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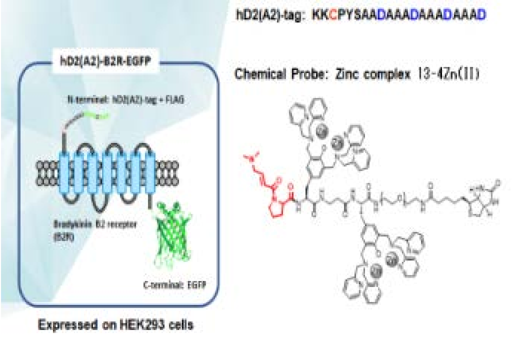
Abstract:	This deliverable is the annual compound of HBP deliveries and results (outputs and outcomes) from Sub-Project SP1 – SP1 Mouse Brain Organisation - Results for SGA1 Period 2. This report outlines the main Key Results of SP1 from April-2017 to March-2018. High-level subcellular and molecular datasets, High-quality datasets of the four brain regions: neocortex, cerebellum, hippocampus and basal ganglia, Whole brain high-level datasets and the experimental methods, IT tools and models developed. In particular, SP1 deliveries include Maps of the vasculature; Whole-brain maps of different cellular types; Microcircuitry analysis, proteins and receptor distributions and fibre architecture; Maps of cellular distributions, long-range axonal projections, and synaptic proteins; reconstructed morphologies of major neuron types; Whole-brain activation maps; Spatial organization principles in brain activation; Functional maps of cortical activity. SP1 deliveries also include strategic data on quantitative description of synaptic connections on neurons; numbers, distributions and relative densities of cells in selected brain regions or across the whole brain; statistical parameters characterizing particular cell types and spatial arrangements between neurons, glia and blood vessels; a high-resolution quantitative synaptic map of exemplar brain regions; EM blocks scans and volume analysis of exemplar brain regions with quantification of the neuropil organization; microcircuit analysis; functional maps of brain activation; morphological and physiological comparative studies of neurons between rodent and human. The live complete catalogue of HBP deliveries is accessible on-line from the HBP portal. The SP1 deliveries are also organized in the SP1 Data catalogue (HBP-SGA1-SP1DC-M23) annexed to this report.
Keywords:	Data, Tools, models, Subcellular and Molecular Level, Cellular Level, Microcircuitry, Whole Brain, Data Integration, Data Catalogue



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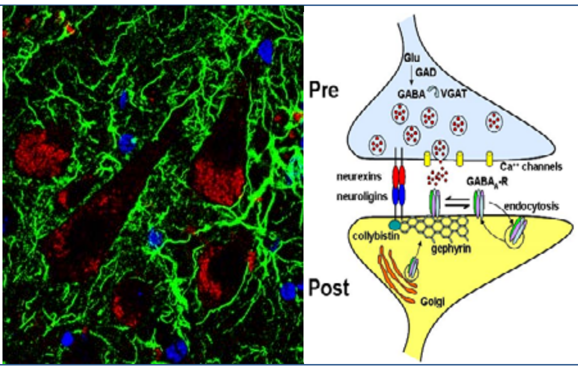

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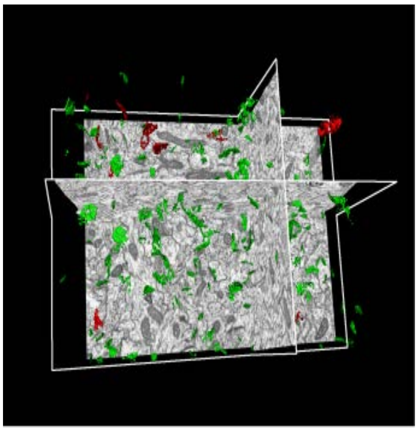
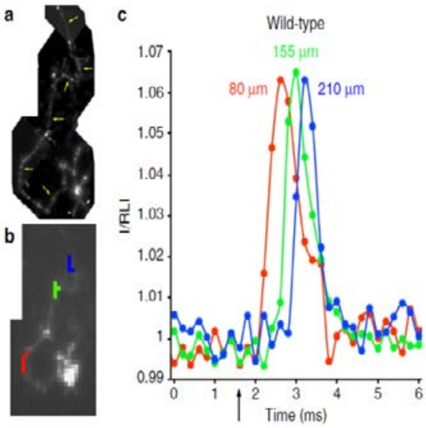
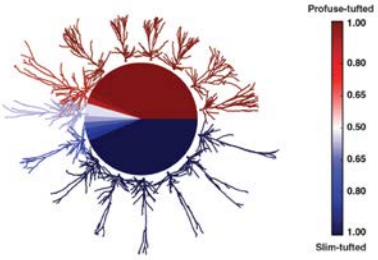


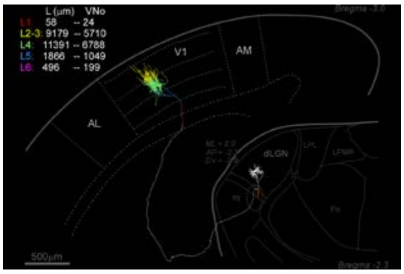
Advanced electron microscopy reconstructions



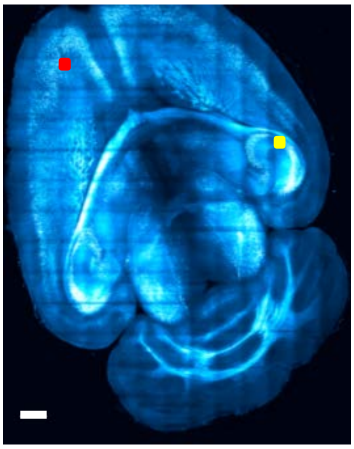
Unique recordings of axon potentials in single axons using voltage-sensitive dye imaging



Matching morphology and electrophysiology



Advanced 3D reconstructions: Individual thalamocortical projection neuron



Adaptive light-sheet microscopy for enhanced neuron and circuit mapping

Staining and imaging protocols for whole-brain vasculature reconstruction

Targeted users/readers	SP2, SP4, SP5, SP6, SP10, other SPs, PCO, Researchers, Policy Makers
Contributing Work-Package(s):	SGA1 WPs 1.1, 1.2, 1.3, 1.4, 1.5
Initially Planned Delivery Date:	SGA1 M24 / 31 Mar 2018 (Date for submission to EC, as set out in DoA)

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1. Introduction

The overarching objective of Subproject 1 (SP1) is to generate neuroscientific concepts, knowledge, experimental datasets and tools, in order to use them to build models for the simulation of the brain. In addition, SP1 provides data and knowledge to support activities undertaken by other Subprojects (SPs) and Co-Design Projects (CDPs), mainly SP6, but also SP4, SP10, CDP1 and CDP2. SP1 generates data mainly on the mouse brain and —to a limited degree— on human brain tissue.

This report outlines the main SP1 highlights during the period M13-M23. Most of them are the final outputs of the activities started in M01. The SP1 main achievements are included in four main SP1 Key Results as follows:

- KR1.1-High-level subcellular and molecular datasets:
  - Quantification of receptors and ion channels density, co-clustering of receptors/ion channels in different neuronal compartments, Intrabody interference and electrophysiological data under neuroligin block, and functional mapping of activated synapses for proteomic analyses
- KR1.2-High-quality datasets of the four brain regions: neocortex, cerebellum, hippocampus and basal ganglia:
  - Neocortex: pyramidal neuron, morphological and physiological comparative studies, EM Data, thalamocortical projections, synaptic maps
  - Cerebellum: plasticity rules
  - Hippocampus: morphological reconstructions, physiological characterization of neurons and synapses, synaptic maps
  - Basal Ganglia: cellular and morphological properties
- KR1.3-Whole brain high-level datasets:
  - A full volumetric atlas of the mouse brain, mesoscale cortical maps in rehabilitated mice after stroke, whole-brain activation and vasculature maps
- KR1.4-Development of experimental methods, IT tools and models:
  - Development of the integrated FIB/SEM and SDS-FRL immuno-electron microscopy technique
  - Generation of IACT small antibody domains for next generation brain imaging
  - Real-time defocus correction for high-resolution light-sheet microscopy
  - MultiMap: spatial analysis and segmentation of synapses from confocal images
  - Software Tools for the Interactive Analysis of Microanatomical Data
  - K channel kinetic and neuronal activity model
  - Computational models to map synapses and proteins

The main Key Results are described below together the main components contributing in each of them as well as the impact achieved. The detailed information regarding the datasets, tools and models generated in SP1 and included in this report is displayed in the SP1 Data Management Plan (D1.5.3: HBP-SGA1-SP1DMP-M23). The datasets generated, tools and models developed in SP1 as well as publications generated during the SGA1 are included in the SP1 Data Catalogue 'HBP-SGA1-SP1DC-M23' (Annex 1).

2. Results

2.1 Key Result 1.1: High-level subcellular and molecular datasets

Nanoscale measurements of distributions of individual receptors and ion channels in cortical neurons have been carried out. In particular, distribution of AMPA-type glutamate receptors, NMDA-type glutamate receptors, P/Q-type (Cav2.1) voltage-dependent calcium channels, GIRK channels, and SK channels have been examined in the cerebellum, hippocampus and other brain regions, by FIB/SEM as examples shown in Figure 2 and by SDS-FRL as examples shown in Figure 1. Existing component used is ID: 653.

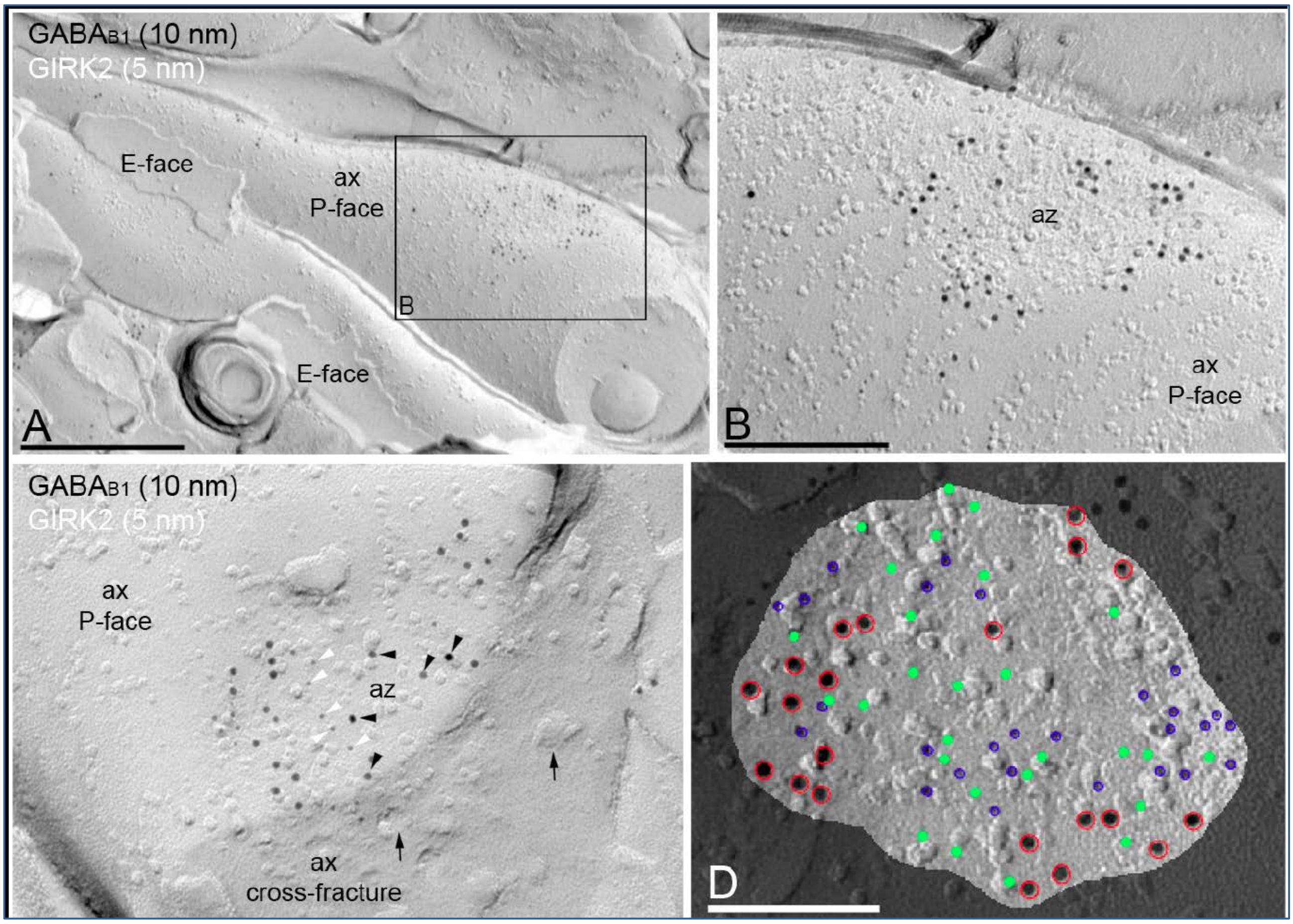


Figure 1: Development and operation of the GPDQ software used for quantitative analyses of immunoparticle distribution

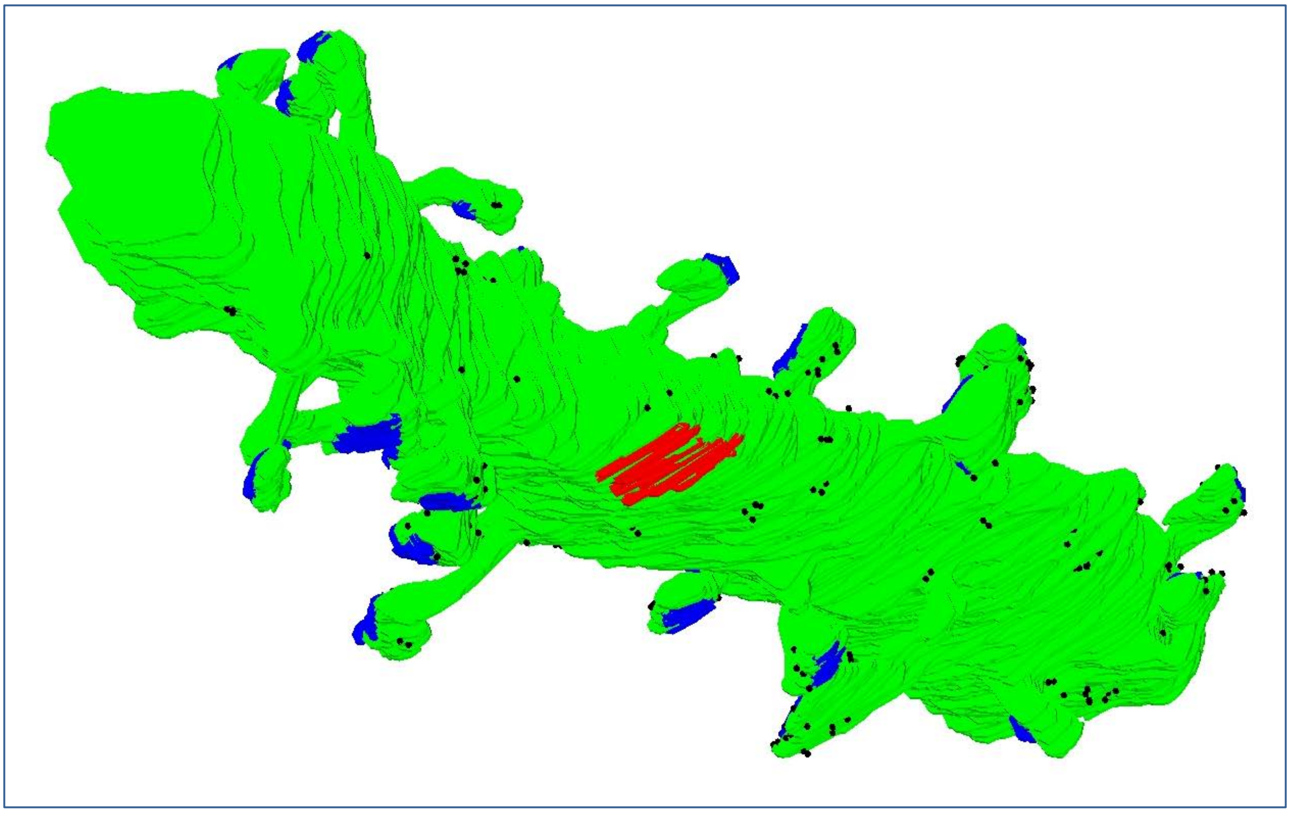


Figure 2: 3D localization of SK2 channels

Moreover, G-protein coupled receptors have different effector ion channels, kinases and others depending on different neuronal membrane compartments. Distinct associations of GABAB receptors to GIRK2/3 and Cav2.1 in spines, dendrites and axons were examined in the cerebellum. Using double-labelling SDS-FRL, co-clustering between $GABA_{B1}$ and GIRK2 was detected in dendritic spines, whereas they were mainly segregated in the dendritic shafts. In contrast, co-clustering of $GABA_{B1}$ and $Ca_V2.1$ was detected in dendritic shafts but not spines. Pre-synaptically, inter-cluster distance for $GABA_{B1}$ and GIRK2 was significantly smaller in the active zone than in the dendritic shafts, and that for $GABA_{B1}$ and $Ca_V2.1$ was significantly smaller in the active zone than in the dendritic shafts and spines. These data provide a better framework for understanding the different roles played by $GABA_B$ receptors and their effector ion channels in the cerebellar network. The existing component used has been *Association (co-clustering) of receptors and their effector ion channels in different neuronal compartments* (ID: 654).

Furthermore, the intrabody interference and electrophysiological data under neuroligin block have also been examined. In the presence of newly selected intrabodies against neuroligin 2 and its partner gephyrin, patch clamp recording from CA1 hippocampal pyramidal neurons unveiled changes in frequency, amplitude and kinetics of synaptic currents and alteration of short term plasticity processes. The generation of in vivo functional data on interactions between Neuroligin and Neurexin synaptic proteins, and their use for the computational modelling of trans-synaptic signalling is mainly aimed to address the functional role of transynaptic signalling in the formation, stabilization and plasticity of the synapses and lastly to generate modelling data used to develop plasticity algorithms, to contribute to the Neuroinformatics Platform and for modelling activities in the Brain Simulation Platform. The components used are the "Electrophysiological data under neuroligin block" (ID: 713) and "STP data" (ID: 711). So far, intrabodies against gephyrin and Neuroligin 2 have been expressed in mouse hippocampal neurons via constitutive lentiviral (dual promoter-EGFP) for biochemical and electrophysiological experiments. Data collected have been used for the ongoing modelling of synaptic signalling at GABAergic synapses. As with anti-gephyrin intrabodies retargeted to the nucleus, anti-NLG2 intrabodies also alter both amplitude and frequency of GABAergic postsynaptic currents. All these experimental data have been used to improve the ongoing modelling of synaptic signalling at GABAergic synapses. Existing component used is ID: 714. Short term plasticity (STP) data from CA1 region of the hippocampus have being collected from organotypic hippocampal slices infected with intrabodies against gephyrin, neuroligin 2 or GFP alone (as controls). Data analysis and their use to implement the computational model are still ongoing. Existing component used is ID: 712.

Finally, main attainments achieved in the studies on the pilot proteome dataset from synapses in the Hippocampus are as follows:

a) Functional mapping of activated synapses in the hippocampus for proteomic analyses

The SYNACTIVE tool has been employed to identify activated spines following chemical and electrical synaptic plasticity protocols in *ex vivo* preparations. The same tool is being exploited both *in vivo* and *ex vivo* to perform proteomic analyses to identify the potentiated spine-specific synaptome, working on both synaptomosomes and immunoprecipitates. Subsequent proteomic analysis is being performed in synaptomes obtained from activated and non-activated spines. The activity “Synapse proteomes and synaptomes” is mainly aimed at comparing the protein composition of constituent, activated synapses, by using the AAV vectors AAV5 hSyn::mPSD95-TAP and AAV5 ESARE::mPSD95-TAP. The data components used are *Activity-dependent proteomic changes occurring at active excitatory synapses* (ID: 2915) and *Proteomic data collection and analysis* (ID: 2916).

b) Extending coverage of published data

We already have a list of 6,500 genes obtained from 30 major synaptic proteomic studies from 2000 to 2016, which we have used to build synaptic protein-protein interaction (PPI) network models. We added data from 5 major postsynaptic studies published in 2017. The addition of these studies increased the total number of human synaptic genes found to 6899, the PPI postsynaptic proteome (PSP) network size to 4,752 (from 3,457), and the PPI PSP reduced network size to 2,156 (from 1,868).

c) Single Cell datasets

Data generated from Single Cell RNA-Seq is growing at a rapid pace; we have begun to integrate this type of annotation data into our synaptic network models. Here we highlight 4 major synaptic studies revealing both coarse and refined-scale functional heterogeneity of cell types (neuronal and non-neuronal) and genes expressed inside these cells in both mouse and human species, at various differential time points (embryotic, juvenile, adult), and at varying regions taken in the Central Nervous System (Cerebral Cortex, ventral midbrain, somatosensory cortex, Hypothalamus). The differentially expressed genes found in each cell type in each published study, has then been mapped back to our 6,500 genes found in the synaptic datasets.

d) Integration of functional data into synapse models

Genotype to phenotype data was obtained from the International Mouse Phenotype Consortium (IMPC). We used the latest release (Release 5.0: ftp://ftp.ebi.ac.uk/pub/databases/impc/release-5.0) to map the completed gene to phenotypes available onto our 6500 genes found in the synaptic datasets. Of the 3343 genes with completed phenotyping available, we find that 980 genes (30%) are found in our synaptic datatsets. This reflects ~12% of the pre-synaptic and PSD network models.

