# **fMRIPrep-next:**

# Preprocessing as a fit-transform model

Christopher J Markiewicz<sup>1</sup>, Mathias Goncalves<sup>1</sup>, John Kruper<sup>2</sup>, Ma Feilong<sup>3</sup>, Guarav H Patel<sup>4</sup>, Juan Sanchez-Pena<sup>4</sup>, Robert E Smith<sup>5</sup>, Lea Waller<sup>6</sup>, Joseph Wexler<sup>1</sup>, Russell Poldrack<sup>1</sup>, Oscar Esteban<sup>7</sup>

<sup>1</sup>Stanford University, Stanford, CA, <sup>2</sup>University of Washington, Seattle, WA, <sup>3</sup>Dartmouth College, Hanover, NH, <sup>4</sup>Columbia University, New York, NY, <sup>5</sup>Florey Institute of Neuroscience and Mental Health, Melbourne, VIC, <sup>6</sup>Charité Universitätsmedizin Berlin, Berlin, Berlin, <sup>7</sup>Lausanne University Hospital and University of Lausanne, Lausanne, VD

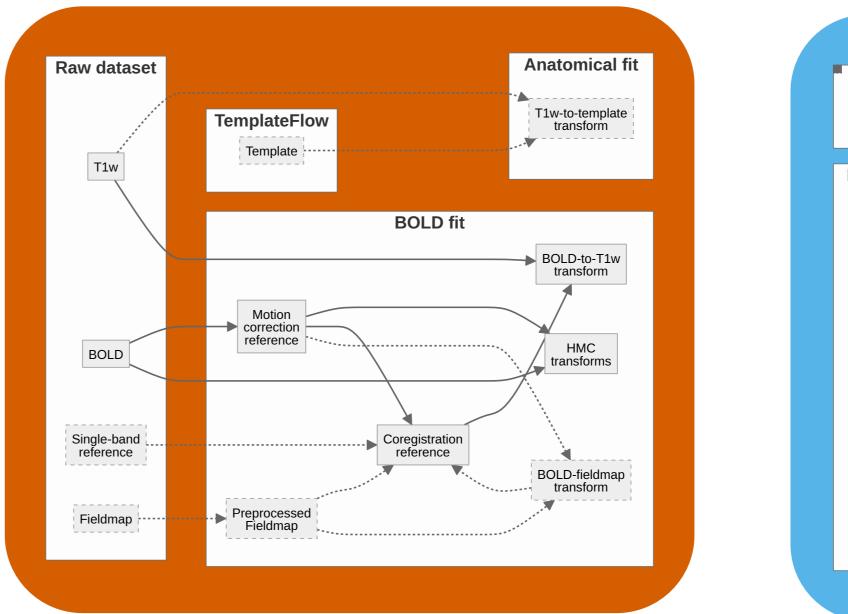
fMRIPrep: https://fmriprep.org NiPreps: https://nipreps.org

