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## Directories

All participant data should be stored in the Participant\_Data directory on Box under the RO1\_Brain\_Mechanisms\_IRB\_5357 study folder. Below you will find a figure depicting the directory structure and specific directory descriptions.

### Folder Tree



### Directory Descriptions

##### 1) Actigraph

Actigraphs collect motion related data during waking and sleeping hours for 1 week for each participant. Here the raw, scored, and validated data are separated into directories during processing

* 1. **RawData**: contains all raw actigraph files
  2. **ScoredData:** contains directories for each individual participant that contain all the processed and scored data
  3. **ValidatedData:** contains an Excel file for each participant with the validated data

##### 2) DXA

Contains pdf outputs from visit 1 and visit 7 dual-energy x-ray absorptiometry (DXA or DEXA) scans.

##### 3) Interoception

Contains all data for the Interoception task and heart rate variability

* 1. **HRV**: contains all raw and processed data and results
     1. **Raw**
  2. **interoception\_heartbeat task:**
     1. **articles**
     2. **old**

##### 4) GNG

The Go-No Go task data follows the same directory tree structure as other experimental computer tasks (‘Task Tree’ on figure).

1. **GNG Task with pseudorandomization**: contains the most up to date E-Prime task and stimuli
2. **GNG\_Databases**: contains 3 databases with performance summary data for all participants—a wide and long format .csv database with the standard summary metrix and one .txt database with summary data needed for Drift Diffusion Modeling.
3. **GNG\_Processed\_Data\_Files**: contains .txt raw data files that have been processed/cleaned up from the raw Eprime output
4. **GNG\_Raw\_Data\_Files**: contains the raw Eprime output (.edat3, .txt, .xml).
   * 1. NOTE: the .txt files do differ. “GNG\_Zoo\_Raw\_###-#” is the exported raw data and is used in data processing; “Go No-Go Zoo Task1-###-#” is the .txt used to re-generate the .edat3 file using the ERecovery program
5. **GNG\_Scripts**: The matlab script “GNG\_Zoo\_neutral\_RO1.m” used to process the raw data is stored here. Also, a ParticipantEdits\_specificScripts directory contains edits of that script to hand participant specific data issues.
   * 1. NOTE: The Kathleen\_nogo\_DDM\_old directory contains shana’s old Drift Diffusion Modeling R scripts. These need to be edited.
6. **GNG\_Task\_old**: old task version

##### 5) SST

The SST task data follows the same directory tree structure as other experimental computer tasks (‘Task Tree’ on figure).

1. **SST\_KellerRO1\_FoodPort**: contains the most up to date Matlab/PsychToolbox task script and stimuli
2. **SST\_Databases**: contains 2 databases with performance summary data for all participants—a wide and long format .csv database
3. **SST\_Processed\_Data\_Files**: contains .txt raw data files that have been processed/cleaned up from the raw task output
4. **SST\_Raw\_Data\_Files**: contains the raw task output .txt files
5. **SST\_Scripts**: The matlab script “SST\_RO1.m” used to process the raw data is stored here.

##### 6) NBack

The NBACK task data follows the same directory tree structure as other experimental computer tasks (‘Task Tree’ on figure).

1. **NBack\_Task**: contains the most up to date Eprime task script and Excel file used to randomize stimuli
2. **NBack\_Databases**: contains 2 databases with performance summary data for all participants—a wide and long format .csv database
3. **NBack\_Processed\_Data\_Files**: contains .txt raw data files that have been processed/cleaned up from the raw task output—there is one per working memory load/task condition per participant
4. **NBack\_Raw\_Data\_Files**: contains the raw Eprime output (.edat3, .txt, .xml).
   * 1. NOTE: the .txt files do differ. ““Nback\_#\_Raw -###-#” is the exported raw data and is used in data processing; ““#-back\_RO1-###-#” is the .txt used to re-generate the .edat3 file using the ERecovery program
5. **NBack\_Scripts**: The matlab script “NBack\_RO1.m” used to process the raw data is stored here.

##### 7) SpaceGame

The SpaceGame task data follows the same directory tree structure as other experimental computer tasks (‘Task Tree’ on figure).

