

Grant Number:	720270	Grant Title:	Human Brain Project SGA1
Deliverable Title:	D1.5.3 - Detailed plan of data usage and the impact of generated data on models		
Contractual Number and type:	SGA1 D1.5.3 - Report (includes SP1 Data Management Plan HBP-SGA1-SP1DMP-M23-v1.3)		
Dissemination Level:	PU (= Public)		
Version / Date:	V4.5 - 20 July 2018 Resubmitted: 30 July 2018; Accepted: 7 Dec 2018		
Abstract:	<p>This Deliverable is SP1's Detailed plan of data usage and the impact of the generated data on models.</p> <p>During SGA1, SP1 has been structured in order to provide the critical data required for modelling (reconstruction and validation) of the 4 main brain subcircuits (cerebral cortex, cerebellum basal ganglia and hippocampus) at the cellular, subcellular, and network level. Conversely, SP1 was not intended to provide full coverage of data for whole-brain reconstruction. From M1 to M24 of SGA1, a detailed plan for data usage via cross-SP working meetings was drawn up as stated in the DoA. This plan includes strategic structural and functional data to model and simulate the four major brain circuits and to set up their use in simulation/modelling at sub-cellular, cellular and circuit levels. Due to time and resource pressures, the data generated was sent to the Platforms as it became available, i.e., not only the initial and intermediate datasets, but also incomplete ones, to test all the pipelines. Identification of the gaps between the data available and the data needed has followed a priority scale established with SP2, SP3, SP4, SP5, SP6, CDP1 and CDP2. The modelling work and the coordination in particular with SP6 and CDP2, ensures that the data generated are critical for the development of specific HBP models/simulations. This plan is based on the document <i>H2020 Programme Guidelines on FAIR Data Management in Horizon 2020</i> (Version 3.0, 26 July 2016). The first version of the SP1 data management plan (SGA1) was delivered in M20 and was updated and submitted by M24 (as scheduled); the current version is an updated version as requested in the SGA1 Final Review that includes further information on the role of the acquired data regarding in which SPs the data are/were going to be used), as well as other required updates. The plan is being implemented in the SGA2 and will continue throughout the project.</p>		
Keywords:	data management plan, datasets, FAIR data, models, reports, software		

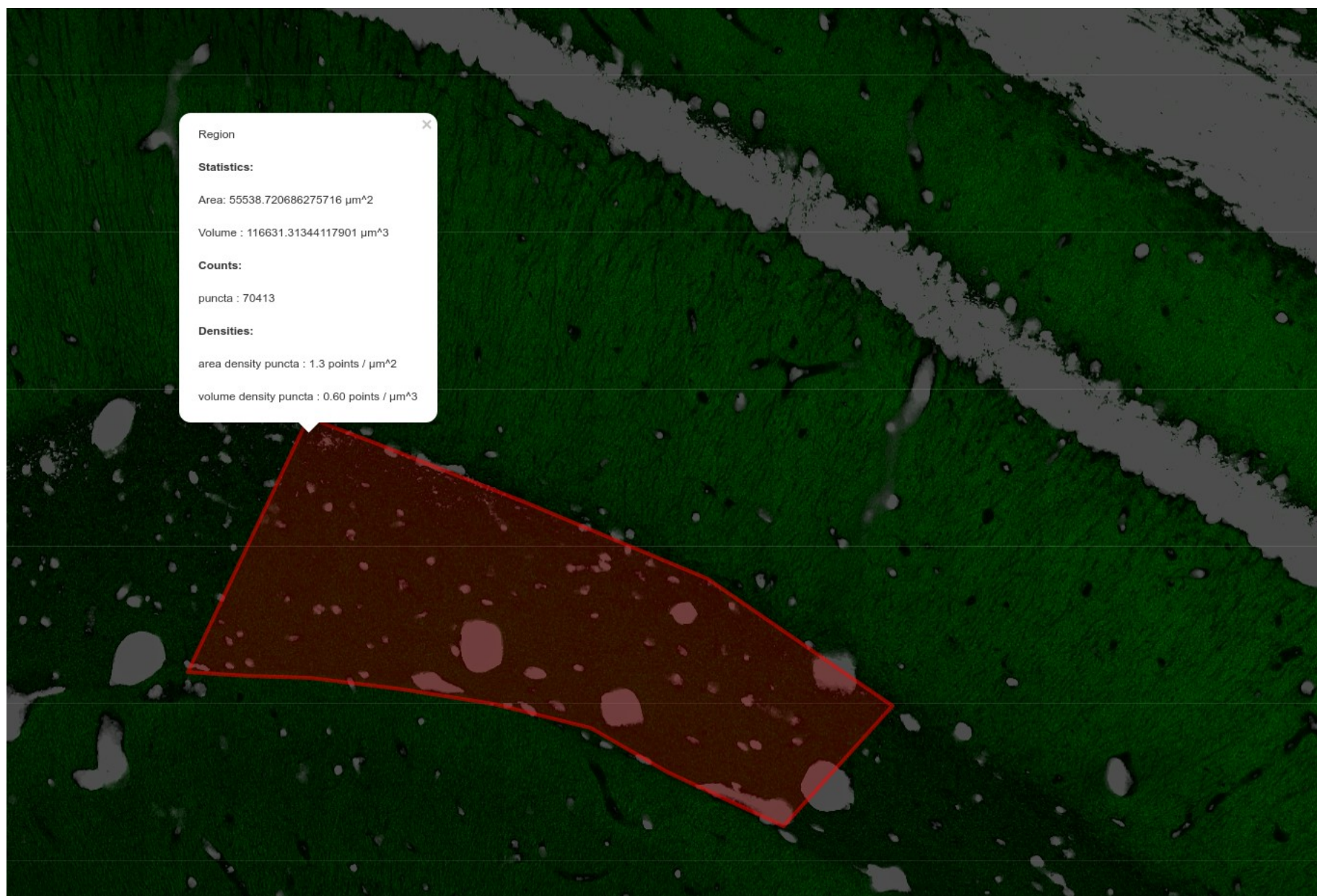


Figure 1: Graphical User Interface Detail from Multimap (SP1 Mouse Brain Organisation)

Targeted users/readers	HBP SPs
Contributing Package(s):	Work- 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) 31 July 2018 8Date for resubmission set out in the SGA1 Review Report)

Authors:	Pilar F. ROMERO, UPM (P68); Javier DEFELIPE (P68)
Compiling Editors:	Pilar F. ROMERO, UPM (P68);
Contributors:	<p>Rafael LUJAN, UCLM (P65)</p> <p>Ryuichi SHIGEMOTO, IST (P31)</p> <p>Simon BERNECHE, SIB (114)</p> <p>Antonino CATTANEO, SNS (P116)</p> <p>Enrico QUERUBINI, EBRI (P115)</p> <p>Michele MIGLIORE, CNR (P12)</p> <p>Douglas ARMSTRONG, UEDIN (P62)</p> <p>Javier DEFELIPE, UPM (P68)</p> <p>Huib MANSVELDER, VU (P113)</p> <p>Sten GRILLNER, KI (P37)</p> <p>Egidio D'ANGELO, UNIPV (P70)</p> <p>Tamás FREUND, Szabolcs KALI, IEM HAS (P30)</p> <p>Zoltan KISVARDAY, UoD (P15)</p> <p>Francisco CLASCA, UAM (P64)</p> <p>Ángel MERCHÁN, UPM (P68)</p> <p>Francesco PAVONE, LENS (P40)</p> <p>Leonardo SACCONI, INO, CNR (P12)</p> <p>Bruno WEBER, UZH (P75)</p> <p>Concha BIELZA, UPM (P68)</p> <p>Luis PASTOR, URJC (P69)</p>
SciTechCoord Review:	EPFL (P1) Jeff MULLER
Editorial Review:	EPFL (P1): Guy WILLIS, Annemieke MICHELS

Table of Contents

Introduction	6
SP1 Data Management Plan	6
1. Data summary	8
1.1 Purpose of data collection/generation	8
1.2 Relationship to SP1's Objectives for SGA1	8
1.3 Types and formats of data generated/collected	9
1.4 Data Re-use	9
1.5 Origin of the data	9
1.6 Expected size of the data:	11
1.7 Data utility	13
2. FAIR data	15
2.1 Data Curation	15
2.2 Making data findable, including provisions for metadata	16
2.2.1 Discoverability of data (metadata provision)	16
2.2.2 Identifiability of data and refer to standard identification mechanism. Do you make use of persistent and unique identifiers such as Digital Object Identifiers?	16
2.2.3 Naming conventions used	16
2.2.4 Approach used for search keywords	16
2.2.5 Approach for clear versioning	17
2.2.6 Standards for metadata creation (if any). If there are no standards in your discipline describe what metadata will be created and how	17
2.3 Making data openly accessible:	17
2.3.1 Data that will be made openly available	17
2.3.2 How the data will be made available	18
2.3.3 Methods or software tools needed to access the data	18
2.3.4 Data and associated metadata location, documentation and code needed	20
2.3.5 How access will be provided in case there are restrictions	20
2.4 Making data interoperable	20
2.4.1 Assess the interoperability of your data	20
2.4.2 Standard vocabulary used for all data types present in a given data set, to allow interdisciplinary interoperability	21
2.5 Increase data re-use (through clarifying licenses)	21
2.5.1 How the data will be licenced to permit the widest reuse possible	21
2.5.2 When the data will be made available for re-use	22
2.5.3 Re-use of the data produced and/or used in the project by third parties, in particular, after the end of the project	22
2.5.4 Data quality assurance processes	22
2.5.5 Length of time for which the data will remain re-usable	22
3. Allocation of resources	22
3.1 Costs estimation for making the data FAIR:	22
3.2 Responsibilities for data management:	23
3.3 Costs and potential value of long-term preservation:	23
4. Data security	24
5. Ethical aspects	24
6. Conclusion and Outlook	24
Annex 1: List of datasets, models and tools	25

Table of Figures

Figure 1: Graphical User Interface Detail from Multimap (SP1 Mouse Brain Organisation).....	2
Figure 2: From Gene to Behaviour.....	14
Figure 3: From SP1 data to HBP models and theories on the human brain.....	14

Table of Tables

Table 1: Component Details for SP1 Data Management Plan	6
Table 2: SP1 Objectives for SGA1	8
Table 3: Types and formats of data generated	9
Table 4: Data re-use	9
Table 5: Data class	10
Table 6: Brain regions.....	10
Table 7: Size of the data	11
Table 8: Methods and Software	18
Table 9: Licensing of data	21
Table 10: Privacy class	22

Introduction

This plan is based on the document *H2020 Programme Guidelines on FAIR Data Management in Horizon 2020* (Version 3.0, 26 July 2016). Each entry includes, among other information, the planned use of data in models; estimated date of delivery; timeline for curation and annotation; and a specification of the target quantity and quality. The plan also includes the mechanism and the periodicity of how the list of deliveries was updated during SGA1 in the Data Catalogue (see below).

A first version of this plan was produced in M18 (HBP-SGA1-SP1DMP-M18-v4) and updated in M23 (HBP-SGA1-SP1DMP-M23-v3.4). In M28, July 2018, the report has been improved and updated via this document as requested. Finally, this plan is in line with and linked to the current version of the HBP Data Management Plan (SGA1 Deliverable D11.3.2).

This plan includes an explicit list of data deliveries by SP1 in SGA1 and is composed of two sections: (i) general information common to all datasets, and (ii) specific information for each dataset (Annex 1: list of datasets)

Detailed information on the role and take up of the data acquired can be found in Annex 1 for each dataset listed as well as in the SP1 Data Catalogue.

This plan is complemented with the SP1 SGA1 Data Catalogue (see document SP1 Data Catalogue Addendum to SGA1 PPR M01-M24) currently including the datasets, as well as tools, reports and models, generated up to M23¹. The updated version of the Data Catalogue was released by M24 as an attachment to the SGA1 M1-M24 Project Periodic Report.

SP1 Data Management Plan

This data management plan (DMP) is for SP1 in the SGA1 phase of the HBP. It has been prepared following the guidance provided by the document *H2020 Programme Guidelines on FAIR Data Management in Horizon 2020* (Version 3.0, 26 July 2016). This implies that the DMP is a living document, and will be updated periodically. The first version produced was HBP-SGA1-SP1DMP-M18-v1.4, an updated version was submitted by M24 (HBP-SGA1-SP1DMP-M23-v3.4), and the current version is HBP-SGA1-SP1DMP-M23-v4.4.

The DMP is complemented with the Data Catalogue (available at <https://collab.humanbrainproject.eu/#/collab/5972/nav/105733> (Storage/SGA1/SP1 Data Catalogue), and also added to the Switch drive)).

As a number of the elements of the DMP are common to the whole HBP, for the sake of brevity, in places this DMP refers to the HBP Data Management Plan (SGA1 Deliverable D11.3.2, delivered on 16 June 2017), which is also a living document and a new version has been submitted in SGA1 M24. This document starts with information that is shared between all SP1 datasets, and then lists datasets produced by SP1, with fields describing information specific to those datasets.

Table 1: Component Details for SP1 Data Management Plan

	Main Meta Data	Comment/title
Component	1015	D1.5.3: Detailed plan of data usage and the impact of generated data on models
Component Type	Report	
Contact	T1.5.1 (DEFELIPE, Javier, F. ROMERO, Pilar)	

¹ M23: target month to submit the deliverables to the PCO according to its instructions

Latest Release	1/03/2018	
TRL	NA	
Location	https://collab.humanbrainproject.eu/#/collab/5972/nav/105733	Also shared with NIP
Maintenance	TBD	
Curation Status	NA	
Validation - QC	Yes	SP1 members, SP5, and SP11
Validation - Already existing users	Yes	SP1, SP2, SP4, SP5, SP6, SP10
Validation - Use in publications	No	
Access privacy	NA	
Access sharing	NA	
Access licence	NA	
URL to access component	https://collab.humanbrainproject.eu/#/collab/5972/nav/105733	
URL to component documentation	https://collab.humanbrainproject.eu/#/collab/5972/nav/105733	
URL to component usage documentation	https://collab.humanbrainproject.eu/#/collab/5972/nav/105733	
URL to dissemination material highlighting component		

HBP-SGA1-SP1DMP-M23-v4.4

Specifically, the SP1-DMP is composed of 7 main sections as follows:

- 1) Data summary: this section outlines the purpose of (i) data collection/generation and (ii) the software and models to be developed. The relation with the SP1 SGA1 objectives is also included. In addition, the information regarding type, formats, re-use, origin, expected size, and utility of the SP1 datasets is included.
- 2) FAIR data: this section outlines how to make data findable, accessible, interoperable, and reusable (FAIR) according to the document *H2020 Programme Guidelines* mentioned above.
- 3) Allocation of resources: this section explains the allocation of resources addressing estimated costs to make SP1 data FAIR, responsibilities of this DMP and the potential value of long term preservation.
- 4) Data security: data recovery as well as secure storage and transfer of data is described.
- 5) Ethical aspects: in this section, the status of the ethical issues is clarified referring to the DoA.
- 6) Other: other relevant information on the SP1 datasets
- 7) Annex 1: List of Datasets

Although this plan is mainly focused on data, the information concerning the IT tools and statistical models that have been — or are currently being — developed in the SGA1 for SP1 is also included in the above items.

The software packages developed in SP1 are also included in the HBP Software Catalogue located at the HBP Collaboratory: <https://collab.humanbrainproject.eu/#/collab/19/nav/2108>

1. Data summary

1.1 Purpose of data collection/generation

In general, SP1 data is collected to support modelling and analysis elsewhere in the HBP, particularly SP6 and SP4, and beyond. SP1 data are critical for internal HBP interactions. SP1 generates data for subcellular modelling, for neuronal model reconstruction and validation, for microcircuit model reconstruction and validation, for whole-brain model reconstruction and validation, and for databasing. We generate data of high granularity that are required for the simulations in SP6 and CDP2 and other SPs and CDPs, and do not exist elsewhere.

Data on the detailed morphology of individual neurons is needed to construct realistic models of neurons, which also requires information on ion channels and receptors expressed in the somatodendritic membrane. Electrophysiological data in terms of membrane properties on the same cells are needed to construct cell models that are as close as possible to their biological counterparts. Data on distributions of synapse types on dendrites and soma, both on individual neurons and throughout the brain is needed, to build realistic models of neuron types and circuit models. The focus in SP1 is to investigate the microcircuits, in four major areas of the brain, the hippocampus, neocortex, basal ganglia and cerebellum. SP1 provides strategic missing pieces required for the modelling efforts in SP6. Data is also collected at the level of the whole brain to link the subcircuit together starting from SGA1 but even more so in subsequent phases on the project. Section 1.7 and the detailed tables below provide more specific information about which datasets are used by whom. Proteomic and molecular interaction data are collected both by experiment and by curating public databases and the literature.

SP1 also develops software packages. The purposes of these packages are (i) to analyse morphological data, where domain knowledge is especially useful for developing software packages; (ii) to analyse protein-protein network structure, where the methods of clustering require domain knowledge; and (iii) to provide a framework to formalise protein-protein interactions in such a way that they may be incorporated easily into subcellular molecular models.

1.2 Relationship to SP1's Objectives for SGA1

All the datasets that SP1 expects to collect, as well as the software and models it has developed in SGA1 are directly linked to SP1's objectives in this project phase.

Table 2: SP1 Objectives for SGA1

SP1	SGA1 Objective
1a	Maps of the vasculature of the whole mouse brain.
1b	Whole-brain maps of different cellular types based on gene expression.
1c	Microcircuitry analysis, proteins and receptor distributions, fibre architecture in a specific large area brain region.
1d	Maps of cellular distributions, long-range axonal projections, and synaptic proteins; reconstructed morphologies of major neuron types.
1e	Whole-brain activation maps related to selected behaviours

1f	Spatial organisation principles in brain activation
1g	Functional maps of cortical activity during learning of the motor task after stroke during learning in the robotic platform

The specific relationship of each dataset, software, report or model with the SP1 objectives is displayed the description of each dataset in Annex 1: List of datasets. Some datasets also relate to objectives linked to other HBP Subprojects.

1.3 Types and formats of data generated/collected

We are generating 12 broad types of data, including software and models (see Table 3).

Table 3: Types and formats of data generated

Type	Formats
Image	tiff, jpg, png
Image stack	tiff, mp4
Electrophysiological recording	abf, brw, ,rsh, rsm, rsd, dha, tbk, spd
Morphological reconstruction of neuron	asc, xml, dat
Whole-cell current clamp recording	tsv
Point-clouds of coordinates	txt
Segmentation data	seg, xls
Parameters	csv
Molecular binding and state transition rules	ka
Bioinformatic meta-analysis	tsv, csv
Model	ipynb, py, ka
Software	py, cpp, java

Each type of data can be stored in one or more formats. In Section 2.2.3, we list the software corresponding to each format.

1.4 Data Re-use

Most of datasets are not reusing data, reflecting the focus of the subproject on data collection. Datasets in which data are being re-used include software datasets, which are developing existing code, and molecular curation datasets.

Table 4: Data re-use

Reused	Freq
Maybe	8
No	31
Yes	7

1.5 Origin of the data

The list of datasets (Annex 1) contains information for each dataset, including the data class (e.g. cellular, molecular or electrophysiological), text describing the specimen information and the brain region and subregion.

An analysis of the data class is shown below.

Table 5: Data class

Data class	Number of dataset
Cellular	16
Circuits	1
Electrophysiological	6
Model	1
Molecular	12
Other	3
Software	1
Software and models	1
Subcellular	3
Whole-brain activation maps	1
Whole-brain cell distributions	1

The largest class is "cellular", reflecting a number of tasks that are reconstructing morphologies.

The predominant experimental specimen is the C57/B6J mouse, at a variety of ages, though human postmortem tissue is also being collected in some datasets, and one dataset is collecting data from Wistar rats. Some datasets are partially derived from data in the literature, and the software datasets do not have any origin in this sense.

An initial analysis of the brain regions mentioned is shown below. Some datasets include information from more than one brain region, so the total number is greater than the number of datasets.

Table 6: Brain regions

Brain region	Number
basal ganglia	1
cerebellum	2
Cerebral cortex	1
cortex	3
forebrain	2
hippocampal formation	5
hippocampus	15
hypothalamus	1
motor cortex	1
n/a	1
neocortex	4
not applicable	1
somatosensory cortex	10
temporal cortex	1
thalamus	1
ventral midbrain	1
visual cortex	2
whole brain	2

Once data collection starts, these metadata will be collected as part of the data curation process (see Section 2.0).

1.6 Expected size of the data:

The expected size of the data is about 53 TB for 46 datasets. The expected size per each dataset is displayed below.

Table 7: Size of the data

Task	Dataset Title	Owner	Size (TB)
T1.1.1	Developing the integrated FIB/SEM and SDS-FRL immunoelectron microscopy technique.	Rafael Luján & Riuichi Shigemoto	2.0e-02
T1.1.1	Nanoscale measurements of distribution of individual receptors and ion channels in cortical neurons.	Rafael Luján & Riuichi Shigemoto.	2.0e-02
T1.1.2	Generation of new intrabodies / antibody fragments	Antonino Cattaneo, Giovanni Meli	1.0e-06
T1.1.2	IACT antibody fragments for imaging	Antonino Cattaneo, Giovanni Meli	1.0e-03
T1.1.3	Association (co-clustering) of receptors and their effector ion channels in different neuronal compartments.	Rafael Luján & Riuichi Shigemoto	2.0e-02
T1.1.3	GluA2, GluA3 and GluN1 in CA1	Ryuichi Shigemoto	1.0e-02
T1.1.4	Electrophysiological data-hippocampus	Enrico Cherubini	1.0e-03
T1.1.5	K channel kinetic and activity in a model neuron	Simon Bernèche	1.0e-04
T1.1.6	Curated list of synaptic protein-protein interactions	Oksana Sorokina	1.0e-03
T1.1.6	Computational, dynamic model of LTP and LTD in a wild type Schaffer Collateral synapse	David Sterratt	1.0e-03
T1.1.6	KappaNEURON software package	David Sterratt	1.0e-03
T1.1.6	A mapping of computational models of synapses to proteins	David Sterratt	1.0e-03
T1.1.7	Subcellular proteomics dataset - hippocampus	Antonino Cattaneo	2.0e-03
T1.1.7	Synaptic Plasticity dataset - hippocampus	Enrico Cherubini	1.0e-01
T1.1.7	Extending coverage of published data	Douglas Armstrong, Antonino Cattaneo	1.0e-03
T1.1.7	Genetic mapping to single cell profiles	Douglas Armstrong, Antonino Cattaneo	1.0e-03
T1.1.7	Integration of functional data into synapse models	Douglas Armstrong, Antonino Cattaneo	1.0e-03

Task	Dataset Title	Owner	Size (TB)
T1.2.1	3D reconstructions mouse hippocampus	Javier DeFelipe	5.0e-03
T1.2.1	3D reconstructions rat hippocampus	Javier DeFelipe	5.0e-03
T1.2.1	3D reconstructions pyramidal neurons human cortex	Javier DeFelipe	5.0e-03
T1.2.1	3D reconstructions human hippocampus	Javier DeFelipe	5.0e-03
T1.2.1	3D reconstructions pyramidal neurons mouse cortex	Javier DeFelipe	5.0e-03
T1.2.2	human neurons with matching Ephys	Mansvelder	0.0e+00
T1.2.3	The striatal microcircuit	Sten Grillner	5.0e-03
T1.2.4	Electrophysiological data cerebellum	Egidio D'Angelo	1.0e-03
T1.2.5	Morphological database of major cell types of the mouse hippocampus	Szabolcs Káli	1.0e-01
T1.2.5	Electrophysiological database of major cell types of the mouse hippocampus	Szabolcs Káli	1.0e-03
T1.2.5	Morphological reconstructions of mouse hippocampal neurons filled in vivo	Szabolcs Káli	1.0e-02
T1.2.5	Physiological characterisation of mouse hippocampal neurons recorded in vivo	Szabolcs Káli	5.0e-03
T1.2.6	Database of synaptic physiological properties in the mouse hippocampus	Szabolcs Káli	1.0e-04
T1.2.7	GABAergic neuron subtypes	Zoltán Kisvárdy	1.0e+00
T1.2.8	3D digital Reconstructions of individual thalamocortical neurons	Franciscp Clasca (UAM)	1.0e-02
T1.2.9	Densities and 3D distributions of synapses using FIB/SEM imaging in the human neocortex (Temporal cortex, T2)	MERCHÁN PÉREZ, Ángel	5.0e-03
T1.2.9	Densities and 3D distributions of synapses in the human hippocampus	MERCHÁN PÉREZ, Ángel	5.0e-03
T1.2.9	Densities and 3D distributions of synapses in the mouse neocortex	Angel Merchan Perez	5.0e-03
T1.2.9	Densities and 3D distributions of synapses in the mouse hippocampus (CA1)	Angel Merchan Perez	5.0e-03
T1.2.9	Immunocytochemical detection of excitatory and inhibitory terminals in the mouse somatosensory cortex by confocal microscopy	Alberto Muñoz	5.0e-03
T1.2.9	Immunocytochemical detection of excitatory and inhibitory terminals in the mouse hippocampus (CA1) by confocal microscopy	Alberto Muñoz	5.0e-03
T1.3.1	Whole brain interneuron distributions	Ludovico Silvestri	4.1e+01
T1.3.2	Wide-field imaging of cortical activity during motor learning	Anna Letizia Allegra Mascaro	5.0e-04

Task	Dataset Title	Owner	Size (TB)
T1.3.2	Wide-field imaging of cortical activity one month after stroke and rehabilitation	Anna Letizia Allegra Mascaro	1.1e+01
T1.3.2	Wide-field imaging of cortical activity one month after stroke	Anna Letizia Allegra Mascaro	5.0e-04
T1.3.4	Whole brain maps of resting state brain activation	Ludovico Silvestri	1.1e+01
T1.3.5	3D image of the vascular system of the mouse brain	Velizar Efremov	1.3e-02
T1.3.5	Model of intravascular and tissue partial pressure of oxygen	Velizar Efremov	0.0e+00
T1.3.5	3D reconstruction of the vascular system of the mouse brain	Velizar Efremov	5.0e-04
T1.4.1	Analysis of micro-anatomical data	Concha Bielza	0.0e+00
T1.4.2	Software PyramidalExplorer 1.2 for early exploratory analysis techniques for morphological data.	Universidad Rey Juan Carlos	5.0e-02

1.7 Data utility

SP1, in agreement with the modelling pipeline of the HBP, will focus on four major brain circuits: neocortex (including the thalamocortical system), hippocampus, basal ganglia and cerebellum. The work plan will focus on fundamental questions, coordinated at the HBP level, on structural organisation, neuronal activity, microcircuit dynamics, synaptic plasticity and neuromodulation required to fuel and complement modelling and theory. The data will serve for both model reconstruction and validation in virtuous feed-back cycles between simulations and experimental recordings (data generated models and simulations instruct hypothesis-driven data sampling). The data will also be used to obtain high-quality integrative maps and circuits of the mouse brain at the functional and anatomical levels integrating SP5 databasing and brain atlasing with molecular, morphological and functional data. An analysis that extends from gene to behaviour needs to be based on animal data combined with human experimentation (see Figure 2 and Figure 3).

The particular role of SP1 is to supply strategic information, not yet available, on the molecular, cellular and synaptic level that is needed in particular for the simulations/models of SP6 and SP4 and also other SPs. The simulations of SP6 are of course based predominantly on experimental data from the scientific literature or through e.g. Allen Brain. To supply still missing, specific detailed data required for both the subcellular and the large microcircuit is the task of SP1. It is important to understand that the granularity of the information required for the detailed SP6 simulation cannot be met by general databases such as the Allen Brain, although they contribute importantly to the overall knowledge of these circuits.

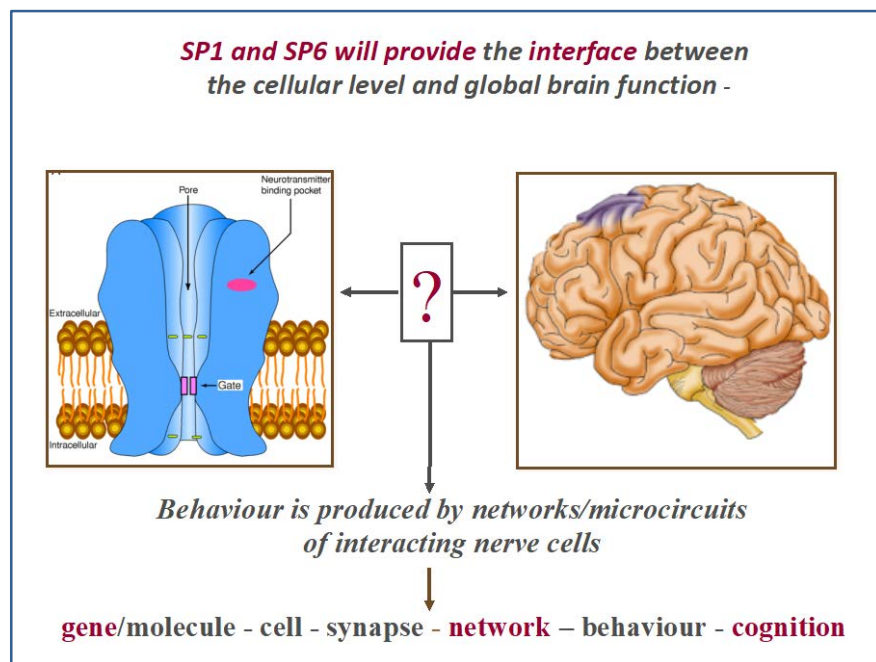


Figure 2: From Gene to Behaviour

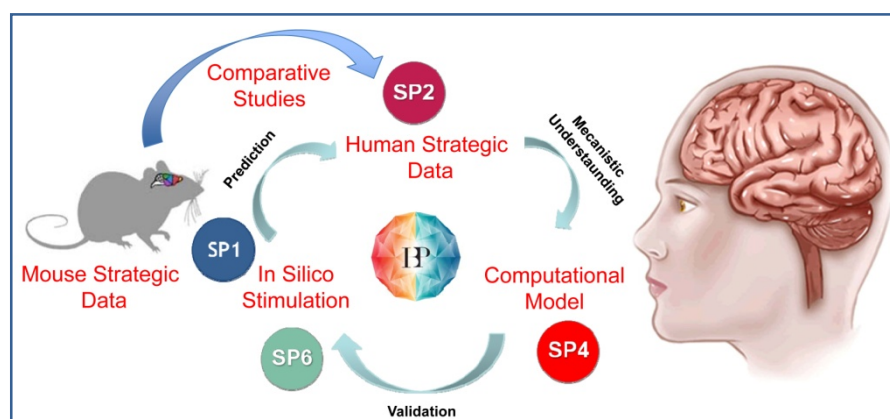


Figure 3: From SP1 data to HBP models and theories on the human brain

Each WP and task in SP1 maps on to the needs of specific tasks in SP6 or SP4 or other SPs as specified in detail in the “*data catalogue*” available at <https://collab.humanbrainproject.eu/#/collab/5972/nav/105733> (Storage/SGA1/SP1 Data Catalogue), and also added to the Switch drive.

- WP 1.1 “*Subcellular and molecular data*” provides strategic information that primarily is critical for both WP6.1. Subcellular and Molecular modelling tasks 6.1.1/1.2/1.3 and WP6.2 (6.2.1 - 6.2.5) and also T 4.1.1. WP1.2
- WP 1.2 *Cell and Microcircuitry: neocortex, hippocampus, basal ganglia and cerebellum*. This WP provides strategic data onto WP 6.2 and tasks 6.2.2 - 6.2.5 which provides models for the four microcircuits, and also to CDP2
- WP1.3 *Whole brain*, this WP delivers data to T6.2.3, T6.2.6, T 4.1.4, T 4.4.5, T 4.4, T 4.5.1, T 4.5.2, T10.1.3
- WP 1.4 “*Microanatomical, structural and functional integration of data in brain circuits*” provides input to in particular T6.2.2, T6.2.3, T6.2.7 and CDP2
- WP1.5 “*Comparative study of cells and microcircuits in the rodent and human brain*” have supported T.4.1, T.6.2.2, T6.2.4

SP1 data collection, organisation and utility are in line with the data objectives for HBP displayed in the HBP DMP, the main purposes of which can be summarised as follows:

- *Collection* - collect data experimentally to satisfy a scientific use case.
- *Organisation* - aggregation and curation for the purpose of making data more readily
- Reusable
- *Model building* - SP1 data are required for developing detailed cellular models of individual neuron types to be used in e.g. microcircuit simulation in SP6.
- Model validation - SP1 data is used to validate existing models.
- Model exploitation - brain-inspired models are used for a variety of use cases, including but not limited to:
 - validating data collection
 - performing *in silico* experiments
 - configuring neuromorphic hardware
 - controlling virtual and real robots
- Tool development - data used for the development of software tools.

The specific utility of the SP1 data is displayed in each of the dataset description in Annex 1: List of datasets). We have indicated the utility to HBP partners and to the wider world.

2. FAIR data

2.1 Data Curation

SP1 Partners and SP5 are jointly responsible for data curation. The curation process can be summarised as follows:

- 1) SP1 Partners submit data and metadata to the HBP Collaboratory (for smaller amounts of data) or the CSCS (SP7) data containers (for larger amounts).
- 2) Basic metadata are organised and stored in the Data Workbench.
- 3) The SP5 Tier 1 curation team validates basic metadata entries for completeness.
- 4) Once metadata curation has been finished for a given dataset, SP5 will know whether the data are suitable for more specialized curation (one of the Tier 2 types).
 - a) SP5 Tier 2A curation teams validate spatial metadata for accuracy and completeness. Spatial coordinates will be assigned in Mouse Brain Atlas space to data, where possible.
 - b) The SP5 Tier 2B curation team validates neural activity data for accuracy and completeness.
- 5) After validation, all metadata are organised and stored in the Knowledge Graph
- 6) Data in the Knowledge Graph are available for query, viewing and analysis through platform services.
- 7) Spatial data are used for displaying data in atlas space.

SP5 estimates that, depending on the demand for and the depth of curation, Tier 1, curation will take 1-2 weeks at present and Tier 2 will take between 2 days and 3 weeks. SP5 estimates the whole curation process to take between 1 and 5 weeks with the current workflow.

