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Authors:	Katrin AMUNTS, JUELICH (P17)
Compiling Editors:	Sabine BRADLER, Timo DICKSCHEID JUELICH (P17), 2.3.1
Contributors:	Cyril POUPON, CEA (P9), T2.1.2 Delphine DUCLAP, CEA (P9), T2.1.2 Jean-François MANGIN, CEA (P9), T2.1.2 Bertrand THIRION, INRIA (P26), T2.1.1 Pieter ROELFSEMA, KNAW (P90), T2.1.8 Wim VANDUFFEL KUL (P89), T2.1.7 Rainer GOEBEL, UM (P53), T2.1.7/T2.1.8 Jean-Philippe LACHAUX, UCBL (P106), T2.1.9/2.2.3
Coordinator Review:	EPFL (P1): Jeff MULLER, Martin TELEFONT UHEI (P45): Sabine SCHNEIDER, Martina SCHMALHOLZ
Editorial Review:	EPFL (P1): Lauren ORWIN

Abstract:	This report describes the second package of the multi-level tools that are ready for HBP-internal integration in the HBP brain atlas as scheduled in Month 30. It provides multi-level *in vivo* data sets of healthy control and patients, and delivers monkey data for comparative analyses.
Keywords:	Data and tools for the human brain atlas, multi-level post mortem and *in vivo* human brain data and tools to integrate into the HBP atlas
Available at:	www.humanbrainproject.eu/ec-deliverables

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1. Introduction

1.1 Aim of this document

This report describes the second package of the multi-level tools that are ready for integration in the HBP brain atlas as scheduled in Month 30. The datasets are described in detail in the following chapters. Additionally, the report provides two tables (20160303_SP2_summarytable.xlsx and 20160318_Methodologies_SP2_D2.3.4.xlsx) summarising task-wise details of the data, tools and methodologies delivered by SP2 in the Ramp-Up Phase.

1.2 Brief overview of data and its scientific significance

The data in this second package covers a wide spectrum of *in vivo* data of the human brain, supplemented by those of the macaque. Human brain data include high-resolution anatomical, diffusion and functional MRI data from subjects, which were measured with 3T MRI and ultra-high field (7T).

The data also include results of measurements of axon density and diameter computed along the tract of the human brain, based on *in vivo* MRI.

In addition, data packages contain comparative data targeting homologies and dissimilarities of human brains and those of other primates including functional data from the awake monkey, which were analysed during the Ramp-Up Phase. To acquire such data is technically particularly challenging. Due to sophisticated protocols in combination with ultra-high resolution MR imaging we were able to reveal the activity and function at the level of cortical layers.

This Deliverable also provides unique multimodal data sets including iEEG (meso- and microrecordings), fMRI, DTI, and cortico-cortical evoked potentials (CCEP) obtained in patients.

Taking advantage of the long-lasting experience in the field of the research groups involved, the datasets show a high to extraordinary quality. They can be seen as unique contributions, and represent the top level of the field.

2. Summary Table of Datasets, Tools and Methodologies

2.1 Summary Table of Datasets and Tools

See Annex B: Summary Table. The table comprises the datasets and tools covering period M1-M30. The original spreadsheet is available as 20160303_SP2_summarytable.xlsx.

2.2 Summary Table of Methodologies and Tools

See Annex C: Methodologies. The table comprises the Methodologies and Tools used and developed in M1-M30. The original spreadsheet is available as 20160318_Methodologies_SP2_D2.3.4.xlsx.

3. Strategic Human Data for the HBP Human Brain Atlas and for Modelling

3.1 High-resolution Anatomical, Diffusion and Functional MRI Images from Subjects Selected for Massive Mapping

3.1.1 Data Description

3.1.1.1 Task(s)/group(s) responsible for generating data

Task 2.1.1. The INRIA Parietal team is responsible for generating the data together with the following units and platform services of Neurospin: UNIACT, UNIRS and UNICOG.