1. **SpaceGame\_Task**: contains the most up to date MATLAB task script. The primary task version that is run is found in the ‘RightConsolePC\_version’ directory and has all instruction spacing optimized for the PC on the right side of the console room in 311. There is also one script under the directory ‘arbitration\_psychtoolbox’ that is the edited version that works on the MacPro in 302—may not be as up to date as new features are first added to the PC version.
2. **SpaceGame\_Databases**: UPDATE
3. **SpaceGame\_Processed\_Data\_Files**: UPDATE FILE STRUCTURE raw data files that have been processed/cleaned up from the raw task output—there is one per working memory load/task condition per participant
4. **SpaceGame\_Raw\_Data\_Files**: contains the raw MATLAB data output (.mat).
5. **SpaceGame\_Scripts**: UPDATE

##### 7) fMRI

This directory contains the imaging data, task, and scripts. Its directory structure is depicted in the figure

* 1. **ImagingData**: contains all raw and processed data and results
     1. **Level1GLM**: directory structure is depicted in the figure in the ‘Level1 Tree’ box. This directory contains all data for the first level general linear model conducted by AFNI.
        1. Session#->ParticipantFolder-> **anat\_warped\***: this directory is created by AFNI’s @SSwarper script, which uses non-linear warping to register the anatomical MPRAGE to a standard MNI template. The snapshots directory contains quality control (QC) images. The directory with “\_ped” will be aligned to the Haskins pediatric template. The other directory is aligned to the MNI152 2009 template.
        2. Session#->ParticipantFolder-> **data\_orig**: this directory is created by a file organization bash/tcsh script that copies raw data into AFNI .BRIK and .HEAD format and labels it correctly.
        3. Session#->ParticipantFolder->**physio:** this directory contains the processed physio files to be used in afni\_proc.py
        4. Session#->ParticipantFolder-> **\*proc.results\***: this directory is created by AFNI’s afni\_proc.py script and contains all first level glm data, the design matrix, motion files, masks, etc. See the data processing section on afni\_proc.py for more information about specific files. Prefixes to the “proc.results” indicate follow-up processing with selected thresholds. The folder with no prefix represents the first processing and is likely not used further. Directories with ‘\_ped’ used the SSwarped anatomical volume that was aligned the Haskins pediatric template. The other directory uses the SSward antatomical volume that was aligned to the MNI152 2009 template.
           1. **AddEdge:** this directory was created by afni\_proc.py and contains anatomical volumes with the edges between tissues enhanced. Can be used for quality control on alignment.
           2. **files\_ACF:** this directory was created by afni\_proc.py and contains the autocorrelation function curve at different radii—used for spatial normalization (blur) after raw signal is extracted
           3. **QC:** this directory was created by 6\_epi\_QC\_snapshots script and contains images to help check the quality of epi-anatomical alignment
           4. **ss\_motion.output**: this folder was created by a motion\_qc script to extract TRs excluded by run at different motion thresholds. Raw output is saved here. This is ONLY in the “proc.results” folder with no pre-amble. It is only run once (i.e., won’t be in a proc.results2 folder).
           5. **ss\_qc.output:** contains snapshots and other information for QC
           6. **stimuli:** this directory was created by afni\_proc.py and contains the copied stimulus onset files.
     2. **Level2GLM**: directory structure TBD. Will be based on the group level statistical models:
        1. **1sampleT**: this directory contains two all past and current 1 sample t-test model results
           1. **Date (##-##-##):** contains the most up to date models
           2. **Old:** all previous date directories are moved here when model is re-run
        2. **2sampleT:** this directory contains all possible 2 sample t-tests (e.g., between groups and stimuli categories)
           1. **Date (##-##-##):** contains the most up to date models
           2. **Old:** all previous date directories are moved here when model is re-run
        3. **ClustExp\_ParList:** this directory contains a file named ParList.csv—this file is a list of all participants that have been processed/are included in group models, their group, and the end of their file path to their stats.001-1+tlrc file (in proc.results) for each contrast/regressor. This is used in Gopt\_ParList\_user to create a file for the specific user who. There is also a user\_AllParStats\_date afni data sets that were made by Gopt\_parDSET\_user—these are datasets where each person and contrast is a brick (i.e., each person will have 6 bricks). The user\_AllParStats\_date can then be used to extract beta values from group model clusters using Gop\_ROIstats\_user.
           1. **Old:** all previous date user specific files are moved here when new ones are created
        4. **ANOVAs:**
     3. **MotionDatasets**: contains processed/cleaned motion datasets and an overall motion database
     4. **PhysioData**:contains all raw physio time courses for each session and participant in their own directory
     5. **RawConverted**: contains converted raw imaging data for each session and participant in their own directory
     6. **RawDicom**: contains raw DICOM files for each session and participant in their own directory
  2. **fMRI\_ProcNotes:** this directory contains template fMRI\_ProcNotes pdf and a R01\_fmri\_processingnotes Excel file to document overall issues/stages of processing.
     1. **Participant\_ProcNotes:** this directory contains all the individual participant ProcNotes .pdfs documenting all processing information
  3. **R:** this directory contains the all R scripts for processing Imaging data
  4. **R01\_fMRI\_task:**
     1. **Scanner\_Task**: contains the most up to date Eprime task script and Excel file used to randomize stimuli
     2. **R01\_fMRI\_Databases**: contains 2 databases with performance summary data for all participants—a wide and long format .csv database
        1. **TaskFixDurations:** this directory contains .txt files with the durations of all inter-block fixations
        2. **TaskOnsetErrors:** this directory contains either a “NoErrors” or “Errors” .txt for each participant listing any errors in their scanner behavioral data
        3. **TaskOnsets\_AFNI:** this directory contains the onset files needed for each participant
     3. **R01\_fMRI\_Processed\_Data\_Files**: contains .txt raw data files that have been processed/cleaned up from the raw task output—there is one per working memory load/task condition per participant
     4. **R01\_fMRI\_Raw\_Data\_Files**: contains the raw Eprime output (.edat3, .txt, .xml).
     5. **R01\_fMRI\_Scripts**: The matlab script “NBack\_RO1.m” used to process the raw data is stored here.
  5. **Scripts:** this directory contains all scripts relevant to processes imaging data
     1. **gen\_proc\_scripts:** template directory that is used to create individual participant proc\_script directories.
     2. **R01\_\*\_proc\_scripts**: These directories (one per participant) contain all individual participant scripts needed to process the imaging activation data on ACI-ICS computing system

