README SALAD Analyses 2020-22 - Lara Wieland, Claudia Ebrahimi & Teresa Katthagen

**Figures from manuscript:**

F1

1. created with draw.io based on study design
2. created from Task\_pptx (SALAD/plots/design) with actually used stimuli (geometrical figures found in SALAD/plot/match\_mri)

F2 created with SALAD\_cortisol.Rmd section

F3 created with SALAD\_fmri section 8)

F4 created with makeFigure\_pxp.m:

F5 created with MRICron on the base of SPM output

**Matlab (cbm) - Modeling (for modeling)**

loop\_SALAD\_Op\_CT.mlx (for 'step 1 model space')

takes behavioral data in .mat files (sorted into ST and CT and 160 trials long) and transforms them for cbm input; model space: 8 models, saved in hbi8models\_CT.mat

loop\_SALAD\_Op\_bothCond.mlx: (for 'step 2 model space')

takes behavioral data in .mat files (appended 1-160: CT, 161-320: ST) and transforms them for cbm input, model space: 4 models, saved in hbi\_bothCond\_scaling\_full.mat

makeFigure\_pxp.m: for F4

**R Markdowns (major analyses scripts accessing data after R Scripts have prepped)**

R scripts can all be found in folders *scripts* and *preps*, behavioral figures in folder *plots*

SALAD\_behav:

* descriptive analyses of demographic/neuropsychological data (reproduced Zsuzsi's scripts)
* repeated measurement ANOVAS and respective plots

SALAD\_hierarchical:

* excludes NA trials (marked by RT = 0) for LME analyses and set contrasts
* sets up mixed models separately + together for HC/AUD (p\_correct, lswitch, wstay and RT)
* post-hoc analyses with emmip

SALAD\_plot\_rep\_mes: (for poster, not manuscript)

* behav plots with single data points and distributions by tutorial

SALAD\_fmri:

* plots of VOI and behav
* plots of VOI and modeling

SALAD\_cortisol

* descriptive plots of cortisol distribution from T1-T6
* plots of correlations between cortisol measures and behav outcomes for correct
* exploratory analyses, dichotomized by WM capacity (wm\_cap) and lifetime stress (PSS)

SALAD\_cbmmodeling:

* plots of behavioral and neuropsychological data + cbm modeling parameters (best model fit: DU model with 2 alphas and 2 betas 'model\_RL\_DU2al\_2betas\_withStress\_NoScaling')

**R Scripts (preparation and import)**

data\_import: imports all behavioral datasets (explanations in README\_filename)

prep\_agg: renames behavioral variables according to order (A = CT first and ST second, B = ST first and CT second day) for full dataset (dat) and just final HC sample (n = 28)

longtowide\_agg: uses datasets created in prep\_agg and transforms behavioral data of 3 major outcome variables (correct, winstay, loseswitch) to long format

import\_singletrial\_data:

* uses *data\_strials* (2\*160 trials per subject in long format) and creates two indices for SALAD\_hierarchical.Rmd  
  - condtrial: 1-55 (1st phase), 1-70 (2nd phase), 1-35 (3rd phase)  
  - volat: 1 (1st phase: pre/stable), 2 (2nd phase: rev/reversal), 3 (3rd phase: post/stable)
* creates *data\_prep* uses Choice\_t (chose Card 1 or 2, directly imported from Matlab): 1/-1 and Outcome (win or loss) 1/0 to calculate  
  switch: always describes next row after change from 1 or -1;  
  w\_stay: if stay = 1 and Outcome = 1

cort\_import: imports *cort\_data* and z*eitablauf\_selection,* calculates two measures for cortisol:   
1. AUC according to Pruessner, 2003  
2. Z\_Peak according to e.g. Luettgau, 2018

prep\_cort\_behav: merges behavioral, cortisol and singletrial datasets (so far only for HC)

rev\_sens\_singletrial: prepares reversal sensitivity index analyses (Cremer, 2020)