

dcant-macaque-pipeline v0.1.0 stages summary

(for nhp-abcd-bids-pipeline v0.2.0, DCAN-labs internal-tools v1.0.0)

updated 22 July 2021

Stage	Key inputs	Key outputs	Description	Notes for troubleshooting
PreliminaryMasking {HCPPIPEDIR}/ PreliminaryMasking/ macaque_masking.py	subject T1w head [subject T2w head]	\${path}/T1w/ T1w_brain.nii.gz (subject T1w brain) [\${path}/T2w/ T2w_brain.nii.gz (subject T2w brain)]	flirt rigid align subject T1w to reference head (MacaqueYerkes19, or study template if specified) ANTs warp subject T1w head to reference head Inverse warp reference brain mask to produce mask for subject T1w [Rigid align subject T1w to subject T2w; apply xfm to T1w mask to produce T2w mask]	If T1w_brain.nii.gz is bad, try specifying a mask to apply to the subject T1w head: use nhp-abcd-bids-pipeline --t1-brain-mask <mask> [If T1w_brain.nii.gz is good but T2w_brain.nii.gz is bad, try --t2-brain-mask <mask>]
PreFreeSurfer {HCPPIPEDIR}/ PreFreeSurfer/ PreFreeSurferPipeline.sh	subject T1w head, brain [subject T2w head, brain]	\${path}/T1w/ T1w_acpc.nii.gz (subject T1w ACPC-aligned to reference) \${path}/T1w/ T1w_acpc_dc.nii.gz (subject T1w ACPC-aligned to reference, readout distortion corrected) \${path}/T1w/ T1w_acpc_dc_restore.nii.gz (ACPC-aligned, readout distortion corrected, bias field corrected)	If multiple anatomical scans of same modality (T1w [and/or T2w]) exist, generate an average image ACPC-align subject T1w [and T2w] to reference T1w Apply HCP's distortion correction (fieldmap or topup depending on gradient/spin echo) to T1w, T2w [Register T2w to T1w] [Compute bias field from	If ACPC alignment is bad, ensure axis labels (LR, DV, PA) are consistent between subject and reference If segmentation (aseg_acpc.nii.gz) is bad, compare \${path}/T1w/T1w_acpc_dc_restore_brain.nii.gz to the JLF templates (default: /opt/pipeline/global/templates/JointLabelCounsil). Consider making a copy of the templates directory that only includes the templates close in age to your subject. Run pipeline with --multi-template-dir <directory>

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		<p><code>\${path}/T1w/aseg_acpc.nii.gz</code> (segmentation generated with AntsJointLabelFusion NOTE: if --aseg is used, the user-specified segmentation is copied to aseg_acpc.nii.gz and the JLF segmentation is written to aseg_acpc_dcn-derived.nii.gz.)</p> <p><code>\${path}/MNINonLinear/T1w_restore.nii.gz</code> (T1w registered to reference)</p> <p><code>[\$path]/T2w/T2w_acpc.nii.gz</code> (subject T2w ACPC-aligned to reference T1w)]</p> <p><code>[\$path]/T1w/T2w_acpc.nii.gz</code> (subject T2w ACPC-aligned to reference, registered to subject ACPC-aligned T1w)]</p> <p><code>[\$path]/T1w/T2w_acpc_dc.nii.gz</code></p>	<p>voxelwise product of T1w, T2w]</p> <p>Register T1w to reference (FLIRT/FNIRT, ANTs w/ or w/o intermediate registration to a study template)</p> <p>Segment T1w with ANTs joint label fusion</p>	<p>to use a custom multi-template directory for JLF.</p> <p>If segmentation is still not satisfactory, copy and manually edit aseg_acpc.nii.gz, then rerun pipeline from FreeSurfer stage with --aseg option to use the edited segmentation. Recommended to edit in coronal view. Try to fix discontinuities in WM, and fix any non-cortical voxels labeled as cortex. It may help to “thicken” WM tracts to be at least 2-3 voxels wide to avoid creating discontinuities when resampling to 1.0 mm for use with FreeSurfer.</p> <p>Option --t1-reg-method is used to select the method used to register T1w_acpc_dc_restore to the reference T1w. Default method is FLIRT_FNIRT to be consistent with nhp-abcd-bids-pipeline <= v0.1.0 and dcn-macaque-pipeline <= v0.0.3, but using ANTS_NO_INTERMEDIATE may be preferable.</p>