##### 8) Noldus Videos

This directory contains all data related to the video recordings during meals in the lab for visits 2-6

1. **Coding**: this directory contains all information needed to code behaviors during visit 2-6 meals. The file Behaviors – Definition.docx contains notes about coding and observation. The Excel sheets Noldus\_Key\_Code\_date contains the Noldus Key for each participant and a place to record notes and dates. The Excel file Noldus\_Boservations\_date contains coded data and observer/coder for each participant and visit. The Excel file RO1 test meals - Identified behaviors & dialogue contains initial observations/vocalization used to create the coding guide.
   * 1. **Noldus Technical Instructions:** contains technical instructions file for video coding meals 2-6
   1. **Vist 2-6 directories**: contain Coded and Raw directories contain the coded and raw videos, respectively

##### 9) QualtricsData\_PDFs

This directory contains all the exported PDFs from Qualtrics stored in directories by visit and the person completing (parent/child)

##### 10) Participant Contacts Database

This directory contains all participant contact information

##### 11) Post-Visit\_Checklists

This directory contains a PDF for each participant, on which data processing/post visit tasks are tracked

##### 12) SPSSDatabases

This directory contains SPSS databases from Qualtrics for each visit for parent and child surveys, SPSS syntax, and the DXA visit 1 and 7 data. Later this will need to be further organized.