In more detail:

The curation team will be led by SP5. When everyone is informed by SP1, SP5 will first have a one-to-one call with the contact person for the group/lab/unit to clarify. SP5 will then ask for a video-conference or Skype call to walk through the data that have been uploaded in the Collaboratory or container. Each group decides how many people will participate. From the curation team, there will be three primary participants in the curation session. Others may also participate - but these three curation team members will be responsible for leading the curation session. SP5 will send out information on any preparation needed, including the testing of an online application for entering metadata. The curation team will ensure that this application meets the needs of all data categories and hierarchies. When metadata are assigned, the complete list will be delivered back to the neuroscience groups for a final check. It will be SP5's responsibility to make the metadata searchable as soon as possible.

Data access: the process outlined above does not result directly in any sharing of data. Before sharing, the groups will be given the opportunity to choose a sharing license.

Embargo: after a license has been chosen, there may still be a need for an embargo period for some data. Details will be worked out taking into account requirements from the European Commission.

2.2 Making data findable, including provisions for metadata

2.2.1 Discoverability of data (metadata provision)

We will supply metadata to SP5 who will then enter it into the Knowledge Graph, to allow us to tag datasets with metadata. This is part of the Tier 1 curation process. <http://interlex.org/>.

2.2.2 Identifiability of data and refer to standard identification mechanism. Do you make use of persistent and unique identifiers such as Digital Object Identifiers?

When data is made public, we will endeavour to provide a DOI for it. The HMP DMP states: "It is a goal to enable data sharing with publicly released datasets given immutable, unique identifiers. However, the details of this capability will vary from storage service to storage service." This item will be discussed with SP5 and SP11.

2.2.3 Naming conventions used

As per the HBP SP11 DMP (SGA1 D11.3.2), file naming conventions are generally not required for data handled by the HBP. Because of the diverse nature of the data contained in SP1, it would be difficult to write a convention. However, it is strongly recommended that, where naming conventions are important for data reuse or interpretation, they should be adequately documented in a file named README, provided with the data.

Any naming conventions will also be documented in the Tier 1 metadata during the curation process.

2.2.4 Approach used for search keywords

The searchability of SP1 data will be assured by following the general approach described in the HBP SP11 DMP (Section 4.1.1) that is as follows:

Data can be discovered through the Web-based user interfaces provided by the SP5 NIP. These interfaces will allow discovery by browsing or by search. Generally speaking, the Access Control Lists of the Collaboratory will be respected to allow user control of privacy settings. In the places where there are caveats to this behaviour, as may be the case in some FENIX data repositories, this will be clearly indicated in the user service documentation. Data will be searchable using SP5 search tools integrated into the HBP Collaboratory. This search will honour Collab membership ACLs in the return of search results. The search will be available on the following content fields:

- Collab metadata (name and description)
- Collab app content (for Collaboratory provided apps, where the app requests indexing)
- Platform app content (where enabled by Platform apps)
- Software Catalogue entries (name, description and tag fields)
- Dataset metadata as defined the by the HBP minimum metadata specifications developed in SP5

2.2.5 *Approach for clear versioning*

The approach for versioning needs to be discussed with SP5.

2.2.6 *Standards for metadata creation (if any). If there are no standards in your discipline describe what metadata will be created and how*

As shown in the Data Summary, we are dealing with diverse types and classes of data. The HBP DMP proposes having a “minimal” or “basic” metadata scheme, common to all datasets, which will be supplemented by domain-specific metadata. The Tier 1 curation undertaken in collaboration with SP5 will collect the basic metadata. The Tier 2 curation will collect domain-specific metadata, such as spatial location.

We have already collected the basic metadata as part of this DMP. We have yet to agree with SP5 which standards to use for domain-specific metadata. As expanded on in Section 2.3, where possible we will use existing ontologies or lexicons to specify items clearly.

2.3 Making data openly accessible:

2.3.1 *Data that will be made openly available*

The SP1 DMP will follow the statement concerning the European policy on Open Data contained in the HBP FPA as a guiding principle of the HBP’s Data Governance Policy and will be respected in all policy and data repository service implementations, as confirmed in the HBP SP11 DMP (SGA1 D11.3.2 Section 4.2.1).

According to the HBP SP11 DMP, in addition to inaccessibility of data required by compliance with European and National legislation, certain classes of data may remain inaccessible for various other reasons. Animal data produced in the HBP may remain temporarily inaccessible to users outside the HBP if:

- Data is a critical competitive dependency for a pending publication.

Human data produced in the HBP may remain temporarily inaccessible to users outside the HBP if:

- Data is a critical competitive dependency for a pending publication.

Human data produced in the HBP may remain permanently inaccessible to users outside the HBP if:

- Data was not collected with sufficient releases to allow sharing outside the HBP.
- Data might be easily re-identifiable when combined with current technology and other readily available datasets.

(See Section 4.2.1 in the HBP SP11 DMP for further information)

2.3.2 *How the data will be made available*

As for the item above, the SP1 DMP will follow the HBP SP11 DMP with regard to accessing data (see HBP DMP, Section 4.2.2 for further information).

2.3.3 *Methods or software tools needed to access the data*

Methods and software to access the data as well as the relevant documentation as describe in the following table:

Table 8: Methods and Software

Extension	Format Name	Documentation URL	Vendor	Software to open format
tiff	Tagged Image File Format	https://en.wikipedia.org/wiki/Tagged_Image_File_Format	Open standard	ImageJ, gimp, many open source libraries
txt	Text file	http://pubs.opengroup.org/onlinepubs/9699919799/basedefs/V1_chap03.html#tag_03_397	Open standard	Many text editors, genral purpose packages (e.g. Python)
jpeg	Joint Photographic Experts Group	https://en.wikipedia.org/wiki/JPEG	Open standard	ImageJ, gimp, many open source libraries
mp4	MPEG-4 Part 14	https://en.wikipedia.org/wiki/MPEG-4_Part_14	Open standard	Many libraries, and packages, e.g. libxml, R XML package
mat	Matlab binary format	https://www.mathworks.com/help/pdf_doc/matlab/matfile_format.pdf	Mathworks	Matlab, R, Octave
xls	Microsoft Excel worksheet sheet (97-2003)	https://msdn.microsoft.com/en-us/library/gg134032.aspx	Microsoft	Microsoft Excel, Libreoffice, R xlsconnect package
dat	NeuroLucida binary format	http://www.mbfbioscience.com/help/si11/Content/About/FileFormats.htm	MBF Bioscience	NeuroConstruct (http://www.neuroconstruct.org/docs/import.html#NeuroLucida) can import ASCII (*.asc) format V3 files
abf	Axon Binary Format	https://moleculardevices.app.box.com/s/iisgk109swvcrwtmy3p13dn3r0vyvasr	Molecular Devices	Abfload (Matlab script; https://uk.mathworks.com/matlabcentral/fileexchange/6190-abfload)
brw	BrainWave	http://www.3brain.com/websites/3brain/downloads/BrainWave-Userguide.pdf	3Brain	http://www.3brain.com/downloads.html#software-and-utilities

Extension	Format Name	Documentation URL	Vendor	Software to open format
mod	nmodl	https://www.neuron.yale.edu/neuron/static/docs/help/neuron/nmodl/nmodl.html	Duke, Yale, BBP	https://www.neuron.yale.edu/neuron/static/docs/help/neuron/nmodl/nmodl.html#ModelDescriptionLanguage
ipynb	IPython Notebook	https://en.wikipedia.org/wiki/IPython	Open source software	Jupyter notebook
rsh	BrainVision	http://www.scimedia.com/files/support/download/ultima/	SciMedia	BV_Ana (http://www.scimedia.com/files/support/download/ultima/)
rsm	BrainVision	http://www.scimedia.com/files/support/download/ultima/	SciMedia	BV_Ana (http://www.scimedia.com/files/support/download/ultima/)
rsd	BrainVision	http://www.scimedia.com/files/support/download/ultima/	SciMedia	BV_Ana (http://www.scimedia.com/files/support/download/ultima/)
dha	BrainVision or Matlab	http://www.scimedia.com/files/support/download/micam01/	SciMedia	BV_Ana (http://www.scimedia.com/files/support/download/micam01/)
tbk	Tucker-Davis Technologies	http://www.tdt.com/files/manuals/OpenEx_User_Supplement_Syn.pdf	Tucker-Davis	OpenEx Software (http://www.tdt.com/openex.html)
spd	SpikeTrain	http://www.neurasmus.com/spiketrain/SpikeTrainUserGuideV1_08.pdf	Neurasmus	SpikeTrain (http://www.neurasmus.com/spiketrain.php)
png	Portable Network Graphic	https://en.wikipedia.org/wiki/Portable_Network_Graphics	Open standard	ImageJ, gimp, many open source libraries
xml	Extensible markup language	https://en.wikipedia.org/wiki/XML	Open standard	Many libraries, and packages, e.g. libxml, R XML package
docx	Microsoft Office XML document	https://en.wikipedia.org/wiki/Microsoft_Office_XML_formats	Microsoft	Microsoft Word, Libreoffice Writer
seg	Espina	http://cajalbbp.cesvima.upm.es/espina/	Universidad Rey Juan Carlos	Espina (http://cajalbbp.cesvima.upm.es/espina/)
csv	ASCII text as comma-separated values	https://en.wikipedia.org/wiki/Comma-separated_values	Open standard	Microsoft Excel, Libreoffice Calc, many general purpose packages (e.g. Python, R, Matlab)
tsv	Tab-Separated Values	https://en.wikipedia.org/wiki/Tab-separated_values	Open standard	Microsoft Excel, Libreoffice Calc, many general purpose packages (e.g. Python, R, Matlab)

Extension	Format Name	Documentation URL	Vendor	Software to open format
ka	Kappa file (SpatialKappa dialect)	https://github.com/lptolik/SpatialKappa/raw/master/docs/manual/SpatialKappaManual-v2.1.0.pdf	Open standard	SpatialKappa (https://github.com/lptolik/SpatialKappa), KappaNEURON (https://github.com/davidcsterratt/KappaNEURON)
gml	Graph Modelling Language	http://www.fim.uni-passau.de/index.php?id=17297&L=1	Open standard	Gephi (https://gephi.org/)

This needs to be documented in the Tier 1 metadata “during the curation process”. Further information will be provided in the next version of this plan.

2.3.4 *Data and associated metadata location, documentation and code needed*

SP1 data will initially exist on laboratory servers. As described in Section 2.1, it will then be moved either to the HBP Collaboratory (for smaller datasets, in the GB size range) or the containers of the CSCS servers (SP7) following the approach set up. In addition, the data may be mirrored on subject-area or institutional repositories.

The metadata will exist in the HBP Knowledge Graph, having been curated by SP5, as described in Section 2.1.

Documentation will be included with the datasets, usually in the form of a README file.

Code in the form of software packages will be deposited in source control repositories, such as GitHub or Launchpad. Code in the form of analysis or model scripts will be deposited with the associated dataset or model. Documentation for software packages should be included with the code.

The SP1 DMP data list will provide concrete data status updates and provide downloadable links to the location of data, as well as the documentation for each respective data set, as available.

2.3.5 *How access will be provided in case there are restrictions*

Any restrictions on access to SP1 data need to be documented in the Tier 1 metadata “during the curation process”. The classes of restriction specified in the SP1 DMP are as follows:

- privacy (e.g. Human data)
- very large file size (e.g. high-resolution images)
- a publication embargo
- other

More details will be provided in the next version of this DMP.

2.4 Making data interoperable

2.4.1 *Assess the interoperability of your data*

There is a common approach for Tier 1 and 2 metadata, based on the formats described above.

The Tier 2a curation, which anchors data in the Brain Atlas, will allow data interoperability.

Regarding vocabularies, we will work with the HBP Ontology Definition Team (Section 4.3.2 of HBP DMP) to determine which existing ontologies to use or which new ones are needed. In the meantime, we will use Interlex (<http://interlex.org>) to identify Brain Regions, Cell Types and Techniques.

2.4.2 *Standard vocabulary used for all data types present in a given data set, to allow inter-disciplinary interoperability*

Much of our data is images or numerical (e.g. electrophysiology recordings) and therefore standard vocabularies are probably not so relevant in our case.

To identify genes in our molecular data, we will use standard gene names, as defined by HGNC (<http://www.genenames.org>) and the Mouse Genome Informatics database (<http://www.informatics.jax.org/>), and federated by the Entrez Global Query Cross-Database Search System (<https://www.ncbi.nlm.nih.gov/>). We are exploring which are the best vocabularies to use for molecules. Work in SGA1 to find a suitable ontology to describe molecules used in models and to map them to genes suggests that such an ontology does not exist. Consistent use of gene identifiers allows us to make use of resources such as OMIM (diseases) and gene ontologies. We will provide mappings from Human to Mouse genes.

2.5 Increase data re-use (through clarifying licenses)

2.5.1 *How the data will be licenced to permit the widest reuse possible*

The HBP SP11 DMP states that "...the HBP strongly encourages public release of any and all reusable experimental data. However, the understanding of the importance and career value for individual researchers is expected to grow slowly outside consortia such as the HBP. As a result, data licences will be chosen by the data providers (both inside and outside the HBP) primarily, selecting from a subset of Creative Commons licenses." It goes on to suggest seven Creative Commons licences. We have suggested these to SP1 Partners, along with an "another" option.

Table 9: Licensing of data

Data licence type	Freq
All rights reserved, Copyright	2
Attribution NonCommercial ShareAlike 4.0 International	4
BY - Attribution alone	2
BY-NC - Attribution + Non-commercial	19
BY-NC- ND - Attribution + Non-commercial + No Derivatives	5
BY-NC-SA - Attribution + Non-commercial + ShareAlike	5
BY-SA - Attribution + ShareAlike	2
CC0 - Freeing content globally without restrictions	1
GPL3	1
MIT	1
We need to match BIOGRID, IntAct and DIP terms & licences to CC licenses	4

A total of 40 datasets are to be licenced under one of these CC licences, most of them under BY-NC, 1 software package is released under GPL3 and the remaining under other licences. The

ramifications of choosing a particular licence took some time to work though, so we planned to have a discussion on this with SP11, to be in line with the general HBP DMP.

2.5.2 *When the data will be made available for re-use*

See “RELEASES” section of each dataset in Annex 1 for expected availability of data and embargo information.

2.5.3 *Re-use of the data produced and/or used in the project by third parties, in particular, after the end of the project*

Data will be re-useable by third parties after the Project, subject to privacy issues and reasonable publication embargoes. Each dataset indicates the privacy class. There may be issues concerning reuse of Human Research data, but we have not yet explored the issues in the datasets marked as being Human Research.

Table 10: Privacy class

Privacy class	Number of datasets
Animal Research	32
Human Research	6
No privacy constraints	7

2.5.4 *Data quality assurance processes*

Each lab has its own quality assurance mechanisms (see per-dataset notes in Annex 1). In general, SP1 data are also of interest in its own right, and will therefore be presented in journal submissions and subject to the usual scientific peer review process. The curation process will encourage further checking of data by producers. Sharing data with HBP Partners also provides a form of peer review of the data.

2.5.5 *Length of time for which the data will remain re-usable*

We understand that reusability involves a commitment to make sure that software is supported to use the files. Most of the formats that we use are open standards (e.g. tiff, csv), which will be readable for the foreseeable future. A number of the proprietary formats have open-source readers available, hosted on sites that are likely to remain live for the foreseeable future (for example, the abfload Matlab script to read abf files). The only format that is developed in-house is the Espina seg format. We can only guarantee that this software will be readable while there are funds to maintain the software, i.e. for the duration of the HBP grant. However, Espina is freely-downloadable, and should developments in operating systems or compilers make it impossible or hard to compile from source, it would be possible to run in a Virtual machine.

3. Allocation of resources

3.1 Costs estimation for making the data FAIR:

We estimate that the cost of the extra work SP1 Partners need to make our data FAIR is 2-5 person-days on average for each dataset. This work comprises transferring data, helping SP5 with

curation, contributing to the DMP and writing better documentation, but it does not include the time SP5 partners will spend on curation or that SP7 partners will spend on infrastructure. Multiplied by the number of datasets (46), this leads to an estimate of 90-225 person days, i.e. 4.5-11.5 person-months. We will update this estimate once we have had more experience of the curation process.

3.2 Responsibilities for data management:

- SP1 partners are responsible for:
 - Producing the datasets
 - Documenting the datasets in line with SP1 and HBP standards
 - Uploading the data to HBP servers (either the Collaboratory or CSCS data buckets)
 - Obtaining necessary ethical approvals from the relevant national ethics authority
 - Working with SP5 to provide metadata for curation
- SP1 management is responsible for:
 - Maintaining the SP1 data management plan
 - Maintaining the list of SP1 datasets, checking that all links are accessible
 - Implementing HBP-wide data management policies contained in the HBP DMP in SP1
 - Where specific SP1 policies are required, deciding on SP1-wide policies or recommendations for data management, in collaboration with SP1 and SP11 partners
- SP5 is responsible for:
 - Assisting with the data curation process, including entering metadata in the Knowledge Graph
- SP11 is responsible for:
 - Drawing up the overall HBP DMP
 - Providing infrastructure to store task-specific DMP information, and generate reports from it, as requested by SP1 and other subprojects
- SP12 is responsible for:
 - Surveying SP1 partners to check whether their datasets are compliant with ethical issues as set out in the developing [SGA2 Data Policy Manual](#) written by the Data Governance Working Group

3.3 Costs and potential value of long-term preservation:

SP1 Partners do not pay directly for the costs of data preservation on HBP servers.

It is difficult to quantify the value of the data in monetary terms, though it might be reasonable to assign to the data a cost based on how much it cost to generate - in which case, the value of the data would be a sizeable fraction of the money awarded to SP1 over the course of the HBP.

The questions concerning potential uses of the data show the value in terms of utility to others inside and out with the Project.

4. Data security

When the data is on laboratory servers, individual Partners are responsible for the security of the data, subject to the regulations of their institutions. Once the data has been transferred to HBP servers (Collaboratory or CSCS data buckets) then HBP policies, as described in Section 6 of the HBP DMP, apply.

5. Ethical aspects

The SGA1 DoA covers ethical issues. Within the list of datasets, we have provided the national ethics approval authority and corresponding ID.

6. Conclusion and Outlook

The SP1 Data Management Plan has been drawn up as a key element of good data management, according to the document *H2020 Programme Guidelines on FAIR Data Management in Horizon 2020* (Version 3.0, 26 July 2016). This DMP describes the data management life cycle for the data generated by SP1, as well as the utility of this data for modelling purposes. In addition, the DMP describes how SP1 should organize its datasets, tools and models generated internally and so facilitate further use of its outputs by other SPs.

The SP1 DMP has been adapted to the new work plan proposed for the next project phase, the SGA2, to be implemented and will continue throughout the project.

Annex 1: List of datasets, models and tools

The list of data sets (see below) will be added to this document as a pdf document generated from the excel spread sheet '200718 SP1 SGA1 Data Management Plan Information,xls'

T1.1.1: Developing the integrated FIB/SEM and SDS-FRL immunoelectron microscopy technique

T1.1.1: Nanoscale measurements of distribution of individual receptors and ion channels in cortical neurons

T1.1.2: Generation of new intrabodies / antibody fragments

T1.1.2: IACT antibody fragments for imaging

T1.1.3: Association (co-clustering) of receptors and their effector ion channels in different neuronal compartments.

T1.1.3: GluA2, GluA3 and GluN1 in CA1

T1.1.4: Electrophysiological data-hippocampus

T1.1.5: K channel kinetic and activity in a model neuron

T1.1.6: Curated list of synaptic protein-protein interactions

T1.1.6: Computational, dynamic model of LTP and LTD in a wild type Schaffer Collateral synapse

T1.1.6: KappaNEURON software package

T1.1.6: A mapping of computational models of synapses to proteins

T1.1.7: Subcellular proteomics dataset - hippocampus

T1.1.7: Synaptic Plasticity dataset - hippocampus

T1.2.1: 3D reconstructions mouse hippocampus

T1.2.1: 3D reconstructions rat hippocampus

T1.2.1: 3D reconstructions pyramidal neurons human cortex

T1.2.1: 3D reconstructions human hippocampus

T1.2.1: 3D reconstructions pyramidal neurons mouse cortex

T1.2.2: human neurons with matching Ephys

T1.2.3: The striatal microcircuit

T1.2.4: Electrophysiological data cerebellum

T1.2.5: Morphological database of major cell types of the mouse hippocampus

T1.2.5: Electrophysiological database of major cell types of the mouse hippocampus

T1.2.5: Morphological reconstructions of mouse hippocampal neurons filled in vivo

T1.2.5: Physiological characterisation of mouse hippocampal neurons recorded in vivo

T1.2.6: Database of synaptic physiological properties in the mouse hippocampus

T1.2.7: GABAergic neuron subtypes

T1.2.8: 3D digital Reconstructions of individual thalamocortical neurons

T1.2.9: Densities and 3D distributions of synapses using FIB/SEM imaging in the human neocortex (Temporal cortex, T2)

T1.2.9: Densities and 3D distributions of synapses in the human hippocampus

T1.2.9: Densities and 3D distributions of synapses in the mouse neocortex

T1.2.9: Densities and 3D distributions of synapses in the mouse hippocampus (CA1)

T1.2.9: Immunocytochemical detection of excitatory and inhibitory terminals in the mouse somatosensory cortex by confocal microscopy

T1.2.9: Immunocytochemical detection of excitatory and inhibitory terminals in the mouse hippocampus (CA1) by confocal microscopy

T1.3.1: Whole brain interneuron distributions

T1.3.2: Wide-field imaging of cortical activity during motor learning

T1.3.2: Wide-field imaging of cortical activity one month after stroke and rehabilitation

T1.3.3: Synthetic images for machine learning

T1.3.4: Whole brain maps of resting state brain activation

T1.3.5: 3D image of the vascular system of the mouse brain

T1.3.5: Model of intravascular and tissue partial pressure of oxygen

T1.3.5: 3D reconstruction of the vascular system of the mouse brain

T1.4.1: Analysis of micro-anatomical data

T1.4.2: Software PyramidalExplorer 1.2 for early exploratory analysis techniques for morphological data.

T1.1.1: Developing the integrated FIB/SEM and SDS-FRL immunoelectron microscopy technique. (ID: 652)**Dataset Owner:** Rafael Luján, Riuchi Shigemoto < Rafael.Lujan@uclm.es > (UCLM)**DATA SUMMARY****Purpose of the data collection/generation**

The purpose is to 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. For that purpose, we will develop and integrate MATLAB-based software for the analyses of clustering of gold particles for receptors and ion channels on replica surface in the somatosensory cortex and hippocampus, as well as new tools (secondary antibodies with different shapes) to perform double-labelling for two proteins with similar sensitivity for SDS-FRL.

Relation to the objectives of the project

The data is directly related to the objective 1c, Microcircuitry analysis, proteins and receptor distribution, fibre architecture in a specific large area brain region.

Types and formats of data generated/collected

Types: Freeze-fracture replica and immunoFIB/SEM images of neuronal compartments **Formats:** Tiff files and tables with density and numbers.

Protocol: Electron microscopy immunolabeling protocol

Existing data being re-used (if any)

No

Origin of the data

Data class: Molecular **Specimen information:** C57BL/6, 4w old male

Brain region: Somatosensory cortex; Hippocampus **Subregion:** Layer III, Layer IV, Layer V, Layer VI, CA1

Expected size of the data

20 GB

Data utility: to whom will it be useful

Within HBP: This receptor and ion channels distribution data is needed for the Development of Whole Mouse Brain Model and Mouse Brain Atlas (CDP1), Mouse-Based Cellular Cortical and Sub cortical Microcircuit Models (CPD2) and Plasticity, Learning and Development: Modelling the Dynamic Brain. Modelling/platform task T6.1.1 (SP6) requires our data for SGA1.

Outwith HBP: NA

FAIR DATA**Accessibility: which data will be made openly available**

Privacy class is: Animal Research. There are no issues sharing data

Accessibility: Methods, software tools and documentation needed to access the data

Fiji, Reconstruct, Excel, MatLab, Powerpoint

Re-use: Data licensing to permit the widest reuse possible

BY-NC- ND - Attribution + Noncommercial + NoDerivatives

Re-use: Data quality assurance processes**ETHICAL ASPECTS**

Ethics approval authority: Local ethical committee **Ethics approval ID:** IACUC entry number: PR-2014-07-05

RELEASES AND PROGRESS**Planned releases:**

Month Shared.with Quality			Completeness	Location	Embargo	Actual.Completeness
M18	Consortium	Candidate final quality	60 out of 100 neurons	CSCS data bucket	Awaiting publication	100%

Any deviation and mitigation: NA

Current location(s) of dataset:

<https://collab.humanbrainproject.eu/#/collab/17117/nav/123763>

DATA USAGE

Transferred to SP5/Shared with modelling tasks: NA

Contribution to Use Cases /other SPs: T1.1.3 for SP6 (T6.1.3-C1 - Hodgkin-Huxley modelling of excitation-inhibition (model), T6.1.3-C2 - Modeling modulation of inhibition downstream calcium signaling (model), T6.1.2-SGA1-Data-Driven Modelling of G Protein-Coupled Receptor-Dependent Cascades (model), T6.2.2-SGA1-Initial model validation tests

implemented to compare rat model with mouse data (data).

What are datasets used for (models, atlas)?: Models (to be used to inform future modelling efforts) and Mouse Brain Atlas

Link to model/Atlas: In progress

How the data transfer has been or is coordinated: Through data curation people and metadata form for the Neuroinformatic platform and the Collab system

Role and take-up of the data acquired: The method developed has been used to generate the datasets acquired in T1.1.1 and T1.1.3 (see the relevant components below)

PUBLICATIONS

- [Aguado C, García-Madrona S, Gil-Minguez M, Luján R. \(2016\) Ontogenic Changes and Differential Localization of T-type Ca\(2+\) Channel Subunits Cav3.1 and Cav3.2 in Mouse Hippocampus and Cerebellum. Frontiers in Neuroanatomy 10:83. doi: 10.3389/fnana.2016.00083](#)
 - [Aguado C, Orlandi C, Fajardo-Serrano A, Gil-Minguez M, Martemyanov KA, Luján R. \(2016\). Cellular and Subcellular Localization of the RGS7/Gβ5/R7BP Complex in the Cerebellar Cortex. Frontiers in Neuroanatomy 10:114](#)
 - [Rafael Luján et al., 2017. Differential association of GABAB receptors with their effector ion channels in Purkinje cells. Brain Structure and Function](#)
 - [Harumi HaradaRyuichi Shigemoto Immunogold Protein Localization on Grid-Glued Freeze-Fracture Replicas](#)
-

T1.1.1: Nanoscale measurements of distribution of individual receptors and ion channels in cortical neurons. (ID: 653)**Dataset Owner:** Rafael Luján, Riuichi Shigemoto. < Rafael.Lujan@uclm.es > (UCLM)**DATA SUMMARY****Purpose of the data collection/generation**

The purpose of this particular data generation and collection is 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. The number and density of AMPA, NMDA, mGlu5, GABAB1, GIRK2 and SK2 will be analysed using large high resolution EM images in somatosensory cortex and hippocampus, with quantification of density of immunogold particles in eleven different compartments of pyramidal cells (axon initial segment, cell body, basal dendrites in stratum oriens, spines, apical dendrites in stratum radiatum, oblique dendrites in the proximal, spines, middle and distal parts of stratum radiatum, spines, and stratum lacunosum-moleculare and spines).

Relation to the objectives of the project

The data is directly related to the objective 1c, Microcircuitry analysis, proteins and receptor distribution, fibre architecture in a specific large area brain region.

Types and formats of data generated/collected

Types: Freeze-fracture replica and immunoFIB/SEM images of neuronal compartments **Formats:** Tiff files and tables with density and numbers.

Protocol: Electron microscopy immunolabeling protocol

Existing data being re-used (if any)

No

Origin of the data

Data class: Molecular **Specimen information:** C57BL/6, 4w old male

Brain region: Somatosensory cortex; Hippocampus **Subregion:** Layer III, Layer IV, Layer V, Layer VI, CA1

Expected size of the data

20 GB

Data utility: to whom will it be useful

Within HBP: This receptor and ion channels distribution data is needed for the Development of Whole Mouse Brain Model and Mouse Brain Atlas (CDP1), Mouse-Based Cellular Cortical and Subcortical Microcircuit Models (CPD2) and Plasticity, Learning and Development: Modelling the Dynamic Brain. Modelling/platform task T6.1.1 (SP6) requires our data for SGA1.

Outwith HBP: NA

FAIR DATA**Accessibility: which data will be made openly available**

Privacy class is: Animal Research. There are no issues sharing data

Accessibility: Methods, software tools and documentation needed to access the data

Fiji, Reconstruct, Excel, MatLab, Powerpoint

Re-use: Data licensing to permit the widest reuse possible

BY-NC- ND - Attribution + Noncommercial + NoDerivatives

Re-use: Data quality assurance processes**ETHICAL ASPECTS**

Ethics approval authority: Local ethical committee **Ethics approval ID:** IACUC entry number: PR-2014-07-05

RELEASES AND PROGRESS**Planned releases:**

Month	Shared.with	Quality	Completeness	Location	Embargo	Actual.Completeness
M18	Consortium	Candidate final quality	60 out of 100 neurons	CSCS data bucket	Awaiting publication	100 out of 100 cell profiles are completed (100%).

Any deviation and mitigation: NA

Current location(s) of dataset:

<https://collab.humanbrainproject.eu/#/collab/7106/nav/54313>

<https://collab.humanbrainproject.eu/#/collab/6382/nav/4919>

<https://collab.humanbrainproject.eu/#/collab/17116/nav/123755>

DATA USAGE

Transferred to SP5/Shared with modelling tasks: NA

Contribution to Use Cases /other SPs: SP6 (T6.1.3-C1 - Hodgkin-Huxley modelling of excitation-inhibition (model), T6.1.3-C2 - Modeling modulation of inhibition downstream calcium signaling (model), T6.1.2-SGA1-Data-Driven Modelling of G Protein-Coupled Receptor-Dependent Cascades (model), T6.2.2-SGA1-Initial model validation tests implemented to compare rat model with mouse data (data).

What are datasets used for (models, atlas)?: Models (to be used to inform future modelling efforts) and Mouse Brain Atlas

Link to model/Atlas: In progress

How the data transfer has been or is coordinated: Through data curation people and metadata form for the Neuroinformatic platform and the Collab system

Role and take-up of the data acquired: The work involves a detailed quantitative EM analysis of different subunits/subtypes belonging to three key neurotransmitter receptors (AMPA, NMDA and GABAB receptors) and key ion channels (SK, GIRK and P/Q-type Ca²⁺ channels) in the different cell classes, different layers and areas of the mice, mainly hippocampus, neocortex and cerebellum. SDS-digested freeze-fracture replica labelling (SDS-FRL) and an automated dual-beam electron microscope combined with pre-embedding immunogold reactions (FIB/SEM immunogold) engendered a highly innovative approach that is providing critical parameters for SP6 Task 6.1.2 (Data-Driven Modelling of G Protein-Coupled Receptor-Dependent Cascades) and Task 6.1.3 (Data-Driven Modelling of Ca²⁺ Dependent Cascades), for example, as well as providing molecular maps complementary to Multi-level Atlas of the Rodent Brain in WP5.2 of SP5. Although these receptor and ion channel maps are now under integration with cellular, connectional and neuroimaging data in the HBP Mouse Brain Atlas, our data is particularly relevant to provide global constraints and validation data for brain models produced by The Brain Simulation Platform (SP6), in which different model cell-types will contain different receptors at different densities. Furthermore, our T1.1.3 is delivering common and differing principles of organization that can be used in algorithms that reconstruct synaptic connections in brain models in WP6.1, WP6.2, WP6.4 and WP6.5 of SP6.

PUBLICATIONS

- Aguado C, García-Madróna S, Gil-Mínguez M, Luján R. (2016) Ontogenic Changes and Differential Localization of T-type Ca(2+) Channel Subunits Cav3.1 and Cav3.2 in Mouse Hippocampus and Cerebellum. *Frontiers in Neuroanatomy* 10:83. doi: 10.3389/fnana.2016.00083
 - Aguado C, Orlandi C, Fajardo-Serrano A, Gil-Mínguez M, Martemyanov KA, Luján R. (2016). Cellular and Subcellular Localization of the RGS7/Gβ5/R7BP Complex in the Cerebellar Cortex. *Frontiers in Neuroanatomy* 10:114
 - Rafael Luján et al., 2017. Differential association of GABAB receptors with their effector ion channels in Purkinje cells. *Brain Structure and Function*
 - Harumi Harada Ryuichi Shigemoto Immunogold Protein Localization on Grid-Glued Freeze-Fracture Replicas
-

T1.1.2: Generation of new intrabodies / antibody fragments (ID: 826)**Dataset Owner:** Antonino Cattaneo, Giovanni Meli < antonino.cattaneo@sns.it > (SNS, EBRI)**DATA SUMMARY****Purpose of the data collection/generation**

Generation of new intrabodies/antibody fragments by IACT and data of biochemical validation

Relation to the objectives of the project

Data concerning the generation and validation of new intrabodies / antibody fragments to study proteins of interest (i.e. Neuroligins). Final uses for imaging and functional interference are related to several objectives (i.e. SP1-1c and 1g)

Types and formats of data generated/collected**Types:** Protein expression analysis, co-immunoprecipitation **Formats:** file extension .xls , docx , pdf**Protocol:** [Western blot assay](#); [Immunoprecipitation assay](#)**Existing data being re-used (if any)**

No

Origin of the data**Data class:** Molecular **Specimen information:** Mouse, C57Bl6, male/female (4 days old for organotypic hippocampal cultures)**Brain region:** [Hippocampus](#) **Subregion:****Expected size of the data**

MB

Data utility: to whom will it be useful**Within HBP:** These data show generation of tools exploited in T1.1.2 and T1.1.4, which have several links to different downstream components (see related DMPs). In detail, a set of these data (biochemical validation) can explain 'per se' molecular mechanisms (i.e. protein-protein interactions of Neuroligins partners) upstream to functional studies of Task 1.1.4 (Generation of in vivo Functional Data on Interactions between Neuroligin and Neuroxin Synaptic Proteins, and their use for the Computational Modelling of Trans-Synaptic Signalling).**Outwith HBP:** NA**FAIR DATA****Accessibility: which data will be made openly available**

Privacy class is: Animal Research. There are no issues sharing data

Accessibility: Methods, software tools and documentation needed to access the data

Excel , Word, Adobe acrobat

Re-use: Data licensing to permit the widest reuse possible

All rights reserved, Copyright

Re-use: Data quality assurance processes**ETHICAL ASPECTS****Ethics approval authority:** Italian Ministry of Health **Ethics approval ID:** Authorization n.5/2015PR**RELEASES AND PROGRESS****Planned releases:**

Month	Shared.with	Quality	Completeness	Location	Embargo	Actual.Completeness
M18	—	—	—	—	—	Antibody generation: 100% 7 out of 7 new intrabodies anti-NLGs; intrabody biochemical validation: 30% 2 out of 7 intrabodies
M23	Collab	Candidate final quality	7 out of 7 new intrabodies / antibody fragments produced	Collaboratory Data	embargoed awaiting publication	Antibody generation: 100% 7 out of 7 new intrabodies anti-NLGs; intrabody biochemical validation: 60% for 2 intrabodies anti-NLG2

Any deviation and mitigation: NA**Current location(s) of dataset:**<https://collab.humanbrainproject.eu/#/collab/11537/nav/86273>**DATA USAGE****Transferred to SP5/Shared with modelling tasks:** NA**Contribution to Use Cases /other SPs:** SGA1: SP6,T6.2.4. SGA2: SP2:T2.3.1, T2.3.2; SP6: T6.1.5.**What are datasets used for (models, atlas)?:** Models (SGA2)**Link to model/Atlas:** In progress (planned for SGA2)

How the data transfer has been or is coordinated: SGA1 mainly focus in generating biochemical data from intrabody interference used by T1.1.4 to be integrated in SP6 models, in detail started with the Computational Modeling of Trans-Synaptic Signalling (SGA1, SP6, T6.2.4). The coordination has already started between the curation team and T1.1.2 / T1.1.4

Role and take-up of the data acquired: This dataset shows: a) the generation of 7 different new IACT anti-NLGs antibody fragments (nanobodies), reported in the collab SGA1 T1.1.2 as DATASET 2_A; b) the biochemical validation as intrabodies of 2 anti-NLG2, reported in the collab SGA1 T1.1.2 as DATASET 2_B. In SGA1 these new tools have been exploited as intrabodies in T1.1.4, allowing the generation of data reported in dataset “T1.1.4: Electrophysiological data-hippocampus”. Intrabody interference data reported in dataset 2_B are useful to decipher new biochemical mechanisms of synaptic interactome of Neuroligins and to integrate, together with T1.1.4 electrophysiological data, the Computational Modelling of Trans-Synaptic Signalling (SP6, T6.2.4). On the basis of this dataset, in SGA2 T1.1.2 further biochemical studies and links with several SP1, SP4 and SP6 tasks will allow achieving a better integration between biochemical intracellular networks and models based on electrical currents.

