

## BIDS Apps for imaging data processing pipelines (D8.7.2 - SGA2)

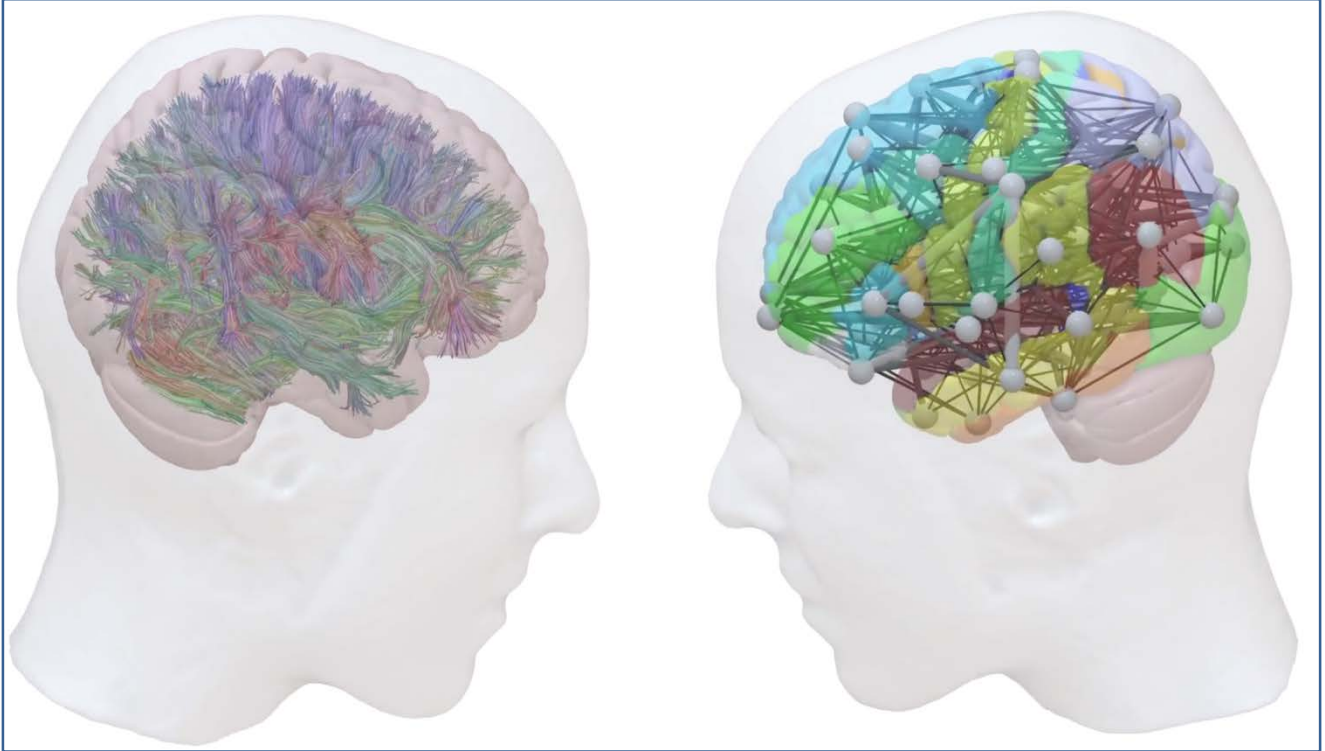


Figure 1: From neuroimaging to brain modelling.

The output of this deliverable is a pipeline that takes structural, functional and diffusion-weighted MRI data and computes functional and structural connectomes (brain networks). Furthermore, brain network models are generated that can be directly imported and used in The Virtual Brain Neuroinformatics Platform for brain simulation. For details, please refer to the HBP Collab Python notebook:

<https://collab.humanbrainproject.eu/#/collab/57720/nav/456763>

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<b>Description in GA:</b>	Applications for the imaging data processing pipelines using the Brain Imaging Data Structure format.		
<b>Abstract:</b>	This deliverable comprises a pipeline that takes structural, functional and diffusion-weighted MRI data as input and computes structural and functional connectomes as output. Furthermore, a BIDS App was developed that takes the output of other BIDS Apps to construct brain network models that can be directly imported into the Neuroinformatics Platform The Virtual Brain		
<b>Keywords:</b>	brain network model, pipeline, neuroimaging, connectome, The Virtual Brain		
<b>Target Users/Readers:</b>	clinicians, computational neuroscience community, computer scientists, consortium members, experts in neuroimaging, funders, general public, HPC community, neuroimaging community, neuroinformaticians, neuroscientific community, neuroscientists, platform users, policymakers, researchers, scientific community, students		

