for direct effects of factors with adjustment for other covariates
4620 mG_RP2 <-
4621   lm(
4622     mean_riskperception2_6 ~
4623       studyarm +
4624       mean_indivhorz +
4625       mean_indivvertical +
4626       mean_collhorz +
4627       mean_collvertical +
4628       bornincanada + #CHANGELOG ASJ: covariate list shortened 2021-08-04
4629       language_1 +
4630       language_2 +
4631       Asian_group +
4632       White_group +
4633       disability_any +
4634       genderidentity +
4635       income +
4636       edhi +
4637       age,
4638     data = datGeneric
4639   )
4640 Anova(mG_RP2,type="III")
4641 summary(mG_RP2)
4642
4643 # Model 3: Check for moderating effects of individualism & collectivism with adjustment
for other covariates
4644 mG_RP3 <-
4645   lm(
4646     mean_riskperception2_6 ~
4647       studyarm * mean_indivhorz +
4648       studyarm * mean_indivvertical +
4649       studyarm * mean_collhorz +
4650       studyarm * mean_collvertical +
4651       bornincanada + #CHANGELOG ASJ: covariate list shortened 2021-08-04
4652       language_1 +
4653       language_2 +
4654       Asian_group +
4655       White_group +
4656       disability_any +
4657       genderidentity +
4658       income +
4659       edhi +
4660       age,
4661     data = datGeneric
4662   )
4663 Anova(mG_RP3,type="III")
4664 summary(mG_RP3)
4665
4666 # CHANGELOG: Model 4 + 5 : To check the interaction between the study arm and education

```

```

4667 # Model 4: Check for interaction studyarm*edhi
4668 mG_RP4 <- lm(mean_riskperception2_6 ~ studyarm*edhi, data=datGeneric)
4669 Anova(mG_RP4,type="III")
4670 summary(mG_RP4)
4671
4672 # Model 5: Check for interaction studyarm*edhi with adjustment for other covariates
4673 mG_RP5 <- lm(mean_riskperception2_6 ~ studyarm*edhi +
4674             mean_indivhorz +
4675             mean_indivvertical +
4676             mean_collhorz +
4677             mean_collvertical +
4678             bornincanada +
4679             language_1 +
4680             language_2 +
4681             Asian_group +
4682             White_group +
4683             disability_any +
4684             genderidentity +
4685             income +
4686             age, data=datGeneric)
4687 Anova(mG_RP5,type="III")
4688 summary(mG_RP5)
4689
4690 ##### ++ Validating assumptions #####
4691
4692 # Check to see if the assumptions of the models are respected. If not, we will
4693 # transform the
4694 # outcome.
4695
4696 checkassumptions(mG_RP1)
4697 checkassumptions(mG_RP2)
4698 checkassumptions(mG_RP3)
4699 checkassumptions(mG_RP4)
4700 checkassumptions(mG_RP5)
4701
4702 ##### ++ Interpretation #####
4703
4704 mG_RP1_arm <- emmeans(mG_RP1,~studyarm)
4705 mG_RP1_arm
4706 pairs(mG_RP1_arm)
4707 plot(mG_RP1_arm)
4708
4709 mG_RP2_arm <- emmeans(mG_RP2,~studyarm)
4710 mG_RP2_arm
4711 pairs(mG_RP2_arm)
4712 plot(mG_RP2_arm)
4713
4714 emmip(mG_RP3, studyarm ~ mean_indivhorz, cov.reduce = range)
4715 emmip(mG_RP3, studyarm ~ mean_indivvertical, cov.reduce = range)
4716 emmip(mG_RP3, studyarm ~ mean_collvertical, cov.reduce = range)
4717
4718 mG_RP4_v <- emmeans(mG_RP4,~studyarm|edhi)
4719 mG_RP4_v
4720 pairs(mG_RP4_v)
4721 mG_RP4_e <- emmeans(mG_RP4,~edhi|studyarm)
4722 mG_RP4_e
4723 pairs(mG_RP4_e)
4724
4725 emmeans(mG_RP5,~studyarm|edhi)
4726
4727
4728
4729 # Now running models on imputed data.
4730 #CHANGELOG ASJ: No missing data for mean_riskperception2_6, no model with imputation
4731 #performed, 21-09-20.
4732
4733 ##### + Measles #####

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```

4734
4735 # Model 1: Check for direct effects of factors without any covariates
4736 mM_RP26_1 <- lm(mean_riskperception2_6 ~ studyarm, data=datMeasles)
4737 Anova(mM_RP26_1,type="III")
4738 summary(mM_RP26_1)
4739
4740 # Model 2: Check for direct effects of factors with adjustment for other covariates
4741 mM_RP26_2 <-
4742   lm(
4743     mean_riskperception2_6 ~
4744       studyarm +
4745       mean_indivhorz +
4746       mean_indivvertical +
4747       mean_collhorz +
4748       mean_collvertical +
4749       bornincanada + #CHANGELOG ASJ: covariate list shortened 2021-08-04
4750       language_1 +
4751       language_2 +
4752       Asian_group +
4753       White_group +
4754       disability_any +
4755       genderidentity +
4756       income +
4757       edhi +
4758       age,
4759     data = datMeasles
4760   )
4761 Anova(mM_RP26_2,type="III")
4762 summary(mM_RP26_2)
4763
4764 # Model 3: Check for moderating effects of individualism & collectivism with adjustment
4765 # for other covariates
4766 mM_RP26_3 <-
4767   lm(
4768     mean_riskperception2_6 ~
4769       studyarm * mean_indivhorz +
4770       studyarm * mean_indivvertical +
4771       studyarm * mean_collhorz +
4772       studyarm * mean_collvertical +
4773       bornincanada + #CHANGELOG ASJ: covariate list shortened 2021-08-04
4774       language_1 +
4775       language_2 +
4776       Asian_group +
4777       White_group +
4778       disability_any +
4779       genderidentity +
4780       income +
4781       edhi +
4782       age,
4783     data = datMeasles
4784   )
4785 Anova(mM_RP26_3,type="III")
4786 summary(mM_RP26_3)
4787
4788 # CHANGELOG: Model 4 + 5 : To check the interaction between the study arm and education
4789 # Model 4: Check for interaction studyarm*edhi
4790 mM_RP26_4 <- lm(mean_riskperception2_6 ~ studyarm*edhi, data=datMeasles)
4791 Anova(mM_RP26_4,type="III")
4792 summary(mM_RP26_4)
4793
4794 # Model 5: Check for interaction studyarm*edhi with adjustment for other covariates
4795 mM_RP26_5 <- lm(mean_riskperception2_6 ~ studyarm*edhi +
4796   mean_indivhorz +
4797   mean_indivvertical +
4798   mean_collhorz +
4799   mean_collvertical +
4800   bornincanada +
4801   language_1 +
4802   language_2 +

```



```

4802         Asian_group +
4803         White_group +
4804         disability_any +
4805         genderidentity +
4806         income +
4807         age, data=datMeasles)
4808 Anova(mM_RP26_5,type="III")
4809 summary(mM_RP26_5)
4810
4811 ##### ++ Validating assumptions #####
4812
4813 # Check to see if the assumptions of the models are respected. If not, we will
4814 # transform the
4815 # outcome.
4816
4816 checkassumptions(mM_RP26_1)
4817 checkassumptions(mM_RP26_2)
4818 checkassumptions(mM_RP26_3)
4819 checkassumptions(mM_RP26_4)
4820 checkassumptions(mM_RP26_5)
4821
4822 ##### ++ Interpretation #####
4823 #CHANGELOG ASJ: adapt relevant functions depending on results of global tests,
4824 2021-08-11.
4824 mM_RP26_1_arm <- emmeans(mM_RP26_1,~studyarm)
4825 mM_RP26_1_arm
4826 pairs(mM_RP26_1_arm)
4827
4828 emmeans(mM_RP26_2,~studyarm)
4829
4830 emmip(mM_RP26_3, studyarm ~ mean_indivvertical, cov.reduce = range)
4831
4832 emmeans(mM_RP26_4,~studyarm|edhi)
4833
4834 emmeans(mM_RP26_5,~studyarm|edhi)
4835
4836
4837
4838 # Now running models on imputed data.
4839 #CHANGELOG ASJ: No missing data for mean_riskperception2_6, no model with imputation
4840 performed, 21-09-20.
4841
4842
4843 ##### + Flu #####
4844
4845 # Model 1: Check for direct effects of factors without any covariates
4846 mF_RP26_1 <- lm(mean_riskperception2_6 ~ studyarm, data=datFlu)
4847 Anova(mF_RP26_1,type="III")
4848 summary(mF_RP26_1)
4849
4850 # Model 2: Check for direct effects of factors with adjustment for other covariates
4851 mF_RP26_2 <-
4852   lm(
4853     mean_riskperception2_6 ~
4854     studyarm +
4855     mean_indivhorz +
4856     mean_indivvertical +
4857     mean_collhorz +
4858     mean_collvertical +
4859     bornincanada + #CHANGELOG ASJ: covariate list shortened 2021-08-04
4860     language_1 +
4861     language_2 +
4862     Asian_group +
4863     White_group +
4864     disability_any +
4865     genderidentity +
4866     income +
4867     edhi +

```

```

4868     age,
4869     data = datFlu
4870 )
4871 Anova(mF_RP26_2,type="III")
4872 summary(mF_RP26_2)
4873
4874 # Model 3: Check for moderating effects of individualism & collectivism with adjustment
4875 # for other covariates
4876 mF_RP26_3 <-
4877   lm(
4878     mean_riskperception2_6 ~
4879     studyarm * mean_indivhorz +
4880     studyarm * mean_indivvertical +
4881     studyarm * mean_collhorz +
4882     studyarm * mean_collvertical +
4883     bornincanada + #CHANGELOG ASJ: covariate list shortened 2021-08-04
4884     language_1 +
4885     language_2 +
4886     Asian_group +
4887     White_group +
4888     disability_any +
4889     genderidentity +
4890     income +
4891     edhi +
4892     age,
4893     data = datFlu
4894   )
4895 Anova(mF_RP26_3,type="III")
4896 summary(mF_RP26_3)
4897
4898 # CHANGELOG: Model 4 + 5 : To check the interaction between the study arm and education
4899 # Model 4: Check for interaction studyarm*edhi
4900 mF_RP26_4 <- lm(mean_riskperception2_6 ~ studyarm*edhi, data=datFlu)
4901 Anova(mF_RP26_4,type="III")
4902 summary(mF_RP26_4)
4903
4904 # Model 5: Check for interaction studyarm*edhi with adjustment for other covariates
4905 mF_RP26_5 <- lm(mean_riskperception2_6 ~ studyarm*edhi +
4906     mean_indivhorz +
4907     mean_indivvertical +
4908     mean_collhorz +
4909     mean_collvertical +
4910     bornincanada +
4911     language_1 +
4912     language_2 +
4913     Asian_group +
4914     White_group +
4915     disability_any +
4916     genderidentity +
4917     income +
4918     age, data=datFlu)
4919 Anova(mF_RP26_5,type="III")
4920 summary(mF_RP26_5)
4921
4922
4923 #### ++ Validating assumptions ####
4924
4925 # Check to see if the assumptions of the models are respected. If not, we will
4926 # transform the
4927 # outcome.
4928
4929 checkassumptions(mF_RP26_1)
4930 checkassumptions(mF_RP26_2)
4931 checkassumptions(mF_RP26_3)
4932 checkassumptions(mF_RP26_4)
4933 checkassumptions(mF_RP26_5)
4934
4935 #### ++ Interpretation ####

```

```

4935 #CHANGELOG ASJ: adapt relevant functions depending on results of global tests,
4936 2021-08-11.
4937
4937 mF_RP26_1_arm <- emmeans(mF_RP26_1,~studyarm)
4938 mF_RP26_1_arm
4939 pairs(mF_RP26_1_arm)
4940
4941 mF_RP26_2_arm <- emmeans(mF_RP26_2,~studyarm)
4942 mF_RP26_2_arm
4943 pairs(mF_RP26_2_arm)
4944
4945 emmip(mF_RP26_3, studyarm ~ mean_indivhorz, cov.reduce = range)
4946 emmip(mF_RP26_3, studyarm ~ mean_indivvertical, cov.reduce = range)
4947
4948 emmeans(mF_RP26_4,~studyarm|edhi)
4949
4950 emmeans(mF_RP26_5,~studyarm|edhi)
4951
4952
4953
4954
4955 # Now running models on imputed data.
4956 #CHANGELOG ASJ: No missing data for mean_riskperception2_6, no model with imputation
4957 performed, 21-09-20.
4958
4959
4960 #CHANGELOG ASJ: Added for secondary outcomes, 21-09-03.
4961 ##### +++ ONE WAY ANOVA FOR EMOTIONS #####
4962 ##### + Generic #####
4963
4964 # Model 1: Check for direct effects of factors without any covariates
4965 options(contrasts=c("contr.sum", "contr.poly"))
4966 mG_E1 <- lm(mean_emotion ~ studyarm, data=datGeneric)
4967 Anova(mG_E1,type="III")
4968 summary(mG_E1)
4969
4970 # Model 2: Check for direct effects of factors with adjustment for other covariates
4971 mG_E2 <-
4972   lm(
4973     mean_emotion ~
4974       studyarm +
4975       mean_indivhorz +
4976       mean_indivvertical +
4977       mean_collhorz +
4978       mean_collvertical +
4979       bornincanada +
4980       language_1 +
4981       language_2 +
4982       Asian_group +
4983       White_group +
4984       disability_any +
4985       genderidentity +
4986       income +
4987       edhi +
4988       age,
4989     data = datGeneric
4990   )
4991 Anova(mG_E2,type="III")
4992 summary(mG_E2)
4993
4994 # Model 3: Check for moderating effects of individualism & collectivism with adjustment
4995 for other covariates
4996 mG_E3 <-
4997   lm(
4998     mean_emotion ~
4999       studyarm * mean_indivhorz +
5000       studyarm * mean_indivvertical +
5001       studyarm * mean_collhorz +

```

```

5001     studyarm * mean_collvertical +
5002     bornincanada +
5003     language_1 +
5004     language_2 +
5005     Asian_group +
5006     White_group +
5007     disability_any +
5008     genderidentity +
5009     income +
5010     edhi +
5011     age,
5012     data = datGeneric
5013 )
5014 Anova(mG_E3,type="III")
5015 summary(mG_E3)
5016
5017 # CHANGELOG: Model 4 + 5 : To check the interaction between the study arm and education
5018 # Model 4: Check for interaction studyarm*edhi
5019 mG_E4 <- lm(mean_emotion ~ studyarm*edhi, data=datGeneric)
5020 Anova(mG_E4,type="III")
5021 summary(mG_E4)
5022
5023 # Model 5: Check for interaction studyarm*edhi with adjustment for other covariates
5024 mG_E5 <- lm(mean_emotion ~ studyarm*edhi +
5025             mean_indivhorz +
5026             mean_indivvertical +
5027             mean_collhorz +
5028             mean_collvertical +
5029             bornincanada +
5030             language_1 +
5031             language_2 +
5032             Asian_group +
5033             White_group +
5034             disability_any +
5035             genderidentity +
5036             income +
5037             age, data=datGeneric)
5038 Anova(mG_E5,type="III")
5039 summary(mG_E5)
5040
5041 ##### ++ Validating assumptions #####
5042
5043 # Check to see if the assumptions of the models are respected. If not, we will
5044 # transform the
5045 # outcome.
5046
5047 checkassumptions(mG_E1)
5048 checkassumptions(mG_E2)
5049 checkassumptions(mG_E3)
5050 checkassumptions(mG_E4)
5051 checkassumptions(mG_E5)
5052
5053 ##### ++ Interpretation #####
5054
5055 mG_E1_arm <- emmeans(mG_E1,~studyarm)
5056 plot(mG_E1_arm)
5057
5058 mG_E2_arm <- emmeans(mG_E2,~studyarm)
5059 plot(mG_E2_arm)
5060
5061 emmip(mG_E3, studyarm ~ mean_indivhorz, cov.reduce = range)
5062 emmip(mG_E3, studyarm ~ mean_collhorz, cov.reduce = range)
5063
5064 emmeans(mG_E4,~studyarm|edhi)
5065
5066 emmeans(mG_E5,~studyarm|edhi)
5067
5068

```

```

5069
5070
5071
5072 # Now running models on imputed data.
5073 #CHANGELOG ASJ: No missing data for mean_emotion, no model with imputation performed,
21-09-20.
5074
5075
5076
5077 ##### + Measles #####
5078
5079 # Model 1: Check for direct effects of factors without any covariates
5080 mM_E_1 <- lm(mean_emotion ~ studyarm, data=datMeasles)
5081 Anova(mM_E_1,type="III")
5082 summary(mM_E_1)
5083
5084 # Model 2: Check for direct effects of factors with adjustment for other covariates
5085 mM_E_2 <-
5086   lm(
5087     mean_emotion ~
5088       studyarm +
5089       mean_indivhorz +
5090       mean_indivvertical +
5091       mean_collhorz +
5092       mean_collvertical +
5093       bornincanada +
5094       language_1 +
5095       language_2 +
5096       Asian_group +
5097       White_group +
5098       disability_any +
5099       genderidentity +
5100       income +
5101       edhi +
5102       age,
5103     data = datMeasles
5104   )
5105 Anova(mM_E_2,type="III")
5106 summary(mM_E_2)
5107
5108 # Model 3: Check for moderating effects of individualism & collectivism with adjustment
for other covariates
5109 mM_E_3 <-
5110   lm(
5111     mean_emotion ~
5112       studyarm * mean_indivhorz +
5113       studyarm * mean_indivvertical +
5114       studyarm * mean_collhorz +
5115       studyarm * mean_collvertical +
5116       bornincanada +
5117       language_1 +
5118       language_2 +
5119       Asian_group +
5120       White_group +
5121       disability_any +
5122       genderidentity +
5123       income +
5124       edhi +
5125       age,
5126     data = datMeasles
5127   )
5128 Anova(mM_E_3,type="III")
5129 summary(mM_E_3)
5130
5131 # CHANGELOG: Model 4 + 5 : To check the interaction between the study arm and education
5132 # Model 4: Check for interaction studyarm*edhi
5133 mM_E_4 <- lm(mean_emotion ~ studyarm*edhi, data=datMeasles)
5134 Anova(mM_E_4,type="III")
5135 summary(mM_E_4)

```

```

5136
5137 # Model 5: Check for interaction studyarm*edhi with adjustment for other covariates
5138 mM_E_5 <- lm(mean_emotion ~ studyarm*edhi +
5139               mean_indivhorz +
5140               mean_indivvertical +
5141               mean_collhorz +
5142               mean_collvertical +
5143               bornincanada +
5144               language_1 +
5145               language_2 +
5146               Asian_group +
5147               White_group +
5148               disability_any +
5149               genderidentity +
5150               income +
5151               age, data=datMeasles)
5152 Anova(mM_E_5,type="III")
5153 summary(mM_E_5)
5154
5155 ##### ++ Validating assumptions #####
5156
5157 # Check to see if the assumptions of the models are respected. If not, we will
transform the
5158 # outcome.
5159
5160 checkassumptions(mM_E_1)
5161 checkassumptions(mM_E_2)
5162 checkassumptions(mM_E_3)
5163 checkassumptions(mM_E_4)
5164 checkassumptions(mM_E_5)
5165
5166 ##### ++ Interpretation #####
5167 #CHANGELOG ASJ: adapt relevant functions depending on results of global tests,
2021-08-11.
5168 mM_E_1_arm <- emmeans(mM_E_1,~studyarm)
5169 mM_E_1_arm
5170 pairs(mM_E_1_arm)
5171
5172 mM_E_2_arm <- emmeans(mM_E_2,~studyarm)
5173 mM_E_2_arm
5174 pairs(mM_E_2_arm)
5175
5176 emmeans(mM_E_4,~studyarm|edhi)
5177
5178 emmeans(mM_E_5,~studyarm|edhi)
5179
5180
5181
5182 # Now running models on imputed data.
5183 #CHANGELOG ASJ: No missing data for mean_emotion, no model with imputation performed,
21-09-20.
5184
5185
5186 ##### + Flu #####
5187
5188 # Model 1: Check for direct effects of factors without any covariates
5189 mF_E_1 <- lm(mean_emotion ~ studyarm, data=datFlu)
5190 Anova(mF_E_1,type="III")
5191 summary(mF_E_1)
5192
5193 # Model 2: Check for direct effects of factors with adjustment for other covariates
5194 mF_E_2 <-
5195   lm(
5196     mean_emotion ~
5197       studyarm +
5198       mean_indivhorz +
5199       mean_indivvertical +
5200       mean_collhorz +
5201       mean_collvertical +

```

```

5202     bornincanada +
5203     language_1 +
5204     language_2 +
5205     Asian_group +
5206     White_group +
5207     disability_any +
5208     genderidentity +
5209     income +
5210     edhi +
5211     age,
5212     data = datFlu
5213 )
5214 Anova(mF_E_2,type="III")
5215 summary(mF_E_2)
5216
5217 # Model 3: Check for moderating effects of individualism & collectivism with adjustment
for other covariates
5218 mF_E_3 <-
5219   lm(
5220     mean_emotion ~
5221       studyarm * mean_indivhorz +
5222       studyarm * mean_indivvertical +
5223       studyarm * mean_collhorz +
5224       studyarm * mean_collvertical +
5225       bornincanada +
5226       language_1 +
5227       language_2 +
5228       Asian_group +
5229       White_group +
5230       disability_any +
5231       genderidentity +
5232       income +
5233       edhi +
5234       age,
5235     data = datFlu
5236   )
5237 Anova(mF_E_3,type="III")
5238 summary(mF_E_3)
5239
5240
5241 # CHANGELOG: Model 4 + 5 : To check the interaction between the study arm and education
5242 # Model 4: Check for interaction studyarm*edhi
5243 mF_E_4 <- lm(mean_emotion ~ studyarm*edhi, data=datFlu)
5244 Anova(mF_E_4,type="III")
5245 summary(mF_E_4)
5246
5247 # Model 5: Check for interaction studyarm*edhi with adjustment for other covariates
5248 mF_E_5 <- lm(mean_emotion ~ studyarm*edhi +
5249     mean_indivhorz +
5250     mean_indivvertical +
5251     mean_collhorz +
5252     mean_collvertical +
5253     bornincanada +
5254     language_1 +
5255     language_2 +
5256     Asian_group +
5257     White_group +
5258     disability_any +
5259     genderidentity +
5260     income +
5261     age, data=datFlu)
5262 Anova(mF_E_5,type="III")
5263 summary(mF_E_5)
5264
5265
5266 #### ++ Validating assumptions ####
5267
5268 # Check to see if the assumptions of the models are respected. If not, we will
transform the

```

