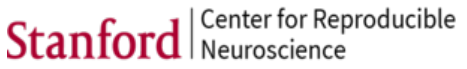
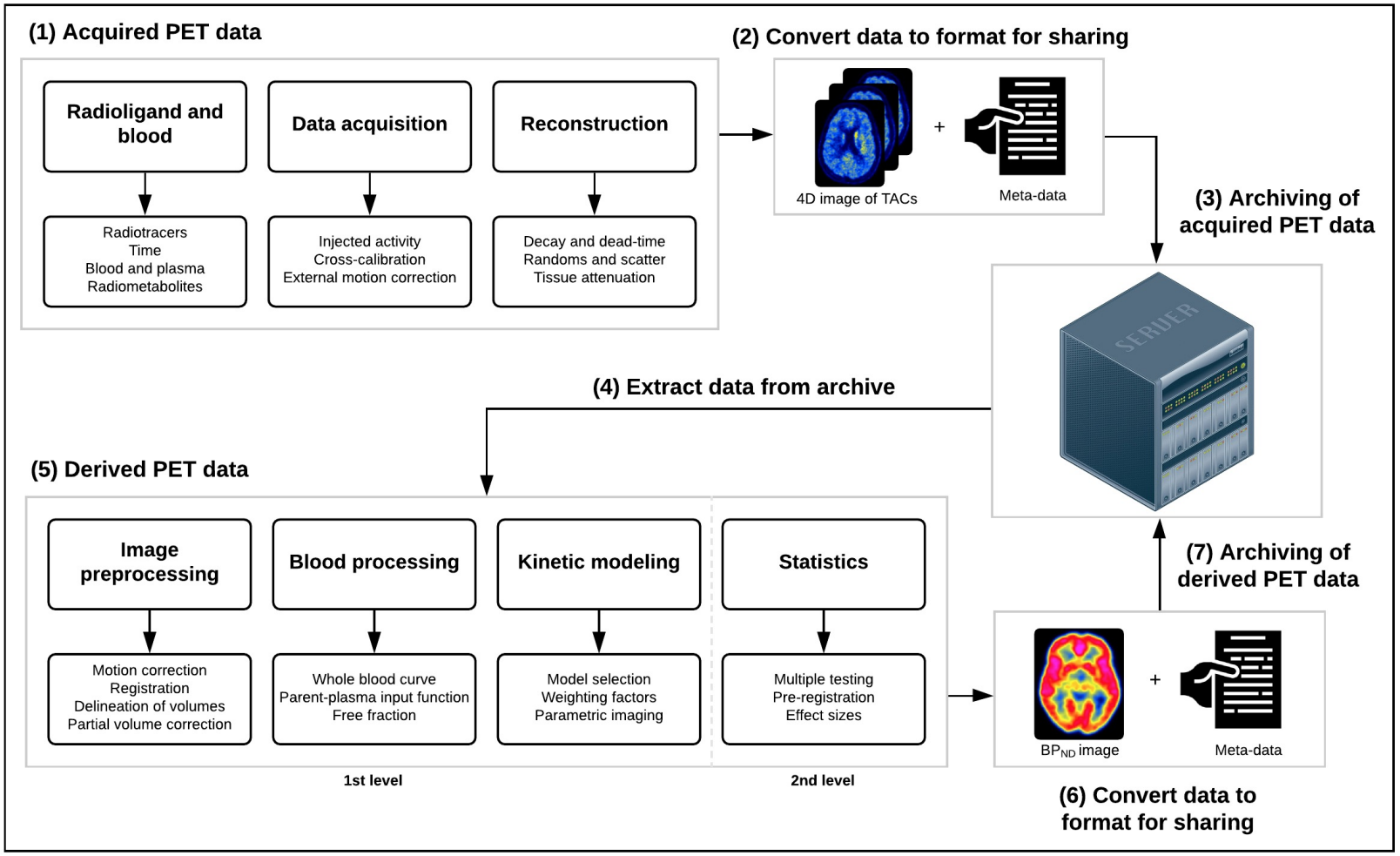
# Moving Forward with (PET-)BIDS Derivatives