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# 1. Overview

The aim of Codesign Project 8 (CDP8) - The Virtual Brain (TVB) is to add tools for large-scale brain network simulation to the HBP. Instead of simulating individual neurons, TVB uses neural masses and mean-field neural population models for efficient simulation of the entire brain. The main goal of the CDP is to provide software that is based on the existing infrastructure of HBP and that bridges to the existing infrastructure provided by the HBP's Brain Simulation Platform (BSP, SP6), Neuroinformatics Platform (NIP, SP5) and High-Performance Analytics and Computing Platform (HPAC, SP7). More specifically, TVB's large-scale simulation facilities will be added to the HBP's code-base in order to provide software for parallelised, high-performance, multi-scale brain simulation.

The basis for brain simulation are structural models of large-scale brain networks. A major component of the CDP is, therefore, to provide users with connectome extraction pipelines and preprocessed connectomes extracted from major public data repositories, along with educational aids to help users to get quickly acquainted with TVB tools.

## 2. Introduction

In this report, we summarise the work performed by CDP8 for the Deliverable D8.7.2 "BIDS Apps for imaging data processing pipelines" until the end of the first year of SGA2. The work revolves around the implementation of a neuroimaging pipeline that generates structural and functional connectomes from MRI data.

This work produced one Key Result:

- KRc8.1: Pipeline for connectome extraction and brain model construction

## 3. Key Result KRc8.1: Pipeline for connectome extraction and brain model construction

### 3.1. Outputs

#### 3.1.1. *Overview of outputs*

- BIDS Container App *tvb\_converter*
- HBP Collab neuroimaging Pipeline and HPC interface

#### 3.1.2. *BIDS Container App tvb\_converter*

A Docker Container BIDS App was implemented that takes the outputs of other BIDS Apps (currently: *fmriprep* and *mrtrix3\_connectome*) as input and converts them into input for TVB. BIDS provides a standard for the specification and format of neuroimaging data as well as an ecosystem of containerised software modules (Apps) that enable a more robust and platform-independent processing of neuroimaging data as all the software necessary to perform the preprocessing are packaged in different containers that are maintained and regularly updated according to best practices.