```

5269 # outcome.
5270
5271 checkassumptions(mF_E_1)
5272 checkassumptions(mF_E_2)
5273 checkassumptions(mF_E_3)
5274 checkassumptions(mF_E_4)
5275 checkassumptions(mF_E_5)
5276
5277 ##### ++ Interpretation #####
5278 #CHANGELOG ASJ: adapt relevant functions depending on results of global tests,
5279 2021-08-11.
5280
5281 emmeans(mF_E_1,~studyarm)
5282
5283 emmeans(mF_E_2,~studyarm)
5284
5285 mF_E4_s<-emmeans(mF_E_4,~studyarm|edhi)
5286 mF_E4_s
5287 pairs(mF_E4_s)
5288
5289 mF_E4_e<-emmeans(mF_E_4,~edhi|studyarm)
5290 pairs(mF_E4_e)
5291
5292 emmeans(mF_E_5,~studyarm|edhi)
5293
5294
5295
5296 # Now running models on imputed data.
5297 #CHANGELOG ASJ: No missing data for mean_emotion, no model with imputation performed,
5298 21-09-20.
5299
5300 ##### +++ ONE WAY ANOVA FOR KNOWLEDGE #####
5301 ##### + Generic #####
5302
5303 # Model 1: Check for direct effects of factors without any covariates
5304 options(contrasts=c("contr.sum", "contr.poly"))
5305 mG_K1 <- lm(sum_knowledge ~ studyarm, data=datGeneric)
5306 Anova(mG_K1,type="III")
5307 summary(mG_K1)
5308
5309 # Model 2: Check for direct effects of factors with adjustment for other covariates
5310 mG_K2 <-
5311   lm(
5312     sum_knowledge ~
5313       studyarm +
5314       mean_indivhorz +
5315       mean_indivvertical +
5316       mean_collhorz +
5317       mean_collvertical +
5318       bornincanada +
5319       language_1 +
5320       language_2 +
5321       Asian_group +
5322       White_group +
5323       disability_any +
5324       genderidentity +
5325       income +
5326       edhi +
5327       age,
5328     data = datGeneric
5329   )
5330 Anova(mG_K2,type="III")
5331 summary(mG_K2)
5332
5333 # Model 3: Check for moderating effects of individualism & collectivism with adjustment
5334 for other covariates
5335 mG_K3 <-

```



```

5335     lm(
5336       sum_knowledge ~
5337         studyarm * mean_indivhorz +
5338         studyarm * mean_indivvertical +
5339         studyarm * mean_collhorz +
5340         studyarm * mean_collvertical +
5341         bornincanada +
5342         language_1 +
5343         language_2 +
5344         Asian_group +
5345         White_group +
5346         disability_any +
5347         genderidentity +
5348         income +
5349         edhi +
5350         age,
5351       data = datGeneric
5352     )
5353 Anova(mG_K3,type="III")
5354 summary(mG_K3)
5355
5356 # CHANGELOG: Model 4 + 5 : To check the interaction between the study arm and education
5357 # Model 4: Check for interaction studyarm*edhi
5358 mG_K4 <- lm(sum_knowledge ~ studyarm*edhi, data=datGeneric)
5359 Anova(mG_K4,type="III")
5360 summary(mG_K4)
5361
5362 # Model 5: Check for interaction studyarm*edhi with adjustment for other covariates
5363 mG_K5 <- lm(sum_knowledge ~ studyarm*edhi +
5364             mean_indivhorz +
5365             mean_indivvertical +
5366             mean_collhorz +
5367             mean_collvertical +
5368             bornincanada +
5369             language_1 +
5370             language_2 +
5371             Asian_group +
5372             White_group +
5373             disability_any +
5374             genderidentity +
5375             income +
5376             age, data=datGeneric)
5377 Anova(mG_K5,type="III")
5378 summary(mG_K5)
5379
5380 ##### ++ Validating assumptions #####
5381
5382 # Check to see if the assumptions of the models are respected. If not, we will
5383 # transform the
5384 # outcome.
5385
5386 checkassumptions(mG_K1)
5387 checkassumptions(mG_K2)
5388 checkassumptions(mG_K3)
5389 checkassumptions(mG_K4)
5390 checkassumptions(mG_K5)
5391
5392 ##### ++ Interpretation #####
5393
5394 mG_K1_arm <- emmeans(mG_K1,~studyarm)
5395 mG_K1_arm
5396 pairs(mG_K1_arm)
5397
5398 mG_K2_arm <- emmeans(mG_K2,~studyarm)
5399 mG_K2_arm
5400 pairs(mG_K2_arm)
5401
5402 emmeans(mG_K4,~studyarm|edhi)
5403

```

```

5403 emmeans(mG_K5, ~studyarm|edhi)
5404
5405
5406 # Now running models on imputed data.
5407 #CHANGELOG ASJ: No missing data for sum_knowledge, no model with imputation performed,
5408 21-09-20.
5409
5410
5411 ##### + Measles #####
5412
5413 # Model 1: Check for direct effects of factors without any covariates
5414 mM_K_1 <- lm(sum_knowledge ~ studyarm, data=datMeasles)
5415 Anova(mM_K_1, type="III")
5416 summary(mM_K_1)
5417
5418 # Model 2: Check for direct effects of factors with adjustment for other covariates
5419 mM_K_2 <-
5420   lm(
5421     sum_knowledge ~
5422       studyarm +
5423       mean_indivhorz +
5424       mean_indivvertical +
5425       mean_collhorz +
5426       mean_collvertical +
5427       bornincanada +
5428       language_1 +
5429       language_2 +
5430       Asian_group +
5431       White_group +
5432       disability_any +
5433       genderidentity +
5434       income +
5435       edhi +
5436       age,
5437     data = datMeasles
5438   )
5439 Anova(mM_K_2, type="III")
5440 summary(mM_K_2)
5441
5442 # Model 3: Check for moderating effects of individualism & collectivism with adjustment
5443 for other covariates
5444 mM_K_3 <-
5445   lm(
5446     sum_knowledge ~
5447       studyarm * mean_indivhorz +
5448       studyarm * mean_indivvertical +
5449       studyarm * mean_collhorz +
5450       studyarm * mean_collvertical +
5451       bornincanada +
5452       language_1 +
5453       language_2 +
5454       Asian_group +
5455       White_group +
5456       disability_any +
5457       genderidentity +
5458       income +
5459       edhi +
5460       age,
5461     data = datMeasles
5462   )
5463 Anova(mM_K_3, type="III")
5464 summary(mM_K_3)
5465
5466 # CHANGELOG: Model 4 + 5 : To check the interaction between the study arm and education
5467 # Model 4: Check for interaction studyarm*edhi
5468 mM_K_4 <- lm(sum_knowledge ~ studyarm*edhi, data=datMeasles)
5469 Anova(mM_K_4, type="III")
5470 summary(mM_K_4)

```

```

5470
5471 # Model 5: Check for interaction studyarm*edhi with adjustment for other covariates
5472 mM_K_5 <- lm(sum_knowledge ~ studyarm*edhi +
5473             mean_indivhorz +
5474             mean_indivvertical +
5475             mean_collhorz +
5476             mean_collvertical +
5477             bornincanada +
5478             language_1 +
5479             language_2 +
5480             Asian_group +
5481             White_group +
5482             disability_any +
5483             genderidentity +
5484             income +
5485             age, data=datMeasles)
5486 Anova(mM_K_5,type="III")
5487 summary(mM_K_5)
5488
5489 ##### ++ Validating assumptions #####
5490
5491 # Check to see if the assumptions of the models are respected. If not, we will
5492 # transform the
5493
5494 checkassumptions(mM_K_1)
5495 checkassumptions(mM_K_2)
5496 checkassumptions(mM_K_3)
5497 checkassumptions(mM_K_4)
5498 checkassumptions(mM_K_5)
5499
5500 ##### ++ Interpretation #####
5501 #CHANGELOG ASJ: adapt relevant functions depending on results of global tests,
5502 #2021-08-11.
5503 mM_K_1_arm <- emmeans(mM_K_1,~studyarm)
5504 mM_K_1_arm
5505 pairs(mM_K_1_arm)
5506
5507 mM_K_2_arm <- emmeans(mM_K_2,~studyarm)
5508 mM_K_2_arm
5509 pairs(mM_K_2_arm)
5510
5511 emmip(mM_K_3, studyarm ~ mean_indivvertical, cov.reduce = range)
5512
5513 emmeans(mM_K_4,~studyarm|edhi)
5514
5515 emmeans(mM_K_5,~studyarm|edhi)
5516
5517
5518 # Now running models on imputed data.
5519 #CHANGELOG ASJ: No missing data for sum_knowledge, no model with imputation performed,
5520 #21-09-20.
5521
5522
5523
5524 ##### + Flu #####
5525
5526 # Model 1: Check for direct effects of factors without any covariates
5527 mF_K_1 <- lm(sum_knowledge ~ studyarm, data=datFlu)
5528 Anova(mF_K_1,type="III")
5529 summary(mF_K_1)
5530
5531 # Model 2: Check for direct effects of factors with adjustment for other covariates
5532 mF_K_2 <-
5533   lm(
5534     sum_knowledge ~
5535     studyarm +

```

```

5536     mean_indivhorz +
5537     mean_indivvertical +
5538     mean_collhorz +
5539     mean_collvertical +
5540     bornincanada +
5541     language_1 +
5542     language_2 +
5543     Asian_group +
5544     White_group +
5545     disability_any +
5546     genderidentity +
5547     income +
5548     edhi +
5549     age,
5550     data = datFlu
5551 )
5552 Anova(mF_K_2,type="III")
5553 summary(mF_K_2)
5554
5555 # Model 3: Check for moderating effects of individualism & collectivism with adjustment
for other covariates
5556 mF_K_3 <-
5557   lm(
5558     sum_knowledge ~
5559     studyarm * mean_indivhorz +
5560     studyarm * mean_indivvertical +
5561     studyarm * mean_collhorz +
5562     studyarm * mean_collvertical +
5563     bornincanada +
5564     language_1 +
5565     language_2 +
5566     Asian_group +
5567     White_group +
5568     disability_any +
5569     genderidentity +
5570     income +
5571     edhi +
5572     age,
5573     data = datFlu
5574   )
5575 Anova(mF_K_3,type="III")
5576 summary(mF_K_3)
5577
5578
5579 # CHANGELOG: Model 4 + 5 : To check the interaction between the study arm and education
5580 # Model 4: Check for interaction studyarm*edhi
5581 mF_K_4 <- lm(sum_knowledge ~ studyarm*edhi, data=datFlu)
5582 Anova(mF_K_4,type="III")
5583 summary(mF_K_4)
5584
5585 # Model 5: Check for interaction studyarm*edhi with adjustment for other covariates
5586 mF_K_5 <- lm(sum_knowledge ~ studyarm*edhi +
5587               mean_indivhorz +
5588               mean_indivvertical +
5589               mean_collhorz +
5590               mean_collvertical +
5591               bornincanada +
5592               language_1 +
5593               language_2 +
5594               Asian_group +
5595               White_group +
5596               disability_any +
5597               genderidentity +
5598               income +
5599               age, data=datFlu)
5600 Anova(mF_K_5,type="III")
5601 summary(mF_K_5)
5602
5603

```

```

5604 ##### ++ Validating assumptions #####
5605
5606 # Check to see if the assumptions of the models are respected. If not, we will
transform the
5607 # outcome.
5608
5609 checkassumptions(mF_K_1)
5610 checkassumptions(mF_K_2)
5611 checkassumptions(mF_K_3)
5612 checkassumptions(mF_K_4)
5613 checkassumptions(mF_K_5)
5614
5615 ##### ++ Interpretation #####
5616 #CHANGELOG ASJ: adapt relevant functions depending on results of global tests,
2021-08-11.
5617
5618 mF_K_1_arm <- emmeans(mF_K_1,~studyarm)
5619 mF_K_1_arm
5620 pairs(mF_K_1_arm)
5621
5622 mF_K_2_arm <- emmeans(mF_K_2,~studyarm)
5623 mF_K_2_arm
5624 pairs(mF_K_2_arm)
5625
5626 emmip(mF_K_3, studyarm ~ mean_indivvertical, cov.reduce = range)
5627
5628 emmeans(mF_K_4,~studyarm|edhi)
5629
5630 mF_K_5_arm <- emmeans(mF_K_5,~studyarm|edhi)
5631 mF_K_5_arm
5632 pairs(mF_K_5_arm)
5633 pairs(emmeans(mF_K_5,~edhi|studyarm))
5634
5635
5636
5637 # Now running models on imputed data.
5638 #CHANGELOG ASJ: No missing data for sum_knowledge, no model with imputation performed,
21-09-20.
5639
5640
5641
5642
5643
5644
5645 #CHANGELOG ASJ: Add logistic regression models for dichotomous outcomes, 2021-08-11.
5646
5647 ##### +++ Logistic regression for RP1 #####
5648
5649 #Create relevel before model to avoid problems with pairs function.
5650 datGeneric$RP1_dicho <- relevel(datGeneric$RP1_dicho,ref = "Low")
5651 datMeasles$RP1_dicho <- relevel(datMeasles$RP1_dicho,ref = "Low")
5652 datFlu$RP1_dicho <- relevel(datFlu$RP1_dicho,ref = "Low")
5653
5654 ##### ++ Generic #####
5655
5656 ##### + Model 1: Check for direct effects of factors without any covariates #####
5657
5658 options(contrasts=c("contr.sum", "contr.poly"))
5659 rlogG_RP1_1 <- glm(RP1_dicho ~ studyarm, data = datGeneric,family=binomial("logit"))
5660 Anova(rlogG_RP1_1,type="III")
5661 summary(rlogG_RP1_1)
5662
5663 mgRP1 <- emmeans(rlogG_RP1_1,~studyarm,type = "response") #proportions
5664 mgRP1
5665 confint(pairs(mgRP1,reverse = TRUE)) #Odds ratios
5666 pairs(mgRP1,reverse = TRUE, type = "response")
5667
5668 # Model 2: Check for direct effects of factors with adjustment for other covariates
5669 rlogG_RP1_2 <-

```

```

5670     glm(RP1_dicho ~ studyarm +
5671         mean_indivhorz +
5672         mean_indivvertical +
5673         mean_collhorz +
5674         mean_collvertical +
5675         bornincanada +
5676         language_1 +
5677         language_2 +
5678         Asian_group +
5679         White_group +
5680         disability_any +
5681         genderidentity +
5682         income +
5683         edhi +
5684         age,
5685         data = datGeneric,family=binomial("logit")
5686     )
5687     Anova(rlogG_RP1_2, type = "III")
5688     summary(rlogG_RP1_2)
5689
5690     mgRP1_2 <- emmeans(rlogG_RP1_2,~studyarm,type = "response")
5691     mgRP1_2
5692     confint(pairs(mgRP1_2,reverse = TRUE))
5693     pairs(mgRP1_2,reverse = TRUE,type = "response")
5694
5695
5696     # Model 3: Check for moderating effects of individualism & collectivism with adjustment
for other covariates
5697     rlogG_RP1_3 <-
5698         glm(RP1_dicho ~
5699             studyarm * mean_indivhorz +
5700             studyarm * mean_indivvertical +
5701             studyarm * mean_collhorz +
5702             studyarm * mean_collvertical +
5703             bornincanada +
5704             language_1 +
5705             language_2 +
5706             Asian_group +
5707             White_group +
5708             disability_any +
5709             genderidentity +
5710             income +
5711             edhi +
5712             age,
5713             data = datGeneric,family=binomial("logit")
5714         )
5715     Anova(rlogG_RP1_3, type = "III")
5716     summary(rlogG_RP1_3)
5717
5718     #No interaction with moderator to interpret
5719
5720     ##### + Model 4: Check for interaction viz*edhi without any covariates #####
5721
5722     rlogG_RP1_4 <- glm(RP1_dicho ~ studyarm * edhi, data =
datGeneric,family=binomial("logit"))
5723     Anova(rlogG_RP1_4,type="III")
5724     summary(rlogG_RP1_4)
5725
5726     mgRP1_4_s <- emmeans(rlogG_RP1_4,~studyarm|edhi,type = "response")
5727     mgRP1_4_s
5728     confint(pairs(mgRP1_4_s,reverse = TRUE))
5729
5730     mgRP1_4_e <- emmeans(rlogG_RP1_4, ~ edhi|studyarm, type = "response")
5731     confint(pairs(mgRP1_4_e,reverse = TRUE))
5732
5733
5734     # Model 5: Check for interaction viz*edhi with adjustment for other covariates
5735
5736     rlogG_RP1_5 <-

```

```

5737     glm(RP1_dicho ~ studyarm*edhi +
5738         mean_indivhorz +
5739         mean_indivvertical +
5740         mean_collhorz +
5741         mean_collvertical +
5742         bornincanada +
5743         language_1 +
5744         language_2 +
5745         Asian_group +
5746         White_group +
5747         disability_any +
5748         genderidentity +
5749         income +
5750         age,
5751     data = datGeneric, family=binomial("logit")
5752 )
5753 Anova(rlogG_RP1_5, type = "III")
5754 summary(rlogG_RP1_5)
5755
5756 mgRP1_5_s <- emmeans(rlogG_RP1_5, ~studyarm|edhi, type = "response")
5757 mgRP1_5_s
5758 confint(pairs(mgRP1_5_s, reverse = TRUE))
5759
5760 mgRP1_5_e <- emmeans(rlogG_RP1_5, ~ edhi|studyarm, type = "response")
5761 confint(pairs(mgRP1_5_e, reverse = TRUE))
5762
5763 # Now running models on imputed data.
5764
5765 imprlogG_RP1_1 <-
5766     with(data = datGenericImputed,
5767         exp = glm(relevel(RP1_dicho, ref="Low") ~ studyarm, family = binomial("logit")))
5768 combineimprlogG_RP1_1 <- pool(imprlogG_RP1_1)
5769 summary(combineimprlogG_RP1_1)
5770
5771
5772 ##### ++ Measles #####
5773
5774 ##### + Model 1: Check for direct effects of factors without any covariates #####
5775
5776 options(contrasts=c("contr.sum", "contr.poly"))
5777 rlogM_RP1_1 <- glm(RP1_dicho ~ studyarm, data = datMeasles, family=binomial("logit"))
5778 Anova(rlogM_RP1_1, type="III")
5779 summary(rlogM_RP1_1)
5780
5781 mmRP1 <- emmeans(rlogM_RP1_1, ~studyarm, type = "response") #proportions
5782 mmRP1
5783 confint(pairs(mmRP1, reverse = TRUE)) #Odds ratios
5784 pairs(mmRP1, reverse = TRUE, type = "response")
5785
5786 # Model 2: Check for direct effects of factors with adjustment for other covariates
5787 rlogM_RP1_2 <-
5788     glm(RP1_dicho ~ studyarm +
5789         mean_indivhorz +
5790         mean_indivvertical +
5791         mean_collhorz +
5792         mean_collvertical +
5793         bornincanada +
5794         language_1 +
5795         language_2 +
5796         Asian_group +
5797         White_group +
5798         disability_any +
5799         genderidentity +
5800         income +
5801         edhi +
5802         age,
5803     data = datMeasles, family=binomial("logit")
5804 )
5805 Anova(rlogM_RP1_2, type = "III")

```

```

5806 summary(rlogM_RP1_2)
5807
5808 mmRP1_2 <- emmeans(rlogM_RP1_2,~studyarm,type = "response")
5809 mmRP1_2
5810 confint(pairs(mmRP1_2,reverse = TRUE))
5811 pairs(mmRP1_2,reverse = TRUE,type = "response")
5812
5813
5814 # Model 3: Check for moderating effects of individualism & collectivism with adjustment
for other covariates
5815 rlogM_RP1_3 <-
5816   glm(RP1_dicho ~
5817     studyarm * mean_indivhorz +
5818     studyarm * mean_indivvertical +
5819     studyarm * mean_collhorz +
5820     studyarm * mean_collvertical +
5821     bornincanada +
5822     language_1 +
5823     language_2 +
5824     Asian_group +
5825     White_group +
5826     disability_any +
5827     genderidentity +
5828     income +
5829     edhi +
5830     age,
5831     data = datMeasles,family=binomial("logit")
5832   )
5833 Anova(rlogM_RP1_3, type = "III")
5834 summary(rlogM_RP1_3)
5835
5836 #No interaction with moderator to interpret
5837
5838 ##### + Model 4: Check for interaction viz*edhi without any covariates #####
5839
5840 rlogM_RP1_4 <- glm(RP1_dicho ~ studyarm * edhi, data =
datMeasles,family=binomial("logit"))
5841 Anova(rlogM_RP1_4,type="III")
5842 summary(rlogM_RP1_4)
5843
5844 mmRP1_4_s <- emmeans(rlogM_RP1_4,~studyarm|edhi,type = "response")
5845 mmRP1_4_s
5846 confint(pairs(mmRP1_4_s,reverse = TRUE))
5847
5848 mmRP1_4_e <- emmeans(rlogM_RP1_4, ~ edhi|studyarm, type = "response")
5849 confint(pairs(mmRP1_4_e,reverse = TRUE))
5850
5851
5852 # Model 5: Check for interaction viz*edhi with adjustment for other covariates
5853
5854 rlogM_RP1_5 <-
5855   glm(RP1_dicho ~ studyarm*edhi +
5856     mean_indivhorz +
5857     mean_indivvertical +
5858     mean_collhorz +
5859     mean_collvertical +
5860     bornincanada +
5861     language_1 +
5862     language_2 +
5863     Asian_group +
5864     White_group +
5865     disability_any +
5866     genderidentity +
5867     income +
5868     age,
5869     data = datMeasles,family=binomial("logit")
5870   )
5871 Anova(rlogM_RP1_5, type = "III")
5872 summary(rlogM_RP1_5)

```



```

5873
5874 mmRP1_5_s <- emmeans(rlogM_RP1_5,~studyarm|edhi,type = "response")
5875 mmRP1_5_s
5876 confint(pairs(mmRP1_5_s,reverse = TRUE))
5877
5878 mmRP1_5_e <- emmeans(rlogM_RP1_5, ~ edhi|studyarm, type = "response")
5879 confint(pairs(mmRP1_5_e,reverse = TRUE))
5880
5881 # Now running models on imputed data.
5882
5883 imprlogM_RP1_1 <-
5884   with(data = datMeaslesImputed,
5885         exp = glm(relevel(RP1_dicho,ref="Low") ~ studyarm,family = binomial("logit"))))
5886 combineimprlogM_RP1_1 <- pool(imprlogM_RP1_1)
5887 summary(combineimprlogM_RP1_1)
5888
5889
5890 ##### ++ Flu #####
5891
5892 ##### + Model 1: Check for direct effects of factors without any covariates #####
5893
5894 options(contrasts=c("contr.sum", "contr.poly"))
5895 rlogF_RP1_1 <- glm(RP1_dicho ~ studyarm, data = datFlu,family=binomial("logit"))
5896 Anova(rlogF_RP1_1,type="III")
5897 summary(rlogF_RP1_1)
5898
5899 mFRP1_1 <- emmeans(rlogF_RP1_1,~studyarm,type = "response") #proportions
5900 mFRP1_1
5901 confint(pairs(mFRP1_1,reverse = TRUE)) #Odds ratios
5902 pairs(mFRP1_1,reverse = TRUE, type = "response")
5903
5904 # Model 2: Check for direct effects of factors with adjustment for other covariates
5905 rlogF_RP1_2 <-
5906   glm(RP1_dicho ~ studyarm +
5907         mean_indivhorz +
5908         mean_indivvertical +
5909         mean_collhorz +
5910         mean_collvertical +
5911         bornincanada +
5912         language_1 +
5913         language_2 +
5914         Asian_group +
5915         White_group +
5916         disability_any +
5917         genderidentity +
5918         income +
5919         edhi +
5920         age,
5921         data = datFlu,family=binomial("logit")
5922   )
5923 Anova(rlogF_RP1_2, type = "III")
5924 summary(rlogF_RP1_2)
5925
5926 mFRP1_2 <- emmeans(rlogF_RP1_2,~studyarm,type = "response")
5927 mFRP1_2
5928 confint(pairs(mFRP1_2,reverse = TRUE))
5929 pairs(mFRP1_2,reverse = TRUE,type = "response")
5930
5931
5932 # Model 3: Check for moderating effects of individualism & collectivism with adjustment
# for other covariates
5933 rlogF_RP1_3 <-
5934   glm(RP1_dicho ~
5935         studyarm * mean_indivhorz +
5936         studyarm * mean_indivvertical +
5937         studyarm * mean_collhorz +
5938         studyarm * mean_collvertical +
5939         bornincanada +
5940         language_1 +

```