3.1.1.2 Data, tools and methodologies storage location(s)

The Ramp-Up Phase was used to set up the basis for a seven-year long acquisition protocol for the so-called "Individual Brain Charting" (IBC) project. We have written the medical protocols, obtained the medical and legal authorisation to run the project, and hired the participants. In parallel, we have taken decisions on the optimal acquisition parameters, gathered cognitive protocols to be used for optimal brain mapping, and set up the analysis pipeline. We have started to acquire the data, check their quality and analyse them (pre-processing – distortion and motion correction, co-registration between modalities and to anatomical templates – and derivation of functional contrast maps). The acquired data and results are uploaded on the Jade server (Jülich) to deliver it to the HBP Consortium.

3.1.1.3 Description of data

11 human participants (9 males) have been screened, right-handed, age range: 27-40 years.

The data are MRI images with a resolution of 1.5mm (functional and diffusion images) or 0.75-1 mm (anatomical images). They cover the full brain, with a typical field of view of 192*192*141 mm.

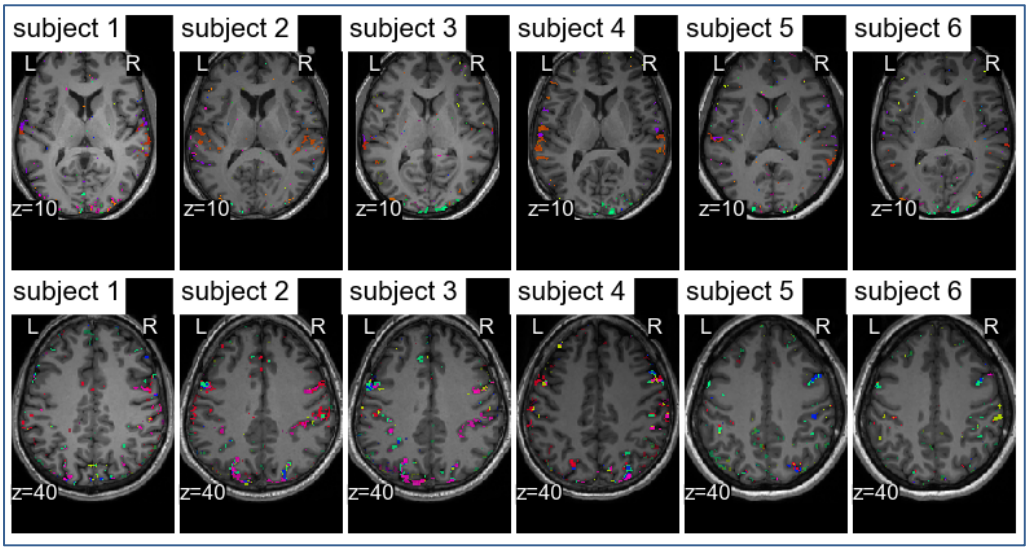

Figure 1: Active areas for a set of reference contrasts in six representative subjects. The two rows represent two different sets of functional contrasts.

The functional images display the BOLD contrast associated with brain activation following various cognitive conditions. They yield a view of brain organisation that encompasses the functional specialisation of brain territories (segregation) and the large-scale network organisation (integration). The anatomical images display anatomical contrasts that define brain structures and provide some means to localise functional and connectivity characteristics. The diffusion data provide some measurements on the structure of the white matter, which is then used to derive models of the brain tracts connecting brain regions, yielding an anatomical model of brain connectivity.

