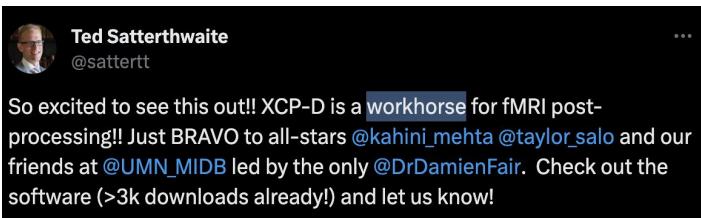


XCP-D: Extensible Connectivity Pipeline-DCAN

XCP-D: A Robust Pipeline for the post-processing of fMRI data

 Kahini Pankaj Mehta, Taylor Salo, Thomas Madison, Azeez Adebimpe,  Danielle S Bassett, Max Bertolero,  Matthew Cieslak, Sydney Covitz, Audrey Houghton, Arielle S Keller,  Audrey Luo, Oscar Miranda Dominguez, Steve Nelson,  Golia Shafiei, Sheila Shanmugan, Russell Shinohara, Valerie Jill Sydnor, Eric Feczko, Damien A Fair,  Theodore D Satterthwaite

doi: <https://doi.org/10.1101/2023.11.20.567926>



This fMRI post-processing and noise regression pipeline is developed by the [Satterthwaite lab at the University of Pennsylvania](#) (XCP; eXtensible Connectivity Pipeline) and [Developmental Cognition and Neuroimaging lab at the University of Minnesota](#) (-DCAN) for open-source software distribution.


About

XCP-D paves the final section of the reproducible and scalable route from the MRI scanner to functional connectivity data in the hands of neuroscientists. We developed XCP-D to extend the BIDS and NiPrep apparatus to the point where data is most commonly consumed and analyzed by neuroscientists studying functional connectivity. Thus, with the development of XCP-D, data can be automatically preprocessed and analyzed in BIDS format, using NiPrep-style containerized code, all the way from the scanner to functional connectivity matrices.

Ciric et al., 2018 in *Nature*

Protocol | [Published: 16 November 2018](#)

Mitigating head motion artifact in functional connectivity MRI

[Rastko Ciric](#), [Adon F. G. Rosen](#), [Guray Erus](#), [Matthew Cieslak](#), [Azeez Adebimpe](#), [Philip A. Cook](#), [Danielle S. Bassett](#), [Christos Davatzikos](#), [Daniel H. Wolf](#) & [Theodore D. Satterthwaite](#) 

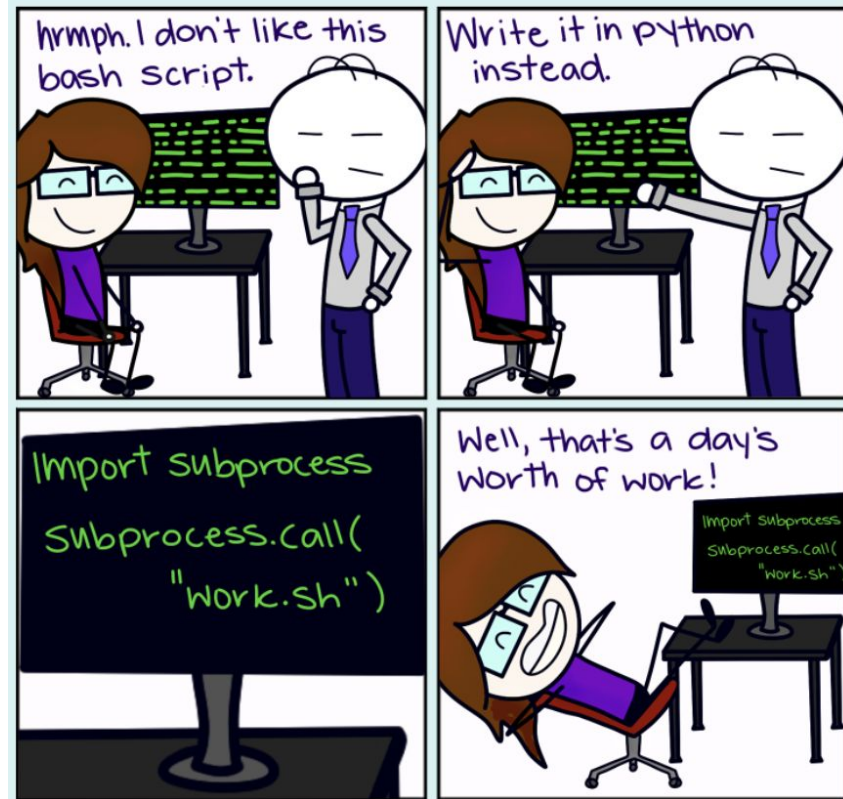
[Nature Protocols](#) **13**, 2801–2826 (2018) | [Cite this article](#)