```

5941         language_2 +
5942         Asian_group +
5943         White_group +
5944         disability_any +
5945         genderidentity +
5946         income +
5947         edhi +
5948         age,
5949         data = datFlu, family=binomial("logit")
5950     )
5951     Anova(rlogF_RP1_3, type = "III")
5952     summary(rlogF_RP1_3)
5953
5954     emmip(rlogF_RP1_3, studyarm ~ mean_collhorz, cov.reduce = range, type = "response")
5955     emmip(rlogF_RP1_3, studyarm ~ mean_collvertical, cov.reduce = range, type = "response")
5956
5957
5958     #### + Model 4: Check for interaction viz*edhi without any covariates ####
5959
5960     rlogF_RP1_4 <- glm(RP1_dicho ~ studyarm * edhi, data =
5961     datMeasles, family=binomial("logit"))
5962     Anova(rlogF_RP1_4, type="III")
5963     summary(rlogF_RP1_4)
5964
5965     mfRP1_4_s <- emmeans(rlogF_RP1_4, ~studyarm|edhi, type = "response")
5966     mfRP1_4_s
5967     confint(pairs(mfRP1_4_s, reverse = TRUE))
5968
5969     mfRP1_4_e <- emmeans(rlogF_RP1_4, ~ edhi|studyarm, type = "response")
5970     confint(pairs(mfRP1_4_e, reverse = TRUE))
5971
5972     # Model 5: Check for interaction viz*edhi with adjustment for other covariates
5973
5974     rlogF_RP1_5 <-
5975     glm(RP1_dicho ~ studyarm*edhi +
5976         mean_indivhorz +
5977         mean_indivvertical +
5978         mean_collhorz +
5979         mean_collvertical +
5980         bornincanada +
5981         language_1 +
5982         language_2 +
5983         Asian_group +
5984         White_group +
5985         disability_any +
5986         genderidentity +
5987         income +
5988         age,
5989         data = datFlu, family=binomial("logit")
5990     )
5991     Anova(rlogF_RP1_5, type = "III")
5992     summary(rlogF_RP1_5)
5993
5994     mfRP1_5_s <- emmeans(rlogF_RP1_5, ~studyarm|edhi, type = "response")
5995     mfRP1_5_s
5996     confint(pairs(mfRP1_5_s, reverse = TRUE))
5997
5998     mfRP1_5_e <- emmeans(rlogF_RP1_5, ~ edhi|studyarm, type = "response")
5999     confint(pairs(mfRP1_5_e, reverse = TRUE))
6000
6001     # Now running models on imputed data.
6002
6003     imprlogF_RP1_1 <-
6004     with(data = datFluImputed,
6005         exp = glm(relevel(RP1_dicho, ref="Low") ~ studyarm, family = binomial("logit")))
6006     combineimprlogF_RP1_1 <- pool(imprlogF_RP1_1)
6007     summary(combineimprlogF_RP1_1)
6008

```

```

6009
6010 ##### +++ Logistic regression for VaxIntention #####
6011
6012 #Create relevel before model to avoid problems with pairs function.
6013 datGeneric$vaxintent <- relevel(datGeneric$vaxintent,ref = "Low")
6014 datMeasles$vaxintent <- relevel(datMeasles$vaxintent,ref = "Low")
6015 datFlu$vaxintent <- relevel(datFlu$vaxintent,ref = "Low")
6016
6017 ##### ++ Generic #####
6018
6019 ##### + Model 1: Check for direct effects of factors without any covariates #####
6020
6021 options(contrasts=c("contr.sum", "contr.poly"))
6022 rlogG_vi_1 <- glm(vaxintent ~ studyarm, data = datGeneric,family=binomial("logit"))
6023 Anova(rlogG_vi_1,type="III")
6024 summary(rlogG_vi_1)
6025
6026 mgvi_1 <- emmeans(rlogG_vi_1,~studyarm,type = "response") #proportions
6027 mgvi_1
6028 confint(pairs(mgvi_1,reverse = TRUE)) #Odds ratios
6029
6030 # Model 2: Check for direct effects of factors with adjustment for other covariates
6031 rlogG_vi_2 <-
6032   glm(vaxintent ~ studyarm +
6033     mean_indivhorz +
6034     mean_indivvertical +
6035     mean_collhorz +
6036     mean_collvertical +
6037     bornincanada +
6038     language_1 +
6039     language_2 +
6040     Asian_group +
6041     White_group +
6042     disability_any +
6043     genderidentity +
6044     income +
6045     edhi +
6046     age,
6047     data = datGeneric,family=binomial("logit")
6048   )
6049 Anova(rlogG_vi_2, type = "III")
6050 summary(rlogG_vi_2)
6051
6052 mgvi_2 <- emmeans(rlogG_vi_2,~studyarm,type = "response")
6053 mgvi_2
6054 confint(pairs(mgvi_2,reverse = TRUE))
6055
6056
6057 # Model 3: Check for moderating effects of individualism & collectivism with adjustment
for other covariates
6058 rlogG_vi_3 <-
6059   glm(vaxintent ~
6060     studyarm * mean_indivhorz +
6061     studyarm * mean_indivvertical +
6062     studyarm * mean_collhorz +
6063     studyarm * mean_collvertical +
6064     bornincanada +
6065     language_1 +
6066     language_2 +
6067     Asian_group +
6068     White_group +
6069     disability_any +
6070     genderidentity +
6071     income +
6072     edhi +
6073     age,
6074     data = datGeneric,family=binomial("logit")
6075   )
6076 Anova(rlogG_vi_3, type = "III")

```

```

6077 summary(rlogG_vi_3)
6078
6079 #No interaction with moderator to interpret
6080
6081 ##### + Model 4: Check for interaction viz*edhi without any covariates #####
6082
6083 rlogG_vi_4 <- glm(vaxintent ~ studyarm * edhi, data =
datGeneric,family=binomial("logit"))
6084 Anova(rlogG_vi_4,type="III")
6085 summary(rlogG_vi_4)
6086
6087 mgvi_4_s <- emmeans(rlogG_vi_4,~studyarm|edhi,type = "response")
6088 mgvi_4_s
6089 confint(pairs(mgvi_4_s,reverse = TRUE))
6090
6091 mgvi_4_e <- emmeans(rlogG_vi_4, ~ edhi|studyarm, type = "response")
6092 confint(pairs(mgvi_4_e,reverse = TRUE))
6093
6094
6095 # Model 5: Check for interaction viz*edhi with adjustment for other covariates
6096
6097 rlogG_vi_5 <-
6098   glm(vaxintent ~ studyarm*edhi +
6099     mean_indivhorz +
6100     mean_indivvertical +
6101     mean_collhorz +
6102     mean_collvertical +
6103     bornincanada +
6104     language_1 +
6105     language_2 +
6106     Asian_group +
6107     White_group +
6108     disability_any +
6109     genderidentity +
6110     income +
6111     age,
6112     data = datGeneric,family=binomial("logit")
6113   )
6114 Anova(rlogG_vi_5, type = "III")
6115 summary(rlogG_vi_5)
6116
6117 mgvi_5_s <- emmeans(rlogG_vi_5,~studyarm|edhi,type = "response")
6118 mgvi_5_s
6119 confint(pairs(mgvi_5_s,reverse = TRUE))
6120
6121 mgvi_5_e <- emmeans(rlogG_vi_5, ~ edhi|studyarm, type = "response")
6122 confint(pairs(mgvi_5_e,reverse = TRUE))
6123
6124 # Now running models on imputed data.
6125
6126 imprlogG_vi_1 <-
6127   with(data = datGenericImputed,
6128     exp = glm(relevel(vaxintent,ref="Low") ~ studyarm,family = binomial("logit")))
6129 combineimprlogG_vi_1 <- pool(imprlogG_vi_1)
6130 summary(combineimprlogG_vi_1)
6131
6132 #CHANGELOG ASJ: add test to check if global test result changes or not, 21-09-20.
6133 imprlogG_vi_vide <-
6134   with(data = datGenericImputed,
6135     exp = glm(relevel(vaxintent,ref="Low") ~ 1,family = binomial("logit"))) #model
6136     with intercept only
6137 combineimprlogG_vi_vide <- pool(imprlogG_vi_vide)
6138 summary(combineimprlogG_vi_vide)
6139 test_sig<-D2(imprlogG_vi_1,imprlogG_vi_vide) #compare model with studyarm vs model with
intercept only
6139 summary(test_sig)
6140
6141
6142

```

```

6143
6144 ##### ++ Measles #####
6145
6146 ##### + Model 1: Check for direct effects of factors without any covariates #####
6147
6148 options(contrasts=c("contr.sum", "contr.poly"))
6149 rlogM_vi_1 <- glm(vaxintent ~ studyarm, data = datMeasles, family=binomial("logit"))
6150 Anova(rlogM_vi_1, type="III")
6151 summary(rlogM_vi_1)
6152
6153 mmvi <- emmeans(rlogM_vi_1, ~studyarm, type = "response") #proportions
6154 mmvi
6155 confint(pairs(mmvi, reverse = TRUE)) #Odds ratios
6156 pairs(mmvi, reverse = TRUE, type = "response")
6157
6158 # Model 2: Check for direct effects of factors with adjustment for other covariates
6159 rlogM_vi_2 <-
6160   glm(vaxintent ~ studyarm +
6161     mean_indivhorz +
6162     mean_indivvertical +
6163     mean_collhorz +
6164     mean_collvertical +
6165     bornincanada +
6166     language_1 +
6167     language_2 +
6168     Asian_group +
6169     White_group +
6170     disability_any +
6171     genderidentity +
6172     income +
6173     edhi +
6174     age,
6175     data = datMeasles, family=binomial("logit")
6176   )
6177 Anova(rlogM_vi_2, type = "III")
6178 summary(rlogM_vi_2)
6179
6180 mmvi_2 <- emmeans(rlogM_vi_2, ~studyarm, type = "response")
6181 mmvi_2
6182 confint(pairs(mmvi_2, reverse = TRUE))
6183
6184
6185 # Model 3: Check for moderating effects of individualism & collectivism with adjustment
for other covariates
6186 rlogM_vi_3 <-
6187   glm(vaxintent ~
6188     studyarm * mean_indivhorz +
6189     studyarm * mean_indivvertical +
6190     studyarm * mean_collhorz +
6191     studyarm * mean_collvertical +
6192     bornincanada +
6193     language_1 +
6194     language_2 +
6195     Asian_group +
6196     White_group +
6197     disability_any +
6198     genderidentity +
6199     income +
6200     edhi +
6201     age,
6202     data = datMeasles, family=binomial("logit")
6203   )
6204 Anova(rlogM_vi_3, type = "III")
6205 summary(rlogM_vi_3)
6206
6207 #No interaction with moderator to interpret
6208
6209 ##### + Model 4: Check for interaction viz*edhi without any covariates #####
6210

```

```

6211 rlogM_vi_4 <- glm(vaxintent ~ studyarm * edhi, data =
datMeasles, family=binomial("logit"))
6212 Anova(rlogM_vi_4, type="III")
6213 summary(rlogM_vi_4)
6214
6215 mmvi_4_s <- emmeans(rlogM_vi_4, ~studyarm|edhi, type = "response")
6216 mmvi_4_s
6217 confint(pairs(mmvi_4_s, reverse = TRUE))
6218
6219 mmvi_4_e <- emmeans(rlogM_vi_4, ~ edhi|studyarm, type = "response")
6220 confint(pairs(mmvi_4_e, reverse = TRUE))
6221
6222
6223 # Model 5: Check for interaction viz*edhi with adjustment for other covariates
6224
6225 rlogM_vi_5 <-
6226   glm(vaxintent ~ studyarm*edhi +
6227     mean_indivhorz +
6228     mean_indivvertical +
6229     mean_collhorz +
6230     mean_collvertical +
6231     bornincanada +
6232     language_1 +
6233     language_2 +
6234     Asian_group +
6235     White_group +
6236     disability_any +
6237     genderidentity +
6238     income +
6239     age,
6240     data = datMeasles, family=binomial("logit")
6241   )
6242 Anova(rlogM_vi_5, type = "III")
6243 summary(rlogM_vi_5)
6244
6245 mmvi_5_s <- emmeans(rlogM_vi_5, ~studyarm|edhi, type = "response")
6246 mmvi_5_s
6247 confint(pairs(mmvi_5_s, reverse = TRUE))
6248
6249 mmvi_5_e <- emmeans(rlogM_vi_5, ~ edhi|studyarm, type = "response")
6250 confint(pairs(mmvi_5_e, reverse = TRUE))
6251
6252 # Now running models on imputed data.
6253 imprlogM_vi_1 <-
6254   with(data = datMeaslesImputed,
6255     exp = glm(relevel(vaxintent, ref="Low") ~ studyarm, family = binomial("logit")))
6256 combineimprlogM_vi_1 <- pool(imprlogM_vi_1)
6257 summary(combineimprlogM_vi_1)
6258
6259
6260 ##### ++ Flu #####
6261
6262 ##### + Model 1: Check for direct effects of factors without any covariates #####
6263
6264 options(contrasts=c("contr.sum", "contr.poly"))
6265 rlogF_vi_1 <- glm(vaxintent ~ studyarm, data = datFlu, family=binomial("logit"))
6266 Anova(rlogF_vi_1, type="III")
6267 summary(rlogF_vi_1)
6268
6269 mfvi_1 <- emmeans(rlogF_vi_1, ~studyarm, type = "response") #proportions
6270 mfvi_1
6271 confint(pairs(mfvi_1, reverse = TRUE)) #Odds ratios
6272
6273
6274 # Model 2: Check for direct effects of factors with adjustment for other covariates
6275 rlogF_vi_2 <-
6276   glm(vaxintent ~ studyarm +
6277     mean_indivhorz +
6278     mean_indivvertical +

```

```

6279         mean_collhorz +
6280         mean_collvertical +
6281         bornincanada +
6282         language_1 +
6283         language_2 +
6284         Asian_group +
6285         White_group +
6286         disability_any +
6287         genderidentity +
6288         income +
6289         edhi +
6290         age,
6291         data = datFlu,family=binomial("logit")
6292     )
6293     Anova(rlogF_vi_2, type = "III")
6294     summary(rlogF_vi_2)
6295
6296     mfvi_2 <- emmeans(rlogF_vi_2,~studyarm,type = "response")
6297     mfvi_2
6298     confint(pairs(mfvi_2,reverse = TRUE))
6299
6300
6301     # Model 3: Check for moderating effects of individualism & collectivism with adjustment
6302     # for other covariates
6303     rlogF_vi_3 <-
6304         glm(vaxintent ~
6305             studyarm * mean_indivhorz +
6306             studyarm * mean_indivvertical +
6307             studyarm * mean_collhorz +
6308             studyarm * mean_collvertical +
6309             bornincanada +
6310             language_1 +
6311             language_2 +
6312             Asian_group +
6313             White_group +
6314             disability_any +
6315             genderidentity +
6316             income +
6317             edhi +
6318             age,
6319             data = datFlu,family=binomial("logit")
6320         )
6321     Anova(rlogF_vi_3, type = "III")
6322     summary(rlogF_vi_3)
6323
6324     emmip(rlogF_vi_3, studyarm ~ mean_indivvertical, cov.reduce = range, type = "response")
6325
6326     ##### + Model 4: Check for interaction viz*edhi without any covariates #####
6327
6328     rlogF_vi_4 <- glm(vaxintent ~ studyarm * edhi, data = datFlu,family=binomial("logit"))
6329     Anova(rlogF_vi_4,type="III")
6330     summary(rlogF_vi_4)
6331
6332     mfvi_4_s <- emmeans(rlogF_vi_4,~studyarm|edhi,type = "response")
6333     mfvi_4_s
6334     confint(pairs(mfvi_4_s,reverse = TRUE))
6335
6336     mfvi_4_e <- emmeans(rlogF_vi_4, ~ edhi|studyarm, type = "response")
6337     confint(pairs(mfvi_4_e,reverse = TRUE))
6338
6339
6340     # Model 5: Check for interaction viz*edhi with adjustment for other covariates
6341
6342     rlogF_vi_5 <-
6343         glm(vaxintent ~ studyarm*edhi +
6344             mean_indivhorz +
6345             mean_indivvertical +
6346             mean_collhorz +

```

```

6347         mean_collvertical +
6348         bornincanada +
6349         language_1 +
6350         language_2 +
6351         Asian_group +
6352         White_group +
6353         disability_any +
6354         genderidentity +
6355         income +
6356         age,
6357         data = datFlu, family=binomial("logit")
6358     )
6359 Anova(rlogF_vi_5, type = "III")
6360 summary(rlogF_vi_5)
6361
6362 mfvi_5_s <- emmeans(rlogF_vi_5, ~studyarm|edhi, type = "response")
6363 mfvi_5_s
6364 confint(pairs(mfvi_5_s, reverse = TRUE))
6365
6366 mfvi_5_e <- emmeans(rlogF_vi_5, ~ edhi|studyarm, type = "response")
6367 confint(pairs(mfvi_5_e, reverse = TRUE))
6368
6369 # Now running models on imputed data.
6370 imprlogF_vi_1 <-
6371     with(data = datFluImputed,
6372         exp = glm(relevel(vaxintent, ref="Low") ~ studyarm, family = binomial("logit")))
6373 combineimprlogF_vi_1 <- pool(imprlogF_vi_1)
6374 summary(combineimprlogF_vi_1)
6375
6376 ##### +++ Logistic regression for C19VaxIntention #####
6377
6378 #Create relevel before model to avoid problems with pairs function.
6379 datGeneric$c19vaxintent <- relevel(datGeneric$c19vaxintent, ref = "Low")
6380 datMeasles$c19vaxintent <- relevel(datMeasles$c19vaxintent, ref = "Low")
6381 datFlu$c19vaxintent <- relevel(datFlu$c19vaxintent, ref = "Low")
6382
6383 ##### ++ Generic #####
6384
6385 ##### + Model 1: Check for direct effects of factors without any covariates #####
6386
6387 options(contrasts=c("contr.sum", "contr.poly"))
6388 rlogG_c19vi_1 <- glm(c19vaxintent ~ studyarm, data =
6389     datGeneric, family=binomial("logit"))
6390 Anova(rlogG_c19vi_1, type="III")
6391 summary(rlogG_c19vi_1)
6392
6393 mgc19vi_1 <- emmeans(rlogG_c19vi_1, ~studyarm, type = "response") #proportions
6394 mgc19vi_1
6395 confint(pairs(mgc19vi_1, reverse = TRUE)) #Odds ratios
6396
6397 # Model 2: Check for direct effects of factors with adjustment for other covariates
6398 rlogG_c19vi_2 <-
6399     glm(c19vaxintent ~ studyarm +
6400         mean_indivhorz +
6401         mean_indivvertical +
6402         mean_collhorz +
6403         mean_collvertical +
6404         bornincanada +
6405         language_1 +
6406         language_2 +
6407         Asian_group +
6408         White_group +
6409         disability_any +
6410         genderidentity +
6411         income +
6412         edhi +
6413         age,
6414         data = datGeneric, family=binomial("logit")
6415     )

```



```

6415 Anova(rlogG_c19vi_2, type = "III")
6416 summary(rlogG_c19vi_2)
6417
6418 mgc19vi_2 <- emmeans(rlogG_c19vi_2,~studyarm,type = "response")
6419 mgc19vi_2
6420 confint(pairs(mgc19vi_2,reverse = TRUE))
6421 pairs(mgc19vi_2,reverse = TRUE, type = "response")
6422
6423 # Model 3: Check for moderating effects of individualism & collectivism with adjustment
for other covariates
6424 rlogG_c19vi_3 <-
6425   glm(c19vaxintent ~
6426     studyarm * mean_indivhorz +
6427     studyarm * mean_indivvertical +
6428     studyarm * mean_collhorz +
6429     studyarm * mean_collvertical +
6430     bornincanada +
6431     language_1 +
6432     language_2 +
6433     Asian_group +
6434     White_group +
6435     disability_any +
6436     genderidentity +
6437     income +
6438     edhi +
6439     age,
6440     data = datGeneric,family=binomial("logit")
6441   )
6442 Anova(rlogG_c19vi_3, type = "III")
6443 summary(rlogG_c19vi_3)
6444
6445 #No interaction with moderator to interpret
6446
6447 ##### + Model 4: Check for interaction viz*edhi without any covariates #####
6448
6449 rlogG_c19vi_4 <- glm(c19vaxintent ~ studyarm * edhi, data =
datGeneric,family=binomial("logit"))
6450 Anova(rlogG_c19vi_4,type="III")
6451 summary(rlogG_c19vi_4)
6452
6453 mgc19vi_4_s <- emmeans(rlogG_c19vi_4,~studyarm|edhi,type = "response")
6454 mgc19vi_4_s
6455 confint(pairs(mgc19vi_4_s,reverse = TRUE))
6456
6457 mgc19vi_4_e <- emmeans(rlogG_c19vi_4, ~ edhi|studyarm, type = "response")
6458 confint(pairs(mgc19vi_4_e,reverse = TRUE))
6459
6460
6461 # Model 5: Check for interaction viz*edhi with adjustment for other covariates
6462
6463 rlogG_c19vi_5 <-
6464   glm(c19vaxintent ~ studyarm*edhi +
6465     mean_indivhorz +
6466     mean_indivvertical +
6467     mean_collhorz +
6468     mean_collvertical +
6469     bornincanada +
6470     language_1 +
6471     language_2 +
6472     Asian_group +
6473     White_group +
6474     disability_any +
6475     genderidentity +
6476     income +
6477     age,
6478     data = datGeneric,family=binomial("logit")
6479   )
6480 Anova(rlogG_c19vi_5, type = "III")
6481 summary(rlogG_c19vi_5)

```

```

6482
6483 mgc19vi_5_s <- emmeans(rlogG_c19vi_5,~studyarm|edhi,type = "response")
6484 mgc19vi_5_s
6485 confint(pairs(mgc19vi_5_s,reverse = TRUE))
6486
6487 mgc19vi_5_e <- emmeans(rlogG_c19vi_5, ~ edhi|studyarm, type = "response")
6488 confint(pairs(mgc19vi_5_e,reverse = TRUE))
6489
6490 ##### ++ Measles #####
6491
6492 ##### + Model 1: Check for direct effects of factors without any covariates #####
6493
6494 options(contrasts=c("contr.sum", "contr.poly"))
6495 rlogM_c19vi_1 <- glm(c19vaxintent ~ studyarm, data =
6496   datMeasles,family=binomial("logit"))
6497 Anova(rlogM_c19vi_1,type="III")
6498 summary(rlogM_c19vi_1)
6499
6500 mmc19vi_1 <- emmeans(rlogM_c19vi_1,~studyarm,type = "response") #proportions
6501 mmc19vi_1
6502 confint(pairs(mmc19vi_1,reverse = TRUE)) #Odds ratios
6503
6504 # Model 2: Check for direct effects of factors with adjustment for other covariates
6505 rlogM_c19vi_2 <-
6506   glm(c19vaxintent ~ studyarm +
6507     mean_indivhorz +
6508     mean_indivvertical +
6509     mean_collhorz +
6510     mean_collvertical +
6511     bornincanada +
6512     language_1 +
6513     language_2 +
6514     Asian_group +
6515     White_group +
6516     disability_any +
6517     genderidentity +
6518     income +
6519     edhi +
6520     age,
6521     data = datMeasles,family=binomial("logit")
6522   )
6523 Anova(rlogM_c19vi_2, type = "III")
6524 summary(rlogM_c19vi_2)
6525
6526 mmc19vi_2 <- emmeans(rlogM_c19vi_2,~studyarm,type = "response")
6527 mmc19vi_2
6528 confint(pairs(mmc19vi_2,reverse = TRUE))
6529
6530 # Model 3: Check for moderating effects of individualism & collectivism with adjustment
6531   for other covariates
6532 rlogM_c19vi_3 <-
6533   glm(c19vaxintent ~
6534     studyarm * mean_indivhorz +
6535     studyarm * mean_indivvertical +
6536     studyarm * mean_collhorz +
6537     studyarm * mean_collvertical +
6538     bornincanada +
6539     language_1 +
6540     language_2 +
6541     Asian_group +
6542     White_group +
6543     disability_any +
6544     genderidentity +
6545     income +
6546     edhi +
6547     age,
6548     data = datMeasles,family=binomial("logit")

```

