Data prep script 2: Compute NIH Toolbox Flanker Score

Template Rmd

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Contents

About

This script computes the NIH Toolbox Flanker score

1. Get Setup

1.1. Clear everything & set width

```
options(width=80, Ncpus = 6) #Set width
rm(list=ls())     #Remove everything from environment
cat("\014")       #Clear Console
```

1.2. Load Libraries

```
  # renv::restore()     #restore environment
  library(knitr)      #allows rmarkdown files
  library(haven)      #helps import stata
  library(questionr)  #allows lookfor function
  library(MASS)       #calculate residualized scores
  library(tidyverse)  #plotting/cleaning, etc.
  library(broom)      #nice statistical output
  library(here)       #nice file paths
  library(expss)      #labeling variables/values
  library(psych)      #used for statistical analyses
  library(workflowr)  #helps with workflow
```

1.3. Get the Working Directory

```
  here()
```

```
## [1] "/Users/brentrappaport/Documents/temp_files/DDM/work"
```

1.4. Set seed

```
     set.seed(312)    #Set seed
```

1.5 Load Data

Remember to immediately rename and remove. Avoid overwriting old data.

```
here::i_am("work/management/data02_LDDM_rdoc.Rmd")
```

```
## here() starts at /Users/brentrappaport/Documents/temp_files/DDM
```

```
LDDM_cleaning04_fullbeh_rdoc <- read.csv(here("./RDoC/DDM_Trialwise_Prepped/Block-Based/RDoC_ERN_HDDM_da
```

3.1 All trials

```
# Setup the dataset with the needed variables (eg., ID, block # 1-11, trial # 1-30 per block)
LDDM_cleaning04_rdoc_calc1 <- LDDM_cleaning04_fullbeh_rdoc %>%
  group_by(subj_idx) %>%
  mutate(block = c(rep(1,30),rep(2,30),rep(3,30),rep(4,30),rep(5,30),rep(6,30),rep(7,30),rep(8,30),rep(
  group_by(subj_idx, block) %>%
  mutate(trial = 1:30) %>%
  filter(rt<999)

# Calculate the accuracy per subject (according to NIH toolbox this should be the number of correct res
LDDM_cleaning04_rdoc_calc2 <- LDDM_cleaning04_rdoc_calc1 %>%
  group_by(subj_idx) %>%
  reframe(accuracy_score = sum(response==1)*(5/length(trial)))

LDDM_cleaning04_rdoc_ind <-  LDDM_cleaning04_rdoc_calc1 %>%
  group_by(subj_idx) %>% # per subject
  filter(stim=="incongruent" & response==1) %>% #incongruent trials with correct response
  mutate(mean_rt = mean(rt),
         sd_rt = sd(rt)) %>% # compute individual mean and sd RT
  filter(rt>=0.1 & rt>(mean_rt - 3*sd_rt) & rt<(mean_rt + 3*sd_rt)) %>% #remove trials less than 100ms
  reframe(med_rt = median(rt)*1000) %>% # compute individual level median RT
  mutate(rt_score = 5-(5*((log(med_rt)-log(250))/(log(1000)-log(250)))),
         rt_score_truncated = 5-(5*((log(med_rt)-log(500))/(log(3000)-log(500)))))

LDDM_cleaning04_rdoc_calc3 <- LDDM_cleaning04_rdoc_calc1 %>%
  full_join(LDDM_cleaning04_rdoc_ind, by = 'subj_idx') %>%
  full_join(LDDM_cleaning04_rdoc_calc2, by='subj_idx') %>%
  group_by(subj_idx) %>% # per subject
  mutate(total_accuracy_perc = sum(response==1)/length(response)) %>% # compute total accuracy percenta
  reframe(flanker_score_list_rdoc = if_else(total_accuracy_perc>0.8, accuracy_score+rt_score, accuracy_
          flanker_score_list_rdoc_truncated = if_else(total_accuracy_perc>0.8, accuracy_score+rt_scor
          accuracy = mean(total_accuracy_perc)) %>%# if accuracy is above 80% then add accuracy and r
  transmute(ID=subj_idx, flanker_score_list_rdoc=flanker_score_list_rdoc, flanker_score_list_rdoc_trunca
  group_by(ID) %>% # per subject
  reframe(flanker_score_rdoc = mean(flanker_score_list_rdoc),
          flanker_score_rdoc_truncated = mean(flanker_score_list_rdoc_truncated),
          accuracy = mean(accuracy))

LDDM_cleaning04_rdoc_accuracy_by_condition <- LDDM_cleaning04_rdoc_calc1 %>%
  full_join(LDDM_cleaning04_rdoc_ind, by = 'subj_idx') %>%
  full_join(LDDM_cleaning04_rdoc_calc2, by='subj_idx') %>%
  group_by(subj_idx, stim) %>% # per subject
  mutate(total_accuracy_perc = sum(response==1)/length(response)) %>% # compute total accuracy percenta
  reframe(accuracy_by_stim = mean(total_accuracy_perc)) %>%
  pivot_wider(names_from=stim, values_from=accuracy_by_stim, id_cols=subj_idx, names_prefix="accuracy_"
  mutate(ID=subj_idx,
         accuracy_congruent_log = log(accuracy_congruent))

LDDM_cleaning04_rdoc_calc4 <- full_join(LDDM_cleaning04_rdoc_calc3, LDDM_cleaning04_rdoc_accuracy_by_con
  select(-subj_idx)
```