Also included are the annotation, Interpro families and domains for GO Molecular Function (MF), Biological Process (BP), Cellular Component (CC) and Human Disease Ontology (HDO) for each synaptic PPI network model.

We provide an interoperable Jupyter notebook to extract information associated with a gene of interest (“JupyterNotebook_functions”). The HBP Collab 'synaptic_data_integration' (https://collab.humanbrainproject.eu/#/collab/7076/nav/54104) contains all the required data, python functions, a Jupyter notebook to search through available datasets, and a simple user demonstration video ("use_example.ogv"). Available information focuses on synaptic genes/proteins and can be queried with a human EntrezID. Currently included datasets are:

- **synaptic proteome** – it can be checked if a gene is found in any one of the synaptic proteome sets – the output specifies in which, if any, of the synaptic datasets the protein was expressed: presynapse, postsynapse, synaptosome.
- **protein-protein interaction information** – the tool supplies information of any human, direct, interactions the gene of interest is part of. Currently the "interaction type" is displayed, but metadata fulfilling mitab25 standards is available in the deposited raw file.
- **single cell gene expression data** (separated by individual studies) – the tool displays if the gene of interest is expressed in neuronal or non-neuronal cells and specifies the prototypic cell type as well as cell type (e.g. oligodenrocytes, microglia, glutamatergic).
- **IMPC genotype-phenotype information** – information regarding the "mpath_term" (id and name), "top_level_mp" (id and name), and "mp_term" (id and name) associated with the gene of interest is displayed.
- **list of genes extracted from synaptic models** – checks if the gene of interest is part of one of the models we analysed in our paper submitted to PloS Comp. Biol. (Preprint at https://www.biorxiv.org/content/early/2018/01/28/254094).

2.1.1 Achieved Impact

The data collected in KR1.1 enables the use of gene expression data to predict features of the brain that have not been measured experimentally, drastically reducing the number of experiments necessary to build high fidelity reconstructions of the brain. As well as that, the generation of molecular maps provides vital information for the reconstruction and simulation of the healthy brain, and for the exploration and simulation of hundreds of brain diseases. In addition, the integration of molecular maps with cellular scale maps will allow cell classification and modelling of different types of cells.

The data collected provides the initial scaffolding and validation tests for high-fidelity reconstructions and simulations of the mouse brain, to be filled in with data from the HBP's European and International collaborations and with predictions from reconstructions.

2.1.2 Component Dependencies

Component ID	Component Name	HBP Internal	Comment
653	Nanoscale measurements of distributions of individual receptors and ion channels in cortical neurons.	*Yes*	Data generation and collection to provide 2D and 3D mapping along the neuronal surface by revealing the precise quantitative localization of receptors (AMPA, NMDA, mGlu5 and GABAB1) and ion channels (GIRK1, GIRK2, SK2 and Cav2.1) at the electron microscopic level.
654	Association (co-clustering) of receptors and their effector ion channels in different neuronal compartments	*Yes*	Data generation on the co-localization of different subunits of receptors and ion channels in the hippocampus and neocortex.
711	STP data	*Yes*	Ex-vivo electrophysiological recordings
713	Electrophysiological data under neuroligin block	*Yes*	Data generated on spontaneous action potential dependent and

			independent post synaptic current, inhibitory and excitatory (sIPSC, mIPSC, sEPSC and mEPSC) and short term plasticity in control and under gephyrin/neuroligin block.
2915	Activity-dependent proteomic changes occurring at active excitatory synapses	*Yes*	Data on the activity-dependent local translation of reporter proteins at activated dendritic spines, via a combination of RNA targeting and protein targeting sequences (Synaptic current).
2916	Proteomic data collection and analysis	*Yes*	Data on subcellular proteome: differential analysis between samples.
2917	Extending coverage of published data	*Yes*	PPI Network models
2918	Genetic mapping to single cell profiles	*Yes*	Copies of datasets on single cell transcriptomic profiles of mouse neurons.
2919	Integration of functional data into synapse models	*Yes*	Generation of prototype data

2.2 Key Result 1.2: High-quality datasets of the four brain regions: neocortex, cerebellum, hippocampus and basal ganglia

2.2.1 Neocortex

2.2.1.1 The pyramidal neuron

A major goal in neuroscience is the study of pyramidal cells as they represent the main type of neuron in the neocortex and hippocampus. A key question posed by Gordon Shepherd is 'what is the minimum architecture necessary to capture the integrative structure of the pyramidal neuron in order to build realistic neuronal and network models to simulate brain functions?' To answer this question, we are closely collaborating with several laboratories of the HBP by combining experimental (anatomy and physiology) and computational studies. In particular, morphological and physiological datasets from same neurons in adult mouse and adult human has been generated. These datasets from the same neurons in adult mouse and adult human neocortex have been matched and have been shared with HBP laboratories from the Brain Simulation Platform

This model of pyramidal cell will be integrated in a model of cortical microcircuit in which the main types of GABAergic interneurons will be included. Indeed, the study of interneurons is another major aim as GABA-mediated inhibition regulates synaptic integration, probability and timing of action potential generation of pyramidal cells. Accordingly, these neurons are crucial in establishing the functional balance and computational design of neural circuits. In SP1, six GABAergic subtypes: parvalbumin, calbindin, calretinin, vasoactive intestinal polypeptide, somatostatin and choline-acetyltransferase have been identified. Also, the utmost ultrastructure in specimen aimed for quantitative electron microscopy (qEM) has been achieved and the "mirror" technique has been implemented on these neurons.

Concerning the pyramidal neuron studies, these have used the existing data components IDs: 955-959 and has generated several publications that are included in the SP1 Data catalogue (see in Annex 1 publications linked to T1.2.1). The comparative studies of neural morphology and physiology have used the existing components IDs: 757, 759 and has generated several publications that are included in the SP1 Data Catalogue (see in Annex 1 publications linked to T1.2.2). The identification of the GABAergic subtypes has used the existing data component used is ID: 784.

Moreover, 3D Reconstructions of individually labelled thalamocortical projection neurons' axons have been generated. A total of 17 valid transfection-labelled individual thalamocortical projection neurons in somatosensory and visual thalamic nuclei from adult (2-3month-old) C57B/L6 wild-type male mice have been analysed. We have digitally reconstructed their complete axon morphology over large series of histological sections to accurately measure key functionally-relevant structural parameters such as axonal length and varicosity number (as a proxy for synaptic sites) in their cortical and subcortical target regions. The 3D reconstruction data files include references to key brain landmarks that are necessary for precise 3D atlasing of these cells in the Allen Mouse Brain Atlas. Finally, we produced serial "virtual slice" image stacks of the labelled neuronal cell body and of each of the terminal axonal arborisation fields. Internally, these datasets are being used to develop automated 3D mouse brain atlasing tools, as well as) to guide multi-electrode array mapping of somatomotor cortex dynamics. Externally, these data have been shared with the Blue Brain Project group in Geneva to develop a biologically accurate mouse model of the thalamo-reticular circuitry. The existing component ID: 732 has been used. Several publications have been generated that are included in the SP1 Data catalogue (see in Annex 1 publications linked to T1.2.8).

Furthermore, synaptic maps at the meso and nanoscopic levels in the neocortex of the mouse and human have also been generated at Cellular level. The densities of synapses and their spatial distribution have been determined in the six layers of the mouse neocortex (primary somatosensory cortex) and in layer III of the human neocortex (temporal cortex, T2). Data have been obtained by confocal microscopy and electron microscopy (FIB/SEM), and have been analysed with dedicated software (Espina). Key quantitative information on the distribution of excitatory and inhibitory synapses has been obtained at different scales from the mouse and human neocortex. At the confocal microscopy level, we have determined the distribution of immunocytochemically labelled axon terminals (VGlut1 and vGAT for excitatory and inhibitory terminals, respectively) in strata oriens, pyramidale, radiatum and lacunosum-moleculare from the six layers of the mouse somatosensory cortex. At the ultrastructural level, we have used three-dimensional electron microscopy to quantify the distribution of excitatory and inhibitory synapses in the same regions. Datasets from confocal imaging studies have been correlated to electron microscopy data. Knowing the number and distribution of different types of synapses in different areas of the brain is important to better understand brain connectivity, since we have found that different brain regions and cortical layers show different densities of synaptic connections. As well as that, these differences can be mapped to their corresponding bran regions, so they are useful for atlasing efforts. Finally, the quantitative information on the densities and distributions of synapses can be used in the design, building, validation and refining of realistic brain models. The existing data components 962, 964, 966 have been used and several publications have been generated that are included in the SP1 Data catalogue (see in Annex 1 publications linked to T1.2.9)

2.2.2 Cerebellum

We have determined a set of novel forms of synaptic plasticity that are needed to develop the model of the mouse cerebellum and Mouse-Based Cellular Cortical and Subcortical Microcircuit Models. These include STDP at the mossy fibre - granule cell synapse (Sgritta et al., 2017), bidirectional anti-Hebbian plasticity at the mossy fibre-Golgi cell synapse (in preparation), low-frequency resonance plasticity at DCN synapses (submitted), and alterations of LTP in the IB2 mouse model of autism (submitted).

This achievement has used the existing data components IDs 810 and 811 and has generated several publications that are included in the SP1 Data catalogue (see in Annex 1 publications linked to T1.2.4)

2.2.3 Hippocampus

Based on more than 300 experiments in SGA1 and the ramp-up phase, a database of the morphological and physiological features of the main classes of hippocampal neurons in the mouse has been constructed. The database includes 3-dimensional image stacks and reconstructions of the somata, dendritic arbors and axonal bouton clouds of approximately 200 cells filled in the hippocampal slice, and about 500 recordings and extracted physiological features from a partially overlapping cell population (new internal Component ID: 805). In addition, the database contains reconstructions and physiological data from hippocampal neurons recorded in awake, head-fixed mice (new internal component ID: 806).

Moreover, using paired whole-cell recordings in hippocampal slices, the basal transmission properties and short-term plasticity parameters for several major classes of hippocampal connections have been determined and stored in a database (new internal Component 926). In order to increase the generalization power of the dataset, explicit comparison of different hippocampal subfields (CA3 vs. CA1) and animal ages (young vs. adult) has also been carried out.

Furthermore, synaptic maps of the mouse and human have also been generated at the meso and nanoscopic levels. The densities of synapses and their spatial distribution have been determined in the mouse and human hippocampus (CA1 area). Data have been obtained by confocal microscopy and electron microscopy (FIB/SEM), and have been analysed with dedicated software (Espina). Key quantitative information on the distribution of excitatory and inhibitory synapses has been obtained at different scales. At the confocal microscopy level, we have determined the distribution of immunocytochemically labelled axon terminals (VGlut1 and vGAT for excitatory and inhibitory terminals, respectively) in strata oriens, pyramidale, radiatum and lacunosum-moleculare. At the ultrastructural level, we have used three-dimensional electron microscopy to quantify the distribution of excitatory and inhibitory synapses in the same regions. Datasets from confocal imaging studies have been correlated to electron microscopy data. Knowing the number and distribution of different types of synapses in different areas of the brain is important to better understand brain connectivity, since we have found that different brain regions and cortical layers show different densities of synaptic connections. As well as that, these differences can be mapped to their corresponding bran regions, so they are useful for atlasing efforts. Finally, the quantitative information on the densities and distributions of synapses can be used in the design, building, validation and refining of realistic brain models. The existing data components IDs 961, 963, 965 have been used and several publications have been generated that are included in the SP1 Data catalogue (see in Annex 1 publications linked to T1.2.9)

2.2.4 Basal Ganglia

The morphology of the two types of medium spiny neurons (expressing D1 and D2 dopamine receptors, respectively) are described in parallel with their membrane properties. Fast-spiking and cholinergic interneurons have been described in a similar way. The soma-dendritic morphology combined with the detailed membrane properties are critical for allowing a detailed simulation of the different neuronal subtypes with Hodgkin-Huxley compartmental models. In order to understand the processing in the basal ganglia, which is of fundamental importance for decision making, selection of behaviour and motor learning, it is critical to understand the underlying networks. Of particular importance is the input layer of the basal ganglia, i.e. the striatum. The data produced under this activity is critical for the simulations of the model of basal ganglia. The existing components used are Connectivity and morphology of neurons within striatum (ID: 938) and Cellular properties of neurons within striatum (ID: 940)

2.2.5 Achieved Impact

Data generated in this KR allows the implementation of detailed neuron and microcircuitry reconstruction and physiological analysis for example by intracellular injections of markers, 3D reconstructions, and physiological recordings of cellular properties in vivo and in vitro. This multilevel approach has been applied to four brain regions, neocortex (including thalamocortical projections), cerebellum, basal ganglia, and hippocampus to generate multiscale molecular, anatomical and functional maps. The integration of molecular maps with cellular scale maps will allow cell classification and modelling of different types of cells, as mention in KR1.1.

Furthermore, the data collected in this KR makes a vital contribution to the Multi-level Atlas of the Mouse Brain, created in SP5. As well as that, the data collected in this KR provides the initial scaffolding and validation tests for high-fidelity reconstructions and simulations of the mouse brain, to be filled in with data from the HBP's European and International collaborations and with predictions from reconstructions.

Finally, the comparative assessment of the data generated in this KR SP1 and other KRs from SP2 can identify principles allowing the use of mouse data to predict features of the human brain for which experimental data are not available.

2.2.6 Component Dependencies

Component ID	Component Name	HBP Internal	Comment
955, 956, 957, 958, 959	955 3D reconstructions of 300 pyramidal neurons from the mouse somatosensory cortex across layers II-VI 956 3D reconstructions of 50 cells in mouse hippocampal CA1 region 957 3D reconstructions of 50 cells in rat hippocampal CA1 region 958 3D reconstructions of 50 cells in human hippocampal formation (CA1) 959 3D reconstructions of 200 cells in human neocortex (temporal, cingulate and frontal)	Yes	Data generation on 3D reconstructions of cell of the mouse and human neocortex and mouse, rat and human hippocampus for modelling circuits
757 , 759	Morphological and physiological data from the same neurons in adult mouse	Yes	Generation of morphological and physiological data in temporal and frontal cortex in adult mouse and human for modelling human neocortical circuits, theory and simulation
784	Quantitative electron microscopic (qEM) database of synaptic coverage of GABAergic neuron subtypes	Yes	Generation of quantitative data on the synaptic input morphologies for GABAergic populations of interneurons
732	3D reconstruction of thalamocortical neurons	Yes	Generation of quantitative data on axonal length terminal bouton number of thalamocortical neurons innervating V1 and S1 cortices
962, 964, 966	962 Immunocytochemical detection of excitatory and inhibitory terminals in the mouse neocortex (somatosensory cortex) by confocal microscopy (data)	Yes	Generation of high-resolution synaptic maps in the neocortex of mouse and human

	964 Densities and 3D distributions of synapses using FIB/SEM imaging in the mouse neocortex (somatosensory cortex) (data) 966 Densities and 3D distributions of synapses using FIB/SEM imaging in the human neocortex (Temporal cortex, T2) (data)		
810, 811	Patch-clamp recordings from cerebellar neurons Combined optogenetics, two-photon imaging and electrophysiological recordings from cerebellar neurons	Yes	Generation of morphological, electrophysiological data for cerebellar modelling
805	Database of all the major excitatory and inhibitory cell types of the mouse hippocampus, using a combination of morphological and electrophysiological classification	Yes	Generation of a database of all the major excitatory and inhibitory cell types of the mouse hippocampus
926	Database of paired recordings in hippocampal slices which display in vivo-like activity levels and patterns	Yes	Generation of a electrophysiological database of major cell types of the mouse hippocampus
961, 963, 965	965 Densities and 3D distributions of synapses using FIB/SEM imaging in the human hippocampus (CA1) (data) 963 Densities and 3D distributions of synapses using FIB/SEM imaging in the mouse hippocampus (CA1) (data) 961 Immunocytochemical detection of excitatory and inhibitory terminals in the mouse hippocampus (CA1) by confocal microscopy (data)	Yes	Generation of high-resolution synaptic maps in the hippocampus of mouse and human
938	Connectivity and morphology of neurons within striatum	Yes	Generation of data on the striatum to develop model of basal ganglia and models of motor control
940	Cellular properties of neurons within striatum	Yes	Generation of data on the striatum to develop model of basal ganglia and models of motor control

2.3 Key Result 1.3: Whole brain high-level datasets

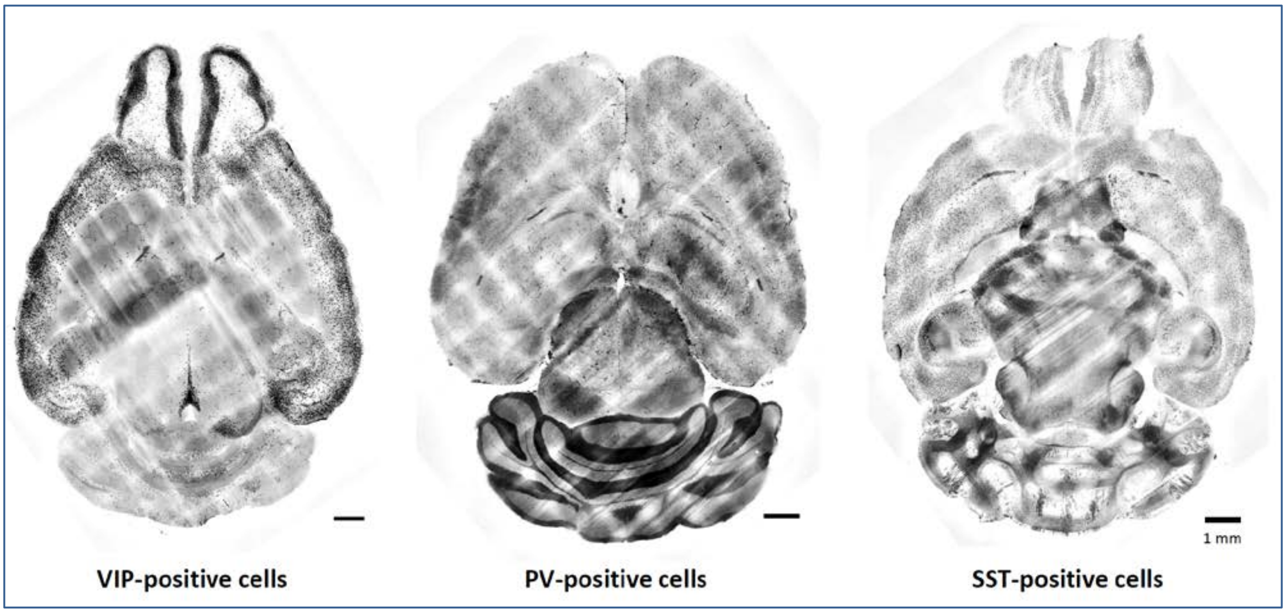
Main achievements accomplished at whole brain level are as follows:

2.3.1 A full volumetric atlas of the mouse brain

HBP researchers combined high-resolution light-sheet microscopy with deep learning-based image analysis to obtain a cell-resolution map of different neuronal types in the entire mouse brain. In detail, we focused on three interneuron populations: parvalbumin-positive, somatostatin positive and vasoactive intestinal peptide-positive. We used transgenic animals where these neurons express fluorescent protein, cleared the sample and imaged with a custom-made light-sheet microscope. Full resolution datasets are available on CINECA, whereas low-res one has been uploaded on the Collab.

Constituting components are: Whole-brain images of selected neuronal types (existing, ID: 932), Whole-brain maps of selected neuronal types, Optimization of Clarity for whole brain imaging, Improved light-sheet microscopy for whole brain imaging (existing, ID: 892), SP1 - Software for cell counting and shape recognition, LocaliZoom: viewer for series of 2D images with reference atlas superimposed (Component 85-11), MeshView: online 3-D surface and custom slice viewer for Allen mouse brain atlas, MeshView v2.0: updated functionality, viewing of annotations from LocaliZoom (Component 86-12). Components accessible via with the following tools (available through a UIO webserver): LOCALIZOOM and MESHVIEW.

The impact obtained thanks to this delivery has been, internally, data that can be used to build realistic brain models, and outside HBP, these data are reference data about brain cytoarchitecture, and reference images for the development of image processing methods.



VIP-positive cells PV-positive cells SST-positive cells

Figure 3: Representative whole-brain cell distribution data. Virtual transversal slices extracted from whole-brain volume.

2.3.2 Mesoscale cortical maps in rehabilitated mice after stroke

Through a wide-field microscope HBP researchers recorded calcium activity after stroke in resting state and during the pulling task on the robotic platform, in order to obtain cortical maps of activation in the peri-infarct area. We studied the functional plasticity using a wide-field microscope revealing the calcium dynamic over a large area while the mice perform the motor task on the robotic platform. By analysing the maps of activation, we observe that the rehabilitation protocol promotes the refocus of cortical output. To evaluate the interhemispheric remapping, we apply an all optical approach on Thy1-GCaMP6f mice expressing in the primary motor cortex the light sensitive protein Channelrodopsin 2. By analysing the activation profiles during the stimulation, we reveal after 4 weeks of rehabilitation a strengthened interhemispheric connectivity, compared to non-treated mice.