Beginning to refactor...



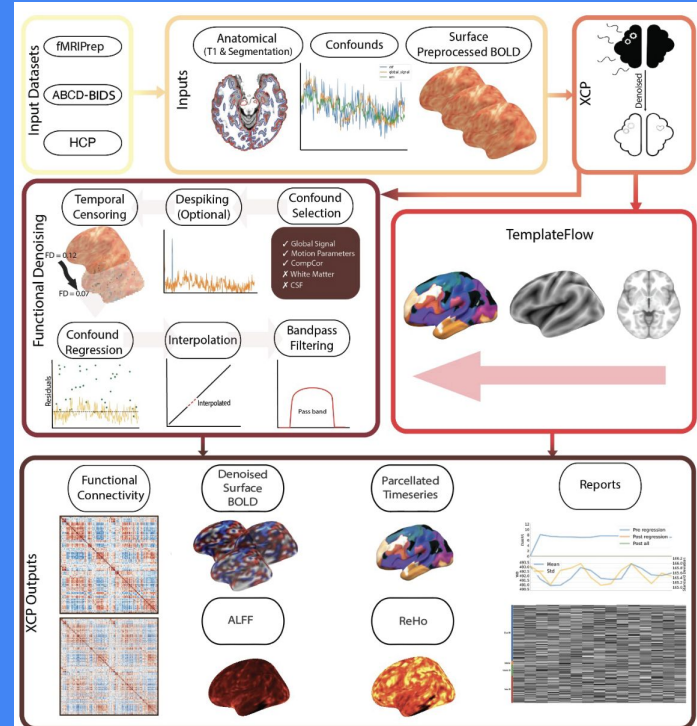
Why the refactor?

1. Substantial technical debt accumulated - easier to maintain in Python than bash
2. Ensuring modularity via Nipype
3. BIDS compliance
4. Allowing ingestion from HCP-YA, ABCD-BIDS and fMRIPrep
5. Allowing for a more flexible denoising pipeline
6. Ensuring all modules are tested
7. Ensuring best software engineering practices (eg: reviews required before merging, Circle CI testing)

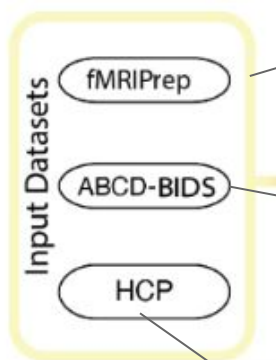


Alternative solutions

So what does
XCP-D do now?



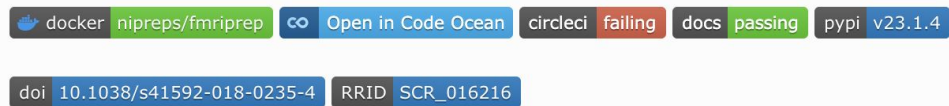
Ingestion



Default

fMRIPrep. A Robust Preprocessing Pipeline for fMRI Data

fMRIPrep is a *NiPreps* (*NeuroImaging PREProcessing tools*) application (www.nipreps.org) for the preprocessing of task-based and resting-state functional MRI (fMRI).