3.1.1.4 Completeness of data

We currently have data on 8 subjects. Ultimately, 12 subjects will be included. The purpose of the project is to derive functional atlases of the brain based on responses measured with non-invasive imaging at high resolution. This requires a wide coverage of cognitive functions, based on well-targeted protocols, together with detailed measurements of brain anatomical organisation and connectivity. This is an "individual" brain charting procedure, meaning that the analysis is carried out at the individual level, is in order to not compromise the high spatial resolution obtained in our acquisitions. This requires a high signal-to-noise ration in the individual data, hence we have made sure to rely on a sufficiently large number of repetitions to obtain unambiguous results in the analysis, i.e. for each individual brain we will achieve a very robust and detailed map of cognitive functions. In a second stage, the individual features will be compared across individuals to uncover the most stable features across the sample of subjects. Our strategy was not to target the between-subject variability in contrast to several existing cohort studies in the neuroimaging community (e.g. the Human Connectome Project; see below also). Instead, we aim to address fundamental questions on brain organisation, namely the functional asymmetry across hemispheres, the comparison of functional responses and connectivity, the number of modules that can be identified reliably, the decoding of brain activities at the individual and group level, and the existence or non-existence of homeomorphic mappings across individuals. Such information is also relevant for the development of alignment tools, a topic in common with SP8. In each subject, we have the basic anatomical definition, and a relatively large amount of functional data, namely 43 functional contrasts that provide a rich functional fingerprint to define brain territories. This corresponds to 3 acquisitions (4.5 hours) per subject (but more in some of the subjects).

3.1.1.5 Current data set versus a projected full data set to be generated by the research community

In the next 12 months, we will raise the number of acquisitions to about 10 acquisitions (15 hours scanning time) per subject. At the end of the IBC project, we will have performed about 50 acquisitions per subject. What makes this dataset unique is that is shows individual activations in a small number of subjects, collected over a large time frame. For obvious reasons, this research can only be run in close proximity with the location of the participants, hence at Neurospin.