Some anti-NLGs nanobodies reported in this dataset are also planned to be developed as tools of imaging in SGA2 T1.1.1 and its linked tasks.

Specific list of propagation to other SPs and CDPs: SGA1: SP1 T.1.1.4; SP6,T6.2.4. SGA2: SP1: T1.1.1, T1.1.2, T1.1.3, T1.3.2, T1.3.3; SP2:T2.3.1, T2.3.2; SP6: T6.1.5

PUBLICATIONS

- [Chirichella M, Lisi S Fantini M Goracci M Calvello M, Brandi R, Arisi I, D'Onofrio M, Di Primio C, Cattaneo A. Post-translational selective intracellular silencing of acetylated proteins with de novo selected intrabodies. Nat Methods. 2017 Mar;14\(3\):279-282. doi: 10.1038/nmeth.4144. Epub 2017 Jan 16](#)
-

T1.1.2: IACT antibody fragments for imaging (ID: 826A)**Dataset Owner:** Antonino Cattaneo, Giovanni Meli < antonino.cattaneo@sns.it > (SNS, EBRI)**DATA SUMMARY****Purpose of the data collection/generation**

Collection of imaging data generated by the use of IACT-selected small antibody domains. Data show representative results of immunofluorescence-confocal images demonstrating the novelty of IACT small antibody fragments such as their specificity and better penetration in tissues.

Relation to the objectives of the project

Analysis of proteins of interest in brain sections by exploiting new IACT antibody fragments: major relation to the objective SP1-1c

Types and formats of data generated/collected

Types: Confocal images of brain tissues **Formats:** .tiff , pdf

Protocol: [Confocal imaging protocol](#); [Immunolabeling protocol](#); [Immunohistochemical protocol](#)

Existing data being re-used (if any)

No

Origin of the data

Data class: Cellular **Specimen information:** Post mortem human brains of controls and pathological cases of interest (i.e. Alzheimer's Dementia, AD) from public Brain Banks

Brain region: [Neocortex](#) **Subregion:** NA

Expected size of the data

1GB

Data utility: to whom will it be useful

Within HBP: Final data will show the novelty of IACT small antibody fragments for imaging studies. Then, the validated antibody domains can be distributed to interested HBP users. In order to be fully developed in next SGA2, some pilot collaborations are planned with SGA1 (possible linking downstream to this component were hypothesized with the following tasks : T1.1.4 Generation of in vivo Functional Data on Interactions between Neuroligin and Neuroxin Synaptic Proteins, and their use for the Computational Modelling of Trans-Synaptic Signalling, T1.3.3 Methodical development in optical imaging, data analysis, integration and atlasing - Optimization of Clarity for whole brain imaging, T2.2.2 Cell types, synapses, and their quantitative characterization in the human brain and T2.2.3 Transmitter receptors in cortical and subcortical regions and layers of the human brain).

Outwith HBP: NA

FAIR DATA**Accessibility: which data will be made openly available**

Privacy class is: Human Research. There may be issues sharing data openly

Accessibility: Methods, software tools and documentation needed to access the data

Common software of imaging management and modification (tiff) , Adobe Acrobat (pdf)

Re-use: Data licensing to permit the widest reuse possible

All rights reserved, Copyright

Re-use: Data quality assurance processes**ETHICAL ASPECTS**

Ethics approval authority: Post-mortem human brain specimens are obtained from Brain Banks approved by their National Research Ethics Services **Ethics approval ID:** NA

RELEASES AND PROGRESS**Planned releases:**

Month	Shared.with	Quality	Completeness	Location	Embargo	Actual.Completeness
M18	—	—	—	—	—	Imaging 50% ; 5 out 10 brain slices
M23	Partner	Candidate final quality	10 out 10 brain slices	Collaboratory	Data embargoed awaiting publication	Imaging 100% ; 11 out 10 brain slices

Any deviation and mitigation: NA

Current location(s) of dataset:

<https://collab.humanbrainproject.eu/#/collab/11537/nav/86273>

DATA USAGE

Transferred to SP5/Shared with modelling tasks: NA

Contribution to Use Cases /other SPs: SGA2: SP2:T2.3.1, T2.3.2; SP5: T5.6.1; SP6: T6.1.5

What are datasets used for (models, atlas)?: Atlas and Models(SGA2)

Link to model/Atlas: In progress (planned for SGA2)

How the data transfer has been or is coordinated: SGA1 mainly focus in pilot studies of imaging with nanobodies and datasets have not been used for atlas yet. The coordination has already started between the curation team and T1.1.2

Role and take-up of the data acquired: Innovative strategies for brain imaging and mapping are crucial in HBP. In this dataset we showed the proof of concept of IACT nanobodies for improved brain imaging due to their specificity, better penetration in tissues (reported in the collab SGA1 T1.1.2 as DATASET1) and easy molecular engineering (i.e. tagging for direct labeling, reported in the collab SGA1 T1.1.2 as DATASET2_C). Data generated in SGA1 pilot studies with anti-AbOs nanobodies, used jointly with well-established antibodies against neuronal and glial markers, are planned to be transferred to SP5, on the basis of already agreed procedures.

On this basis, activity started in SGA1 T1.1.2 will be continued and improved in SGA2 T1.1.1 to generate micro- and macro-anatomical maps of the proteins of interest with a translational value in HBP i) from mouse and human brains, ii) from normal to impaired brains in different pathological conditions. Different levels of nanobody imaging resolution will be achieved as advanced electron microscopy with SP1 T1.1.3, or whole brain imaging linked with tasks SP1 T1.3.2, T1.3.3 and SP2 T2.3.1, T2.3.2. Data of improved resolution and specificity, elaborated by SP5 T5.6.1, will be useful not only for SP5 atlasing but also to provide constraints for SP6 modeling. For instance, nanobody brain mapping of Gephyrin and Neuroligins will support SGA2 T1.1.2 data to better constrain the computational model of the hippocampus circuits in SP6, that already is using data from SGA1 T1.1.2 and T1.1.4. Furthermore, new nanobodies against proteins of major and general interest in HBP (i.e. receptors, cell type markers) will be generated in SGA2 (to be shared with linked SP1 and SP2 tasks, above mentioned).

Specific list of propagation to other SPs and CDPs: SGA2: SP1: T1.1.2, T1.1.3, T1.3.2, T1.3.3; SP2:T2.3.1, T2.3.2; SP5: T5.6.1; SP6: T6.1.5.

PUBLICATIONS

- [Chirichella M, Lisi S Fantini M Goracci M Calvello M, Brandi R, Arisi I, D'Onofrio M, Di Primio C, Cattaneo A. Post-translational selective intracellular silencing of acetylated proteins with de novo selected intrabodies. Nat Methods. 2017 Mar;14\(3\):279-282. doi: 10.1038/nmeth.4144. Epub 2017 Jan 16](#)
-

T1.1.3: GluA2, GluA3 and GluN1 in CA1 (ID: 6)**Dataset Owner:** Ryuichi Shigemoto < ryuichi.shigemoto@ist.ac.at > (IST)**DATA SUMMARY****Purpose of the data collection/generation**

To provide realistic parameters for neuronal modelling

Relation to the objectives of the project

The data is directly related to the objective 1c, Microcircuitry analysis, proteins and receptor distributions, fibre architecture in a specific large area brain region

Types and formats of data generated/collected**Types:** images, density measurements **Formats:** TIF, Excel**Protocol:** Electron microscopy**Existing data being re-used (if any)**

No

Origin of the data**Data class:** Molecular **Specimen information:** C57BL/6 adult male mice**Brain region:** Somatosensory cortex, hippocampus, cerebellum **Subregion:** CA1, somatosensory, cerebellar cortex**Expected size of the data**

10GB

Data utility: to whom will it be useful**Within HBP:** This data is needed to constrain neuronal models**Outwith HBP:** NA**FAIR DATA****Accessibility: which data will be made openly available**

Privacy class is: Animal Research. There are no issues sharing data

Accessibility: Methods, software tools and documentation needed to access the data**Re-use: Data licensing to permit the widest reuse possible**

BY-NC- ND - Attribution + Noncommercial + NoDerivatives

Re-use: Data quality assurance processes**ETHICAL ASPECTS****Ethics approval authority:** bmfwf **Ethics approval ID:** BMWFW-66.018/0009-WF/II/3b/2014**RELEASES AND PROGRESS****Planned releases:**

Month	Shared.with	Quality	Completeness	Location	Embargo	Actual.Completeness
M18	—	—	—	—	—	10 cells (100%)
M23	Consortium	Final quality	10 cells	Collaboratory		Ditto

Any deviation and mitigation: NA**Current location(s) of dataset:**<https://collab.humanbrainproject.eu/#/collab/17119/nav/123775>**DATA USAGE****Transferred to SP5/Shared with modelling tasks:** NA**Contribution to Use Cases /other SPs:** SP6 (T6.1.3-C1 - Hodgkin-Huxley modelling of excitation-inhibition (model), T6.1.3-C2 - Modeling modulation of inhibition downstream calcium signaling (model), T6.1.2-SGA1-Data-Driven Modelling of G Protein-Coupled Receptor-Dependent Cascades (model), T6.2.2-SGA1-Initial model validation tests implemented to compare rat model with mouse data (data).**What are datasets used for (models, atlas)?:** Models (to be used to inform future modelling efforts) and Mouse Brain Atlas**Link to model/Atlas:** In progress**How the data transfer has been or is coordinated:** Through data curation people and metadata form for the Neuroinformatic platform and the Collab system**Role and take-up of the data acquired:** The work involves a detailed quantitative EM analysis of different subunits/subtypes belonging to three key neurotransmitter receptors (AMPA, NMDA and GABAB receptors) and key ion channels (SK, GIRK and P/Q-type Ca²⁺ channels) in the different cell classes, different layers and areas of the mice, mainly hippocampus, neocortex and cerebellum. SDS-digested freeze-fracture replica labelling (SDS-FRL) and an automated dual-beam electron microscope combined with pre-embedding immunogold reactions (FIB/SEM immunogold) engendered a highly innovative approach that is providing critical parameters for SP6 Task 6.1.2 (Data-Driven Modelling)

of G Protein-Coupled Receptor-Dependent Cascades) and Task 6.1.3 (Data-Driven Modelling of Ca²⁺ Dependent Cascades), for example, as well as providing molecular maps complementary to Multi-level Atlas of the Rodent Brain in WP5.2 of SP5. Although these receptor and ion channel maps are now under integration with cellular, connectional and neuroimaging data in the HBP Mouse Brain Atlas, our data is particularly relevant to provide global constraints and validation data for brain models produced by The Brain Simulation Platform (SP6), in which different model cell-types will contain different receptors at different densities. Furthermore, our T1.1.3 is delivering common and differing principles of organization that can be used in algorithms that reconstruct synaptic connections in brain models in WP6.1, WP6.2, WP6.4 and WP6.5 of SP6.

PUBLICATIONS

- [Aguado C, García-Madróna S, Gil-Minguez M, Luján R. \(2016\) Ontogenic Changes and Differential Localization of T-type Ca\(2+\) Channel Subunits Cav3.1 and Cav3.2 in Mouse Hippocampus and Cerebellum. *Frontiers in Neuroanatomy* 10:83. doi: 10.3389/fnana.2016.00083](#)
 - [Aguado C, Orlandi C, Fajardo-Serrano A, Gil-Minguez M, Martemyanov KA, Luján R. \(2016\). Cellular and Subcellular Localization of the RGS7/Gβ5/R7BP Complex in the Cerebellar Cortex. *Frontiers in Neuroanatomy* 10:114](#)
 - [Rafael Luján et al., 2017. Differential association of GABAB receptors with their effector ion channels in Purkinje cells. *Brain Structure and Function*](#)
 - [Harumi Harada Ryuichi Shigemoto Immunogold Protein Localization on Grid-Glued Freeze-Fracture Replicas](#)
-

T1.1.3: Association (co-clustering) of receptors and their effector ion channels in different neuronal compartments. (ID: 654)

Dataset Owner: Rafael Luján, Riuichi Shigemoto < Rafael.Lujan@uclm.es > (UCLM)

DATA SUMMARY

Purpose of the data collection/generation

Co-localization of receptors and ion channels has a tremendous influence on the functional effects of stimulants. Based on the mapping data of receptors and ion channels obtained in Task 1.1.1 by single labelling, we will investigate principles of co-localization of different subunits of these receptors and channels in the hippocampus and neocortex. Using double-labelling approaches with gold particles of different size, we will determine the association (co-clustering) of receptors and their effector ion channels in different neuronal compartments and the spatial relationships and composition of immunoparticle clusters for the receptor and associated ion channels, and how these parameters differ in different compartment and for different effector channels. 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, in different subcellular compartments.

Relation to the objectives of the project

The data is directly related to the objective 1c, Microcircuitry analysis, proteins and receptor distribution, fibre architecture in a specific large area brain region.

Types and formats of data generated/collected

Types: Freeze-fracture replica images of neuronal compartments **Formats:** Tiff files and tables with density and numbers

Protocol: Electron microscopy immunolabeling protocol

Existing data being re-used (if any)

No

Origin of the data

Data class: Molecular **Specimen information:** C57BL/6, 4w old male

Brain region: Somatosensory cortex; Hippocampus **Subregion:** Layer III, Layer IV, Layer V, Layer VI, CA1

Expected size of the data

20 GB

Data utility: to whom will it be useful

Within HBP: This receptor and ion channels distribution data is needed for the Development of Whole Mouse Brain Model and Mouse Brain Atlas (CDP1), Mouse-Based Cellular Cortical and Subcortical Microcircuit Models (CPD2) and Plasticity, Learning and Development: Modelling the Dynamic Brain. Modelling/platform task T6.1.1 (SP6) requires our data for SGA1.

Outwith HBP: NA

FAIR DATA

Accessibility: which data will be made openly available

Privacy class is: Animal Research. There are no issues sharing data

Accessibility: Methods, software tools and documentation needed to access the data

Fiji, Reconstruct, Excel, MatLab, Powerpoint

Re-use: Data licensing to permit the widest reuse possible

BY-NC- ND - Attribution + Noncommercial + NoDerivatives

Re-use: Data quality assurance processes

ETHICAL ASPECTS

Ethics approval authority: Local ethical committee **Ethics approval ID:** IACUC entry number: PR-2014-07-05

RELEASES AND PROGRESS

Planned releases:

Month	Shared.with	Quality	Completeness	Location	Embargo	Actual.Completeness
M18	Consortium	Candidate final quality	60 out of 100 neurons	CSCS data bucket	Awaiting publication	50 out of 100 cell profiles are completed (50%).
M23	Ditto	Ditto	Ditto	Ditto	Ditto	100%

Any deviation and mitigation: NA

Current location(s) of dataset:

<https://collab.humanbrainproject.eu/#/collab/6380/nav/49179>

DATA USAGE

Transferred to SP5/Shared with modelling tasks: NA

Contribution to Use Cases /other SPs: SP6 (T6.1.3-C1 - Hodgkin-Huxley modelling of excitation-inhibition (model), T6.1.3-C2 - Modeling modulation of inhibition downstream calcium signaling (model), T6.1.2-SGA1-Data-Driven Modelling of G Protein-Coupled Receptor-Dependent Cascades (model), T6.2.2-SGA1-Initial model validation tests implemented to compare rat model with mouse data (data).

What are datasets used for (models, atlas)?: Models (to be used to inform future modelling efforts))

Link to model/Atlas: In progress

How the data transfer has been or is coordinated: Through data curation people and metadata form for the Neuroinformatic platform and the Collab system

Role and take-up of the data acquired: T1.1.3 is related with component Association (co-clustering) of receptors and their effector ion channels in different neuronal, which involves a detailed quantitative EM analysis on the spatial relation of functionally associated neurotransmitter receptors and ion channels (for instance, GABAB receptors with GIRK channels or Cav channels, and NMDA receptors with SK channels) in specific neuronal compartments using SDS-digested freeze-fracture replica labelling (SDS-FRL) and an automated dual-beam electron microscope with double-labelling approaches. This sophisticated approach will provide key information on the functional and molecular association of two different proteins essential for SP6 Task 6.1.2 (Data-Driven Modelling of G Protein-Coupled Receptor-Dependent Cascades) and Task 6.1.3 (Data-Driven Modelling of Ca²⁺ Dependent Cascades). Furthermore, this Task is delivering common and differing principles of organization that can be used in algorithms that reconstruct synaptic connections in brain models in WP6.1, WP6.2, WP6.4 and WP6.5 of SP6.

PUBLICATIONS

- [Aguado C, García-Madrona S, Gil-Minguez M, Luján R. \(2016\) Ontogenic Changes and Differential Localization of T-type Ca\(2+\) Channel Subunits Cav3.1 and Cav3.2 in Mouse Hippocampus and Cerebellum. Frontiers in Neuroanatomy 10:83. doi: 10.3389/fnana.2016.00083](#)
 - [Aguado C, Orlandi C, Fajardo-Serrano A, Gil-Minguez M, Martemyanov KA, Luján R. \(2016\). Cellular and Subcellular Localization of the RGS7/Gβ5/R7BP Complex in the Cerebellar Cortex. Frontiers in Neuroanatomy 10:114](#)
 - [Rafael Luján et al., 2017. Differential association of GABAB receptors with their effector ion channels in Purkinje cells. Brain Structure and Function](#)
 - [Harumi HaradaRyuichi Shigemoto Immunogold Protein Localization on Grid-Glued Freeze-Fracture Replicas](#)
-

T1.1.4: Electrophysiological data - hippocampus (ID: 713)**Dataset Owner:** Enrico Cherubini < e.cherubini@ebri.it > (SNS, EBRI, CNR)**DATA SUMMARY****Purpose of the data collection/generation**

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/neuroigin block, will be collected and used for modelling which than will feed the Brain Simulation Platform. These data are important for the understanding of the trans-synaptic signalling at both inhibitory and excitatory synapses. In addition, short term plasticity data will be relevant for this signalling on CA1 Schaffer collateral synaptic efficacy changes.

Relation to the objectives of the project**Types and formats of data generated/collected****Types:** Ex-vivo electrophysiological recording **Formats:** abf; txts**Protocol:** [Electrical recording assay](#); [Electrical recording protocol](#); [Extracellular electrode recording protocol](#); [Single-electrode voltage clamp recording protocol](#); [Whole-cell voltage clamp recording protocol](#)**Existing data being re-used (if any)**

No

Origin of the data**Data class:** Electrophysiological **Specimen information:** Mouse, C57Bl6, male/female, 4 days old (for organotypic hippocampal cultures), pups, 5 gr, Plaisant**Brain region:** [Hippocampus](#) **Subregion:** [Hippocampus CA1 pyramidal cell](#)**Expected size of the data**

GB

Data utility: to whom will it be useful**Within HBP:** These electrophysiological data are needed to constrain functional models of hippocampal synaptic neurotransmission and plasticity (T1.1.4, T6.2.4)**Outwith HBP:** NA**FAIR DATA****Accessibility: which data will be made openly available**

Privacy class is: Animal Research. There are no issues sharing data

Accessibility: Methods, software tools and documentation needed to access the data

Clampfit (molecular device); Graficuser interface

Re-use: Data licensing to permit the widest reuse possible

BY-NC

Re-use: Data quality assurance processes**ETHICAL ASPECTS****Ethics approval authority:** Minister of Health **Ethics approval ID:** Authorization n.5/2015PR**RELEASES AND PROGRESS****Planned releases:**

Month	Shared.with	Quality	Completeness	Location	Embargo	Actual.Completeness
M18	—	—	—	—	—	38%; 86 out of 215 recordings
M23	Consortium	Final quality	10 out of 15 recordings	Collaboratory; CSCS data bucket	awaiting publication	162 out of 215 recordings; 75%

Any deviation and mitigation: NA**Current location(s) of dataset:**<https://collab.humanbrainproject.eu/#/collab/914/nav/8073>**DATA USAGE****Transferred to SP5/Shared with modelling tasks:** NA**Contribution to Use Cases /other SPs:** SP1-UC04: Fitting individual synaptic events;Biophysical model of LTP and LTD in wild type and mutant hippocampal CA1 synapses; SP6: T6.2.4 Models of Hippocampus**What are datasets used for (models, atlas)?:** Models**Link to model/Atlas:**https://object.cscs.ch/v1/AUTH_63ea6845b1d34ad7a43c8158d9572867/Migliore_SGA1_T1.1.6/hbp-00010/Gephyrin/hbp-00010_Gephyrin__ProbGABAAB_EMS_GEPH_g.mod**How the data transfer has been or is coordinated:** data curation has been coordinated by MilicaMarkovic (SP5)

Role and take-up of the data acquired: Data from experimental models of synaptic interference with neuroligins and gephyrin (obtained both with intrabodies and knock-out methods) are essential for modelling trans-synaptic signaling, synapse stabilization and maintenance of an appropriate excitatory/inhibitory balance within the hippocampal network. Indeed, any realistic model of synaptic transmission and synaptic plasticity in the hippocampus have to include modeling of feedback signals connecting the post-synaptic to the presynaptic signaling. This dataset on inhibitory synaptic currents of hippocampus has been used to model transynaptic signaling at inhibitory synapses. This is part of the hippocampus model in SP6 (T6.2.4, T6.4.5, T6.4.6) and is available for HBP users through a Graphical User Interface (GUI). In addition, data on short term synaptic plasticity data are being used to implement a quantitative computational model and will be extended for plasticity algorithms (T4.3.1). Dataset generated in SGA1 T1.1.4 has been uploaded on the Knowledge Graph (WP5.1) and a model has been already implemented using the Brain simulation platform tools (T6.5.1). For SGA2, an ongoing acquisition of this type of data, also extended to in vivo experiments will be used in CDP2 -T6.2.4 and CDP5-SP3, to constrain and/or validate the model circuit. In collaboration with SP5 (WP5.1) and SP6 (T6.1.4, T6.1.2, T6.1.5, T6.2.3, T6.2.7, CDP2) we intend to integrate in a single computational model both the electrical and biochemical components of synaptic plasticity.

Specific list of propagation to other SPs and CDPs: SGA1: T5.1, T6.1.4, T6.2.4, T6.4.5, T6.5.1; SGA2: T4.3.1, T5.1, T6.1.2,, T6.1.5, T6.2.3, T6.2.7, CDP2

PUBLICATIONS

- Lupascu CA, Morabito A, Merenda E, Marinelli S, Marchetti C, Migliore R, Cherubini E, Migliore M. A General Procedure to Study Subcellular Models of Transsynaptic Signaling at Inhibitory Synapses. *Front Neuroinform.* 2016 Jun 30;10:23. doi: 10.3389/fninf.2016.00023. eCollection 2016
 - Cellot G, Maggi L, Di Castro MA, Catalano M, Migliore R, Migliore M, Scattoni ML, Calamandrei G, Cherubini E (2016) Premature changes in neuronal excitability account for hippocampal network impairment and autistic-like behavior in neonatal BTBR T+tf/J mice. *Sci Rep.* 2016 Aug 16;6:31696. doi: 10.1038/srep31696
 - Griguoli M and Cherubini E (2017) Early Correlated Network Activity in the Hippocampus: Its Putative Role in Shaping Neuronal Circuits. *Front. Cell. Neurosci.* 11:255.doi: 10.3389/fncel.2017.00255
 - Francesco Gobbo, Laura Marchetti Ajesh Jacob, Bruno Pinto, Noemi Binini, Federico Pecoraro Bisogni, Claudia Alia, Stefano Luin, Matteo Caleo, Tommaso Fellin, Laura Cancedda and Antonino Cattaneo (2017) Activity-dependent expression of Channelrhodopsin at neuronal synapses. *Nature Communications*, accepted for publication
-

T1.1.5: K channel kinetic and activity in a model neuron (ID: 575)**Dataset Owner:** Simon Bernèche < simon.berneche@unibas.ch > (SIB)**DATA SUMMARY****Purpose of the data collection/generation**

Provide kinetic models that better represent the specific properties of the different K channels. Illustrate how these channels can modulate propagated signals.

Relation to the objectives of the project**Types and formats of data generated/collected****Types:** multi-state ion channel models **Formats:** csv, Neuron model (.mod)**Protocol:****Existing data being re-used (if any)**

Electrophysiological data from the Blue Brain Project

Origin of the data**Data class:** Model **Specimen information:** NA**Brain region:** NA **Subregion:** NA**Expected size of the data**

<100MB

Data utility: to whom will it be useful**Within HBP:** These kinetic models would add a layer of granularity to neuron models (T6.2.1,T6.2.2,T6.2.4)**Outwith HBP:** NA**FAIR DATA****Accessibility: which data will be made openly available**

Privacy class is: No privacy constraints. There are no issues sharing data

Accessibility: Methods, software tools and documentation needed to access the data

NA

Re-use: Data licensing to permit the widest reuse possible

CC0 - Freeing content globally without restrictions

Re-use: Data quality assurance processes**ETHICAL ASPECTS****Ethics approval authority:** NA **Ethics approval ID:** NA**RELEASES AND PROGRESS****Planned releases:**

Month	Shared.with	Quality	Completeness	Location	Embargo	Actual.Completeness
M18	—	—	—	—	—	80% (25 datasets)
M23	Anonymous	Candidate final quality	Models were defined for all K channels for which reliable and sufficient data are available (20/20).	Lab server	NA	90%

Any deviation and mitigation: NA**Current location(s) of dataset:**<https://github.com/njohnner/Kv-kinetic-models>**DATA USAGE****Transferred to SP5/Shared with modelling tasks:** NA

Contribution to Use Cases /other SPs: SP6 (T6.1.3-C1 - Hodgkin-Huxley modelling of excitation-inhibition (model); T6.2.2: Initial model validation tests implemented to compare rat model with mouse data (data); T6.2.4: Models of mouse hippocampal neurons (model).

What are datasets used for (models, atlas)?: To be included in sub-cellular models**Link to model/Atlas:** In progress**How the data transfer has been or is coordinated:** Through the CSCS data infrastructure

Role and take-up of the data acquired: Current neuron models integrate the function of K channels in a general way that summarizes the activity of K channels in only a few mathematical models, typically following the Hodgkin-Huxley formalism. Our goal is to provide a greater granularity allowing for a better understanding of the role played by each of the channels.

T1.1.5 provides kinetic models of a broad variety of K channels based on exhaustive electrophysiological recordings. These models can readily be integrated in the Neuron modeling environment. Neuron models developed in SP6, which will eventually combine these specific kinetic models with the experimental distribution of the different channels in various

neuron types, can reproduce the neuronal electrophysiological activity using a more realistic biophysical description (SP6).

Such detailed modeling work, taking into account the specific properties of locally expressed channels, reveals unforeseen neuronal functions (e.g. precise modulation of the propagated signal). Such high level functions can be implemented in phenomenological models as developed in SP4.

PUBLICATIONS

- [F.T. Heer, D.J. Posson, W. Wojtas-Niziurski, C.M. Nimigean, S. Bernèche. Mechanism of Activation at the Selectivity Filter of the KcsA Channel. eLife In press. DOI: 10.7554/eLife.25844](#)
-

T1.1.6: KappaNEURON software package (ID: 34)**Dataset Owner:** David Sterratt < david.c.sterratt@ed.ac.uk > (UEDIN)**DATA SUMMARY****Purpose of the data collection/generation**

The purpose of KappaNEURON is to enable detailed molecular simulations, particularly at synapses, described using the concise, rule-based language “kappa” in the context of electrophysiological simulations of neurons. The work here is to make KappaNEURON compatible with NEURON 7.4.

Relation to the objectives of the project

Objective 6b (Scaffold models of molecular-level principal neurons, cellular-level reconstructions of selected cortical and sub-cortical regions.)

Types and formats of data generated/collected**Types:** Software **Formats:** Java, Python, Kappa**Protocol:****Existing data being re-used (if any)****Origin of the data****Data class:** Software **Specimen information:** NA**Brain region:** NA **Subregion:** NA**Expected size of the data**

1GB

Data utility: to whom will it be useful

Within HBP: This software is needed to run a proof of concept detailed rule-based synaptic plasticity model, and will facilitate molecular simulations in future phases of HBP.

Outwith HBP: NA**FAIR DATA****Accessibility: which data will be made openly available**

Privacy class is: No privacy constraints. There are no issues sharing data

Accessibility: Methods, software tools and documentation needed to access the data

KappaNEURON depends on NEURON, Python, Java and SpatialKappa, all of which are open source tools. It would not be appropriate to include these packages; the installation docs specify which versions are needed.

Re-use: Data licensing to permit the widest reuse possible

GPL3

Re-use: Data quality assurance processes**ETHICAL ASPECTS****Ethics approval authority:** NA **Ethics approval ID:** NA**RELEASES AND PROGRESS****Planned releases:**

Month	Shared	with Quality	Completeness	Location	Embargo	Actual.Completeness
M12	Anonymous	Candidate final quality	KappaNEURON upgraded to work with NEURON 7.4	Github		—
M18	Ditto	Ditto	Ditto	Ditto	Ditto	Complete – KappaNEURON updated to work with NEURON 7.4

Any deviation and mitigation: NA**Current location(s) of dataset:**<https://github.com/davidcsterratt/KappaNEURON>**DATA USAGE****Transferred to SP5/Shared with modelling tasks:** NA

Contribution to Use Cases /other SPs: SP1-UC02: Biophysical model of LTP and LTD in wild type and mutant hippocampal CA1 synapses

What are datasets used for (models, atlas)?: This software is awaiting use, pending development of a simpler, purely molecular rule-based model.

Link to model/Atlas:**How the data transfer has been or is coordinated:**

Role and take-up of the data acquired: The software “KappaNEURON software package” will be used to implement rule-based models of synaptic plasticity in the context of neurons; these models will be complementary and compared with the STEPS-based spatial simulations undertaken by SGA2-T6.2.7.

PUBLICATIONS

T1.1.6: A mapping of computational models of synapses to proteins (ID: 420)**Dataset Owner:** David Sterratt < david.c.sterratt@ed.ac.uk > (UEDIN)**DATA SUMMARY****Purpose of the data collection/generation**

The purpose is to relate the constituents (e.g. proteins, ions, second messengers) of published models of synaptic plasticity to standard identifiers, which will then allow comparison with synaptic proteome datasets, and ontologies of biological function and disease.

Relation to the objectives of the project

This will inform the development of models under Objective 6b (Scaffold models of molecular-level principal neurons, cellular-level reconstructions of selected cortical and sub-cortical regions) and it will be possible to link proteins in the mapped models to data collected under Objective 1d (Maps of cellular distributions, long-range axonal projections, and synaptic proteins; reconstructed morphologies of major neuron types).

Types and formats of data generated/collected**Types:** Mapping tables **Formats:** csv**Protocol:****Existing data being re-used (if any)**

Yes, this data uses HGNC mappings from genes to gene families.

Origin of the data**Data class:** Molecular **Specimen information:****Brain region:** Subregion:**Expected size of the data**

1GB

Data utility: to whom will it be useful

Within HBP: This will inform the development of models in SP6 in SGA1 (e.g. T6.1.3, Data-driven modelling of Ca²⁺ dependent cascades controlling synaptic signalling and homeostasis and T6.1.2 Data-Driven Modelling of G Protein-Coupled Receptor-Dependent Cascades).

Outwith HBP: NA**FAIR DATA****Accessibility: which data will be made openly available**

Privacy class is: No privacy constraints. There are no issues sharing data

Accessibility: Methods, software tools and documentation needed to access the data

The data comes with a set of R scripts to reproduce our analysis.

Re-use: Data licensing to permit the widest reuse possible

BY - Attribution alone

Re-use: Data quality assurance processes**ETHICAL ASPECTS****Ethics approval authority:** NA **Ethics approval ID:** NA**RELEASES AND PROGRESS****Planned releases:**

Month	Shared.with	Quality	Completeness	Location	Embargo	Actual.Completeness
M18	Consortium	Final quality	30/30 models curated	Collaboratory		Complete – 30/30 models curated

Any deviation and mitigation: NA**Current location(s) of dataset:**
<https://collab.humanbrainproject.eu/#/collab/6172/nav/47729>
DATA USAGE**Transferred to SP5/Shared with modelling tasks:** NA

Contribution to Use Cases /other SPs: SP1-UC02: Biophysical model of LTP and LTD in wild type and mutant hippocampal CA1 synapses

What are datasets used for (models, atlas)? This dataset is meant to guide future modelling efforts, rather than be used in a model, so it has not fed directly into a model. Jeanette Hellgren-Kotaleski (SP6) has been involved in writing the resulting paper, so knows about the dataset.