```

6549 Anova(rlogM_c19vi_3, type = "III")
6550 summary(rlogM_c19vi_3)
6551
6552 #No interaction with moderator to interpret
6553
6554 ##### + Model 4: Check for interaction viz*edhi without any covariates #####
6555
6556 rlogM_c19vi_4 <- glm(c19vaxintent ~ studyarm * edhi, data =
datMeasles,family=binomial("logit"))
6557 Anova(rlogM_c19vi_4,type="III")
6558 summary(rlogM_c19vi_4)
6559
6560 mmc19vi_4_s <- emmeans(rlogM_c19vi_4,~studyarm|edhi,type = "response")
6561 mmc19vi_4_s
6562 confint(pairs(mmc19vi_4_s,reverse = TRUE))
6563
6564 mmc19vi_4_e <- emmeans(rlogM_c19vi_4, ~ edhi|studyarm, type = "response")
6565 confint(pairs(mmc19vi_4_e,reverse = TRUE))
6566
6567
6568 # Model 5: Check for interaction viz*edhi with adjustment for other covariates
6569
6570 rlogM_c19vi_5 <-
6571   glm(c19vaxintent ~ studyarm*edhi +
6572     mean_indivhorz +
6573     mean_indivvertical +
6574     mean_collhorz +
6575     mean_collvertical +
6576     bornincanada +
6577     language_1 +
6578     language_2 +
6579     Asian_group +
6580     White_group +
6581     disability_any +
6582     genderidentity +
6583     income +
6584     age,
6585     data = datMeasles,family=binomial("logit")
6586   )
6587 Anova(rlogM_c19vi_5, type = "III")
6588 summary(rlogM_c19vi_5)
6589
6590 mmc19vi_5_s <- emmeans(rlogM_c19vi_5,~studyarm|edhi,type = "response")
6591 mmc19vi_5_s
6592 confint(pairs(mmc19vi_5_s,reverse = TRUE))
6593
6594 mmc19vi_5_e <- emmeans(rlogM_c19vi_5, ~ edhi|studyarm, type = "response")
6595 confint(pairs(mmc19vi_5_e,reverse = TRUE))
6596
6597
6598
6599 ##### ++ Flu #####
6600
6601 ##### + Model 1: Check for direct effects of factors without any covariates #####
6602
6603 options(contrasts=c("contr.sum", "contr.poly"))
6604 rlogF_c19vi_1 <- glm(c19vaxintent ~ studyarm, data = datFlu,family=binomial("logit"))
6605 Anova(rlogF_c19vi_1,type="III")
6606 summary(rlogF_c19vi_1)
6607
6608 mfc19vi_1 <- emmeans(rlogF_c19vi_1,~studyarm,type = "response") #proportions
6609 mfc19vi_1
6610 confint(pairs(mfc19vi_1,reverse = TRUE)) #Odds ratios
6611
6612
6613 # Model 2: Check for direct effects of factors with adjustment for other covariates
6614 rlogF_c19vi_2 <-
6615   glm(c19vaxintent ~ studyarm +
6616     mean_indivhorz +

```

```

6617         mean_indivvertical +
6618         mean_collhorz +
6619         mean_collvertical +
6620         bornincanada +
6621         language_1 +
6622         language_2 +
6623         Asian_group +
6624         White_group +
6625         disability_any +
6626         genderidentity +
6627         income +
6628         edhi +
6629         age,
6630         data = datFlu,family=binomial("logit")
6631     )
6632     Anova(rlogF_c19vi_2, type = "III")
6633     summary(rlogF_c19vi_2)
6634
6635     mfc19vi_2 <- emmeans(rlogF_c19vi_2,~studyarm,type = "response")
6636     mfc19vi_2
6637     confint(pairs(mfc19vi_2,reverse = TRUE))
6638
6639
6640     # Model 3: Check for moderating effects of individualism & collectivism with adjustment
for other covariates
6641     rlogF_c19vi_3 <-
6642         glm(c19vaxintent ~
6643             studyarm * mean_indivhorz +
6644             studyarm * mean_indivvertical +
6645             studyarm * mean_collhorz +
6646             studyarm * mean_collvertical +
6647             bornincanada +
6648             language_1 +
6649             language_2 +
6650             Asian_group +
6651             White_group +
6652             disability_any +
6653             genderidentity +
6654             income +
6655             edhi +
6656             age,
6657             data = datFlu,family=binomial("logit")
6658         )
6659     Anova(rlogF_c19vi_3, type = "III")
6660     summary(rlogF_c19vi_3)
6661
6662     #No interaction with moderator to interpret
6663
6664     ##### + Model 4: Check for interaction viz*edhi without any covariates #####
6665
6666     rlogF_c19vi_4 <- glm(c19vaxintent ~ studyarm * edhi, data =
datFlu,family=binomial("logit"))
6667     Anova(rlogF_c19vi_4,type="III")
6668     summary(rlogF_c19vi_4)
6669
6670     mfc19vi_4_s <- emmeans(rlogF_c19vi_4,~studyarm|edhi,type = "response")
6671     mfc19vi_4_s
6672     confint(pairs(mfc19vi_4_s,reverse = TRUE))
6673
6674     mfc19vi_4_e <- emmeans(rlogF_c19vi_4, ~ edhi|studyarm, type = "response")
6675     confint(pairs(mfc19vi_4_e,reverse = TRUE))
6676
6677
6678     # Model 5: Check for interaction viz*edhi with adjustment for other covariates
6679
6680     rlogF_c19vi_5 <-
6681         glm(c19vaxintent ~ studyarm*edhi +
6682             mean_indivhorz +
6683             mean_indivvertical +

```

```

6684         mean_collhorz +
6685         mean_collvertical +
6686         bornincanada +
6687         language_1 +
6688         language_2 +
6689         Asian_group +
6690         White_group +
6691         disability_any +
6692         genderidentity +
6693         income +
6694         age,
6695         data = datFlu, family=binomial("logit")
6696     )
6697     Anova(rlogF_c19vi_5, type = "III")
6698     summary(rlogF_c19vi_5)
6699
6700     mfc19vi_5_s <- emmeans(rlogF_c19vi_5, ~studyarm|edhi, type = "response")
6701     mfc19vi_5_s
6702     confint(pairs(mfc19vi_5_s, reverse = TRUE))
6703
6704     mfc19vi_5_e <- emmeans(rlogF_c19vi_5, ~ edhi|studyarm, type = "response")
6705     confint(pairs(mfc19vi_5_e, reverse = TRUE))
6706
6707
6708
6709
6710
6711
6712
6713     ##### +++ Logistic regression for Trust Info #####
6714
6715     #Create relelevel before model to avoid problems with pairs function.
6716     datGeneric$Htrustinfo <- relelevel(datGeneric$Htrustinfo, ref = "No")
6717     datMeasles$Htrustinfo <- relelevel(datMeasles$Htrustinfo, ref = "No")
6718     datFlu$Htrustinfo <- relelevel(datFlu$Htrustinfo, ref = "No")
6719
6720     ##### ++ Generic #####
6721
6722     ##### + Model 1: Check for direct effects of factors without any covariates #####
6723
6724     options(contrasts=c("contr.sum", "contr.poly"))
6725     rlogG_ti_1 <- glm(Htrustinfo ~ studyarm, data = datGeneric, family=binomial("logit"))
6726     Anova(rlogG_ti_1, type="III")
6727     summary(rlogG_ti_1)
6728
6729     mgti_1 <- emmeans(rlogG_ti_1, ~studyarm, type = "response") #proportions
6730     mgti_1
6731     confint(pairs(mgti_1, reverse = TRUE)) #Odds ratios
6732     pairs(mgti_1, reverse = TRUE, type="response")
6733
6734     # Model 2: Check for direct effects of factors with adjustment for other covariates
6735     rlogG_ti_2 <-
6736         glm(Htrustinfo ~ studyarm +
6737             mean_indivhorz +
6738             mean_indivvertical +
6739             mean_collhorz +
6740             mean_collvertical +
6741             bornincanada +
6742             language_1 +
6743             language_2 +
6744             Asian_group +
6745             White_group +
6746             disability_any +
6747             genderidentity +
6748             income +
6749             edhi +
6750             age,
6751             data = datGeneric, family=binomial("logit")
6752         )

```

```

6753 Anova(rlogG_ti_2, type = "III")
6754 summary(rlogG_ti_2)
6755
6756 mgti_2 <- emmeans(rlogG_ti_2,~studyarm,type = "response")
6757 mgti_2
6758 confint(pairs(mgti_2,reverse = TRUE))
6759 pairs(mgti_2,reverse = TRUE,type="response")
6760
6761 # Model 3: Check for moderating effects of individualism & collectivism with adjustment
for other covariates
6762 rlogG_ti_3 <-
6763   glm(Htrustinfo ~
6764     studyarm * mean_indivhorz +
6765     studyarm * mean_indivvertical +
6766     studyarm * mean_collhorz +
6767     studyarm * mean_collvertical +
6768     bornincanada +
6769     language_1 +
6770     language_2 +
6771     Asian_group +
6772     White_group +
6773     disability_any +
6774     genderidentity +
6775     income +
6776     edhi +
6777     age,
6778     data = datGeneric,family=binomial("logit")
6779   )
6780 Anova(rlogG_ti_3, type = "III")
6781 summary(rlogG_ti_3)
6782
6783 #No interaction with moderator to interpret
6784
6785 ##### + Model 4: Check for interaction viz*edhi without any covariates #####
6786
6787 rlogG_ti_4 <- glm(Htrustinfo ~ studyarm * edhi, data =
datGeneric,family=binomial("logit"))
6788 Anova(rlogG_ti_4,type="III")
6789 summary(rlogG_ti_4)
6790
6791 mgti_4_s <- emmeans(rlogG_ti_4,~studyarm|edhi,type = "response")
6792 mgti_4_s
6793 confint(pairs(mgti_4_s,reverse = TRUE))
6794
6795 mgti_4_e <- emmeans(rlogG_ti_4, ~ edhi|studyarm, type = "response")
6796 confint(pairs(mgti_4_e,reverse = TRUE))
6797
6798
6799 # Model 5: Check for interaction viz*edhi with adjustment for other covariates
6800
6801 rlogG_ti_5 <-
6802   glm(Htrustinfo ~ studyarm*edhi +
6803     mean_indivhorz +
6804     mean_indivvertical +
6805     mean_collhorz +
6806     mean_collvertical +
6807     bornincanada +
6808     language_1 +
6809     language_2 +
6810     Asian_group +
6811     White_group +
6812     disability_any +
6813     genderidentity +
6814     income +
6815     age,
6816     data = datGeneric,family=binomial("logit")
6817   )
6818 Anova(rlogG_ti_5, type = "III")
6819 summary(rlogG_ti_5)

```

```

6820
6821 mgti_5_s <- emmeans(rlogG_ti_5,~studyarm|edhi,type = "response")
6822 mgti_5_s
6823 confint(pairs(mgti_5_s,reverse = TRUE))
6824
6825 mgti_5_e <- emmeans(rlogG_ti_5, ~ edhi|studyarm, type = "response")
6826 confint(pairs(mgti_5_e,reverse = TRUE))
6827
6828 # Now running models on imputed data.
6829 imprlogG_ti_1 <-
6830   with(data = datGenericImputed,
6831         exp = glm(relevel(Htrustinfo,ref="No") ~ studyarm,family = binomial("logit")))
6832 combineimprlogG_ti_1 <- pool(imprlogG_ti_1)
6833 summary(combineimprlogG_ti_1)
6834
6835
6836 ##### ++ Measles #####
6837
6838 ##### + Model 1: Check for direct effects of factors without any covariates #####
6839
6840 options(contrasts=c("contr.sum", "contr.poly"))
6841 rlogM_ti_1 <- glm(Htrustinfo ~ studyarm, data = datMeasles,family=binomial("logit"))
6842 Anova(rlogM_ti_1,type="III")
6843 summary(rlogM_ti_1)
6844
6845 mmti_1 <- emmeans(rlogM_ti_1,~studyarm,type = "response") #proportions
6846 mmti_1
6847 confint(pairs(mmti_1,reverse = TRUE)) #Odds ratios
6848 pairs(mmti_1,reverse = TRUE, type = "response")
6849
6850 # Model 2: Check for direct effects of factors with adjustment for other covariates
6851 rlogM_ti_2 <-
6852   glm(Htrustinfo ~ studyarm +
6853       mean_indivhorz +
6854       mean_indivvertical +
6855       mean_collhorz +
6856       mean_collvertical +
6857       bornincanada +
6858       language_1 +
6859       language_2 +
6860       Asian_group +
6861       White_group +
6862       disability_any +
6863       genderidentity +
6864       income +
6865       edhi +
6866       age,
6867       data = datMeasles,family=binomial("logit")
6868   )
6869 Anova(rlogM_ti_2, type = "III")
6870 summary(rlogM_ti_2)
6871
6872 mmti_2 <- emmeans(rlogM_ti_2,~studyarm,type = "response")
6873 mmti_2
6874 confint(pairs(mmti_2,reverse = TRUE))
6875 pairs(mmti_2,reverse = TRUE,type = "response")
6876
6877 # Model 3: Check for moderating effects of individualism & collectivism with adjustment
for other covariates
6878 rlogM_ti_3 <-
6879   glm(Htrustinfo ~
6880       studyarm * mean_indivhorz +
6881       studyarm * mean_indivvertical +
6882       studyarm * mean_collhorz +
6883       studyarm * mean_collvertical +
6884       bornincanada +
6885       language_1 +
6886       language_2 +
6887       Asian_group +

```

```

6888         White_group +
6889         disability_any +
6890         genderidentity +
6891         income +
6892         edhi +
6893         age,
6894         data = datMeasles,family=binomial("logit")
6895     )
6896     Anova(rlogM_ti_3, type = "III")
6897     summary(rlogM_ti_3)
6898
6899     #No interaction with moderator to interpret
6900
6901     ##### + Model 4: Check for interaction viz*edhi without any covariates #####
6902
6903     rlogM_ti_4 <- glm(Htrustinfo ~ studyarm * edhi, data =
6904     datMeasles,family=binomial("logit"))
6905     Anova(rlogM_ti_4,type="III")
6906     summary(rlogM_ti_4)
6907
6908     mmti_4_s <- emmeans(rlogM_ti_4,~studyarm|edhi,type = "response")
6909     mmti_4_s
6910     confint(pairs(mmti_4_s,reverse = TRUE))
6911
6912     mmti_4_e <- emmeans(rlogM_ti_4, ~ edhi|studyarm, type = "response")
6913     confint(pairs(mmti_4_e,reverse = TRUE))
6914
6915     # Model 5: Check for interaction viz*edhi with adjustment for other covariates
6916
6917     rlogM_ti_5 <-
6918         glm(Htrustinfo ~ studyarm*edhi +
6919             mean_indivhorz +
6920             mean_indivvertical +
6921             mean_collhorz +
6922             mean_collvertical +
6923             bornincanada +
6924             language_1 +
6925             language_2 +
6926             Asian_group +
6927             White_group +
6928             disability_any +
6929             genderidentity +
6930             income +
6931             age,
6932             data = datMeasles,family=binomial("logit")
6933         )
6934     Anova(rlogM_ti_5, type = "III")
6935     summary(rlogM_ti_5)
6936
6937     mmti_5_s <- emmeans(rlogM_ti_5,~studyarm|edhi,type = "response")
6938     mmti_5_s
6939     confint(pairs(mmti_5_s,reverse = TRUE))
6940
6941     mmti_5_e <- emmeans(rlogM_ti_5, ~ edhi|studyarm, type = "response")
6942     confint(pairs(mmti_5_e,reverse = TRUE))
6943
6944     # Now running models on imputed data.
6945     #CHANGELOG ASJ: No missing data for htrustinfo in measles, no model with imputation
6946     performed, 21-09-20.
6947
6948
6949     ##### ++ Flu #####
6950
6951     ##### + Model 1: Check for direct effects of factors without any covariates #####
6952
6953     options(contrasts=c("contr.sum", "contr.poly"))
6954     rlogF_ti_1 <- glm(Htrustinfo ~ studyarm, data = datFlu,family=binomial("logit"))

```



```

6955 Anova(rlogF_ti_1,type="III")
6956 summary(rlogF_ti_1)
6957
6958 mfti_1 <- emmeans(rlogF_ti_1,~studyarm,type = "response") #proportions
6959 mfti_1
6960 confint(pairs(mfti_1,reverse = TRUE)) #Odds ratios
6961 pairs(mfti_1,reverse = TRUE,type="response")
6962
6963 # Model 2: Check for direct effects of factors with adjustment for other covariates
6964 rlogF_ti_2 <-
6965   glm(Htrustinfo ~ studyarm +
6966     mean_indivhorz +
6967     mean_indivvertical +
6968     mean_collhorz +
6969     mean_collvertical +
6970     bornincanada +
6971     language_1 +
6972     language_2 +
6973     Asian_group +
6974     White_group +
6975     disability_any +
6976     genderidentity +
6977     income +
6978     edhi +
6979     age,
6980     data = datFlu,family=binomial("logit")
6981   )
6982 Anova(rlogF_ti_2, type = "III")
6983 summary(rlogF_ti_2)
6984
6985 mfti_2 <- emmeans(rlogF_ti_2,~studyarm,type = "response")
6986 mfti_2
6987 confint(pairs(mfti_2,reverse = TRUE))
6988 pairs(mfti_2,reverse = TRUE,type="response")
6989
6990
6991 # Model 3: Check for moderating effects of individualism & collectivism with adjustment
6992 # for other covariates
6993 rlogF_ti_3 <-
6994   glm(Htrustinfo ~
6995     studyarm * mean_indivhorz +
6996     studyarm * mean_indivvertical +
6997     studyarm * mean_collhorz +
6998     studyarm * mean_collvertical +
6999     bornincanada +
7000     language_1 +
7001     language_2 +
7002     Asian_group +
7003     White_group +
7004     disability_any +
7005     genderidentity +
7006     income +
7007     edhi +
7008     age,
7009     data = datFlu,family=binomial("logit")
7010   )
7011 Anova(rlogF_ti_3, type = "III")
7012 summary(rlogF_ti_3)
7013
7014 #No interaction with moderators to interpret
7015
7016 #### + Model 4: Check for interaction viz*edhi without any covariates ####
7017
7018 rlogF_ti_4 <- glm(Htrustinfo ~ studyarm * edhi, data = datFlu,family=binomial("logit"))
7019 Anova(rlogF_ti_4,type="III")
7020 summary(rlogF_ti_4)
7021
7022 mfti_4_s <- emmeans(rlogF_ti_4,~studyarm|edhi,type = "response")
7023 mfti_4_s

```

```

7023 confint(pairs(mfti_4_s,reverse = TRUE))
7024
7025 mfti_4_e <- emmeans(rlogF_ti_4, ~ edhi|studyarm, type = "response")
7026 confint(pairs(mfti_4_e,reverse = TRUE))
7027
7028
7029 # Model 5: Check for interaction viz*edhi with adjustment for other covariates
7030
7031 rlogF_ti_5 <-
7032   glm(Htrustinfo ~ studyarm*edhi +
7033     mean_indivhorz +
7034     mean_indivvertical +
7035     mean_collhorz +
7036     mean_collvertical +
7037     bornincanada +
7038     language_1 +
7039     language_2 +
7040     Asian_group +
7041     White_group +
7042     disability_any +
7043     genderidentity +
7044     income +
7045     age,
7046     data = datFlu,family=binomial("logit")
7047   )
7048 Anova(rlogF_ti_5, type = "III")
7049 summary(rlogF_ti_5)
7050
7051 mfti_5_s <- emmeans(rlogF_ti_5,~studyarm|edhi,type = "response")
7052 mfti_5_s
7053 confint(pairs(mfti_5_s,reverse = TRUE))
7054
7055 mfti_5_e <- emmeans(rlogF_ti_5, ~ edhi|studyarm, type = "response")
7056 confint(pairs(mfti_5_e,reverse = TRUE))
7057
7058 # Now running models on imputed data.
7059 #CHANGELOG ASJ: No missing data for htrustinfo in flu, no model with imputation
7060 #performed, 21-09-20.
7061
7062
7063 ##### +++ Logistic regression for C5 Confidence #####
7064
7065 #Create relevel before model to avoid problems with pairs function.
7066 datGeneric$mean_C5_conf2 <- relevel(as.factor(datGeneric$mean_C5_conf2),ref = "0")
7067 datMeasles$mean_C5_conf2 <- relevel(as.factor(datMeasles$mean_C5_conf2),ref = "0")
7068 datFlu$mean_C5_conf2 <- relevel(as.factor(datFlu$mean_C5_conf2),ref = "0")
7069
7070 ##### ++ Generic #####
7071
7072 ##### + Model 1: Check for direct effects of factors without any covariates #####
7073
7074 options(contrasts=c("contr.sum", "contr.poly"))
7075 rlogG_C5conf_1 <- glm(mean_C5_conf2 ~ studyarm, data =
7076   datGeneric,family=binomial("logit"))
7077 Anova(rlogG_C5conf_1,type="III")
7078 summary(rlogG_C5conf_1)
7079
7079 mgC5conf <- emmeans(rlogG_C5conf_1,~studyarm,type = "response") #proportions
7080 mgC5conf
7081 confint(pairs(mgC5conf,reverse = TRUE)) #Odds ratios
7082
7083 # Model 2: Check for direct effects of factors with adjustment for other covariates
7084 rlogG_C5conf_2 <-
7085   glm(mean_C5_conf2 ~ studyarm +
7086     mean_indivhorz +
7087     mean_indivvertical +
7088     mean_collhorz +
7089     mean_collvertical +

```

```

7090         bornincanada +
7091         language_1 +
7092         language_2 +
7093         Asian_group +
7094         White_group +
7095         disability_any +
7096         genderidentity +
7097         income +
7098         edhi +
7099         age,
7100         data = datGeneric,family=binomial("logit")
7101     )
7102     Anova(rlogG_C5conf_2, type = "III")
7103     summary(rlogG_C5conf_2)
7104
7105     mgC5conf_2 <- emmeans(rlogG_C5conf_2,~studyarm,type = "response")
7106     mgC5conf_2
7107     confint(pairs(mgC5conf_2,reverse = TRUE))
7108
7109
7110     # Model 3: Check for moderating effects of individualism & collectivism with adjustment
for other covariates
7111     rlogG_C5conf_3 <-
7112         glm(mean_C5_conf2 ~
7113             studyarm * mean_indivhorz +
7114             studyarm * mean_indivvertical +
7115             studyarm * mean_collhorz +
7116             studyarm * mean_collvertical +
7117             bornincanada +
7118             language_1 +
7119             language_2 +
7120             Asian_group +
7121             White_group +
7122             disability_any +
7123             genderidentity +
7124             income +
7125             edhi +
7126             age,
7127             data = datGeneric,family=binomial("logit")
7128         )
7129     Anova(rlogG_C5conf_3, type = "III")
7130     summary(rlogG_C5conf_3)
7131
7132     #No interaction with moderator to interpret
7133
7134     #### + Model 4: Check for interaction viz*edhi without any covariates ####
7135
7136     rlogG_C5conf_4 <- glm(mean_C5_conf2 ~ studyarm * edhi, data =
datGeneric,family=binomial("logit"))
7137     Anova(rlogG_C5conf_4,type="III")
7138     summary(rlogG_C5conf_4)
7139
7140     mgC5conf_4_s <- emmeans(rlogG_C5conf_4,~studyarm|edhi,type = "response")
7141     mgC5conf_4_s
7142     confint(pairs(mgC5conf_4_s,reverse = TRUE))
7143
7144     mgC5conf_4_e <- emmeans(rlogG_C5conf_4, ~ edhi|studyarm, type = "response")
7145     confint(pairs(mgC5conf_4_e,reverse = TRUE))
7146
7147
7148     # Model 5: Check for interaction viz*edhi with adjustment for other covariates
7149
7150     rlogG_C5conf_5 <-
7151         glm(mean_C5_conf2 ~ studyarm*edhi +
7152             mean_indivhorz +
7153             mean_indivvertical +
7154             mean_collhorz +
7155             mean_collvertical +
7156             bornincanada +

```

