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Version 1

DATA STRUCTURE AND QUALITY CONTROL NEUROCHEMISTRY_H PIPELINE (CONNExIN 2025) V.1

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Protocol status: Working

We use this protocol and it's working

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Abstract

CONNEXIN 2025 Neurochemistry H team analysis pipeline



DATA STRUCTURE

- 1 **Define project directories:**
\$BIDS_DIR- root of BIDS dataset (e.g., "~/bids_dataset")
\$RAW_DICOM_DIR- source DICOMs (e.g., "~/raw_dicom/sub-064/ses-03/func")
- 2 **Create subject/session folders**
sub-064/ses-03/func
- 3 **Convert DICOM to NIfTI:**
NIfTI + JSON (keep BIDS names)
- 4 **Validate BIDS Structure**
bids-validator /neurodesktop-storage/bids/

QUALITY CONTROL

- 5 **Motion assessment:**
Calculate frame wise displacement using FSL (e.g. mcflirt -in "\$FMRI" -out motion_corrected -plots -rmsrel -rmsabs)

QUALITY CONTROL

- 6 **Generate motion plots:**
Create motion parameter visualization (e.g. fsL_motion_outliers -i "\$FMRI" -o motion_outliers.txt --fd --thresh=0.2 -p motion_plot)
- 7 **Signal-To-Noise-Ratio:**
Calculate temporal SNR using AFNI (available in NeuroDesktop) (e.g. 3dTstat -cvarinv -prefix tSNR "\$FMRI")