Link to model/Atlas:

How the data transfer has been or is coordinated: As we are writing the paper, the coordination is being done in-house

Role and take-up of the data acquired: The dataset “A mapping of computational models of synapses to proteins” will be used to inform future modelling efforts in SP6, in particular which proteins have not been modelled extensively and are particularly relevant for disease. The raw data will be released as part of a publication.

PUBLICATIONS

- [Katharina F. Heil, Emilia M. Wysocka Oksana Sorokina, Jeanette HällgrenKotaleski, T. Ian Simpson,B](#)
-

T1.1.6: Curated list of synaptic protein-protein interactions (ID: 422)**Dataset Owner:** Oksana Sorokina < osorokin@inf.ed.ac.uk > (UEDIN)**DATA SUMMARY****Purpose of the data collection/generation**

A definitive (as of June 2016) curated list of synaptic protein-protein interactions (PPIs), derived from selected PPI databases (currently BIOGRID, INTACT and DIP). Each PPI will be labelled according to whether it is presynaptic and or postsynaptic. This will enable various types of inference on protein networks to take place.

Relation to the objectives of the project

Objective 1c (Microcircuitry analysis, proteins and receptor distributions, fibre architecture in a specific large area brain region)

Types and formats of data generated/collected

Types: Curated protein-protein interactions **Formats:** csv

Protocol:

Existing data being re-used (if any)

Yes. The IntAct, BioGRID and DIP databases.

Origin of the data

Data class: Molecular **Specimen information:** Human

Brain region: [Forebrain](#) **Subregion:**

Expected size of the data

1GB

Data utility: to whom will it be useful

Within HBP: Cluster analysis of protein networks can be combined with functional gene annotation (T8.4.1) to find protein subnetworks associated with biological function and disease. It will also help to constrain dynamic models of protein-protein networks (T1.1.6).

Outwith HBP: NA

FAIR DATA**Accessibility: which data will be made openly available**

Privacy class is: No privacy constraints. There are no issues sharing data

Accessibility: Methods, software tools and documentation needed to access the data

Software to read tables, e.g. Excel, R, python

Re-use: Data licensing to permit the widest reuse possible

We need to match BIOGRID, IntAct and DIP terms & licences to CC licenses

Re-use: Data quality assurance processes**ETHICAL ASPECTS**

Ethics approval authority: NA **Ethics approval ID:** NA

RELEASES AND PROGRESS**Planned releases:**

Month	Shared.with	Quality	Completeness	Location	Embargo	Actual.Completeness
M06	Public authenticated	Final quality	Definitive as of June 2016	Collaboratory	—	
M18	Ditto	Ditto	Ditto	Ditto	Ditto	Complete – List updated to June 2016 versions of databases

Any deviation and mitigation: NA

Current location(s) of dataset:

<https://collab.humanbrainproject.eu/#/collab/3389/nav/27146>

DATA USAGE

Transferred to SP5/Shared with modelling tasks: NA

Contribution to Use Cases /other SPs: SP1-UC02: Biophysical model of LTP and LTD in wild type and mutant hippocampal CA1 synapses

What are datasets used for (models, atlas)?: This dataset has been shared with Paolo Carloni's group (SP6). The group has started to identify the effect of disease-linked mutations on the protein interactome at the human synapse by bioinformatics and molecular simulation. This work will continue in SGA2.

Link to model/Atlas: No model yet.

How the data transfer has been or is coordinated: The data transfer has been coordinated by Skype meetings and email, with the data itself being shared via the collab.

Role and take-up of the data acquired: See “what datasets are used for”

PUBLICATIONS

- [Marcia Roy, Oksana Sorokina, Nathan Skene, Clemence Simonnet, Francesca Mazzo, Ruud Zwart, Emanuele Sher, Colin Smith, J Douglas Armstrong and Seth GN Grant \(2018\) Proteomic analysis of postsynaptic proteins in regions of the human neocortex. Nature Neuroscience 21:130–138](#)
-

T1.1.6: Computational, dynamic model of LTP and LTD in a wild type Schaffer Collateral synapse (ID: 560)**Dataset Owner:** David Sterratt < david.c.sterratt@ed.ac.uk > (UEDIN)**DATA SUMMARY****Purpose of the data collection/generation**

Data-driven models of synaptic plasticity and transmission at the molecular level will allow brain simulations to reflect synaptic diversity accurately and can be related directly to genetic manipulations and drug application. This work is will include proteins proteins such as PSD-95, mutations of which affect long term potentiation and long term depression. Also, the model will trial use of second generation rule-based languages such as Kappa or BNGL for synaptic simulations.

Relation to the objectives of the project

Objective 6b (Scaffold models of molecular-level principal neurons, cellular-level reconstructions of selected cortical and sub-cortical regions.)

Types and formats of data generated/collected**Types:** Model **Formats:** .ka**Protocol:****Existing data being re-used (if any)**

No

Origin of the data**Data class:** Molecular **Specimen information:** NA**Brain region:** [Hippocampus](#) **Subregion:** NA**Expected size of the data**

1GB

Data utility: to whom will it be useful

Within HBP: The model will trial 2nd generation rule-based methods that could be used by Task 4.3.1 ("Plasticity algorithms"), Task 6.1.2 (Data-driven modelling of G protein coupled receptor dependent cascades involved in neuromodulation and synaptic signalling) and Task 6.1.3 (Data-driven modelling of Ca²⁺ dependent cascades controlling synaptic signalling and homeostasis).

Outwith HBP: NA**FAIR DATA****Accessibility: which data will be made openly available**

Privacy class is: No privacy constraints. There are no issues sharing data

Accessibility: Methods, software tools and documentation needed to access the dataKaSim (<http://dev.executableknowledge.org>)**Re-use: Data licensing to permit the widest reuse possible**

BY - Attribution alone

Re-use: Data quality assurance processes**ETHICAL ASPECTS****Ethics approval authority:** NA **Ethics approval ID:** NA**RELEASES AND PROGRESS****Planned releases:**

Month	Shared.with Quality		Completeness	Location	Embargo	Actual.Completeness
M18	—	—	—	—	—	Complete – there is an executable model with a fit to the data
M22	Anonymous	Candidate final quality	Executable model	Github		Ditto

Any deviation and mitigation: NA**Current location(s) of dataset:**<https://github.com/davidcsterratt/ltp-ltd-sc>**DATA USAGE****Transferred to SP5/Shared with modelling tasks:** NA**Contribution to Use Cases /other SPs:** SP1-UC02: Biophysical model of LTP and LTD in wild type and mutant hippocampal CA1 synapses**What are datasets used for (models, atlas)?:** NA**Link to model/Atlas:** <https://github.com/davidcsterratt/ltp-ltd-sc>**How the data transfer has been or is coordinated:** NA

Role and take-up of the data acquired: The model “Computational, dynamic model of wild-type and PSD-95 KO LTP and LTD in a Schaffer Collateral synapse” will form the basis of work with Jeanette Hellgren Kotaleski (SGA2-T6.2.7 Models of subcellular signalling) and Dan Keller on models of calcium- and GCPR-dependent cascades, and models of synaptic plasticity.

PUBLICATIONS

T1.1.7: Synaptic plasticity dataset - hippocampus (ID: 2915)**Dataset Owner:** Enrico Cherubini < e.cherubini@ebri.it > (SNS, EBRI, CNR)**DATA SUMMARY****Purpose of the data collection/generation**

Ex vivo synaptic plasticity data will be collected and used for modelling. These data are relevant for the knowledge of potentiated spine specific pattern in relation to a defined protocol of stimuli. These data will give a link between synaptic plasticity (memory), circuit and activation at spine level

Relation to the objectives of the project

Plasticity data gathered in this task will also result in a selective activation of specific spines complying with the SO13 objective : spatial organization principles in brain activation

Types and formats of data generated/collected

Types: synaptic current **Formats:** .abf; .txts

Protocol: [Current clamp voltage recording protocol](#); [Electrical recording assay](#); [Electrical recording protocol](#); [Single electrode extracellular recording protocol](#); [Whole-cell voltage clamp recording protocol](#)

Existing data being re-used (if any)

No

Origin of the data

Data class: Electrophysiological **Specimen information:** Mouse, C57Bl6, male/female, 4 days old (for organotypic hippocampal cultures), pups, 5 gr, Plaisant

Brain region: [Hippocampus](#) **Subregion:** [CA1](#); [Hippocampus CA3 pyramidal cell](#)

Expected size of the data

GBs

Data utility: to whom will it be useful

Within HBP: This proteomic data is needed to constrain molecular models of synaptic plasticity (T1.1.6 and T6.2.4)

Outwith HBP: NA

FAIR DATA**Accessibility: which data will be made openly available**

Privacy class is: Animal Research. There are no issues sharing data

Accessibility: Methods, software tools and documentation needed to access the data

Microsoft Excel ; Clampfit (molecular device)

Re-use: Data licensing to permit the widest reuse possible

BY-NC-SA - Attribution + Noncommercial + ShareAlike

Re-use: Data quality assurance processes**ETHICAL ASPECTS**

Ethics approval authority: Italian Health Ministry **Ethics approval ID:** Authorization n.5/2015PR

RELEASES AND PROGRESS**Planned releases:**

Month	Shared	with Quality	Completeness	Location	Embargo	Actual Completeness
M18	—	—	—	—	—	The work in the new task on the activity-dependent synaptic proteome has already started and is progressing well; a paper on the underlying technique has been accepted for publication.
M23	Collab	Final quality	10 out of 15 recordings for each dataset	Collaboratory; awaiting CSCS data bucket	publication	Hippocampus: 50% (task started at M18, covering the gap of external call on proteomics that was not implemented)

Any deviation and mitigation: NA

Current location(s) of dataset:

<https://collab.humanbrainproject.eu/#/collab/11209/nav/83847>

DATA USAGE

Transferred to SP5/Shared with modelling tasks: NA

Contribution to Use Cases /other SPs: SGA2: SP6 T6.1.2, T6.1.5, T6.2.3

What are datasets used for (models, atlas)?: Models (to be used to inform future modelling efforts)

Link to model/Atlas: No model yet

How the data transfer has been or is coordinated: The coordination is in progress

Role and take-up of the data acquired: Ex vivo synaptic plasticity data (related to the proteome of activated spines) are relevant to link proteomic patterns specific to potentiated spines with defined plasticity inducing protocols. These data integrate with proteomic data of ex vivo potentiated synapses, providing a link between synaptic plasticity and activation at spine level. Plasticity data gathered in this task will also result in a selective activation of specific spines complying with the SO13 objective: spatial organization principles in brain activation. In collaboration with SP5 (WP5.1) these data are being curated to establish a container.

These datasets are instrumental to SP6 T6.2.4, T6.1.3, T6.1.4, SP1 T1.1.6 (SGA1) and they will be for SGA2 (SP6 T6.2.3) to implement models of the hippocampus, in both basal and learning/memory –activated conditions. Being the electrophysiological correlate of proteomic data, these synaptic plasticity data will provide the physiological substrate to model synaptic plasticity processes integrating the sub cellular and synaptic level (SP1 T1.4.3, SP4 WP4.3, SP5 WP5.1, SP6 T6.1.2, T6.1.5).
Specific list of propagation to other SPs and CDPs: SGA1: T1.1.6, T4.3, T5.1, T6.1.3, T6.1.4. T6.2.4. SGA2: T1.4.3, T4.3, T5.1, T6.1.2, T6.1.5, T6.2.3

PUBLICATIONS

T1.1.7: Subcellular proteomics dataset - hippocampus (ID: 2916)**Dataset Owner:** Antonino Cattaneo < antonino.cattaneo@sns.it > (SNS)**DATA SUMMARY****Purpose of the data collection/generation**

Functional potentiation of synapse transmission is underlied by a number of modifications in protein content of the synapse, particularly on the postsynaptic side. These include: (i) re-localization of proteins between the spine and the dendrite regions, (ii) modifications of pre-existing proteins, (iii) new synthesis of proteins, and (iv) selective degradation of proteins. A number of proteins that fall into one of these categories have been identified, although many other members are likely to be still undiscovered. A hub of postsynaptic proteome, organizing structural modifications instrumental to synaptic plasticity, is PSD95. This task aims at collecting data to perform a direct, unbiased comparison between the synaptic proteomes of resting and potentiated synapses. This will provide a complete list of proteins whose levels are changed in potentiated synapses (either up- or downregulated). In addition, a novel method to purify synaptosomes will be set up to compare the synaptomes of resting and potentiated synapses, thus extending our understanding of the molecular underpinnings of structural plasticity beyond the PSD95 interactome.

Relation to the objectives of the project

Accomplishment of this task will result in a nanoscale analysis of the proteome of potentiated synapses, thus fulfilling objective SO13. In addition, comparative analysis of potentiated and resting synapses will shed light on the nanoscopic principles of structural organization of the brain, thus contributing to SO16.

Types and formats of data generated/collected

Types: Subcellular proteome (differential analysis between samples). **Formats:** .csv, .txt, .docx, .xlsx

Protocol: [Biochemical specimen preparation protocol](#); [Immunoprecipitation protocol](#); [Immunohistochemical protocol](#); [Western blot protocol](#); AAV infection LS/MS proteomics

Existing data being re-used (if any)

No

Origin of the data

Data class: Molecular **Specimen information:** Mouse, C57BL/6J, both sexes, 2 months old, 25 gr, Jackson lab Mouse, C57Bl6, male/female, 4 days old (for organotypic hippocampal cultures), pups, 5 gr, Plaisant

Brain region: [Hippocampus](#) **Subregion:** [CA1](#); [Hippocampus CA3 pyramidal cell](#)

Expected size of the data

0.5-2 GB

Data utility: to whom will it be useful

Within HBP: This proteomic data is needed to constrain molecular models of synaptic plasticity (T1.1.6 and T6.2.4) and for the physiological characterization of hippocampal synapses (T1.2.6) and for the whole-brain cell- resolution activity maps (T1.3.4)

Outwith HBP: NA

FAIR DATA**Accessibility: which data will be made openly available**

Privacy class is: Animal Research. There are no issues sharing data

Accessibility: Methods, software tools and documentation needed to access the data

Microsoft Excel and Word; Open Office package

Re-use: Data licensing to permit the widest reuse possible

BY-NC-SA - Attribution + Noncommercial + ShareAlike

Re-use: Data quality assurance processes**ETHICAL ASPECTS**

Ethics approval authority: Italian Health Ministry **Ethics approval ID:** Authorization n.5/2015PR

RELEASES AND PROGRESS**Planned releases:**

Month	Shared.with	Quality	Completeness	Location	Embargo	Actual.Completeness
M22	Collab	Candidate final quality	3 biological replicates per sample	Collaboratory	Awaiting publication	—
M23	Collab	Final quality	A total of 5 biological replicates per experimental group.	CSCS data bucket	Awaiting publication	Hippocampus: 70% (task started at M18, covering the gap of external call on proteomics that was not implemented)

Any deviation and mitigation: NA

Current location(s) of dataset:

<https://collab.humanbrainproject.eu/#/collab/11209/nav/83847>

DATA USAGE

Transferred to SP5/Shared with modelling tasks: NA

Contribution to Use Cases /other SPs: SGA2: SP6 T6.1.2, T6.1.3, T6.1.5, T6.2.3

What are datasets used for (models, atlas)?: Models (to be used to inform future modelling efforts)

Link to model/Atlas: No model yet

How the data transfer has been or is coordinated: The coordination is in progress

Role and take-up of the data acquired: We have generated a first proteomic dataset from potentiated synapses in the hippocampus, along with a control dataset. This allows, for the first time, to perform a differential screening to extract the activity-dependent interactome of the PSD-95 synaptic hub from in vivo samples. In addition, we have also started collecting proteomic datasets from the whole synaptome (the entire proteome of a synapse) of potentiated synapses and this will be further pursued in SGA2.

These new strategic proteomic datasets complement curated datasets from published studies (SGA1 T1.1.6) and have already been integrated into the HBP collab 11209/nav/83847. With regard to other SP's, these datasets are instrumental to (i) SP6 T6.1.3 (SGA1); T6.1.2 (SGA2), as activation of calcium-dependent cascades is key to synaptic plasticity; (ii) SP6 T6.1.4 (SGA1); T6.1.5 (SGA2), as we are providing information on a specific subcellular domain to be integrated in the single neuron model; (iii) SP T6.2.4 (SGA1); T6.2.3 (SGA2), as we are contributing data to model the hippocampal functioning in both basal and learning-activated conditions; (iv) SP4 WP4.3 (SGA1;SGA2), as we are providing the molecular and cellular substrate to model synaptic plasticity and learning/memory processes.

Specific list of propagation to other SPs and CDPs: SGA1: T1.1.6, T4.3, T5.1, T6.1.3, T6.1.4, T6.2.4. SGA2: T1.4.3, T4.3, T5.1, T6.1.2, T6.1.5, T6.2.3

PUBLICATIONS

T1.1.7: Extending coverage of published data (ID: 2917)

Dataset Owner: Douglas Armstrong, Antonino Cattaneo < douglas.armstrong@ed.ac.uk; antonino.cattaneo@sns.it > (UEDIN)

DATA SUMMARY**Purpose of the data collection/generation**

All proteomics lists maintained (including T1.1.7, ID 422) 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

Relation to the objectives of the project

Objective 1c (Microcircuitry analysis, proteins and receptor distributions, fibre architecture in a specific large area brain region)

Types and formats of data generated/collected

Types: Tables of PPIs, mitab25 standard **Formats:** csv, gml, xls

Protocol:**Existing data being re-used (if any)**

Yes. The IntAct, BioGRID and DIP databases.

Origin of the data

Data class: Molecular **Specimen information:** Human, Mouse (gene mappings)

Brain region: [Forebrain](#) **Subregion:**

Expected size of the data

1GB

Data utility: to whom will it be useful

Within HBP: Cluster analysis of protein networks can be combined with functional gene annotation (T8.4.1; T1.1.7) to find protein subnetworks associated with biological function and disease. It will also help to constrain dynamic models of protein-protein networks in SGA2 SP6 submolecular tasks.

Outwith HBP: NA

FAIR DATA**Accessibility: which data will be made openly available**

Privacy class is: No privacy constraints. There are no issues sharing data

Accessibility: Methods, software tools and documentation needed to access the data

Software to read tables, e.g. Excel, R, python

Re-use: Data licensing to permit the widest reuse possible

We need to match BIOGRID, IntAct and DIP terms & licences to CC licenses

Re-use: Data quality assurance processes**ETHICAL ASPECTS**

Ethics approval authority: NA **Ethics approval ID:** NA

RELEASES AND PROGRESS**Planned releases:**

Month	Shared.with	Quality	Completeness	Location	Embargo	Actual.Completeness
M23	Consortium	Final quality	Integrated and up to date set of published proteomics	Collaboratory	Awaiting publication	5 datasets added; number of genes increased to 6899 (from 6500); PPI postsynaptic proteome (PSP) network size to 4752 (from 3457), and the PPI PSP reduced network size to 2156 (from 1868); 100% of current availability.

Any deviation and mitigation: NA

Current location(s) of dataset:

4

DATA USAGE

Transferred to SP5/Shared with modelling tasks: NA

Contribution to Use Cases /other SPs: NA

What are datasets used for (models, atlas)? This dataset has been shared with Paolo Carloni's group (SP6). The group has started to identify the effect of disease-linked mutations on the protein interactome at the human synapse by bioinformatics and molecular simulation. This work will continue in SGA2.

Link to model/Atlas: No model yet

How the data transfer has been or is coordinated: The data transfer has been coordinated by Skype meetings and email, with the data itself being shared via the collab.

Role and take-up of the data acquired: See “what datasets are used for”

PUBLICATIONS

- [Marcia Roy, Oksana Sorokina, Nathan Skene, Clemence Simonnet, Francesca Mazzo, Ruud Zwart, Emanuele Sher, Colin Smith, J Douglas Armstrong and Seth GN Grant \(2018\) Proteomic analysis of postsynaptic proteins in regions of the human neocortex. Nature Neuroscience 21:130–138](#)
-

T1.1.7: Genetic mapping to single cell profiles (ID: 2918)

Dataset Owner: Douglas Armstrong, Antonino Cattaneo < douglas.armstrong@ed.ac.uk; antonino.cattaneo@sns.it > (UEDIN)

DATA SUMMARY**Purpose of the data collection/generation**

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.

Relation to the objectives of the project

Objective 1c (Microcircuitry analysis, proteins and receptor distributions, fibre architecture in a specific large area brain region)

Types and formats of data generated/collected

Types: Mapping tables **Formats:** xls

Protocol:

Existing data being re-used (if any)

Yes

Origin of the data

Data class: Molecular **Specimen information:** Human, Mouse

Brain region: [Cerebral cortex](#); [Ventral midbrain](#); [Hypothalamus](#) **Subregion:**

Expected size of the data

1GB

Data utility: to whom will it be useful

Within HBP:

Outwith HBP: NA

FAIR DATA**Accessibility: which data will be made openly available**

Privacy class is: No privacy constraints. There are no issues sharing data

Accessibility: Methods, software tools and documentation needed to access the data

Software to read tables, e.g. Excel, R, python

Re-use: Data licensing to permit the widest reuse possible

We need to match BIOGRID, IntAct and DIP terms & licences to CC licenses

Re-use: Data quality assurance processes**ETHICAL ASPECTS**

Ethics approval authority: NA **Ethics approval ID:** NA

RELEASES AND PROGRESS**Planned releases:**

Month	Shared.with	Quality	Completeness	Location	Embargo	Actual.Completeness
M23	Consortium	Final quality	Extraction of mouse single cell transcriptome data and cross-referencing with synaptic proteins	Collaboratory	Awaiting publication	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.

Any deviation and mitigation: NA

Current location(s) of dataset:

<https://collab.humanbrainproject.eu/#/collab/5961/nav/46154>

DATA USAGE

Transferred to SP5/Shared with modelling tasks: NA

Contribution to Use Cases /other SPs: NA

What are datasets used for (models, atlas)?: This dataset will be used to inform modelling efforts in SP6 and will feed into our own bioinformatic analyses.

Link to model/Atlas: No model yet

How the data transfer has been or is coordinated: NA

Role and take-up of the data acquired: See “what datasets are used for”

PUBLICATIONS

T1.1.7: Integration of functional data into synapse models (ID: 2919)

Dataset Owner: Douglas Armstrong, Antonino Cattaneo < douglas.armstrong@ed.ac.uk; antonino.cattaneo@sns.it > (UEDIN)

DATA SUMMARY**Purpose of the data collection/generation**

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.

Relation to the objectives of the project

Objective 1c (Microcircuitry analysis, proteins and receptor distributions, fibre architecture in a specific large area brain region)

Types and formats of data generated/collected

Types: Mapping tables **Formats:** xls

Protocol:

Existing data being re-used (if any)

Yes

Origin of the data

Data class: Molecular **Specimen information:** Human, Mouse (gene mappings)

Brain region: Subregion:

Expected size of the data

1GB

Data utility: to whom will it be useful

Within HBP:

Outwith HBP: NA

FAIR DATA**Accessibility: which data will be made openly available**

Privacy class is: No privacy constraints. There are no issues sharing data

Accessibility: Methods, software tools and documentation needed to access the data

Software to read tables, e.g. Excel, R, python

Re-use: Data licensing to permit the widest reuse possible

We need to match BIOGRID, IntAct and DIP terms & licences to CC licenses

Re-use: Data quality assurance processes**ETHICAL ASPECTS**

Ethics approval authority: NA **Ethics approval ID:** NA

RELEASES AND PROGRESS**Planned releases:**

Month	Shared.with	Quality	Completeness	Location	Embargo	Actual.Completeness
M23	Consortium	Final quality	Mapping of IMPC phenotype terms linked to mutations in identified genes to synaptic protein datasets	Collaboratory	Awaiting publication	Of 3343 genes with completed phenotyping available from IMPC version 5.0, 980 genes (30%) found in synaptic datasets. 100% mapped to last release of IMPC.

Any deviation and mitigation: NA

Current location(s) of dataset:

<https://collab.humanbrainproject.eu/#/collab/5961/nav/46154>

DATA USAGE

Transferred to SP5/Shared with modelling tasks: NA

Contribution to Use Cases /other SPs: NA

What are datasets used for (models, atlas)? This dataset has been shared with Paolo Carloni's group (SP6). The group has started to identify the effect of disease-linked mutations on the protein interactome at the human synapse by bioinformatics and molecular simulation. This work will continue in SGA2.

Link to model/Atlas: No model yet.

How the data transfer has been or is coordinated: The data transfer has been coordinated by Skype meetings and email, with the data itself being shared via the collab.

Role and take-up of the data acquired: We are in discussions with Sven Cichon (SP8) about how this data could be used to assist with relating subnetworks of proteins to disease.

PUBLICATIONS

T1.2.1: 3D reconstructions pyramidal neurons mouse cortex (ID: 955)**Dataset Owner:** Javier DeFelipe < defelipe@cajal.csic.es > (UPM)**DATA SUMMARY****Purpose of the data collection/generation**

We will produce 3D reconstructions of 300 pyramidal neurons from the mouse somatosensory cortex across layers II-VI using Neurolucida software from 3D confocal stack of images.

Relation to the objectives of the project

The data is directly related to the objectives 1c and 1d, Microcircuitry analysis, proteins and receptor distributions, fibre architecture in a specific large area brain region and Maps of cellular distributions, long-range axonal projections, and synaptic proteins; reconstructed morphologies of major neuron types

Types and formats of data generated/collected

Types: 3D cell reconstructions **Formats:** .xls, .DAT

Protocol: 3D reconstructions of intracellularly injected cells using confocal microscopy

Existing data being re-used (if any)

No

Origin of the data

Data class: Cellular **Specimen information:** Mouse C57Bl male, adult, 8 weeks

Brain region: Somatosensory cortex **Subregion:** Primary somatosensory cortex

Expected size of the data

5 GB

Data utility: to whom will it be useful

Within HBP: Data from 3D reconstructions of pyramidal cells in mouse neocortex will be useful to modelling and integration of anatomical data with functional studies in mouse brain. Data will be useful for example for tasks 6.1.3, T1.5.5, T 1.3.4, T6.2.2.

Outwith HBP: NA

FAIR DATA**Accessibility: which data will be made openly available**

Privacy class is: Animal Research. There are no issues sharing data

Accessibility: Methods, software tools and documentation needed to access the data

Neurolucida explorer, Microsoft excel

Re-use: Data licensing to permit the widest reuse possible

BY-NC

Re-use: Data quality assurance processes**ETHICAL ASPECTS**

Ethics approval authority: Local Ethics Committee (CSIC) ES280790000184 **Ethics approval ID:** CEAA-IC Approval

RELEASES AND PROGRESS**Planned releases:**

Month	Shared.with	Quality	Completeness	Location	Embargo	Actual.Completeness
M18	Collab	Candidate final quality	70 out of 300 3D reconstructions of cells	Collaboratory	Awaiting publication	At M18, 70 cells reconstructed.
M23	Collab	Candidate final quality	120 out of 300 3D reconstructions of cells	Collaboratory	Awaiting publication	169 cells reconstructed

Any deviation and mitigation: NA

Current location(s) of dataset:

<https://collab.humanbrainproject.eu/#/collab/17043/nav/123272>

DATA USAGE

Transferred to SP5/Shared with modelling tasks: NA

Contribution to Use Cases /other SPs: SP1-UC01: 3D reconstruction and visualization of microanatomical parameters of pyramidal cells: PyramidalExplorer; SP4 (T4.1.1): complex to simplified models (model) and T1.4.3; SP6 (T6.2.2)

What are datasets used for (models, atlas)?: Models (SP4) Simplified Dendritic Neuron Models & Input-Output Transfer Functions of Morphologically Detailed Neuronal Models

Link to model/Atlas: <https://collab.humanbrainproject.eu/#/collab/1655/nav/75901>

How the data transfer has been or is coordinated: It has been coordinated with the Data Curation Team (Krister Andersson) and with meetings with model builders

Role and take-up of the data acquired: This dataset has been generated by task T1.2.1. Pyramidal neurons are key components of the cerebral cortex, where they are the predominant cell type. The structural design of brain circuits depends on the type, number and position of neurons, as well as the synaptic connections that they establish. During SGA1 we have obtained quantitative information about several relevant features of pyramidal neurons, such as the extension of their dendritic trees, their branching patterns, and the density of dendritic spines, from which the number of synaptic inputs can be derived. These data have been obtained from the hippocampus and the neocortex of rodents and humans. Knowing these structural properties is crucial for building, validating and refining brain models. This dataset has been used in SP1 (T1.2.2), SP2 (T1.2.5) and SP4 (T1.4.3 for comparative studies and integration,; in SP2 (T1.2.6 for comparative studies); and the dataset has been used or will be used for modeling proposes in SP4 (T4.1.1, T4.1.2, T4.2.1, T4.5.1), SP6 (T6.2.1, T6.2.2, T6.2.3, T6.3.3, T6.2.4, T6.2.5) and CDP2. See the list of SP1 publications.

PUBLICATIONS

- [Fernandez-Gonzalez P, Benavides-Piccione R, Leguey I, Bielza C, Larrañaga P, DeFelipe J. \(2016\). Dendritic-branching angles of pyramidal neurons of the human cerebral cortex. *Brain Struct Funct.* 2016 Sep 30.](#)
 - [Eyal G, Verhoog MB, Testa-Silva G, Deitcher Y, Lodder JC, Benavides-Piccione R, Morales J, DeFelipe J, de Kock CP, Mansvelder HD, Segev I. Unique membrane properties and enhanced signal processing in human neocortical neurons. *Elife.* 2016 Oct 6;5. pii: e16553. doi: 10.7554/eLife.16553.](#)
 - [Rodríguez-Lopez C., Clasca F, Prensa L. \(2017\) The Mesoaccumbens Pathway: A Retrograde Labeling and Single-Cell Axon Tracing Analysis in the Mouse. \(2017\) *Front. Neuroanat.* 2017 March 27 11:25 eCollection Mar 27 <https://doi.org/10.3389/fnana.2017.00025>](#)
 - [Alejandro Antón-Fernández, Guillermo Aparicio-Torres, Silvia Tapia, Javier DeFelipe, Alberto Muñoz \(2016\). Morphometric alterations of Golgi apparatus in Alzheimer's disease are related to tau hyperphosphorylation. *Neurobiology of Disease* \(97\) 2017 11-23](#)
 - [Carolina Gonzalez-Riano, Silvia Tapia-Gonzalez, Antonia García, Alberto Muñoz, Javier DeFelipe, Coral Barbas \(2017\). Metabolomics and neuroanatomical evaluation of post mortem changes in the hippocampus. *Brain Struct Funct.* DOI: 10.1007/s00429-017-1375-5](#)
 - [Bosch C, Masachs N, Exposito-Alonso D, Martínez A, Teixeira CM, Feraud I, Pujadas L, Ulloa F, Comella JX, DeFelipe J, Merchán-Pérez A, Soriano E. \(2016\). Reelin Regulates the Maturation of Dendritic Spines, Synaptogenesis and Glial Ensheathment of Newborn Granule Cells. *Cereb Cortex.* 2016 Sep 13.](#)
 - [Anton-Sanchez L, Bielza C, Benavides-Piccione R, DeFelipe J, Larrañaga P. \(2016\). Dendritic and Axonal Wiring Optimization of Cortical GABAergic Interneurons. *Neuroinformatics.* 2016 Oct; 14 \(4\):453-64. doi: 10.1007/s12021-016-9309-6](#)
 - [Anton-Sanchez, L., P. Larrañaga, R. Benavides-Piccione, I. Feraud, J. DeFelipe, and C. Bielza, "Three-dimensional spatial modeling of spines along dendritic networks in human cortical pyramidal neurons", *PLoS ONE* 12\(6\): e0180400, 2017](#)
 - [Barth et al., Comment on "Principles of connectivity among morphologically defined cell types in adult neocortex" *Science* 09 Sep 2016: Vol. 353, Issue 6304, pp. 1108](#)
-

T1.2.1: 3D reconstructions mouse hippocampus (ID: 956)**Dataset Owner:** Javier DeFelipe < defelipe@cajal.csic.es > (UPM)**DATA SUMMARY****Purpose of the data collection/generation**

We will produce 3D reconstructions of 50 cells in mouse hippocampal CA1 region using Neurolucida software from 3D confocal stack of images.

Relation to the objectives of the project

The data is directly related to the objectives 1c and 1d, Microcircuitry analysis, proteins and receptor distributions, fibre architecture in a specific large area brain region and Maps of cellular distributions, long-range axonal projections, and synaptic proteins; reconstructed morphologies of major neuron types

Types and formats of data generated/collected

Types: 3D cell reconstructions **Formats:** .xls, .DAT

Protocol: 3D reconstructions of intracellularly injected cells using confocal microscopy

Existing data being re-used (if any)

No

Origin of the data

Data class: Cellular **Specimen information:** Mouse C57Bl male, adult, 8 weeks

Brain region: Hippocampus **Subregion:** CA1

Expected size of the data

5 GB

Data utility: to whom will it be useful

Within HBP: Data from 3D reconstructions of pyramidal cells in mouse hippocampus will be useful to modelling and integration of anatomical data with functional studies in mouse hippocampus. Data will be useful for example for tasks 6.1.3, T6.2.3, T 1.5.5, T6.2.4.