Adolescent Brain Cognitive Development (ABCD) Community MRI Collection and Utilities

 Eric Feczko, Greg Conan, Scott Marek, Brenden Tervo-Clemmens, Michaela Cordova, Olivia Doyle, Eric Earl, Anders Perrone, Darrick Sturgeon, Rachel Klein, Gareth Harman, Dakota Kilamovich, Robert Hermosillo, Oscar Miranda-Dominguez, Azeez Adebimpe, Maxwell Bertolero, Matthew Cieslak, Sydney Covitz, Timothy Hendrickson, Anthony C. Juliano, Kathy Snider, Lucille A. Moore, Johnny Uriarte, Alice M. Graham, Finn Calabro, Monica D. Rosenberg, Kristina M. Rapuano, BJ Casey, Richard Watts, Donald Hagler, Wesley K. Thompson, Thomas E. Nichols, Elizabeth Hoffman, Beatriz Luna, Hugh Garavan, Theodore D. Satterthwaite, Sarah Feldstein Ewing, Bonnie Nagel, Nico U.F. Dosenbach, Damien A. Fair
doi: <https://doi.org/10.1101/2021.07.09.451638>

Young Adult HCP

1200 Subjects (2010-2016)

The Human Connectome Project (HCP) has tackled one of the great scientific challenges of the 21st century: mapping the human brain, aiming to connect its structure to function and behavior.

Removal of non-steady state (dummy) volumes



Hello,

I've been collecting data recently off our Siemens Prisma scanner, which automatically discards the first 8 "dummy" volumes. That being said, I've noticed that occasionally in the confounds files a volume or two is designated as a non-steady state volume. For a first level regression analysis, is it appropriate (or at least acceptable) to censor these volumes out, or is there a different method?

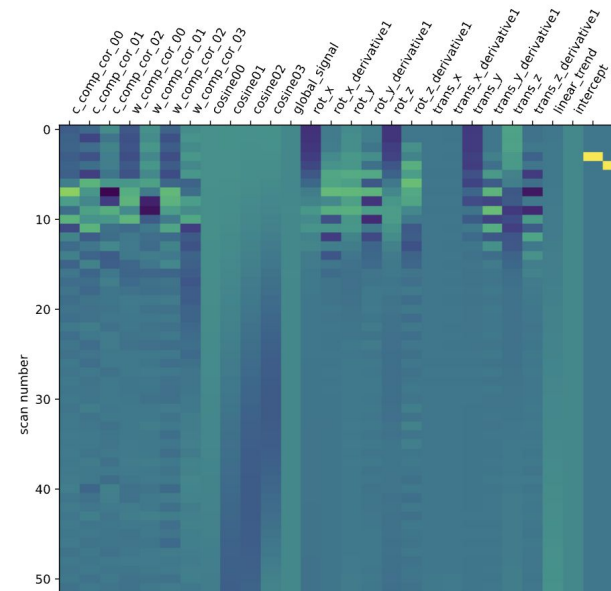
Thanks!

Despiking

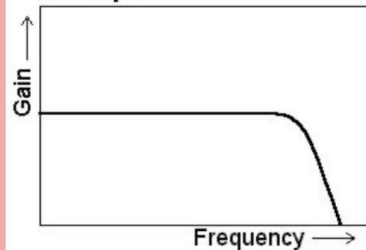
spike



Filtering of realignment parameters

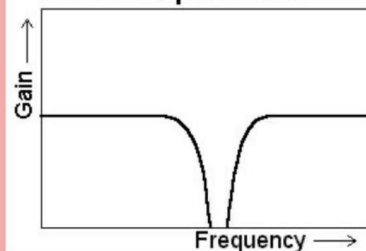


Low pass



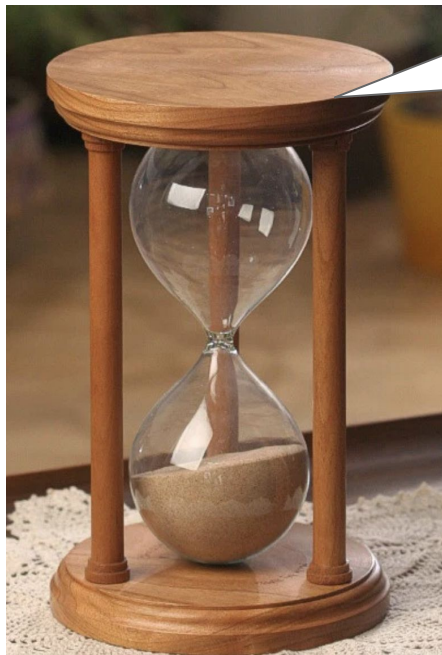
SINGLE-BAND
(Gratton et al., 2020)