```

7157         language_1 +
7158         language_2 +
7159         Asian_group +
7160         White_group +
7161         disability_any +
7162         genderidentity +
7163         income +
7164         age,
7165         data = datGeneric,family=binomial("logit")
7166     )
7167     Anova(rlogG_C5conf_5, type = "III")
7168     summary(rlogG_C5conf_5)
7169
7170     mgC5conf_5_s <- emmeans(rlogG_C5conf_5,~studyarm|edhi,type = "response")
7171     mgC5conf_5_s
7172     confint(pairs(mgC5conf_5_s,reverse = TRUE))
7173
7174     mgC5conf_5_e <- emmeans(rlogG_C5conf_5, ~ edhi|studyarm, type = "response")
7175     confint(pairs(mgC5conf_5_e,reverse = TRUE))
7176
7177     # Now running models on imputed data.
7178     #CHANGELOG ASJ: No missing data for c5conf, no model with imputation performed, 21-09-20.
7179
7180
7181
7182     ##### ++ Measles #####
7183
7184     ##### + Model 1: Check for direct effects of factors without any covariates #####
7185
7186     options(contrasts=c("contr.sum", "contr.poly"))
7187     rlogM_C5conf_1 <- glm(mean_C5_conf2 ~ studyarm, data =
7188     datMeasles,family=binomial("logit"))
7189     Anova(rlogM_C5conf_1,type="III")
7190     summary(rlogM_C5conf_1)
7191
7192     mmC5conf <- emmeans(rlogM_C5conf_1,~studyarm,type = "response") #proportions
7193     mmC5conf
7194     confint(pairs(mmC5conf,reverse = TRUE)) #Odds ratios
7195
7196     # Model 2: Check for direct effects of factors with adjustment for other covariates
7197     rlogM_C5conf_2 <-
7198     glm(mean_C5_conf2 ~ studyarm +
7199         mean_indivhorz +
7200         mean_indivvertical +
7201         mean_collhorz +
7202         mean_collvertical +
7203         bornincanada +
7204         language_1 +
7205         language_2 +
7206         Asian_group +
7207         White_group +
7208         disability_any +
7209         genderidentity +
7210         income +
7211         edhi +
7212         age,
7213         data = datMeasles,family=binomial("logit")
7214     )
7215     Anova(rlogM_C5conf_2, type = "III")
7216     summary(rlogM_C5conf_2)
7217
7218     mmC5conf_2 <- emmeans(rlogM_C5conf_2,~studyarm,type = "response")
7219     mmC5conf_2
7220     confint(pairs(mmC5conf_2,reverse = TRUE))
7221
7222     # Model 3: Check for moderating effects of individualism & collectivism with adjustment
7223     for other covariates
7224     rlogM_C5conf_3 <-

```

```

7224     glm(mean_C5_conf2 ~
7225         studyarm * mean_indivhorz +
7226         studyarm * mean_indivvertical +
7227         studyarm * mean_collhorz +
7228         studyarm * mean_collvertical +
7229         bornincanada +
7230         language_1 +
7231         language_2 +
7232         Asian_group +
7233         White_group +
7234         disability_any +
7235         genderidentity +
7236         income +
7237         edhi +
7238         age,
7239         data = datMeasles, family=binomial("logit")
7240     )
7241 Anova(rlogM_C5conf_3, type = "III")
7242 summary(rlogM_C5conf_3)
7243
7244 #No interaction with moderator to interpret
7245
7246 ##### + Model 4: Check for interaction viz*edhi without any covariates #####
7247
7248 rlogM_C5conf_4 <- glm(mean_C5_conf2 ~ studyarm * edhi, data =
7249     datMeasles, family=binomial("logit"))
7250 Anova(rlogM_C5conf_4, type="III")
7251 summary(rlogM_C5conf_4)
7252
7253 mmC5conf_4_s <- emmeans(rlogM_C5conf_4, ~studyarm|edhi, type = "response")
7254 confint(pairs(mmC5conf_4_s, reverse = TRUE))
7255
7256 mmC5conf_4_e <- emmeans(rlogM_C5conf_4, ~ edhi|studyarm, type = "response")
7257 confint(pairs(mmC5conf_4_e, reverse = TRUE))
7258
7259
7260 # Model 5: Check for interaction viz*edhi with adjustment for other covariates
7261
7262 rlogM_C5conf_5 <-
7263     glm(mean_C5_conf2 ~ studyarm*edhi +
7264         mean_indivhorz +
7265         mean_indivvertical +
7266         mean_collhorz +
7267         mean_collvertical +
7268         bornincanada +
7269         language_1 +
7270         language_2 +
7271         Asian_group +
7272         White_group +
7273         disability_any +
7274         genderidentity +
7275         income +
7276         age,
7277         data = datMeasles, family=binomial("logit")
7278     )
7279 Anova(rlogM_C5conf_5, type = "III")
7280 summary(rlogM_C5conf_5)
7281
7282 mmC5conf_5_s <- emmeans(rlogM_C5conf_5, ~studyarm|edhi, type = "response")
7283 mmC5conf_5_s
7284 confint(pairs(mmC5conf_5_s, reverse = TRUE))
7285
7286 mmC5conf_5_e <- emmeans(rlogM_C5conf_5, ~ edhi|studyarm, type = "response")
7287 confint(pairs(mmC5conf_5_e, reverse = TRUE))
7288
7289 # Now running models on imputed data.
7290 #CHANGELOG ASJ: No missing data for c5conf, no model with imputation performed, 21-09-20.
7291

```

```

7292 ##### ++ Flu #####
7293
7294
7295 ##### + Model 1: Check for direct effects of factors without any covariates #####
7296
7297 options(contrasts=c("contr.sum", "contr.poly"))
7298 rlogF_C5conf_1 <- glm(mean_C5_conf2 ~ studyarm, data = datFlu, family=binomial("logit"))
7299 Anova(rlogF_C5conf_1, type="III")
7300 summary(rlogF_C5conf_1)
7301
7302 mfC5conf_1 <- emmeans(rlogF_C5conf_1, ~studyarm, type = "response") #proportions
7303 mfC5conf_1
7304 confint(pairs(mfC5conf_1, reverse = TRUE)) #Odds ratios
7305
7306 # Model 2: Check for direct effects of factors with adjustment for other covariates
7307 rlogF_C5conf_2 <-
7308   glm(mean_C5_conf2 ~ studyarm +
7309     mean_indivhorz +
7310     mean_indivvertical +
7311     mean_collhorz +
7312     mean_collvertical +
7313     bornincanada +
7314     language_1 +
7315     language_2 +
7316     Asian_group +
7317     White_group +
7318     disability_any +
7319     genderidentity +
7320     income +
7321     edhi +
7322     age,
7323     data = datFlu, family=binomial("logit")
7324   )
7325 Anova(rlogF_C5conf_2, type = "III")
7326 summary(rlogF_C5conf_2)
7327
7328 mfC5conf_2 <- emmeans(rlogF_C5conf_2, ~studyarm, type = "response")
7329 mfC5conf_2
7330 confint(pairs(mfC5conf_2, reverse = TRUE))
7331
7332
7333 # Model 3: Check for moderating effects of individualism & collectivism with adjustment
7334 for other covariates
7335 rlogF_C5conf_3 <-
7336   glm(mean_C5_conf2 ~
7337     studyarm * mean_indivhorz +
7338     studyarm * mean_indivvertical +
7339     studyarm * mean_collhorz +
7340     studyarm * mean_collvertical +
7341     bornincanada +
7342     language_1 +
7343     language_2 +
7344     Asian_group +
7345     White_group +
7346     disability_any +
7347     genderidentity +
7348     income +
7349     edhi +
7350     age,
7351     data = datFlu, family=binomial("logit")
7352   )
7353 Anova(rlogF_C5conf_3, type = "III")
7354 summary(rlogF_C5conf_3)
7355
7356 emmip(rlogF_C5conf_3, studyarm ~ mean_indivvertical, cov.reduce = range, type =
7357 "response")
7358
7359 ##### + Model 4: Check for interaction viz*edhi without any covariates #####

```

```

7359
7360 rlogF_C5conf_4 <- glm(mean_C5_conf2 ~ studyarm * edhi, data =
datFlu,family=binomial("logit"))
7361 Anova(rlogF_C5conf_4,type="III")
7362 summary(rlogF_C5conf_4)
7363
7364 mfC5conf_4_s <- emmeans(rlogF_C5conf_4,~studyarm|edhi,type = "response")
7365 mfC5conf_4_s
7366 confint(pairs(mfC5conf_4_s,reverse = TRUE))
7367
7368 mfC5conf_4_e <- emmeans(rlogF_C5conf_4, ~ edhi|studyarm, type = "response")
7369 confint(pairs(mfC5conf_4_e,reverse = TRUE))
7370
7371
7372 # Model 5: Check for interaction viz*edhi with adjustment for other covariates
7373
7374 rlogF_C5conf_5 <-
7375   glm(mean_C5_conf2 ~ studyarm*edhi +
7376     mean_indivhorz +
7377     mean_indivvertical +
7378     mean_collhorz +
7379     mean_collvertical +
7380     bornincanada +
7381     language_1 +
7382     language_2 +
7383     Asian_group +
7384     White_group +
7385     disability_any +
7386     genderidentity +
7387     income +
7388     age,
7389     data = datFlu,family=binomial("logit")
7390   )
7391 Anova(rlogF_C5conf_5, type = "III")
7392 summary(rlogF_C5conf_5)
7393
7394 mfC5conf_5_s <- emmeans(rlogF_C5conf_5,~studyarm|edhi,type = "response")
7395 mfC5conf_5_s
7396 confint(pairs(mfC5conf_5_s,reverse = TRUE))
7397
7398 mfC5conf_5_e <- emmeans(rlogF_C5conf_5, ~ edhi|studyarm, type = "response")
7399 confint(pairs(mfC5conf_5_e,reverse = TRUE))
7400
7401 # Now running models on imputed data.
7402 #CHANGELOG ASJ: No missing data for c5conf, no model with imputation performed, 21-09-20.
7403
7404 ##### +++ Logistic regression for C5 Complacency #####
7405
7406 #Create relevel before model to avoid problems with pairs function.
7407 datGeneric$mean_C5_comp2 <- relevel(as.factor(datGeneric$mean_C5_comp2),ref = "0")
7408 datMeasles$mean_C5_comp2 <- relevel(as.factor(datMeasles$mean_C5_comp2),ref = "0")
7409 datFlu$mean_C5_comp2 <- relevel(as.factor(datFlu$mean_C5_comp2),ref = "0")
7410
7411 ##### ++ Generic #####
7412
7413 ##### + Model 1: Check for direct effects of factors without any covariates #####
7414
7415 options(contrasts=c("contr.sum", "contr.poly"))
7416 rlogG_C5comp_1 <- glm(mean_C5_comp2 ~ studyarm, data =
datGeneric,family=binomial("logit"))
7417 Anova(rlogG_C5comp_1,type="III")
7418 summary(rlogG_C5comp_1)
7419
7420 mgC5comp_1 <- emmeans(rlogG_C5comp_1,~studyarm,type = "response") #proportions
7421 mgC5comp_1
7422 confint(pairs(mgC5comp_1,reverse = TRUE)) #Odds ratios
7423 pairs(mgC5comp_1,reverse = TRUE)
7424
7425 # Model2: Check for direct effects of factors with adjustment for other covariates

```

```

7426 rlogG_C5comp_2 <-
7427   glm(mean_C5_comp2 ~ studyarm +
7428     mean_indivhorz +
7429     mean_indivvertical +
7430     mean_collhorz +
7431     mean_collvertical +
7432     bornincanada +
7433     language_1 +
7434     language_2 +
7435     Asian_group +
7436     White_group +
7437     disability_any +
7438     genderidentity +
7439     income +
7440     edhi +
7441     age,
7442     data = datGeneric, family=binomial("logit")
7443   )
7444 Anova(rlogG_C5comp_2, type = "III")
7445 summary(rlogG_C5comp_2)
7446
7447 mgC5comp_2 <- emmeans(rlogG_C5comp_2, ~studyarm, type = "response")
7448 mgC5comp_2
7449 confint(pairs(mgC5comp_2, reverse = TRUE))
7450 pairs(mgC5comp_2, reverse = TRUE)
7451
7452 # Model 3: Check for moderating effects of individualism & collectivism with adjustment
for other covariates
7453 rlogG_C5comp_3 <-
7454   glm(mean_C5_comp2 ~
7455     studyarm * mean_indivhorz +
7456     studyarm * mean_indivvertical +
7457     studyarm * mean_collhorz +
7458     studyarm * mean_collvertical +
7459     bornincanada +
7460     language_1 +
7461     language_2 +
7462     Asian_group +
7463     White_group +
7464     disability_any +
7465     genderidentity +
7466     income +
7467     edhi +
7468     age,
7469     data = datGeneric, family=binomial("logit")
7470   )
7471 Anova(rlogG_C5comp_3, type = "III")
7472 summary(rlogG_C5comp_3)
7473
7474 #No interaction with moderator to interpret
7475
7476 ##### + Model 4: Check for interaction viz*edhi without any covariates #####
7477
7478 rlogG_C5comp_4 <- glm(mean_C5_comp2 ~ studyarm * edhi, data =
datGeneric, family=binomial("logit"))
7479 Anova(rlogG_C5comp_4, type="III")
7480 summary(rlogG_C5comp_4)
7481
7482 mgC5comp_4_s <- emmeans(rlogG_C5comp_4, ~studyarm|edhi, type = "response")
7483 mgC5comp_4_s
7484 confint(pairs(mgC5comp_4_s, reverse = TRUE))
7485 pairs(mgC5comp_4_s, reverse = TRUE)
7486
7487 mgC5comp_4_e <- emmeans(rlogG_C5comp_4, ~ edhi|studyarm, type = "response")
7488 confint(pairs(mgC5comp_4_e, reverse = TRUE))
7489 pairs(mgC5comp_4_e, reverse = TRUE)
7490
7491 # Model 5: Check for interaction viz*edhi with adjustment for other covariates
7492

```



```

7493 rlogG_C5comp_5 <-
7494   glm(mean_C5_comp2 ~ studyarm*edhi +
7495       mean_indivhorz +
7496       mean_indivvertical +
7497       mean_collhorz +
7498       mean_collvertical +
7499       bornincanada +
7500       language_1 +
7501       language_2 +
7502       Asian_group +
7503       White_group +
7504       disability_any +
7505       genderidentity +
7506       income +
7507       age,
7508       data = datGeneric,family=binomial("logit")
7509   )
7510 Anova(rlogG_C5comp_5, type = "III")
7511 summary(rlogG_C5comp_5)
7512
7513 mgC5comp_5_s <- emmeans(rlogG_C5comp_5,~studyarm|edhi,type = "response")
7514 mgC5comp_5_s
7515 confint(pairs(mgC5comp_5_s,reverse = TRUE))
7516
7517 mgC5comp_5_e <- emmeans(rlogG_C5comp_5, ~ edhi|studyarm, type = "response")
7518 confint(pairs(mgC5comp_5_e,reverse = TRUE))
7519
7520 # Now running models on imputed data.
7521 #CHANGELOG ASJ: No missing data for c5conf, no model with imputation performed, 21-09-20.
7522
7523
7524 ##### ++ Measles #####
7525
7526 ##### + Model 1: Check for direct effects of factors without any covariates #####
7527
7528 options(contrasts=c("contr.sum", "contr.poly"))
7529 rlogM_C5comp_1 <- glm(mean_C5_comp2 ~ studyarm, data =
7530   datMeasles,family=binomial("logit"))
7531 Anova(rlogM_C5comp_1,type="III")
7532 summary(rlogM_C5comp_1)
7533
7534 mmC5comp_1 <- emmeans(rlogM_C5comp_1,~studyarm,type = "response") #proportions
7535 mmC5comp_1
7536 confint(pairs(mmC5comp_1,reverse = TRUE)) #Odds ratios
7537
7538 # Model 2: Check for direct effects of factors with adjustment for other covariates
7539 rlogM_C5comp_2 <-
7540   glm(mean_C5_comp2 ~ studyarm +
7541       mean_indivhorz +
7542       mean_indivvertical +
7543       mean_collhorz +
7544       mean_collvertical +
7545       bornincanada +
7546       language_1 +
7547       language_2 +
7548       Asian_group +
7549       White_group +
7550       disability_any +
7551       genderidentity +
7552       income +
7553       edhi +
7554       age,
7555       data = datMeasles,family=binomial("logit")
7556   )
7557 Anova(rlogM_C5comp_2, type = "III")
7558 summary(rlogM_C5comp_2)
7559
7560 mmC5comp_2 <- emmeans(rlogM_C5comp_2,~studyarm,type = "response")
7561 mmC5comp_2

```

```

7561 confint(pairs(mmC5comp_2,reverse = TRUE))
7562
7563
7564 # Model 3: Check for moderating effects of individualism & collectivism with adjustment
for other covariates
7565 rlogM_C5comp_3 <-
7566   glm(mean_C5_comp2 ~
7567     studyarm * mean_indivhorz +
7568     studyarm * mean_indivvertical +
7569     studyarm * mean_collhorz +
7570     studyarm * mean_collvertical +
7571     bornincanada +
7572     language_1 +
7573     language_2 +
7574     Asian_group +
7575     White_group +
7576     disability_any +
7577     genderidentity +
7578     income +
7579     edhi +
7580     age,
7581     data = datMeasles,family=binomial("logit")
7582   )
7583 Anova(rlogM_C5comp_3, type = "III")
7584 summary(rlogM_C5comp_3)
7585
7586 #No interaction with moderator to interpret
7587
7588 ##### + Model 4: Check for interaction viz*edhi without any covariates #####
7589
7590 rlogM_C5comp_4 <- glm(mean_C5_comp2 ~ studyarm * edhi, data =
datMeasles,family=binomial("logit"))
7591 Anova(rlogM_C5comp_4,type="III")
7592 summary(rlogM_C5comp_4)
7593
7594 mmC5comp_4_s <- emmeans(rlogM_C5comp_4,~studyarm|edhi,type = "response")
7595 mmC5comp_4_s
7596 confint(pairs(mmC5comp_4_s,reverse = TRUE))
7597
7598 mmC5comp_4_e <- emmeans(rlogM_C5comp_4, ~ edhi|studyarm, type = "response")
7599 confint(pairs(mmC5comp_4_e,reverse = TRUE))
7600
7601
7602 # Model 5: Check for interaction viz*edhi with adjustment for other covariates
7603
7604 rlogM_C5comp_5 <-
7605   glm(mean_C5_comp2 ~ studyarm*edhi +
7606     mean_indivhorz +
7607     mean_indivvertical +
7608     mean_collhorz +
7609     mean_collvertical +
7610     bornincanada +
7611     language_1 +
7612     language_2 +
7613     Asian_group +
7614     White_group +
7615     disability_any +
7616     genderidentity +
7617     income +
7618     age,
7619     data = datMeasles,family=binomial("logit")
7620   )
7621 Anova(rlogM_C5comp_5, type = "III")
7622 summary(rlogM_C5comp_5)
7623
7624 mmC5comp_5_s <- emmeans(rlogM_C5comp_5,~studyarm|edhi,type = "response")
7625 mmC5comp_5_s
7626 confint(pairs(mmC5comp_5_s,reverse = TRUE))
7627

```

```

7628 mmC5comp_5_e <- emmeans(rlogM_C5comp_5, ~ edhi|studyarm, type = "response")
7629 confint(pairs(mmC5comp_5_e,reverse = TRUE))
7630
7631 # Now running models on imputed data.
7632 #CHANGELOG ASJ: No missing data for c5conf, no model with imputation performed, 21-09-20.
7633
7634
7635 ##### ++ Flu #####
7636
7637 ##### + Model 1: Check for direct effects of factors without any covariates #####
7638
7639 options(contrasts=c("contr.sum", "contr.poly"))
7640 rlogF_C5comp_1 <- glm(mean_C5_comp2 ~ studyarm, data = datFlu,family=binomial("logit"))
7641 Anova(rlogF_C5comp_1,type="III")
7642 summary(rlogF_C5comp_1)
7643
7644 mfC5comp_1 <- emmeans(rlogF_C5comp_1,~studyarm,type = "response") #proportions
7645 mfC5comp_1
7646 confint(pairs(mfC5comp_1,reverse = TRUE)) #Odds ratios
7647 pairs(mfC5comp_1,reverse = TRUE)
7648
7649 # Model 2: Check for direct effects of factors with adjustment for other covariates
7650 rlogF_C5comp_2 <-
7651   glm(mean_C5_comp2 ~ studyarm +
7652     mean_indivhorz +
7653     mean_indivvertical +
7654     mean_collhorz +
7655     mean_collvertical +
7656     bornincanada +
7657     language_1 +
7658     language_2 +
7659     Asian_group +
7660     White_group +
7661     disability_any +
7662     genderidentity +
7663     income +
7664     edhi +
7665     age,
7666     data = datFlu,family=binomial("logit")
7667   )
7668 Anova(rlogF_C5comp_2, type = "III")
7669 summary(rlogF_C5comp_2)
7670
7671 mfC5comp_2 <- emmeans(rlogF_C5comp_2,~studyarm,type = "response")
7672 mfC5comp_2
7673 confint(pairs(mfC5comp_2,reverse = TRUE))
7674 pairs(mfC5comp_2,reverse = TRUE)
7675
7676 # Model 3: Check for moderating effects of individualism & collectivism with adjustment
for other covariates
7677 rlogF_C5comp_3 <-
7678   glm(mean_C5_comp2 ~
7679     studyarm * mean_indivhorz +
7680     studyarm * mean_indivvertical +
7681     studyarm * mean_collhorz +
7682     studyarm * mean_collvertical +
7683     bornincanada +
7684     language_1 +
7685     language_2 +
7686     Asian_group +
7687     White_group +
7688     disability_any +
7689     genderidentity +
7690     income +
7691     edhi +
7692     age,
7693     data = datFlu,family=binomial("logit")
7694   )
7695 Anova(rlogF_C5comp_3, type = "III")

```