Outwith HBP: NA

FAIR DATA**Accessibility: which data will be made openly available**

Privacy class is: Animal Research. There are no issues sharing data

Accessibility: Methods, software tools and documentation needed to access the data

Neurolucida explorer, Microsoft excel

Re-use: Data licensing to permit the widest reuse possible

BY-NC

Re-use: Data quality assurance processes**ETHICAL ASPECTS**

Ethics approval authority: Local Ethics Committee (CSIC) ES280790000184 **Ethics approval ID:** CEAA-IC Approval

RELEASES AND PROGRESS**Planned releases:**

Month	Shared.with	Quality	Completeness	Location	Embargo	Actual.Completeness
M18	Collab	Candidate final quality	25 out of 50 3D reconstructions of cells	Collaboratory	Awaiting publication	At M18, 25 cells reconstructed.
M23	Collab	Candidate final quality	50 out of 50 3D reconstructions of cells	Collaboratory	Awaiting publication	50 cells reconstructed

Any deviation and mitigation: NA

Current location(s) of dataset:

<https://collab.humanbrainproject.eu/#/collab/17044/nav/123277>

DATA USAGE

Transferred to SP5/Shared with modelling tasks: NA

Contribution to Use Cases /other SPs: 3D reconstruction and visualization of microanatomical parameters of pyramidal cells: PyramidalExplorer SP1-UC01: 3D reconstruction and visualization of microanatomical parameters of pyramidal cells: PyramidalExplorer; SP4 (T4.1.1): complex to simplified models (model) and T1.4.3; SP6 (T6.2.2)

What are datasets used for (models, atlas)?: Models (SP4) Simplified Dendritic Neuron Models & Input-Output Transfer Functions of Morphologically Detailed Neuronal Models

Link to model/Atlas: <https://collab.humanbrainproject.eu/#/collab/1655/nav/75902>

How the data transfer has been or is coordinated: It has been coordinated with the Data Curation Team (Krister Andersson) and with meetings with model builders

Role and take-up of the data acquired: This dataset has been generated by task T1.2.1. See component ID 955 for the information on the role and take up of the acquired data in this task.

PUBLICATIONS

- Fernandez-Gonzalez P, Benavides-Piccione R, Leguey I, Bielza C, Larrañaga P, DeFelipe J. (2016). Dendritic-branching angles of pyramidal neurons of the human cerebral cortex. *Brain Struct Funct.* 2016 Sep 30.
 - Eyal G, Verhoog MB, Testa-Silva G, Deitcher Y, Lodder JC, Benavides-Piccione R, Morales J, DeFelipe J, de Kock CP, Mansvelder HD, Segev I. Unique membrane properties and enhanced signal processing in human neocortical neurons. *Elife.* 2016 Oct 6;5. pii: e16553. doi: 10.7554/eLife.16553.
 - Rodriguez-Lopez C., Clasca F, Prensa L. (2017) The Mesoaccumbens Pathway: A Retrograde Labeling and Single-Cell Axon Tracing Analysis in the Mouse. (2017) *Front. Neuroanat.* 2017 March 27 11:25 eCollection Mar 27 <https://doi.org/10.3389/fnana.2017.00025>
 - Alejandro Antón-Fernández, Guillermo Aparicio-Torres, Silvia Tapia, Javier DeFelipe, Alberto Muñoz (2016). Morphometric alterations of Golgi apparatus in Alzheimer's disease are related to tau hyperphosphorylation. *Neurobiology of Disease* (97) 2017 11-23
 - Carolina Gonzalez-Riano, Silvia Tapia-Gonzalez, Antonia García, Alberto Muñoz, Javier DeFelipe, Coral Barbas (2017). Metabolomics and neuroanatomical evaluation of post mortem changes in the hippocampus. *Brain Struct Funct.* DOI: 10.1007/s00429-017-1375-5
 - Bosch C, Masachs N, Exposito-Alonso D, Martínez A, Teixeira CM, Feraud I, Pujadas L, Ulloa F, Comella JX, DeFelipe J, Merchán-Pérez A, Soriano E. (2016). Reelin Regulates the Maturation of Dendritic Spines, Synaptogenesis and Glial Ensheathment of Newborn Granule Cells. *Cereb Cortex.* 2016 Sep 13.
 - Anton-Sanchez L, Bielza C, Benavides-Piccione R, DeFelipe J, Larrañaga P. (2016). Dendritic and Axonal Wiring Optimization of Cortical GABAergic Interneurons. *Neuroinformatics.* 2016 Oct; 14 (4):453-64. doi: 10.1007/s12021-016-9309-6
 - Anton-Sanchez, L., P. Larrañaga, R. Benavides-Piccione, I. Feraud, J. DeFelipe, and C. Bielza, "Three-dimensional spatial modeling of spines along dendritic networks in human cortical pyramidal neurons", *PLoS ONE* 12(6): e0180400, 2017
 - Barth et al., Comment on "Principles of connectivity among morphologically defined cell types in adult neocortex" *Science* 09 Sep 2016: Vol. 353, Issue 6304, pp. 1108
-

T1.2.1: 3D reconstructions rat hippocampus (ID: 957)**Dataset Owner:** Javier DeFelipe < defelipe@cajal.csic.es > (UPM)**DATA SUMMARY****Purpose of the data collection/generation**

We will produce 3D reconstructions of 50 cells in rat hippocampal CA1 region using Neurolucida software from 3D confocal stack of images.

Relation to the objectives of the project

The data is directly related to the objectives 1c and 1d, Microcircuitry analysis, proteins and receptor distributions, fibre architecture in a specific large area brain region and Maps of cellular distributions, long-range axonal projections, and synaptic proteins; reconstructed morphologies of major neuron types

Types and formats of data generated/collected

Types: 3D cell reconstructions **Formats:** .xls, .DAT

Protocol: 3D reconstructions of intracellularly injected cells using confocal microscopy

Existing data being re-used (if any)

No

Origin of the data

Data class: Cellular **Specimen information:** Wistar rats , male, adult

Brain region: Hippocampus **Subregion:** CA1

Expected size of the data

5 GB

Data utility: to whom will it be useful

Within HBP: Data from 3D reconstructions of pyramidal cells in rat hippocampus will be useful to modelling and integration of anatomical data with functional studies in rat hippocampus. Data will be useful for example for tasks 6.1.3, T6.2.3, T 1.4.1, T6.2.4.

Outwith HBP: NA

FAIR DATA**Accessibility: which data will be made openly available**

Privacy class is: Animal Research. There are no issues sharing data

Accessibility: Methods, software tools and documentation needed to access the data

Neurolucida explorer, Microsoft excel

Re-use: Data licensing to permit the widest reuse possible

BY-NC

Re-use: Data quality assurance processes**ETHICAL ASPECTS**

Ethics approval authority: Local Ethics Committee (CSIC) ES280790000184 **Ethics approval ID:** CEAA-IC Approval

RELEASES AND PROGRESS**Planned releases:**

Month	Shared.with	Quality	Completeness	Location	Embargo	Actual.Completeness
M18	Collab	Candidate final quality	30 out of 50 3D reconstructions of cells	Collaboratory	Awaiting publication	At M18, 30 cells reconstructed .
M23	Collab	Candidate final quality	50 out of 50 3D reconstructions of cells	Collaboratory	Awaiting publication	50 cells reconstructed

Any deviation and mitigation: NA

Current location(s) of dataset:

<https://collab.humanbrainproject.eu/#/collab/17045/nav/123286>

DATA USAGE

Transferred to SP5/Shared with modelling tasks: NA

Contribution to Use Cases /other SPs: SP1-UC01: 3D reconstruction and visualization of microanatomical parameters of pyramidal cells: PyramidalExplorer; SP4 (T4.1.1): complex to simplified models (model) and T1.4.3; SP6 (T6.2.2)

What are datasets used for (models, atlas)?: Models (SP4) Simplified Dendritic Neuron Models & Input-Output Transfer Functions of Morphologically Detailed Neuronal Models

Link to model/Atlas: <https://collab.humanbrainproject.eu/#/collab/1655/nav/75903>

How the data transfer has been or is coordinated: It has been coordinated with the Data Curation Team (Krister Andersson) and with meetings with model builders

Role and take-up of the data acquired: This dataset has been generated by task T1.2.1. See component ID 955 for the information on the role and take up of the acquired data in this task.

PUBLICATIONS

- Fernandez-Gonzalez P, Benavides-Piccione R, Leguey I, Bielza C, Larrañaga P, DeFelipe J. (2016). Dendritic-branching angles of pyramidal neurons of the human cerebral cortex. *Brain Struct Funct.* 2016 Sep 30.
 - Eyal G, Verhoog MB, Testa-Silva G, Deitcher Y, Lodder JC, Benavides-Piccione R, Morales J, DeFelipe J, de Kock CP, Mansvelder HD, Segev I. Unique membrane properties and enhanced signal processing in human neocortical neurons. *Elife.* 2016 Oct 6;5. pii: e16553. doi: 10.7554/eLife.16553.
 - Rodriguez-Lopez C., Clasca F, Prensa L. (2017) The Mesoaccumbens Pathway: A Retrograde Labeling and Single-Cell Axon Tracing Analysis in the Mouse. (2017) *Front. Neuroanat.* 2017 March 27 11:25 eCollection Mar 27 <https://doi.org/10.3389/fnana.2017.00025>
 - Alejandro Antón-Fernández, Guillermo Aparicio-Torres, Silvia Tapia, Javier DeFelipe, Alberto Muñoz (2016). Morphometric alterations of Golgi apparatus in Alzheimer's disease are related to tau hyperphosphorylation. *Neurobiology of Disease* (97) 2017 11-23
 - Carolina Gonzalez-Riano, Silvia Tapia-Gonzalez, Antonia García, Alberto Muñoz, Javier DeFelipe, Coral Barbas (2017). Metabolomics and neuroanatomical evaluation of post mortem changes in the hippocampus. *Brain Struct Funct.* DOI: 10.1007/s00429-017-1375-5
 - Bosch C, Masachs N, Exposito-Alonso D, Martínez A, Teixeira CM, Feraud I, Pujadas L, Ulloa F, Comella JX, DeFelipe J, Merchán-Pérez A, Soriano E. (2016). Reelin Regulates the Maturation of Dendritic Spines, Synaptogenesis and Glial Ensheathment of Newborn Granule Cells. *Cereb Cortex.* 2016 Sep 13.
 - Anton-Sanchez L, Bielza C, Benavides-Piccione R, DeFelipe J, Larrañaga P. (2016). Dendritic and Axonal Wiring Optimization of Cortical GABAergic Interneurons. *Neuroinformatics.* 2016 Oct; 14 (4):453-64. doi: 10.1007/s12021-016-9309-6
 - Anton-Sanchez, L., P. Larrañaga, R. Benavides-Piccione, I. Feraud, J. DeFelipe, and C. Bielza, "Three-dimensional spatial modeling of spines along dendritic networks in human cortical pyramidal neurons", *PLoS ONE* 12(6): e0180400, 2017
 - Barth et al., Comment on "Principles of connectivity among morphologically defined cell types in adult neocortex" *Science* 09 Sep 2016: Vol. 353, Issue 6304, pp. 1108
-

T1.2.1: 3D reconstructions human hippocampus (ID: 958)**Dataset Owner:** Javier DeFelipe < defelipe@cajal.csic.es > (UPM)**DATA SUMMARY****Purpose of the data collection/generation**

We will produce 3D reconstructions of 50 cells in human hippocampal CA1 region using Neurolucida software from 3D confocal stack of images.

Relation to the objectives of the project

The data is directly related to the objectives 1c and 1d, Microcircuitry analysis, proteins and receptor distributions, fibre architecture in a specific large area brain region and Maps of cellular distributions, long-range axonal projections, and synaptic proteins; reconstructed morphologies of major neuron types

Types and formats of data generated/collected

Types: 3D cell reconstructions **Formats:** .xls, .DAT

Protocol: 3D reconstructions of intracellularly injected cells using confocal microscopy

Existing data being re-used (if any)**Origin of the data**

Data class: Cellular **Specimen information:** Human Adult

Brain region: Hippocampus **Subregion:** CA1

Expected size of the data

5 GB

Data utility: to whom will it be useful

Within HBP: Data from 3D reconstructions of pyramidal cells in human hippocampus will be useful to modelling and integration of anatomical data with functional studies in hippocampus. Data will be useful for example for tasks T6.1.3, T1.5.5.

Outwith HBP: NA

FAIR DATA**Accessibility: which data will be made openly available**

Privacy class is: Human Research. There may be issues sharing data openly

Accessibility: Methods, software tools and documentation needed to access the data

Neurolucida explorer, Microsoft excel

Re-use: Data licensing to permit the widest reuse possible

BY-NC

Re-use: Data quality assurance processes**ETHICAL ASPECTS**

Ethics approval authority: Local Ethics Committee (CSIC) ES280790000184 **Ethics approval ID:** CEAA-IC Approval & CEI PI55-2016

RELEASES AND PROGRESS**Planned releases:**

Month	Shared.with	Quality	Completeness	Location	Embargo	Actual.Completeness
M18	Collab	Final quality	50 out of 50 3D reconstructions of cells	Collaboratory	Awaiting publication	At M18, 50 cells reconstructed.
M23	Ditto	Ditto	Ditto	Ditto	Ditto	50 cells reconstructed

Any deviation and mitigation: NA

Current location(s) of dataset:

<https://collab.humanbrainproject.eu/#/collab/17047/nav/123296>

DATA USAGE

Transferred to SP5/Shared with modelling tasks: NA

Contribution to Use Cases /other SPs: SP1-UC01: 3D reconstruction and visualization of microanatomical parameters of pyramidal cells: PyramidalExplorer; SP4 (T4.1.1): complex to simplified models (model) and T1.4.3; SP6 (T6.2.2)

What are datasets used for (models, atlas)?: Models (SP4) Simplified Dendritic Neuron Models & Input-Output Transfer Functions of Morphologically Detailed Neuronal Models

Link to model/Atlas: <https://collab.humanbrainproject.eu/#/collab/1655/nav/75905>

How the data transfer has been or is coordinated: It has been coordinated with the Data Curation Team (Krister Andersson) and with meetings with model builders

Role and take-up of the data acquired: This dataset has been generated by task T1.2.1. See component ID 955 for the information on the role and take up of the acquired data in this task.

PUBLICATIONS

- Fernandez-Gonzalez P, Benavides-Piccione R, Leguey I, Bielza C, Larrañaga P, DeFelipe J. (2016). Dendritic-branching angles of pyramidal neurons of the human cerebral cortex. *Brain Struct Funct.* 2016 Sep 30.
 - Eyal G, Verhoog MB, Testa-Silva G, Deitcher Y, Lodder JC, Benavides-Piccione R, Morales J, DeFelipe J, de Kock CP, Mansvelder HD, Segev I. Unique membrane properties and enhanced signal processing in human neocortical neurons. *Elife.* 2016 Oct 6;5. pii: e16553. doi: 10.7554/eLife.16553.
 - Rodriguez-Lopez C., Clasca F, Prensa L. (2017) The Mesoaccumbens Pathway: A Retrograde Labeling and Single-Cell Axon Tracing Analysis in the Mouse. (2017) *Front. Neuroanat.* 2017 March 27 11:25 eCollection Mar 27 <https://doi.org/10.3389/fnana.2017.00025>
 - Alejandro Antón-Fernández, Guillermo Aparicio-Torres, Silvia Tapia, Javier DeFelipe, Alberto Muñoz (2016). Morphometric alterations of Golgi apparatus in Alzheimer's disease are related to tau hyperphosphorylation. *Neurobiology of Disease* (97) 2017 11-23
 - Carolina Gonzalez-Riano, Silvia Tapia-Gonzalez, Antonia García, Alberto Muñoz, Javier DeFelipe, Coral Barbas (2017). Metabolomics and neuroanatomical evaluation of post mortem changes in the hippocampus. *Brain Struct Funct.* DOI: 10.1007/s00429-017-1375-5
 - Bosch C, Masachs N, Exposito-Alonso D, Martínez A, Teixeira CM, Feraud I, Pujadas L, Ulloa F, Comella JX, DeFelipe J, Merchán-Pérez A, Soriano E. (2016). Reelin Regulates the Maturation of Dendritic Spines, Synaptogenesis and Glial Ensheathment of Newborn Granule Cells. *Cereb Cortex.* 2016 Sep 13.
 - Anton-Sanchez L, Bielza C, Benavides-Piccione R, DeFelipe J, Larrañaga P. (2016). Dendritic and Axonal Wiring Optimization of Cortical GABAergic Interneurons. *Neuroinformatics.* 2016 Oct; 14 (4):453-64. doi: 10.1007/s12021-016-9309-6
 - Anton-Sanchez, L., P. Larrañaga, R. Benavides-Piccione, I. Feraud, J. DeFelipe, and C. Bielza, "Three-dimensional spatial modeling of spines along dendritic networks in human cortical pyramidal neurons", *PLoS ONE* 12(6): e0180400, 2017
 - Barth et al., Comment on "Principles of connectivity among morphologically defined cell types in adult neocortex" *Science* 09 Sep 2016: Vol. 353, Issue 6304, pp. 1108
-

T1.2.1: 3D reconstructions pyramidal neurons human cortex (ID: 959)**Dataset Owner:** Javier DeFelipe < defelipe@cajal.csic.es > (UPM)**DATA SUMMARY****Purpose of the data collection/generation**

We will produce 3D reconstructions of 200 cells in human neocortex (temporal, cingulate and frontal) using Neurolucida software from 3D confocal stack of images.

Relation to the objectives of the project

The data is directly related to the objectives 1c and 1d, Microcircuitry analysis, proteins and receptor distributions, fibre architecture in a specific large area brain region and Maps of cellular distributions, long-range axonal projections, and synaptic proteins; reconstructed morphologies of major neuron types

Types and formats of data generated/collected

Types: 3D cell reconstructions **Formats:** .xls, .DAT

Protocol: 3D reconstructions of intracellularly injected cells using confocal microscopy

Existing data being re-used (if any)

No

Origin of the data

Data class: Cellular **Specimen information:** Human Adult

Brain region: neocortex **Subregion:** Temporal, Cingular and Frontal cortex

Expected size of the data

5 GB

Data utility: to whom will it be useful

Within HBP: Data from 3D reconstructions of pyramidal cells in human neocortex will be useful to modelling and integration of anatomical data with functional studies in different brain regions. Data will be useful for example for tasks 6.1.3, T6.2.1, T6.2.5, T1.5.5, T 1.4.1, T4.1.1.

Outwith HBP: NA

FAIR DATA**Accessibility: which data will be made openly available**

Privacy class is: Human Research. There may be issues sharing data openly

Accessibility: Methods, software tools and documentation needed to access the data

Neurolucida explorer, Microsoft excel

Re-use: Data licensing to permit the widest reuse possible

BY-NC

Re-use: Data quality assurance processes**ETHICAL ASPECTS**

Ethics approval authority: Local Ethics Committee (CSIC) ES280790000184 **Ethics approval ID:** CEAA-IC Approval & CEI PI55-2016

RELEASES AND PROGRESS**Planned releases:**

Month	Shared.with	Quality	Completeness	Location	Embargo	Actual.Completeness
M18	Collab	Final quality	217 out of 200 3D reconstructions of cells	Collaboratory	Awaiting publication	At M18, 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).
M23	Ditto	Ditto	Ditto	Ditto	Ditto	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)

Any deviation and mitigation: NA

Current location(s) of dataset:

<https://collab.humanbrainproject.eu/#/collab/17046/nav/123289>

DATA USAGE

Transferred to SP5/Shared with modelling tasks: NA

Contribution to Use Cases /other SPs: SP1-UC01: 3D reconstruction and visualization of microanatomical parameters of pyramidal cells: PyramidalExplorer; SP4 (T4.1.1): complex to simplified models (model) and T1.4.3; SP6 (T6.2.2)

What are datasets used for (models, atlas)?: Models (SP4) Simplified Dendritic Neuron Models & Input-Output Transfer Functions of Morphologically Detailed Neuronal Models

Link to model/Atlas: <https://collab.humanbrainproject.eu/#/collab/1655/nav/75904>

How the data transfer has been or is coordinated: It has been coordinated with the Data Curation Team (Krister Andersson) and with meetings with model builders

Role and take-up of the data acquired: This dataset has been generated by task T1.2.1. See component ID 955 for the information on the role and take up of the acquired data in this task.

PUBLICATIONS

- Fernandez-Gonzalez P, Benavides-Piccione R, Leguey I, Bielza C, Larrañaga P, DeFelipe J. (2016). Dendritic-branching angles of pyramidal neurons of the human cerebral cortex. *Brain Struct Funct.* 2016 Sep 30.
 - Eyal G, Verhoog MB, Testa-Silva G, Deitcher Y, Lodder JC, Benavides-Piccione R, Morales J, DeFelipe J, de Kock CP, Mansvelder HD, Segev I. Unique membrane properties and enhanced signal processing in human neocortical neurons. *Elife.* 2016 Oct 6;5. pii: e16553. doi: 10.7554/eLife.16553.
 - Rodriguez-Lopez C., Clasca F, Prensa L. (2017) The Mesoaccumbens Pathway: A Retrograde Labeling and Single-Cell Axon Tracing Analysis in the Mouse. (2017) *Front. Neuroanat.* 2017 March 27 11:25 eCollection Mar 27 <https://doi.org/10.3389/fnana.2017.00025>
 - Alejandro Antón-Fernández, Guillermo Aparicio-Torres, Silvia Tapia, Javier DeFelipe, Alberto Muñoz (2016). Morphometric alterations of Golgi apparatus in Alzheimer's disease are related to tau hyperphosphorylation. *Neurobiology of Disease* (97) 2017 11-23
 - Carolina Gonzalez-Riano, Silvia Tapia-Gonzalez, Antonia García, Alberto Muñoz, Javier DeFelipe, Coral Barbas (2017). Metabolomics and neuroanatomical evaluation of post mortem changes in the hippocampus. *Brain Struct Funct.* DOI: 10.1007/s00429-017-1375-5
 - Bosch C, Masachs N, Exposito-Alonso D, Martínez A, Teixeira CM, Feraud I, Pujadas L, Ulloa F, Comella JX, DeFelipe J, Merchán-Pérez A, Soriano E. (2016). Reelin Regulates the Maturation of Dendritic Spines, Synaptogenesis and Glial Ensheathment of Newborn Granule Cells. *Cereb Cortex.* 2016 Sep 13.
 - Anton-Sanchez L, Bielza C, Benavides-Piccione R, DeFelipe J, Larrañaga P. (2016). Dendritic and Axonal Wiring Optimization of Cortical GABAergic Interneurons. *Neuroinformatics.* 2016 Oct; 14 (4):453-64. doi: 10.1007/s12021-016-9309-6
 - Anton-Sanchez, L., P. Larrañaga, R. Benavides-Piccione, I. Feraud, J. DeFelipe, and C. Bielza, "Three-dimensional spatial modeling of spines along dendritic networks in human cortical pyramidal neurons", *PLoS ONE* 12(6): e0180400, 2017
 - Barth et al., Comment on "Principles of connectivity among morphologically defined cell types in adult neocortex" *Science* 09 Sep 2016: Vol. 353, Issue 6304, pp. 1108
-

T1.2.2: Human neurons with matching electrophysiology (ID: 759)**Dataset Owner:** Huib Mansvelder < h.d.mansvelder@vu.nl > (VU)**DATA SUMMARY****Purpose of the data collection/generation**

Modelling human neocortical circuits, theory and simulation

Relation to the objectives of the project

Simulation of human neurons

Types and formats of data generated/collected**Types:** morphology, Ephys **Formats:** txt, abf, mat**Protocol:****Existing data being re-used (if any)****Origin of the data****Data class:** Cellular **Specimen information:** human**Brain region:** temporal cortex **Subregion:** medial temporal gyrus**Expected size of the data****Data utility: to whom will it be useful****Within HBP:** SP4 and SP6**Outwith HBP:** NA**FAIR DATA****Accessibility: which data will be made openly available**

Privacy class is: Human Research. There may be issues sharing data openly

Accessibility: Methods, software tools and documentation needed to access the data**Re-use: Data licensing to permit the widest reuse possible**

BY-NC (TBC)

Re-use: Data quality assurance processes**ETHICAL ASPECTS****Ethics approval authority:** Medical Ethical Committee of the Vrije Universiteit Medical Center (VUmc) **Ethics approval****ID:** Medical Ethical Committee Vumc approval**RELEASES AND PROGRESS****Planned releases:**

Month	Shared	with Quality	Completeness	Location	Embargo	Actual Completeness
M18	—	—	—	—	—	All data have been shared within HBP teams Mansvelder (SP1/SP2), Segev (SP4) and Markram (SP6). Data will be made available through SP5
M23	Partner	Final quality	100%	Collaboratory		100%

Any deviation and mitigation: NA**Current location(s) of dataset:**<https://collab.humanbrainproject.eu/#/collab/17049/nav/123306>**DATA USAGE****Transferred to SP5/Shared with modelling tasks:** NA**Contribution to Use Cases /other SPs:** SP4 (T4.1.1): Simplified neuron models (model); SP6 (t6.2.1: Detailed passive models of human neurons (model). SP6 (T6.2.5: Modeling L2/3-L2/3 synaptic connection (model); T6.2.3-C: Hodgkin-Huxley modelling of excitation-inhibition (model).**What are datasets used for (models, atlas)?:** Models (SP4 & SP6): Simplified Dendritic Neuron Models & Input-Output Transfer Functions of Morphologically Detailed Neuronal Models & Circuits Models**Link to model/Atlas:** <https://collab.humanbrainproject.eu/#/collab/1655/nav/75902>**How the data transfer has been or is coordinated:** It has been coordinated with the Data Curation Team and with meetings with model builders**Role and take-up of the data acquired:** This dataset has been generated by task T1.2.1. See component ID 955 for the information on the role and take up of the acquired data in this task.**PUBLICATIONS**

- Eyal G, Verhoog MB, Testa-Silva G, Deitcher Y, Lodder JC, Benavides-Piccione R, Morales J, DeFelipe J, de Kock CP, Mansvelder HD, Segev I. Unique membrane properties and enhanced signal processing in human neocortical neurons. *Elife*. 2016 Oct 6;5. pii: e16553. doi: 10.7554/eLife.16553.
 - Deitcher Y, Eyal G, Kanari L, Verhoog MB, Atnekeng Kahou GA, Mansvelder HD, de Kock CPJ, Segev I (2017). Comprehensive Morpho-Electrotonic Analysis Shows 2 Distinct Classes of L2 and L3 Pyramidal Neurons in Human Temporal Cortex. *Cerebral Cortex* 15:1-17
 - Obermayer J, Verhoog MB, Luchicchi A, Mansvelder HD. Cholinergic Modulation of Cortical Microcircuits Is Layer-Specific: Evidence from Rodent, Monkey and Human Brain
-

T1.2.3: The striatal microcircuit (ID: 938)**Dataset Owner:** Sten Grillner < sten.grillner@ki.se > (KI)**DATA SUMMARY****Purpose of the data collection/generation**

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 task T1.2.3 is critical for the simulations in SP6, T6.2.5.

Relation to the objectives of the project

The data is directly related to the objectives 1c and 1d, Microcircuitry analysis, proteins and receptor distributions, fibre architecture in a specific large area brain region and Maps of cellular distributions, long-range axonal projections, and synaptic proteins; reconstructed morphologies of major neuron types

Types and formats of data generated/collected

Types: Striatal neurons with morphology and ion channel characteristics. **Formats:** SWC, json

Protocol: [Current clamp voltage recording protocol](#); Neurolucida

Existing data being re-used (if any)

No

Origin of the data

Data class: Cellular **Specimen information:** Slices of striatum

Brain region: [basal ganglia](#) **Subregion:** [striatum](#)

Expected size of the data

Below 5GB

Data utility: to whom will it be useful

Within HBP: T6.2.5

Outwith HBP: NA

FAIR DATA**Accessibility: which data will be made openly available**

Privacy class is: Animal Research. There are no issues sharing data

Accessibility: Methods, software tools and documentation needed to access the data

Will be available through the Neuroinformatics platform (SP5)

Re-use: Data licensing to permit the widest reuse possible

BY-SA - Attribution + ShareAlike

Re-use: Data quality assurance processes**ETHICAL ASPECTS**

Ethics approval authority: Stockholms Norra djurförsöksetiska nämnd **Ethics approval ID:** Tresorit reference:

SP01/T1.2.3

RELEASES AND PROGRESS**Planned releases:**

Month	Shared	with Quality	Completeness	Location	Embargo	Actual Completeness
M18	—	—	—	—	—	Morphologies have been elaborated in interaction with SP6 of medium spiny neurons of the two different varieties expressing the D1 and D2 receptors, respectively, and also of cholinergic and fast-spiking interneurons. Analysis of cell body and dendritic arbors have been performed on MSNs and cholinergic cells and fast-spiking interneurons.

Month	Shared.with	Quality	Completeness	Location	Embargo	Actual.Completeness
M23	Consortium	Candidate final quality	10 each of cholinergic and MSNs of D1 and D2 type.	Collaboratory	The data embargoed until accepted for publication	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%.

Any deviation and mitigation: NA

Current location(s) of dataset:

<https://collab.humanbrainproject.eu/#/collab/376/nav/3797>

<https://collab.humanbrainproject.eu/#/collab/376/nav/43458>

DATA USAGE

Transferred to SP5/Shared with modelling tasks: NA

Contribution to Use Cases /other SPs: SP6 (T6.2.5): Models of basal ganglia

What are datasets used for (models, atlas)?: Models

Link to model/Atlas: D1 MSN, D2 MSN, FS, ChIN

How the data transfer has been or is coordinated: Transfer of data is coordinated with SP6 (T6.2.5): Models of basal ganglia, and has also been made available for SP5.

Role and take-up of the data acquired: The data have been used in SP6, T6.2.5: Models of basal ganglia

PUBLICATIONS

- Grillner S, Robertson B. The Basal Ganglia Over 500 Million Years. *Curr Biol.* 2016 Oct 24; 26;1088-1100
- Perez-Fernandez J, Kardamakis A, Suzuki D, Robertson B, and Grillner S, Direct dopaminergic projections from SNc modulate visuomotor transformation. *Neuron* 2017 (e.pub Oct. 27th)
- StenGrillner, Arndt von Twickel Brita Robertson. The blueprint of the vertebrate forebrain – With special reference to the habenulae
- Du K, Wu YW, Lindroos R, Liu Y, Rózsa B, Katona G, Ding JB, Kotaleski JH. Cell-type-specific inhibition of the dendritic plateau potential in striatal spiny projection neurons. *Proc Natl Acad Sci U S A.* 2017 Sep 5;114(36):E7612-E7621. doi: 10.1073/pnas.1704893114. Epub 2017 Aug 21
- Lindroos R, Dorst MC, Du K, Filipovic M, Keller D, Ketzeff M, Kozlov AK, Kumar A, Lindahl M, Nair AG, Pérez-Fernández J, Grillner S, Silberberg G, Hellgren Kotaleski J. Basal Ganglia Neuromodulation Over Multiple Temporal and Structural Scales—Simulations of Direct Pathway MSNs Investigate the Fast Onset of Dopaminergic Effects and Predict the Role of Kv4.2. *Front. Neural Circuits*, 12:3, 2018

T1.2.4: Electrophysiological data cerebellum (ID: 810)**Dataset Owner:** Egidio D'Angelo < dangelo@unipv.it > (UNIPV)**DATA SUMMARY****Purpose of the data collection/generation**

These data will be directly used for modelling in BSP and will then be useful for the whole scientific community in order to analyse and model the physiological aspects of cerebellar neurons and networks.

Relation to the objectives of the project

The data collected will be used for cerebellar modelling, to clarify the spatio-temporal cell-specific organization principles in brain activation (SO15)

Types and formats of data generated/collected

Types: Electrophysiological recordings (MEA, patch clamp, two-photon, calcium imaging) **Formats:** .abf; .brw; .mod, .ipynb, .mat, .rsh, .rsm, .rsd, .dha, .tbk, .spd, .png

Protocol: [Electrophysiology concept](#)

Existing data being re-used (if any)**Origin of the data**

Data class: Cellular **Specimen information:** acute brain slices; rat/mouse, juvenile, c57Bl6, GLY T2, IB2

Brain region: [Cerebellum](#) **Subregion:** [Cerebellar cortex](#); [Deep cerebellar nuclear complex](#)

Expected size of the data

GB

Data utility: to whom will it be useful

Within HBP: These data will be used into T6.2.3 (cerebellum model) and T6.2.4 (microcircuit level service

Outwith HBP: NA

FAIR DATA**Accessibility: which data will be made openly available**

Privacy class is: Animal Research. There are no issues sharing data

Accessibility: Methods, software tools and documentation needed to access the data

The data can be accessed using software specific for the different instruments used. The file format is indicated. The relevant software can be included as open source only in some cases.

Re-use: Data licensing to permit the widest reuse possible

Attribution-NonCommercial-ShareAlike 4.0 International

Re-use: Data quality assurance processes**ETHICAL ASPECTS**

Ethics approval authority: Italian Health Ministry and UNIPV OPBA **Ethics approval ID:** The Italian Ministry of Health approved our experimental protocols with silence consensus, so we do not have an ID number

RELEASES AND PROGRESS**Planned releases:**

Month	Shared.with	Quality	Completeness	Location	Embargo	Actual.Completeness
M12	Collab	Final quality	All usable cells	Collaboratory; CSCS data bucket	immediate for internal usage; awaiting publication for public access	—
M18	Ditto	Ditto	Ditto	Ditto	Ditto	Representative datasets for each protocol applied to different cerebellar neuronal types; Link: T6.2.3, T6.4.2- Stefano Masoli, Stefano Casali, Claudia Casellato, Martina Rizza
M23	Collab	Final quality		Collaboratory; CSCS data bucket	immediate for internal usage; awaiting publication for public access	100%

Any deviation and mitigation: NA

Current location(s) of dataset:

<https://collab.humanbrainproject.eu/#/collab/5389/nav/41947>

DATA USAGE

Transferred to SP5/Shared with modelling tasks: NA

Contribution to Use Cases /other SPs: SGA1-T6.2.4 - Models of cerebellum SGA2-SP1-UC03: The structural and functional basis of cerebellar dynamics and plasticity

What are datasets used for (models, atlas)?: Models (Cerebellum)

Link to model/Atlas: Model Catalogue: <https://collab.humanbrainproject.eu/#/collab/1655/nav/75901>

How the data transfer has been or is coordinated: Coordination went through the curation team of HPAC, NIP, and SP6

Role and take-up of the data acquired: This component has been generated by T1.2.4. See component ID 811 for information on the role and take up of the acquired data in this task.