Band stop / notch

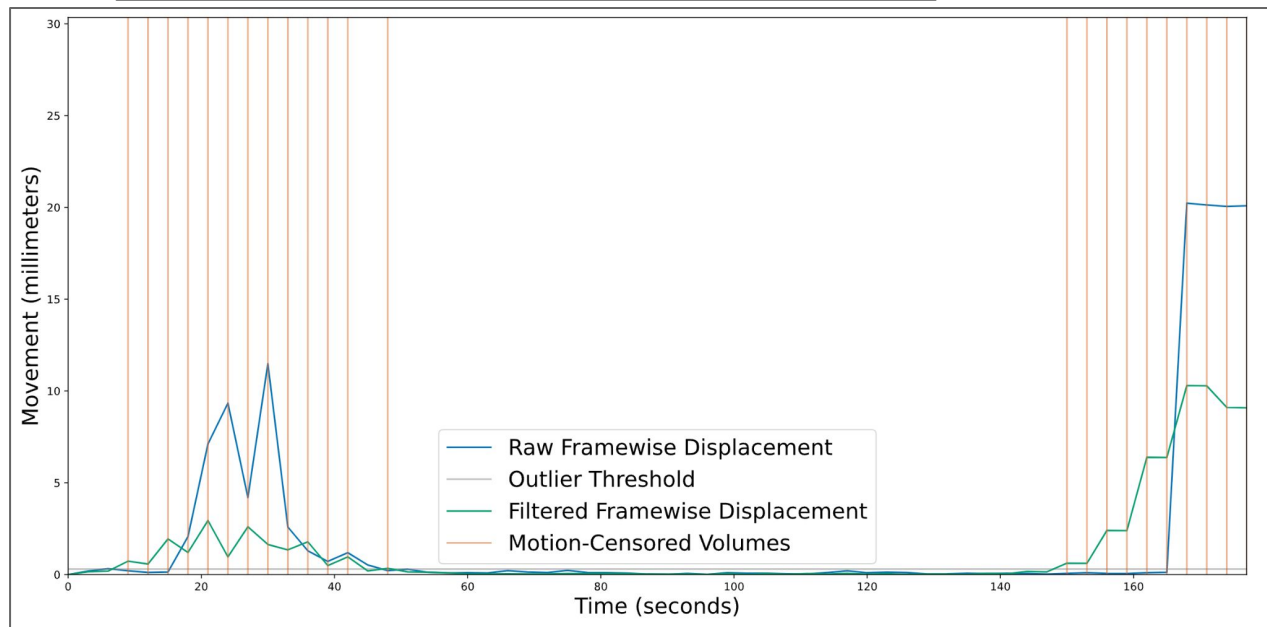


MULTIBAND
(Fair et al., 2020)

Temporal censoring



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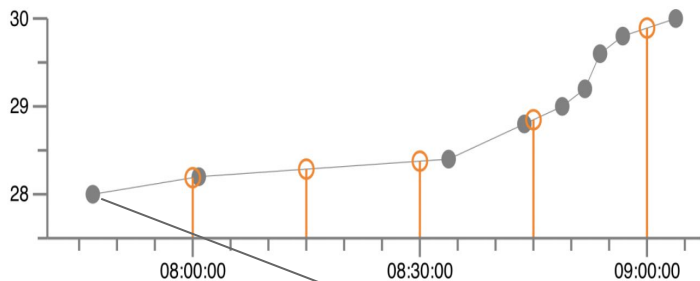
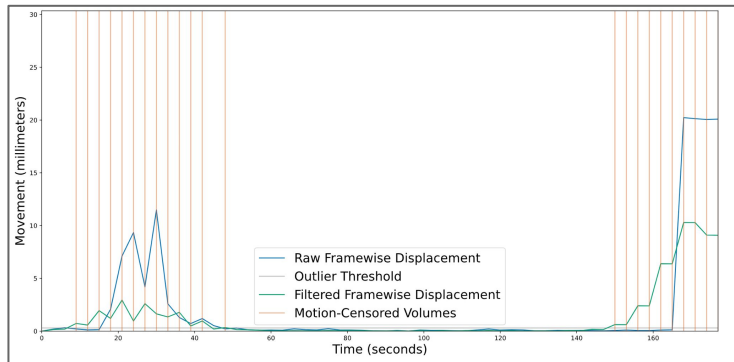