Constituting components are: Fluorescence imaging of cortical activity after stroke (existing, ID: 552), Wide-field mesoscope, Single-photon system for optogenetic actuation, Optimization of rehabilitation platform, Analysis of meso-scale fluorescence functional data. The impact obtained thanks to this delivery includes progressive recovery of cortical activation profiles, the validation of the calcium activity model, the integration of cortical activity maps on the HBP Mouse Brain Atlas and the validation of virtual rehabilitation scenario.

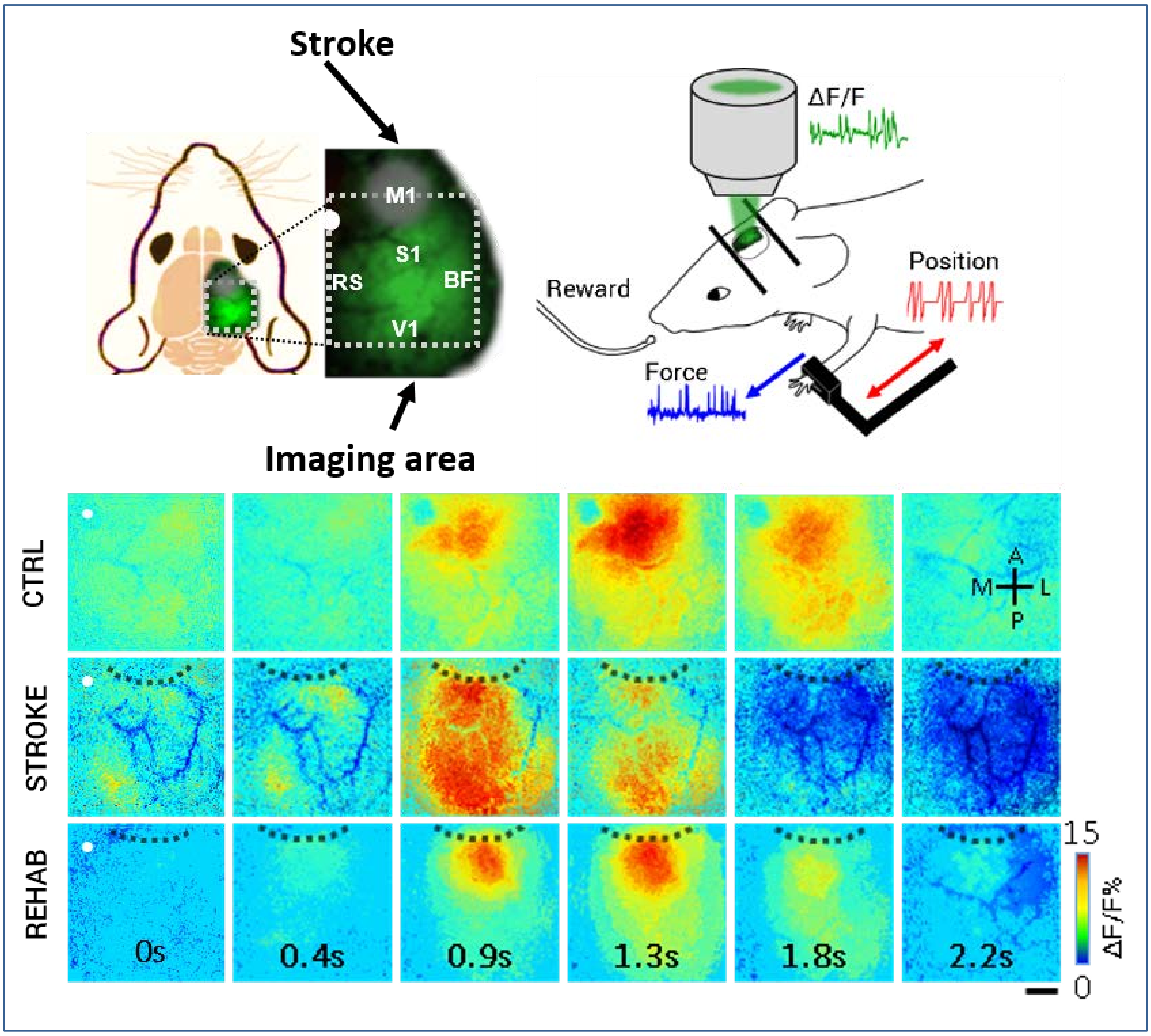


Figure 4: Cortical activation profiles in stroke conditions and after 4 week of rehabilitation.

2.3.3 Whole-brain activation mapped with cellular resolution

HBP researchers exploited activity-dependent fluorescence labelling to obtain the whole-brain distribution of activated neurons in resting mice. Resting-state activity mapping in mice with cellular resolution represent a fundamental reference for model validation inside and outside HBP. Constituting components are: Images of neuronal activation of whole mouse brain (existing, ID: 931), Maps of neuronal activation of whole mouse brain, SP1 - Software for cell counting and shape recognition and Point-neuron model of the whole mouse brain? Concerning the impact obtained thanks to this delivery, internally, these data that can be used to validate brain models. Outside HBP, these data are reference data about brain resting-state activation and reference images for the development of image processing methods.

Figure 5: Representative Dataset of resting-state activation.

Virtual transversal slice extracted from a whole-brain volume

2.3.4 Vasculature maps

One of the areas SP1 focused on in the last 12 months was to acquire large areas of mouse brain vasculature images and improving segmentation and graph extraction methods on them. The goal is creating high-resolution vascular maps using multimodal and multiscale approaches. To achieve this, the methods had to be robust on different inputs. Therefore, the current version of the reconstruction pipeline has been tested using new alternate datasets which differ significantly from the first dataset used (Synchrotron Radiation X-Ray). We achieved good results on these new datasets. We are also developing deep learning based segmentation approaches in collaboration with our partners at TUM to integrate into our pipeline. This will allow us comparison, better performance and possible fusion approaches to improve results. The method is tested with the first dataset used (Synchrotron Radiation X-Ray) with success. Another area of effort is on the side of gathering manual ground truth data. A big issue that is being faced with learning methods (which outperform other methods) is lack of training data. For that we have gathered a team of 4 people from different disciplines and institutions (UZH, TUM, and ETH) including computer science, neuroscience and fluid dynamics (potential end-users of the vasculature graph networks). First annotations of large datasets are done.

Improvements scheduled before the end of SGA1 include the improvement of the performance of learning methods using newly gathered manual ground truth annotations and the integration of an alternative new segmentation method into the reconstruction pipeline. Constituting components are Newly Acquired Raw Data: [new] – 2 different sources of light sheet microscopy images, and Generated Vascular Graph Models: [new] – Large scale vascular models generated from 3 data sources in the size ranging from 26K to 213K vessel segments. Existing components used are IDs: 744 and 755. All components are accessible via with the following tools: Rat Cortex Vasculature Collab

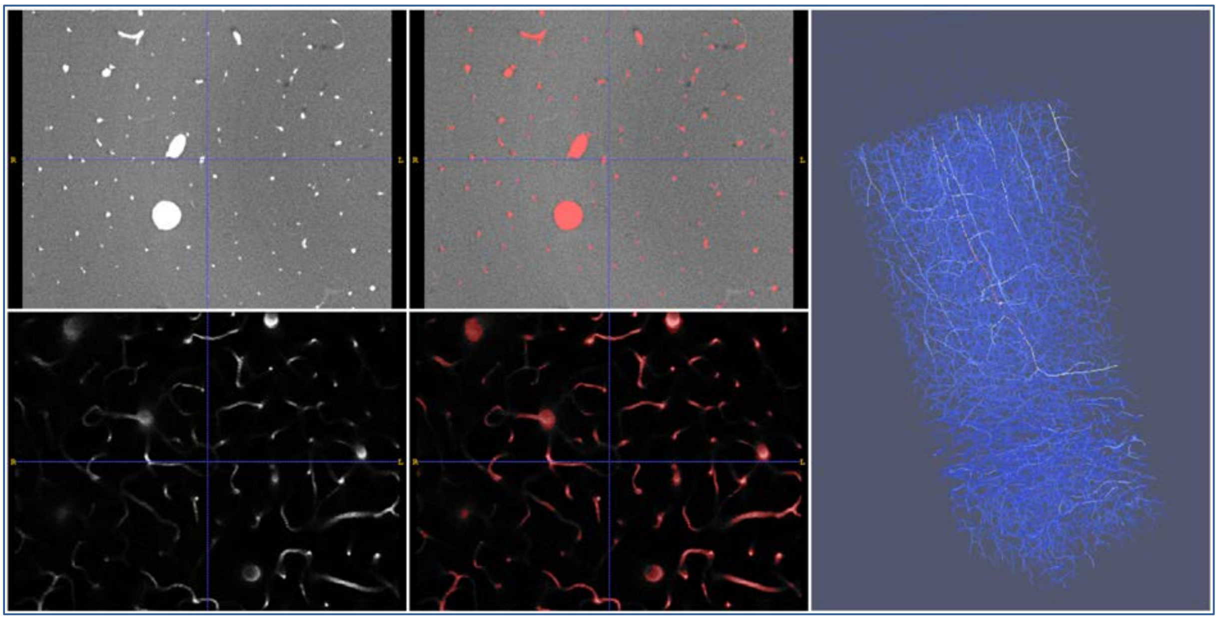


Figure 6: Pipeline of reconstruction.

Left column: raw images from SRXRay and Two-photon microscope. Middle column: segmentations. Right column: vascular reconstruction of part of the cortex (129K vessel segments) including colour coded radius estimates.

2.3.5 Achieved Impact

This KR contributes to the creation of the first multi-level map of the whole mouse brain.

The generation of whole brain cell distribution maps are being integrated with single-cell characterization to allow detailed whole-brain simulations. This KR also contributes to translational research by investigating the remapping of cortical activity triggered by robot-assisted rehabilitation.

The data collected in this KR makes a vital contribution to the Multi-level Atlas of the Mouse Brain, created in SP5. As well as that, the data collected in SP1 will provide the initial scaffolding and validation tests for high-fidelity reconstructions and simulations of the mouse brain, to be filled in with data from the HBP's European and International collaborations and with predictions from reconstructions. As with KR1.2, the comparative assessment of the data collected in this KR and other KRs in SP2 can identify principles allowing the use of mouse data to predict features of the human brain for which experimental data are not available.

2.3.6 Component Dependencies

Component ID	Component Name	HBP Internal	Comment
932	Whole-brain images of selected neuronal types	*Yes*	Generation of whole-brain cell maps
552	Fluorescence imaging of cortical activity after stroke	*Yes*	Data generation on 2D lapse recording of calcium-activity in the cortex of fluorescent mice of three experimental groups: control, stroke, rehabilitated
931	Images of neuronal activation of whole mouse brain	*Yes*	Generation of whole brain activation maps

755	3D reconstruction of the entire vascular system of the mouse brain	*Yes*	Generation of maps of the vasculature of the whole mouse brain
744	3D image of the entire vascular system of the mouse brain	*Yes*	To provide input to methods that will create vasculature models of the brain

2.4 Key Result 1.4: Development of experimental methods, IT tools and model

2.4.1 *Development of the integrated FIB/SEM and SDS-FRL immunoelectron microscopy technique*

A semi-automated image acquisition and analyses software (GPDQ: *Gold Particle Detection and Quantification*) has been developed to *enable* analysis of immunogold distribution on different neuronal compartments. The software is built on MATLAB and Image Processing Toolbox 9.3 (The MathWorks, Inc., Natick, MA, USA) optimised for two-dimensional detection of gold particles of different sizes and allow users to supervise the process of segmentation and counting, modifying the appropriate parameters and validating the results as needed (Figure 1).

Constituting new components are:

- Particle detection module– The particle detection module allows obtaining the radius and position (in nanometres from top-left corner) of the particles in the images. The automated version uses a two-stage procedure that detects the circles of a given diameter in the image with MATLAB’s implementation of the Hough transform, and then determines which of them correspond to actual particles by means of a supervised classification model.
- Analysis and simulation module – This module allows for the processing of all information about images and particle locations, particle clusters and simulations computing the number of particles, nearest neighbour distances to both particles of the same type (intra-type NNDs, e.g. from 5 nm particle to nearest 5 nm particle) and other type (inter-type NNDs, e.g. from 5 nm particle to nearest 10 nm particle). Clusters are obtained by single-linkage. In addition, the second module allows for two types of simulations, termed random and fitted simulation.
- Graph and statistics module – The third module deals with the generation of graphs and statistics, from the parameters computed with the second module.
- Visualization module – The fourth module allows for visualization of the distribution of original particles as well as simulated particles as for example shown in Figure 1.

Fluorescence-guided and grid-glued replica methods (Harada and Shigemoto, 2017) have also developed to facilitate efficient mapping of receptors and ion channels in large brain areas. In addition, new labelling metal reporters are under development to increase the resolution of labelling and multiple labelling for protein complex analyses.

Existing component used is ID: 652.

2.4.2 *Generation of IACT small antibody domains for next generation brain imaging*

IACT small antibody fragments used as tools for brain imaging, due their specificity and better penetration in tissues. The component used is the PLA based "Antibodies against targets identified in all genomic and proteomics tasks" (ID: 826) and data reports are uploaded in an Internal / Provisional repository with a protected access on EBRI lab server (http://151.100.170.9:8080/cgi-bin/), in a dataset called "IACT antibody fragments for imaging".

To date, the main use of small antibody domains in imaging is obtained by exploiting antibody fragments raised against Amyloid beta Oligomers. Publications generated are listed in the SP1 Data catalogue (see in Annex 1 publications linked to T1.1.2).

2.4.3 Real-time defocus correction for high-resolution light-sheet microscopy

HBP researchers devised RAPID, a real-time image-based autofocus method that empowers light-sheet microscopy by maintaining image sharpness without any reduction in imaging speed. RAPID is based on the principle of phase detection, widely used in photography, and is applicable to all wide-field microscopy schemes. An Italian patent application regarding RAPID has been filed, and several microscopy companies have already expressed interest in this technology. Impact obtained is to improve image quality acquisitions with light-sheet microscope and an Italian Patent is pending. Constituting component is ‘Improved light-sheet microscopy for whole brain imaging’ (ID: 892)

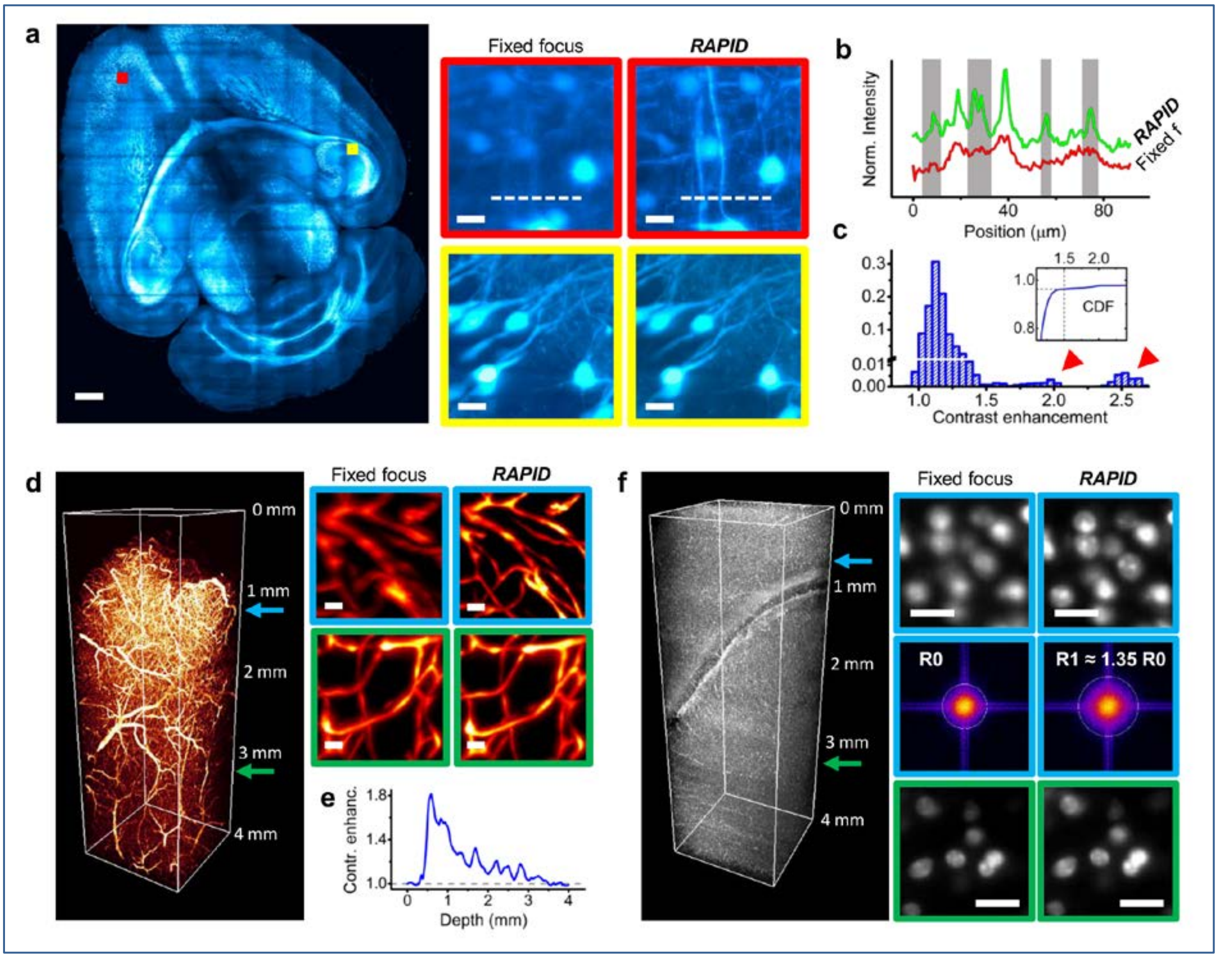


Figure 7: A virtual slab (500 µm thick) from the brain of a thy1-GFP-M transgenic mouse

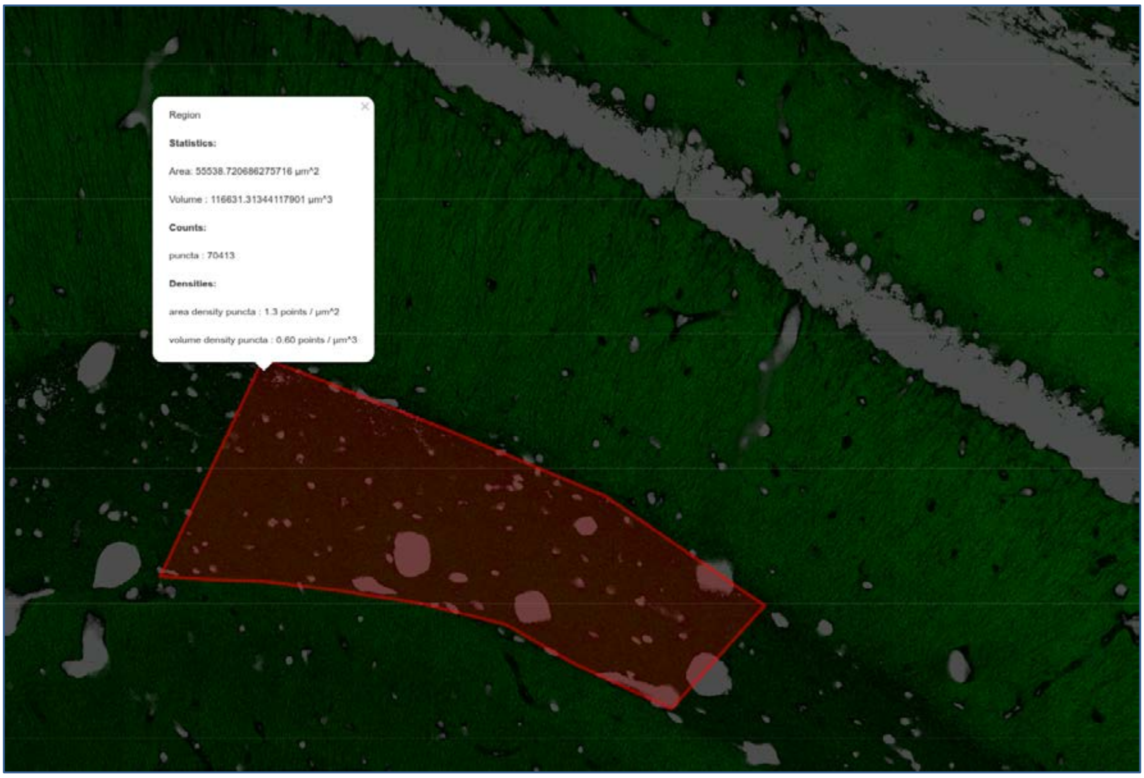
(a). RAPID defocus correction across different tiles (insets). The intensity profiles were obtained along the dashed lines (b). The grey regions denote fine sample details lost without autofocus. Histogram of contrast enhancement using RAPID relative to fixed focus imaging (c) for all the images forming the slab in (a). The red arrowheads indicate positive outliers, and the inset shows the cumulative density function (CDF). Three-dimensional rendering of an image stack from a vasculature-stained mouse brain showing insets at different depths (d). The RAPID contrast enhancement for this stack as a function of depth is shown in (e). Three-dimensional rendering of an image stack from a mouse brain with nuclear staining. The constant shape of the nuclei allows the evaluation of the resolution enhancement achieved with RAPID by examining the radius of the Fourier transforms (insets, middle line). Scale bars: 1 mm (a), 20 µm (insets).