PUBLICATIONS

- Mapelli L, Gagliano G, Soda T, Laforenza U., Moccia F, D'Angelo E. Granular Layer Neurons Control Cerebellar Neurovascular Coupling Through an NMDA Receptor/NO-Dependent System. *J Neurosci.* 2017 Feb 1;37(5):1340-1351. doi:10.1523/JNEUROSCI
 - Sgritta M, Locatelli F, Soda T, Prestori F, D'Angelo E. Hebbian spike-timing dependent plasticity at the cerebellar input stage. *J Neurosci.* 2017 Feb 10. pii: 2079-16. doi: 10.1523/JNEUROSCI.2079-16.2016
 - Gandolfi D, Cerri S, Mapelli J, Polimeni M, Tritto S, Fuzzati-Armentero MT, Bigiani A, Blandini F, Mapelli L, D'Angelo E (2017). Activation of the CREB/c-Fos Pathway during Long-Term Synaptic Plasticity in the Cerebellum Granular Layer. *Front. Cell. Neurosci.* 28 June 2017; <https://doi.org/10.3389/fncel.2017.00184>
 - K. Dover, C. Marra, S. Solinas, M. Popovic, S. Subramaniam, D. Zecevic, E. D'Angelo, M. Goldfarb. FHF-independent conduction of action potentials along the leak-resistant cerebellar granule cell axon. *Nature Communications.* 26 September 2016 doi:10.1038/ncomms12895
 - Masoli S, Rizza MF, Sgritta M, Van Geit W, Schürmann F, D'Angelo E. Single Neuron Optimization as a Basis for Accurate Biophysical Modeling: The Case of Cerebellar Granule Cells. *Front. Cell. Neurosci.*, 15 March 2017|<https://doi.org/10.3389/fncel.2017.0007>
 - Parmar K, Stadelmann C, Rocca MA, Langdon D, D'Angelo E, et al., . The role of the cerebellum in multiple sclerosis-150 years after Charcot. *Neurosci Biobehav Rev.* 2018 Feb 23. pii: S0149-7634(17)30639-5. doi: 10.1016/j.neubiorev.2018.02.012. Review. PubMed PMID: 29477616
 - Palesi F, De Rinaldis A, Castellazzi G, Calamante F, Muhlert N, Chard D, Tournier JD, Magenes G, D'Angelo E, Gandini Wheeler-Kingshott CAM. Contralateral cortico-ponto-cerebellar pathways reconstruction in humans in vivo: implications for reciprocal cerebro-cerebellar structural connectivity in motor and non-motor areas. *Sci Rep.* 2017 Oct 9;7(1):12841. PubMed PMID: 28993670; PubMed Central PMCID: PMC5634467
 - Masoli S, D'Angelo E. Synaptic Activation of a Detailed Purkinje Cell Model Predicts Voltage-Dependent Control of Burst-Pause Responses in Active Dendrites. *Front Cell Neurosci.* 2017 Sep 13;11:278. eCollection 2017. PubMed PMID: 28955206; PubMed Central PMCID: PMC5602117
 - Zuccolo E, Lim D, Kheder DA, Perna A, Catarsi P, Botta L, Rosti V, Riboni L, Sancini G, Tanzi F, D'Angelo E, Guerra G, Moccia F. Acetylcholine induces intracellular Ca(2+) oscillations and nitric oxide release in mouse brain endothelial cells. *Cell Calcium.* 2017 Sep;66:33-47. Epub 2017 Jun 12. PubMed PMID: 28807148
-

T1.2.5: Morphological database of major cell types of the mouse hippocampus (ID: 805)**Dataset Owner:** Szabolcs Káli < kali.szabolcs@koki.mta.hu > (IEM HAS)**DATA SUMMARY****Purpose of the data collection/generation**

Hippocampal circuits perform functions which are critical for learning and memory. Understanding these circuits requires the characterization of their constituent neurons both in terms of their morphology (which defines the underlying substrate of intracellular signal integration as well as the possible patterns of connectivity within the network) and their physiological behaviour (which defines the functional input-output mapping of the neuron). 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 SGA1 phase, we 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.

Relation to the objectives of the project

The data is directly related to the objective 1d, Maps of cellular distributions, long-range axonal projections, and synaptic proteins; reconstructed morphologies of major neuron types

Types and formats of data generated/collected

Types: morphological reconstructions of hippocampal neurons based on confocal image stacks **Formats:** .asc, .xml (NeuroLucida)

Protocol: [Laser scanning confocal imaging protocol](#)

Existing data being re-used (if any)

No

Origin of the data

Data class: Cellular **Specimen information:** C57BL/6 mouse, 8 weeks

Brain region: [Hippocampal formation](#) **Subregion:**

Expected size of the data

10 MB (100 GB including image stacks)

Data utility: to whom will it be useful

Within HBP: These data are required to build models of hippocampal neurons and circuits (SGA1 T6.2.4)

Outwith HBP: NA

FAIR DATA**Accessibility: which data will be made openly available**

Privacy class is: Animal Research. There are no issues sharing data

Accessibility: Methods, software tools and documentation needed to access the data**Re-use: Data licensing to permit the widest reuse possible**

BY-NC - Attribution + Noncommercial

Re-use: Data quality assurance processes**ETHICAL ASPECTS**

Ethics approval authority: Animal experimentation committee of IEM HAS **Ethics approval ID:** N/A (slice experiments do not require specific outside permission)

RELEASES AND PROGRESS**Planned releases:**

Month	Shared	with Quality	Completeness	Location	Embargo	Actual Completeness
M18	—	—	—	—	—	The number of reconstructed neurons has increased to over 130 (We are currently in the process of registering this dataset in the Neuroinformatics Platform (contact person: Andrew Davison). The data have been shared with modelers in SP6 (SGA1 Task 6.2.4: Szabolcs Káli, Michele Migliore, Armando Romani).

Month	Shared.with	Quality	Completeness	Location	Embargo	Actual.Completeness
M23	Consortium	Candidate final quality	80 cells reconstructed	Lab server; Collabatory; CSCS data bucket		The database now 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. We are still in the process of registering this dataset in the Neuroinformatics Platform (contact person: Andrew Davison). The data have been used by modelers in SP6 to build models of several classes of mouse hippocampal neuron (SGA1 Task 6.2.4: Szabolcs Káli, Michele Migliore, Armando Romani)

Any deviation and mitigation: NA

Current location(s) of dataset:

https://kokimta.hu-my.sharepoint.com/:f/g/personal/kali_szabolcs_koki_mta_hu/EkK3A-vyTPpAjsW4q5m00LQBDNCzQYj1tk2uu9lv2AGZkA?e=0dcza1

DATA USAGE

Transferred to SP5/Shared with modelling tasks: NA

Contribution to Use Cases /other SPs: SP6 : T6.2.4-SGA1-Models of mouse hippocampal neurons (model). The data have been shared with modelers in SP6 (SGA1 Task 6.2.4: Szabolcs Káli, Michele Migliore, Armando Romani))

What are datasets used for (models, atlas)? Morphological and electrophysiological data from this data set have been used in Task 6.2.4 (SGA1) to build and optimize the parameters of detailed compartmental models of mouse hippocampal neurons.

Link to model/Atlas: Modeling of mouse neurons in Task 6.2.4 is work in progress, so the models constructed so far have not been publicly released.

How the data transfer has been or is coordinated: Both morphological and electrophysiological data first underwent local quality control at IEM HAS. Releases of the data were prepared regularly (approximately one release every six months), and data were transferred directly to the modelers for further quality control and use.

Role and take-up of the data acquired: This component has been generated by T1.2.5. This task (together with its predecessor in the ramp-up phase) provided 3-dimensional morphological reconstructions and physiological data for the hippocampal modeling task in SP6 (Task 6.2.4 Models of Hippocampus in SGA1). The database now contains data about more than 200 neurons of various types in the adult mouse hippocampus. The majority of the data come from recording and filling cells in acute hippocampal slices. These morphologies and corresponding electrophysiological features are used to create and optimize detailed compartmental models of the different hippocampal cell types, which then provide the fundamental building blocks for models of the hippocampal network. The detailed morphologies are also used in the circuit building process to derive predictions for the connectome of the hippocampus. Although the focus of Task 6.2.4 in SGA1 was the completion of the hippocampal modeling pipeline and its testing through the example of the rat CA1 region, a pilot study for the mouse cells was also carried out, and indicated that the data provided by this task are suitable for building high-quality models of mouse hippocampal neurons. An effort to systematically build models of all the major cell types of the mouse hippocampus based on this experimental database is currently under way, and the morphologies are also evaluated for use by algorithms that predict the connectome. Finally, the database also contains several neurons recorded in head-fixed mice in vivo, where, in addition to intracellular activity, the local field potential and behavioral variables were also measured. These data represent a unique opportunity for the validation of single cell and population activity in the complete circuit model, which will be completed in SGA2.

PUBLICATIONS

- Gulyás AI, Freund TF, Káli S (2016) The Effects of Realistic Synaptic Distribution and 3D Geometry on Signal Integration and Extracellular Field Generation of Hippocampal Pyramidal Cells and Inhibitory Neurons. *Frontiers in Neural Circuits* 10:88. DOI: 10.3389/fncir.2016.00088

T1.2.5: Electrophysiological database of major cell types of the mouse hippocampus (ID: 805)**Dataset Owner:** Szabolcs Káli < kali.szabolcs@koki.mta.hu > (IEM HAS)**DATA SUMMARY****Purpose of the data collection/generation**

Hippocampal circuits perform functions which are critical for learning and memory. Understanding these circuits requires the characterization of their constituent neurons both in terms of their morphology (which defines the underlying substrate of intracellular signal integration as well as the possible patterns of connectivity within the network) and their physiological behaviour (which defines the functional input-output mapping of the neuron). 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 SGA1 phase, we 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.

Relation to the objectives of the project

The data is directly related to the objective 1d, Maps of cellular distributions, long-range axonal projections, and synaptic proteins; reconstructed morphologies of major neuron types

Types and formats of data generated/collected

Types: Whole-cell current-clamp patch recordings **Formats:** Tab-separated text files (.txt)

Protocol: [Current clamp voltage recording protocol](#)

Existing data being re-used (if any)

No

Origin of the data

Data class: Electrophysiological **Specimen information:** C57BL/6 mouse, 8 weeks

Brain region: [Hippocampal formation](#) **Subregion:**

Expected size of the data

1 GB

Data utility: to whom will it be useful

Within HBP: These data are required to build models of hippocampal neurons and circuits (SGA1 T6.2.4)

Outwith HBP: NA

FAIR DATA**Accessibility: which data will be made openly available**

Privacy class is: Animal Research. There are no issues sharing data

Accessibility: Methods, software tools and documentation needed to access the data**Re-use: Data licensing to permit the widest reuse possible**

BY-NC - Attribution + Noncommercial

Re-use: Data quality assurance processes**ETHICAL ASPECTS**

Ethics approval authority: Animal experimentation committee of IEM HAS **Ethics approval ID:** N/A (slice experiments do not require specific outside permission)

RELEASES AND PROGRESS**Planned releases:**

Month	Shared.with	Quality	Completeness	Location	Embargo	Actual.Completeness
M18	—	—	—	—	—	The number of reconstructed neurons has increased to over 130 (We are currently in the process of registering this dataset in the Neuroinformatics Platform (contact person: Andrew Davison). The data have been shared with modelers in SP6 (SGA1 Task 6.2.4: Szabolcs Káli, Michele Migliore, Armando Romani).

Month	Shared.with	Quality	Completeness	Location	Embargo	Actual.Completeness
M23	Public authenticated	Final quality	80 cells recorded	Lab server; Collabatory; CSCS data bucket		The database now 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. We are still in the process of registering this dataset in the Neuroinformatics Platform (contact person: Andrew Davison). The data have been used by modelers in SP6 to build models of several classes of mouse hippocampal neuron (SGA1 Task 6.2.4: Szabolcs Káli, Michele Migliore, Armando Romani)

Any deviation and mitigation: NA

Current location(s) of dataset:

https://kokimtahu-my.sharepoint.com/:f/g/personal/kali_szabolcs_koki_mta_hu/EkK3A-vyTPpAjsW4q5m00LQBDNCzQYj1tk2uu9lv2AGZkA?e=0dcza1

DATA USAGE

Transferred to SP5/Shared with modelling tasks: NA

Contribution to Use Cases /other SPs: SP6 : T6.2.4-SGA1-Models of mouse hippocampal neurons (model). The data have been shared with modelers in SP6 (SGA1 Task 6.2.4: Szabolcs Káli, Michele Migliore, Armando Romani))

What are datasets used for (models, atlas)? Morphological and electrophysiological data from this data set have been used in Task 6.2.4 (SGA1) to build and optimize the parameters of detailed compartmental models of mouse hippocampal neurons.

Link to model/Atlas: Modeling of mouse neurons in Task 6.2.4 is work in progress, so the models constructed so far have not been publicly released.

How the data transfer has been or is coordinated: Both morphological and electrophysiological data first underwent local quality control at IEM HAS. Releases of the data were prepared regularly (approximately one release every six months), and data were transferred directly to the modelers for further quality control and use.

Role and take-up of the data acquired: This component has been generated by T1.2.5. This task (together with its predecessor in the ramp-up phase) provided 3-dimensional morphological reconstructions and physiological data for the hippocampal modeling task in SP6 (Task 6.2.4 Models of Hippocampus in SGA1). The database now contains data about more than 200 neurons of various types in the adult mouse hippocampus. The majority of the data come from recording and filling cells in acute hippocampal slices. These morphologies and corresponding electrophysiological features are used to create and optimize detailed compartmental models of the different hippocampal cell types, which then provide the fundamental building blocks for models of the hippocampal network. The detailed morphologies are also used in the circuit building process to derive predictions for the connectome of the hippocampus. Although the focus of Task 6.2.4 in SGA1 was the completion of the hippocampal modeling pipeline and its testing through the example of the rat CA1 region, a pilot study for the mouse cells was also carried out, and indicated that the data provided by this task are suitable for building high-quality models of mouse hippocampal neurons. An effort to systematically build models of all the major cell types of the mouse hippocampus based on this experimental database is currently under way, and the morphologies are also evaluated for use by algorithms that predict the connectome. Finally, the database also contains several neurons recorded in head-fixed mice in vivo, where, in addition to intracellular activity, the local field potential and behavioral variables were also measured. These data represent a unique opportunity for the validation of single cell and population activity in the complete circuit model, which will be completed in SGA2.

PUBLICATIONS

- [Gulyás AI, Freund TF, Káli S \(2016\) The Effects of Realistic Synaptic Distribution and 3D Geometry on Signal Integration and Extracellular Field Generation of Hippocampal Pyramidal Cells and Inhibitory Neurons. Frontiers in Neural Circuits 10:88. DOI: 10.3389/fncir.2016.00088](#)

T1.2.5: Morphological reconstructions of mouse hippocampal neurons filled in vivo (ID: 806)**Dataset Owner:** Szabolcs Káli < kali.szabolcs@koki.mta.hu > (IEM HAS)**DATA SUMMARY****Purpose of the data collection/generation**

Hippocampal circuits perform functions which are critical for learning and memory. Understanding these circuits requires the characterization of their constituent neurons both in terms of their morphology (which defines the underlying substrate of intracellular signal integration as well as the possible patterns of connectivity within the network) and their physiological behaviour (which defines the functional input-output mapping of the neuron). Recording and filling neurons in vivo, in awake, head-fixed mice allows a more complete reconstruction of the morphology of the neuron.

Relation to the objectives of the project

The data is directly related to the objective 1d, Maps of cellular distributions, long-range axonal projections, and synaptic proteins; reconstructed morphologies of major neuron types

Types and formats of data generated/collected

Types: morphological reconstructions of hippocampal neurons based on confocal image stacks **Formats:** .asc, .xml (NeuroLucida)

Protocol: [Laser scanning confocal imaging protocol](#)

Existing data being re-used (if any)

No

Origin of the data

Data class: Cellular **Specimen information:**

Brain region: [Hippocampal formation](#) **Subregion:**

Expected size of the data

10 MB (10 GB including image stacks)

Data utility: to whom will it be useful

Within HBP: These data are required to build models of hippocampal neurons and circuits (SGA1 T6.2.4)

Outwith HBP: NA

FAIR DATA**Accessibility: which data will be made openly available**

Privacy class is: Animal Research. There are no issues sharing data

Accessibility: Methods, software tools and documentation needed to access the data**Re-use: Data licensing to permit the widest reuse possible**

BY-NC - Attribution + Noncommercial

Re-use: Data quality assurance processes**ETHICAL ASPECTS**

Ethics approval authority: Pest County Government Office **Ethics approval ID:** PEI/001/1308-6/2015

RELEASES AND PROGRESS**Planned releases:**

Month	Shared.with	Quality	Completeness	Location	Embargo	Actual.Completeness
M18	—	—	—	—	—	Overall, eight successful in vivo whole-cell recordings have been made from CA1 pyramidal neurons (We are currently in the process of registering this dataset in the Neuroinformatics Platform (contact person: Andrew Davison)
M23	Public	Final	5 cells	Lab server;		Overall, 29 successful in vivo whole-cell recordings have been made (for a subset of these experiments, LFP recordings and/or basic behavioral data are also available). 18 of the recorded cells could be visually identified and precisely localized. 5 neurons (4 in area CA1, 1 in subiculum) can be reconstructed, and 2 of these reconstructions have been completed. We are in the process of registering this dataset in the Neuroinformatics Platform (contact person: Andrew Davison).
	authenticated	quality	reconstructed	Collabatory;		
				CSCS data		
				bucket		

Any deviation and mitigation: NA

Current location(s) of dataset:<https://kokimtahu->my.sharepoint.com/:f:/g/personal/kali_szabolcs_koki_mta_hu/Enpb97TQi2NLmhJLJ7MPqOEB3Hlw2FcjuKhVhXEBKbyY7Q?e=vh1qyj

DATA USAGE

Transferred to SP5/Shared with modelling tasks: NA**Contribution to Use Cases /other SPs:** SP6 : T6.2.4-SGA1-Models of mouse hippocampal neurons (model)**What are datasets used for (models, atlas)?:** The in vivo electrophysiological data from this task are useful mainly for model validation. This is planned for SGA2, when the hippocampal network model becomes sufficiently mature. The morphological data are currently undergoing quality control and evaluation for inclusion in the morphological dataset produced in the in vitro experiments.**Link to model/Atlas:** Planned for SGA2**How the data transfer has been or is coordinated:** Planned for SGA2**Role and take-up of the data acquired:** This component has been generated by T1.2.5. See component ID 805 for information on the role and take up of the acquired data in this task.

PUBLICATIONS

T1.2.5: Physiological characterisation of mouse hippocampal neurons recorded in vivo (ID: 806)**Dataset Owner:** Szabolcs Káli < kali.szabolcs@koki.mta.hu > (IEM HAS)**DATA SUMMARY****Purpose of the data collection/generation**

Hippocampal circuits perform functions which are critical for learning and memory. Understanding these circuits requires the characterization of their constituent neurons both in terms of their morphology (which defines the underlying substrate of intracellular signal integration as well as the possible patterns of connectivity within the network) and their physiological behaviour (which defines the functional input-output mapping of the neuron). Recording and filling neurons in awake, head-fixed mice allows the electrophysiological properties of the neuron to be determined under in vivo conditions, and the correlation of single cell activity with behavioural variables.

Relation to the objectives of the project

The data is directly related to the objective 1d, Maps of cellular distributions, long-range axonal projections, and synaptic proteins; reconstructed morphologies of major neuron types

Types and formats of data generated/collected

Types: whole-cell recording from single neurons in awake, head-fixed mice **Formats:**

Protocol: [Current clamp voltage recording protocol](#)

Existing data being re-used (if any)

No

Origin of the data

Data class: Electrophysiological **Specimen information:** mouse

Brain region: [Hippocampal formation](#) **Subregion:**

Expected size of the data

5 GB

Data utility: to whom will it be useful

Within HBP: These data are required to validate models of hippocampal neurons and circuits (SGA1 T6.2.4)

Outwith HBP: NA

FAIR DATA**Accessibility: which data will be made openly available**

Privacy class is: Animal Research. There are no issues sharing data

Accessibility: Methods, software tools and documentation needed to access the data**Re-use: Data licensing to permit the widest reuse possible**

BY-NC- ND - Attribution + Noncommercial + NoDerivatives

Re-use: Data quality assurance processes**ETHICAL ASPECTS**

Ethics approval authority: Pest County Government Office **Ethics approval ID:** PEI/001/1308-6/2015

RELEASES AND PROGRESS**Planned releases:****Month Shared.with Quality Completeness Location Embargo Actual.Completeness**

M18	—	—	—	—	—	Overall, eight successful in vivo whole-cell recordings have been made from CA1 pyramidal neurons (We are currently in the process of registering this dataset in the Neuroinformatics Platform (contact person: Andrew Davison)
M23	Public authenticated	Final quality	5 hippocampal neurons recorded and filled	Lab server; CSCS data bucket		Overall, 29 successful in vivo whole-cell recordings have been made (for a subset of these experiments, LFP recordings and/or basic behavioral data are also available). 18 of the recorded cells could be visually identified and precisely localized. 5 neurons (4 in area CA1, 1 in subiculum) can be reconstructed, and 2 of these reconstructions have been completed. We are in the process of registering this dataset in the Neuroinformatics Platform (contact person: Andrew Davison).

Any deviation and mitigation: NA

Current location(s) of dataset:

https://kokimtahu-my.sharepoint.com/:f:/g/personal/kali_szabolcs_koki_mta_hu/Enpb97TQi2NLmhJLJ7MPqOEB3Hlw2FcjuKhVhXEBKbyY7Q?e=vh1qyj

DATA USAGE

Transferred to SP5/Shared with modelling tasks: NA

Contribution to Use Cases /other SPs: SP6 : T6.2.4-SGA1-Models of mouse hippocampal neurons (model)

What are datasets used for (models, atlas)?: The in vivo electrophysiological data from this task are useful mainly for model validation. This is planned for SGA2, when the hippocampal network model becomes sufficiently mature. The morphological data are currently undergoing quality control and evaluation for inclusion in the morphological dataset produced in the in vitro experiments.

Link to model/Atlas: Planned for SGA2

How the data transfer has been or is coordinated: Planned for SGA2

Role and take-up of the data acquired: This component has been generated by T1.2.5. See component ID 805 for information on the role and take up of the acquired data in this task.

PUBLICATIONS

T1.2.6: Database of synaptic physiological properties in the mouse hippocampus (ID: 926)**Dataset Owner:** Szabolcs Káli < kali.szabolcs@koki.mta.hu > (IEM HAS)**DATA SUMMARY****Purpose of the data collection/generation**

State-of-the-art anatomical methods allow the precise mapping of specific types of neuron and their connectivity patterns. However, simulating the function of brain networks also requires a detailed characterization of neuronal interactions at the physiological level, using conditions and activity patterns which are characteristic of the intact brain. The relevant synaptic parameters (including the properties of activity-dependent short-term plasticity) have been determined only for a small and almost arbitrary subset of connections, and mostly under very artificial (silent) conditions. By contrast, we will perform paired recordings in hippocampal slices which display in vivo-like activity levels and patterns. Using this approach, 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.

Relation to the objectives of the project

The data is directly related to the objective 1d, Maps of cellular distributions, long-range axonal projections, and synaptic proteins; reconstructed morphologies of major neuron types

Types and formats of data generated/collected

Types: Whole-cell voltage-clamp patch recordings **Formats:** Tab-separated text files (.txt)

Protocol: Dual whole-cell recordings of hippocampal neurons.

Existing data being re-used (if any)

No

Origin of the data

Data class: Electrophysiological **Specimen information:** mouse

Brain region: [Hippocampal formation](#) **Subregion:**

Expected size of the data

100 MB

Data utility: to whom will it be useful

Within HBP: These data are required to build models of hippocampal circuits (T6.2.4)

Outwith HBP: NA

FAIR DATA**Accessibility: which data will be made openly available**

Privacy class is: Animal Research. There are no issues sharing data

Accessibility: Methods, software tools and documentation needed to access the data**Re-use: Data licensing to permit the widest reuse possible**

BY-NC - Attribution + Noncommercial

Re-use: Data quality assurance processes**ETHICAL ASPECTS**

Ethics approval authority: Animal experimentation committee of IEM HAS **Ethics approval ID:** N/A (slice experiments do not require specific outside permission)

RELEASES AND PROGRESS**Planned releases:**

Month	Shared.with	Quality	Completeness	Location	Embargo	Actual.Completeness
M18	—	—	—	—	—	The database of synaptic properties now contains information on more than 100 connections (We are currently in the process of registering this dataset in the Neuroinformatics Platform (contact person: Andrew Davison). The data have been shared with modelers in SP6 (SGA1 Task 6.2.4: Szabolcs Káli, Michele Migliore, Armando Romani). A subset of the data has also been uploaded to the CRCNS repository).

Month	Shared.with	Quality	Completeness	Location	Embargo	Actual.Completeness
M23	Public authenticated	Final quality	100 connected cell pairs characterized	Lab server; Collabatory; CSCS data bucket		The database of synaptic properties now contains information on more than 50 connections. We are currently in the process of registering this dataset in the Neuroinformatics Platform (contact person: Andrew Davison). The data have been used by modelers in SP6 to build models of several types of hippocampal synaptic connection (SGA1 Task 6.2.4: Szabolcs Káli, Michele Migliore, Armando Romani). A subset of the data has also been uploaded to the CRCNS repository.

Any deviation and mitigation: NA

Current location(s) of dataset:

https://kokimtahu-my.sharepoint.com/:f:/g/personal/kali_szabolcs_koki_mta_hu/Em5A3xNdpEhPpwNxu4w-TyoBi6ccw1fSgA2WGPelGatnGw?e=9wzvFS

DATA USAGE

Transferred to SP5/Shared with modelling tasks: NA

Contribution to Use Cases /other SPs: SP6-T6.2.4-SGA1-Circuit model of the mouse hippocampus (model) The data have been shared with modelers in SP6 (SGA1 Task 6.2.4: Szabolcs Káli, Michele Migliore, Armando Romani). A subset of the data has also been uploaded to the CRCNS repository).

What are datasets used for (models, atlas)?: Synaptic data from this data set have been used in Task 6.2.4 (SGA1) to set the parameters of synapses in network models of the hippocampus.

Link to model/Atlas: <https://collab.humanbrainproject.eu/#/collab/1655/nav/75901?state=model.47606e45-6efc-49adb61d-efcd26d9bb46>

How the data transfer has been or is coordinated: Synaptic electrophysiological data first underwent local quality control at IEM HAS. Releases of the data were prepared regularly, and data were transferred directly to the modelers for further quality control and use.

Role and take-up of the data acquired: Using paired whole-cell recordings in hippocampal slices, the basal transmission properties and short-term plasticity parameters for several major classes of hippocampal connections were determined and stored in a database. 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) was also carried out. These data are used to construct models of the different classes of synaptic connections in the hippocampal modeling task in SP6 (Task 6.2.4 in SGA1). Data from different types of hippocampal synapses can be used to define the classes of connections in the model and thus establish a viable generalization strategy. The kinetics of individual synaptic responses are used to set synaptic time constants in the model, while the dynamics of the responses to repeated stimulation allow the fitting of Tsodyks-Markram-type models of short-term synaptic plasticity. As data on the properties of hippocampal synapses (and especially their short-term plasticity) are extremely sparse, the data collected in this task are fundamental for constraining synapse models in SP6, which is a critical step in the construction of reliable circuit models.

PUBLICATIONS

- [Z. Kohus, S.Káli, L. Rovira-Esteban, D. Schlingloff, O.Papp, T.F.Freund, N.Hájos and A. I. Gulyás, Properties and dynamics of inhibitory synaptic communication within the CA3 microcircuits of pyramidal cells and interneurons expressing parvalbumin or cholecystokinin. The Journal of Physiology, 2016. 594:3745-3774](#)

T1.2.7: GABAergic neuron subtypes (ID: 785)**Dataset Owner:** Zoltán Kisvárdy < kisvarday@anat.med.unideb.hu > (UoD)**DATA SUMMARY****Purpose of the data collection/generation**

Our aim is to quantify the synaptic input morphologies for the considerably diverse and still little known GABAergic populations of interneurons (e.g. PV, CB, CR, VIP, SOM, CCK, nNOS, NPY, ChAT). For establishing a qEM database we are going to accomplish volumetric 3D reconstruction, whereby not only the main parameters (bouton size and shape, vesicle and mitochondria content, surface extent of the active zone), but the exact location, number and type of boutons along the selected dendrite segments of single cells can be determined.

Relation to the objectives of the project

The data is directly related to the objective 1d, Maps of cellular distributions, long-range axonal projections, and synaptic proteins; reconstructed morphologies of major neuron types

Types and formats of data generated/collected

Types: image stacks of single cell dendrites **Formats:** TIFF, Microsoft Word Document, xml

Protocol: Fixation protocol; Immunohistochemical protocol; Nissl staining protocol; TEM imaging protocol; mirror technique: Here we use the “mirror” technique that was originally introduced for double immunohistochemical staining of neuronal cell bodies. Briefly, the surfaces of adjoining sections share cell bodies which are cut by the sectioning plane. For these cell bodies, independent histological treatments are feasible, for example different types of immunohistochemical staining, respectively. We exploited this approach and use such cell bodies of adjoining sections in the following way. One section is stained for a particular GABAergic subtype marker, e.g. calbindin, whereas the adjoining sections are reserved for EM analysis without any immunostaining or histological treatment that would compromise the quality of ultrastructure. Therefore the complement of immunopositive cell bodies and their dendrites retain high quality EM ultrastructure and can be subjected for a quantitative EM analysis.

Existing data being re-used (if any)

No

Origin of the data

Data class: Cellular **Specimen information:** Species: mouse; Strain: Black 6 (C57BL/6J); Sex: male; Age (as category): 8-15 weeks; Age (at time of measurement): 14 weeks

Brain region: Somatosensory cortex; Visual cortex **Subregion:** Primary Somatosensory cortex (S1): Bregma +1.94 and +0.5; Visual cortex primary (V1): Bregma -3.52 and -2.46

Expected size of the data

1 TB

Data utility: to whom will it be useful

Within HBP: SP6: T6.2.2. (UPM); T6.2.6. (EPFL)

Outwith HBP: NA

FAIR DATA**Accessibility: which data will be made openly available**

Privacy class is: Animal Research. There are no issues sharing data

Accessibility: Methods, software tools and documentation needed to access the data**Re-use: Data licensing to permit the widest reuse possible**

BY-NC

Re-use: Data quality assurance processes**ETHICAL ASPECTS**

Ethics approval authority: University of Debrecen; Faculty of Medicine **Ethics approval ID:** 12/2016/DE MÁB
Dr. Kisvárdy Zoltán

RELEASES AND PROGRESS**Planned releases:**

Month	Shared.with	Quality	Completeness	Location	Embargo	Actual.Completeness
M18	—	—	—	—	—	Achievement of the top-ranking quality preservation of ultrastructure; Immunohistochemical characterisation of 6 GABAergic interneuron subtypes from 9 (~65%)
M20	Collab	Prototype data	1 out of 24 (2 areas, 6 layers each, 2 cells per layer)	Collaboratory		Ditto

Month	Shared.with	Quality	Completeness	Location	Embargo	Actual.Completeness
M23	Ditto	Ditto	Ditto	Ditto	Ditto	2-2 series (S1 and V1) of alternate coronal sections of 5 from 6 characterized interneuron subtypes are prepared for electron microscopy, and ready for identification and tracing of dendrites with the help of the “mirror technique” elaborated before. (~80%)

Any deviation and mitigation: NA

Current location(s) of dataset:

<https://collab.humanbrainproject.eu/#/collab/6280/nav/48469>

DATA USAGE

Transferred to SP5/Shared with modelling tasks: NA

Contribution to Use Cases /other SPs: SP1-UC06: High-resolution synaptic maps in the mouse neocortex and hippocampus; SP1-UC07-Polyneuronal innervations of the dendrites: synaptic coverage of subtypes of GABAergic neurons

What are datasets used for (models, atlas)?: Models of SSC

Link to model/Atlas: <https://collab.humanbrainproject.eu/#/collab/1655/nav/75901>

How the data transfer has been or is coordinated:

Role and take-up of the data acquired: This dataset has been generated by task T1.2.7. Quantitative data according to the spatio-temporal topography of synaptic inputs within primary sensory cortices of the mouse are still lacking and essential for modelling of neuronal microcircuits. Electron microscopical 3D reconstruction is the only way to get a detailed view about the synaptic coverage of the neurons. We provide quantitative data about the synaptic coverage of dendrites of the different subpopulations of GABAergic interneurons, and determine the exact location of synaptic inputs with respect to the soma. Our work completes well with the results of the laboratory of R. Shigemoto (SP1, Task 1.1.3), who map the synaptic receptor content of the cortical neurons including GABAergic interneurons. This work provides essential data for 3 tasks of SP6: T6.1.4: Integration of Subcellular Models in Single Neuron Models., T6.2.2: Models of Somatosensory Cortex, and T6.3.3: Tools for Cellular Reconstruction

We use a reliable and well feasible method, the „mirror-technique”, which allows us to determine the exact location of the interneuron in the immuno-labelled and the neighboring “non-labelled” section and preserve the original quality of ultrastructure at the same time. The latter is crucial for following and punctual segmentation of the dendrites. We could identify 6 (calbindin, calretinin, parvalbumin, VIP, somatostatin, CCK) from the 8 subtypes planned in the frame of the first milestone of our Task (M1.2.2.). This milestone is still only partially achieved, because now we focus on the segmentation and 3D reconstruction of the identified dendrites (M1.2.13.). So far, we have 4 identified calbindin-D28K positive interneurons from different neocortical layers (2-4) of the primary visual cortex and 7 dendrites have been traced. According to our plan at least two additional GABAergic subtypes (one calbindin and one calretinin) will be analysed until the end of 2018.

PUBLICATIONS

T1.2.8: 3D digital reconstructions of individual thalamocortical neurons (ID: 732)**Dataset Owner:** Francisco Clasca < francisco.clasca@uam.es > (UAM)**DATA SUMMARY****Purpose of the data collection/generation**

Quantitative data on axonal length terminal bouton number of thalamocortical neurons innervating V1 and S1 cortices

Relation to the objectives of the project

Direct relation to objective 1d, Maps of cellular distributions, long-range axonal projections, and synaptic proteins; reconstructed morphologies of major neuron types

Types and formats of data generated/collected**Types:** 3D Neurolucida reconstruction/measurements **Formats:** .DAT**Protocol:** Single-cell transfection-labeling and whole axon 3D reconstruction**Existing data being re-used (if any)**

No

Origin of the data**Data class:** Cellular **Specimen information:** C57BL6 mice. Male 60-80 day old, normal eyes and whiskers. Wild-type with no previous manipulation. Breed in our University facilities.**Brain region:** Somatosensory cortex, Thalamus, Visual cortex, **Subregion:** S1,S2, Ins, M1, VPM, Po V1, V2 DLG, LP**Expected size of the data**

10 GB

Data utility: to whom will it be useful**Within HBP:** Thalamocortical axon data are needed to constrain predictive, bottom-up models of cortical microcircuitry.T3.1.4 SGA1) and (T1.2.9 SGA1)**Outwith HBP:** NA**FAIR DATA****Accessibility: which data will be made openly available**

Privacy class is: Animal Research. There are no issues sharing data

Accessibility: Methods, software tools and documentation needed to access the data

Neurolucida .DAT files (MBF Neuroscience, Willington, VT, USA)

Re-use: Data licensing to permit the widest reuse possible

BY-NC - Attribution + Noncommercial

Re-use: Data quality assurance processes**ETHICAL ASPECTS****Ethics approval authority:** Comunidad de Madrid, Consejería de Agricultura y Ganadería **Ethics approval ID:** PROEX 175/16 (08/18/2016-08/17/2021)**RELEASES AND PROGRESS****Planned releases:**

Month	Shared	with Quality	Completeness	Location	Embargo	Actual Completeness
M18	—	—	—	—	—	17 cells with axons completely labeled and valid for analysis (9 visual, 8 somatosensory) have been obtained. At M18, 7 of these cells have been Neurolucida-reconstructed (23%). At M18, metadata from the 7 reconstructed cells have been uploaded.
M23	Collab	Candidate final quality	15 out of 30 cells traced	Collaboratory	These data are being submitted for publication as part of two full-length research reports	22 cells with axons completely labeled and valid for analysis (9 visual, 13 somatosensory) have been obtained. At M23, 7 of these cells have been Neurolucida-reconstructed (31%) . At M23, metadata from the 7 reconstructed cells have been uploaded. Besides, image stacks (virtual slices from the soma, dendrites and arborization in the cortex and reticular nucleus) from 3 of these neurons have been uploaded.