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		(Subject T2w, ACPC-aligned, registered to subject ACPC-aligned T1w, readout distortion corrected) [\${path}/T1w/T2w_acpc_dc_restore.nii.gz (Subject T2w, ACPC-aligned, registered to subject ACPC-aligned T1w, readout distortion corrected, bias field corrected) \${path}/MNINonLinear/T2w_restore.nii.gz (T2w registered to reference)]		
FreeSurfer {HCPPIPEDIR}/FreeSurfer/FreeGreyPipeline.sh	\${path}/T1w/T1w_acpc_dc_restore.nii.gz	\${path}/T1w/T1wN_acpc.nii.gz (hypermormalized subject T1w) \${path}/T1w/\${subject}N (FreeSurfer work directory for hypernormalized T1w) \${path}/T1w/\${subject}_1mm ("main" FreeSurfer work directory, uses T1w resampled to 1.0 mm)	Applies hypernormalization to T1w: image is resampled such that its histogram of voxel intensities matches an adult human reference Anatomical images and segmentation are resampled to 1.0 mm, 256 x 256 x 256 for input to FreeSurfer. (Our FreeSurfer implementation is largely unchanged from Glasser,	For issues with bad surfaces/surface generation errors, recommended to look at the CIFTI outputs from the next stage (PostFreeSurfer) instead of the FreeSurfer 1mm output.

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		<code>\${path}/T1w/\${subject}</code> (Directory for FreeSurfer output resampled to reference)	<p>et al, 2013 “The minimal preprocessing pipelines for the Human Connectome Project.” with the exception of our use of the MacaqueYerkes19 templates/coordinate space)</p> <p>Resample FreeSurfer output to reference template resolution</p>	
PostFreeSurfer <code>{HCPPIPEDIR}/PostFreeSurfer/PostFreeSurferPipeline.sh</code>	<code>\${path}/T1w/\${subject}</code> (FreeSurfer output resampled to reference)	<code>\${path}/MNINonLinear/fsaverage_LR32k</code> (CIFTI output in reference space; surfaces resampled to standard meshes) <code>\${path}/MNINonLinear/wmparc.nii.gz</code> (Segmentation volume derived from <code>aseg_acpc.nii.gz</code> , in reference space)	<p>Generate CIFTI surface files from FreeSurfer output.</p> <p>Resample surfaces to standard meshes.</p> <p>Output volumes and surfaces in both subject’s native space and standard reference space(s)</p>	<p>(NOTE: Output in the “MNINonLinear” directory is actually in MacaqueYerkes19 0.5 mm space; the name “MNINonLinear” was inherited from the DCAN ABCD and original HCP pipelines)</p> <p>To inspect surfaces, load the <code>wb_spec</code> file in <code>\${path}/MNINonLinear/fsaverage_LR32k</code>, and also load <code>\${path}/MNINonLinear/wmparc.nii.gz</code></p> <p>If either white or pial surface looks bad, <code>aseg_acpc.nii.gz</code> in the T1w directory may need correcting (see PreFreeSurfer).</p> <p>If issues persist with the pial surface, also try <code>--single-pass-pial</code> (instead of making pial</p>

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				<p>surfaces in two passes, the first using the hypernormalized T1w to create a prior and the second with the non-normalized, save the output of the first pass as the final surface)</p> <p>For the white surface, there is also <code>--make-white-from-norm-t1</code> (use hypernormalized T1 instead of non-normalized for initial white surface creation)</p> <p>If <code>T1w_acpc_dc_restore.nii.gz</code> has susceptibility artifacts impacting FreeSurfer's ability to segment matter, also try <code>--hyper-normalization-method ROI_IPS</code> (histogram-match intensities to adult human reference on a per-matter-type basis) together with <code>--norm-gm-std-dev-scale 0.5</code>, <code>--norm-wm-std-dev-scale 0.5</code>, <code>--norm-csf-std-dev-scale 0.5</code> to reduce standard deviation of intensity within each matter type by half.</p>
FMRIVolume <code>{HCPPIPEDIR}/ fMRIVolume/ GenericfMRIVolumePr ocessingPipeline.sh</code>	Functional data from subject's func/ and fmap/ input directories	In directory <code>\${path}/ses-\${ses}_task-\${task}[_run-\${run}]</code>: <code>ses-\${ses}_task-\${task}[_run-\${run}]_orig.nii.gz</code>	<p>Apply motion correction (MCFLIRT) to functional data</p> <p>Apply distortion correction (fieldmap or topup)</p>	Pipeline errors at this stage are most commonly caused by bad NifTI files or JSON sidecars, or missing other required files due to a non-fatal error from a previous stage.