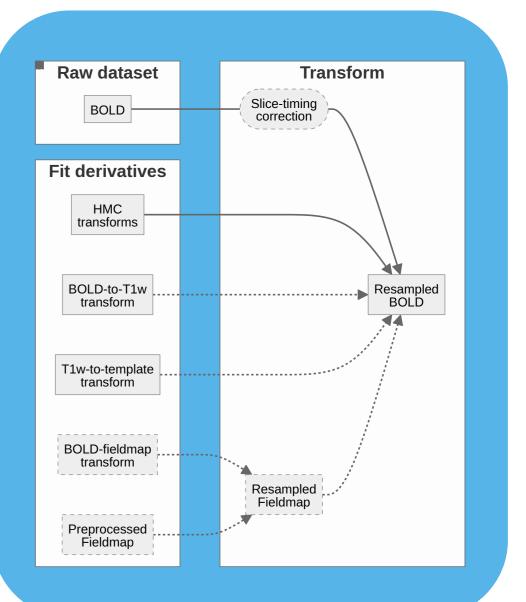
OHBM Poster #2257

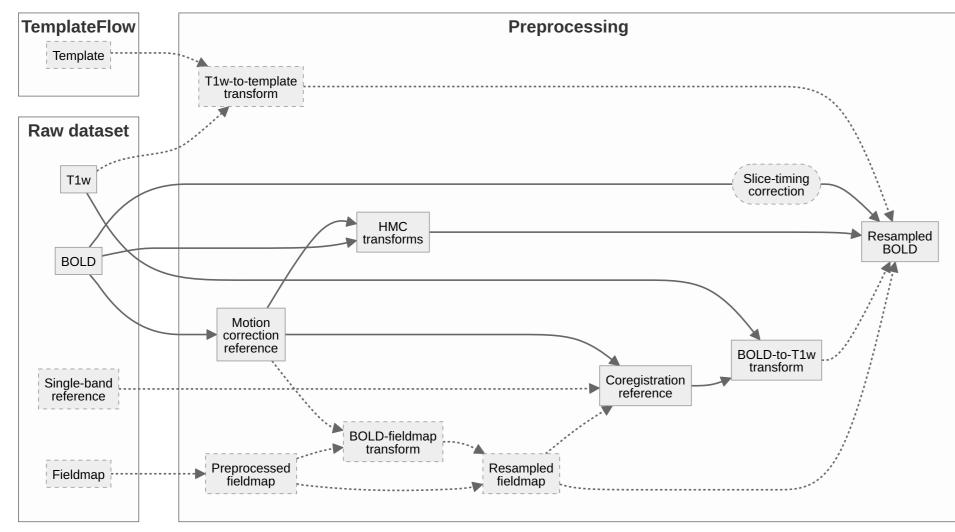
# End-to-end fMRI preprocessing pipelines are best suited to *small workloads*

- Data are preprocessed and analyzed on one system
- Subjects can be run all-at-once
- Little to no customization or modification is needed
- Derivative BOLD series can easily be stored together

#### Minimal derivatives enable new use cases







Schematic overview of the preprocessing workflow to generated a BOLD series resampled into a target space. Arrows indicate data dependencies, and dashes indicate optional inputs or steps.

When processing **large datasets**, or targetting **multiple output spaces**, generating derivative BOLD series demands **significant storage resources**.

Such workflows can be conceptually split into two parts (borrowing terms from scikit-learn): FIT - Expensive estimates of required corrections

Running only the **FIT** workflow produces a compact set of derivatives. More target spaces can be selected with only a small impact on storage requirements.

Running only the **TRANSFORM** workflow avoids unnecessary recomputation. Resampling targets may be chosen for the specific analysis.

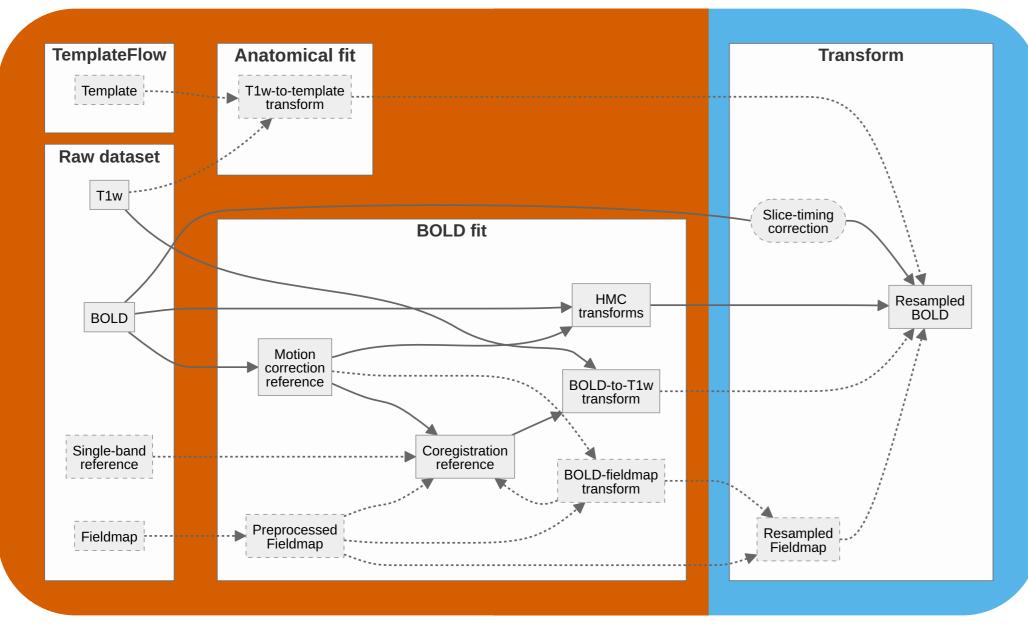
#### Use Case: Secondary research

Alice publishes her raw data and the **FIT** workflow derivatives to a public archive. She provides transforms to multiple volumetric and surface templates. Bob and Carol each fetch the data and run the **TRANSFORM** workflow to reconstruct identical BOLD series in MNI space for analysis.

