

GROUP DIRECTORY CONTENTS /om/group/saxelab/OpenAutism

Location of TIER directory:

/om/group/saxelab/OpenAutism/TIER_OpenAutism

TIER_OpenAutism: the TIER directory, which contains all pilot_data and analysis_data (see the TIER directory pdf)

Location of group MRIQC bash scripts:

/om/group/saxelab/OpenAutism/submit_mriqc_group_job_EIB.sh

submit_mriqc_group_job_<site>.sh: runs the group level MRIQC

Location of parcels:

/om/group/saxelab/OpenAutism/Analysis/PARCELS

PARCELS: folder that contains a copy of the parcels. The parcels called from the script are within the TIER directory (see TIER directory PDF)

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All ipynb scripts:

ALL_METRICS: main script; extracts all metrics for all runs & saves csvs

Acquisition_Site_Info: returns protocol info from dicom of specific site, subject, task

autoxy_mriqc_plots: script shared with us from Mathias but was not used. Builds off mriqc statistics (e.g. fd_mean by run boxplots; fd_mean and dvars per task per subject; lookup definitions of MRIQC values). See *Replotting_MRIQC_output* script for our use.

Creating_TIER_Directory: script that creates the TIER subdirectory within OpenAutism -> analysis_data/pilot_data, called SUBJECTS. This SUBJECTS folder contains all first level and second level analyses information

Generate_Motion_Histograms: makes the histograms for motion

Identify_Missing_Files: Identifies missing files using master list

Intra_site_variance: compares principal components within sites and creates glass brains to represent regions of high variance between subjects

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All ipynb scripts:

[Motion_Threshold](#): script that generates text files with details about each run's motion. Uses FMRIprep output confound files. The script creates INCLUDE.csv file and the motion text files in the subfolder MotionTextFiles

[MRIQC_site_variance_metrics](#): Looking at IQMs that are correlated by site (Oscar Esteban)

[ppca.ipynb](#): script taken from cangermueller; this is a probabilistic pca that I thought would be useful to have. Normal PCA was ultimately used for site variance analyses for follow Murcia et al

[Replotting_MRIQC_output](#): replotting MRIQC based on included/excluded runs

[Replotting_MRIQC_output_GROUP](#): replotting MRIQC based on group (ASD vs. NT)

[Sample_ROIs.ipynb](#): script that plots the parcels on the brain for example presentations

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All ipynb scripts:

[swpca.ipynb](#): actual script used in Murcia et al looking at site variance by pca

[Testing_Site_Variance](#): tests site variance and classifies principal components (Murcia et al) based on the mean functional image by comparing two of any specified sites. Look at the following differences (sites, tasks, runs).

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All Folders:

_modules: contains a few modules that I needed to import before using I started to use the singularity image

Acquisition_Dicom_Info: contains site folders, and text files with extracted dicom info per task within site

anaconda3: software download

EVColumns: explanatory variable info for first level analyses design matrices (timestamp & duration per condition)

Histograms_Motion: all the plots in .png format describing frequency of motion outliers, percent exclusion based on different criteria, and average motion

MotionTextFiles: Files with information about motion per run

MRIQC_Scripts_Results: this is MRIQC folder with bash scripts and the results for all individuals and the group batch job

neurodocker: folder that contains all files needed to create singularity image. See notes.txt for more info

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All Folders (continued):

Old_Analysis: Initial scripts (outdated) analyzing data; updates and additions included in METRICS script

OpenAutism_latex: contains all pdf and tex files, as well as image folders for compilation

PARCELS_not_scaled: includes original SPM parcels (before dimension transformations) and scripts for parcels that were pulled from outside of mindhive

Probably_Trash: contains old versions of scripts and unneeded files

Python2Latex_Example: script and output of an example of generate a latex through python code from online resource. *Note: need a compiler for this .tex document to be produced as a PDF (e.g. can view this example .tex document with texShop on a mac)*

Site_Variance_Plots: plots features of intra and inter site variance, both through PCA classification (Murcia et al) and MRIQC site-related IQM distributions & correlation/covariance matrices

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All Folders (continued):

tmpXDG: needed for python

ToddGit_OpenAutism: folder with local repo organized to pull/push to github OpenAutism remote repo

TOMLOC_INFO: holding place for all demographic and task files Dima created. The internal versions are available inside TIER. All of the versions (internal and external) are found in this folder. *Please make sure these are the latest versions—because these scripts are generated manually!*

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All Files:

INCLUDE.csv: contains all information about each run (# FD outliers, binary exclusion criteria based on 0.2 and 0.4 threshold)

INCLUDE_final.csv: static copy of INCLUDE (can delete)

list_of_missing_files.csv: file that flags missing information in analysis data

list_of_missing_tomloc_files: file that flags missing information in pilot data

nipype_env.simg: singularity image used to run python etc.

Subject_Conversion_Table.csv: file with the old subject IDs and new subject IDs. Used in many scripts. *Please note that this is manually updated by Dima on a version on her local machine, so need to confirm that latest file is in use.*