2.4.4 MultiMap: spatial analysis and segmentation of synapses from confocal images

MultiMap is a new tool that allows the visualization, 3D segmentation and quantification of fluorescent structures selectively in the neuropil from large stacks of confocal microscopy images. The major contribution of this tool is the possibility to easily navigate and create regions of interest of any shape and size within a large brain area that will be automatically 3D segmented and quantified to determine the density of puncta in the neuropil. Figure 8 illustrates estimating point density over a region. The current version of the software (released in M12) already contains most of the intended functionality. A final release is due in M24.

Constituting components used have been Synapse segmentation ImageJ plugin and macro (new).The plugin filters a stack of images from confocal microscopy to separate background from foreground. Foreground pixels are further connected to create 3D objects, the synapses, and Interactive synaptic map (new): Web-based end-user interface to interactively analyse regions of the brain previously segmented to detect synapses. Error model is used to validate segmentation. All components are installable locally as their code is available from GitHub.

The existing components used have been IDs: 433 and 434. This tool has been applied to analyse glutamatergic and GABAergic presynaptic axon terminals in the mouse hippocampal region and provide putative excitatory and inhibitory synaptic maps and a paper has been submitted to Frontiers in Neuroanatomy



Region

Statistics:

Area: 55538.720686275716 µm^2

Volume : 116631.31344117901 µm^3

Counts:

puncta : 70413

Densities:

area density puncta : 1.3 points / µm^2

volume density puncta : 0.60 points / µm^3

Figure 8: Detail of the Graphical Interface of MultiMap

Detail of the Graphical Interface of MultiMap, showing the computed holes layer and the result of the density estimation over a region

2.4.5 Software tools for the interactive analysis of micro-anatomical data

This key result includes a framework of interactive tools that have been specifically developed for the visual analysis of micro-anatomical data (Pyramidal Explorer, DC Explorer, mi Explorer and Clint Explorer). Different captures from the framework are shown in Figure 9. Their goal is to help users to gain insight into the complex datasets acquired with modern neuroscience laboratory techniques. Even though the developments were specifically focused on micro-anatomical data, the tools have been designed with a general purpose. In consequence, they can be applied to different kinds of information or datasets. Constituting component (existing) is 'Tools for the early analysis of morphological data' (ID: 906), including Pyramidal Explorer, DCExplorer, InToolExplorer, ClintExplorer.

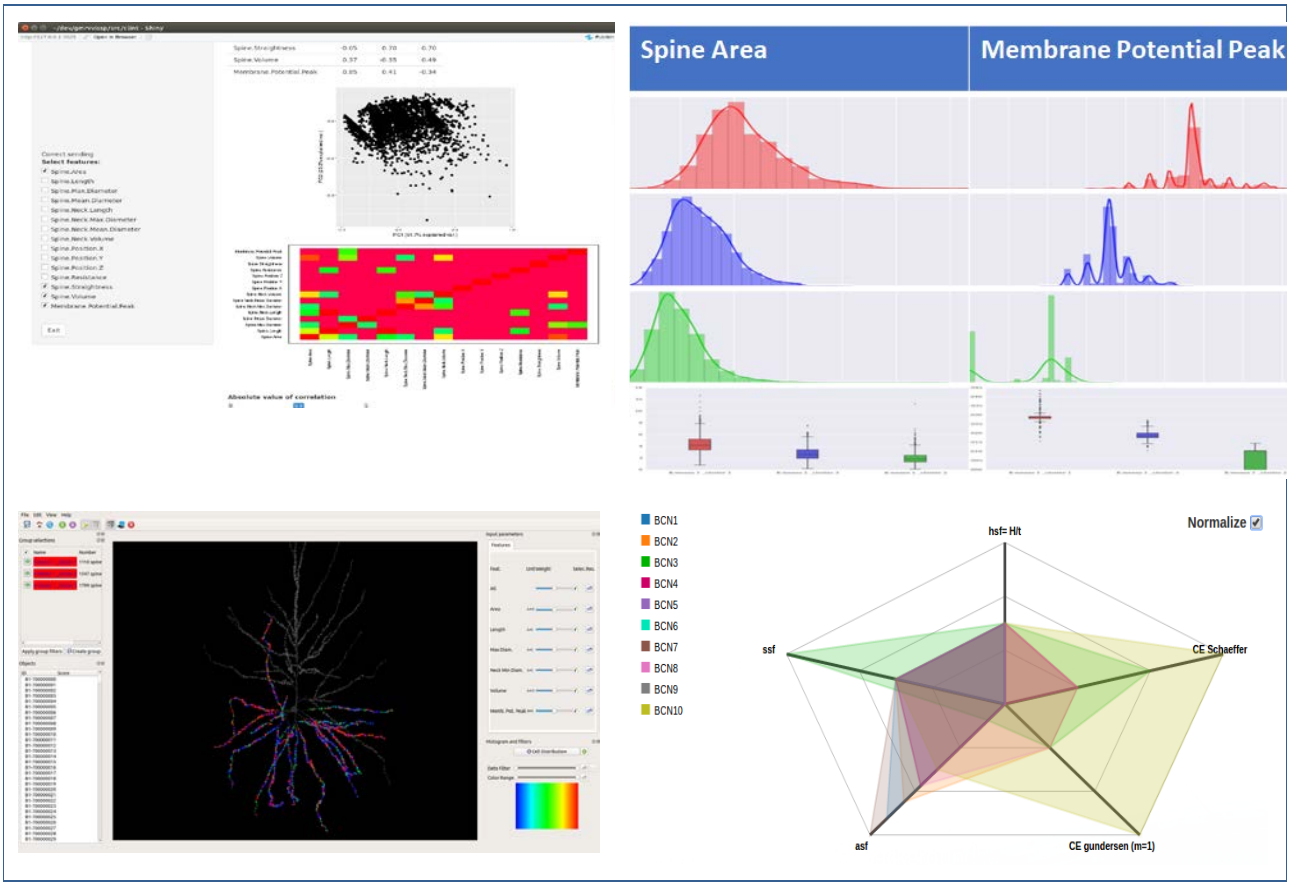


Figure 9: Overview of the interactive visualization tools framework

2.4.6 K channel kinetic and neuronal activity model

Kinetic models using different number of functional states were fitted to electrophysiology data for 23 K channel genes for which electrophysiological data were available. Such kinetic models were later included in a generic neuron model to simulate action potential propagation in presence of different density ratio of the K channel of interest and the generic K channels of the neuron model. The single neuron simulations illustrate how each channel can modulate the shape of action potentials and the frequency of the signal. The study of K channels down to the minute details allows for models of different complexity and accuracy. The comparison of the different models illustrates the compromises that are made when a simple kinetic model is used instead of a potentially more detailed one. The analysis of the functional properties of the different channels also illustrate to which extent it is important to integrate each channel individually in a neuron model. These kinetic models would add a layer of granularity to neuron models (T6.2.1, T6.2.2, and T6.2.4). Constituting component is *K channel activity within neuron models* (ID: 575)

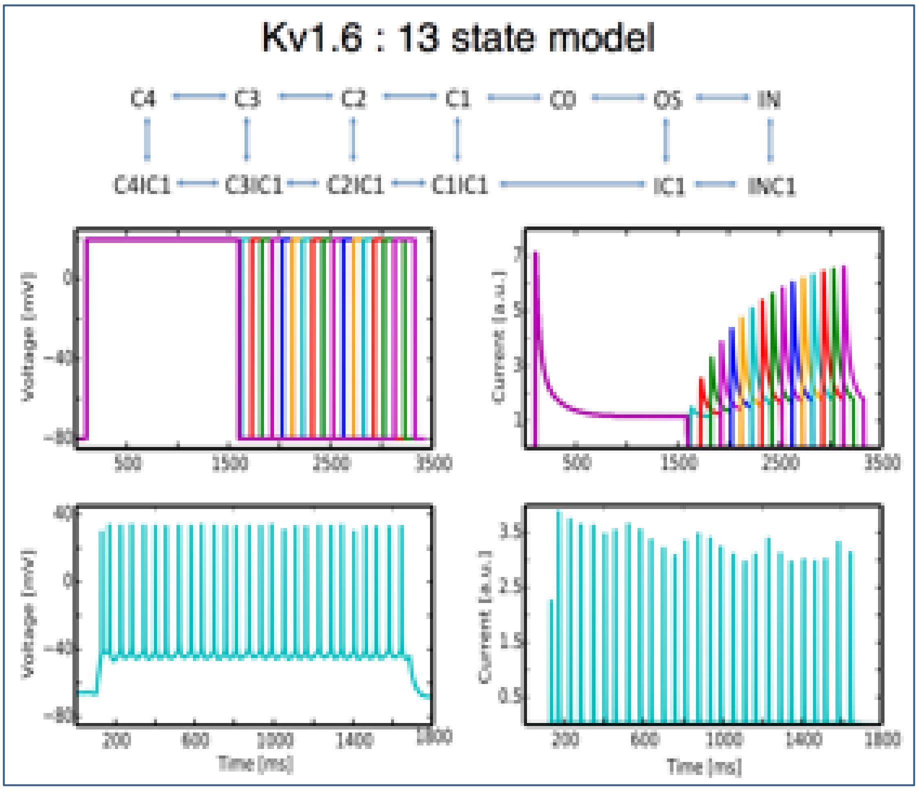


Figure 10: Kinetic model of a Kv channel and associated electrophysiological traces

Kinetic model of a Kv channel and associated electrophysiological traces with the applied voltage on the left and the resulting current on the right

2.4.7 Computational models to map synapses and proteins

HBP is investigating plasticity, and a crucial question is which of the many proteins identified in synapses to bring into models, so as to build models with high explanatory power and relevance to disease. This work is designed to start the process of prioritizing proteins in a principled, systematic manner. As a data component, no components have been used to create this data. The data are in CSV and text files so can be accessed using many general purpose mathematical and statistical packages. We have provided scripts in R that read the files, and generate many of the plots in the paper that accompanies the data.

We have used the files to perform an analysis of proteins represented in models of synaptic plasticity (manuscript submitted; available on bioRxiv: https://doi.org/10.1101/254094**Error! Hyperlink reference not valid.**We were able to map 4.2% of previously reported synaptic proteins to entities in biophysical models. Linking the modelled protein list to Gene Ontology terms shows that modelled proteins are focused on functions such as calmodulin binding, cellular responses to glucagon stimulus, G-alpha signalling and DARPP-32 events. We cross-linked the set of modelled proteins with sets of genes associated with common neurological diseases. We find some examples of disease-associated molecules that are well represented in models, such as voltage-dependent calcium channel family CACNA1C, dopamine D1 receptor, and glutamate ionotropic NMDA type 2A and 2B receptors. Many other disease-associated genes have not been included in models of synaptic plasticity, for example, catechol-O-methyltransferase COMT and MAOA. By incorporating pathway enrichment results, we identify LAMTOR, a gene uniquely associated with Schizophrenia, which is closely linked to the MAPK pathway found in some models. Our analysis provides a map of how molecular pathways underpinning neurological diseases relate to synaptic biophysical models that can in turn be used to explore how these molecular events might bridge scales into cellular processes and beyond. The map illustrates disease areas where biophysical models have good coverage as well as domain gaps that require significant further research.

2.4.8 Achieved Impact

This KR involves the experimental methods, tools and models developed in SP1 in the SGA1 at molecular, cellular and whole brain level. These outputs are crucial to generate and analysis data that contribute to the reconstructions and simulations of the mouse brain, for comparative assessment using mouse data to predict features of the human brain for which experimental data are not available, and make a vital contribution to the Multi-level Atlas of the Mouse Brain, created in SP5.

Innovative imaging techniques have been developed. The development of these techniques beyond the state-of-the-art allows dissection of unresolved scientific questions, such as recovery mechanisms after brain injury and whole brain connectivity at single cell level. In addition, the application of statistical and machine learning techniques allows to infer principles of human and mouse neuron morphology and neuroanatomical organization. Finally, novel workflows within the morphological data extraction process have been developed that can be applied to different types of information or datasets.

2.4.9 Component Dependencies

Component ID	Component Name	HBP Internal	Comment
652	Development of the integrated FIB/SEM and SDS-FRL immunoelectron microscopy technique	*Yes*	This technique allows the analysis of immunogold distribution on different neuronal compartments. It has been used to generate molecular data (KR1.1).
826	Antibodies against targets identified in all genomic and proteomics tasks	*Yes*	IACT small antibody fragments used as tools for brain imaging, due their specificity and better penetration in tissues. It has been used to generate molecular data (KR1.1).
892	Improved light-sheet microscopy for whole brain imaging	*Yes*	This innovative technique improves image quality acquisitions with light-sheet microscope for whole brain imaging. It has been used to generate data at the whole-brain level (KR1.3).
433	Synapse segmentation ImageJ plugin and macro	*Yes*	This is a new tool that allows the visualization, 3D segmentation and quantification of fluorescent structures selectively in the neuropil from large stacks of confocal microscopy images. It has been used to analysis anatomical data (KR1.2).
434	Interactive synaptic maps	*Yes*	This tool is a Web-based end-user interface to interactively analyse regions of the brain previously segmented to detect synapses. It has been used to analysis anatomical data (KR1.2).
906	Tools for the early analysis of morphological data (Pyramidal Explorer, DCExplorer, InToolExplorer, ClintExplorer)	*Yes*	This component involves a framework of interactive tools that have been specifically developed for the visual analysis of micro-anatomical data. It has been used to analysis anatomical data (KR1.2).

575	K channel activity within neuron models (model)	*Yes*	This model represents the specific properties of the different K channels and illustrates how these channels can modulate propagated Signals. This model adds a layer of granularity to neuron models and allows for more detailed neuron modelling.
420	A mapping of computational models of synapses to proteins	*Yes*	This component is a data component that implies an analysis of what proteins are contained in existing models of synaptic plasticity. This has been used to generate computational models to map synapses and proteins.

3. Component Details

The following is a list of the newly released internal Components for this deliverable.

3.1 Nanoscale measurements of distributions of individual receptors and ion channels in cortical neurons

Field Name	Field Content	Additional Information
ID	653	
Component Type	Data	
Contact	LUJAN, Rafael (UCLM)	
Component Description	This highly innovative approach will provide, for the first time, a mapping and comprehensive characterization of the cellular and subcellular localization of specific ion channel subunits and neurotransmitter receptors along the entire surface of cortical neurons, using single labelling experiments for each receptor and ion channel.	
Latest Release	2017/12/01	
TRL	NA	
Location	CSCS (via Collaboratory)	
Format	Tiff files and tables with densities and numbers	
Curation Status	NIP curation storage	NA
Validation - QC	Pass	Comparable with the available literature
Validation – Users	Yes	The users were hand selected.

Validation - Publications	No	Manuscripts have been submitted.
Privacy Constraints	Animal Research	
Sharing	Publically anonymous. There are no issues sharing data	
License	BY-NC-ND	
Component Access URL	https://www.dropbox.com/sh/6ljw2obd654z733/AADlMFLU9uqMcQlIAkt5zu7Ya?dl=0; https://www.dropbox.com/sh/zjj8kxtcs0pixlm/AAAlkHC-4peGakzyuI0Aa7qTa?dl=0	Also, NIP curation storage
Technical documentation URL	https://www.dropbox.com/sh/6ljw2obd654z733/AADlMFLU9uqMcQlIAkt5zu7Ya?dl=0; https://www.dropbox.com/sh/zjj8kxtcs0pixlm/AAAlkHC-4peGakzyuI0Aa7qTa?dl=0	
Usage documentation URL	NA	
Component dissemination material URL	NA	

3.2 Association (co-clustering) of receptors and their effector ion channels in different neuronal compartments

Field Name	Field Content	Additional Information
ID	654	
Component Type	Data	
Contact	LUJAN, Rafael (UCLM)	
Component Description	We will provide individual channel distances for the two related receptors and ion channels (for example, GABAB and GIRK, Cav2.1 and SK, NMDA and SK), their co-clustering, and channel cluster distances for two kinds of clusters in different neuronal compartments together with size of these co-clusters, their composition, and spatial relation of the co-clusters to synapses obtained from more than 100 neurons, in different subcellular compartments.	
Latest Release	2018/03/01	100%
TRL	NA	
Location	CSCS (via Collaboratory)	
Format	Tiff files and tables with density and numbers	
Curation Status	NIP curation storage	
Validation - QC	Pass	NA

Validation – Users	Yes	The users were hand selected.
Validation – Publications	No	Manuscripts have been submitted.
Privacy Constraints	Animal research	
Sharing	There are no issues sharing data. Publically anonymous	
License	BY-NC-ND	
Component Access URL	https://www.dropbox.com/sh/6ljw2obd654z733/AADIMFLU9uqMcQIIAkt5zu7Ya?dl=0	Also, NIP curation storage
Technical documentation URL	https://www.dropbox.com/sh/6ljw2obd654z733/AADIMFLU9uqMcQIIAkt5zu7Ya?dl=0	
Usage documentation URL	NA	
Component dissemination material URL	NA	

3.3 STP data

Field Name	Field Content	Additional Information
ID	711	
Component Type	Data	
Contact	Cherubini, Enrico	
Component Description	This component will generate data on STP under control and under NLGN/ NRXN proteins block, to test short- and long term plasticity at CA3-CA1 synapses. Patch clamp recordings will be performed from principal cells of the CA1 region of the hippocampus.	
Latest Release	MS1.1.5 & 2018/03/01	Ex vivo expression of NLG1 and NLG3 intrabodies in hippocampus of mice and their functional characteristics.
TRL	NA	
Location	data hosted by Collaboratory storage	
Format	abf; txts	
Curation Status	uploaded to Collab storage	
Validation - QC	Pass - Cherubini (Blind experiments and data analyses. Experiments performed by two different experimenters. Comparison with data in literature, statistical power Analyses)	
Validation – Users	Yes	T.1.1.4
Validation – Publications	1: Marchionni I, Kasap Z, Mozrzymas JW, Sieghart W, Cherubini E, Zacchi P. New insights on the role of	

	gephyrin in regulating both phasic and tonic GABAergic inhibition in rat hippocampal neurons in culture. Neuroscience. 2009 Dec 1;164(2):552-62. 2: Varley ZK, Pizzarelli R, Antonelli R, Stancheva SH, Kneussel M, Cherubini E, Zacchi P. Gephyrin regulates GABAergic and glutamatergic synaptic transmission in hippocampal cell cultures. J Biol Chem. 2011 Jun 10;286(23):20942-51.	
Privacy Constraints	Animal Research	
Sharing	consortium - share with any consortium members	There are no issues sharing data
License	BY-NC (TBC)	NA
Component Access URL	https://collab.humanbrainproject.eu/#/collab/914/nav/8073	HBP Collaboratory
Technical documentation URL	https://collab.humanbrainproject.eu/#/collab/914/nav/8073	HBP Collaboratory
Usage documentation URL	https://collab.humanbrainproject.eu/#/collab/914/nav/8073	HBP Collaboratory
Component dissemination material URL		

3.4 Electrophysiological data under neuroligin block

Field Name	Field Content	Additional Information
ID	713	
Component Type	Data	
Contact	Cherubini, Enrico	
Component Description	This component will provide electrophysiological data to study the role played by NLGN-NRXN connections in regulating signalling between post- and pre-synaptic processing.	
Latest Release	MS1.1.5 &2018/03/01	Ex vivo expression of NLG1 and NLG3 intrabodies in hippocampus of mice and their functional characteristics.
TRL	NA	
Location	data hosted by Collaboratory storage	
Format	abf; txts	
Curation Status	NIP curation storage	
Validation - QC	Pass - Cherubini (Blind experiments and data analyses. Experiments performed by two different experimenters. Comparison with data in literature, statistical power Analyses)	

Validation – Users	1: Marchionni I, Kasap Z, Mozrzymas JW, Sieghart W, Cherubini E, Zacchi P. New insights on the role of gephyrin in regulating both phasic and tonic GABAergic inhibition in rat hippocampal neurons in culture. Neuroscience. 2009 Dec 1;164(2):552-62. 2: Varley ZK, Pizzarelli R, Antonelli R, Stancheva SH, Kneussel M, Cherubini E, Zacchi P. Gephyrin regulates GABAergic and glutamatergic synaptic transmission in hippocampal cell cultures. J Biol Chem. 2011 Jun 10;286(23):20942-51.	
Validation – Publications	1: Marchionni I, Kasap Z, Mozrzymas JW, Sieghart W, Cherubini E, Zacchi P. New insights on the role of gephyrin in regulating both phasic and tonic GABAergic inhibition in rat hippocampal neurons in culture. Neuroscience. 2009 Dec 1;164(2):552-62. 2: Varley ZK, Pizzarelli R, Antonelli R, Stancheva SH, Kneussel M, Cherubini E, Zacchi P. Gephyrin regulates GABAergic and glutamatergic synaptic transmission in hippocampal cell cultures. J Biol Chem. 2011 Jun 10;286(23):20942-51.	
Privacy Constraints	Animal Research	
Sharing	consortium - share with any consortium members	There are no issues sharing data
License	BY-NC (TBC)	NA
Component Access URL	https://collab.humanbrainproject.eu/#/collab/914/nav/8073	HBP Collaboratory
Technical documentation URL	https://collab.humanbrainproject.eu/#/collab/914/nav/8073	HBP Collaboratory
Usage documentation URL	https://collab.humanbrainproject.eu/#/collab/914/nav/8073	HBP Collaboratory
Component dissemination material URL		