Confound selection & regression (Satterthwaite et al., 2013; Ciric et al., 2017)

Pipelines	Six Motion Estimates	White Matter	CSF	Global Signal	ACompCor	AROMA	Linear Trend	Intercept
24P	X, X ² , dX, dX ²						X	X
27P	X, X ² , dX, dX ²	X	X	X			X	X
36P	X, X ² , dX, dX ²	X, X ² , dX, dX ²	X, X ² , dX, dX ²	X, X ² , dX, dX ²			X	X
acompcor_gsr	X, dX			X	10 com, 5WM, 5CSF		X	X
acompcor	X, dX				10 com, 5WM, 5CSF		X	X
aroma_gsr	X, dX	X	X	X		X	X	X
aroma	X, dX	X	X			X	X	X
none								

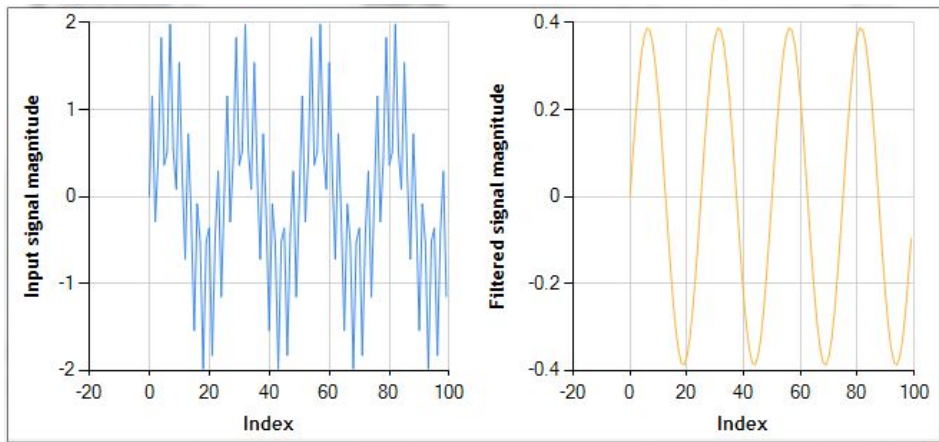
Interpolation & filtering

Interpolated Timeseries

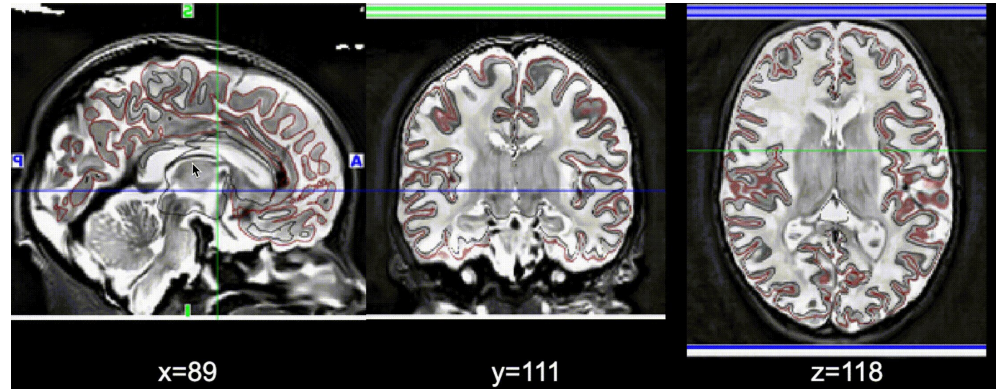
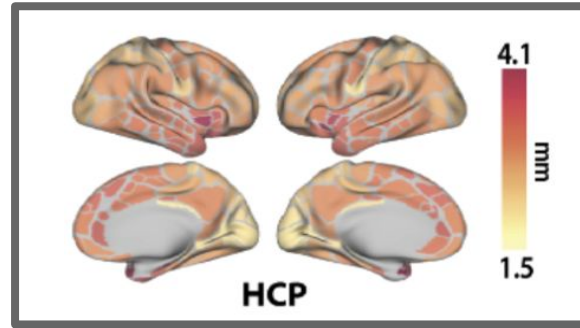


