Statistical Analysis Plan for:

Olfactory contributions to sleep-dependent food craving and calorie intake

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fMRI data pre-processing

Pre-processing of fMRI data was performed using SPM12 (http://www.fil.ion.ucl.ac.uk/spm/software/spm12/). For each participant, we aligned all functional volumes for both sleep sessions to the first acquired functional volume to correct for head motion. We then realigned and averaged the ten whole-brain EPI volumes, and co-registered the mean whole-brain EPI to the anatomical T1 image. The mean functional volume was then co-registered to the mean whole-brain EPI, and this transformation was applied to all functional volumes. Spatial normalization was performed by normalizing the T1 anatomical images to the MNI (Montreal Neurological Institute) space using the six tissue probability map provided by SPM12. For multivariate analysis, the resulting deformation fields were applied to searchlight-based maps of decoding accuracy (see below). The normalized decoding accuracy maps were spatially smoothed with a 6 x 6 x 6 mm full-width half-maximum (FWHM) Gaussian kernel before group-level statistical testing. For functional connectivity and univariate analyses (see below), the motion-corrected and co-registered functional images were normalized to MNI space using the previously estimated deformation fields and spatially smoothed with a 6 x 6 x 6 mm FWHM Gaussian kernel.

Multivoxel pattern analysis

We implemented a searchlight-based multi-voxel pattern analysis (MVPA) (Howard & Kahnt, 2018; Kahnt, Grueschow, Speck, & Haynes, 2011) to decode information about food vs. non-food odors. We first estimated general linear models (GLM) for each subject, separately for each session, using the non-normalized and un-smoothed functional images. The GLM included three regressors of interest specifying onset times for the following conditions: 1) food odors, 2) non-food odors, 3) clean air. We also included the following nuisance regressors: the smoothed and normalized respiratory trace, down-sampled to scanner temporal resolution (0.5 Hz); the 6 realignment parameters (3 translations, 3 rotations), calculated for each volume during motion correction; the derivate, square, and the square of the derivative of each realignment regressor; the absolute signal difference between even and odd slices, and the variance across slices in each functional volume (to account for fMRI signal fluctuation caused by within-volume head motion); additional regressors as needed to model out individual volumes in which particularly strong head motion occurred (absolute difference between odd and even slices >5 SD or slice variance >4 SD). The parameter estimates from the first two regressors of this GLM reflect the voxel-wise response amplitudes for food and non-food odors, separately for each run and sleep session.

Next, we used these voxel-wise parameter estimates in a searchlight-based, leave-one-run-out cross-validated decoding approach. We decoded food vs. non-food odors from patterns of odor-evoked activity, separately for each of the two sleep sessions. We used The Decoding Toolbox (TDT) to implement the searchlight (Hebart, Gorgen, & Haynes, 2014) and LIBSVM (Chang & Lin, 2011) for the linear support vector machine (SVM) classifier. To test for brain regions that encoded food vs. non-food odors, at each searchlight (sphere with 8 mm radius), we trained a SVM to discriminate between activity patterns evoked by food vs. non-food odors in three of the four runs per session (DS or NDS), and tested it on activity patterns evoked by food vs. non-food from the fourth “left out” run of the same session. The procedure was repeated four times leaving a different run out, and decoding accuracies were averaged and mapped to the center voxel of the searchlight. This procedure was repeated for every voxel within a 10% gray-matter mask (based on SPMs tissue probability map that was inverse-normalized into the individual native space, as described in (Howard & Kahnt, 2018)). The resulting accuracy maps for food vs. non-food odors for DS and NDS sessions were subtracted (DS > NDS), normalized, and smoothed (6mm FWHM). We tested for significant differences between DS and NDS sessions at the group level using voxel-wise one-sample t-tests. Statistical thresholds were set to $P<0.05$, family-wise error (FWE)

small-volume corrected for multiple comparisons at the voxel-level in a functional mask of piriform cortex that was obtained from a one-sample t-test of decoding accuracy for food vs. non-food odors, averaged across sleep sessions.

Analysis of food intake

Food items were weighed before and after eating to determine the amount of food consumed. Total calorie and energy density (kcal/g) of consumed food was calculated from the product nutrition labels. Changes in food intake in the deprived sleep (DS) session were computed as percentage change from non-sleep deprived baseline (NSD) and tested against zero using one-sample t-tests.

Analysis of hormones

Ghrelin, leptin, insulin, and cortisol were measured in blood samples collected at each session. Changes in hormone levels in the deprived sleep (DS) session were computed as percentage change from non-sleep deprived baseline (NSD) and tested against zero using one-sample t-tests.

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