3.5 Activity-dependent proteomic changes occurring at active excitatory synapses

Field Name	Field Content	Additional Information
ID	2915	
Component Type	Data (Synaptic current)	
Contact	Cattaneo, Antonino Marinelli, Silvia and Cherubini, Enrico (EBRI)	Component Owner Reference persons
Component Description	We shall take advantage of a new method developed Gobbo et al (2016, BioRxiv (http://biorxiv.org/content/early/2016/12/21/095984), based on the expression vector pSYNACTIVE, that allows to effectively achieve the activity-dependent local translation of reporter proteins at activated dendritic spines, via a combination of RNA targeting and protein targeting sequences.	For the electrical stimulation, organotypic hippocampal slices will be stimulated by two high frequency trains (1 s at 100 Hz at 10 s interval) delivered to the

	The method allows to express at synapses, in a spatially localized and activity-dependent manner, a number of different reporter proteins of interest. Depending on the reporter protein expressed, different applications of the method can be envisaged. In this Task, the reporter proteins expressed from the pSYNACTIVE vector, expressed in organotypic hippocampal slices by viral infection, will be tailored for the downstream proteomic analysis of activated synapses. The definition of the synaptic proteome of hippocampal slices in basal conditions and after theta burst stimulation will be the starting point for the analysis of the other components. This will provide one of the reference database for the proteome analysis of slice infected with pSYNACTIVE. We shall then epitope-tag activated excitatory synapses for downstream purification and proteomic profiling. We shall exploit a membrane form of GFP reporter, tagged with HA-FLAG epitopes for TAP, and displayed on the postsynaptic membrane of excitatory synapses. This reporter will be expressed from the pSYNACTIVE vector and from a non-activity-dependent control vector. In an alternative approach, we shall exploit the activity-dependent nascent translation of a synaptic protein hub (PSD-95) as a molecular handle to probe a sample of the PSD-95-connected proteome of an activated glutamatergic synapse. To this aim, we shall use an HA and FLAG tagged PSD-95 reporter (as in Grant, 2009, Mol Syst Biol), expressed from the pSYNACTIVE vector. Experiments will be performed in organotypic hippocampal slices (method of Stoppini) infected with lentiviruses or AAV driving the expression of the Synactive reporters. Organotypic hippocampal slices expressing the SYNACTIVE reporters (and controls) will be stimulated with electrical stimulation of the CA3-CA1 pathway or pharmacologically.	Schaffer collateral in current clamp conditions to persistently modify synaptic strength (long-term potentiation) in the targeted neurons (CA1 principal cells). Synaptic currents will be recorded before and after the stimulation trains and changes in their slope will be measured as a function of time and the expression of the SYNACTIVE reporter will be imaged by confocal microscopy. On a preparative scale, stimulated slices will be processed for the purification of synaptosomes and of post-synaptic densities (Distler, 2014, Proteomics) by immunopurification (TAP) and by fluorescent activated sorting (Biesmann et al EMBO J 2014).
Latest Release	2018/03/01	
TRL	NA	
Location	data hosted by Collaboratory storage	
Format	.abf .txts	
Curation Status	NIP curation storage	
Validation - QC	Pass - Cattaneo (Comparison with data in the literature. Statistical power analysis.)	
Validation – Users	Collaborators internal (EBRI) and external to HBP consortium	
Validation – Publications	Gobbo F, Marchetti L, Jacob A, Pinto B, Binini N, Pecoraro Bisogni F, Alia C, Luin S, Caleo M, Fellin T, Cancedda L, Cattaneo A. Activity-dependent expression of Channelrhodopsin at neuronal synapses. Nat Commun. 2017 Nov 20;8(1):1629.	
Privacy Constraints	Animal Research	

Sharing	consortium - share with any consortium members	There are no issues sharing data
License	BY-NC-SA	
Component Access URL	https://collab.humanbrainproject.eu/#/collab/914/nav/8073	HBP Collaboratory
Technical documentation URL	https://collab.humanbrainproject.eu/#/collab/914/nav/8073	HBP Collaboratory
Usage documentation URL	https://collab.humanbrainproject.eu/#/collab/914/nav/8073	HBP Collaboratory
Component dissemination material URL	https://collab.humanbrainproject.eu/#/collab/914/nav/8073	HBP Collaboratory

3.6 Proteomic data collection and analysis

Field Name	Field Content	Additional Information
ID	2916	
Component Type	Data	
Contact	Cattaneo, Antonino Mainardi, Marco	Component Owner Reference person
Component Description	Both synaptosomes and PSD-95 interactomes will be analysed by label free proteomic quantification. Given the relatively low complexity of the samples and the dynamic range of detection a state-of-the-art mass spectrometer (at least 4 orders of magnitude), a single-shot analysis will be sufficient for both analyses. Isolations from activated and control cells will be performed in at least biological quadruplicates to enable robust statistical evaluation of protein abundance in activated synapses. Thus, protein intensities will be log2 transformed and normalized across runs to take into account variability in the efficiency of the isolation procedures. For TAP data, the usage of data imputation will be evaluated in order not to miss interacting partners that are exclusively detected in either activated or control samples. Downstream analysis will be based on Gene Ontology and gene set enrichment analysis and network approaches. Specific algorithms aimed at analysing the stoichiometry of protein complexes will be also applied (Ori, 2016, Genome Biology) in collaboration with UEDIN, components “Extending coverage of published data” and “Analysis of activated synapses”.	
Latest Release	2018/03/01	N/A
TRL	NA	
Location	Data hosted by task providing dataset http://151.100.170.9:8080/cgi-bin/	Internal / Provisional repository with a protected access on EBRI lab server. Username: hbp; Password: nanobodies

Format	.csv, .txt, .docx, .xlsx	
Curation Status	These data have not been sent to SP5 yet	NIP curation storage planned
Validation - QC	Pass	Cattaneo (Comparison with data in the literature. Statistical power analysis.)
Validation – Users	Collaborators internal (EBRI and UEDIN) and external to HBP consortium (A. Ori at Lipman Institute for Ageing, JENA, Germany)	
Validation – Publications	Gobbo F, Marchetti L, Jacob A, Pinto B, Binini N, Pecoraro Bisogni F, Alia C, Luin S, Caleo M, Fellin T, Cancedda L, Cattaneo A. Activity-dependent expression of Channelrhodopsin at neuronal synapses. Nat Commun. 2017 Nov 20;8(1)	
Privacy Constraints	Animal Research	
Sharing	consortium - share with any consortium members	There are no issues sharing data
License	BY-NC-SA	N/A
Component Access URL	http://151.100.170.9:8080/cgi-bin/	Internal / Provisional repository with a protected access on EBRI lab server; Username: hbp; Password: nanobodies
Technical documentation URL	http://151.100.170.9:8080/cgi-bin/	Internal / Provisional repository with a protected access on EBRI lab server; Username: hbp; Password: nanobodies
Usage documentation URL	http://151.100.170.9:8080/cgi-bin/	Internal / Provisional repository with a protected access on EBRI lab server; Username: hbp; Password: nanobodies
Component dissemination material URL	http://151.100.170.9:8080/cgi-bin/	Internal / Provisional repository with a protected access on EBRI lab server; Username: hbp; Password: nanobodies

3.7 Extending coverage of published data

Field Name	Field Content	Additional Information
ID	2917	
Component Type	Data	

Contact	ARMSTRONG, Douglas	
Component Description	All proteomics lists maintained will be extended through the addition of the latest literature. Since the ramp-up phase several new high quality and large coverage proteomic studies have been added to the literature that we do not have in the HBP curated sets (e.g. Uezu et al., 1021 synapse proteins; Focking et al., 2033 synaptic proteins). We also know of several other studies of mouse and human synapses submitted/in press. Raw and metadata will be extracted and added to a synapse proteomic database. At UEDIN we maintain a lightweight SQL database which we will extend and then deposit in the Neuroinformatics Platform so that the data can be queried as required. While we have to rely on the external availability of suitable and relevant datasets this does represent very good value for money and maximises re-use of data obtained from animal studies. As the proteomics results from component "Proteomic data collection and analysis" above become available we will integrate these data as well.	
Latest Release	Release ID: N/A & Release date: 2017/12/15	5 datasets added
TRL	NA	
Location	data hosted by Collaboratory storage Synaptic PPI Collab: https://collab.humanbrainproject.eu/#/collab/5961/nav/46154	
Format	Excel (.xls), Graph modelling language (.gml)	
Curation Status	NIP curation storage	
Validation - QC	Unchecked	
Validation – Users	Yes - Paolo Carloni's group in Juelich	
Validation – Publications	Not yet – publication in preparation	
Privacy Constraints	No privacy constraints	
Sharing	Public authenticated	
License	We need to investigate how to licence data that is already in the public domain	N/A
Component Access URL	https://collab.humanbrainproject.eu/#/collab/5961/nav/46154	
Technical documentation URL	https://collab.humanbrainproject.eu/#/collab/5961/nav/46156	
Usage documentation URL	https://collab.humanbrainproject.eu/#/collab/5961/nav/46156	
Component dissemination material URL		

3.8 Genetic mapping to single cell profiles

Field Name	Field Content	Additional Information
ID	2918	
Component Type	Data	
Contact	ARMSTRONG, Douglas	
Component Description	Single cell transcriptomic profiles of mouse neurons are now widely available with a whole mouse brain dataset due for completion this year (Linnarsson pers. comm.). We will obtain copies of these datasets and map them onto the proteomic datasets available. This work will form the basis of a bridging mechanism between cellular identity and the types of synaptic profile that can be supported by a neuron. Where available we will also incorporate protein expression data to link cell type transcript to synapse class.	
Latest Release	2018/03/01	Single Cell RNA-Seq from 4 major synaptic studies. The differentially expressed genes found in each cell type in each published study mapped back to 6500 genes in synaptic datasets. % complete is not applicable as this is a proof of concept.
TRL	NA	
Location	data hosted by Collaboratory storage	Main Hosting location Synaptic PPI Collab https://collab.humanbrainproject.eu/#/collab/5961/nav/46154 In Storage, folder “Single Cell Data 20_11_2017”
Format	.xlsx	
Curation Status	NIP curation storage	
Validation - QC	Unchecked	
Validation – Users	Yes	Used in-house
Validation – Publications	No?	
Privacy Constraints	No privacy constraints	
Sharing	Public authenticated	
License	CC-BY 4.0 planned (TBC)	

Component Access URL	https://project-lifecycle.herokuapp.com/component/2918	
Technical documentation URL	https://collab.humanbrainproject.eu/#/collab/5961/nav/46156	
Usage documentation URL	https://collab.humanbrainproject.eu/#/collab/5961/nav/46156	
Component dissemination material URL		

3.9 Integration of functional data into synapse models

Field Name	Field Content	Additional Information
ID	2919	
Component Type	Data	
Contact	ARMSTRONG, Douglas	
Component Description	We routinely extend the coverage of molecular complexes by curating additional molecular interaction and functional information. Gene Ontology and (through orthology mapping) Disease Association terms will be exacted and added so that molecular network models can be constructed that include a core level of functional annotation. Since the start of the HBP, the International Mouse Phenotyping Consortium (IMPC) have been generating mutants and releasing phenotype information. We will work with the IMPC informatics groups at MRC Harwell to cross-link the IMPC functional information with the HBP synapse proteomics lists so that we can readily identify known mouse phenotypes associated with synaptic proteins and also identify available genetic resources (i.e. mouse strains) for future studies.	
Latest Release	2018/03/01	Of 3,343 genes with completed phenotyping available from IMPC version 5.0, 980 genes (30%) found in synaptic datatsets. 100% mapped to last release of IMPC.
TRL	NA	
Location	synaptic_data_integration Collab https://collab.humanbrainproject.eu/#/collab/7076/nav/54104	data hosted by Collaboratory storage
Format	.tsv/csv files python functions and Juypter notebook	
Curation Status	NIP curation storage	NA
Validation - QC	Unchecked	

Validation – Users	Yes	Used in-house
Validation – Publications	No?	Publication in preparation
Privacy Constraints	No privacy constraints	
Sharing	Public authenticated	
License	CC-BY 4.0	
Component Access URL	synaptic_data_integration Collab: https://collab.humanbrainproject.eu/#/collab/7076/nav/54104	
Technical documentation URL	The notebook itself contains “readme/help” text explaining the details: https://collab.humanbrainproject.eu/#/collab/7076/nav/54107	
Usage documentation URL	The short video illustrates usage: file “use_example.ogv” in Collab storage (should be this link: https://collab.humanbrainproject.eu/#/collab/7076/nav/54104?state=uuid%3D2f86f35b-33ff-4dd9-a134-e5bf7f24044a)	
Component dissemination material URL		

3.10 3D reconstructions of 300 pyramidal neurons from the mouse somatosensory cortex across layers II-VI

Field Name	Field Content	Additional Information
ID	955	
Component Type	Data	
Contact	DEFELIPE, Javier BENAVIDES-PICCIONE, Ruth	
Component Description	3D reconstructions of 300 pyramidal neurons from the mouse somatosensory cortex across layers II-VI Related milestones: MS1.2.3 Reconstruction of pyramidal neurons M12 MS1.2.8 Reconstruction of dendritic arbors and dendritic spines of pyramidal neurons M24 Verification: Data released and data quality validated Related task: Task 1.2.1 The pyramidal neuron in the cerebral cortex of humans and rodents	
Latest Release	CP-SSC & 2018/03/01	169 cells reconstructed
TRL	NA	
Location	Data hosted by task providing dataset add	HBP storage: NIP curation storage

	https://www.dropbox.com/sh/96gx9guevrdsom8/AAAGyS2g739YqY9uenlQF5oBa?dl=0	
Format	.xls, .DAT	
Curation Status	NIP curation storage	
Validation - QC	Pass	DeFelipe, Peer review
Validation – Users	Yes	SP4, SP5, SP6
Validation – Publications	Alejandro Antón-Fernández, et al., Neurobiology of Disease (97) 2017 11-23. Carolina Gonzalez-Riano, et al., (2017) Brain Struct Funct. DOI: 10.1007/s00429-017-1375-5; Bosch C, et al. Cereb Cortex. 2016 Sep 13; Fernandez-Gonzalez P, et al., (2016). Brain Struct Funct. 2016 Sep 30; Eyal G, et al., Elife. 2016 Oct 6; 5; Anton-Sanchez L, et al., Neuroinformatics. 2016 Oct; 14 (4):453-64. doi: 10.1007/s12021-016-9309-6; Anton-Sanchez, L., et al., PLoS ONE 12(6): e0180400, 2017.	
Privacy Constraints	Animal research	
Sharing	There are no issues sharing data	
License	BY-NC (TBC)	
Component Access URL	https://www.dropbox.com/sh/96gx9guevrdsom8/AAAGyS2g739YqY9uenlQF5oBa?dl=0	
Technical documentation URL	https://www.dropbox.com/sh/96gx9guevrdsom8/AAAGyS2g739YqY9uenlQF5oBa?dl=0	
Usage documentation URL	https://www.dropbox.com/sh/96gx9guevrdsom8/AAAGyS2g739YqY9uenlQF5oBa?dl=0	
Component dissemination material URL		

3.11 3D reconstructions of 50 cells in mouse hippocampal CA1 region

Field Name	Field Content	Additional Information
ID	956	
Component Type	Data	
Contact	DFELIPE, Javier BENAVIDES-PICCIONE, Ruth	
Component Description	3D reconstructions of 50 cells in mouse hippocampal CA1 region Related milestones: MS1.2.3 Reconstruction of pyramidal neurons M12 MS1.2.8 Reconstruction of dendritic arbors and dendritic spines of pyramidal neurons M24Verification: Data released and data quality validated Related task: Task 1.2.1 The pyramidal neuron in the cerebral cortex of humans and rodents	

Latest Release	CA1-M & 2018/03/01	50 cells reconstructed
TRL	NA	
Location	Data hosted by task providing dataset https://www.dropbox.com/sh/96gx9guevrdsom8/AAAGyS2g739YqY9uenIQF5oBa?dl=0	HBP storage: NIP curation storage
Format	.xls, .DAT	
Curation Status	NIP curation storage	
Validation - QC	Pass	DeFelipe, Merchán; Peer review
Validation – Users	Yes	SP4, SP5, SP6
Validation – Publications	Alejandro Antón-Fernández, et al., Neurobiology of Disease (97) 2017 11-23. Carolina Gonzalez-Riano, et al., (2017) Brain Struct Funct. DOI: 10.1007/s00429-017-1375-5; Bosch C, et al., Cereb Cortex. 2016 Sep 13; Fernandez-Gonzalez P, et al., (2016). Brain Struct Funct. 2016 Sep 30; Eyal G, et al., Elife. 2016 Oct 6; 5; Anton-Sanchez L, et al., Neuroinformatics. 2016 Oct; 14 (4):453-64. doi: 10.1007/s12021-016-9309-6; Anton-Sanchez, L., et al., PLoS ONE 12(6): e0180400, 2017.	
Privacy Constraints	Animal research	
Sharing	There are no issues sharing data	
License	BY-NC (TBC)	
Component Access URL	https://www.dropbox.com/sh/96gx9guevrdsom8/AAAGyS2g739YqY9uenIQF5oBa?dl=0	
Technical documentation URL	https://www.dropbox.com/sh/96gx9guevrdsom8/AAAGyS2g739YqY9uenIQF5oBa?dl=0	
Usage documentation URL	https://www.dropbox.com/sh/96gx9guevrdsom8/AAAGyS2g739YqY9uenIQF5oBa?dl=0	
Component dissemination material URL		

3.12 3D reconstructions of 50 cells in rat hippocampal CA1 region

Field Name	Field Content	Additional Information
ID	957	
Component Type	Data	
Contact	DFELIPE, Javier BENAVIDES-PICCIONE, Ruth	
Component Description	3D reconstructions of 50 cells in rat hippocampal CA1 region Related milestones: MS1.2.3 Reconstruction of pyramidal neurons M12	

	MS1.2.8 Reconstruction of dendritic arbors and dendritic spines of pyramidal neurons M24 Verification: Data released and data quality validated Related task: Task 1.2.1 The pyramidal neuron in the cerebral cortex of humans and rodents	
Latest Release	CA1-R & 2018/03/01	50 cells reconstructed
TRL	NA	
Location	Data hosted by task providing dataset https://www.dropbox.com/sh/96gx9guevrdsom8/AAAGyS2g739YqY9uenIQF5oBa?dl=0	HBP storage: NIP curation storage
Format	.xls, .DAT	
Curation Status	NIP curation storage	
Validation - QC	Pass	DeFelipe, Merchán; Peer review
Validation – Users	Yes	SP4, SP5, SP6
Validation – Publications	Alejandro Antón-Fernández, et al., Neurobiology of Disease (97) 2017 11-23. Carolina Gonzalez-Riano, et al., (2017) Brain Struct Funct. DOI: 10.1007/s00429-017-1375-5; Bosch C, et al., Cereb Cortex. 2016 Sep 13; Fernandez-Gonzalez P, et al., (2016). Brain Struct Funct. 2016 Sep 30; Eyal G, et al., Elife. 2016 Oct 6; 5; Anton-Sanchez L, et al., Neuroinformatics. 2016 Oct; 14 (4):453-64. doi: 10.1007/s12021-016-9309-6; Anton-Sanchez, L., et al., PLoS ONE 12(6): e0180400, 2017.	
Privacy Constraints	Animal Research	
Sharing	There are no issues sharing data	
License	BY-NC (TBC)	
Component Access URL	https://www.dropbox.com/sh/96gx9guevrdsom8/AAAGyS2g739YqY9uenIQF5oBa?dl=0	
Technical documentation URL	https://www.dropbox.com/sh/96gx9guevrdsom8/AAAGyS2g739YqY9uenIQF5oBa?dl=0	
Usage documentation URL	https://www.dropbox.com/sh/96gx9guevrdsom8/AAAGyS2g739YqY9uenIQF5oBa?dl=0	
Component dissemination material URL		

3.13 3D reconstructions of 50 cells in human hippocampal formation (CA1)