## Data Processing

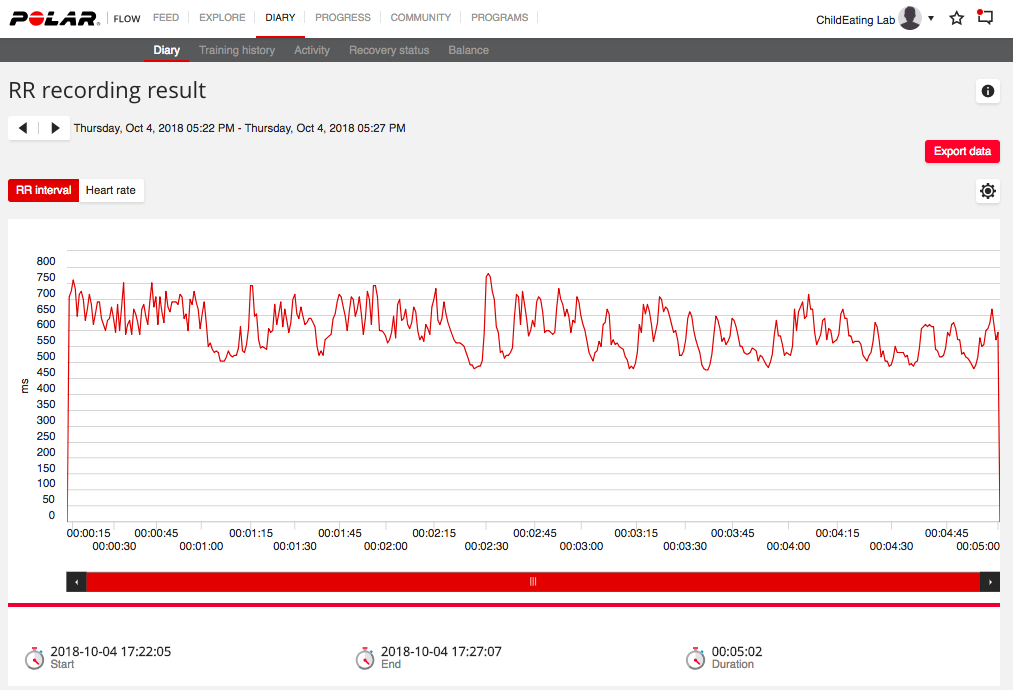
### Actigraph Data

1. Scoring Parameters
   1. EE - Use Freedson Combination (1998)
   2. METs - Use Freedson Children (2005)
   3. Cut points - Evenson Children (2008)
   4. Bouts – Checked
   5. Sedentary Analysis – Checked
   6. NO HREE
   7. Exclude Non-wear time from analysis – Checked

### DXA

### Interoception

##### Exporting data



### GNG

##### Task Design

Instructions…

12 practice trials. 5 blocks of 40 trials (30 Go/10 NoGo). Timing info… Between blocks…

##### Processing Steps

* 1. Export the file from E-Prime as a .txt files to the correct folder on Box (GNG\_Raw\_Data\_Files)
  2. Open Matlab and navigate the “Current Folder” window pane to the Box folder with the SST script (ParticipantData->GNG/GNG\_Scripts). You should see the script entitled “GNG\_Zoo\_neutral\_RO1”
     1. To run, type in the “Command Window” pane. You can process 1 participant at a time or multiple—see below:
        1. Single Participant: GNG\_Zoo\_neutral\_RO1(*participant#, session#*), where participant# is the ID number (e.g., 1) and session# is either 1 (first time completed) or 2 (completed at follow up in visit 7). Hit return.

e.g.: GNG\_Zoo\_neutral\_RO1(1, 1)

* + - 1. Multiple Participants: GNG\_Zoo\_neutral\_RO1([*participant#, participant#], 1*), where participant# is the ID number (e.g., [1, 2]) and session# is either 1 (first time completed) or 2 (completed at follow up in visit 7). Can only processes participants from same session at a time. Participant IDs must be in square brackets (e.g., [ ]) with commas separating them. A comma must also separate the end of the brackets and the session#.

e.g.: GNG\_Zoo\_neutral\_RO1([1, 2, 3], 1).

##### Standard Performance Metrics

Performace on the GNG task is typicall assessed based on correct responses and errors. Correct responses are often called ‘Hits’. There are two primary errors that can occur in the GNG task. Omission errors are when the participant failed to respond to a target/go stimuli while commission errors occur when the participant response to a NoGo trial. These types of errors are often called ‘misses’ and ‘false alarms’, respectively. In addition to response correctness, reaction time is also used to look at differences between correct responses and false alarms. The following standard measures were computed overall and by block.

1. nACC: total number of trials with a correct response or no response
2. pACC: total percent correct response and no responses
3. nGo\_Hit: total number of trials where participants correctly responded to Go stimuli
4. nNoGo\_Corr: total number of trials where participant correctly withheld/did not response to NoGo stimuli
5. nNoGo\_FA: total number of trials where participant incorrectly responded to NoGo stimuli
6. pGo\_Hit: percent of trials where participants correctly responded to Go stimuli
7. pNoGo\_Corr: percent of trials where participant correctly withheld/did not response to NoGo stimuli
8. pNoGo\_FA: percent of trials where participant incorrectly responded to NoGo stimuli
9. RTmeanGo\_Hit: mean reaction time to correct Go responses
10. RTmean NoGo\_FA: mean reaction time to incorrect responses on NoGo trials (false alarms)
11. RTmedGo\_Hit: median reaction time to correct Go responses
12. RTmed NoGo\_FA: median reaction time to incorrect responses on NoGo trials (false alarms)