Data interpolated into censored timepoint

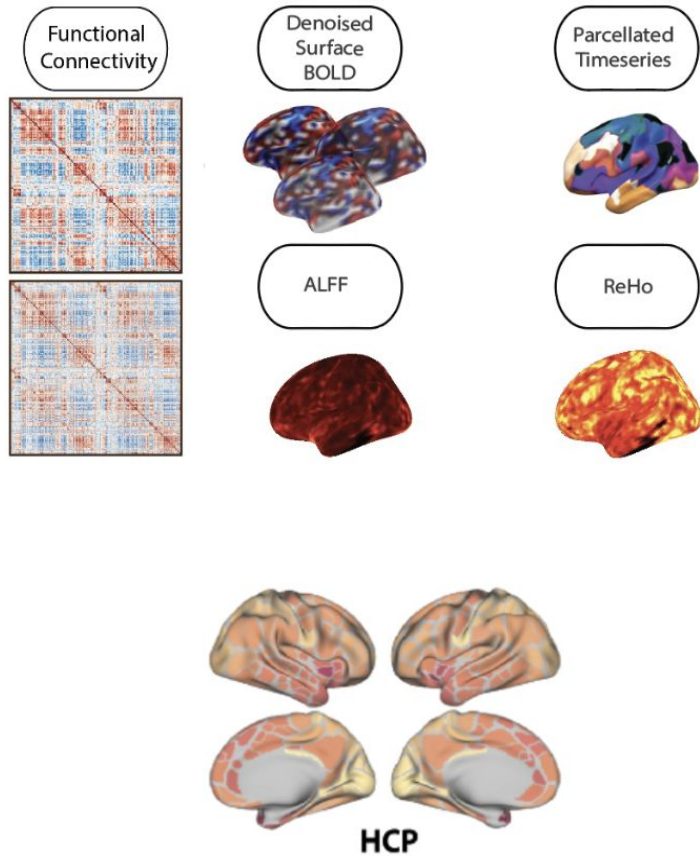
Butterworth filter



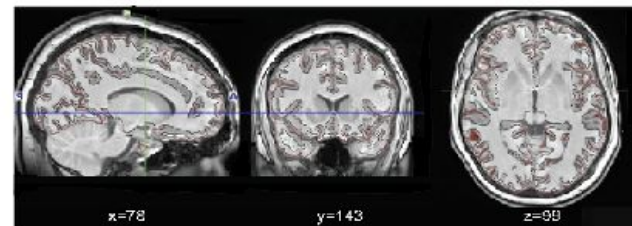
Experimental/other options: Anatomical Workflow + Concatenation