Field Name	Field Content	Additional Information
ID	958	
Component Type	Data	

Contact	DFELIPE, Javier BENAVIDES-PICCIONE, Ruth	
Component Description	3D reconstructions of 50 cells in human hippocampal formation (CA1) Related milestones: MS1.2.3 Reconstruction of pyramidal neurons M12 MS1.2.8 Reconstruction of dendritic arbors and dendritic spines of pyramidal neurons M24 Verification: Data released and data quality validated Related task: Task 1.2.1 The pyramidal neuron in the cerebral cortex of humans and rodents	
Latest Release	CA1-H & 2018/03/01	50 cells reconstructed
TRL	NA	
Location	Data hosted by task providing dataset https://www.dropbox.com/sh/96gx9guevrdsom8/AAAGyS2g739YqY9uenIQF5oBa?dl=0	HBP storage: NIP curation storage
Format	.xls, .DAT	
Curation Status	NIP curation storage	
Validation - QC	Pass	DeFelipe, Merchán, Peer review
Validation – Users	Yes	SP4, SP5, SP6
Validation – Publications	Alejandro Antón-Fernández, et al., Neurobiology of Disease (97) 2017 11-23. Carolina Gonzalez-Riano, et al., (2017) Brain Struct Funct. DOI: 10.1007/s00429-017-1375-5; Bosch C, et al., Cereb Cortex. 2016 Sep 13; Fernandez-Gonzalez P, et al., (2016). Brain Struct Funct. 2016 Sep 30; Eyal G, et al., Elife. 2016 Oct 6; 5; Anton-Sanchez L, et al., Neuroinformatics. 2016 Oct; 14 (4):453-64. doi: 10.1007/s12021-016-9309-6; Anton-Sanchez, L., et al., PLoS ONE 12(6): e0180400, 2017.	
Privacy Constraints	Human research	
Sharing	There are no issues sharing data	
License	BY-NC (TBC)	
Component Access URL	https://www.dropbox.com/sh/96gx9guevrdsom8/AAAGyS2g739YqY9uenIQF5oBa?dl=0	
Technical documentation URL	https://www.dropbox.com/sh/96gx9guevrdsom8/AAAGyS2g739YqY9uenIQF5oBa?dl=0	
Usage documentation URL	https://www.dropbox.com/sh/96gx9guevrdsom8/AAAGyS2g739YqY9uenIQF5oBa?dl=0	
Component dissemination material URL		

3.14 3D reconstructions of 200 cells in human neocortex (temporal, cingulate and frontal)

Field Name	Field Content	Additional Information
ID	959	
Component Type	Data	
Contact	DFELIPE, Javier BENAVIDES-PICCIONE, Ruth	
Component Description	3D reconstructions of 200 cells in human neocortex (temporal, cingulate and frontal) Related milestones: MS1.2.3 Reconstruction of pyramidal neurons M12 MS1.2.8 Reconstruction of dendritic arbors and dendritic spines of pyramidal neurons M24 Verification: Data released and data quality validated Related task: Task 1.2.1 The pyramidal neuron in the cerebral cortex of humans and rodents	
Latest Release	NC-H & 2018/03/01	The number of reconstructed cells to date is 217 (94 in the temporal cortex, 64 in the cingular cortex and 59 in the frontal cortex)
TRL	NA	
Location	Data hosted by task providing dataset https://www.dropbox.com/sh/96gx9guevrdsom8/AAAGyS2g739YqY9uenIQF5oBa?dl=0	HBP storage: NIP curation storage
Format	.xls, .DAT	
Curation Status	NIP curation storage	
Validation - QC	Pass	DeFelipe, Merchán; Peer review
Validation – Users	Yes	SP4, SP5, SP6
Validation – Publications	Alejandro Antón-Fernández, et al., Neurobiology of Disease (97) 2017 11-23. Carolina Gonzalez-Riano, et al., (2017) Brain Struct Funct. DOI: 10.1007/s00429-017-1375-5; Bosch C, et al., Cereb Cortex. 2016 Sep 13; Fernandez-Gonzalez P, et al., (2016). Brain Struct Funct. 2016 Sep 30; Eyal G, et al., Elife. 2016 Oct 6; 5; Anton-Sanchez L, et al., Neuroinformatics. 2016 Oct; 14 (4):453-64. doi: 10.1007/s12021-016-9309-6; Anton-Sanchez, L., et al., PLoS ONE 12(6): e0180400, 2017.	
Privacy Constraints	Animal research	
Sharing	There are no issues sharing data	
License	BY-NC	
Component Access URL	https://www.dropbox.com/sh/96gx9guevrdsom8/AAAGyS2g739YqY9uenIQF5oBa?dl=0	
Technical documentation URL	https://www.dropbox.com/sh/96gx9guevrdsom8/AAAGyS2g739YqY9uenIQF5oBa?dl=0	

Usage documentation URL	https://www.dropbox.com/sh/96gx9guevrdsom8/AAAGyS2g739YqY9uenIQF5oBa?dl=0	
Component dissemination material URL		

3.15 Morphological and physiological data from the same neurons in adult mouse

Field Name	Field Content	Additional Information
ID	757	
Component Type	Data	
Contact	MANSVELDER, Huib	
Component Description	Morphological (dendrites AND axons) and physiological data (e-codes) from the same cortical pyramidal neurons in different layers in temporal and frontal cortex of the adult rodent will be recorded.	
Latest Release	2018/03/01	100%
TRL	NA	
Location	Data hosted by task providing dataset https://www.dropbox.com/home/HBPmansvelder	https://www.dropbox.com/s/hhp07tgdlq7odf3/Boudewijns_etal_FrontCellNeurosci2013_DigitalReconstructions.zip?dl=0
Format	Txt, abf, mat	
Curation Status	NIP curation storage	
Validation - QC	Unchecked	
Validation – Users	Yes	SP6, SP4
Validation – Publications	Eyal et al., ELife 2016 Deitcher et al., Cerebral Cortex 2017	
Privacy Constraints	Animal research	
Sharing	There may be issues sharing data openly	
License	BY-NC (TBC)	
Component Access URL	https://www.dropbox.com/home/HBPmansvelder	
Technical documentation URL		
Usage documentation URL		
Component dissemination material URL		

3.16 Morphological and physiological data from the same neurons in adult human

Field Name	Field Content	Additional Information
ID	759	
Component Type	Data	
Contact	MANSVELDER, Huib	
Component Description	Description: Morphological (dendrites AND axons) and physiological data (e-codes) from the same cortical pyramidal neurons in different layers in temporal and frontal cortex of the adult human will be recorded.	
Latest Release	2018/03/01	100%
TRL	NA	
Location	Data hosted by task providing dataset https://www.dropbox.com/home/HBPmansvelder	https://www.dropbox.com/s/hhp07tgdlq7odf3/Boudewijns_etal_FrontCellNeurosci2013_DigitalReconstructions.zip?dl=0
Format	Txt, abf, mat	
Curation Status	NIP curation storage	
Validation - QC	Unchecked	
Validation – Users	Yes	SP6, SP4
Validation – Publications	Eyal et al., ELife 2016 Deitcher et al., Cerebral Cortex 2017	
Privacy Constraints	Human research	
Sharing	There may be issues sharing data openly	
License	BY-NC (TBC)	
Component Access URL	https://www.dropbox.com/home/HBPmansvelder	
Technical documentation URL		
Usage documentation URL		
Component dissemination material URL		

3.17 Quantitative electron microscopic (qEM) database of Synaptic Coverage of GABAergic Neuron Subtypes

Field Name	Field Content	Additional Information
ID	784	
Component Type	Data	
Contact	KISVARDAY, Zoltan	
Component Description	Neocortical GABAergic neurons will be labelled in vivo and characterised post hoc for chemical content using a battery of immunohistochemical markers for somatostatin, parvalbumin, calretinin, calbindin, vasoactive intestinal polypeptide, cholecystokinin, and neuropeptide Y, choline-acetyltransferase and NO-synthase in adult mice. Our aim is to establish a quantitative electron microscopic (qEM) database of the complete synaptic coverage of subtypes of GABAergic neurons. To generate a qEM database, a representative number of subtypes of GABAergic neurons will be selected to map out synaptic coverage along the soma-dendritic surface and estimate the contribution of various input types. This immunostaining will be carried out in brain tissue of C57BL/6J adult mice (8-week-old male) and for GABAergic cells of Slc32a1tm2 (cre) Lowl and Ai14 mice strains. Tissue samples will include the primary visual cortex (V1) and the primary somatosensory cortex (SI). Labelled cells of all six cortical layers will be selected for a detailed EM analysis. At least two labelled cells per cortical layer will be subjected to qEM.	
Latest Release	6280 – 2018-01-30	One more Calbindin-DK28-positive neuron and its dendrite located in layer 2/3 of the primary visual cortex was identified. (9 subtypes, 2 areas, 6 layers each, 2 cells per layer) (Use case 2) (~5%)
TRL	NA	
Location	data hosted by Collaboratory storage http://collab.humanbrainproject.eu/#/collab/6280/nav/48469	
Format	TIFF, Microsoft Word Document, xml	
Curation Status	NIP curation storage	
Validation - QC	Pass - Kisvarday, Method for data analysis validated	
Validation – Users	No	SP6 (T6.2.2, T6.2.6) planned
Validation – Publications	No	
Privacy Constraints	Animal Research	
Sharing	No issues on sharing data	

License	BY-NC	
Component Access URL	http://collab.humanbrainproject.eu/#/collab/6280/nav/48469	
Technical documentation URL		
Usage documentation URL		
Component dissemination material URL		

3.18 3D reconstruction of thalamocortical neurons

Field Name	Field Content	Additional Information
ID	732	
Component Type	Data	
Contact	Garcia-Amado, Maria	
Component Description	We will produce 3D digital reconstruction and quantification of a significant number (30-40) of individual cells from 4 populations of thalamocortical LRPNs (40 in total), each from a different thalamic nucleus, (two specific/sensory and two multi-specific/higher order nuclei), with particular focus on their terminal synaptic site in different cortical layers. We chose thalamocortical cells because of their "hub" position in forebrain networks and because the homogeneity in cellular composition of thalamic nuclei makes it technically easier to obtain a significant number of well-labelled cells of the same axonal type.	
Latest Release	CLAS-Neuron number-Case number / 2017/09/27	Features of the release: 3D vectorial computer reconstruction of neuronal morphology (.DAT file), metadata, serial colour 400X brightfield microscope image stacks of axonal arborizations and somatodendritic domain (.jpx)
TRL	NA	
Location	data hosted by Collaboratory storage https://collab.humanbrainproject.eu/#/collab/5346/nav/41581	
Format	DAT	
Curation Status	SP5 Tier category 2	

Validation - QC	Pass	Kriester Andersson
Validation – Users	SP5 (UOI, Dr. T. Brauns) and (SKU, Dr. P. Tiesinga) for developing automated 3D mouse brain atlasing tools, as well as by SP6 (UB, Dr. MV Sánchez Vives) for guiding multi-electrode array studies of mouse somatomotor cortex dynamics.	
Validation – Publications	underway	2 manuscripts in preparation
Privacy Constraints	Animal Research	
Sharing	consortium - share with any consortium members	
License	Private (Attribution Non-commercial)	
Component Access URL	https://collab.humanbrainproject.eu/#/collab/5346/nav/41581	
Technical documentation URL	https://docs.google.com/spreadsheets/d/1r4HZPUb0m6maRJh57qbyv4zeM9XlZBI0YOV4d6VhDgE/edit#gid=0	
Usage documentation URL		
Component dissemination material URL		

3.19 Immunocytochemical detection of excitatory and inhibitory terminals in the mouse neocortex (somatosensory cortex) by confocal microscopy

Field Name	Field Content	Additional Information
ID	962	
Component Type	Data	
Contact	MERCHÁN, Ángel	
Component Description	Immunocytochemical detection of excitatory and inhibitory terminals in the mouse neocortex (somatosensory cortex) by confocal microscopy. Five animals, 15 confocal stacks per layer. Related milestone: MS1.2.4 Synaptic maps (mesoscopic level) M12 Verification: Data released and data quality validated Related milestone: MS1.2.7 High-resolution synaptic maps in neocortex and hippocampus M16 Verification: Segmented images released; correct light microscopy reconstructions validated with correlative FIB/SEM electron microscopy 3D reconstructions, also with real images labelled by experts; software released and tested Related task: Task 1.2.9: High-resolution synaptic maps in the neocortex and hippocampus using confocal microscopy and FIB/SEM	

Latest Release	SM & 2017/08/01	Completed at M16; Analysis from 15 confocal stacks per cortical layer in 5 animals (100%)
TRL	NA	
Location	Data hosted by task providing dataset	HBP storage: NIP curation storage
Format	Excel files	
Curation Status	NIP curation storage	
Validation - QC	Pass	Muñoz; Peer review
Validation – Users	Yes	SP5, SP6
Validation – Publications	Alejandro Antón-Fernández, et al., Neurobiology of Disease (97) 2017 11-23. Carolina Gonzalez-Riano, et al., (2017) Brain Struct Funct. DOI: 10.1007/s00429-017-1375-5. Santuy A, et al. Brain Struct Funct. 2017 Jul 18. doi: 10.1007/s00429-017-1470-7 Bosch C, et al., Cereb Cortex. 2016 Sep 13. Urrecha M, et al., PLoS One. 2017 Feb 15;12 (2)	
Privacy Constraints	Animal Research	
Sharing	consortium - share with any consortium members	There may be issues sharing data openly
License	BY-NC (TBC)	
Component Access URL	https://www.dropbox.com/sh/2iyy7s6ahf32fqu/AABSKbJTTIUTACNxTtdvSyjMa?dl=0	
Technical documentation URL		
Usage documentation URL		
Component dissemination material URL		

3.20 Densities and 3D distributions of synapses using FIB/SEM imaging in the mouse neocortex (somatosensory cortex)

Field Name	Field Content	Additional Information
ID	964	
Component Type	Data	
Contact	MERCHÁN, Ángel	
Component Description	Densities and 3D distributions of synapses using FIB/SEM imaging in the mouse neocortex	

	(somatosensory cortex). Three animals, one FIB/SEM stack per layer Related milestone: MS1.2.7 High-resolution synaptic maps in neocortex and hippocampus M16 Verification: Segmented images released; correct light microscopy reconstructions validated with correlative FIB/SEM electron microscopy 3D reconstructions, also with real images labelled by experts; software released and tested Related milestone: MS1.2.9 Synaptic maps (nanoscopic level) M24 Verification: Data released and data quality validated Related Task: Task 1.2.9: High-resolution synaptic maps in the neocortex and hippocampus using confocal microscopy and FIB/SEM	
Latest Release	SM & 2018/03/01	At M23 we have acquired 21 FIB/SEM stacks of images from the six cortical layers, from three animals. This is 100% of the stacks required. Segmentation has been completed and analysis is in progress
TRL	NA	
Location	data hosted by task providing dataset	HBP storage: NIP curation storage
Format	.seg files (created with Espina software); Excel files	
Curation Status	NIP curation storage	
Validation - QC	Pass	Merchán, Peer review
Validation – Users	Yes	SP5, SP6
Validation – Publications	Alejandro Antón-Fernández, et al., Neurobiology of Disease (97) 2017 11-23. Carolina Gonzalez-Riano, et al., (2017) Brain Struct Funct. DOI: 10.1007/s00429-017-1375-5. Santuy A, et al. Brain Struct Funct. 2017 Jul 18. doi: 10.1007/s00429-017-1470-7 Bosch C, et al., Cereb Cortex. 2016 Sep 13. Urrecha M, et al., PLoS One. 2017 Feb 15;12 (2)	
Privacy Constraints	Animal Research	
Sharing	consortium - share with any consortium members	There may be issues sharing data openly
License	BY-NC (TBC)	
Component Access URL	https://www.dropbox.com/sh/2iyy7s6ahf32fqu/AABSKbJTTlUTACNxTtdvSyjMa?dl=0	
Technical documentation URL		
Usage documentation URL		

Component dissemination material URL		

3.21 Densities and 3D distributions of synapses using FIB/SEM imaging in the human neocortex (Temporal cortex, T2)

Field Name	Field Content	Additional Information
ID	966	
Component Type	Data	
Contact	MERCHÁN, Ángel	
Component Description	Densities and 3D distributions of synapses using FIB/SEM imaging in the human neocortex (Temporal cortex, T2). Three human subjects, nine FIB/SEM stacks Related milestone: MS1.2.9 Synaptic maps (nanoscopic level) M24 Verification: Data released and data quality validated Related Task: Task 1.2.9: High-resolution synaptic maps in the neocortex and hippocampus using confocal microscopy and FIB/SEM	
Latest Release	SM & 2018/03/01	At M23, we acquired 9 FIB/SEM stacks of images from the layer 3 of the T2 neocortex. This is 100% of the stacks required. Segmentation is completed and analysis is in progress
TRL	NA	
Location	data hosted by task providing dataset	HBP storage: NIP curation storage
Format	.seg files (created with Espina software); Excel files	
Curation Status	NIP curation storage	
Validation - QC	Pass	Merchán, Peer review
Validation – Users	Yes	SP5, SP6
Validation – Publications	Alejandro Antón-Fernández, et al., Neurobiology of Disease (97) 2017 11-23. Carolina Gonzalez-Riano, et al., (2017) Brain Struct Funct. DOI: 10.1007/s00429-017-1375-5. Santuy A, et al. Brain Struct Funct. 2017 Jul 18. doi: 10.1007/s00429-017-1470-7 Bosch C, et al., Cereb Cortex. 2016 Sep 13. Urrecha M, et al., PLoS One. 2017 Feb 15;12 (2)	

Privacy Constraints	Human Research	
Sharing	consortium - share with any consortium members	There maybe issues sharing data openly
License	BY-NC (TBC)	
Component Access URL	https://www.dropbox.com/sh/2iyy7s6ahf32fqu/AABSKbJTTIUTACNxTtdvSyjMa?dl=0	
Technical documentation URL		
Usage documentation URL		
Component dissemination material URL		

3.22 Patch-clamp recordings from cerebellar neurons

Field Name	Field Content	Additional Information
ID	810	
Component Type	Data	
Contact	D'ANGELO, Egidio	
Component Description	Patch-clamp recordings from cerebellar neurons will be made to assist with constructing advanced Purkinje cell models and stellate cell models. The experiments will be designed to achieve optimal alignment with HBP cerebellar modelling, thus allowing efficient model construction. About 50 neurons will be recorded and analysed.	
Latest Release	M23	100%
TRL	NA	
Location	data hosted by HPC platform data hosted by Collaboratory storage	
Format	abf; .brw; .mod, .ipynb, .mat, .rsh, .rsm, .rsd, .dha, .tbk, .spd, .png	
Curation Status	NIP curation storage	
Validation - QC	Pass	D'ANGELO, Egidio; Best lab practice, statistical power analysis, internal cross-relation of parameters, literature comparison, double-blind checking
Validation – Users	Yes	These data have been use for model building in SP6 task 6.2.3 and 6.4.2

Validation – Publications	Masoli S, et al., Front Cell Neurosci. 2017 Sep 13;11:278. doi: 10.3389/fncel.2017.00278. eCollection 2017. Masoli S, et al., Front Cell Neurosci. 2017 Mar 15;11:71. doi: 10.3389/fncel.2017.00071. eCollection 2017. D'Angelo E, et al., Front Cell Neurosci. 2016 Jul 8;10:176. doi: 10.3389/fncel.2016.00176. eCollection 2016. Revie.	
Privacy Constraints	Animal Research	
Sharing	consortium - share with any consortium members	There are no issues sharing data.
License	All rights reserved, copyright. BY-NC	
Component Access URL	https://collab.humanbrainproject.eu/#/collab/5389/nav/41945	
Technical documentation URL	https://collab.humanbrainproject.eu/#/collab/5389/nav/41945	
Usage documentation URL		
Component dissemination material URL		

3.23 Combined optogenetics, two-photon imaging and electrophysiological recordings from cerebellar neurons

Field Name	Field Content	Additional Information
ID	811	
Component Type	Data	
Contact	D’ANGELO, Egidio	
Component Description	Combined optogenetic, two-photon imaging and electrophysiological recordings from cerebellar neurons will be made in order to determine microcircuit dynamics and plasticity in response to the specific patterns used for simulations in modelling tasks. About 50 experimental recordings will be performed.	
Latest Release	M23	100%
TRL	NA	
Location	data hosted by HPC platform data hosted by Collaboratory storage	
Format	abf; .brw; .mod, .ipynb, .mat, .rsh, .rsm, .rsd, .dha, .tbk, .spd, .png	
Curation Status	NIP curation storage	
Validation - QC	Pass	D’ANGELO, Egidio; Best lab practice,

		statistical power analysis, internal cross-relation of parameters, literature comparison, double-blind checking
Validation – Users	Yes	These data have been use for model building in SP6 task 6.2.3 and 6.4.2
Validation – Publications	Masoli S, et al., Front Cell Neurosci. 2017 Sep 13;11:278. doi: 10.3389/fncel.2017.00278. eCollection 2017. Masoli S, et al., Front Cell Neurosci. 2017 Mar 15;11:71. doi: 10.3389/fncel.2017.00071. eCollection 2017. D'Angelo E, et al., Front Cell Neurosci. 2016 Jul 8;10:176. doi: 10.3389/fncel.2016.00176. eCollection 2016. Revie.	
Privacy Constraints	Animal Research	
Sharing	consortium - share with any consortium members	There are no issues sharing data
License	All rights reserved, copyright. BY-NC	
Component Access URL	https://collab.humanbrainproject.eu/#/collab/5389/nav/41945	
Technical documentation URL	https://collab.humanbrainproject.eu/#/collab/5389/nav/41945	
Usage documentation URL		
Component dissemination material URL		

3.24 Database of all the major excitatory and inhibitory cell types of the mouse hippocampus, using a combination of morphological and electrophysiological classification