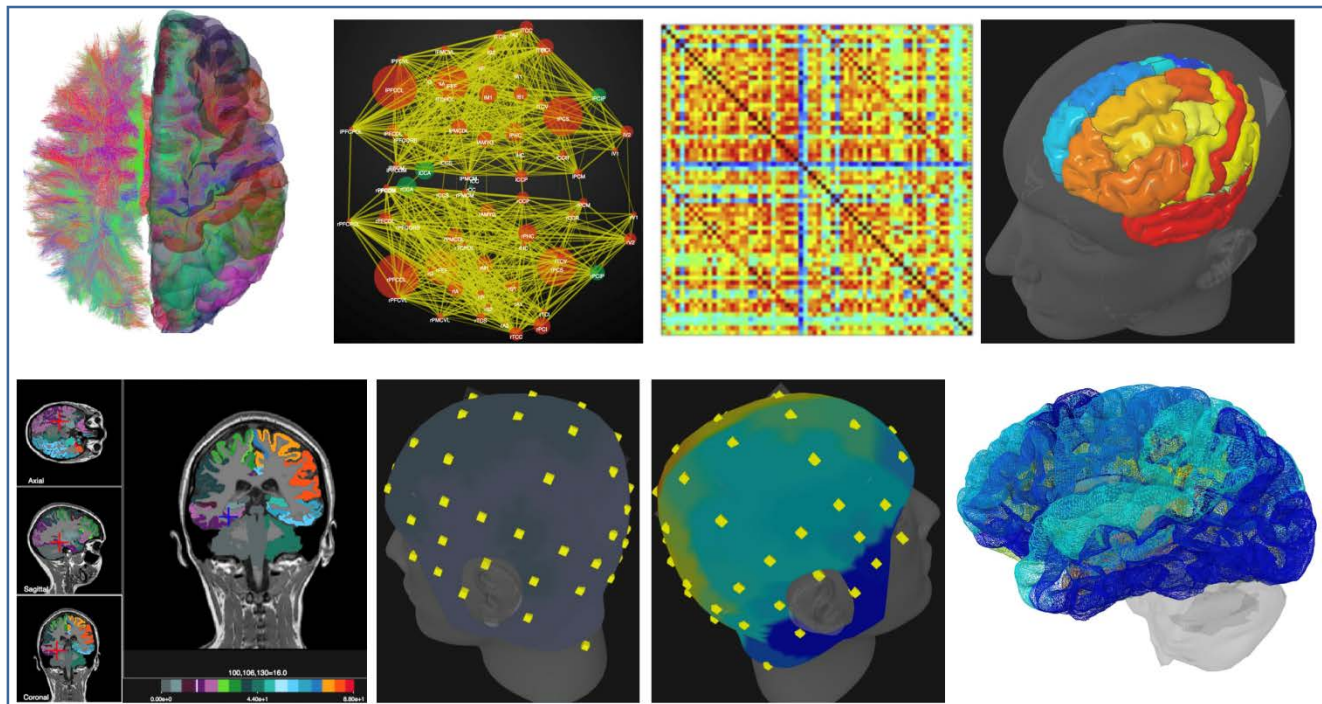


Figure 2: Some of the *tvb\_converter* BIDS App outputs.

Top row, from left to right: tractograms, structural connectomes, functional connectomes, region-average fMRI activity. Bottom row, from left to right: brain parcellations, M/EEG head and sensor models, source space / forward model, cortical surface triangulations.

The *tvb\_converter* BIDS App performs several postprocessing operations on the outputs of upstream structural/functional connectome BIDS Apps such as: non-aggressive cleaning of fMRI data using AROMA noise components, resampling of parcellation image from MRtrix docker pipeline to fMRI resolution, extraction of region-average fMRI time series, create region-mapping for volume-based parcellations, create cortical-surface and region-mapping. In addition, M/EEG source models are generated involving the computation of BEM head models and dipole forward model to compute leadfield models importable to TVB.

The outputs of this BIDS App are:

- a region map that maps source space (cortical surface) with parcellation regions
- cortical surface triangulation (source space)
- BEM inner skull, outer skull, outer skin surface triangulation
- EEG sensor locations
- structural connectome: connection weights, distances and region centres
- region orientations
- region areas
- Upon creation, these output data are converted into TVB-importable format.

### 3.1.3. HBP Collab Neuroimaging Pipeline and HPC Interface

The HBP Collab environment provides workspaces for HBP users where HBP software can be conveniently imported and executed. It also provides an interface for supercomputers based on the PyUnicore Api. We used this framework to implement a pipeline that generates structural connectomes, region-average fMRI time series and functional connectomes for simulation within The Virtual Brain, currently hosted at:

<https://collab.humanbrainproject.eu/#/collab/57720/nav/456763>

In this exhaustively documented Python notebook we showcase users in a tutorial-style how these goals can be realised step-by-step and provide further explanations on the usage of the involved software. Specifically, we make users acquainted with the usage of the HBP Collab framework, e.g., how BIDS data sets can be uploaded to Collab Storage and from there imported into the Jupyter client virtual filesystem; how datasets can be uploaded and downloaded from HBP supercomputers via PyUnicore and how PyUnicore can be used to create and execute batch job scripts on the supercomputer. After preparing the environment, the pipeline commences to process diffusion-weighted MRI data, using the state-of-the-art diffusion tractography software MRtrix3, implemented in the BIDS App `mrtrix3_connectome`, to produce structural full-brain connectomes. The workflow begins with denoising, artifact reduction and distortion corrections (e.g. correction of EPI susceptibility distortions); spherical deconvolution is performed to estimate fibre orientation distributions; diffusion-weighted and structural MRI are co-registered, tissues segmented and atlas-based parcellations applied to constrain tractography; Anatomically-Constrained Tractography ensures biological plausibility of generated streamlines; probabilistic tractography is used to generate full-brain tractograms and SIFT2 is used to generate connection weights.