```

7696 summary(rlogF_C5comp_3)
7697
7698 emmip(rlogF_C5comp_3, studyarm ~ mean_collhorz, cov.reduce = range, type = "response")
7699
7700
7701 ##### + Model 4: Check for interaction viz*edhi without any covariates #####
7702
7703 rlogF_C5comp_4 <- glm(mean_C5_comp2 ~ studyarm * edhi, data =
datFlu, family=binomial("logit"))
7704 Anova(rlogF_C5comp_4, type="III")
7705 summary(rlogF_C5comp_4)
7706
7707 mfC5comp_4_s <- emmeans(rlogF_C5comp_4, ~studyarm|edhi, type = "response")
7708 mfC5comp_4_s
7709 confint(pairs(mfC5comp_4_s, reverse = TRUE))
7710
7711 mfC5comp_4_e <- emmeans(rlogF_C5comp_4, ~ edhi|studyarm, type = "response")
7712 confint(pairs(mfC5comp_4_e, reverse = TRUE))
7713
7714
7715 # Model 5: Check for interaction viz*edhi with adjustment for other covariates
7716
7717 rlogF_C5comp_5 <-
7718   glm(mean_C5_comp2 ~ studyarm*edhi +
7719     mean_indivhorz +
7720     mean_indivvertical +
7721     mean_collhorz +
7722     mean_collvertical +
7723     bornincanada +
7724     language_1 +
7725     language_2 +
7726     Asian_group +
7727     White_group +
7728     disability_any +
7729     genderidentity +
7730     income +
7731     age,
7732     data = datFlu, family=binomial("logit")
7733   )
7734 Anova(rlogF_C5comp_5, type = "III")
7735 summary(rlogF_C5comp_5)
7736
7737 mfC5comp_5_s <- emmeans(rlogF_C5comp_5, ~studyarm|edhi, type = "response")
7738 mfC5comp_5_s
7739 confint(pairs(mfC5comp_5_s, reverse = TRUE))
7740
7741 mfC5comp_5_e <- emmeans(rlogF_C5comp_5, ~ edhi|studyarm, type = "response")
7742 confint(pairs(mfC5comp_5_e, reverse = TRUE))
7743
7744 # Now running models on imputed data.
7745 #CHANGELOG ASJ: No missing data for c5conf, no model with imputation performed, 21-09-20.
7746
7747
7748 ##### +++ Logistic regression for C5 Constraints #####
7749
7750 #Create relevel before model to avoid problems with pairs function.
7751 datGeneric$mean_C5_cons2 <- relevel(as.factor(datGeneric$mean_C5_cons2), ref = "0")
7752 datMeasles$mean_C5_cons2 <- relevel(as.factor(datMeasles$mean_C5_cons2), ref = "0")
7753 datFlu$mean_C5_cons2 <- relevel(as.factor(datFlu$mean_C5_cons2), ref = "0")
7754
7755 ##### ++ Generic #####
7756
7757 ##### + Model 1: Check for direct effects of factors without any covariates #####
7758
7759 options(contrasts=c("contr.sum", "contr.poly"))
7760 rlogG_C5cons_1 <- glm(mean_C5_cons2 ~ studyarm, data =
datGeneric, family=binomial("logit"))
7761 Anova(rlogG_C5cons_1, type="III")
7762 summary(rlogG_C5cons_1)

```

```

7763 mgC5cons_1 <- emmeans(rlogG_C5cons_1,~studyarm,type = "response") #proportions
7764 mgC5cons_1
7765 confint(pairs(mgC5cons_1,reverse = TRUE)) #Odds ratios
7766 pairs(mgC5cons_1,reverse = TRUE)
7767
7768
7769 # Model 2: Check for direct effects of factors with adjustment for other covariates
7770 rlogG_C5cons_2 <-
7771   glm(mean_C5_cons2 ~ studyarm +
7772     mean_indivhorz +
7773     mean_indivvertical +
7774     mean_collhorz +
7775     mean_collvertical +
7776     bornincanada +
7777     language_1 +
7778     language_2 +
7779     Asian_group +
7780     White_group +
7781     disability_any +
7782     genderidentity +
7783     income +
7784     edhi +
7785     age,
7786     data = datGeneric,family=binomial("logit")  )
7787 Anova(rlogG_C5cons_2, type = "III")
7788 summary(rlogG_C5cons_2)
7789
7790 mgC5cons_2 <- emmeans(rlogG_C5cons_2,~studyarm,type = "response")
7791 mgC5cons_2
7792 confint(pairs(mgC5cons_2,reverse = TRUE))
7793 pairs(mgC5cons_2,reverse = TRUE)
7794
7795 # Model 3: Check for moderating effects of individualism & collectivism with adjustment
for other covariates
7796 rlogG_C5cons_3 <-
7797   glm(mean_C5_cons2 ~
7798     studyarm * mean_indivhorz +
7799     studyarm * mean_indivvertical +
7800     studyarm * mean_collhorz +
7801     studyarm * mean_collvertical +
7802     bornincanada +
7803     language_1 +
7804     language_2 +
7805     Asian_group +
7806     White_group +
7807     disability_any +
7808     genderidentity +
7809     income +
7810     edhi +
7811     age,
7812     data = datGeneric,family=binomial("logit")
7813   )
7814 Anova(rlogG_C5cons_3, type = "III")
7815 summary(rlogG_C5cons_3)
7816
7817 emmip(rlogG_C5cons_3, studyarm ~ mean_indivvertical, cov.reduce = range, type =
"response")
7818
7819
7820 ##### + Model 4: Check for interaction viz*edhi without any covariates #####
7821
7822 rlogG_C5cons_4 <- glm(mean_C5_cons2 ~ studyarm * edhi, data =
datGeneric,family=binomial("logit"))
7823 Anova(rlogG_C5cons_4,type="III")
7824 summary(rlogG_C5cons_4)
7825
7826 mgC5cons_4_s <- emmeans(rlogG_C5cons_4,~studyarm|edhi,type = "response")
7827 mgC5cons_4_s
7828 confint(pairs(mgC5cons_4_s,reverse = TRUE))

```

```

7829
7830 mgC5cons_4_e <- emmeans(rlogG_C5cons_4, ~ edhi|studyarm, type = "response")
7831 confint(pairs(mgC5cons_4_e,reverse = TRUE))
7832
7833 # Model 5: Check for interaction viz*edhi with adjustment for other covariates
7834
7835 rlogG_C5cons_5 <-
7836   glm(mean_C5_cons2 ~ studyarm*edhi +
7837     mean_indivhorz +
7838     mean_indivvertical +
7839     mean_collhorz +
7840     mean_collvertical +
7841     bornincanada +
7842     language_1 +
7843     language_2 +
7844     Asian_group +
7845     White_group +
7846     disability_any +
7847     genderidentity +
7848     income +
7849     age,
7850     data = datGeneric,family=binomial("logit")
7851   )
7852 Anova(rlogG_C5cons_5, type = "III")
7853 summary(rlogG_C5cons_5)
7854
7855 mgC5cons_5_s <- emmeans(rlogG_C5cons_5,~studyarm|edhi,type = "response")
7856 mgC5cons_5_s
7857 confint(pairs(mgC5cons_5_s,reverse = TRUE))
7858
7859 mgC5cons_5_e <- emmeans(rlogG_C5cons_5, ~ edhi|studyarm, type = "response")
7860 confint(pairs(mgC5cons_5_e,reverse = TRUE))
7861
7862 # Now running models on imputed data.
7863 #CHANGELOG ASJ: No missing data for c5conf, no model with imputation performed, 21-09-20.
7864
7865
7866 ##### ++ Measles #####
7867
7868 ##### + Model 1: Check for direct effects of factors without any covariates #####
7869
7870 options(contrasts=c("contr.sum", "contr.poly"))
7871 rlogM_C5cons_1 <- glm(mean_C5_cons2 ~ studyarm, data =
7872   datMeasles,family=binomial("logit"))
7873 Anova(rlogM_C5cons_1,type="III")
7874 summary(rlogM_C5cons_1)
7875
7876 mmC5cons_1 <- emmeans(rlogM_C5cons_1,~studyarm,type = "response") #proportions
7877 mmC5cons_1
7878 confint(pairs(mmC5cons_1,reverse = TRUE)) #Odds ratios
7879
7880 # Model 2: Check for direct effects of factors with adjustment for other covariates
7881 rlogM_C5cons_2 <-
7882   glm(mean_C5_cons2 ~ studyarm +
7883     mean_indivhorz +
7884     mean_indivvertical +
7885     mean_collhorz +
7886     mean_collvertical +
7887     bornincanada +
7888     language_1 +
7889     language_2 +
7890     Asian_group +
7891     White_group +
7892     disability_any +
7893     genderidentity +
7894     income +
7895     edhi +
7896     age,
7897     data = datMeasles,family=binomial("logit")

```

```

7897     )
7898     Anova(rlogM_C5cons_2, type = "III")
7899     summary(rlogM_C5cons_2)
7900
7901     mmC5cons_2 <- emmeans(rlogM_C5cons_2, ~studyarm, type = "response")
7902     mmC5cons_2
7903     confint(pairs(mmC5cons_2, reverse = TRUE))
7904
7905
7906     # Model 3: Check for moderating effects of individualism & collectivism with adjustment
for other covariates
7907     rlogM_C5cons_3 <-
7908         glm(mean_C5_cons2 ~
7909             studyarm * mean_indivhorz +
7910             studyarm * mean_indivvertical +
7911             studyarm * mean_collhorz +
7912             studyarm * mean_collvertical +
7913             bornincanada +
7914             language_1 +
7915             language_2 +
7916             Asian_group +
7917             White_group +
7918             disability_any +
7919             genderidentity +
7920             income +
7921             edhi +
7922             age,
7923             data = datMeasles, family=binomial("logit")
7924         )
7925     Anova(rlogM_C5cons_3, type = "III")
7926     summary(rlogM_C5cons_3)
7927
7928     emmip(rlogM_C5cons_3, studyarm ~ mean_indivvertical, cov.reduce = range, type =
"response")
7929
7930
7931     ##### + Model 4: Check for interaction viz*edhi without any covariates #####
7932
7933     rlogM_C5cons_4 <- glm(mean_C5_cons2 ~ studyarm * edhi, data =
datMeasles, family=binomial("logit"))
7934     Anova(rlogM_C5cons_4, type="III")
7935     summary(rlogM_C5cons_4)
7936
7937     mmC5cons_4_s <- emmeans(rlogM_C5cons_4, ~studyarm|edhi, type = "response")
7938     mmC5cons_4_s
7939     confint(pairs(mmC5cons_4_s, reverse = TRUE))
7940
7941     mmC5cons_4_e <- emmeans(rlogM_C5cons_4, ~ edhi|studyarm, type = "response")
7942     confint(pairs(mmC5cons_4_e, reverse = TRUE))
7943
7944
7945     # Model 5: Check for interaction viz*edhi with adjustment for other covariates
7946
7947     rlogM_C5cons_5 <-
7948         glm(mean_C5_cons2 ~ studyarm*edhi +
7949             mean_indivhorz +
7950             mean_indivvertical +
7951             mean_collhorz +
7952             mean_collvertical +
7953             bornincanada +
7954             language_1 +
7955             language_2 +
7956             Asian_group +
7957             White_group +
7958             disability_any +
7959             genderidentity +
7960             income +
7961             age,
7962             data = datMeasles, family=binomial("logit")

```

```

7963     )
7964     Anova(rlogM_C5cons_5, type = "III")
7965     summary(rlogM_C5cons_5)
7966
7967     mmC5cons_5_s <- emmeans(rlogM_C5cons_5, ~studyarm|edhi, type = "response")
7968     mmC5cons_5_s
7969     confint(pairs(mmC5cons_5_s, reverse = TRUE))
7970
7971     mmC5cons_5_e <- emmeans(rlogM_C5cons_5, ~ edhi|studyarm, type = "response")
7972     confint(pairs(mmC5cons_5_e, reverse = TRUE))
7973
7974     # Now running models on imputed data.
7975     #CHANGELOG ASJ: No missing data for c5conf, no model with imputation performed, 21-09-20.
7976
7977
7978     #### ++ Flu ####
7979
7980     #### + Model 1: Check for direct effects of factors without any covariates ####
7981
7982     options(contrasts=c("contr.sum", "contr.poly"))
7983     rlogF_C5cons_1 <- glm(mean_C5_cons2 ~ studyarm, data = datFlu, family=binomial("logit"))
7984     Anova(rlogF_C5cons_1, type="III")
7985     summary(rlogF_C5cons_1)
7986
7987     mfC5cons_1 <- emmeans(rlogF_C5cons_1, ~studyarm, type = "response") #proportions
7988     mfC5cons_1
7989     confint(pairs(mfC5cons_1, reverse = TRUE)) #Odds ratios
7990
7991     # Model 2: Check for direct effects of factors with adjustment for other covariates
7992     rlogF_C5cons_2 <-
7993         glm(mean_C5_cons2 ~ studyarm +
7994             mean_indivhorz +
7995             mean_indivvertical +
7996             mean_collhorz +
7997             mean_collvertical +
7998             bornincanada +
7999             language_1 +
8000             language_2 +
8001             Asian_group +
8002             White_group +
8003             disability_any +
8004             genderidentity +
8005             income +
8006             edhi +
8007             age,
8008             data = datFlu, family=binomial("logit")
8009         )
8010     Anova(rlogF_C5cons_2, type = "III")
8011     summary(rlogF_C5cons_2)
8012
8013     mfC5cons_2 <- emmeans(rlogF_C5cons_2, ~studyarm, type = "response")
8014     mfC5cons_2
8015     confint(pairs(mfC5cons_2, reverse = TRUE))
8016     pairs(mfC5cons_2, reverse = TRUE)
8017
8018     # Model 3: Check for moderating effects of individualism & collectivism with adjustment
8019     # for other covariates
8020     rlogF_C5cons_3 <-
8021         glm(mean_C5_cons2 ~
8022             studyarm * mean_indivhorz +
8023             studyarm * mean_indivvertical +
8024             studyarm * mean_collhorz +
8025             studyarm * mean_collvertical +
8026             bornincanada +
8027             language_1 +
8028             language_2 +
8029             Asian_group +
8030             White_group +
8031             disability_any +

```



```

8031         genderidentity +
8032         income +
8033         edhi +
8034         age,
8035         data = datFlu,family=binomial("logit")
8036     )
8037     Anova(rlogF_C5cons_3, type = "III")
8038     summary(rlogF_C5cons_3)
8039
8040     emmip(rlogF_C5cons_3, studyarm ~ mean_collhorz, cov.reduce = range, type = "response")
8041
8042
8043     ##### + Model 4: Check for interaction viz*edhi without any covariates #####
8044
8045     rlogF_C5cons_4 <- glm(mean_C5_cons2 ~ studyarm * edhi, data =
8046     datFlu,family=binomial("logit"))
8047     Anova(rlogF_C5cons_4,type="III")
8048     summary(rlogF_C5cons_4)
8049
8049     mfC5cons_4_s <- emmeans(rlogF_C5cons_4,~studyarm|edhi,type = "response")
8050     mfC5cons_4_s
8051     confint(pairs(mfC5cons_4_s,reverse = TRUE))
8052
8053     mfC5cons_4_e <- emmeans(rlogF_C5cons_4, ~ edhi|studyarm, type = "response")
8054     confint(pairs(mfC5cons_4_e,reverse = TRUE))
8055
8056
8057     # Model 5: Check for interaction viz*edhi with adjustment for other covariates
8058
8059     rlogF_C5cons_5 <-
8060         glm(mean_C5_cons2 ~ studyarm*edhi +
8061             mean_indivhorz +
8062             mean_indivvertical +
8063             mean_collhorz +
8064             mean_collvertical +
8065             bornincanada +
8066             language_1 +
8067             language_2 +
8068             Asian_group +
8069             White_group +
8070             disability_any +
8071             genderidentity +
8072             income +
8073             age,
8074             data = datFlu,family=binomial("logit")
8075         )
8076     Anova(rlogF_C5cons_5, type = "III")
8077     summary(rlogF_C5cons_5)
8078
8079     mfC5cons_5_s <- emmeans(rlogF_C5cons_5,~studyarm|edhi,type = "response")
8080     mfC5cons_5_s
8081     confint(pairs(mfC5cons_5_s,reverse = TRUE))
8082
8083     mfC5cons_5_e <- emmeans(rlogF_C5cons_5, ~ edhi|studyarm, type = "response")
8084     confint(pairs(mfC5cons_5_e,reverse = TRUE))
8085
8086
8087     # Now running models on imputed data.
8088     #CHANGELOG ASJ: No missing data for c5conf, no model with imputation performed, 21-09-20.
8089
8090     ##### +++ Logistic regression for C5 Calculation #####
8091
8092     #Create relevel before model to avoid problems with pairs function.
8093     datGeneric$mean_C5_calc2 <- relevel(as.factor(datGeneric$mean_C5_calc2),ref = "0")
8094     datMeasles$mean_C5_calc2 <- relevel(as.factor(datMeasles$mean_C5_calc2),ref = "0")
8095     datFlu$mean_C5_calc2 <- relevel(as.factor(datFlu$mean_C5_calc2),ref = "0")
8096
8097     ##### ++ Generic #####
8098

```

```

8099 ##### + Model 1: Check for direct effects of factors without any covariates #####
8100
8101 options(contrasts=c("contr.sum", "contr.poly"))
8102 rlogG_C5calc_1 <- glm(mean_C5_calc2 ~ studyarm, data =
8103   datGeneric, family=binomial("logit"))
8104 Anova(rlogG_C5calc_1, type="III")
8105 summary(rlogG_C5calc_1)
8106
8107 mgC5calc_1 <- emmeans(rlogG_C5calc_1, ~studyarm, type = "response") #proportions
8108 confint(pairs(mgC5calc_1, reverse = TRUE)) #Odds ratios
8109
8110 # Model 2: Check for direct effects of factors with adjustment for other covariates
8111 rlogG_C5calc_2 <-
8112   glm(mean_C5_calc2 ~ studyarm +
8113     mean_indivhorz +
8114     mean_indivvertical +
8115     mean_collhorz +
8116     mean_collvertical +
8117     bornincanada +
8118     language_1 +
8119     language_2 +
8120     Asian_group +
8121     White_group +
8122     disability_any +
8123     genderidentity +
8124     income +
8125     edhi +
8126     age,
8127     data = datGeneric, family=binomial("logit") )
8128 Anova(rlogG_C5calc_2, type = "III")
8129 summary(rlogG_C5calc_2)
8130
8131 mgC5calc_2 <- emmeans(rlogG_C5calc_2, ~studyarm, type = "response")
8132 mgC5calc_2
8133 confint(pairs(mgC5calc_2, reverse = TRUE))
8134
8135 # Model 3: Check for moderating effects of individualism & collectivism with adjustment
8136 # for other covariates
8137 rlogG_C5calc_3 <-
8138   glm(mean_C5_calc2 ~
8139     studyarm * mean_indivhorz +
8140     studyarm * mean_indivvertical +
8141     studyarm * mean_collhorz +
8142     studyarm * mean_collvertical +
8143     bornincanada +
8144     language_1 +
8145     language_2 +
8146     Asian_group +
8147     White_group +
8148     disability_any +
8149     genderidentity +
8150     income +
8151     edhi +
8152     age,
8153     data = datGeneric, family=binomial("logit")
8154   )
8155 Anova(rlogG_C5calc_3, type = "III")
8156 summary(rlogG_C5calc_3)
8157
8158 #No interaction to interpret
8159
8160 ##### + Model 4: Check for interaction viz*edhi without any covariates #####
8161
8162 rlogG_C5calc_4 <- glm(mean_C5_calc2 ~ studyarm * edhi, data =
8163   datGeneric, family=binomial("logit"))
8164 Anova(rlogG_C5calc_4, type="III")
8165 summary(rlogG_C5calc_4)
8166

```

```

8165 mgC5calc_4_s <- emmeans(rlogG_C5calc_4,~studyarm|edhi,type = "response")
8166 mgC5calc_4_s
8167 confint(pairs(mgC5calc_4_s,reverse = TRUE))
8168
8169 mgC5calc_4_e <- emmeans(rlogG_C5calc_4, ~ edhi|studyarm, type = "response")
8170 confint(pairs(mgC5calc_4_e,reverse = TRUE))
8171
8172 # Model 5: Check for interaction viz*edhi with adjustment for other covariates
8173
8174 rlogG_C5calc_5 <-
8175   glm(mean_C5_calc2 ~ studyarm*edhi +
8176       mean_indivhorz +
8177       mean_indivvertical +
8178       mean_collhorz +
8179       mean_collvertical +
8180       bornincanada +
8181       language_1 +
8182       language_2 +
8183       Asian_group +
8184       White_group +
8185       disability_any +
8186       genderidentity +
8187       income +
8188       age,
8189       data = datGeneric,family=binomial("logit")
8190   )
8191 Anova(rlogG_C5calc_5, type = "III")
8192 summary(rlogG_C5calc_5)
8193
8194 mgC5calc_5_s <- emmeans(rlogG_C5calc_5,~studyarm|edhi,type = "response")
8195 mgC5calc_5_s
8196 confint(pairs(mgC5calc_5_s,reverse = TRUE))
8197
8198 mgC5calc_5_e <- emmeans(rlogG_C5calc_5, ~ edhi|studyarm, type = "response")
8199 confint(pairs(mgC5calc_5_e,reverse = TRUE))
8200
8201 # Now running models on imputed data.
8202 #CHANGELOG ASJ: No missing data for c5conf, no model with imputation performed, 21-09-20.
8203
8204
8205 ##### ++ Measles #####
8206
8207 ##### + Model 1: Check for direct effects of factors without any covariates #####
8208
8209 options(contrasts=c("contr.sum", "contr.poly"))
8210 rlogM_C5calc_1 <- glm(mean_C5_calc2 ~ studyarm, data =
8211   datMeasles,family=binomial("logit"))
8212 Anova(rlogM_C5calc_1,type="III")
8213 summary(rlogM_C5calc_1)
8214
8215 mmC5calc_1 <- emmeans(rlogM_C5calc_1,~studyarm,type = "response") #proportions
8216 mmC5calc_1
8217 confint(pairs(mmC5calc_1,reverse = TRUE)) #Odds ratios
8218 pairs(mmC5calc_1,reverse = TRUE)
8219
8220 # Model 2: Check for direct effects of factors with adjustment for other covariates
8221 rlogM_C5calc_2 <-
8222   glm(mean_C5_calc2 ~ studyarm +
8223       mean_indivhorz +
8224       mean_indivvertical +
8225       mean_collhorz +
8226       mean_collvertical +
8227       bornincanada +
8228       language_1 +
8229       language_2 +
8230       Asian_group +
8231       White_group +
8232       disability_any +
8233       genderidentity +

```

```

8233         income +
8234         edhi +
8235         age,
8236         data = datMeasles, family=binomial("logit")
8237     )
8238     Anova(rlogM_C5calc_2, type = "III")
8239     summary(rlogM_C5calc_2)
8240
8241     mmC5calc_2 <- emmeans(rlogM_C5calc_2, ~studyarm, type = "response")
8242     mmC5calc_2
8243     confint(pairs(mmC5calc_2, reverse = TRUE))
8244
8245
8246     # Model 3: Check for moderating effects of individualism & collectivism with adjustment
for other covariates
8247     rlogM_C5calc_3 <-
8248         glm(mean_C5_calc2 ~
8249             studyarm * mean_indivhorz +
8250             studyarm * mean_indivvertical +
8251             studyarm * mean_collhorz +
8252             studyarm * mean_collvertical +
8253             bornincanada +
8254             language_1 +
8255             language_2 +
8256             Asian_group +
8257             White_group +
8258             disability_any +
8259             genderidentity +
8260             income +
8261             edhi +
8262             age,
8263             data = datMeasles, family=binomial("logit")
8264         )
8265     Anova(rlogM_C5calc_3, type = "III")
8266     summary(rlogM_C5calc_3)
8267
8268     #No interaction to interpret
8269
8270     #### + Model 4: Check for interaction viz*edhi without any covariates ####
8271
8272     rlogM_C5calc_4 <- glm(mean_C5_calc2 ~ studyarm * edhi, data =
datMeasles, family=binomial("logit"))
8273     Anova(rlogM_C5calc_4, type="III")
8274     summary(rlogM_C5calc_4)
8275
8276     mmC5calc_4_s <- emmeans(rlogM_C5calc_4, ~studyarm|edhi, type = "response")
8277     mmC5calc_4_s
8278     confint(pairs(mmC5calc_4_s, reverse = TRUE))
8279
8280     mmC5calc_4_e <- emmeans(rlogM_C5calc_4, ~ edhi|studyarm, type = "response")
8281     confint(pairs(mmC5calc_4_e, reverse = TRUE))
8282
8283
8284     # Model 5: Check for interaction viz*edhi with adjustment for other covariates
8285
8286     rlogM_C5calc_5 <-
8287         glm(mean_C5_calc2 ~ studyarm*edhi +
8288             mean_indivhorz +
8289             mean_indivvertical +
8290             mean_collhorz +
8291             mean_collvertical +
8292             bornincanada +
8293             language_1 +
8294             language_2 +
8295             Asian_group +
8296             White_group +
8297             disability_any +
8298             genderidentity +
8299             income +

```

