

Project title:

Effekten av högintensiv träning på vita blodkroppar, med speciellt fokus på funktion kopplad till att bekämpa cancerceller.

Date: 18th of June 2024

SAP – statistical analysis plan

In general, statistical analysis is performed using GraphPad Prism version 10.1.12 (324). The statistical analysis of the RNAseq data was performed by the core facility BEA at Karolinska Institutet. In brief, Fastq-files were aligned to GRCh38 using STAR. Gene counts were processed using DESeq2 and the Wald test, with the apeglm method for log fold change shrinkage. The design was ~individual+condition (pre- or post-exercise). Benjamini & Hochberg was employed to adjust for multiple testing. Gene set enrichment analysis was performed using the fgsea package and the function fsgseaMultilevel in R version 4.1.2 to compare the signature of genes in CD8+ cells post and pre-exercise versus the GO signatures from the Molecular Signatures Database.

For the blood gas data and the absolute cell number data, one-way RM ANOVA with Tukey´s multiple comparisons test was utilized. For analysis of flow cytometry data, paired t-test was used both for pre/post comparison of individual surface marker expressions and for the cluster analysis. For metabolism assays using SeaHorse, RM two-way ANOVA with Sídáks multiple comparison test and paired t-test was used. For the analysis of IFN-gamma expression, paired t-test was used. For the cytotoxicity data, RM two-way ANOVA with Sídáks multiple comparison test was used.