Field Name	Field Content	Additional Information
ID	805	
Component Type	Data	
Contact	KÁLI, Szabolcs	
Component Description	During the Ramp-Up phase of HBP (Task 1.2.4), we developed and fine-tuned procedures for precise morphological reconstruction and electrophysiological characterization of hippocampal neurons in 600-micrometer-thick slices from 8-week-old Black6 mice. In the next phase, we aim to further apply these	

	methods to start building systematically a database of all the major excitatory and inhibitory cell types of the hippocampus, using a combination of morphological and electrophysiological classification, and also utilizing transgenic animals expressing cell-type-specific fluorescent markers.	
Latest Release	Morphological and physiological database of major cell types in the mouse hippocampus (SGA1 M24) 2018/03/01	Data released and data quality validated
TRL	NA	
Location	data hosted by HPAC Platform	
Format	asc, .xml (Neurolucida)	
Curation Status	SP5 Tier 1	
Validation - QC	Pass - GULYÁS, Attila – inspection of the reconstructions and images KÁLI, Szabolcs – automated feature extraction and manual validation of electrophysiological recordings	
Validation – Users	Using the data from this component, detailed biophysical models of mouse hippocampal neurons are constructed in Task 6.2.4.	Using the data from this component, detailed biophysical models of mouse hippocampal neurons are constructed in Task 6.2.4.
Validation – Publications	No	
Privacy Constraints	Animal research	
Sharing	Anonymous	
License	Attribution Non-Commercial	
Component Access URL	https://www.dropbox.com/sh/cxseu9c2qstsgl0/AACIJwmw6rYehjApK3O6tzpAa?dl=0	
Technical documentation URL	https://www.dropbox.com/sh/cxseu9c2qstsgl0/AACIJwmw6rYehjApK3O6tzpAa?dl=0	
Usage documentation URL		
Component dissemination material URL	NA	

3.25 Database of paired recordings in hippocampal slices which display in vivo-like activity levels and patterns

Field Name	Field Content	Additional Information
ID	926	
Component Type	Data	

Contact	KÁLI, Szabolcs	
Component Description	Using our protocol for performing paired recordings in hippocampal slices which display in vivo-like activity levels and patterns, we will describe the basic properties of synaptic transmission and characterize short-term synaptic plasticity between identified cells, employing morphological and electrophysiological classification as well as transgenic animals expressing cell-type-specific fluorescent markers to target specific connections.	
Latest Release	Database of synaptic physiological properties in the mouse hippocampus (SGA1 M24) 2018/03/01	
TRL	NA	
Location	data hosted by HPC platform	
Format	Tab-separated text files (.txt)	
Curation Status	SP5 Tier 1	
Validation - QC	Pass - GULYÁS, Attila – inspection of the recordings	
Validation – Users	Using the data from this component, detailed biophysical models of hippocampal synapses are constructed in Task 6.2.4.	
Validation – Publications	Kohus Z, Káli S, Rovira-Esteban L, Schlingloff D, Papp O, Freund TF, Hájos N, Gulyás AI. (2016) Properties and dynamics of inhibitory synaptic communication within the CA3 microcircuits of pyramidal cells and interneurons expressing parvalbumin or cholecystokinin. J Physiol. 594:3745-74. doi: 10.1113/JP272231.	
Privacy Constraints	Animal research	
Sharing	Anonymous	
License	Attribution Non-Commercial	
Component Access URL	https://crcns.org/data-sets/hc/hc-7/about-hc-7	
Technical documentation URL	https://crcns.org/data-sets/hc/hc-7/about-hc-7	
Usage documentation URL		
Component dissemination material URL		

3.26 Immunocytochemical detection of excitatory and inhibitory terminals in the mouse hippocampus (CA1) by confocal microscopy

Field Name	Field Content	Additional Information
ID	926	

Component Type	Data	
Contact	KÁLI, Szabolcs	
Component Description	Using our protocol for performing paired recordings in hippocampal slices which display in vivo-like activity levels and patterns, we will describe the basic properties of synaptic transmission and characterize short-term synaptic plasticity between identified cells, employing morphological and electrophysiological classification as well as transgenic animals expressing cell-type-specific fluorescent markers to target specific connections.	
Latest Release	Database of synaptic physiological properties in the mouse hippocampus (SGA1 M24) 2018/03/01	
TRL	NA	
Location	data hosted by HPC platform	
Format	Tab-separated text files (.txt)	
Curation Status	SP5 Tier 1	
Validation - QC	Pass - GULYÁS, Attila – inspection of the recordings	
Validation – Users	Using the data from this component, detailed biophysical models of hippocampal synapses are constructed in Task 6.2.4.	
Validation – Publications	Kohus Z, Káli S, Rovira-Esteban L, Schlingloff D, Papp O, Freund TF, Hájos N, Gulyás AI. (2016) Properties and dynamics of inhibitory synaptic communication within the CA3 microcircuits of pyramidal cells and interneurons expressing parvalbumin or cholecystokinin. J Physiol. 594:3745-74. doi: 10.1113/JP272231.	
Privacy Constraints	Animal research	
Sharing	Anonymous	
License	Attribution Non-Commercial	
Component Access URL	https://crcns.org/data-sets/hc/hc-7/about-hc-7	
Technical documentation URL	https://crcns.org/data-sets/hc/hc-7/about-hc-7	
Usage documentation URL		
Component dissemination material URL		

3.27 Densities and 3D distributions of synapses using FIB/SEM imaging in the mouse hippocampus (CA1)

Field Name	Field Content	Additional Information
ID	963	

Component Type	Data	
Contact	MERCHÁN, Ángel	
Component Description	Densities and 3D distributions of synapses using FIB/SEM imaging in the mouse hippocampus (CA1). Three animals, one FIB/SEM stack per layer Related milestone: MS1.2.7 High-resolution synaptic maps in neocortex and hippocampus M16 Verification: Segmented images released; correct light microscopy reconstructions validated with correlative FIB/SEM electron microscopy 3D reconstructions, also with real images labelled by experts; software released and tested Related milestone: MS1.2.9 Synaptic maps (nanoscopic level) M24 Verification: Data released and data quality validated. Related Task: Task 1.2.9: High-resolution synaptic maps in the neocortex and hippocampus using confocal microscopy and FIB/SEM	
Latest Release	SM & 2018/03/01	At M23, we acquired 12 FIB/SEM stacks of images from str. Oriens, radiatum and lacunosum moleculare, from 3 animals. This is 100% of the stacks required. Segmentation has been completed and analysis is in progress.
TRL	NA	
Location	Data hosted by task providing dataset	HBP storage: NIP curation storage
Format	Excel files	
Curation Status	NIP curation storage	
Validation - QC	Pass	Merchán; peer review
Validation – Users	Yes	SP5, SP6
Validation – Publications	Alejandro Antón-Fernández, et al., Neurobiology of Disease (97) 2017 11-23. Carolina Gonzalez-Riano, et al., (2017) Brain Struct Funct. DOI: 10.1007/s00429-017-1375-5. Santuy A, et al. Brain Struct Funct. 2017 Jul 18. doi: 10.1007/s00429-017-1470-7 Bosch C, et al., Cereb Cortex. 2016 Sep 13. Urrecha M, et al., PLoS One. 2017 Feb 15;12 (2)	
Privacy Constraints	Animal Research	
Sharing	consortium - share with any consortium members	There may be issues sharing data openly
License	BY-NC	

Component Access URL	https://www.dropbox.com/sh/2iyy7s6ahf32fqu/AABSKbJTTIUTACNxTtdvSyjMa?dl=0	
Technical documentation URL	NA	
Usage documentation URL	NA	
Component dissemination material URL	NA	

3.28 Densities and 3D distributions of synapses using FIB/SEM imaging in the human hippocampus (CA1)

Field Name	Field Content	Additional Information
ID	965	
Component Type	Data	
Contact	MERCHÁN, Ángel	
Component Description	Densities and 3D distributions of synapses using FIB/SEM imaging in the human hippocampus (CA1). Three human subjects, one FIB/SEM stack per layer Related milestone: MS1.2.9 Synaptic maps (nanoscopic level) M24 Verification: Data released and data quality validated Related task: Task 1.2.9: High-resolution synaptic maps in the neocortex and hippocampus using confocal microscopy and FIB/SEM	
Latest Release	SM & 2018/03/01	At M23, we acquired 18 FIB/SEM stacks of images from stratum pyramidal and radiatum of human CA1. This is 100% of the stacks required. Segmentation has been completed and analysis is in progress.
TRL	NA	
Location	Data hosted by task providing dataset	HBP storage: NIP curation storage
Format	Espina .seg; Excel .xls	
Curation Status	NIP curation storage	
Validation - QC	Pass - Another lab colleague checks all segmentations	
Validation – Users	Yes	SP5, SP6
Validation – Publications	Alejandro Antón-Fernández, et al., Neurobiology of Disease (97) 2017 11-23. Carolina Gonzalez-Riano, et al., (2017) Brain Struct Funct. DOI: 10.1007/s00429-017-1375-5.	

	Santuy A, et al. Brain Struct Funct. 2017 Jul 18. doi: 10.1007/s00429-017-1470-7 Bosch C, et al., Cereb Cortex. 2016 Sep 13. Urrecha M, et al., PLoS One. 2017 Feb 15;12 (2)	
Privacy Constraints	Human Research	
Sharing	consortium - share with any consortium members	There may be issues sharing data openly
License	BY-NC (TBC)	
Component Access URL	https://www.dropbox.com/sh/2iyy7s6ahf32fqu/AABSKbJTTlUTACNxTtdvSyjMa?dl=0	
Technical documentation URL		
Usage documentation URL		
Component dissemination material URL		

3.29 Connectivity and morphology of neurons within striatum

Field Name	Field Content	Additional Information
ID	938	
Component Type	Data	
Contact	GRILLNER, Sten (KI)	
Component Description	The connectivity and morphology properties of neurons within striatum and the output stage of the basal ganglia will be addressed, as well as the projection patterns of the different types of neurons from cortex as well as thalamus. The techniques that will be used to capture the data include morphological reconstructions with neuronal labelling and tracing using fluorescence bright field and confocal microscopy, immunolabelling, two-photon microscopy, live-cell imaging.	
Latest Release	Internal release to SP1 (2018/03/01) and SP6. HBP Collab, Basal ganglia data. Detailed morphologies have been obtained of medium spiny neurons of the two different varieties expressing the D1 and D2 receptors, respectively, and also of cholinergic and fast-spiking interneurons. Five full reconstructions of cholinergic interneurons are completed. A first complete reconstruction with all spines of one D1 MSN has been achieved in collaboration with Javier DEFELIPE (UPM). Morphological features of reconstructed neurons are validated against publicly available data. Completeness 90%.	
TRL	NA	

Location	data hosted by Collaboratory storage	
Format	Reconstructed morphologies of striatal D1 and D2 projection neurons and cholinergic and fast-spiking interneurons	
Curation Status	NIP curation storage	
Validation - QC	The data are validated against data in the literature	
Validation – Users	Yes	SP6, T6.2.5, T6.4.1
Validation – Publications	Lindroos et al., 2018, Frontiers in Neural Circuits, in press.	
Privacy Constraints	HBP Internal	
Sharing	With SP6	
License	CC Attribution ShareAlike 4.0 International	
Component Access URL	https://collab.humanbrainproject.eu/#/collab/376/nav/3797, https://collab.humanbrainproject.eu/#/collab/376/nav/43458	
Technical documentation URL	https://collab.humanbrainproject.eu/#/collab/376/nav/3797, https://collab.humanbrainproject.eu/#/collab/376/nav/43458	
Usage documentation URL	https://collab.humanbrainproject.eu/#/collab/376/nav/3797, https://collab.humanbrainproject.eu/#/collab/376/nav/43458	
Component dissemination material URL	http://neuroinformatics2017.org/	Poster, INCF 2017, Lindroos et al, 2018

3.30 Cellular properties of neurons within striatum

Field Name	Field Content	Additional Information
ID	940	
Component Type	Data	
Contact	GRILLNER, Sten (KI)	
Component Description	The cellular properties of neurons within striatum and the output stage of the basal ganglia will be addressed, as well as the projection patterns of the different types of neurons from cortex as well as thalamus. The techniques that will be used to capture the data include single- and multi-electrode whole cell patch clamp.	
Latest Release	Internal release to SP1 (2018/03/01) and SP6. Private HBP Collab, Basal ganglia data. Ion channel composition has been analysed physiologically and with RNA-seq through collaboration. Available	

	databases of have been analysed for striatal cells. Completed.	
TRL	NA	
Location	data hosted by Collaboratory storage	
Format	SWC, json	Cellular properties of striatal D1 and D2 projection neurons and cholinergic and fast-spiking interneurons
Curation Status	NIP curation storage	
Validation - QC	Pass	QC according to experimental standards
Validation – Users	Yes	SP6, T6.2.5, T6.4.1
Validation – Publications	Lindroos et al., 2018, Frontiers in Neural Circuits, in press.	
Privacy Constraints	Anima Research	
Sharing	consortium - share with any consortium members	SP6
License	CC Attribution ShareAlike 4.0 International	
Component Access URL	SP6 Basal ganglia: https://collab.humanbrainproject.eu/#/collab/376/nav/12695, https://collab.humanbrainproject.eu/#/collab/376/nav/4425	
Technical documentation URL	https://collab.humanbrainproject.eu/#/collab/376/nav/12695, https://collab.humanbrainproject.eu/#/collab/376/nav/4425	
Usage documentation URL	https://collab.humanbrainproject.eu/#/collab/376/nav/12695, https://collab.humanbrainproject.eu/#/collab/376/nav/4425	
Component dissemination material URL	http://neuroinformatics2017.org/	Poster, INCF 2017 Lindroos et al, 2018

3.31 Whole-brain images of selected neuronal types

Field Name	Field Content	Additional Information
ID	932	
Component Type	Data	
Contact	SILVESTRI, Ludovico (LENS)	
Component Description	Image stack of different cell types (parvalbumin interneurons, somatostatin interneurons, VIP	

	interneurons and pyramidal cells) across the entire mouse brain	
Latest Release	MS1.3.9 & 30.11.2017 11 whole-brain datasets (4 with parvalbumin-positive neurons labelled, 4 with VIP-positive and 3 with somatostatin-positive) have been collected. Raw data.	
TRL	N. A.	
Location	data hosted by Collaboratory storage	
Format	Image stack of different cell types (parvalbumin interneurons, somatostatin interneurons, VIP interneurons and pyramidal cells) across the entire mouse brain	
Curation Status	SP5 Tier 2	
Validation - QC	Pass	Silvestri Ludovico, QC based on visual inspection
Validation – Users	No	
Validation – Publications	No	
Privacy Constraints	Anima Research	
Sharing	Collab - share only with members of private Collab	
License	CC	
Component Access URL	LOCALIZOOM	
Technical documentation URL		
Usage documentation URL		
Component dissemination material URL		

3.32 Fluorescence imaging of cortical activity after stroke

Field Name	Field Content	Additional Information
ID	552	
Component Type	Data	
Contact	ALLEGRA MASCARO, Anna Letizia	
Component Description	2D lapse recording of calcium-activity in the cortex of fluorescent mice of three experimental groups: control, stroke, rehabilitated. 3 mice per group, 5 days each, 15 datasets total.	
Latest Release	MS1.3.5 - 30.09.2017	

	Multi-tiff format files for each mouse (4), we have daily (5 days tot) imaging sessions lasting 40 sec, 25 Hz framerate acquisition	
TRL	N. A.	
Location	data hosted by Collaboratory storage	
Format	2D Time lapse cortical recording maps	
Curation Status	SP5 Tier 2	
Validation - QC	Pass - ALLEGRA MASCARO, QC based on visual inspection	
Validation – Users	Yes - Viktor Jirsa (SP4)	
Validation – Publications	No	
Privacy Constraints	Anima Research	
Sharing	Collab - share only with members of private Collab	
License	CC	
Component Access URL	https://ksproxy.cscs.ch:13000/Pavone_SGA1_1.3.2 https://collab.humanbrainproject.eu/#/collab/5340/nav/41538	
Technical documentation URL		
Usage documentation URL		
Component dissemination material URL		

3.33 Images of neuronal activation of whole mouse brain

Field Name	Field Content	Additional Information
ID	931	
Component Type	Data	
Contact	SILVESTRI, Ludovico	
Component Description	Whole-brain images of neuronal activation in mouse brain acquired with light-sheet microscopy. Animal models will be used to detect immediate early genes (IEGs) expression.	
Latest Release	MS1.3.4 - 31.05.2017 two first images of neuronal activation based on early-genes expression (cFos) mapping	
TRL	N.A.	
Location	CINECA	HBP Collaboratory

Format	txt file for point cloud, jpeg for lossy-compressed images, mp4 for lossless-compressed data	
Curation Status	SP5 Tier 2	
Validation - QC	Pass - Silvestri Ludovico, QC based on visual inspection	
Validation – Users	No	
Validation – Publications	No	
Privacy Constraints	Animal Research	
Sharing	Collab - share only with members of private Collab	
License	CC	
Component Access URL	https://collab.humanbrainproject.eu/#/collab/5340/nav/41538	
Technical documentation URL		
Usage documentation URL		
Component dissemination material URL		

3.34 3D reconstruction of the entire vascular system of the mouse brain

Field Name	Field Content	Additional Information
ID	745	
Component Type	Data	
Contact	WEBER, Bruno (UZH)	
Component Description	Supporting community activities in SP3. These activities will include dissemination, outreach, organizing community workshops and industry events.	
Latest Release	Release ID – 2017-12 Graph networks from 3 different datasets of varying size available	
TRL	TRL 5	
Location	Data hosted by HPAC Platform, accessible via Collaboratory	
Format	Vasculature Graph Network	
Curation Status	NIP curation storage	
Validation - QC	Pass - Weber, method for data analysis tested	
Validation – Users	No	

Validation – Publications	No	
Privacy Constraints	No privacy constraints – Animal Research	
Sharing	Collab Only	
License	Attribution Non-commercial ShareAlike 4.0 International	
Component Access URL	Cortex Vasculature Collab - Data	
Technical documentation URL		
Usage documentation URL		
Component dissemination material URL		

3.35 3D image of the entire vascular system of the mouse brain

Field Name	Field Content	Additional Information
ID	744	
Component Type	Data	
Contact	WEBER, Bruno (UZH)	
Component Description	For SGA1, the main objective will be to achieve a three dimensional image of the entire vascular system of the mouse brain for the first time. This will be achieved by using light-sheet microscopy and/or synchrotron-radiation based X- ray microscopy. Very big data sets (~ 15 TB per mouse brain) will be generated.	
Latest Release	Release ID – 2017-12 Raw data of 2 different datasets (two-photon microscopy)	
TRL	NA	
Location	Data hosted by HPAC Platform, accessible via Collaboratory	
Format	Raw microscopy images	
Curation Status	NIP curation storage	
Validation - QC	Pass - Weber, method for data analysis tested	
Validation – Users	Yes - We are currently using it on the component 3D reconstruction of the entire vascular system of the mouse brain	
Validation – Publications	No	
Privacy Constraints	No privacy constraints – Animal Research	

Sharing	Collab Only	
License	Attribution Non-commercial ShareAlike 4.0 International	
Component Access URL	Cortex Vasculature Collab - Data	
Technical documentation URL		
Usage documentation URL		
Component dissemination material URL		

3.36 Developing the integrated FIB/SEM and SDS-FRL immunoelectron microscopy technique

Field Name	Field Content	Additional Information
ID	652	
Component Type	Report	
Contact	LUJÁN, Rafael	Component owner Reference person
Component Description	We will integrate two newly developed immunoelectron microscopy techniques: 1) an automated dual-beam electron microscope that combines focused ion beam milling and scanning electron microscopy, and 2), we will combine this technology with pre-embedding immunogold reactions (FIB/SEM immunogold) to obtain three-dimensional reconstruction, and with SDS-digested freeze-fracture replica labelling (SDS-FRL) to obtain two-dimensional views of molecular distribution on surface of neurons	
Latest Release	2017/09/30	100%
TRL	NA	
Location	data hosted by task providing dataset: https://www.dropbox.com/sh/6ljw2obd654z733/AADIMFLU9uqMcQlIAkt5zu7Ya?dl=0; https://www.dropbox.com/sh/zjj8kxtcs0pixlm/AAAIkHC-4peGakzyuI0Aa7qTa?dl=0 HBP storage: NIP curation storage	
Format	Tiff files and tables with density and numbers	
Curation Status	NIP curation storage	NA
Validation - QC	Pass - Luján: Method tested	
Validation – Users	Yes - Collaborators external to HBP consortium	
Validation – Publications	No	
Privacy Constraints	Animal Research	

Sharing	consortium - share with any consortium members	There are no issues sharing data
License	BY-NC- ND	NA
Component Access URL	https://www.dropbox.com/sh/6ljw2obd654z733/AADlMFLU9uqMcQIIAkt5zu7Ya?dl=0; https://www.dropbox.com/sh/zjj8kxtcs0pixlm/AAAIkHC-4peGakzyuI0Aa7qTa?dl=0	
Technical documentation URL	https://www.dropbox.com/sh/6ljw2obd654z733/AADlMFLU9uqMcQIIAkt5zu7Ya?dl=0; https://www.dropbox.com/sh/zjj8kxtcs0pixlm/AAAIkHC-4peGakzyuI0Aa7qTa?dl=0	
Usage documentation URL		
Component dissemination material URL		

3.37 Antibodies against targets identified in all genomic and proteomics tasks

Field Name	Field Content	Additional Information
ID	826	
Component Type	Data	
Contact	CATTANEO, Antonino MELI, Giovanni	Component owner Reference person
Component Description	We will use IACT-SPLINT (Intracellular Antibody Capture Technology - Single Pot Library of Intracellular Antibodies) to obtain, in a validated manner, antibodies against targets identified in genomic and proteomics tasks, without the need to express the proteins (from genes to antibodies), with the additional bonus that also the genes coding for the antibody domain are concurrently isolated, so that the selected antibodies can be used either as proteins (classical use, but with improved properties) or as genes (intrabodies for functional interference).	IACT antibody fragments for imaging; Generation of new intrabodies/antibody fragments
Latest Release	Release ID: MS1.1.4 and MS1.1.9 Release Date: 2018/03/01 Detection of antigens of interest; Antibody generation: 100% 7 out of 7 new intrabodies anti-NLGs; Imaging 100% ; 11 out 10 brain slices; intrabody biochemical validation: 60% for 2 intrabodies anti-NLG2	
TRL	NA	
Location	data hosted by task providing dataset http://151.100.170.9:8080/cgi-bin/ Provisional internal repository with protected access on EBRI lab server.	Username: hbp Password: nanobodies
Format	.tiff, .pdf .xlsx , .docx	IACT antibody fragments for imaging;

		Generation of new intrabodies/antibody fragments
Curation Status	These data have not been sent to SP5 yet	NIP curation storage planned
Validation - QC	Pass - MELI, Giovanni – QC test; validation in different laboratories by different operators	
Validation – Users	Yes - Collaborators external to HBP consortium	
Validation – Publications	No	Manuscript in preparation
Privacy Constraints	Human Research Animal Research	Human research Animal research
Sharing	consortium - share with any consortium members	Data are planned to be shared openly within consortium
License	All rights reserved, Copyright	
Component Access URL	http://151.100.170.9:8080/cgi-bin/ Provisional internal repository with protected access on EBRI lab server	
Technical documentation URL	http://151.100.170.9:8080/cgi-bin/ Provisional internal repository with protected access on EBRI lab server	
Usage documentation URL	http://151.100.170.9:8080/cgi-bin/ Provisional internal repository with protected access on EBRI lab server	
Component dissemination material URL	http://151.100.170.9:8080/cgi-bin/ Provisional internal repository with protected access on EBRI lab server	

3.38 Improved light-sheet microscopy for whole brain imaging

Field Name	Field Content	Additional Information
ID	892	
Component Type	Report	
Contact	SILVESTRI, Ludovico	
Component Description	Set-up of Improved light-sheet microscopy for whole brain imaging	
Latest Release	MS1.3.1 31.05.2017	Preprint publication
TRL	N.A.	
Location	data hosted by Collaboratory storage	
Format	set-up description of improved light-sheet microscopy for whole brain imaging	
Curation Status	N.A.	