##### Signal Detection

Signal Detection Theory (SDT) attempts to determine thresholds at which a person can distinguish a pattern (e.g., signal) from random patterns of noise. In the context of GNG, it is a technique to assess the ability to detect the NoGo signal during the task. Below are metrics that can be used to test signal detection and the accompanying equations. Non-parametric measures were included due to the fact because it is likely that the signal and noise distributions do not meet the following assumptions: 1) both are normal; and 2) have the same SD. It is not possible to test these assumptions with Yes/No tasks like GNG. When these assumptions are not met, sensory sensitivity will vary with differing response biases. See the following paper for an explanation of the selected measures and has excellent references for further reading: (Stanislaw & Todorov, 1999).

d’: d-prime is a parametric measure of sensory sensitivity—it is equal to the distance between the noise distribution and the signal and noise distribution

A’: A-prime is a non-parametric measure of sensory sensitivity; generally between 0.5 - 1

c: is a measure of bias—distance between the criterion and a neutral point where neither response is favored—the neutral point is where the signal and noise distributions overlap. Negative values correspond to bias to respond ‘yes’ (i.e., press for Go) and positive corresponds to bias to respond ‘No’

’’ Geir’s ): is a non-parametric measure of response bias—it is the ratio of the ordinate (i.e., height) of the signal and noise distribution at the criterion to the the ordinate of the noise distribution

The following measures were added to the database based on SDT:

* + - 1. Z\_Hit: z score derived from the Normal inverse cumulative distribution function for the probability of correct responses (percent hits)
      2. Z\_FA: z score derived from the Normal inverse cumulative distribution function for the probability of incorrect responses (percent false alarms)
      3. Z\_Hit\_mm: Macmillian corrected z score for hits for extreme values (hit rate =1, FA rate = 0)
      4. Z\_Hit\_ll: loglinear adjusted z scores for hits
      5. Z\_FA\_mm: Macmillian corrected z score for false alarms for extreme values (hit rate =1, FA rate = 0)
      6. Z\_FA\_ll: loglinear adjusted z scores for false alarms
      7. d\_prime\_mm: d’ calculated from the Macmillian adjusted z values
      8. d\_prime\_ll: d’ calculated from the loglinear adjusted z values
      9. A\_prime\_mm: A’ calculated from the Macmillian adjusted z values
      10. A\_prime\_ll: A’ calculated from the loglinear adjusted z values
      11. c\_mm: c calculated from the Macmillian adjusted z values
      12. c\_ll: c calculated from the loglinear adjusted z values
      13. Grier\_beta\_mm: ’’ calculated from the Macmillian adjusted z values
      14. Grier\_beta\_ll: ’’ calculated from the loglinear adjusted z values

##### 

##### Drift Diffusion Models

### SST

##### Task Design

##### Processing Steps

* 1. Copy all output .txt files to the correct folder on Box (SST\_Raw\_Data\_Files)
  2. Open Matlab and navigate the “Current Folder” window pane to the Box folder with the SST script (ParticipantData->SST/SST\_Scripts). You should see the script entitled “SST\_RO1”
     1. To run, type in the “Command Window” pane. You can process 1 participant at a time or multiple—see below:
        1. Single Participant: SST\_RO1(*participant###, session#*), where participant# is the 3 digit ID number (e.g., 001) and session# is either 1 (first time completed) or 2 (completed at follow up in visit 7). Hit return.

e.g.: SST\_RO1(001, 1)

* + - 1. Multiple Participants: SST\_RO1([*participant###, participant###], 1*), where participant# is the 3 digit ID number (e.g., [001, 002]) and session# is either 1 (first time completed) or 2 (completed at follow up in visit 7). Can only processes participants from same session at a time. Participant IDs must be in square brackets (e.g., [ ]) with commas separating them. A comma must also separate the end of the brackets and the session#.

e.g.: SST\_RO1([001, 002, 006], 1)

##### Standard Performance Metrics

The SST is based a measure of reactive response inhibition and adapted from the implementation in (Verbruggen, Logan, & Stevens, 2008). For a thorough discussion of the theoretical basis for the race-horse model of response inhibition see (Verbruggen & Logan, 2009). The basic premise is that participants will first activate a go-response to a stimuli. After seeing the stop stimuli, they will activate a nogo-response. If they are successful in inhibiting the go-response, the nogo-response was faster. If they fail to inhibit the go-response, the nogo-response was too slow. In this task, inhibition can be measured by manipulating the delay of the stop signal using a step-like function to hold successful stopping at a .5 probability. All data were processed as recommended in the recent consensus paper (Verbruggen et al., 2019). Below is a description of the primary performance metrics output in from the SST\_RO1.m script. They are computed for each block and labeled so a \* is used to indicate that in the name.