BIDS DERIVATIVES MEETING COPENHAGEN
June 21-23, 2023



# Guidelines for the format and content of PET data




Knudsen & Innis et al. 2020, JCBFM

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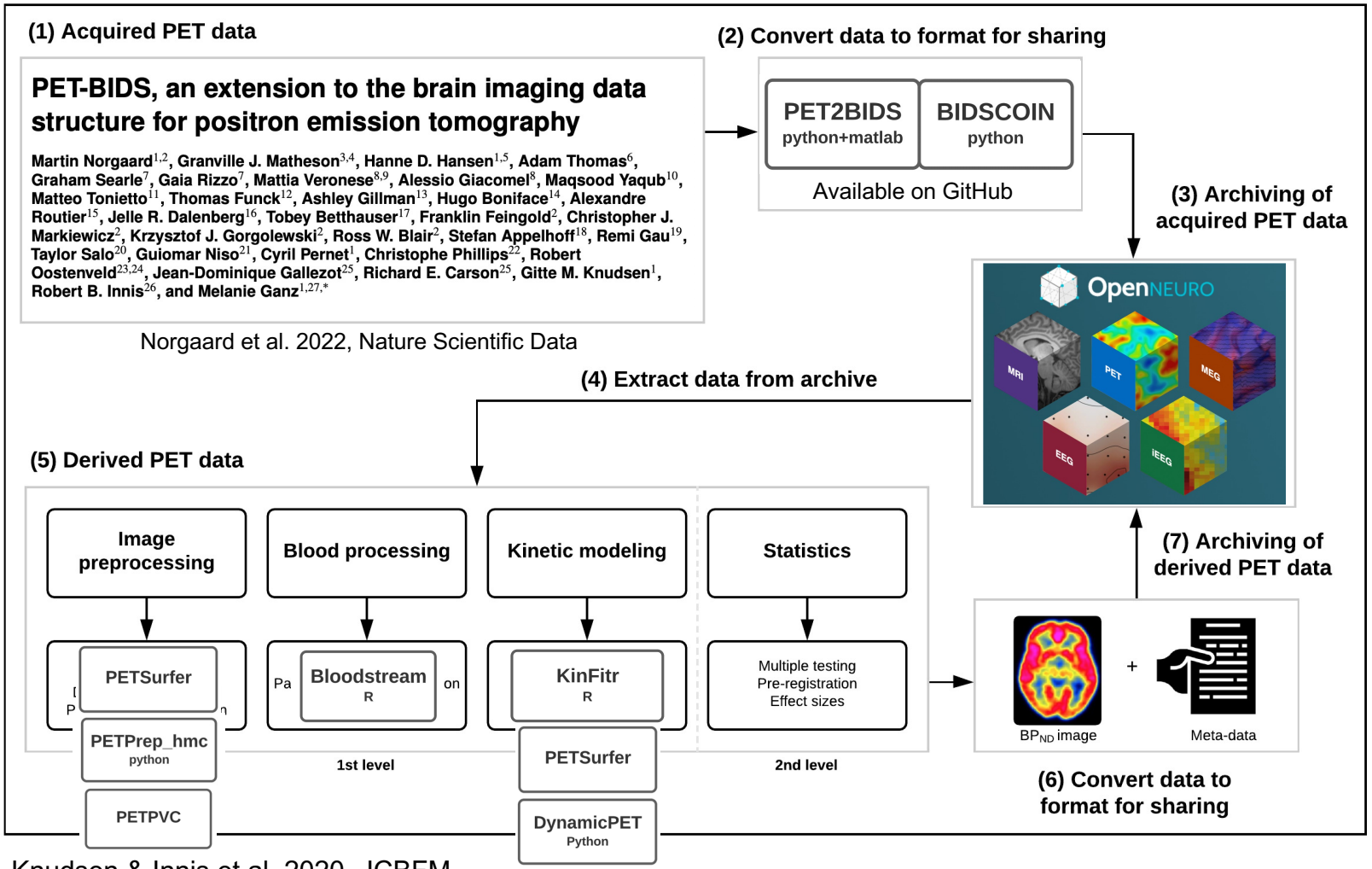
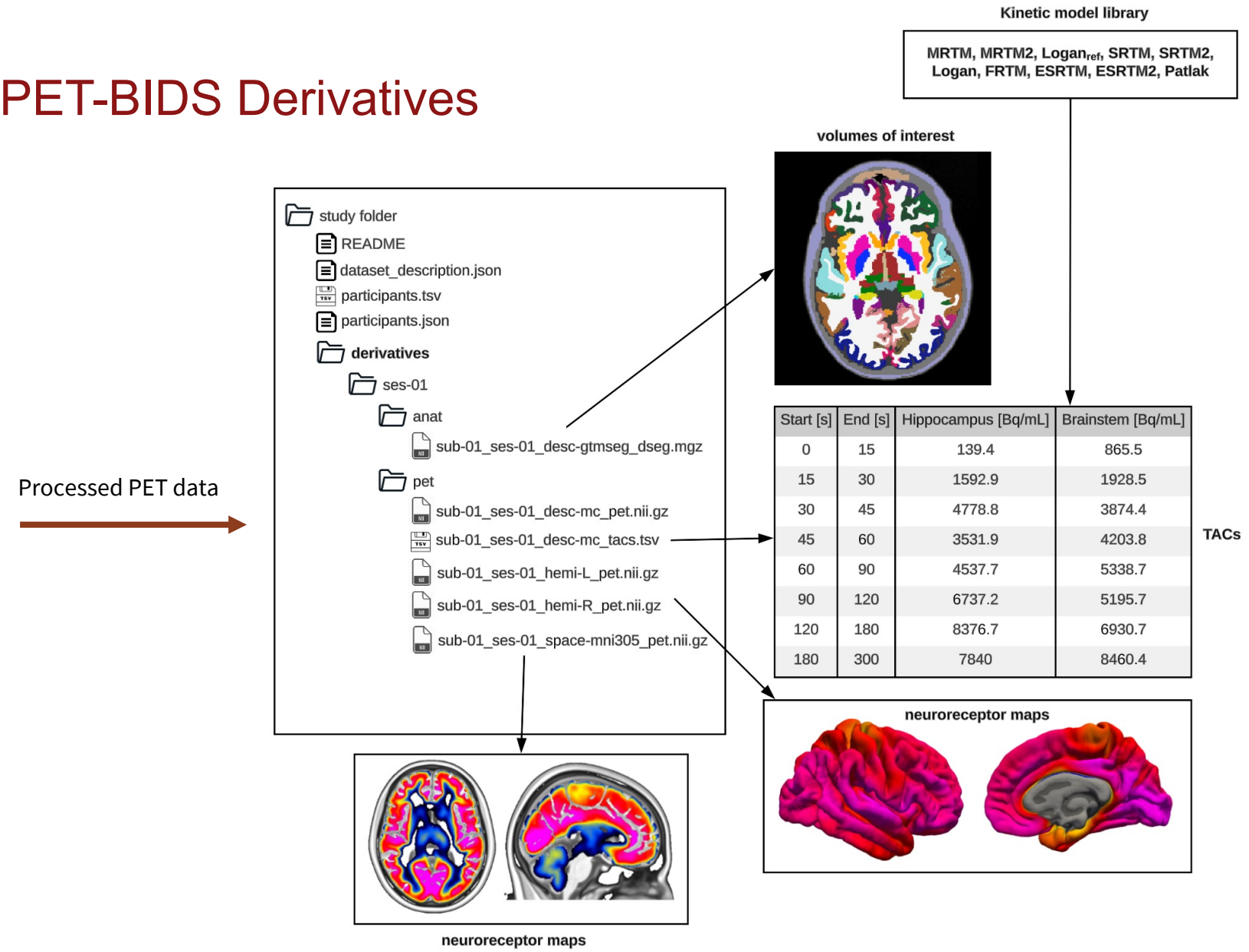