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		(Copy of input functional data) ses-\${ses}_task-\${task}[_run-\${run}].mc.nii.gz (Motion-corrected functional data) ses-\${ses}_task-\${task}[_run-\${run}].mc.nii.gz (Motion corrected functional data, resampled, in reference space) T1w_restore_\${res}.nii.gz (downsampled atlas-registered T1w)	[Register functional data to T2w] (use T1w if no T2w available) Resample functional data into standard space (use downsampled atlas-registered T1w as reference)	
FMRISurface {HCPPIPEDIR}/ fMRISurface/ GenericfMRISurfaceProcessingPipeline.sh	Functional data from subject's func/ and fmap/ input directories	In `\${path}/MNINonLinear/Results`: ses-\${ses}_task-\${task}[_run-\${run}]/ ses-\${ses}_task-\${task}[_run-\${run}].Atlas.dtseries.nii (dtseries functional data per run, in reference space) ses-\${ses}_task-\${task}[_run-\${run}]/	Map functional data to low-res ("32k") surfaces Apply spatial smoothing to subcortical volume and surface-mapped functional data (default FWHM = 1.5 mm) Compile volumes and surfaces into CIFTI dtseries	To visualize power spectra of motion-related artifacts, Movement_Regressors.txt can be input to the power_per_RestingRegressors Power Plots utility (https://github.com/DCAN-Labs/movement_regressors_power_plots) By identifying the peak in power spectra due to respiration-related motion, an appropriate band-stop filter can be applied in DCANBOLDProcessing to filter out the motion artifact.

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		Movement_Regressors.txt (movement regressors) which may be input to the power_per_Resting function of the Movement Regressors Power Plots utility to visualize power spectra of motion-related artifact https://github.com/DCAN-Labs/movement_regressors_power_plots		
DCANBOLDProcessing	dtseries functional data (output of FMRISurface) various motion and signal regressors, framewise displacement statistics	In `\${path}/MNINonLinear/Results`: ses-\${ses}_task-\${task}[_run-\${run}]/DCANBOLDProc_\${ver}/ ses-\${ses}_task-\${task}[_run-\${run}]/DCANBOLDProc_\${ver}_Atlas.dtseries.nii (processed dtseries data per run) ses-\${ses}_task-\${task}_run-DCANBOLDProc_\${ver}_Atlas.dtseries.nii (concatenated, processed dtseries data per task type)	Demean/detrend, GLM denoise (regressors include both signal and movement variables), apply bandpass filter (2 nd order Butterworth 0.008 Hz < f < 0.09 Hz) Optional: bandstop respiratory filter Motion censoring (remove frames with framewise displacement above threshold, plus "outlier" frames) Concatenate runs by task type, generate parcellated timeseries data (ptseries)	See this issue for help generating parcellated output: https://github.com/DCAN-Labs/dcn-macaque-pipeline/issues/5 (DCANBOLDProcessing does not include macaque parcellations, so a workaround is to bind a directory containing your macaque parcellations to the default parcellations directory) Check output logs for non-fatal errors due to inability to open or write required files. (May be an issue with multithreading; running the pipeline single-threaded seems to help avoid this) If using the bandstop filter (--bandstop <lower bound> <upper bound>), ensure that

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		ses-\${ses}_task-\${task}_run- _DCANBOLDProc_\${ver}_\${parcellation}.ptseries.nii (concatenated, processed, parcellated ptseries data per task type)		(1) bounds are entered in breaths-per-minute and not Hz; (2) the upper bound does not exceed the Nyquist frequency (one-half the sampling rate, or $30 / TR$)
ExecutiveSummary	<various output from DCANBOLDProcessing and other stages>	\${path}/summary_DCANBOLDProc_\${ver}/executivesummary/executive_summary_sub-\${sub}_ses-\${ses}.html (executive summary)	Compile executive summary from outputs of DCANBOLDProcessing and other stages	BrainSprite viewer has known issues rendering T1w/T2w; this does not mean the source images are bad.