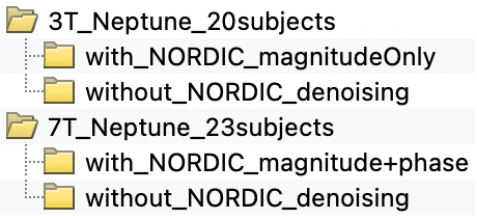
Description of 3T and 7T spinal cord functional MRI data directories

We provide data obtained from distinct participant pools at 3 Tesla and 7 Tesla. Within each, we provide data separately with and without NORDIC denoising. For the 3T data, images were acquired with partial Fourier sampling; hence, phase images were unavailable. For this reason, NORDIC denoising was performed using only the magnitude images (which is reflected in the folder name). For the 7T data, partial Fourier sampling was not chosen; hence, NORDIC denoising was performed using both magnitude and phase images.



3T data

Two separate runs were performed for each of the 20 participants (during the same scan session). Physiological data were available and used for denoising using the RETROICOR method. Temporal bandpass filtering was performed with lower and upper cutoff frequencies of 0.01 and 0.1 Hz, respectively. The sampling rate was 2.08 s, which was sufficient to perform HRF deconvolution. Static functional connectivity (SFC) was calculated between all quadrant pairs (both within and between slices) using Pearson's correlation. In addition, within-slice connectivity was also computed (as is customary in the spinal cord literature) between the four quadrants of a given slice. Temporal signal-to-noise ratio (tSNR) was calculated across slices as well as across pre-processing steps. Lastly, fractional amplitude of low-frequency fluctuations (fALFF) was computed too. With this background, we next describe the files found within each subject's folder. As an example, the following figure shows the files provided within sub-01's directory.

QC

A directory containing the quality control (QC) output figures, which can be browsed using the HTML webpage found within the directory (report_neptune_sub-01.html).

anat.nii.gz

Anatomical image.

anat_reduced_all_masks.mat

Anatomical segmentation masks for gray matter (GM), white matter (WM), and cerebrospinal fluid (CSF) regions.

cord_quadrants.mat

Anatomical masks defining each of the four quadrants of each slice separately for gray and white matter. These masks represent the cord quadrants used during post-processing.

cross_sectional_areas_Neptune.mat

Cross-sectional areas (CSA) obtained through manual segmentation in Neptune. Unlike CSA values obtained using the Spinal Cord Toolbox, these are not validated measures.

motion_parameters.mat

Slice-wise motion parameters (two translation parameters in the X-Y plane). It also contains aggregate relative motion (framewise displacement, FD) values, as well as mean and maximum FD.

covariates_denoise5_COVregress.mat

It contains the covariates used during Neptune's step-15 (additional covariates regression).

rest*.nii.gz (here, rest* corresponds to rest1 and rest2 – runs 1 and 2, respectively)

Unprocessed resting-state fMRI data.

rest*.log

Physiological data (pulse and respiration). To avoid repetition, these are not provided in the data without NORDIC denoising.

rest*_mask_NS.mat

The 'not-cord' mask (in the functional space) generated in Neptune's step-5, which is used as a mask during motion correction.

rest*_denoised50WMcov_deconv_BPF10.mat

Fully pre-processed data. Here, 'denoised50' indicates Neptune's step-12 (CSF regression), 'WM' indicates step-13 (WM regression), 'cov' indicates step-14 (additional covariates regression), 'deconv' refers to step-17 (HRF deconvolution), and 'BPF10' refers to temporal bandpass filtering (upper cutoff = 0.10 Hz) performed after deconvolution.

rest*_denoised50WMcov_deconv_BPF10_quads_timeseries.mat

Voxel-level quadrant time series obtained from each of the cord quadrants.

rest*_denoised50WMcov_deconv_BPF10_SFC_betweenslice.mat

Between-slice functional connectivity outputs.

rest*_denoised50WMcov_deconv_BPF10_SFC_withinslice.mat

Within-slice functional connectivity outputs.

rest*_denoised50WMcov_HPF01_deconv_fALFF.mat

FALFF output. It is computed using high-pass filtered deconvolved data (HPF01, with a cutoff frequency of 0.01 Hz).

rest*_denoised50WMcov_HRFparams.mat

HRF parameters obtained during step-17 (deconvolution).