Any deviation and mitigation: NA

Current location(s) of dataset:

<https://collab.humanbrainproject.eu/#/collab/5346/nav/41583>

<https://docs.google.com/spreadsheets/d/1r4HZPUB0m6maRJh57qbyv4zeM9XIZBI0YOV4d6VhDgE/edit#gid=0>

DATA USAGE

Transferred to SP5/Shared with modelling tasks: NA

Contribution to Use Cases /other SPs: Reconstructions released to two SP5 groups (SKU, UIO)

<http://dx.doi.org/10.7490/f1000research.1114766.1>>; SP5-UC05: Prediction of axonal termination patterns of long-range projection neurons (LRPN)

What are datasets used for (models, atlas)?: Atlas

Link to model/Atlas: <https://collab.humanbrainproject.eu/#/collab/5401/nav/82073>

How the data transfer has been or is coordinated: 3D reconstructions of thalamocortical projection neurons were delineated based on Franklin and Paxinos (2007) by María García-Amado Sancho in Francisco Clascá's laboratory. Coordinate positions of the soma for each neuronal reconstruction were registered in the Allen mouse brain atlas (v3). The dataset is available for download in Storage: Example datasets (Neuronal soma coordinates.txt) and can be visualised in 3D mouse brain atlas space with the Meshview tool.

Role and take-up of the data acquired: This dataset has been used in the Atlas. Link:

<https://collab.humanbrainproject.eu/#/collab/5401/nav/82073>. 3D reconstructions of thalamocortical projection neurons were delineated based on Franklin and Paxinos (2007) by María García-Amado Sancho in Francisco Clascá's laboratory. Coordinate positions of the soma for each neuronal reconstruction were registered in the Allen mouse brain atlas (v3). The dataset is available for download in Storage: Example datasets (Neuronal soma coordinates.txt) and can be visualized in 3D mouse brain atlas space with the Meshview tool.

In addition, this dataset has contributed to SP5-UC05. In particular, reconstructions released to two SP5 groups (SKU, UIO) <http://dx.doi.org/10.7490/f1000research.1114766.1>>; SP5-UC05: Prediction of axonal termination patterns of long-range projection neurons (LRPN)

This metadata has been generated by task T1.2.7. See component ID 732 for information on the role and take up of the acquired data of this task.

PUBLICATIONS

- Cazemier JL, Clascá F, Tiesinga PH. (2016) Connectomic Analysis of Brain Networks: Novel Techniques and Future Directions. *Front Neuroanat.* 2016 Nov 9;10:110. eCollection 2016 Nov 9 Open Access <https://doi.org/10.3389/fnana.2016.00110>
 - Rodriguez-Lopez C., Clasca F, Prensa L. (2017) The Mesoaccumbens Pathway: A Retrograde Labeling and Single-Cell Axon Tracing Analysis in the Mouse. (2017) *Front. Neuroanat.* 2017 March 27 11:25 eCollection Mar 27 <https://doi.org/10.3389/fnana.2017.00025>
 - Rodriguez Moreno J., J, Rollengaen A., Arlandis J, Santuy A, Merchán-Pérez A, DeFelipe J, Lubke JHR, Clasca F (2017) Quantitative 3D ultrastructure of thalamocortical synapses from the 'lemniscal' ventral posteromedial nucleus in mouse barrel cortex. *Cerebral Cortex.* <https://doi.org/10.1093/cercor/bhx187>
 - Casas-Torremocha D, Clascá F and Núñez Á (2017) Posterior Thalamic Nucleus Modulation of Tactile Stimuli Processing in Rat Motor and Primary Somatosensory Cortices. *Front. Neural Circuits* 11:69. doi: 10.3389/fncir.2017.00069
-

T1.2.9: Immunocytochemical detection of excitatory and inhibitory terminals in the mouse hippocampus (CA1) by confocal microscopy (ID: 961)

Dataset Owner: Alberto Muñoz < amunozc@bio.ucm.es > (UPM)

DATA SUMMARY

Purpose of the data collection/generation

Number of excitatory and inhibitory axon terminals per unit volume in the three strata of the adult mouse CA1 region

Relation to the objectives of the project

The data is directly related to the objectives 1c and 1d, Microcircuitry analysis, proteins and receptor distributions, fibre architecture in a specific large area brain region and Maps of cellular distributions, long-range axonal projections, and synaptic proteins; reconstructed morphologies of major neuron types

Types and formats of data generated/collected

Types: Files containing number and morphological features of excitatory and inhibitory axon terminals **Formats:** Excel files

Protocol: Immunofluorescence, confocal microscopy

Existing data being re-used (if any)

No

Origin of the data

Data class: Cellular **Specimen information:** Male adult (8 weeks) C57 mouse

Brain region: Hippocampus **Subregion:** CA1

Expected size of the data

5GB

Data utility: to whom will it be useful

Within HBP: The number of axon terminals and their distribution in the different strata of CA1 is necessary to build and refine brain models. This is important for T6.2.3 (SGA2) Models of hippocampus & community, T6.2.4 (SGA1) Models of hippocampus, and for T1.2.1 (SGA1) The pyramidal neuron in the cerebral cortex of humans and rodents

Outwith HBP: NA

FAIR DATA

Accessibility: which data will be made openly available

Privacy class is: Animal Research. There are no issues sharing data

Accessibility: Methods, software tools and documentation needed to access the data

Excel

Re-use: Data licensing to permit the widest reuse possible

BY-NC

Re-use: Data quality assurance processes

ETHICAL ASPECTS

Ethics approval authority: Local Ethics Committee (CSIC) ES280790000184 **Ethics approval ID:** CEAA-IC Approval

RELEASES AND PROGRESS

Planned releases:

Month	Shared.with	Quality	Completeness	Location	Embargo	Actual.Completeness
M16	Collab	Candidate final quality	Complete.15 stacks analysed per stratum and animal	Collaboratory	Until publication	—
M18	Ditto	Ditto	Ditto	Ditto	Ditto	Completed at M16; Analysis from 15 confocal stacks per CA1 hippocampal stratum in 5 animals (100%)

Any deviation and mitigation: NA

Current location(s) of dataset:

<https://collab.humanbrainproject.eu/#/collab/17051/nav/123316>

DATA USAGE

Transferred to SP5/Shared with modelling tasks: NA

Contribution to Use Cases /other SPs: SP1-UC03: Connectivity skeletons to explore local synaptic rules; SP4 (T1.4.1) and SP6 (T6.2.2 - Models of Somatosensory Cortex and T6.2.4 - Models of Hippocampus).

What are datasets used for (models, atlas)?: Models

Link to model/Atlas: <https://collab.humanbrainproject.eu/#/collab/1655/nav/75902>

How the data transfer has been or is coordinated: It has been coordinated with the Data Curation Team (Krister Andersson) and with meetings with model builders

Role and take-up of the data acquired: This dataset has been generated by task T1.2.9. See component iD 962 for information on the role and take up of the acquired data of this task.

PUBLICATIONS

- [Alejandro Antón-Fernández, Guillermo Aparicio-Torres, Silvia Tapia, Javier DeFelipe, Alberto Muñoz \(2016\). Morphometric alterations of Golgi apparatus in Alzheimer's disease are related to tau hyperphosphorylation. Neurobiology of Disease \(97\) 2017 11-23](#)
 - [Carolina Gonzalez-Riano, Silvia Tapia-Gonzalez, Antonia García, Alberto Muñoz, Javier DeFelipe, Coral Barbas \(2017\). Metabolomics and neuroanatomical evaluation of post mortem changes in the hippocampus. Brain Struct Funct. DOI: 10.1007/s00429-017-1375-5](#)
 - [Santuy A, Rodriguez JR, DeFelipe J, Merchán-Pérez A \(2017\) Volume electron microscopy of the distribution of synapses in the neuropil of the juvenile rat somatosensory cortex. Brain Struct Funct. 2017 Jul 18. doi: 10.1007/s00429-017-1470-7.](#)
 - [Bosch C, Masachs N, Exposito-Alonso D, Martínez A, Teixeira CM, Feraud I, Pujadas L, Ulloa F, Comella JX, DeFelipe J, Merchán-Pérez A, Soriano E. \(2016\). Reelin Regulates the Maturation of Dendritic Spines, Synaptogenesis and Glial Ensheathment of Newborn Granule Cells. Cereb Cortex. 2016 Sep 13.](#)
 - [Urrecha M, Romero I1, DeFelipe J, Merchán-Pérez A. Influence of cerebral blood vessel movements on the position of perivascular synapses. PLoS One. 2017 Feb 15;12\(2\):e0172368. doi: 10.1371/journal.pone.0172368](#)
-

T1.2.9: Immunocytochemical detection of excitatory and inhibitory terminals in the mouse somatosensory cortex by confocal microscopy (ID: 962)

Dataset Owner: Alberto Muñoz < amunozc@bio.ucm.es > (UPM)

DATA SUMMARY

Purpose of the data collection/generation

Number of excitatory and inhibitory axon terminals per unit volume in the six cortical layers of the adult mouse somatosensory cortex

Relation to the objectives of the project

The data is directly related to the objectives 1c and 1d, Microcircuitry analysis, proteins and receptor distributions, fibre architecture in a specific large area brain region and Maps of cellular distributions, long-range axonal projections, and synaptic proteins; reconstructed morphologies of major neuron types

Types and formats of data generated/collected

Types: Files containing number and morphological features of excitatory and inhibitory axon terminals **Formats:** Excel files

Protocol: Immunofluorescence, confocal microscopy

Existing data being re-used (if any)

No

Origin of the data

Data class: Cellular **Specimen information:** Male adult (8 weeks) C57 mouse

Brain region: Somatosensory cortex **Subregion:** Hindlimb representation

Expected size of the data

5GB

Data utility: to whom will it be useful

Within HBP: The number of axon terminals and their distribution in the different cortical layers of the mouse somatosensory cortex is necessary to build and refine brain models. This is essential for T6.2.2 (SGA1) Models of somatosensory cortex, important for T1.2.1 (SGA1) The pyramidal neuron in the cerebral cortex of humans and rodents and added value for T3.1.4 (SGA1) Animal model for context-sensitive amplification - dendritic mechanisms of feedback interactions

Outwith HBP: NA

FAIR DATA

Accessibility: which data will be made openly available

Privacy class is: Animal Research. There are no issues sharing data

Accessibility: Methods, software tools and documentation needed to access the data

Excel

Re-use: Data licensing to permit the widest reuse possible

BY-NC

Re-use: Data quality assurance processes

ETHICAL ASPECTS

Ethics approval authority: Local Ethics Committee (CSIC) ES280790000184 **Ethics approval ID:** CEAA-IC Approval

RELEASES AND PROGRESS

Planned releases:

Month	Shared.with	Quality	Completeness	Location	Embargo	Actual.Completeness
M16	Collab	Candidate final quality	Complete.15 stacks analysed per cortical layer and animal	Collaboratory	Until publication	—
M18	Ditto	Ditto	Ditto	Ditto	Ditto	Completed at M16; Analysis from 15 confocal stacks per cortical layer in 5 animals (100%)

Any deviation and mitigation: NA

Current location(s) of dataset:

<https://collab.humanbrainproject.eu/#/collab/17051/nav/123316>

DATA USAGE

Transferred to SP5/Shared with modelling tasks: NA

Contribution to Use Cases /other SPs: SP1-UC03: Connectivity skeletons to explore local synaptic rules; SP4 (T1.4.1) and SP6 (T6.2.2 - Models of Somatosensory Cortex and T6.2.4 - Models of Hippocampus).

What are datasets used for (models, atlas)?: Models

Link to model/Atlas: <https://collab.humanbrainproject.eu/#/collab/1655/nav/75901>

How the data transfer has been or is coordinated: It has been coordinated with the Data Curation Team (Krister Andersson) and with meetings with model builders

Role and take-up of the data acquired: This dataset has been generated by T1.2.9. The number and distribution of synaptic contacts are key features of brain circuits. In brain models, once the neurons are placed in the appropriate locations, it is necessary to connect them with the appropriate number of synapses. At the cellular scale (using confocal microscopy) large areas of the brain can be surveyed and the number of excitatory and inhibitory synapses can be estimated using immunocytochemical methods. Better estimates can be obtained at the subcellular scale (using FIB/SEM), although the sampled regions are bound to be smaller. We have combined both methods to obtain information on the number and distribution of excitatory and inhibitory synapses in the different layers of the hippocampus and the neocortex of the mouse and human. These data are very interesting in model building since the density of synapses present in any given region, as well as the proportion of excitatory and inhibitory synapses, are crucial from the structural and functional points of view. This dataset has been used in T1.4.1 to identify common and differing principles of organization that can be used in algorithms that reconstruct synaptic connections for use in brain models. In addition, this data has been delivered to the HBP Mouse Brain Atlas, and will complement the data obtained by the Allen Institute in order to further develop the HBP Mouse Brain Atlas. As well as that, the data has been and will be used by SP6 (T6.2.2 - Models of Somatosensory Cortex and T6.2.4 - Models of Hippocampus).

PUBLICATIONS

- [Alejandro Antón-Fernández, Guillermo Aparicio-Torres, Silvia Tapia, Javier DeFelipe, Alberto Muñoz \(2016\). Morphometric alterations of Golgi apparatus in Alzheimer's disease are related to tau hyperphosphorylation. Neurobiology of Disease \(97\) 2017 11-23](#)
 - [Carolina Gonzalez-Riano, Silvia Tapia-Gonzalez, Antonia García, Alberto Muñoz, Javier DeFelipe, Coral Barbas \(2017\). Metabolomics and neuroanatomical evaluation of post mortem changes in the hippocampus. Brain Struct Funct. DOI: 10.1007/s00429-017-1375-5](#)
 - [Santuy A, Rodriguez JR, DeFelipe J, Merchán-Pérez A \(2017\) Volume electron microscopy of the distribution of synapses in the neuropil of the juvenile rat somatosensory cortex. Brain Struct Funct. 2017 Jul 18. doi: 10.1007/s00429-017-1470-7.](#)
 - [Bosch C, Masachs N, Exposito-Alonso D, Martínez A, Teixeira CM, Feraud I, Pujadas L, Ulloa F, Comella JX, DeFelipe J, Merchán-Pérez A, Soriano E. \(2016\). Reelin Regulates the Maturation of Dendritic Spines, Synaptogenesis and Glial Ensheathment of Newborn Granule Cells. Cereb Cortex. 2016 Sep 13.](#)
 - [Urrecha M, Romero I1, DeFelipe J, Merchán-Pérez A. Influence of cerebral blood vessel movements on the position of perivascular synapses. PLoS One. 2017 Feb 15;12\(2\):e0172368. doi: 10.1371/journal.pone.0172368](#)
-

T1.2.9: Densities and 3D distributions of synapses in the mouse hippocampus (CA1) (ID: 963)**Dataset Owner:** Angel Merchan Perez < amerchan@fi.upm.es > (UPM)**DATA SUMMARY****Purpose of the data collection/generation**

Number of synapses per unit volume in stratum oriens, stratum radiatum and stratum moleculare-lacunosum of the adult mouse hippocampus (CA1)

Relation to the objectives of the project

The data is directly related to the objectives 1c and 1d, Microcircuitry analysis, proteins and receptor distributions, fibre architecture in a specific large area brain region and Maps of cellular distributions, long-range axonal projections, and synaptic proteins; reconstructed morphologies of major neuron types

Types and formats of data generated/collected

Types: 3D files containing the segmentations of synaptic junctions. Raw data containing the numbers and positions of synaptic junctions **Formats:** .seg files (created with Espina software); Excel files

Protocol: FIB/SEM imaging

Existing data being re-used (if any)

No

Origin of the data

Data class: Electrophysiological **Specimen information:** Male adult (8 weeks) C57 mouse

Brain region: Hippocampus **Subregion:** CA1

Expected size of the data

5GB

Data utility: to whom will it be useful

Within HBP: The number of synapses in their distribution in the different cortical layers of the mouse somatosensory cortex is necessary to build and refine models of the hippocampus. This is important for T6.2.4 (SGA1) "Models of hippocampus"; important for T1.2.1 (SGA1) "The pyramidal neuron in the cerebral cortex of humans and rodents"; essential for T1.5.5 (SGA2) "Machine learning-based comparative studies of microanatomy and physiology of mice and humans"

Outwith HBP: NA

FAIR DATA**Accessibility: which data will be made openly available**

Privacy class is: Animal Research. There are no issues sharing data

Accessibility: Methods, software tools and documentation needed to access the data

Espina; Excel

Re-use: Data licensing to permit the widest reuse possible

BY-NC

Re-use: Data quality assurance processes**ETHICAL ASPECTS**

Ethics approval authority: Local Ethics Committee (CSIC) ES280790000184 **Ethics approval ID:** CEAA-IC Approval

RELEASES AND PROGRESS**Planned releases:**

Month	Shared.with	Quality	Completeness	Location	Embargo	Actual.Completeness
M18	—	—	—	—	—	At M18 we have aquired 12 FIB/SEM stacks of images from str. Oriens, radiatum and lacunosum moleculare, from three animals. This is 100% of the stacks required. Segmentation and analysis is in progress
M23	Collab	Candidate final quality	At least one FIB-SEM sample from each of the three layers, from three animals analysed	Collaboratory	Until publication	At M23 we have aquired 12 FIB/SEM stacks of images from str. Oriens, radiatum and lacunosum moleculare, from three animals. This is 100% of the stacks required. Segmentation has been completed and analysis is in progress

Any deviation and mitigation: NA

Current location(s) of dataset:

<https://collab.humanbrainproject.eu/#/collab/17053/nav/123326>

DATA USAGE

Transferred to SP5/Shared with modelling tasks: NA

Contribution to Use Cases /other SPs: SP1-UC03: Connectivity skeletons to explore local synaptic rules; SP4 (T1.4.1) and SP6 (T6.2.2 - Models of Somatosensory Cortex and T6.2.4 - Models of Hippocampus).

What are datasets used for (models, atlas)?: Models

Link to model/Atlas: <https://collab.humanbrainproject.eu/#/collab/1655/nav/75904>

How the data transfer has been or is coordinated: It has been coordinated with the Data Curation Team (Krister Andersson) and with meetings with model builders

Role and take-up of the data acquired: This dataset has been generated by task T1.2.9. See component iD 962 for information on the role and take up of the acquired data of this task.

PUBLICATIONS

- [Alejandro Antón-Fernández, Guillermo Aparicio-Torres, Silvia Tapia, Javier DeFelipe, Alberto Muñoz \(2016\). Morphometric alterations of Golgi apparatus in Alzheimer's disease are related to tau hyperphosphorylation. Neurobiology of Disease \(97\) 2017 11-23](#)
- [Carolina Gonzalez-Riano, Silvia Tapia-Gonzalez, Antonia García, Alberto Muñoz, Javier DeFelipe, Coral Barbas \(2017\). Metabolomics and neuroanatomical evaluation of post mortem changes in the hippocampus. Brain Struct Funct. DOI: 10.1007/s00429-017-1375-5](#)
- [Santuy A, Rodriguez JR, DeFelipe J, Merchán-Pérez A \(2017\) Volume electron microscopy of the distribution of synapses in the neuropil of the juvenile rat somatosensory cortex. Brain Struct Funct. 2017 Jul 18. doi: 10.1007/s00429-017-1470-7.](#)
- [Bosch C, Masachs N, Exposito-Alonso D, Martínez A, Teixeira CM, Feraud I, Pujadas L, Ulloa F, Comella JX, DeFelipe J, Merchán-Pérez A, Soriano E. \(2016\). Reelin Regulates the Maturation of Dendritic Spines, Synaptogenesis and Glial Ensheathment of Newborn Granule Cells. Cereb Cortex. 2016 Sep 13.](#)
- [Urrecha M, Romero I1, DeFelipe J, Merchán-Pérez A. Influence of cerebral blood vessel movements on the position of perivascular synapses. PLoS One. 2017 Feb 15;12\(2\):e0172368. doi: 10.1371/journal.pone.0172368](#)

T1.2.9: Densities and 3D distributions of synapses in the mouse neocortex (ID: 964)**Dataset Owner:** Ángel Merchán Pérez < amerchan@fi.upm.es > (UPM)**DATA SUMMARY****Purpose of the data collection/generation**

Number of synapses per unit volume in the six cortical layers of the adult mouse somatosensory cortex (layers I, II, III, IV, Va, Vb and VI)

Relation to the objectives of the project

The data is directly related to the objectives 1c and 1d, Microcircuitry analysis, proteins and receptor distributions, fibre architecture in a specific large area brain region and Maps of cellular distributions, long-range axonal projections, and synaptic proteins; reconstructed morphologies of major neuron types

Types and formats of data generated/collected

Types: 3D files containing the segmentations of synaptic junctions. Raw data containing the numbers and positions of synaptic junctions **Formats:** .seg files (created with Espina software); Excel files

Protocol: FIB/SEM imaging

Existing data being re-used (if any)

No

Origin of the data

Data class: Subcellular **Specimen information:** Male adult (8 weeks) C57 mouse

Brain region: Somatosensory cortex **Subregion:** Hindlimb representation

Expected size of the data

5GB

Data utility: to whom will it be useful

Within HBP: The number of synapses in their distribution in the different cortical layers of the mouse somatosensory cortex is necessary to build and refine brain models. This is essential for T6.2.2 (SGA1) "Models of somatosensory cortex"; important for T1.2.1 (SGA1) "The pyramidal neuron in the cerebral cortex of humans and rodents"; essential for T1.5.5 (SGA2) "Machine learning-based comparative studies of microanatomy and physiology of mice and humans"

Outwith HBP: NA

FAIR DATA**Accessibility: which data will be made openly available**

Privacy class is: Animal Research. There are no issues sharing data

Accessibility: Methods, software tools and documentation needed to access the data

Espina; Excel

Re-use: Data licensing to permit the widest reuse possible

BY-NC

Re-use: Data quality assurance processes**ETHICAL ASPECTS**

Ethics approval authority: Local Ethics Committee (CSIC) **Ethics approval ID:** ES280790000184

RELEASES AND PROGRESS**Planned releases:**

Month	Shared	with Quality	Completeness	Location	Embargo	Actual.Completeness
M18	—	—	—	—	—	At M18 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 and analysis is in progress
M23	Collab	Candidate final quality	At least one FIB-SEM sample from each of the six cortical layers, from three animals analysed	Collaboratory	Until publication	At M23 we have acquired 21 FIB/SEM stacks of images from the six cortical layers, of three animals. This is 100% of the stacks required. Segmentation has been completed and analysis is in progress

Any deviation and mitigation: NA

Current location(s) of dataset:

<https://collab.humanbrainproject.eu/#/collab/17052/nav/123321>

DATA USAGE

Transferred to SP5/Shared with modelling tasks: NA

Contribution to Use Cases /other SPs: SP1-UC03: Connectivity skeletons to explore local synaptic rules; SP4 (T1.4.1) and SP6 (T6.2.2 - Models of Somatosensory Cortex and T6.2.4 - Models of Hippocampus).

What are datasets used for (models, atlas)?: Models

Link to model/Atlas: <https://collab.humanbrainproject.eu/#/collab/1655/nav/75903>

How the data transfer has been or is coordinated: It has been coordinated with the Data Curation Team (Krister Andersson) and with meetings with model builders

Role and take-up of the data acquired: This dataset has been generated by task T1.2.9. See component iD 962 for information on the role and take up of the acquired data of this task.

PUBLICATIONS

- [Alejandro Antón-Fernández, Guillermo Aparicio-Torres, Silvia Tapia, Javier DeFelipe, Alberto Muñoz \(2016\). Morphometric alterations of Golgi apparatus in Alzheimer's disease are related to tau hyperphosphorylation. Neurobiology of Disease \(97\) 2017 11-23](#)
 - [Carolina Gonzalez-Riano, Silvia Tapia-Gonzalez, Antonia García, Alberto Muñoz, Javier DeFelipe, Coral Barbas \(2017\). Metabolomics and neuroanatomical evaluation of post mortem changes in the hippocampus. Brain Struct Funct. DOI: 10.1007/s00429-017-1375-5](#)
 - [Santuy A, Rodriguez JR, DeFelipe J, Merchan-Perez A \(2017\) Volume electron microscopy of the distribution of synapses in the neuropil of the juvenile rat somatosensory cortex. Brain Struct Funct. 2017 Jul 18. doi: 10.1007/s00429-017-1470-7.](#)
 - [Bosch C, Masachs N, Exposito-Alonso D, Martínez A, Teixeira CM, Feraud I, Pujadas L, Ulloa F, Comella JX, DeFelipe J, Merchán-Pérez A, Soriano E. \(2016\). Reelin Regulates the Maturation of Dendritic Spines, Synptogenesis and Glial Ensheatment of Newborn Granule Cells. Cereb Cortex. 2016 Sep 13.](#)
 - [Urrecha M, Romero I1, DeFelipe J, Merchán-Pérez A. Influence of cerebral blood vessel movements on the position of perivascular synapses. PLoS One. 2017 Feb 15;12\(2\):e0172368. doi: 10.1371/journal.pone.0172368](#)
-

T1.2.9: Densities and 3D distributions of synapses in the human hippocampus (ID: 965)**Dataset Owner:** Ángel Merchán Pérez < amerchan@fi.upm.es > (UPM)**DATA SUMMARY****Purpose of the data collection/generation**

Obtaining densities and 3D distributions of synapses using FIB/SEM in the neuropil of CA1 region from human hippocampus provides details of the synaptic organization in a critical brain region

Relation to the objectives of the project

The data is directly related to the objective 1c, Microcircuitry analysis, proteins and receptor distributions, fibre architecture in a specific large area brain region

Types and formats of data generated/collected

Types: Segmentation data of FIB/SEM stacks **Formats:** Espina .seg; Excel .xls

Protocol: Focused Ion Beam Milling / Scanning Electron Microscopy

Existing data being re-used (if any)

No

Origin of the data

Data class: Subcellular **Specimen information:** Human, adult

Brain region: Hippocampus **Subregion:** CA1

Expected size of the data

5GB

Data utility: to whom will it be useful

Within HBP: Data will be used to complete synaptic comparative models (T1.4.1)

Outwith HBP: NA

FAIR DATA**Accessibility: which data will be made openly available**

Privacy class is: Human Research. There may be issues sharing data openly

Accessibility: Methods, software tools and documentation needed to access the data

Espina; Excel

Re-use: Data licensing to permit the widest reuse possible

BY-NC

Re-use: Data quality assurance processes**ETHICAL ASPECTS**

Ethics approval authority: Local Ethics Committee (CSIC) ES280790000184 **Ethics approval ID:** CEAA-IC Approval & CEI PI55-2016

RELEASES AND PROGRESS**Planned releases:**

Month	Shared	with Quality	Completeness	Location	Embargo	Actual.Completeness
M18	—	—	—	—	—	At M18 we have acquired 18 FIB/SEM stacks of images from stratum pyramidal and radiatum of human CA1. This is 100% of the stacks required. Segmentation and analysis is in progress
M23	Collab	Candidate final quality	18 FIB/SEM images stacks segmented	Collaboratory	Awaiting publication	At M23 we have 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

Any deviation and mitigation: NA

Current location(s) of dataset:

<https://collab.humanbrainproject.eu/#/collab/17085/nav/123536>

DATA USAGE

Transferred to SP5/Shared with modelling tasks: NA

Contribution to Use Cases /other SPs: SP1-UC03: Connectivity skeletons to explore local synaptic rules; SP4 (T1.4.1) and SP6 (T6.2.2 - Models of Somatosensory Cortex and T6.2.4 - Models of Hippocampus).

What are datasets used for (models, atlas)?: Models

Link to model/Atlas: <https://collab.humanbrainproject.eu/#/collab/1655/nav/75906>

How the data transfer has been or is coordinated: It has been coordinated with the Data Curation Team (Krister Andersson) and with meetings with model builders

Role and take-up of the data acquired: This dataset has been generated by task T1.2.9. See component iD 962 for information on the role and take up of the acquired data of this task.

PUBLICATIONS

- [Alejandro Antón-Fernández, Guillermo Aparicio-Torres, Silvia Tapia, Javier DeFelipe, Alberto Muñoz \(2016\). Morphometric alterations of Golgi apparatus in Alzheimer's disease are related to tau hyperphosphorylation. Neurobiology of Disease \(97\) 2017 11-23](#)
 - [Carolina Gonzalez-Riano, Silvia Tapia-Gonzalez, Antonia García, Alberto Muñoz, Javier DeFelipe, Coral Barbas \(2017\). Metabolomics and neuroanatomical evaluation of post mortem changes in the hippocampus. Brain Struct Funct. DOI: 10.1007/s00429-017-1375-5](#)
 - [Santuy A, Rodriguez JR, DeFelipe J, Merchán-Pérez A \(2017\) Volume electron microscopy of the distribution of synapses in the neuropil of the juvenile rat somatosensory cortex. Brain Struct Funct. 2017 Jul 18. doi: 10.1007/s00429-017-1470-7.](#)
 - [Bosch C, Masachs N, Exposito-Alonso D, Martínez A, Teixeira CM, Feraud I, Pujadas L, Ulloa F, Comella JX, DeFelipe J, Merchán-Pérez A, Soriano E. \(2016\). Reelin Regulates the Maturation of Dendritic Spines, Synaptogenesis and Glial Ensheathment of Newborn Granule Cells. Cereb Cortex. 2016 Sep 13.](#)
 - [Urrecha M, Romero I1, DeFelipe J, Merchán-Pérez A. Influence of cerebral blood vessel movements on the position of perivascular synapses. PLoS One. 2017 Feb 15;12\(2\):e0172368. doi: 10.1371/journal.pone.0172368](#)
-

T1.2.9: Densities and 3D distributions of synapses using FIB/SEM imaging in the human neocortex (Temporal cortex, T2) (ID: 966)

Dataset Owner: Ángel Merchán Pérez < amerchan@fi.upm.es > (UPM)

DATA SUMMARY

Purpose of the data collection/generation

We will produce 3D reconstructions of as synapses at the ultrastructural level in the neuropil of neocortex from temporal associative area 21 in non-pathological human brain tissue using FIB/SEM technology

Relation to the objectives of the project

The data is directly related to the objective 1c, Microcircuitry analysis, proteins and receptor distributions, fibre architecture in a specific large area brain region

Types and formats of data generated/collected

Types: Segmentation data of FIB/SEM stacks **Formats:** Espina .seg; Excel .xls

Protocol: Focused Ion Beam Milling / Scanning Electron Microscopy

Existing data being re-used (if any)

No

Origin of the data

Data class: Subcellular **Specimen information:** Human, adult

Brain region: Neocortex **Subregion:** Temporal cortex

Expected size of the data

5GB

Data utility: to whom will it be useful

Within HBP: Data will be used to complete synaptic comparative models (T1.4.1)

Outwith HBP: NA

FAIR DATA

Accessibility: which data will be made openly available

Privacy class is: Human Research. There may be issues sharing data openly

Accessibility: Methods, software tools and documentation needed to access the data

Espina; Excel

Re-use: Data licensing to permit the widest reuse possible

BY-NC

Re-use: Data quality assurance processes

ETHICAL ASPECTS

Ethics approval authority: Local Ethics Committee (CSIC) ES280790000184 **Ethics approval ID:** CEAA-IC Approval & CEI PI55-2016

RELEASES AND PROGRESS

Planned releases:

Month	Shared.with	Quality	Completeness	Location	Embargo	Actual.Completeness
M18	—	—	—	—	—	At M18 we have aquired 9 FIB/SEM stacks of images from the layer 3 of the T2 neocortex. This is 100% of the stacks required. Segmentation and analysis is in progress
M23	Collab	Candidate final quality	9 of 9 FIB/SEM images stacks segmented	Collaboratory	Awaiting publication	At M23 we have aquired 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

Any deviation and mitigation: NA

Current location(s) of dataset:

<https://collab.humanbrainproject.eu/#/collab/17084/nav/123531>

DATA USAGE

Transferred to SP5/Shared with modelling tasks: NA

Contribution to Use Cases /other SPs: SP1-UC03: Connectivity skeletons to explore local synaptic rules; SP4 (T1.4.1) and SP6 (T6.2.2 - Models of Somatosensory Cortex and T6.2.4 - Models of Hippocampus).

What are datasets used for (models, atlas)?: Models

Link to model/Atlas: <https://collab.humanbrainproject.eu/#/collab/1655/nav/75905>

How the data transfer has been or is coordinated: It has been coordinated with the Data Curation Team (Krister Andersson) and with meetings with model builders

Role and take-up of the data acquired: This dataset has been generated by task T1.2.9. See component iD 962 for information on the role and take up of the acquired data of this task.