```

8300         age,
8301         data = datMeasles,family=binomial("logit")
8302     )
8303     Anova(rlogM_C5calc_5, type = "III")
8304     summary(rlogM_C5calc_5)
8305
8306     mmC5calc_5_s <- emmeans(rlogM_C5calc_5,~studyarm|edhi,type = "response")
8307     mmC5calc_5_s
8308     confint(pairs(mmC5calc_5_s,reverse = TRUE))
8309
8310     mmC5calc_5_e <- emmeans(rlogM_C5calc_5, ~ edhi|studyarm, type = "response")
8311     confint(pairs(mmC5calc_5_e,reverse = TRUE))
8312
8313     # Now running models on imputed data.
8314     #CHANGELOG ASJ: No missing data for c5conf, no model with imputation performed, 21-09-20.
8315
8316
8317     ##### ++ Flu #####
8318
8319     ##### + Model 1: Check for direct effects of factors without any covariates #####
8320
8321     options(contrasts=c("contr.sum", "contr.poly"))
8322     rlogF_C5calc_1 <- glm(mean_C5_calc2 ~ studyarm, data = datFlu,family=binomial("logit"))
8323     Anova(rlogF_C5calc_1,type="III")
8324     summary(rlogF_C5calc_1)
8325
8326     mfC5calc_1 <- emmeans(rlogF_C5calc_1,~studyarm,type = "response") #proportions
8327     mfC5calc_1
8328     confint(pairs(mfC5calc_1,reverse = TRUE)) #Odds ratios
8329
8330     # Model 2: Check for direct effects of factors with adjustment for other covariates
8331     rlogF_C5calc_2 <-
8332         glm(mean_C5_calc2 ~ studyarm +
8333             mean_indivhorz +
8334             mean_indivvertical +
8335             mean_collhorz +
8336             mean_collvertical +
8337             bornincanada +
8338             language_1 +
8339             language_2 +
8340             Asian_group +
8341             White_group +
8342             disability_any +
8343             genderidentity +
8344             income +
8345             edhi +
8346             age,
8347             data = datFlu,family=binomial("logit")
8348         )
8349     Anova(rlogF_C5calc_2, type = "III")
8350     summary(rlogF_C5calc_2)
8351
8352     mfC5calc_2 <- emmeans(rlogF_C5calc_2,~studyarm,type = "response")
8353     mfC5calc_2
8354     confint(pairs(mfC5calc_2,reverse = TRUE))
8355
8356     # Model 3: Check for moderating effects of individualism & collectivism with adjustment
8357     # for other covariates
8358     rlogF_C5calc_3 <-
8359         glm(mean_C5_calc2 ~
8360             studyarm * mean_indivhorz +
8361             studyarm * mean_indivvertical +
8362             studyarm * mean_collhorz +
8363             studyarm * mean_collvertical +
8364             bornincanada +
8365             language_1 +
8366             language_2 +
8367             Asian_group +
8368             White_group +

```

```

8368         disability_any +
8369         genderidentity +
8370         income +
8371         edhi +
8372         age,
8373         data = datFlu,family=binomial("logit")
8374     )
8375     Anova(rlogF_C5calc_3, type = "III")
8376     summary(rlogF_C5calc_3)
8377
8378     #No interaction to interpret
8379
8380     ##### + Model 4: Check for interaction viz*edhi without any covariates #####
8381
8382     rlogF_C5calc_4 <- glm(mean_C5_calc2 ~ studyarm * edhi, data =
8383     datFlu,family=binomial("logit"))
8384     Anova(rlogF_C5calc_4,type="III")
8385     summary(rlogF_C5calc_4)
8386
8387     mfC5calc_4_s <- emmeans(rlogF_C5calc_4,~studyarm|edhi,type = "response")
8388     mfC5calc_4_s
8389     confint(pairs(mfC5calc_4_s,reverse = TRUE))
8390
8391     mfC5calc_4_e <- emmeans(rlogF_C5calc_4, ~ edhi|studyarm, type = "response")
8392     confint(pairs(mfC5calc_4_e,reverse = TRUE))
8393
8394     # Model 5: Check for interaction viz*edhi with adjustment for other covariates
8395
8396     rlogF_C5calc_5 <-
8397     glm(mean_C5_calc2 ~ studyarm*edhi +
8398         mean_indivhorz +
8399         mean_indivvertical +
8400         mean_collhorz +
8401         mean_collvertical +
8402         bornincanada +
8403         language_1 +
8404         language_2 +
8405         Asian_group +
8406         White_group +
8407         disability_any +
8408         genderidentity +
8409         income +
8410         age,
8411         data = datFlu,family=binomial("logit")
8412     )
8413     Anova(rlogF_C5calc_5, type = "III")
8414     summary(rlogF_C5calc_5)
8415
8416     mfC5calc_5_s <- emmeans(rlogF_C5calc_5,~studyarm|edhi,type = "response")
8417     mfC5calc_5_s
8418     confint(pairs(mfC5calc_5_s,reverse = TRUE))
8419
8420     mfC5calc_5_e <- emmeans(rlogF_C5calc_5, ~ edhi|studyarm, type = "response")
8421     confint(pairs(mfC5calc_5_e,reverse = TRUE))
8422
8423     # Now running models on imputed data.
8424     #CHANGELOG ASJ: No missing data for c5conf, no model with imputation performed, 21-09-20.
8425
8426
8427
8428     ##### +++ Logistic regression for C5 Collective Response #####
8429
8430     #Create relevel before model to avoid problems with pairs function.
8431     datGeneric$mean_C5_coll2 <- relevel(as.factor(datGeneric$mean_C5_coll2),ref = "0")
8432     datMeasles$mean_C5_coll2 <- relevel(as.factor(datMeasles$mean_C5_coll2),ref = "0")
8433     datFlu$mean_C5_coll2 <- relevel(as.factor(datFlu$mean_C5_coll2),ref = "0")
8434
8435     ##### ++Generic #####

```

```

8436
8437 ##### + Model 1: Check for direct effects of factors without any covariates #####
8438
8439 options(contrasts=c("contr.sum", "contr.poly"))
8440 rlogG_C5coll_1 <- glm(mean_C5_coll2 ~ studyarm, data =
datGeneric,family=binomial("logit"))
8441 Anova(rlogG_C5coll_1,type="III")
8442 summary(rlogG_C5coll_1)
8443
8444 mgC5coll_1 <- emmeans(rlogG_C5coll_1,~studyarm,type = "response") #proportions
8445 mgC5coll_1
8446 confint(pairs(mgC5coll_1,reverse = TRUE)) #Odds ratios
8447 pairs(mgC5coll_1,reverse = TRUE)
8448
8449
8450 # Model 2: Check for direct effects of factors with adjustment for other covariates
8451 rlogG_C5coll_2 <-
8452   glm(mean_C5_coll2 ~ studyarm +
8453     mean_indivhorz +
8454     mean_indivvertical +
8455     mean_collhorz +
8456     mean_collvertical +
8457     bornincanada +
8458     language_1 +
8459     language_2 +
8460     Asian_group +
8461     White_group +
8462     disability_any +
8463     genderidentity +
8464     income +
8465     edhi +
8466     age,
8467     data = datGeneric,family=binomial("logit") )
8468 Anova(rlogG_C5coll_2, type = "III")
8469 summary(rlogG_C5coll_2)
8470
8471 mgC5coll_2 <- emmeans(rlogG_C5coll_2,~studyarm,type = "response")
8472 mgC5coll_2
8473 confint(pairs(mgC5coll_2,reverse = TRUE))
8474 pairs(mgC5coll_2,reverse = TRUE)
8475
8476 # Model 3: Check for moderating effects of individualism & collectivism with adjustment
for other covariates
8477 rlogG_C5coll_3 <-
8478   glm(mean_C5_coll2 ~
8479     studyarm * mean_indivhorz +
8480     studyarm * mean_indivvertical +
8481     studyarm * mean_collhorz +
8482     studyarm * mean_collvertical +
8483     bornincanada +
8484     language_1 +
8485     language_2 +
8486     Asian_group +
8487     White_group +
8488     disability_any +
8489     genderidentity +
8490     income +
8491     edhi +
8492     age,
8493     data = datGeneric,family=binomial("logit")
8494   )
8495 Anova(rlogG_C5coll_3, type = "III")
8496 summary(rlogG_C5coll_3)
8497
8498 emmip(rlogG_C5coll_3, studyarm ~ mean_indivvertical, cov.reduce = range, type =
"response")
8499 emmip(rlogG_C5coll_3, studyarm ~ mean_collhorz, cov.reduce = range, type = "response")
8500
8501 ##### + Model 4: Check for interaction viz*edhi without any covariates #####

```

```

8502
8503 rlogG_C5coll_4 <- glm(mean_C5_coll2 ~ studyarm * edhi, data =
datGeneric,family=binomial("logit"))
8504 Anova(rlogG_C5coll_4,type="III")
8505 summary(rlogG_C5coll_4)
8506
8507 mgC5coll_4_s <- emmeans(rlogG_C5coll_4,~studyarm|edhi,type = "response")
8508 mgC5coll_4_s
8509 confint(pairs(mgC5coll_4_s,reverse = TRUE))
8510 pairs(mgC5coll_4_s,reverse = TRUE)
8511
8512 mgC5coll_4_e <- emmeans(rlogG_C5coll_4, ~ edhi|studyarm, type = "response")
8513 confint(pairs(mgC5coll_4_e,reverse = TRUE))
8514 pairs(mgC5coll_4_e,reverse = TRUE)
8515
8516 # Model 5: Check for interaction viz*edhi with adjustment for other covariates
8517
8518 rlogG_C5coll_5 <-
8519   glm(mean_C5_coll2 ~ studyarm*edhi +
8520       mean_indivhorz +
8521       mean_indivvertical +
8522       mean_collhorz +
8523       mean_collvertical +
8524       bornincanada +
8525       language_1 +
8526       language_2 +
8527       Asian_group +
8528       White_group +
8529       disability_any +
8530       genderidentity +
8531       income +
8532       age,
8533   data = datGeneric,family=binomial("logit")
8534   )
8535 Anova(rlogG_C5coll_5, type = "III")
8536 summary(rlogG_C5coll_5)
8537
8538 mgC5coll_5_s <- emmeans(rlogG_C5coll_5,~studyarm|edhi,type = "response")
8539 mgC5coll_5_s
8540 confint(pairs(mgC5coll_5_s,reverse = TRUE))
8541
8542 mgC5coll_5_e <- emmeans(rlogG_C5coll_5, ~ edhi|studyarm, type = "response")
8543 confint(pairs(mgC5coll_5_e,reverse = TRUE))
8544
8545 # Now running models on imputed data.
8546 #CHANGELOG ASJ: No missing data for c5conf, no model with imputation performed, 21-09-20.
8547
8548
8549 ##### ++ Measles #####
8550
8551 ##### + Model 1: Check for direct effects of factors without any covariates #####
8552
8553 options(contrasts=c("contr.sum", "contr.poly"))
8554 rlogM_C5coll_1 <- glm(mean_C5_coll2 ~ studyarm, data =
datMeasles,family=binomial("logit"))
8555 Anova(rlogM_C5coll_1,type="III")
8556 summary(rlogM_C5coll_1)
8557
8558 mmC5coll_1 <- emmeans(rlogM_C5coll_1,~studyarm,type = "response") #proportions
8559 mmC5coll_1
8560 confint(pairs(mmC5coll_1,reverse = TRUE)) #Odds ratios
8561
8562 # Model 2: Check for direct effects of factors with adjustment for other covariates
8563 rlogM_C5coll_2 <-
8564   glm(mean_C5_coll2 ~ studyarm +
8565       mean_indivhorz +
8566       mean_indivvertical +
8567       mean_collhorz +
8568       mean_collvertical +

```



```

8569         bornincanada +
8570         language_1 +
8571         language_2 +
8572         Asian_group +
8573         White_group +
8574         disability_any +
8575         genderidentity +
8576         income +
8577         edhi +
8578         age,
8579         data = datMeasles, family=binomial("logit")
8580     )
8581     Anova(rlogM_C5coll_2, type = "III")
8582     summary(rlogM_C5coll_2)
8583
8584     mmC5coll_2 <- emmeans(rlogM_C5coll_2, ~studyarm, type = "response")
8585     mmC5coll_2
8586     confint(pairs(mmC5coll_2, reverse = TRUE))
8587
8588
8589     # Model 3: Check for moderating effects of individualism & collectivism with adjustment
for other covariates
8590     rlogM_C5coll_3 <-
8591         glm(mean_C5_coll2 ~
8592             studyarm * mean_indivhorz +
8593             studyarm * mean_indivvertical +
8594             studyarm * mean_collhorz +
8595             studyarm * mean_collvertical +
8596             bornincanada +
8597             language_1 +
8598             language_2 +
8599             Asian_group +
8600             White_group +
8601             disability_any +
8602             genderidentity +
8603             income +
8604             edhi +
8605             age,
8606             data = datMeasles, family=binomial("logit")
8607         )
8608     Anova(rlogM_C5coll_3, type = "III")
8609     summary(rlogM_C5coll_3)
8610
8611     #No interaction to interpret
8612
8613     #### + Model 4: Check for interaction viz*edhi without any covariates ####
8614
8615     rlogM_C5coll_4 <- glm(mean_C5_coll2 ~ studyarm * edhi, data =
datMeasles, family=binomial("logit"))
8616     Anova(rlogM_C5coll_4, type="III")
8617     summary(rlogM_C5coll_4)
8618
8619     mmC5coll_4_s <- emmeans(rlogM_C5coll_4, ~studyarm|edhi, type = "response")
8620     mmC5coll_4_s
8621     confint(pairs(mmC5coll_4_s, reverse = TRUE))
8622
8623     mmC5coll_4_e <- emmeans(rlogM_C5coll_4, ~ edhi|studyarm, type = "response")
8624     confint(pairs(mmC5coll_4_e, reverse = TRUE))
8625
8626
8627     # Model 5: Check for interaction viz*edhi with adjustment for other covariates
8628
8629     rlogM_C5coll_5 <-
8630         glm(mean_C5_coll2 ~ studyarm*edhi +
8631             mean_indivhorz +
8632             mean_indivvertical +
8633             mean_collhorz +
8634             mean_collvertical +
8635             bornincanada +

```

```

8636     language_1 +
8637     language_2 +
8638     Asian_group +
8639     White_group +
8640     disability_any +
8641     genderidentity +
8642     income +
8643     age,
8644     data = datMeasles, family=binomial("logit")
8645 )
8646 Anova(rlogM_C5coll_5, type = "III")
8647 summary(rlogM_C5coll_5)
8648
8649 mmC5coll_5_s <- emmeans(rlogM_C5coll_5, ~studyarm|edhi, type = "response")
8650 mmC5coll_5_s
8651 confint(pairs(mmC5coll_5_s, reverse = TRUE))
8652
8653 mmC5coll_5_e <- emmeans(rlogM_C5coll_5, ~ edhi|studyarm, type = "response")
8654 confint(pairs(mmC5coll_5_e, reverse = TRUE))
8655
8656 # Now running models on imputed data.
8657 #CHANGELOG ASJ: No missing data for c5conf, no model with imputation performed, 21-09-20.
8658
8659
8660 ##### ++ Flu #####
8661
8662 ##### + Model 1: Check for direct effects of factors without any covariates #####
8663
8664 options(contrasts=c("contr.sum", "contr.poly"))
8665 rlogF_C5coll_1 <- glm(mean_C5_coll2 ~ studyarm, data = datFlu, family=binomial("logit"))
8666 Anova(rlogF_C5coll_1, type="III")
8667 summary(rlogF_C5coll_1)
8668
8669 mfc5coll_1 <- emmeans(rlogF_C5coll_1, ~studyarm, type = "response") #proportions
8670 mfc5coll_1
8671 confint(pairs(mfc5coll_1, reverse = TRUE)) #Odds ratios
8672
8673 # Model 2: Check for direct effects of factors with adjustment for other covariates
8674 rlogF_C5coll_2 <-
8675   glm(mean_C5_coll2 ~ studyarm +
8676     mean_indivhorz +
8677     mean_indivvertical +
8678     mean_collhorz +
8679     mean_collvertical +
8680     bornincanada +
8681     language_1 +
8682     language_2 +
8683     Asian_group +
8684     White_group +
8685     disability_any +
8686     genderidentity +
8687     income +
8688     edhi +
8689     age,
8690     data = datFlu, family=binomial("logit")
8691   )
8692 Anova(rlogF_C5coll_2, type = "III")
8693 summary(rlogF_C5coll_2)
8694
8695 mfc5coll_2 <- emmeans(rlogF_C5coll_2, ~studyarm, type = "response")
8696 mfc5coll_2
8697 confint(pairs(mfc5coll_2, reverse = TRUE))
8698
8699 # Model 3: Check for moderating effects of individualism & collectivism with adjustment
for other covariates
8700 rlogF_C5coll_3 <-
8701   glm(mean_C5_coll2 ~
8702     studyarm * mean_indivhorz +
8703     studyarm * mean_indivvertical +

```

```

8704     studyarm * mean_collhorz +
8705     studyarm * mean_collvertical +
8706     bornincanada +
8707     language_1 +
8708     language_2 +
8709     Asian_group +
8710     White_group +
8711     disability_any +
8712     genderidentity +
8713     income +
8714     edhi +
8715     age,
8716     data = datFlu, family=binomial("logit")
8717 )
8718 Anova(rlogF_C5coll_3, type = "III")
8719 summary(rlogF_C5coll_3)
8720
8721 emmip(rlogF_C5coll_3, studyarm ~ mean_collhorz, cov.reduce = range, type = "response")
8722
8723
8724 #### + Model 4: Check for interaction viz*edhi without any covariates ####
8725
8726 rlogF_C5coll_4 <- glm(mean_C5_coll2 ~ studyarm * edhi, data =
8727   datFlu, family=binomial("logit"))
8728 Anova(rlogF_C5coll_4, type="III")
8729 summary(rlogF_C5coll_4)
8730
8731 mfC5coll_4_s <- emmeans(rlogF_C5coll_4, ~studyarm|edhi, type = "response")
8732 mfC5coll_4_s
8733 confint(pairs(mfC5coll_4_s, reverse = TRUE))
8734
8735 mfC5coll_4_e <- emmeans(rlogF_C5coll_4, ~ edhi|studyarm, type = "response")
8736 confint(pairs(mfC5coll_4_e, reverse = TRUE))
8737
8738 # Model 5: Check for interaction viz*edhi with adjustment for other covariates
8739
8740 rlogF_C5coll_5 <-
8741   glm(mean_C5_coll2 ~ studyarm*edhi +
8742     mean_indivhorz +
8743     mean_indivvertical +
8744     mean_collhorz +
8745     mean_collvertical +
8746     bornincanada +
8747     language_1 +
8748     language_2 +
8749     Asian_group +
8750     White_group +
8751     disability_any +
8752     genderidentity +
8753     income +
8754     age,
8755     data = datFlu, family=binomial("logit")
8756   )
8757 Anova(rlogF_C5coll_5, type = "III")
8758 summary(rlogF_C5coll_5)
8759
8760 mfC5coll_5_s <- emmeans(rlogF_C5coll_5, ~studyarm|edhi, type = "response")
8761 mfC5coll_5_s
8762 confint(pairs(mfC5coll_5_s, reverse = TRUE))
8763
8764 mfC5coll_5_e <- emmeans(rlogF_C5coll_5, ~ edhi|studyarm, type = "response")
8765 confint(pairs(mfC5coll_5_e, reverse = TRUE))
8766
8767 # Now running models on imputed data.
8768 #CHANGELOG ASJ: No missing data for c5conf, no model with imputation performed, 21-09-20.
8769
8770
8771 #### COMPLETES VS INCOMPLETES ####

```

```

8772
8773 # Here we test for differences between people who finished the survey (completes) and
8774 # those who
8775 # started but did not finish (incompletes) to explore potential issues or limitations
8776 # introduced by
8777 # imputing missing data. To do this, we run Chi-squared tests on categorical variables
8778 # and Wilcoxon
8779 # tests on continuous variables, comparing people who did and did not complete the
8780 # survey. We ran
8781 # the sociodemographic panel of questions first to maximally enable this comparison but
8782 # we won't be
8783 # able to compare with people who never clicked on the survey or who started to read
8784 # and didn't
8785 # answer anything.
8786
8787 #CHANGELOG ASJ: Compare people analysed who finished with quality answer VS (did not
8788 # finished or finished with poor quality), 2021-08-06.
8789 table(datConsent$used) #CHANGELOG ASJ: changed finished to used, and everywhere below
8790 2021-08-06
8791 prop.table(table(datConsent$used))*100
8792
8793 #CHANGELOG ASJ: Apply the same changes to the variables as in the dataset dat, 2021-09-01
8794 datConsent$yearofbirth <- as.numeric(datConsent$yearofbirth)
8795 datConsent$yearofbirth[datConsent$yearofbirth==888] <- NA
8796 datConsent$age <- 2021 - datConsent$yearofbirth
8797
8798 cols.num <-
8799   c(
8800     "bornincanada",
8801     "language_1",
8802     "language_2",
8803     "language_3",
8804     "language_888",
8805     "ethnicity_1",
8806     "ethnicity_2",
8807     "ethnicity_3",
8808     "ethnicity_4",
8809     "ethnicity_5",
8810     "ethnicity_6",
8811     "ethnicity_7",
8812     "ethnicity_8",
8813     "ethnicity_9",
8814     "ethnicity_10",
8815     "ethnicity_11",
8816     "ethnicity_12",
8817     "ethnicity_13",
8818     "ethnicity_14",
8819     "ethnicity_15",
8820     "ethnicity_16",
8821     "ethnicity_17",
8822     "ethnicity_888",
8823     "disability",
8824     "techdisability",
8825     "sexatbirth",
8826     "genderidentity",
8827     "supportedbyincome",
8828     "educationlevel",
8829     "studyarm",
8830     "viz",
8831     "disease",
8832     "immune",
8833     "c19vax"
8834   )
8835 datConsent[cols.num] <- lapply(datConsent[cols.num], as.numeric)
8836
8837 datConsent$language_1[is.na(datConsent$language_1)] <- 0
8838 datConsent$language_2[is.na(datConsent$language_2)] <- 0
8839 datConsent$language_3[is.na(datConsent$language_3)] <- 0

```