fmriprep raw/ out/ participant --level minimal \
 --output-spaces ...

fmriprep raw/ out/ participant --level full \
 --derivatives minimal/ --output-spaces ...

## **TRANSFORM** - Cheap application of corrections

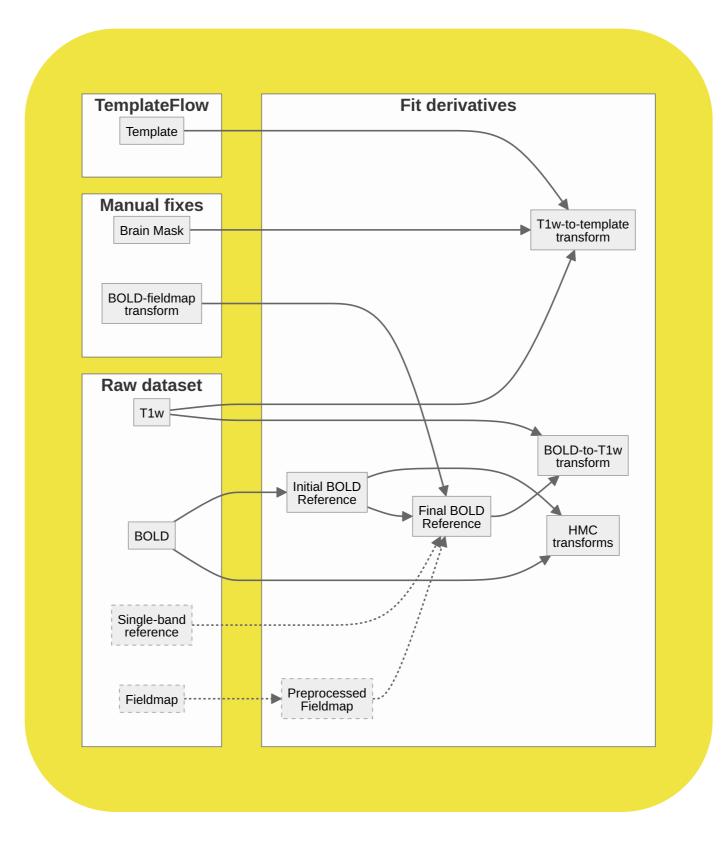


The **FIT** workflow contains most computationally intensive and all non-deterministic components of the preprocessing workflow. The **TRANSFORM** workflow generates most of the space-consuming derivatives.

We rewrote fMRIPrep to create a minimal set of derivatives, from which the output BOLD series can be generated

#### Use Case: Manual intervention

Dave uses an alternative brain mask and BOLD-to-fieldmap registration to improve the quality of his preprocessing. He reruns fMRIPrep with these derivatives as inputs.



fmriprep raw/ out/ \
participant \
--level minimal \
--derivatives fixes/ \
-output-spaces ...

- The minimal derivatives for BOLD series include transforms, reference volumes, and fieldmaps. and the files needed to calculate them.
- Minimal derivatives are expensive to calculate, but small in storage size (e.g., head motion estimates).
- Fit-only workflows reduce runtime by >20% and storage requirements by >90% by size (>80% by file count).

### Space/time comparisons:

https://fmriprep.org/en/latest/benchmarks.html



#### **Future directions**

- Extend the fit-transform model to other nipreps tools. It has been adopted in ASLPrep already.
- fMRIPost library to generate secondary derivatives on-the-fly in downstream tools.
- Convert transform workflow into a standalone tool that is lighter than the fMRIPrep container.

## Acknowlegements

NiPreps development, including fMRIPrep supported by the BRAIN Initiative award 1RF1MH121867-01A1. This research is part of the Frontera computing project at the Texas Advanced Computing Center. Frontera is made possible by National Science Foundation award OAC-1818253.