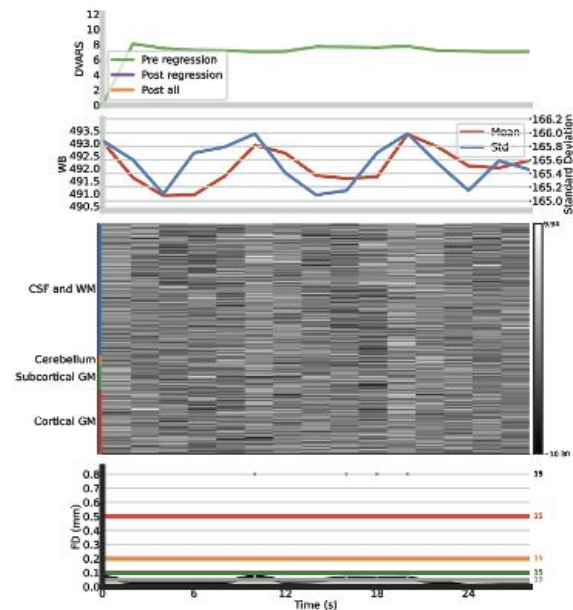
Outputs generated



A. BrainSprite

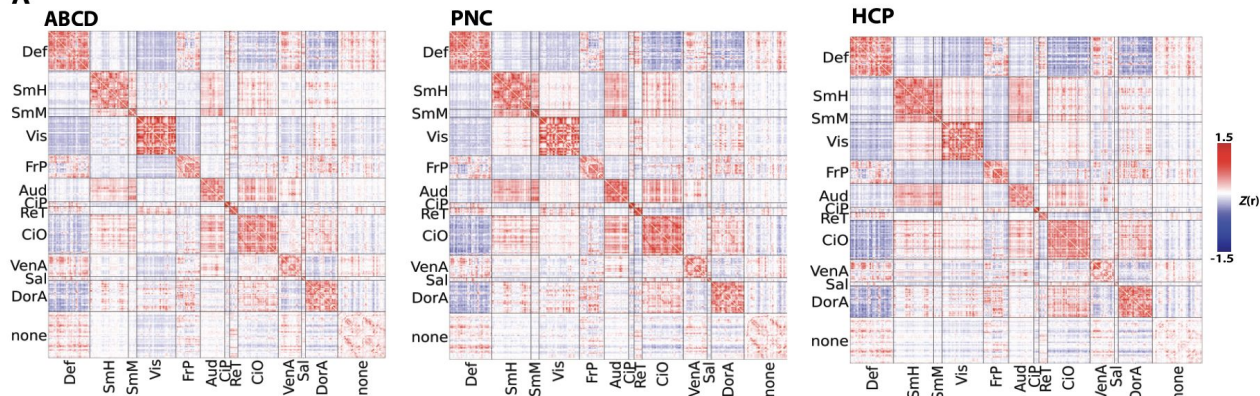


B. DVARS Graph, Carpet Plots, and Framewise Displacement Graph

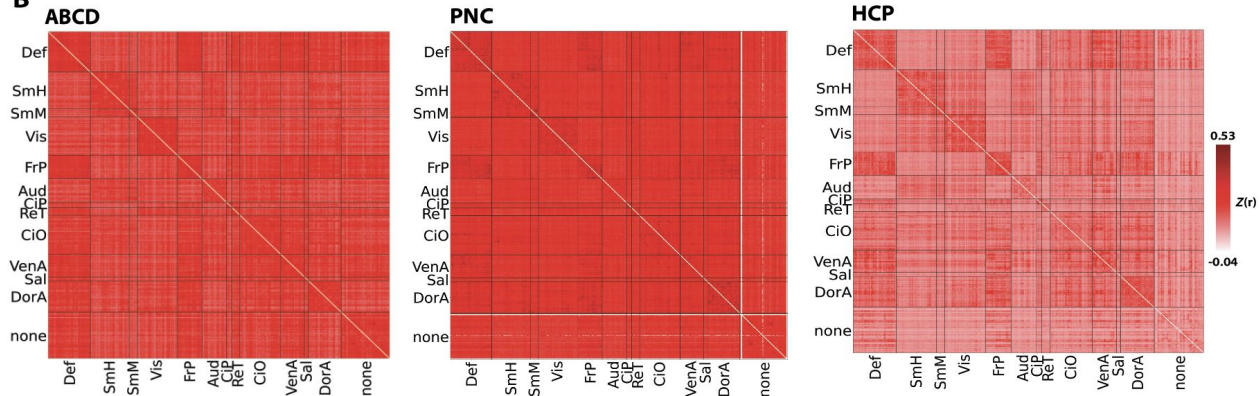


Demonstration of efficacy in N=600

A



B



Mean (**Panel A**) and standard deviation (**Panel B**) functional connectivity generated by XCP-D for each dataset in our large-scale application, displayed after Fisher's Z transformation. Data are displayed using the Gordon atlas (Gordon et al., 2016). *Def*: default mode network; *SmH*: somatomotor hands network; *SmM*: somatomotor mouth network; *Vis*: visual network; *FrP*: Frontoparietal network; *Aud*: auditory network; *CiP*: cinguloparietal network; *CiO*: cingulo-opercular network; *VenA*: ventral attention network; *Sal*: salience network; *DorA*: dorsal attention network