Only 20 trials

```
# Setup the dataset with the needed variables (eg., ID, block # 1-11, trial # 1-30 per block)
LDDM_cleaning04_rdoc_calc1_short_incon <- LDDM_cleaning04_rdoc_calc1 %>%
  group_by(subj_idx) %>%
  filter(stim=="incongruent") %>%
  slice_head(n=8)

LDDM_cleaning04_rdoc_calc1_short_con <- LDDM_cleaning04_rdoc_calc1 %>%
  group_by(subj_idx) %>%
  filter(stim=="congruent") %>%
  slice_head(n=12)

LDDM_cleaning04_rdoc_calc1_short <- rbind(LDDM_cleaning04_rdoc_calc1_short_incon, LDDM_cleaning04_rdoc_c
  arrange(subj_idx)

# Calculate the accuracy per subject (according to NIH toolbox this should be the number of correct res
LDDM_cleaning04_rdoc_calc2_short <- LDDM_cleaning04_rdoc_calc1_short %>%
  group_by(subj_idx) %>%
  reframe(accuracy_score = sum(response==1)*(5/length(trial)))

LDDM_cleaning04_rdoc_ind_short <-  LDDM_cleaning04_rdoc_calc1_short %>%
  group_by(subj_idx) %>% # per subject
  filter(stim=="incongruent" & response==1) %>% #incongruent trials with correct response
  mutate(mean_rt = mean(rt),
         sd_rt = sd(rt)) %>% # compute individual mean and sd RT
  filter(rt>=0.1 & rt>(mean_rt - 3*sd_rt) & rt<(mean_rt + 3*sd_rt)) %>% #remove trials less than 100ms
  reframe(med_rt = median(rt)*1000) %>% # compute individual level median RT
  mutate(rt_score = 5-(5*((log(med_rt)-log(250))/(log(1000)-log(250)))),
         rt_score_truncated = 5-(5*((log(med_rt)-log(500))/(log(3000)-log(500)))))

LDDM_cleaning04_rdoc_calc3_short <- LDDM_cleaning04_rdoc_calc1_short %>%
  full_join(LDDM_cleaning04_rdoc_ind, by = 'subj_idx') %>%
  full_join(LDDM_cleaning04_rdoc_calc2, by='subj_idx') %>%
  group_by(subj_idx) %>% # per subject
  mutate(total_accuracy_perc = sum(response==1)/length(response)) %>% # compute total accuracy percenta
  reframe(flanker_score_list_rdoc = if_else(total_accuracy_perc>0.8, accuracy_score+rt_score, accuracy_s
          flanker_score_list_rdoc_truncated = if_else(total_accuracy_perc>0.8, accuracy_score+rt_scor
          accuracy = mean(total_accuracy_perc)) %>%# if accuracy is above 80% then add accuracy and r
  transmute(ID=subj_idx, flanker_score_list_rdoc=flanker_score_list_rdoc, flanker_score_list_rdoc_trunca
  group_by(ID) %>% # per subject
  reframe(flanker_score_rdoc = mean(flanker_score_list_rdoc),
          flanker_score_rdoc_truncated = mean(flanker_score_list_rdoc_truncated),
          accuracy = mean(accuracy))
```

4. Closing out

In this step, go ahead and close out of the file and quit R without saving the work space.

```
save(LDDM_cleaning04_fullbeh_rdoc, file=here("./work/data/LDDM_cleaning04_fullbeh_rdoc.RData"))

save(LDDM_cleaning04_rdoc_calc4, LDDM_cleaning04_rdoc_calc1, LDDM_cleaning04_rdoc_calc3_short, LDDM_clea
   # renv::snapshot()   #Take a snapshot of environment
```