run*_final_reg.mat

Co-registration transformation matrices output by AFNI during step-17 for runs 1 and 2.

tSNR_across_preproc_steps_run*.mat

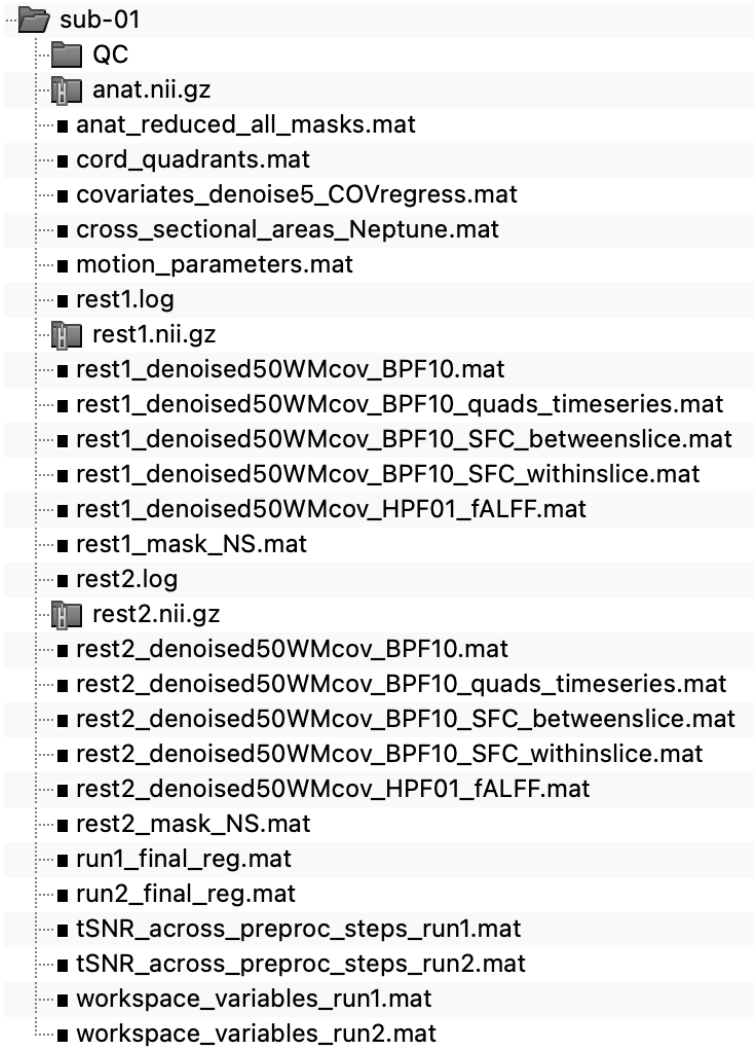
TSNR values across pre-processing steps as well as across slices.

workspace_variables_run*.mat

Certain parameter choices used during Neptune processing are saved here.

7T data

As with the 3T data, two separate runs were performed for each of the 23 participants (during the same scan session). The sampling rate was 3.34 s, which was insufficient to reliably estimate HRF parameters (especially time-to-peak and full-width-at-half-max, which directly depend on temporal resolution). Hence, HRF deconvolution was not performed, as reflected in the file naming convention (i.e., the '_deconv' suffix was not used). The rest of the details are consistent with the above description for the 3T data. As an example, the following figure shows the files provided within sub-01's directory.


sub-01
QC
anat.nii.gz
anat_reduced_all_masks.mat
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rest1_denoised50WMcov_BPF10_SFC_betweenslice.mat
rest1_denoised50WMcov_BPF10_SFC_withinslice.mat
rest1_denoised50WMcov_HPF01_fALFF.mat
rest1_mask_NS.mat
rest2.log
rest2.nii.gz
rest2_denoised50WMcov_BPF10.mat
rest2_denoised50WMcov_BPF10_quads_timeseries.mat
rest2_denoised50WMcov_BPF10_SFC_betweenslice.mat
rest2_denoised50WMcov_BPF10_SFC_withinslice.mat
rest2_denoised50WMcov_HPF01_fALFF.mat
rest2_mask_NS.mat
run1_final_reg.mat
run2_final_reg.mat
tSNR_across_preproc_steps_run1.mat
tSNR_across_preproc_steps_run2.mat
workspace_variables_run1.mat
workspace_variables_run2.mat