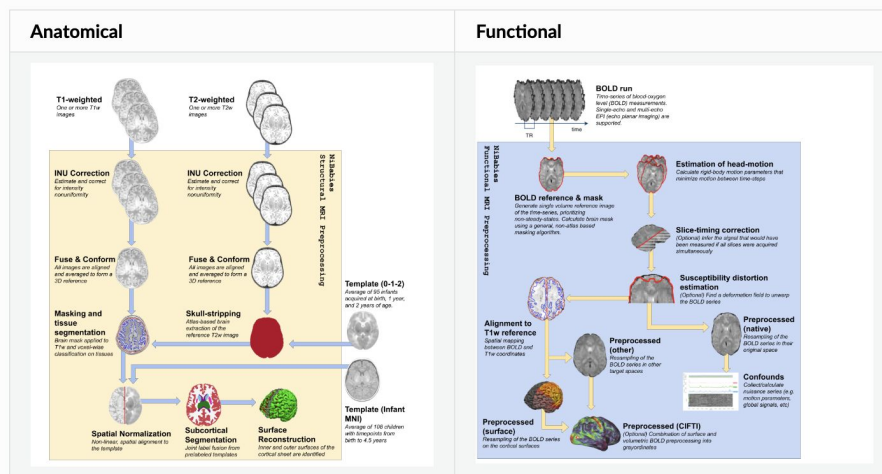
Limitations + future directions

1. Does not support physiological confounds - roadmap
2. Does not support task data - out of scope for now
3. Or Nibabies - plans to implement this in the future.

Contributions always welcome via pull requests :)

NiBabies: A robust preprocessing workflow tailored for neonate and infant MRI

Pytest passing circleci passing docker nipy/nibabies codecov 33% docs passing
DOI 10.5281/zenodo.10105213



Reflections



- Learning an existing codebase
- Following best coding practices
- Working on the software with team members
 - Collaborating across institutions
 - Writing a paper on evolving software

Questions?

Preprint:



read-the-docs:

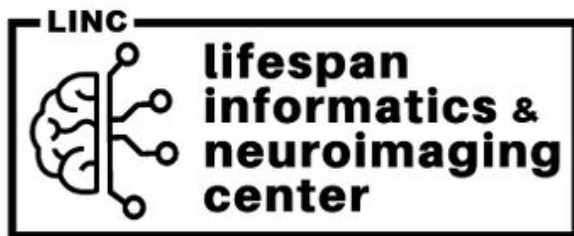


Github:



List/location of datasets run through XCP available via internal lab documentation.

THANK YOU!



XCP-D: A Robust Pipeline for the post-processing of fMRI data

Kahini Mehta^{1,2,3*}, Taylor Salo^{1,2,3*}, Thomas J. Madison⁴, Azeez Adebimpe^{1,2,3}, Danielle S. Bassett^{7,8,9,10,11}, Max Bertolero^{1,2,3}, Matthew Cieslak^{1,2,3}, Sydney Covitz^{1,2,3}, Audrey Houghton⁴, Arielle S. Keller^{1,2,3}, Jacob T. Lundquist⁴, Audrey Luo^{1,2,3}, Oscar Miranda-Dominguez^{4,5}, Steve M. Nelson^{4,5}, Golia Shafiei^{1,2,3}, Sheila Shanmugan^{1,2,3}, Russell T. Shinohara^{12,13}, Valerie J. Sydnor^{1,2,3}, Kimberly B. Weldon⁴, Eric Feczko^{4,5}, Damien A. Fair^{4,5,6**}, Theodore D. Satterthwaite^{1,2,3,12,13**}

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**Contributed equally as senior authors

Keywords: fMRI, software, post-processing, functional connectivity, resting-state

Category: fMRI, software, reproducibility, functional connectivity, image processing, denoising