Stanford University

# PET-BIDS Derivatives




PET-BIDS Derivatives specification (BEP23):
https://docs.google.com/document/d/1yzsd1J9GT-aA0DWhdlgNr5LCu6_gvbjLyfvYq2FuxlY/edit#heading=h.mqkmyp254xh6

# How to move forward with PET-BIDS Derivatives

We need to cover 8 steps of potential processing steps

1. Motion correction
2. Co-registration
3. Delineation of Volumes of Interest
4. Partial Volume Correction
5. Kinetic Modeling
6. Smoothing
7. Blood processing
8. Parametric Images (voxelwise and surface-based)

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**Common across many modalities**

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# PET-BIDS Derivatives (defining output files)

**Motion Correction (*_desc)**

**Files:**
*_desc-confounds_timeseries.tsv
*_desc-confounds_timeseries.json
*_desc-mc_pet.nii.gz
*_desc-mc_pet.json
* figures/QC (redundant?)?

**Registration (*_space-)**

**Files:**
*_from-pet_to-T1w_reg.xfm
*_from-pet_to-T1w_reg.json
*_space-T1w_desc-brain_mask.nii.gz
*_space-T1w_desc-ref_pet.nii.gz
*_space-T1w_desc-ref_pet.json
*_space-T1w_pet.nii.gz

**Delineation of Volumes of Interest (*_desc-)**

**Files:**
*_desc-gtmseg_dseg.nii.gz
*_desc-gtmseg_dseg.tsv
*_desc-gtmseg_tacs.tsv
*_desc-gtmseg_morph.tsv
*_desc-brainstem_dseg.nii.gz
*_desc-brainstem_dseg.tsv ....

**Kinetic modeling (*_km-)**

**Files:**
*_km-mrtm2_desc-gtmseg_kinpar-BPnd_pet.tsv
*_km-mrtm2_desc-gtmseg_kinpar-BPnd_pet.json
*_km-srtm_desc-gtmseg_kinpar-BPnd_pet.tsv
*_km-srtm_desc-gtmseg_kinpar-BPnd_pet.json
*_km-srtm_desc-brainstem_kinpar-R1_pet.tsv
*_km-srtm_desc-brainstem_kinpar-R1_pet.json ...

**Smoothing (*_sm-)**

**Files:**
*_sm-8_pet.nii.gz
*_sm-8_pet.json

**Partial Volume Correction (*_pvc-)**

**Files:**
*_pvc-mg_pet.nii.gz
*_pvc-mg_pet.json
*_pvc-mg_desc-gm_mask.nii.gz
*_pvc-mg_desc-wm_mask.nii.gz
*_pvc-mg_desc-csf_mask.nii.gz

**Blood derivatives**

**Files:**
*_config.json
*_inputfunction.json
*_inputfunction.tsv

**Parametric images (volumes and surfaces)**

**Files:**
*_space-MNI305_res-2_km-mrtm2_kinpar-BPnd_pet.nii.gz
*_space-fsaverage_hemi-L_km-mrtm2_kinpar-BPnd_pet.nii.gz
*_space-fsaverage_hemi-R_km-mrtm2_kinpar-BPnd_pet.nii.gz

Example outputs available here:
https://github.com/openneuropet/pet-bids-derivatives-data/tree/main

# Software for PET analysis pipelines

**SOFTWARE for analyzing PET (and MR) data**

| SOFTWARE | Motion correction | Registration | Smoothing | Delineation of Volumes of Interest | Partial Volume Correction (PVC) | Pharmacokinetic Modeling | **Open source** |
|---|---|---|---|---|---|---|---|
| AIR | x | x | | | | | x |
| FreeSurfer | x | x | x | x | x | x | x |
| FSL | x | x | x | x | | | x |
| SPM* | x | x | X | x | | | |
| PMOD | x | x | x | x | x | x | |
| MIAKAT* | x | x | x | x | x | x | |
| PVElab* | | x | | x | x | | |
| APPIAN | | x | | x | x | x | x |
| Kinfitr | | | | | | x | x |
| PETPVC | | | | | x | | x |

*Runs via MATLAB, and is therefore not open source.

**REFERENCES**

AIR: http://air.bmap.ucla.edu/AIR5/index.html
FreeSurfer: https://surfer.nmr.mgh.harvard.edu/
FSL: https://fsl.fmrib.ox.ac.uk/fsl/fslwiki
SPM: https://www.fil.ion.ucl.ac.uk/spm/
PMOD: https://www.pmod.com/web/
MIAKAT: http://www.miakat.org/MIAKAT2/index.html
PVElab: https://xtra.nru.dk/pveout/
APPIAN: https://github.com/APPIAN-PET/APPIAN
Kinfitr: https://github.com/mathesong/kinfitr
PETPVC: https://github.com/UCL/PETPVC

**Statistics from Nørgaard et al. 2019 (review of 105 published DASB papers):**
AIR (N=7), FreeSurfer (N=2), FSL (N=3), SPM (N=60), PMOD (N=34), MIAKAT (N=0), PVElab (N=15), APPIAN (N=0), Kinfitr (N=0), PETPVC (N=0).

# How to move forward with PET-BIDS Derivatives

1. We need to align steps with other modalities to move forward
2. Have to make some choices on provenance