1. racehorse\_good: checks the racehorse assumption as stated in (Verbruggen et al., 2019); if 0, then participant performance does not match the assumptions of the model
2. \*\_go\_RTmean: average go (i.e., no signal) reaction time
3. \*\_go\_RTsd: standard deviation of go reaction times
4. \*\_go\_correct: number correct for sorting images by pressing the L/R arrow keys during no-signal/go trials
5. \*\_go\_RTmean\_correct: average go reation time for correct trials (i.e., L/R correct)
6. \*\_go\_error: number incorrect for sorting images by pressing the L/R arrow keys during no-signal/go trials
7. \*\_go\_RTmean\_error: average go reaction time for incorrect trials (i.e., L/R incorrect)
8. \*\_go\_missed: number of no-signal/go trials were response was too slow for to be recorded—if there are many of these it may indicate the participant was attempting to slow down or wait to see if the stop signal would appear
9. \*\_usRT: average uncessessful stop reaction time (i.e., reaction times for responding on stop trials)
10. \*\_signal\_probResp: this is the calculated probability of successful inhibition on trials with stop-signal. Goal is to approximate 0.5. Can use t-test against the value of 0.5 to see if differ significantly
11. \*\_ssd: average stop-signal delay
12. \*\_ssrtMean: the stop-signal response time calculated by subtraction method (go RT mean (all only) – SSD)
13. \*\_ssrtInt: the stop-signal response time calculated by the integral method
    * 1. First, this methods calculates participants probability of responding given a stop-signal (number 6 above), then it uses that value to find the nth percentile of go RT with the percentile value matching the probability of responding. Then the subtraction nth percentile RT – SSD.

### NBack

##### Processing Steps

##### Standard Performance Metrics

### fMRI

##### Processing Steps

##### Non-Linear Registration

##### afni\_proc.py

##### Quality Checks and Motion

### Noldus Videos

### Qualtrics Data

##### General

##### Household Demographics

##### Child Puberty & Tanner

##### Child Physical Activity

##### Parent Portion Size Survey (PSS)

##### Feeding Strategies

##### Portion Size Discrimination (PSD)

##### Child Portion Size Survey (CSS)

##### Child Behavior Questionnaire (CBQ)

##### Child Eating Behavior Questionnaire (CEBQ)

##### Binge Eating Scale (BES)

##### Family Food Behavior (FFB)

##### Child Sleep Habits Questionnaire (CSHQ)

##### Kid’s Food Questionnaire (KFQ)

##### Tempest Self-Regulation of Eating (TESQE)

##### Revised Children’s Manifest Anxiety Scale (RCMAS)

##### Lifestyle Behavior Checklist (LBC)

##### Parent Sensitivity to Reward and Punishment (SRSPQP)

##### Parent Weight Loss Behavior (PWLB)

##### Three Factor Eating Questionnaire (TFEQ)

##### Delay Discounting

##### Household Food Security Survey Module (HFFSM)

##### Household Food Insecurity Access Scale (HFIAS)

##### Community Childhood Hunger Identification Project (CCHIP)

##### Behavioral Rating Inventory of Executive Function-2 (BRIEF-2)

The Behavioral Rating Index of Executive Function-2 (BRIEF-2; ) is a parent-report measure of everyday executive behaviors that is normed for age and gender. T scores of 60 or greater indicate high risk/clinical relevance for symptoms. There are 9 subscales, 4 index measures, and 3 parental response checks that are calculated.

Subscales:

1. Inhibit
2. Self-Monitor
3. Shift
4. Emotional Control
5. Initiate
6. Working Memory
7. Plan/Organize
8. Task-Monitor
9. Organization of Materials

Index Measures:

1. Behavioral Regulation Index: Inhibit and Self-Monitor
2. Emotional Regulation Index: Shift and Emotional Control
3. Cognitive Regulation Index: Initiate, Working Memory, Plan/Organize, and Task-Monitor
4. General Executive Composite: all scales

Parental Response Checks:

1. Inconsistency
2. Negativity
3. Infrequency

##### Child Weight Concerns (CWC)

##### Child Body Image Scale (CBIS)

##### Parent Responsiveness (PRM/PRF)

##### Alcohol Use Disorders Identification Test (AUDIT)

##### Loss of Control Eating (LOC)

##### Communities that Care (CtC)

##### WASI

In SPSS syntax, raw scores for Matrix Reasoning and Vocabulary scales are calculated based on individual item scores. Child’s exact age in years and months is calculated based on date WASI was completed. Matrix, Vocab and FSIQ t scores and FSIQ percentiles are then calculated.

## References

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