```

8833
8834 datConsent$language_1[datConsent$language_888==1&datConsent$language_1==0&datConsent$language_2==0&datConsent$language_3==0] <- NA
8835 datConsent$language_2[datConsent$language_888==1&datConsent$language_1==0&datConsent$language_2==0&datConsent$language_3==0] <- NA
8836 datConsent$language_3[datConsent$language_888==1&datConsent$language_1==0&datConsent$language_2==0&datConsent$language_3==0] <- NA
8837
8838 datConsent$ethnicity_1[is.na(datConsent$ethnicity_1)] <- 0
8839 datConsent$ethnicity_2[is.na(datConsent$ethnicity_2)] <- 0
8840 datConsent$ethnicity_3[is.na(datConsent$ethnicity_3)] <- 0
8841 datConsent$ethnicity_4[is.na(datConsent$ethnicity_4)] <- 0
8842 datConsent$ethnicity_5[is.na(datConsent$ethnicity_5)] <- 0
8843 datConsent$ethnicity_6[is.na(datConsent$ethnicity_6)] <- 0
8844 datConsent$ethnicity_7[is.na(datConsent$ethnicity_7)] <- 0
8845 datConsent$ethnicity_8[is.na(datConsent$ethnicity_8)] <- 0
8846 datConsent$ethnicity_9[is.na(datConsent$ethnicity_9)] <- 0
8847 datConsent$ethnicity_10[is.na(datConsent$ethnicity_10)] <- 0
8848 datConsent$ethnicity_11[is.na(datConsent$ethnicity_11)] <- 0
8849 datConsent$ethnicity_12[is.na(datConsent$ethnicity_12)] <- 0
8850 datConsent$ethnicity_13[is.na(datConsent$ethnicity_13)] <- 0
8851 datConsent$ethnicity_14[is.na(datConsent$ethnicity_14)] <- 0
8852 datConsent$ethnicity_15[is.na(datConsent$ethnicity_15)] <- 0
8853 datConsent$ethnicity_16[is.na(datConsent$ethnicity_16)] <- 0
8854 datConsent$ethnicity_17[is.na(datConsent$ethnicity_17)] <- 0
8855
8856
8857 datConsent_ethnicity <-
8858   subset(
8859     datConsent,
8860     select = c(
8861       ethnicity_1,
8862       ethnicity_2,
8863       ethnicity_3,
8864       ethnicity_4,
8865       ethnicity_5,
8866       ethnicity_6,
8867       ethnicity_7,
8868       ethnicity_8,
8869       ethnicity_9,
8870       ethnicity_10,
8871       ethnicity_11,
8872       ethnicity_12,
8873       ethnicity_13,
8874       ethnicity_14,
8875       ethnicity_15,
8876       ethnicity_16,
8877       ethnicity_17
8878     )
8879   )
8880
8881 datConsent$sum_ethnicity <- rowSums(datConsent_ethnicity, na.rm=T)
8882
8883 datConsent$ethnicity_1[datConsent$ethnicity_888==1&datConsent$sum_ethnicity==0] <- NA
8884 datConsent$ethnicity_2[datConsent$ethnicity_888==1&datConsent$sum_ethnicity==0] <- NA
8885 datConsent$ethnicity_3[datConsent$ethnicity_888==1&datConsent$sum_ethnicity==0] <- NA
8886 datConsent$ethnicity_4[datConsent$ethnicity_888==1&datConsent$sum_ethnicity==0] <- NA
8887 datConsent$ethnicity_5[datConsent$ethnicity_888==1&datConsent$sum_ethnicity==0] <- NA
8888 datConsent$ethnicity_6[datConsent$ethnicity_888==1&datConsent$sum_ethnicity==0] <- NA
8889 datConsent$ethnicity_7[datConsent$ethnicity_888==1&datConsent$sum_ethnicity==0] <- NA
8890 datConsent$ethnicity_8[datConsent$ethnicity_888==1&datConsent$sum_ethnicity==0] <- NA
8891 datConsent$ethnicity_9[datConsent$ethnicity_888==1&datConsent$sum_ethnicity==0] <- NA
8892 datConsent$ethnicity_10[datConsent$ethnicity_888==1&datConsent$sum_ethnicity==0] <- NA
8893 datConsent$ethnicity_11[datConsent$ethnicity_888==1&datConsent$sum_ethnicity==0] <- NA
8894 datConsent$ethnicity_12[datConsent$ethnicity_888==1&datConsent$sum_ethnicity==0] <- NA
8895 datConsent$ethnicity_13[datConsent$ethnicity_888==1&datConsent$sum_ethnicity==0] <- NA
8896 datConsent$ethnicity_14[datConsent$ethnicity_888==1&datConsent$sum_ethnicity==0] <- NA
8897 datConsent$ethnicity_15[datConsent$ethnicity_888==1&datConsent$sum_ethnicity==0] <- NA
8898 datConsent$ethnicity_16[datConsent$ethnicity_888==1&datConsent$sum_ethnicity==0] <- NA

```

```

8899 datConsent$ethnicity_17[datConsent$ethnicity_888==1&datConsent$sum_ethnicity==0] <- NA
8900
8901 datConsent$Asian_group <-
8902   ifelse(
8903     datConsent$ethnicity_1 == 1 |
8904     datConsent$ethnicity_2 == 1 |
8905     datConsent$ethnicity_3 == 1 |
8906     datConsent$ethnicity_4 == 1,
8907     1,
8908     0
8909   )
8910
8911
8912 datConsent$White_group <-
8913   ifelse(
8914     datConsent$ethnicity_6 == 1 |
8915     datConsent$ethnicity_7 == 1,
8916     1,
8917     0
8918   )
8919
8920 datConsent$edhi <- ifelse(datConsent$educationlevel == 4 |
8921                           datConsent$educationlevel == 5 |
8922                           datConsent$educationlevel == 6 |
8923                           datConsent$educationlevel == 7, TRUE,
8924                           ifelse(datConsent$educationlevel == 8 |
8925                                   datConsent$educationlevel == 888, NA, FALSE))
8926
8927 datConsent$bornincanada[datConsent$bornincanada==888] <- NA
8928 datConsent$disability[datConsent$disability==888] <- NA
8929 datConsent$techdisability[datConsent$techdisability==888] <- NA
8930 datConsent$sexatbirth[datConsent$sexatbirth==888] <- NA
8931 datConsent$genderidentity[datConsent$genderidentity==888] <- NA
8932 datConsent$income[datConsent$income==888] <- NA
8933 datConsent$income[datConsent$income==5] <- NA
8934 datConsent$supportedbyincome[datConsent$supportedbyincome==888] <- NA
8935 datConsent$educationlevel[datConsent$educationlevel==888] <- NA
8936 datConsent$educationlevel[datConsent$educationlevel==8] <- NA
8937
8938 datConsent$agecat[datConsent$agecat==888 | datConsent$agecat==1] <- NA
8939
8940
8941 datConsent$bornincanada <-
8942   factor(datConsent$bornincanada,
8943         levels = c(1, 0),
8944         labels = c("Yes", "No"))
8945
8946 datConsent$language_1 <-
8947   factor(datConsent$language_1,
8948         levels = c(1, 0),
8949         labels = c("Yes", "No"))
8950
8951 datConsent$language_2 <-
8952   factor(datConsent$language_2,
8953         levels = c(1, 0),
8954         labels = c("Yes", "No"))
8955
8956 datConsent$Asian_group <-
8957   factor(datConsent$Asian_group,
8958         levels = c(1, 0),
8959         labels = c("Yes", "No"))
8960
8961
8962 datConsent$White_group <-
8963   factor(datConsent$White_group,
8964         levels = c(1, 0),
8965         labels = c("Yes", "No"))
8966

```

```

8967
8968 datConsent$disability <-
8969     factor(
8970         datConsent$disability,
8971         levels = c(0, 1),
8972         labels = c("No disability", "yes,at least one")
8973     )
8974
8975 datConsent$techdisability <-
8976     factor(datConsent$techdisability,
8977         levels = c(0, 1),
8978         labels = c("No", "Yes"))
8979
8980 datConsent$sexatbirth <-
8981     factor(datConsent$sexatbirth,
8982         levels = c(1, 2),
8983         labels = c("Female", "Male"))
8984
8985 datConsent$genderidentity <- factor(
8986     datConsent$genderidentity,
8987     levels = c(1, 2, 3, 4),
8988     labels = c(
8989         "Female",
8990         "Male",
8991         "Indigenous or other cultural gender minority identity",
8992         "Something else"
8993     )
8994 )
8995
8996 datConsent$income <-
8997     factor(
8998         datConsent$income,
8999         levels = c(1, 2, 3, 4),
9000         labels = c("24 999 or less", "25 000 to 49 999",
9001             "50 000 to 99 999", "100 000 or more")
9002     )
9003
9004 datConsent$educationlevel <- factor(
9005     datConsent$educationlevel,
9006     levels = c(1, 2, 3, 4, 5, 6, 7),
9007     labels = c(
9008         "Some Elementary School",
9009         "High School Diploma",
9010         "Apprenticeship or trade certificate or diploma",
9011         "College or polytechnical school certificate or diploma",
9012         "University degree bachelor level or below",
9013         "University graduate degree Master level",
9014         "University graduate degree Doctorate level"
9015     )
9016 )
9017
9018 datConsent$agecat<-
9019     factor(
9020         datConsent$agecat,
9021         levels = c(2, 3, 4),
9022         labels = c("18-34 years", "35-49 years", "50 years and more")
9023     )
9024
9025 datConsent$UserLanguage <- as.factor(datConsent$UserLanguage)
9026
9027 datConsent$studyarm <-
9028     factor (
9029         datConsent$studyarm,
9030         levels = c(0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 11, 12, 13),
9031         labels = c(
9032             "controlgeneric",
9033             "controlmeasles",
9034             "controlpertussis",
9035             "controlflu",

```

```

9036     "herdimmgeneric",
9037     "herdimmmeasles",
9038     "herdimpertussis",
9039     "herdimmflu",
9040     "robertkochgeneric",
9041     "sbsnewsgeneric",
9042     "guardianmeasles",
9043     "theotheredmundmeasles",
9044     "publichealthagencycanadaflu"
9045   )
9046 )
9047
9048 datConsent$viz <- factor (
9049   datConsent$viz,
9050   levels = c(0, 1, 2, 3, 5, 6, 7),
9051   labels = c(
9052     "no visualization",
9053     "herdimm",
9054     "robertkoch",
9055     "sbsnews",
9056     "guardian",
9057     "theotheredmund",
9058     "publichealthagencycanada"
9059   )
9060 )
9061
9062 datConsent$disease <-
9063   factor (
9064     datConsent$disease,
9065     levels = c(0, 1, 2, 3),
9066     labels = c("Generic", "Measles", "Pertussis", "Flu")
9067   )
9068
9069
9070 datConsent$genderidentity[datConsent$genderidentity == "Something else" |
9071   datConsent$genderidentity == "Indigenous or other cultural
   gender minority identity"] <- NA
9072
9073 datConsent$genderidentity <- droplevels(datConsent$genderidentity)
9074
9075
9076 datConsent$disability_any <-ifelse(datConsent$disability == "yes,at least one" |
9077   datConsent$techdisability == "Yes", 1, 0)
9078 datConsent$disability_any <-
9079   factor(
9080     datConsent$disability_any,
9081     levels = c(1, 0),
9082     labels = c("Yes", "No")
9083   )
9084
9085 datConsent$agecat <- as.numeric(datConsent$agecat)
9086
9087 datConsent$used <-
9088   factor(
9089     datConsent$used,
9090     levels = c(1, 0),
9091     labels = c("Yes", "No")
9092   )
9093
9094 # For each categorical demographic to do along with the next step of chi square
9095 #CHANGELOG ASJ: Add table for other demographic variables 21-08-31
9096 t1<-data.frame(datConsent$used,datConsent$studyarm)
9097 table(t1)
9098 prop.table(table(t1), 1) * 100
9099
9100 t1<-data.frame(datConsent$used,datConsent$viz)
9101 table(t1)
9102 prop.table(table(t1), 1) * 100
9103
9104 t1<-data.frame(datConsent$used,datConsent$disease)

```



```

9103   table(t1)
9104   prop.table(table(t1), 1) * 100
9105
9106   t1<-data.frame(datConsent$used,datConsent$bornincanada)
9107   table(t1)
9108   prop.table(table(t1), 1) * 100
9109
9110   t1<-data.frame(datConsent$used,datConsent$language_1)
9111   table(t1)
9112   prop.table(table(t1), 1) * 100
9113
9114   t1<-data.frame(datConsent$used,datConsent$language_2)
9115   table(t1)
9116   prop.table(table(t1), 1) * 100
9117
9118   t1<-data.frame(datConsent$used,datConsent$White_group)
9119   table(t1)
9120   prop.table(table(t1), 1) * 100
9121
9122   t1<-data.frame(datConsent$used,datConsent$Asian_group)
9123   table(t1)
9124   prop.table(table(t1), 1) * 100
9125
9126   t1<-data.frame(datConsent$used,datConsent$disability)
9127   table(t1)
9128   prop.table(table(t1), 1) * 100
9129
9130   t1<-data.frame(datConsent$used,datConsent$techdisability)
9131   table(t1)
9132   prop.table(table(t1), 1) * 100
9133
9134   t1<-data.frame(datConsent$used,datConsent$disability_any)
9135   table(t1)
9136   prop.table(table(t1), 1) * 100
9137
9138   t1<-data.frame(datConsent$used,datConsent$sexatbirth)
9139   table(t1)
9140   prop.table(table(t1), 1) * 100
9141
9142   t1<-data.frame(datConsent$used,datConsent$genderidentity)
9143   table(t1)
9144   prop.table(table(t1), 1) * 100
9145
9146   t1<-data.frame(datConsent$used,datConsent$income)
9147   table(t1)
9148   prop.table(table(t1), 1) * 100
9149
9150   t1<-data.frame(datConsent$used,datConsent$educationlevel)
9151   table(t1)
9152   prop.table(table(t1), 1) * 100
9153
9154   t1<-data.frame(datConsent$used,datConsent$edhi)
9155   table(t1)
9156   prop.table(table(t1), 1) * 100
9157
9158   #Comparison for continuous demographics
9159   describeBy(datConsent$age,datConsent$used)
9160   wilcox.test(datConsent$age~datConsent$used)
9161
9162   #CHANGELOG ASJ: Only keep variables analysed with >5% and dichotomous versions 2021-08-06
9163   chisq.test(datConsent$used,datConsent$studyarm, correct=FALSE)
9164   chisq.test(datConsent$used,datConsent$viz, correct=FALSE)
9165   chisq.test(datConsent$used,datConsent$disease, correct=FALSE)
9166   chisq.test(datConsent$used,datConsent$bornincanada, correct=FALSE)
9167   chisq.test(datConsent$used,datConsent$language_1, correct=FALSE)
9168   chisq.test(datConsent$used,datConsent$language_2, correct=FALSE)
9169   chisq.test(datConsent$used,datConsent$Asian_group, correct=FALSE)
9170   chisq.test(datConsent$used,datConsent$White_group, correct=FALSE)
9171   chisq.test(datConsent$used,datConsent$disability, correct=FALSE)

```

```

9172 chisq.test(datConsent$used,datConsent$techdisability, correct=FALSE)
9173 chisq.test(datConsent$used,datConsent$disability_any, correct=FALSE)
9174 chisq.test(datConsent$used,datConsent$sexatbirth, correct=FALSE)
9175 chisq.test(datConsent$used,datConsent$genderidentity, correct=FALSE)
9176 chisq.test(datConsent$used,datConsent$income, correct=FALSE)
9177 chisq.test(datConsent$used,datConsent$educationlevel, correct=FALSE)
9178 chisq.test(datConsent$used,datConsent$edhi, correct=FALSE)
9179
9180
9181 ##### RESEARCH QUESTION 4: Effects of male vs female voice #####
9182
9183 # Recall: Research question 4 (add-on, may be reported separately from Hina Hakim's
9184 # thesis): Are the
9185 # effects of the herdimmm intervention different when the narration uses a female or
9186 # male voice?
9187
9188 # Force this variable to be read as a factor and define the labels (this could be up in
9189 # the data
9190 # cleaning section but we are keeping it separate in case we don't include this in
9191 # Hina's thesis.)
9192
9193 dat$voice <- factor(dat$voice,levels = c(1,2),labels = c("Male", "Female"))
9194
9195 # Create 2 new variables combining voice and study arm to facilitate analyses
9196
9197 dat$viz_voice <- as.factor(paste(dat$viz,dat$voice,sep="_"))
9198 dat$studyarm_voice <- as.factor(paste(dat$studyarm,dat$voice,sep="_"))
9199
9200 # Effect of male versus female voice in herdimmm narration
9201
9202 datHerdimm <-
9203   subset(
9204     dat,
9205     dat$studyarm == "herdimmmgeneric" |
9206     dat$studyarm == "herdimmmmeasles" |
9207     dat$studyarm == "herdimmpertussis" |
9208     dat$studyarm == "herdimmmflu"
9209   )
9210
9211 # Analysis for risk perception, adjusted for covariates and moderators, with
9212 # interaction of gender
9213 # of respondents
9214 options(contrasts=c("contr.sum", "contr.poly")) # CHANGELOG: Added to calculate
9215 properly the type III sum of squares with lm 2021-07-27
9216 mHV_RP <- lm(
9217   mean_riskperception2_6 ~
9218     studyarm * voice * genderidentity +
9219     mean_indivhorz +
9220     mean_indivvertical +
9221     mean_collhorz +
9222     mean_collvertical +
9223     bornincanada + #CHANGELOG ASJ: covariate list shortened 2021-08-04
9224     language_1 +
9225     language_2 +
9226     Asian_group +
9227     White_group +
9228     disability_any +
9229     income +
9230     edhi +
9231     age,
9232   data = datHerdimm
9233 )
9234 Anova(mHV_RP,type="III")
9235 summary(mHV_RP)
9236
9237 # The same analysis will be done for the other outcomes, and the model will be
9238 # validated as for the
9239 # main analyses. If there is an effect of voice in the above model, the 2-way ANOVA

```

```

model
9234 # (viz*disease) and one-way anova model (studyarm) per disease will be done again. In
these new
9235 # models, Herdimm technique will be divided according to the voice gender. The factors
for the
9236 # two-way anova will be viz_voice and disease. The factor for the one-way anova will be
9237 # studyarm_voice.
9238
9239 #CHANGELOG ASJ: Add this model for other continuous outcomes, 2021-08-05.
9240
9241 mHV_emot <- lm(
9242   mean_emotion ~
9243     studyarm * voice * genderidentity +
9244     mean_indivhorz +
9245     mean_indivvertical +
9246     mean_collhorz +
9247     mean_collvertical +
9248     bornincanada +
9249     language_1 +
9250     language_2 +
9251     Asian_group +
9252     White_group +
9253     disability_any +
9254     income +
9255     edhi +
9256     age,
9257   data = datHerdimm
9258 )
9259 Anova(mHV_emot,type="III")
9260
9261 mHV_know <- lm(
9262   sum_knowledge ~
9263     studyarm * voice * genderidentity +
9264     mean_indivhorz +
9265     mean_indivvertical +
9266     mean_collhorz +
9267     mean_collvertical +
9268     bornincanada +
9269     language_1 +
9270     language_2 +
9271     Asian_group +
9272     White_group +
9273     disability_any +
9274     income +
9275     edhi +
9276     age,
9277   data = datHerdimm
9278 )
9279 Anova(mHV_know,type="III")
9280
9281 #Logistic regressions
9282 rlHV_RP1 <- glm(
9283   relevel(RP1_dicho,ref="Low") ~
9284     studyarm * voice * genderidentity +
9285     mean_indivhorz +
9286     mean_indivvertical +
9287     mean_collhorz +
9288     mean_collvertical +
9289     bornincanada +
9290     language_1 +
9291     language_2 +
9292     Asian_group +
9293     White_group +
9294     disability_any +
9295     income +
9296     edhi +
9297     age,
9298   data = datHerdimm,family=binomial("logit")
9299 )

```

```

9300 Anova(rlHV_RP1,type="III")
9301
9302 rlHV_c19vi <- glm(
9303   relevel(c19vaxintent,ref="Low") ~
9304     studyarm * voice * genderidentity +
9305     mean_indivhorz +
9306     mean_indivvertical +
9307     mean_collhorz +
9308     mean_collvertical +
9309     bornincanada +
9310     language_1 +
9311     language_2 +
9312     Asian_group +
9313     White_group +
9314     disability_any +
9315     income +
9316     edhi +
9317     age,
9318   data = datHerdimm,family=binomial("logit")
9319 )
9320 Anova(rlHV_c19vi,type="III")
9321
9322
9323 rlHV_vi <- glm(
9324   relevel(vaxintent,ref="Low") ~
9325     studyarm * voice * genderidentity +
9326     mean_indivhorz +
9327     mean_indivvertical +
9328     mean_collhorz +
9329     mean_collvertical +
9330     bornincanada +
9331     language_1 +
9332     language_2 +
9333     Asian_group +
9334     White_group +
9335     disability_any +
9336     income +
9337     edhi +
9338     age,
9339   data = datHerdimm,family=binomial("logit")
9340 )
9341 Anova(rlHV_vi,type="III")
9342
9343 rlHV_Hti <- glm(
9344   relevel(Htrustinfo,ref="No") ~
9345     studyarm * voice * genderidentity +
9346     mean_indivhorz +
9347     mean_indivvertical +
9348     mean_collhorz +
9349     mean_collvertical +
9350     bornincanada +
9351     language_1 +
9352     language_2 +
9353     Asian_group +
9354     White_group +
9355     disability_any +
9356     income +
9357     edhi +
9358     age,
9359   data = datHerdimm,family=binomial("logit")
9360 )
9361 Anova(rlHV_Hti,type="III")
9362
9363 #CHANGELOG ASJ: Add same analysis for C5 subscales, 21-09-20.
9364 rlHV_C5conf <- glm(
9365   relevel(as.factor(mean_C5_conf2),ref="0") ~
9366     studyarm * voice * genderidentity +
9367     mean_indivhorz +
9368     mean_indivvertical +

```

```

9369     mean_collhorz +
9370     mean_collvertical +
9371     bornincanada +
9372     language_1 +
9373     language_2 +
9374     Asian_group +
9375     White_group +
9376     disability_any +
9377     income +
9378     edhi +
9379     age,
9380     data = datHerdimm, family=binomial("logit")
9381 )
9382 Anova(rlHV_C5conf, type="III")
9383
9384 rlHV_C5cons <- glm(
9385     relevel(as.factor(mean_C5_cons2), ref="0") ~
9386     studyarm * voice * genderidentity +
9387     mean_indivhorz +
9388     mean_indivvertical +
9389     mean_collhorz +
9390     mean_collvertical +
9391     bornincanada +
9392     language_1 +
9393     language_2 +
9394     Asian_group +
9395     White_group +
9396     disability_any +
9397     income +
9398     edhi +
9399     age,
9400     data = datHerdimm, family=binomial("logit")
9401 )
9402 Anova(rlHV_C5cons, type="III")
9403
9404 rlHV_C5comp <- glm(
9405     relevel(as.factor(mean_C5_comp2), ref="0") ~
9406     studyarm * voice * genderidentity +
9407     mean_indivhorz +
9408     mean_indivvertical +
9409     mean_collhorz +
9410     mean_collvertical +
9411     bornincanada +
9412     language_1 +
9413     language_2 +
9414     Asian_group +
9415     White_group +
9416     disability_any +
9417     income +
9418     edhi +
9419     age,
9420     data = datHerdimm, family=binomial("logit")
9421 )
9422 Anova(rlHV_C5comp, type="III")
9423
9424
9425 rlHV_C5calc <- glm(
9426     relevel(as.factor(mean_C5_calc2), ref="0") ~
9427     studyarm * voice * genderidentity +
9428     mean_indivhorz +
9429     mean_indivvertical +
9430     mean_collhorz +
9431     mean_collvertical +
9432     bornincanada +
9433     language_1 +
9434     language_2 +
9435     Asian_group +
9436     White_group +
9437     disability_any +

```

```
9438     income +
9439     edhi +
9440     age,
9441     data = datHerdimm, family=binomial("logit")
9442 )
9443 Anova(r1HV_C5calc, type="III")
9444
9445
9446 r1HV_C5coll <- glm(
9447     relevel(as.factor(mean_C5_coll2), ref="0") ~
9448     studyarm * voice * genderidentity +
9449     mean_indivhorz +
9450     mean_indivvertical +
9451     mean_collhorz +
9452     mean_collvertical +
9453     bornincanada +
9454     language_1 +
9455     language_2 +
9456     Asian_group +
9457     White_group +
9458     disability_any +
9459     income +
9460     edhi +
9461     age,
9462     data = datHerdimm, family=binomial("logit")
9463 )
9464 Anova(r1HV_C5coll, type="III")
9465
9466
9467 ##### END #####
9468
9469
```