Next, the `fmrip` BIDS App is used to preprocess functional MRI data with the goal to extract region-average fMRI time series and associated functional connectomes. The preprocessing involves intensity nonuniformity correction, skull stripping, spatial normalisation, atlassing/parcellation, brain extraction and tissue segmentation, spatial normalisation, surface reconstruction, motion correction, slice time correction, susceptibility distortion correction, multimodal registration, (“one-shot”) resampling into standard spaces and on FreeSurfer surfaces, confounds estimation and ICA-AROMA. The pipeline provides spatial and temporal preprocessed fMRI data, as well as estimated noise components. Noise components will be used to regress associated variance out of the fMRI data.

## 3.2. Validation and Impact

### 3.2.1. *Actual Use of Output(s) / Exploitation*

The pipeline is currently used to generate brain models from 10,000 subjects from the UK Biobank, which will be used to simulate person-specific activity in order to derive Biomarkers for neurological diseases.

### 3.2.2. *Potential Use of Output(s)*

As of October 2019, TVB was downloaded over 23,000 times. Researchers that use TVB could in principle use standard brain models for simulation, but the more interesting applications lie in the simulation of person-specific brain models to reveal inter-individual differences in brain dynamics, e.g. related to pathologies or behavioural features. Personalised medicine has a high demand for causal models that explain pathological brain dynamics on the basis of biophysical mechanisms in order to aid the creation of novel treatments for brain diseases. However, brain model creation is a tedious process, typically involving several different software packages and the use of supercomputers. The core result of this Deliverable makes a neuroimaging pipeline accessible to researchers and general public that enables the construction of person-specific brain models on supercomputers in an accessible and reproducible way. Researchers working in biomarker development (e.g. Alzheimer’s Disease), surgical planning (e.g. tumour, epilepsy), therapy development, diagnosis, etc. can benefit from high-quality brain models as those are only scarcely available today compared to the amount of existing neuroimaging data sets. Integration with the Medical Informatics Platform would augment the data available for researchers for modelling.

### 3.2.3. *Publications*

- 1) Aerts, Schirner, Jeurissen, Van Roost, Achten, Ritter, Marinazzo (2018) Modeling brain dynamics in brain tumor patients using The Virtual Brain. *eNeuro*
- 2) Leon Stefanovski, Paul Triebkorn, Andreas Spiegler, Margarita-Arimatea Diaz-Cortes, Ana Solodkin, Viktor Jirsa, Anthony Randal McIntosh, Petra Ritter; for the Alzheimer's Disease Neuroimaging Initiative (2019). Linking molecular pathways and large-scale computational modeling to assess candidate disease mechanisms and pharmacodynamics in Alzheimer's disease. *Frontiers Computational Neuroscience*
- 3) Poldrack, Feingold, Frank, Gleeson, de Hollander, Huys, Love, Markiewicz, Moran, Ritter, Turner, Yarkoni, Zhang, Cohen. (2019) The importance of standards for sharing of computational models and data. *Computational Brain & Behavior*
- 4) Ritter, P., M. Schirner, A. R. McIntosh and V. K. Jirsa (2013). The virtual brain integrates computational modeling and multimodal neuroimaging. *Brain Connect* 3(2): 121-145
- 5) Schirner, McIntosh, Jirsa, Deco, Ritter (2018) Inferring multi-scale neural mechanisms with brain network modelling. *eLife*
- 6) Schirner, M., S. Rothmeier, V. Jirsa, A. R. McIntosh and Ritter, P. (2015). An automated pipeline for constructing personalised virtual brains from multimodal neuroimaging data. *Neuroimage*.
- 7) Shen K, Bezgin G, Schirner M, Ritter P, Everling S, McIntosh AR (2019) A macaque connectome for large-scale network simulations in TheVirtualBrain *Nature Scientific Data*
- 8) Zimmermann, Perry, Breakspear, Schirner, Sachdev, Wen, Kochan, Mapstone, Ritter, McIntosh, Solodkin (2018) Differentiation of Alzheimer's disease based on local and global parameters in personalized Virtual Brain models. *Neuroimage Clinical*

### 3.2.4. *Measures to Increase Impact of Output(s): Dissemination*

In August 2019 CDP8 has organised the TVB-Node 9 at the annual INCF conference in Warsaw, Poland where a beta version of the pipeline was presented to participants. Participants obtained



**Figure 3: At TVB-Node 9 during the annual INCF conference in Warsaw, Poland**

At TVB-Node 9 during the annual INCF conference in Warsaw, Poland, a beta version of the pipeline was presented to participants.