Validation - QC	N.A.	
Validation – Users	Yes - T1.3.1, T1.3.4	
Validation – Publications	Silvestri et al., https://doi.org/10.1101/170555	
Privacy Constraints	No Privacy Constraint	
Sharing	anonymous - share with anonymous non-consortium members	
License	All Rights Reserved, Copyright	
Component Access URL	Online preprint	
Technical documentation URL		
Usage documentation URL		
Component dissemination material URL		

3.39 Synapse segmentation ImageJ plugin and macro

Field Name	Field Content	Additional Information
ID	433	
Component Type	Software	
Contact	Bielza, Concha (UPM)	
Component Description	The plugin filters a stack of images from confocal microscopy to separate background from foreground. Foreground pixels are further connected to create 3D objects, the synapses.	
Latest Release	2016/11/30 (Final Release)	
TRL	TRL5	
Location	data hosted by other non-HBP 3rd party	
Format	ImageJ plug-in	
Curation Status		
Validation - QC	Unchecked	
Validation – Users	Yes - Users from Laboratorio Cajal de Circuitos Corticales, Instituto Cajal, Spain	
Validation – Publications	No	Manuscript submitted.
Privacy Constraints	No privacy constraint	
Sharing	Publically anonymous.	No issues sharing data
License	MIT	

Component Access URL	https://github.com/ComputationalIntelligenceGroup/ObjCounter	Installable locally, not available within the Platform.
Technical documentation URL		
Usage documentation URL	https://github.com/ComputationalIntelligenceGroup/obj_detection_toolset	
Component dissemination material URL		

3.40 Interactive synaptic map

Field Name	Field Content	Additional Information
ID	434	
Component Type	Software	
Contact	Bielza, Concha (UPM)	
Component Description	Web-based end-user interface to interactively analyse regions of the brain previously segmented to detect synapses. Error model is used to validate segmentation.	
Latest Release	2017/03/31 (Internal Release)	
TRL	TRL5	
Location	data hosted by other non-HBP 3rd party	
Format	User interface application	
Curation Status	NA	
Validation - QC	NA	No quality check performed.
Validation – Users	Yes	Users from Laboratorio Cajal de Circuitos Corticales, Instituto Cajal, Spain
Validation – Publications	No	Manuscript has been submitted.
Privacy Constraints	No privacy constraint	
Sharing	Publically anonymous. There are no issues in sharing data.	
License	MIT	
Component Access URL	https://github.com/ComputationalIntelligenceGroup/MultiMap	Installable locally, not available within the platform.
Technical documentation URL		
Usage documentation URL	https://computationalintelligencegroup.github.io/MultiMap-documentation/	

Component dissemination material URL		

3.41 Tools for the early analysis of morphological data (Pyramidal Explorer)

Field Name	Field Content	Additional Information
ID	906	
Component Type	Software	Pyramidal Explorer, DCExplorer, InToolExplorer, ClintExplorer
Contact	GALINDO, Sergio (URJC), GARCÍA, Marcos (URJC), TRINCADO, Fernando (URJC)	
Component Description	Tools for the 1) early analysis of morphological data, in order to provide feedback to steer the data extraction process and to correct possible errors or even redesign experiments if necessary, 2) analysis of complex systems, exploiting the ability of the human visual system to extract information from visual scenarios.	
Latest Release	2018/03/01	100%
TRL	Pyramidal Explorer and InToolExplorer: TRL-4, DCExplorer: TRL-5, ClintExplorer: TRL-3	
Location	data hosted by task providing dataset http://gmrv.es/pyramidalexplorer/PyramidalExplorer-0.2.0-TestData.zip https://cajalbbp.es/dcexplorer https://cajalbbp.es/intoolexplorer	
Format	NA	
Curation Status	NA	
Validation - QC	Pass - GALINDO, Sergio (URJC)); CI Platform and prototype validation; GARCÍA, Marcos (URJC); CI Platform and prototype validation; TRINCADO, Fernando (URJC)	
Validation – Users	Yes - SP1 collaborators	
Validation – Publications	"PyramidalExplorer: A new interactive tool to explore morpho-functional relations of pyramidal neurons". Pablo Toharia1,5, Oscar D. Robles Sanchez1,5, Isabel Fernaud2, Julia Markova3, Sergio Galindo1, Angel Rodriguez4,5, Luis Pastor1,5, Oscar Herreras3, Javier DeFelipe2,3, Ruth Benavides-Piccione2,3 https://www.frontiersin.org/articles/10.3389/fnana.2015.00159/full	
Privacy Constraints	No privacy constraint	
Sharing	Publically anonymous	

License	GNU GPL	
Component Access URL	http://gmrv.es/gmrvvis/pyramidalexplorer/ https://cajalbbp.es/dcexplorer https://cajalbbp.es/intoolexplorer	
Technical documentation URL	http://gmrv.es/gmrvvis/pyramidalexplorer/ http://cajalbbp.es/dcexplorer_web/ http://cajalbbp.es/intoolexplorer_web/	
Usage documentation URL	http://gmrv.es/gmrvvis/pyramidalexplorer/ http://cajalbbp.es/dcexplorer_web/ http://cajalbbp.es/intoolexplorer_web/	
Component dissemination material URL	http://gmrv.es/gmrvvis/pyramidalexplorer/ http://cajalbbp.es/dcexplorer_web/ http://cajalbbp.es/intoolexplorer_web/	

3.42 K channel activity within neuron models (model)

Field Name	Field Content	Additional Information
ID	575	
Component Type	Model	
Contact	BERNECHE, Simon (SIB)	
Component Description	NEURON model that illustrates to what extent neuron signalling can be modulated by the action of K channels using realistic channel distributions and kinetics.	
Latest Release	2018/03/01	90%
TRL	N/A	
Location	data hosted by HPAC Platform (accessible via Collaboratory) data hosted by other non-HBP 3rd party (https://github.com/njohner/Kv-kinetic-models/tree/master/AP_propagation)	
Format	multi-state ion channel models (csv, Neuron .mod)	
Curation Status	N/A	
Validation - QC	Pass	Berneche, model validated
Validation – Users	No	
Validation – Publications	No	
Privacy Constraints	No privacy constraint	

Sharing	Publically anonymous	
License	CCO-Freeing content globally without restriction	
Component Access URL	https://collab.humanbrainproject.eu/#/collab/6245/nav/48248 https://collab.humanbrainproject.eu/#/collab/6247/nav/48253	
Technical documentation URL	https://collab.humanbrainproject.eu/#/collab/6245/nav/48248 https://collab.humanbrainproject.eu/#/collab/6247/nav/48253	
Usage documentation URL	NA	
Component dissemination material URL	NA	

3.43 A mapping of computational models of synapses to proteins

Field Name	Field Content	Additional Information
ID	420	
Component Type	Data	
Contact	STERRATT, David	
Component Description	An analysis of what proteins are contained in 15+ existing biophysical models of synaptic plasticity that contain more than one signalling pathway (as defined by Manninen et al 2010, Front Comp. Neur 4). This requires a number of tables: (1) A table of "entities". An "entity" may be: a Protein; a Protein Multimer, which can comprise multiple proteins, (e.g. AMPAR, which contains a combination of GluR1-4); a Protein family (e.g. Calmodulin, which may correspond to one of Calmodulin-1, Calmodulin-2 or Calmodulin-3); an ion, or a second messenger. Each protein entity has a standard, meaningful ID, a full name, and mappings to HGNC Family ID, ENTREZ IDs, and MGI IDs (2) A table of mappings of models to entities. Each row contains a the PMID of the paper, the standard name of the entity and the name used for the entity in the paper. There is one row for each entity-paper combination. (3) Additional mappings to resolve mappings of Protein Families and Protein Multimers to genes. There are entities that are implicitly considered protein families by modellers that do not have official protein families in the HGNC or Interpro databases, e.g. SOS. Ideally, mappings we generate will be fed back into the community databases. (4) A table of model characteristics, e.g. region of the brain specified, approximate size of model, simulator used. Some of these data will already exist, e.g. in	

	modeldb or OpenSourceBrain, and these databases would be free to incorporate data we extract. These tables will be processed to give various views on the data.	
Latest Release	2018/02/01	Version of data tables used in the version of the manuscript sent for review
TRL	N/A	
Location	data hosted by HPAC Platform (via Collaboratory)	Supplemental information of PloS Comput. Biol. paper (if published). GitHub
Format	Tables of entities in models and mappings of entities to gene names	
Curation Status	Uploaded to an approved HBP data repository location	
Validation - QC	Unchecked	
Validation – Users	Yes - The authors, who have used the data to assess coverage of molecules in synaptic models	
Validation – Publications	We have published but not yet peer-reviewed results at https://www.biorxiv.org/content/early/2018/01/28/254094.article-info	
Privacy Constraints	No privacy constraint	
Sharing	Publically anonymous	
License	CC-BY 4.0 International Licence	
Component Access URL	https://collab.humanbrainproject.eu/#/collab/6172/nav/47729	
Technical documentation URL	https://www.biorxiv.org/content/early/2018/01/28/254094.article-info	
Usage documentation URL	https://www.biorxiv.org/content/early/2018/01/28/254094.article-info	
Component dissemination material URL	https://www.biorxiv.org/content/early/2018/01/28/254094.article-info	

4. Conclusion and Outlook

In line with the SP1 objectives we have obtained four main groups of results that have been divided in the following key results: High-level subcellular and molecular datasets: High-quality datasets of the four brain regions (neocortex, cerebellum, hippocampus and basal ganglia): Whole brain high-level datasets: Development of experimental methods, IT tools and models. Furthermore, the datasets generated, tools and models developed have been included in a SP1 Data Catalogue 'HBP-SGA1-SP1DC-M23' that was generated to organize the data and to make more accessible the tools and models used in SP1.

Regarding the high-level subcellular and molecular datasets we have obtained high-level datasets, at molecular and subcellular level, in terms of, localization and distribution of receptors, synaptic proteins and synaptic plasticity have been achieved. These datasets have contributed to the generation of models including; modelling activity and use cases such as Hodgkin-Huxley modelling of excitation-inhibition; Modelling modulation of inhibition downstream calcium signalling; Data-Driven Modelling of G Protein-Coupled Receptor-Dependent Cascades; Data-driven modelling of Ca2+ dependent cascades controlling synaptic signalling and homeostasis; Initial model validation tests implemented to compare rat model with mouse data; Models of mouse hippocampal neurons, Fitting individual synaptic events; Biophysical model of LTP and LTD in wild type and mutant hippocampal CA1 synapses.

Concerning to the high-quality datasets at cellular and microcircuit level of focusing on the neocortex, cerebellum, hippocampus and basal ganglia, we have been able to obtain detailed reconstructions of pyramidal cells in different cortical regions and species which will enable us to characterize the differences and similarities between these cells in these cortical regions and species. Furthermore, these reconstructions are being used to generate realistic models of pyramidal cells. The plasticity rules of the cerebellum have been determined. A database of the morphological and physiological features of the main classes of hippocampal neurons in the mouse has been constructed and the basal transmission properties and short-term plasticity parameters for several major classes of hippocampal connections have been determined. As well as that, synaptic maps of the mouse and human hippocampus have also been generated at the meso and nanoscopic levels have been generated. Furthermore, the connectivity and morphology of neurons and cellular properties of neurons within striatum have been determined.

The investigation at whole brain level has achieved its goals, albeit with some delay mainly due to the late signing of the SGA1. For the next phase, we want to establish from the beginning the data curation process learned during SGA1, and expand our datasets to different cell types (concerning structure) and different behaviours (concerning function). From the technology development point of view, we will continue the virtuous circle started in SGA1, hoping to provide ever better optical and computational tools to explore brain structure and function that can also lead to further IP. To maximize the impact of obtained results, besides the traditional channels of dissemination (publications, conferences, etc.) we want to explore with SP5 the possibility of open access to our data from people outside HBP.

Another major aim has been the integration of multi-level data. During this project phase, this integration has been focused on the micro-anatomical data in line with the SP objectives*. Statistical and machine-learning techniques have been applied to infer principles of human and mouse neuron morphology and neuroanatomical organization. In addition, new workflows have been developed within the morphological data extraction process. In the SGA2, SP1 aims to further develop data analysis methods and visual analysis tools to carry out a multiscale investigation on brain physiology and long-range connectivity. The neuroanatomical information will be integrated with genetic, molecular and physiological data. This integration would allow the generation of models to reason about the data, make predictions and suggest new hypotheses to discover new aspects of the structural and functional organization of the brain.

* It should be pointed out, that the description and objectives outlined in the DoA for the integration studies are extended to other types of data such as genetic, electrophysiological, etc. In the end, the research laboratories in charge of the tasks to generate these data left the project

before starting the SGA1. This is the reason why only morphological data have been involved in the integration activities.

Furthermore, the datasets generated in the SGA1 together with those planned in the next project phase will be used to obtain critical comparative information about differences and similarities in brain organization across species.

In general, the SP1 KRs have produced significant advances beyond the state of the art. The generation of molecular maps provides crucial information for the reconstruction and simulation of the healthy brain, and for the exploration and simulation of hundreds of brain diseases. The integration of molecular maps with cellular scale maps will allow cell classification and modelling of different types of cells. At cellular and microcircuit level, the data generated allow to perform detailed neuron and microcircuitry reconstruction and physiological analysis. The multi-level approach followed can be applied to generate multiscale molecular, anatomical and functional maps. At whole-brain level, it has contributed to the creation of the first multi-level map of the mouse brain. The generation of whole brain cell distribution maps integrated with single-cell characterization allow detailed whole-brain simulations. The development of innovative imaging techniques beyond the state-of-the-art contributes to resolved scientific questions, such as recovery mechanisms after brain injury and whole brain connectivity at single cell level. The application of statistical and machine learning techniques has allowed to infer principles of human and mouse neuron morphology and neuroanatomical organization. The models developed allow more detailed neuron modelling and novel workflows have been implemented for the visual analysis of micro-anatomical data that can be applied to different types of data and information.

The impact achieved with the KRs obtained has been as planned. The data generated are a crucial contribution to the Multi-level Atlas of the Mouse Brain, created in SP5; they also provide the initial scaffolding and validation tests for high-fidelity reconstructions and simulations of the mouse brain, to be filled in with data from the HBP’s European and International collaborations and with predictions from reconstructions. In addition, these datasets have allowed the implementation of comparative assessments between rodents and human to predict features of the human brain for which experimental data are not available.

On a different issue, the dissemination plan of SP1 will be used as the main tool to facilitate the use of the SP1 results internally and to maximize the impact of these results outside the HBP. The general objective of the SP1 plan is to identify and organize the activities to be performed in order to promote the use of the SP’s results and the widest dissemination of knowledge from this SP. The plan is intended to be expanded in three directions: (i) towards the communication of the project results in the scientific and general RTD sector, (ii) towards the marketing activities in order to enhance the SP’s results, (iii) towards the general public to promote science. In SP1, dissemination is a horizontal activity and concentrates on disseminating the results of the project itself to a wide range of existing or potential users. SP1 result will be used as a key messages with a targeted audience and will be disseminated via different mechanisms implementing diverse activities.

In addition, other aspect related to the dissemination plan of SP1 is the key goal that has been achieved in the SGA1, the generation of a Data Management Plan, —according to the document *H2020 Programme Guidelines on FAIR Data Management in Horizon 2020* (Version 3.0, 26 July 2016)—. This DMP is in line and linked to the HBP general DMP. The SP1 DMP describes the data management life cycle for the data generated by SP1 as well as the utility of this data for modelling purposes. The DMP has supposed a useful system to organize the datasets, tools and models generated internally and to facilitate further use of the SP1 outputs by other SPs, maximizing their impact. The SP1 DMP will be also used in the next project phase, the SGA2, and will continue throughout the project.

Annex A: Component Field Guidelines

For all URLs, the URL must be visible so as to be usable from a printed paper copy. URLs should not have another text displayed in their place.

4.1 Component ID

The PLA ID for the component. Interim versions might contain a PLA URL for the component, but final versions shared with people outside HBP ***MUST NOT*** include a PLA URL.

4.2 Component Type

- Field Content*:*
  - Select one of the standard PLA component types: data, model, software, service, report or hardware.
- Additional Information:
  - Provide the following additional information dependent on the component type:

4.3 Latest Release

- Field Content
  - Released software semantic version (https://semver.org/).
- Additional Information
  - If a link to a Collaboratory software catalogue release page is available, please include this link as well.

4.4 TRL

Current TRL for the component if applicable. For datasets or reports, this can be set to “Not Applicable”.

The TRLs set out below correspond to the standard European Commission TRLs and previous versions of the following table has been included in the FPA, SGA1 and SGA2 proposals. The properties required of an infrastructure component at each TRL are also defined. The TRLs are intended to be applied, not only to systems delivered as RI, but also to the systems producing key datasets as well.

Table 1: Technology Readiness Levels (TRLs)

Technology Readiness Level	Expected Properties
TRL 1 Project Initiation	• Project owner identified • Project principles and high-level objectives defined • Use case definitions (includes target users and activities)
TRL 2 Conceptualization	• Analytic study of the problem space • Identify key functions which must be validated in Component Implementation • Formulate validation criteria for critical components • Formulate validation criteria of complete prototype system

	• Prototype Epic planning
TRL 3 Proof of Concept Implementation	• Implementations of key functions • Validation of critical concepts • Identification of additional validation criteria for TRL4
TRL 4 Prototype Component	• Validation of prototype components in Lab • Proof of Concept has become prototype components • System technology selection has been made • Load testing of components under key load criteria • Identification of additional validation criteria for TRL5
TRL 5 Prototype Integration	• Validation of integrated system in a real-world environment • Tested in restricted environment with a small number of real users • Data formats specified • Identification of additional validation criteria for TRL6
TRL 6 Prototype-to-Real-world Integration	• Validation of integrated system in a real-world environment • Load testing of integrated system under expected load • Tested in a real-world environment with a small number of real users • Initial System documentation • Initial User documentation • System monitoring points specified (for services) • Identification of additional validation criteria for TRL7
TRL 7 Operational Integration	• Validation of integrated system in a real-world environment • Tested in a real-world environment with a small number of real users (canary testing for SoA) • System monitoring implemented (for services) • No expected data format or API changes without suitable deprecation period (for services or software components) • Load testing of integrated system under expected load • SLA monitored (for services)
TRL 8 Deployment	• Validation of integrated system in a real-world environment • Tested in a real-world environment with a small number of real users • SLA enforced (for services)
TRL 9 Production	• Validation of integrated system in a real-world environment • Tested in a real-world environment with a target number of real users