PUBLICATIONS

- [Alejandro Antón-Fernández, Guillermo Aparicio-Torres, Silvia Tapia, Javier DeFelipe, Alberto Muñoz \(2016\). Morphometric alterations of Golgi apparatus in Alzheimer's disease are related to tau hyperphosphorylation. Neurobiology of Disease \(97\) 2017 11-23](#)
 - [Carolina Gonzalez-Riano, Silvia Tapia-Gonzalez, Antonia García, Alberto Muñoz, Javier DeFelipe, Coral Barbas \(2017\). Metabolomics and neuroanatomical evaluation of post mortem changes in the hippocampus. Brain Struct Funct. DOI: 10.1007/s00429-017-1375-5](#)
 - [Santuy A, Rodriguez JR, DeFelipe J, Merchán-Pérez A \(2017\) Volume electron microscopy of the distribution of synapses in the neuropil of the juvenile rat somatosensory cortex. Brain Struct Funct. 2017 Jul 18. doi: 10.1007/s00429-017-1470-7.](#)
 - [Bosch C, Masachs N, Exposito-Alonso D, Martínez A, Teixeira CM, Feraud I, Pujadas L, Ulloa F, Comella JX, DeFelipe J, Merchán-Pérez A, Soriano E. \(2016\). Reelin Regulates the Maturation of Dendritic Spines, Synaptogenesis and Glial Ensheathment of Newborn Granule Cells. Cereb Cortex. 2016 Sep 13.](#)
 - [Urrecha M, Romero I1, DeFelipe J, Merchán-Pérez A. Influence of cerebral blood vessel movements on the position of perivascular synapses. PLoS One. 2017 Feb 15;12\(2\):e0172368. doi: 10.1371/journal.pone.0172368](#)
-

T1.3.1: Whole-brain images of selected neuronal types (ID: 932)**Dataset Owner:** Ludovico Silvestri < silvestri@lens.unifi.it > (LENS)**DATA SUMMARY****Purpose of the data collection/generation**

Whole-brain comprehensive distribution maps of selected neuronal types based on specific staining are not available. Allen has gene expression maps consisting only of images (no cell localisation data) sampled with coarse sagittal resolution (about 100 microns). CSHL has gene expression maps with localization data, but still on a sampling base (50 microns step).

Relation to the objectives of the project

The whole-brain cell maps are a keystone to achieve objective 1c, and will be also useful to achieve objectives 1b (because the resolution is high enough to investigate cellular organization in subregions) and 1e (because similar technology is being used in SP2).

Types and formats of data generated/collected

Types: Initial data will be whole-brain images, final analysis will deliver point-clouds of various cell types in Allen reference space coordinates **Formats:** txt file for point cloud, jpeg for lossy-compressed images, mp4 for lossless-compressed data **Protocol:** We are using transgenic animals where different interneuron populations (parvalbumin-, somatostatin- and VIP-positive cells) are labelled with fluorescent proteins. Whole brains are extracted around post-natal day 56, and are processed using CLARITY-TDE method (Chung et al. 2013, Costantini et al. 2015). We then image the entire brain with high resolution using cutting-edge light-sheet microscopy. Afterwards, we apply a deep learning software for cell localization (Frasconi et al. 2014).

Existing data being re-used (if any)

No

Origin of the data

Data class: Whole-brain cell distributions **Specimen information:** Mouse (mus musculus), C57/B6J, age PND50-PND60, bought from mainstream Jackson

Brain region: Whole brain **Subregion:** Whole brain

Expected size of the data

About 40 TB of lossless-compressed raw data (for long-term archiving), about 200 GB of lossy-compressed images (for visualization and sharing purpose), and 3-4 GB of point cloud data (for simulation, meta-analysis, atlas building)

Data utility: to whom will it be useful

Within HBP: The cell maps serve: 1) The building of whole mouse brain simulations performed in SP6/SP10 and SP4 to be used in CDP1; 2) The building of whole mouse brain atlas performed in SP5. This will be useful for the scientific community because will provide quantitative information (complementary to Allen Atlas) and will be an essential part of CDP1

Outwith HBP: NA

FAIR DATA**Accessibility: which data will be made openly available**

Privacy class is: Animal Research. There are no issues sharing data

Accessibility: Methods, software tools and documentation needed to access the data

Images can be accessed with standard viewers (e.g. ImageJ). Point clouds can be visualized using specialized software (e.g. CloudCompare). Raw image data can be explored using an API we are internally developing and that will be released within SGA1.

Re-use: Data licensing to permit the widest reuse possible

Attribution NonCommercial ShareAlike 4.0

Re-use: Data quality assurance processes**ETHICAL ASPECTS**

Ethics approval authority: Italian Ministry of Health **Ethics approval ID:** 790/2016-PR

RELEASES AND PROGRESS**Planned releases:**

Month	Shared	with Quality	Completeness	Location	Embargo	Actual Completeness
M18	—	—	—	—	—	At M18, 11 whole-brain datasets (4 with parvalbumin-positive neurons labeled, 4 with VIP-positive and 3 with somatostatin-positive) have been collected. All raw data have been stored at CINECA. 100% of raw data, 25% of processed data

Month	Shared.with Quality	Completeness	Location	Embargo	Actual.Completeness
M23	Consortium	Candidate final quality	15 of 15 brains processed	Collaboratory; UIO Navigator	Awaiting publication
					At M23, 75% of raw data have been processed to obtain point cloud maps. Downsampled data have been stored in the Collaboratory, all raw and processed data have been stored at CINECA.

Any deviation and mitigation: NA

Current location(s) of dataset:

<https://collab.humanbrainproject.eu/#/collab/5340/nav/41538>

DATA USAGE

Transferred to SP5/Shared with modelling tasks: NA

Contribution to Use Cases /other SPs: CDP1-P2: A virtual anatomy lab app

What are datasets used for (models, atlas)?: 3D light-sheet whole brain map with propidium-iodide labeled cells has been used to test and adapt the SP5 workflows, developed for integrating data and metedata in the Mouse Brain Atlas (NIP).

Interneuron maps are used to refine whole-brain point-neuron models

Link to model/Atlas: Link to Filmstrip atlas viewer of an exemplar acquisition (Pseudo-coronal view of the brain. Voxel size 10.4x10.4x10 microns): <http://cmbn-navigator.uio.no/navigator/filmstripzoom/filmstripzoom.html?atlas=300000&series=4106&preview=ABAMousev2Preview.png>

Links to whole brain model:

<https://collab.humanbrainproject.eu/#/collab/1655/nav/75901?state=model.45fd93ed-7ce4-4ee5-90f6-1f985bfa92d5>

<https://collab.humanbrainproject.eu/#/collab/1655/nav/75901?state=model.111bc309-ba88-4aa9-9ea1-1c9dcdf75a13>

How the data transfer has been or is coordinated: Data has been transferred via ftp from LENS to a UIO repository. Down sampled data and related metadata has been uploaded via HBP Collaboratory (<https://collab.humanbrainproject.eu/#/collab/5340/nav/41538>)

Role and take-up of the data acquired: 3D light-sheet whole brain map with propidium-iodide labeled cells has been used to test and adapt the SP5 workflows, developed for integrating data and metedata in the Mouse Brain Atlas (NIP). Interneuron maps are used to refine whole-brain point-neuron models. Link to Filmstrip atlas viewer (Pseudo-coronal view of the brain. Voxel size 10.4x10.4x10 microns): <http://cmbn-navigator.uio.no/navigator/filmstripzoom/filmstripzoom.html?atlas=300000&series=4106&preview=ABAMousev2Preview.png>

The data have also contributed to CDP1-P2: A virtual anatomy lab app. Data has been transferred via ftp from LENS to a UIO repository. Down sampled data and aelated metedata has been uploaded via HBP Collaboratory (<https://collab.humanbrainproject.eu/#/collab/5340/nav/41538>)

PUBLICATIONS

- Adam et al., "Confocal multi-spot microscope for fast and deep imaging in semi-cleared tissues", J. Biomed. Opt., in press

T1.3.2: Wide-field imaging of cortical activity during motor learning (ID: 552)**Dataset Owner:** Anna Letizia Allegra Mascaro < allegra@lens.unifi.it > (LENS)**DATA SUMMARY****Purpose of the data collection/generation**

We will obtain cortical maps based on calcium neuronal activity in awake mice, in either resting state or during motor tasks (pulling a lever). We will use wide-field microscopy to investigate the functional connectivity of cortical neurons either over the cortical hemisphere contralateral to the trained forelimb. In detail, mice expressing calcium indicators (e.g. GCaMP6) in excitatory neurons will be longitudinally monitored for 5 training sessions performed over a week. These activities are part of the CDP1.

Relation to the objectives of the project

This task fulfil the objective 1g, Functional maps of cortical activity during learning of the motor task after stroke during learning in the robotic platform

Types and formats of data generated/collected

Types: wide-field images **Formats:** .tif

Protocol: [Wide-field fluorescence imaging protocol](#)

Existing data being re-used (if any)

No

Origin of the data

Data class: Circuits **Specimen information:** Mouse, Adult, males and females, approx 30g, Jackson Laboratory

Brain region: [Neocortex](#); [Motor cortex](#); [Somatosensory cortex](#) **Subregion:**

Expected size of the data

0.5T

Data utility: to whom will it be useful

Within HBP: The data collected from the above-described experiments will be used for validation of neuronal simulations performed in SP4, SP6 and SP10. In detail, the data provided in this task will be essential for the building and validation of models of spontaneous activity and brain states in mouse within T4.4.1. The entire experiment, from the lab environment to the muscle contraction and the brain activation will be simulated within T6.2.6 and T10.1.6, and fully integrated on the NRP. These data will be extensively used in CDP1 for closed-loop experiment and simulation and will be essential to link CDP1.

Outwith HBP: NA

FAIR DATA**Accessibility: which data will be made openly available**

Privacy class is: Animal Research. There are no issues sharing data

Accessibility: Methods, software tools and documentation needed to access the data

A lot of different software can be used to access the data, like Matlab or ImageJ or standard image processing tools

Re-use: Data licensing to permit the widest reuse possible

Attribution NonCommercial ShareAlike 4.0

Re-use: Data quality assurance processes**ETHICAL ASPECTS**

Ethics approval authority: Italian Minister of Health **Ethics approval ID:** 183/2016-PR

RELEASES AND PROGRESS**Planned releases:**

Month	Shared.with	Quality	Completeness	Location	Embargo	Actual.Completeness
M09	Collab	Candidate final quality	All data on learning should be acquired	Collaboratory	awaiting publication	—
M18	Consortium	Candidate final quality	All data on stroke mice (3 mice, 5 days of imaging sessions each) will be shared	Collaboratory	awaiting publication	At M18, 15 datasets (1/day, 5 days, 3 mice) of calcium activity in awake mice after stroke have been acquired 100% completed
M23	Consortium	Final quality	All data on rehab mice (3 mice, 5 imaging sessions over 5 days each) will be shared	Collaboratory	awaiting publication	already completed at M18

Any deviation and mitigation: NA

Current location(s) of dataset:

<https://collab.humanbrainproject.eu/#/collab/5340/nav/41538> https://ksproxy.cscs.ch:13000/Pavone_SGA1_1.3.2

DATA USAGE

Transferred to SP5/Shared with modelling tasks: NA

Contribution to Use Cases /other SPs: CDP1-P1: Reference set-up of the experiment, CDP1-P2: A virtual anatomy lab app, CDP1-P3: A virtual imaging lab app, CDP1-P6: In silico setup of the motor rehabilitation experiment

What are datasets used for (models, atlas)?: 15 datasets of 2D lapse recording of calcium activity from Thy1-GCaMP6f mice have been used to:

- a) close-loop validation of the cortical activity model developed by SP4
- b) Mapping mouse brain cortical activity maps to reference atlas space (SP5)

Link to model/Atlas: <https://collab.humanbrainproject.eu/#/collab/47/nav/85822?state=model.b05c3d3c-889d-4d04-9854-a1b9b9ae5c1e> and <https://collab.humanbrainproject.eu/#/collab/47/nav/85822?state=model.95d27a2a-14ab-48ec-8dba-62bc8002a8a0>

How the data transfer has been or is coordinated: The data have been shared to other SPs collaborators via Google drive/HBP Collab.

All data are stored in CSCS repository (https://ksproxy.cscs.ch:13000/Pavone_SGA1_1.3.2) and related metadata has been uploaded via HBP Collaboratory (<https://collab.humanbrainproject.eu/#/collab/5340/nav/41538>)

Role and take-up of the data acquired: 15 datasets of 2D lapse recording of calcium activity from Thy1-GCaMP6f mice have been used to:

- a) close-loop validation of the cortical activity model developed by SP4
- b) Mapping mouse brain cortical activity maps to reference atlas space (SP5)

Links are as follows:

<https://collab.humanbrainproject.eu/#/collab/47/nav/85822?state=model.b05c3d3c-889d-4d04-9854-a1b9b9ae5c1e>

<https://collab.humanbrainproject.eu/#/collab/47/nav/85822?state=model.95d27a2a-14ab-48ec-8dba-62bc8002a8a0>

In addition, the data have contributed to CDP1-P1: Reference set-up of the experiment, CDP1-P2: A virtual anatomy lab app, CDP1-P3: A virtual imaging lab app, CDP1-P6: In silico setup of the motor rehabilitation experiment

PUBLICATIONS

- Allegra Mascaro A. L., Conti E., Lai S., Di Giovanna A. P., Spalletti C., Alia C., Quarta E., Panarese A., Sacconi L., Micera S., Caleo M., Pavone F. S., Rehabilitation promotes the recovery of distinct functional and structural features of healthy neuronal networks after stroke, submitted. Preprint available on <https://www.biorxiv.org/content/early/2017/08/02/141697>
- Allegra-Mascaro et al., Label-free NIR reflectance imaging as a complimentary tool for two-photon fluorescence microscopy: multimodal investigation of stroke

T1.3.4: Whole brain maps of resting state brain activation (ID: 931)**Dataset Owner:** Ludovico Silvestri < silvestri@lens.unifi.it > (LENS)**DATA SUMMARY****Purpose of the data collection/generation**

Available data on whole-brain activation via cFos or other immediate early genes do not include detailed quantification of the spatial distribution of activated maps (usually only averages are presented). The data obtained here will thus unveil possible unknown spatial motifs of neuronal activation at the meso- to micro-scale, contributing a significant advancement in the neuroscience.

Relation to the objectives of the project

These data will be fundamental to achieve objective 1c, and will also be very important towards objective 1b because they will help inferring neuronal co-activation between different regions, helping the placement of local circuits in a wider context.

Types and formats of data generated/collected

Types: Initial data will be whole-brain images, final analysis will deliver point-clouds of various cell types in Allen reference space coordinates **Formats:** txt file for point cloud, jpeg for lossy-compressed images, mp4 for lossless-compressed data **Protocol:** We obtain the activation maps by observing expression of the immediate early gene cFos. We use mice where cFos expression is temporally constrained by tamoxifen induction (TRAP mice), sample clearing (CLARITY-TDE, Costantini et al. 2015), cutting-edge adaptive light sheet microscopy (Silvestri et al., submitted), and neuron localisation methods based on deep learning (Frasconi et al., 2014).

Existing data being re-used (if any)

No

Origin of the data

Data class: Whole-brain activation maps **Specimen information:** Mouse (mus musculus), C57/B6J TRAP mice, age PND50-PND60, colony provided by courtesy of Graff lab (EPFL)

Brain region: Whole brain **Subregion:** Whole brain

Expected size of the data

About 10 TB of lossless-compressed raw data (for long-term archiving), about 50 GB of lossy-compressed images (for visualization and sharing purpose), and few GB of point cloud data (for simulation, meta-analysis, models validation)

Data utility: to whom will it be useful

Within HBP: Whole-brain neuronal activation maps in the resting state will provide an important scaffold for multiscale modelling of brain subcircuits (WP1.4), and to generate whole-brain network and population models in SP4.

Outwith HBP: NA

FAIR DATA**Accessibility: which data will be made openly available**

Privacy class is: Animal Research. There are no issues sharing data

Accessibility: Methods, software tools and documentation needed to access the data

Images can be accessed with standard viewers (e.g. ImageJ). Point clouds can be visualized using specialized software (e.g. CloudCompare). Raw image data can be explored using an API we are internally developing and that will be released within SGA1.

Re-use: Data licensing to permit the widest reuse possible

Attribution NonCommercial ShareAlike 4.0

Re-use: Data quality assurance processes**ETHICAL ASPECTS**

Ethics approval authority: Italian Ministry of Health **Ethics approval ID:** 790/2016-PR

RELEASES AND PROGRESS**Planned releases:**

Month	Shared.with	Quality	Completeness	Location	Embargo	Actual.Completeness
M18	—	—	—	—	—	At M18, 2 representative datasets related to visual stimulation and visual deprivation conditions have been acquired. All data are stored at CINECA 100% of raw data, 25% of processed data

Month	Shared.with	Quality	Completeness	Location	Embargo	Actual.Completeness
M23	Consortium	Candidate final quality	2 of 2 brains processed	Collabatory; UIO Navigator	Awaiting publication	At M23, 85% of raw data have been processed to obtain point cloud maps. Downsampled data have been stored in the Collaboratory, all raw and processed data have been stored at CINECA.

Any deviation and mitigation: NA

Current location(s) of dataset:

<https://collab.humanbrainproject.eu/#/collab/5340/nav/41538>

DATA USAGE

Transferred to SP5/Shared with modelling tasks: NA

Contribution to Use Cases /other SPs: CDP1-P1: Reference set-up of the experiment, CDP1-P3: A virtual imaging lab app

What are datasets used for (models, atlas)?: Whole-brain activation maps are used to validate whole-brain point-neuron models

Link to model/Atlas: <https://collab.humanbrainproject.eu/#/collab/47/nav/85822?state=model.b05c3d3c-889d-4d04-9854-a1b9b9ae5c1e> and <https://collab.humanbrainproject.eu/#/collab/47/nav/85822?state=model.95d27a2a-14ab-48ec-8dba-62bc8002a8a0>

How the data transfer has been or is coordinated: Data has been transferred via ftp from LENS to a UIO repository. Related metedata has been uploaded via HBP Collaboratory

Role and take-up of the data acquired: Whole-brain activation maps are used to validate whole-brain point-neuron models. Relevant links to whole brain model:

<https://collab.humanbrainproject.eu/#/collab/47/nav/85822?state=model.b05c3d3c-889d-4d04-9854-a1b9b9ae5c1e>

<https://collab.humanbrainproject.eu/#/collab/1655/nav/75901?state=model.45fd93ed-7ce4-4ee5-90f6-1f985bfa92d5>

<https://collab.humanbrainproject.eu/#/collab/1655/nav/75901?state=model.111bc309-ba88-4aa9-9ea1-1c9dcf75a13>

The data have also contributed to CDP1-P1: Reference set-up of the experiment, CDP1-P3: A virtual imaging lab app
Data has been transferred via ftp from LENS to a UIO repository. Down sampled data and related metadata has been uploaded via HBP Collaboratory (<https://collab.humanbrainproject.eu/#/collab/5340/nav/41538>)

PUBLICATIONS

- Adam et al., "Confocal multi-spot microscope for fast and deep imaging in semi-cleared tissues", J. Biomed. Opt., in press

T1.3.5: 3D image of the vascular system of the mouse brain (ID: 744)**Dataset Owner:** Velizar Efremov < velizar.efremov@pharma.uzh.ch > (UZH)**DATA SUMMARY****Purpose of the data collection/generation**

To provide input to methods that will create vasculature models of the brain.

Relation to the objectives of the project

Maps of the vasculature of the whole mouse brain (1a)

Types and formats of data generated/collected**Types:** Two Photon Microscopy of Vasculature of Rat Cortex **Formats:** tiff image array**Protocol:****Existing data being re-used (if any)****Origin of the data****Data class:** Vasculature **Specimen information:** Rat**Brain region:** Cortex **Subregion:****Expected size of the data**

13GB

Data utility: to whom will it be useful**Within HBP:****Outwith HBP:** NA**FAIR DATA****Accessibility: which data will be made openly available**

Privacy class is: Animal Research. There are no issues sharing data

Accessibility: Methods, software tools and documentation needed to access the data

Any image viewer that can view tiff files.

Re-use: Data licensing to permit the widest reuse possible

BY-NC-SA - Attribution + Noncommercial + ShareAlike

Re-use: Data quality assurance processes**ETHICAL ASPECTS****Ethics approval authority:** NA **Ethics approval ID:** NA**RELEASES AND PROGRESS****Planned releases:**

Month	Shared.with	Quality	Completeness	Location	Embargo	Actual.Completeness
M18	—	—	—	—	—	At M18 2 Dataset with larger area of view is acquired.
M23	Collab	Prototype data	the whole depth of the cortex	Collaboratory		No new full brain dataset has been acquired up to now. One sample has been prepared and is currently being imaged using serial confocal microscopy.

Any deviation and mitigation: NA**Current location(s) of dataset:**<https://collab.humanbrainproject.eu/#/collab/6168/nav/47699>**DATA USAGE****Transferred to SP5/Shared with modelling tasks:** NA**Contribution to Use Cases /other SPs:** CDP1-P1: Reference set-up of the experiment**What are datasets used for (models, atlas)?:** Atlas (mouse brain)**Link to model/Atlas:** Under Raw folder:<https://collab.humanbrainproject.eu/#/collab/6168/nav/47699>**How the data transfer has been or is coordinated:** Data Curation is has been coordinated with Milica Markovic and it is also shared in Collab

Role and take-up of the data acquired: This dataset has been generated in T1.3.5. What is the detailed architecture of the vasculature that directs blood within the brain? What is the structural relationship between neurons, glia and vessels? How do changes in neurons alter the properties of vessels and vice versa? These questions remain unanswered, albeit they are at the basis of the brains high energy usage and maintenance of energetic homeostasis. We have worked on a customized software framework. This technology development was necessary because (1) available software is not able to reliably segment the images derived from either synchrotron-radiation based x-ray tomography and/or confocal light

sheet microscopy and (2) the requirements in terms of precision for microvascular reconstruction are not met by available software and (3) that the available software is not able to handle the big data scope of our newly acquired data. The vascular reconstruction in combination with detailed astrocytic morphology of single astrocytes enabled us to produce invaluable data required for SP6, in which the Neuronal-Glial-Vascular structural architecture is required for in-silico microcircuit simulations. Raw data and reconstructed vascular data (in a standard graph format) are made available for SP6 (T6.2.1: Models of Human Cells , and T6.2.6: Models of Whole Mouse Brain). There is an increasing general need for vascular and astrocytic anatomical data for simulating cerebral blood flow and transport of oxygen and energy substrates in health and disease. The data will be made available to groups outside HBP.

PUBLICATIONS

T1.3.5: 3D reconstruction of the vascular system of the mouse brain (ID: 745)**Dataset Owner:** Velizar Efremov < velizar.efremov@pharma.uzh.ch > (UZH)**DATA SUMMARY****Purpose of the data collection/generation****Relation to the objectives of the project**

Maps of the vasculature of the whole mouse brain (1a)

Types and formats of data generated/collected**Types:** Discreet Graph Structure **Formats:** vtk file**Protocol:****Existing data being re-used (if any)****Origin of the data****Data class:** Vasculature **Specimen information:** Rat**Brain region:** Cortex **Subregion:****Expected size of the data**

10's of MBs

Data utility: to whom will it be useful**Within HBP:****Outwith HBP:** NA**FAIR DATA****Accessibility: which data will be made openly available**

Privacy class is: Animal Research. There are no issues sharing data

Accessibility: Methods, software tools and documentation needed to access the data

ParaView

Re-use: Data licensing to permit the widest reuse possible

BY-NC-SA - Attribution + Noncommercial + ShareAlike

Re-use: Data quality assurance processes**ETHICAL ASPECTS****Ethics approval authority:** NA **Ethics approval ID:** NA**RELEASES AND PROGRESS****Planned releases:**

Month	Shared.with	Quality	Completeness	Location	Embargo	Actual.Completeness
M18	—	—	—	—	—	At M18 we have achieved completion rate of 100% and 80% on main parts of reconstruction pipeline. Vessel Segmentation (100% completed) methods have been improved and are ready to work on a full mouse brain. Network Extraction (80% completed) methods have scalability issues for larger data which are being currently addressed. Partial mouse brain reconstructions have been done.
M23	Collab	Prototype data	85-90 percent F1 score on vasculature segmentation	Collaboratory		90% of reconstruction pipeline is achieved. Network extraction method is now 90% achieved. We have added a new approach including deep-learning algorithms. Two new in vivo two-photon microscopy datasets have been uplaoded, providing important complementary information on small vessel calibers. These two datasets have been processed and networks were generated.

Any deviation and mitigation: NA**Current location(s) of dataset:**<https://collab.humanbrainproject.eu/#/collab/6168/nav/47699>**DATA USAGE****Transferred to SP5/Shared with modelling tasks:** NA**Contribution to Use Cases /other SPs:** CDP1-P1: Reference set-up of the experiment

What are datasets used for (models, atlas)?: Model (mouse brain vasculature)

Link to model/Atlas: Under Networks folder:

<https://collab.humanbrainproject.eu/#/collab/6168/nav/47699>

How the data transfer has been or is coordinated: Data Curation is has been coordinated with Milica Markovic and it is also shared in Collab

Role and take-up of the data acquired: This dataset has been generated in T1.3.5. See component ID 744 for the role of this task.

PUBLICATIONS

- Schmid F, Barrett MJP, Jenny P, Weber B. Vascular density and distribution in neocortex. *NeuroImage* 2017; pii: S1053-8119(17)30516-5. DOI:10.1016/j.neuroimage.2017.06.046
-

T1.3.5: Model of intravascular and tissue partial pressure of oxygen (ID: 747)**Dataset Owner:** Velizar Efremov < velizar.efremov@pharma.uzh.ch > (UZH)**DATA SUMMARY****Purpose of the data collection/generation****Relation to the objectives of the project****Types and formats of data generated/collected****Types: Formats:****Protocol:****Existing data being re-used (if any)****Origin of the data****Data class:** Vasculature **Specimen information:** Rat**Brain region:** Cortex **Subregion:****Expected size of the data****Data utility: to whom will it be useful****Within HBP:****Outwith HBP:** NA**FAIR DATA****Accessibility: which data will be made openly available**

Privacy class is: Animal Research. There are no issues sharing data

Accessibility: Methods, software tools and documentation needed to access the data**Re-use: Data licensing to permit the widest reuse possible**

BY-NC-SA - Attribution + Noncommercial + ShareAlike

Re-use: Data quality assurance processes**ETHICAL ASPECTS****Ethics approval authority:** NA **Ethics approval ID:** NA**RELEASES AND PROGRESS****Planned releases:**

Month	Shared.with	Quality	Completeness	Location	Embargo
M23	Collab	Prototype data	-	Collaboratory	

Any deviation and mitigation: NA**Current location(s) of dataset:****DATA USAGE****Transferred to SP5/Shared with modelling tasks:** NA**Contribution to Use Cases /other SPs:****What are datasets used for (models, atlas)?:****Link to model/Atlas:****How the data transfer has been or is coordinated:** Data Curation is has been coordinated with Milica Markovic and it is also shared in Collab**Role and take-up of the data acquired:** This prototype data has been generated in T1.3.5. See component ID 744 for the role of this task.**PUBLICATIONS**

T1.4.1: Analysis of micro-anatomical data (ID: 434)**Dataset Owner:** Concha Bielza < mcbielza@gmail.com > (UPM)**DATA SUMMARY****Purpose of the data collection/generation****Relation to the objectives of the project**

This task relates to objective 1d. It will provide tools to segment synapses from confocal microscopy and analyse synaptic distribution across brain regions, to automatically identify morphological types of cortical interneurons, and an extensible tool for quantifying neuronal morphology.

Types and formats of data generated/collected

Types: Software (R, C++, web-based tools, Java, ImageJ,) and statistical models. **Formats:**

Protocol:

Existing data being re-used (if any)

Yes, from T1.2.1, T1.2.9

Origin of the data

Data class: Software and models **Specimen information:**

Brain region: Subregion:

Expected size of the data**Data utility: to whom will it be useful**

Within HBP: The tools can be useful to T1.4.7 “Visual analysis tools for microanatomical data”, T4.1.1 “Simplified dendritic neuron models”, T4.5.1 “Comparing models with mouse and human brains”, T5.3.8 “Prediction of cellular, synaptic and connectomic composition, distributions and properties of the human brain”, T6.2.1 “Models of human cells”, and T6.3.2 “Tools for subcellular and cellular reconstruction”.

Outwith HBP: NA

FAIR DATA**Accessibility: which data will be made openly available**

Privacy class is: No privacy constraints. There are no issues sharing data

Accessibility: Methods, software tools and documentation needed to access the data

Yes, all code for the models will be released as open-source on Github.

Re-use: Data licensing to permit the widest reuse possible

MIT

Re-use: Data quality assurance processes**ETHICAL ASPECTS**

Ethics approval authority: NA **Ethics approval ID:** NA

RELEASES AND PROGRESS**Planned releases:**

Month	Shared.with	Quality	Completeness	Location	Embargo	Actual.Completeness
M18	—	—	—	—	—	0.8
M23	Collab	Final quality	All models and software complete	Github		100%

Any deviation and mitigation: NA

Current location(s) of dataset:

<https://github.com/ComputationalIntelligenceGroup/MultiMap>

DATA USAGE

Transferred to SP5/Shared with modelling tasks: NA

Contribution to Use Cases /other SPs: SP1-UC-06: High-resolution synaptic maps in the mouse neocortex and hippocampus

What are datasets used for (models, atlas)?: NA

Link to model/Atlas: NA

How the data transfer has been or is coordinated: NA

Role and take-up of the data acquired: This tool has been generated in T1.4.1. Our task generates mathematical models of cell morphology and tools for morphology analysis and microscopy image segmentation. The main applications of our models and tools are 1) the simulation of neuronal morphologies, which in turn allows for better modeling in SP6 when actual data are scarce, and 2) guiding FIB/SEM electron microscopy data extraction by point density estimation from confocal microscopy. Namely, our models of spine distribution over dendritic shafts, as well as our NeuroSTR C++ neuroanatomy library, are useful for the simulation of dendritic morphologies. NeuroSTR has also been used in SP5 to simulate dendritic spines and arbors, as well as for repairing incomplete dendrites. Our MultiMap tool allows for automatic

point density estimation across custom brain regions. For example, a user can estimate synaptic point densities from confocal images across custom region of the hippocampus. The estimates can guide FIB/SEM electron microscopy towards certain custom regions, thus efficiently enabling high-resolution synaptic maps, a key issue when building brain atlases (SP5).

PUBLICATIONS

- [Juan J. Garcia-Cantero, Juan P. Brito, Susana Mata, Sofia Bayona, Luis Pastor](#)Article Title: Neuron Mesh Generation and Adaptive On The Fly Refinement Publication Name: Frontiers in Neuroinformatics Date: 22.06.2017
 - [Galindo SE, Toharia P, Robles OD, Pastor L.](#) Article Title: ViSimpl: Multi-View Visual Analysis of Brain Simulation Data. Publication Name: Frontiers in Neuroinformatics 07.10.2016
 - [Florian Leitner, Concha Bielza, Sean L. Hill and Pedro Larrañaga.](#) Data Publications Correlate with Citation Impact
-

T1.4.2: Software PyramidalExplorer 1.2 for early exploratory analysis techniques for morphological data (ID: 906)**Dataset Owner:** Luis Pastor < luis.pastor@urjc.es > (URJC)**DATA SUMMARY****Purpose of the data collection/generation**

To offer tools for the early analysis of morphological data and to provide feedback to steer the data extraction process and to correct possible errors or even redesign experiments if necessary. Additionally, the software allows the analysis of complex systems, exploiting the ability of the human visual system to extract information from visual scenarios.

Relation to the objectives of the project

This software is designed for facilitating the early analysis of morphological data and it is related with SGA1 Objective 1d (SO14), since it will help to reconstruct and to perform an early analysis of morphologies of major neuron types.

Types and formats of data generated/collected

Types: Software **Formats:** Not applicable

Protocol: Our software will be developed using a user-centered design methodology.

Existing data being re-used (if any)

Yes, the developed software includes previous software and improves old software versions.

Origin of the data

Data class: Cellular **Specimen information:** Not applicable

Brain region: Not applicable **Subregion:** Not applicable

Expected size of the data

Less than 50GB

Data utility: to whom will it be useful

Within HBP: This software is useful for the analysis of 3D distributions of synapses in the mouse and human neocortex. This software is needed to obtain and early analyse 3D reconstructions of pyramidal neurons from the mouse somatosensory cortex and from the human neocortex.

Outwith HBP: NA

FAIR DATA**Accessibility: which data will be made openly available**

Privacy class is: No privacy constraints. There are no issues sharing data

Accessibility: Methods, software tools and documentation needed to access the data

All the software developed will be released under an open source license for Windows and Linux Operating Systems

Re-use: Data licensing to permit the widest reuse possible

BY-SA - Attribution + ShareAlike

Re-use: Data quality assurance processes**ETHICAL ASPECTS**

Ethics approval authority: NA **Ethics approval ID:** NA

RELEASES AND PROGRESS**Planned releases:**

Month	Shared.with	Quality	Completeness	Location	Embargo	Actual.Completeness
M18	—	—	—	—	—	0.8
M23	Anonymous	Final quality	Not applicable	Lab server	The software will be published	100%

Any deviation and mitigation: NA

Current location(s) of dataset:

<https://gmr.es/pyramidalexplorer/>

<https://cajalbbp.es/dcexplorer>

<https://cajalbbp.es/intooexplorer>

DATA USAGE

Transferred to SP5/Shared with modelling tasks: NA

Contribution to Use Cases /other SPs: SP1-UC01: 3D reconstruction and visualization of microanatomical parameters of pyramidal cells: PyramidalExplorer 1.2

SP1-UC03: Connectivity skeletons to explore local synaptic rules

What are datasets used for (models, atlas)?: The tools are being used for the analysis of neuronal morphological and functional data, acquired within HBP experimental procedures

Link to model/Atlas: not applicable

How the data transfer has been or is coordinated: The software was developed in coordination with the final users (CBB Group) and is available at the following addresses:

<https://gmr.v.es/pyramidalexplorer/>

<https://cajalbbp.es/dcexplorer>

<https://cajalbbp.es/intooexplorer>

Role and take-up of the data acquired: This tools have been used to analysis the microanatomical data generated in this SP1 (WP1.2)

PUBLICATIONS

- Anton-Sanchez L, Bielza C, Benavides-Piccione R, DeFelipe J, Larrañaga P. (2016). Dendritic and Axonal Wiring Optimization of Cortical GABAergic Interneurons. *Neuroinformatics*. 2016 Oct; 14 (4):453-64. doi: 10.1007/s12021-016-9309-6
 - Anton-Sanchez, L., P. Larrañaga, R. Benavides-Piccione, I. Feraud, J. DeFelipe, and C. Bielza, "Three-dimensional spatial modeling of spines along dendritic networks in human cortical pyramidal neurons", *PLoS ONE* 12(6): e0180400, 2017
-