HBP accounts and learned to use the pipeline from HBP Neuroinformatics Platform Collabs to generate brain models that were then simulated on HBP Brain Simulation Platform.

In September 2019, the pipeline was showcased at the Bernstein Conference satellite event “Brain Circuit Insight” in Berlin, Germany, as well as at the Summer School in Computational and Theoretical Models in Neuroscience in Venice, Italy and The Barcelona Cognition Brain and Technology summer school.

The Educational Brain Atlas, based on derivative data from the pipeline is part of the HBP travelling exhibition in Jerusalem and is now available on the HBP Collab platform.

<https://collab.humanbrainproject.eu/#/collab/47/nav/12368?state=software,TVBBrainAtlasViewer>

<https://www.brainsimulation.org/atlasweb/>

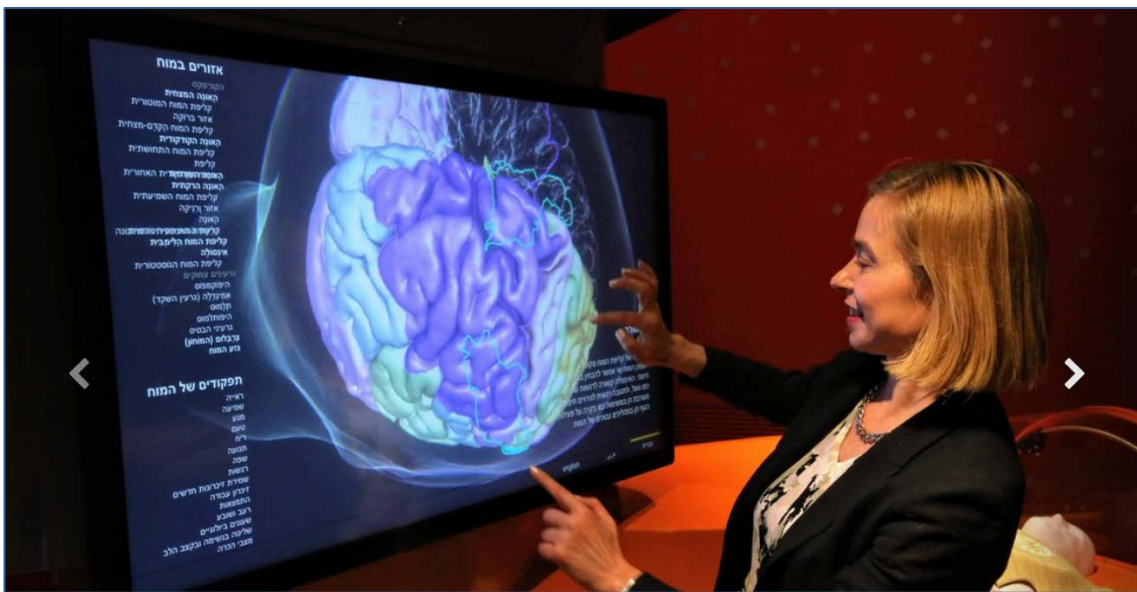


Figure 4: Educational Brain Atlas,

Educational Brain Atlas, based on derivative data from the pipeline, is part of the HBP travelling exhibition in Jerusalem.

## 4. Conclusion and Outlook

The pipeline described in this deliverable report is part of several contributions developed in CDP8. Other legs of this project include, among several others, the BSP-TVB pipeline which is a framework for multiscale brain simulation that enables the co-simulation of spiking networks with NEST and large-scale networks with TVB and the exchange of activity between the two. Another important aspect of this work is the HPAC-TVB pipeline where we implemented TVB’s simulator engine as a high-performance, parallelised C code that exploits supercomputing architectures. Together, these three modules comprise a powerful framework for brain simulation – from macroscopic to microscopic scales – based on person-specific large-scale brain architecture and using massively optimised codes.

Upcoming work deals with the connection of the pipeline with SP5 pipelines for metadata extraction and annotation in HBP Knowledge Graph.