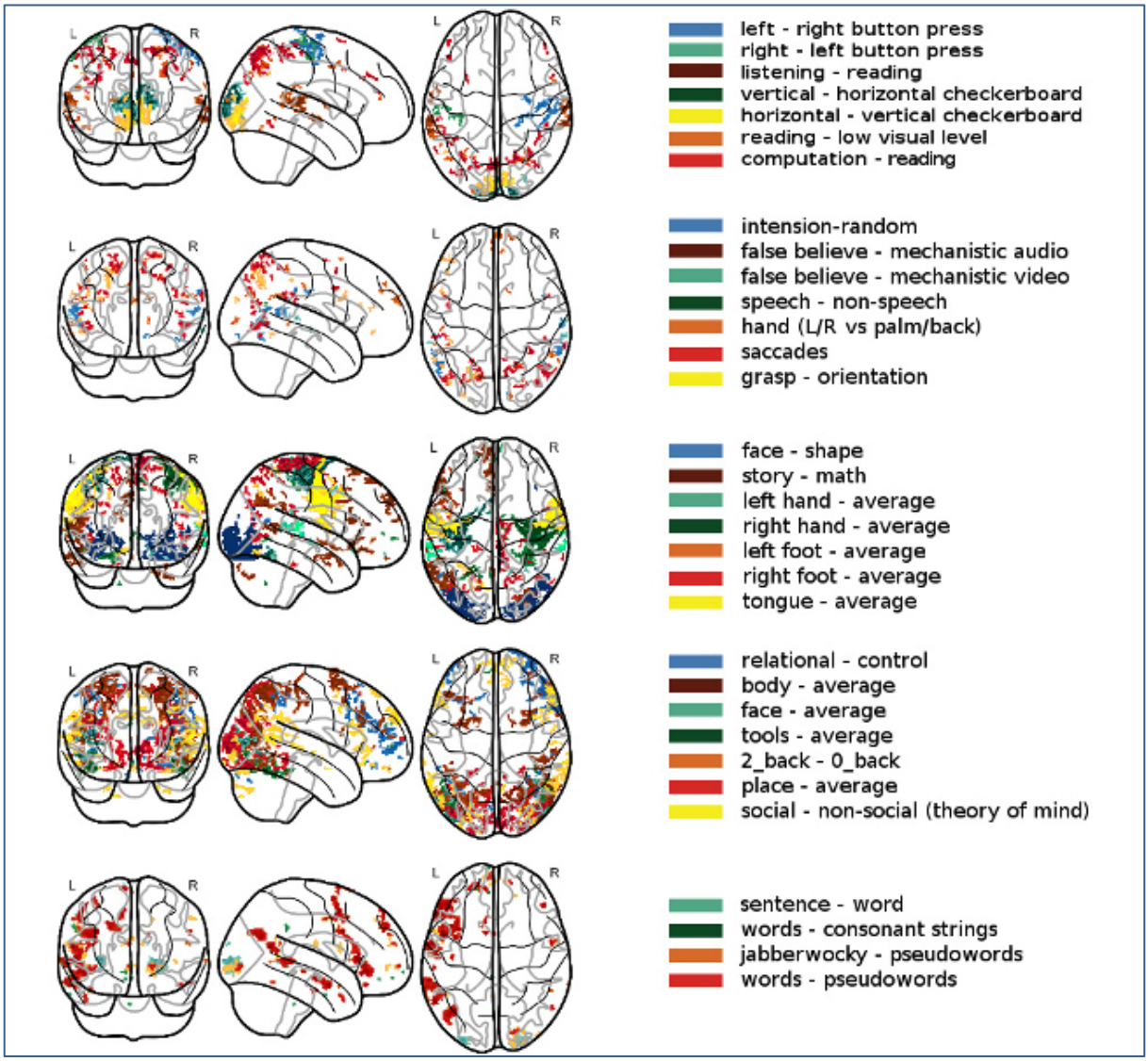

Figure 2: Summary of the main functional contrasts acquired in the group of subjects so far.

In the domain, the main efforts (Human Connectome Project, projects related to various brain diseases or risk factors, Imagen, EU-AIMS etc., UKbiobank) currently address large population aspects, and not at all individualised analysis. Dataset repositories (openfMRI and NeuroVault) offer a large set of functional contrasts, but they are not acquired on the same individuals, and thus suffer from the large inter-subject variability encountered in brain imaging. The data also have standard resolution (3mm) and quality, while IBC-data show a considerably higher resolution and quality; the IBC the protocols have been optimised to increase the SNR within subject and obtain reliable data in each individual participant. The closest project is the Allen Brain Atlas, although they cannot obtain individual functional “fingerprints”. The project is unique in analysing the segregation of the human brain in terms of multiple functions with high spatial accuracy – a necessary prerequisite to address the relationship of cognitive processes and the underlying brain architecture. Such data is prerequisite to develop top-down driven models of cognition, and to inform in the future bottom-up models with human brain data.

The obvious avenue for data analysis and comparison is to compare the results of IBC with those of OpenfMRI and NeuroVault.

3.1.1.6 Data Quality and Value

We have generated reports based on the data pre-processing using the pypreprocess library. These reports will be released with the data. We have made sure that the data are properly aligned and that no large motion (2mm or more) corrupts the acquired images.

Then we check *a posteriori* that the activations obtained after each experiment are in line with our expectations. This *posteriori* check has remained qualitative so far.

Overall, the data have a very high resolution and quality.

The value of the data is (i) to provide an objective reference for the mapping of cognitive parameters to brain activity. This reference is better than existing meta-analytic based systems thanks to the much higher resolution, allowing us to distinguish activation clusters from each other, which would be "lumped together" in meta analyses. Furthermore, the release of actual images makes it possible to run analyses on the effects size, something that does not use current meta-analytic steps. (ii) The quality, resolution and homogeneity of the data are also much higher than those of existing functional public functional data repositories: NeuroVault, http://neurovault.org, that yields activations maps related to different cognitive concepts and OpenfMRI (https://openfmri.org/) that yields complete fMRI datasets). Note, that these repositories are fed by the community and that IBC maps will be added to those in the long term. (iii) The experimental protocols will be released together with the image data, making it possible for neuroscientists to re-use some of our protocols, reproduce our results and compare them with their own protocols.

3.1.1.7 Data usage to date

The data have been uploaded on the Jade server (Jülich) to feed the estimation of a common human brain atlas that is currently being performed in a collaboration between SP2 and SP5.

In the SGA1, the data will used in:

- Task 2.1.1 to define target regions for the study of the impact of genetic variability.
- Task 2.3.1, to release a first functional brain atlas and run large-scale analyses of brain activation data.
- Task 2.3.2 to refine and clarify the definition of brain regions in local analyses.
- Task 2.3.3 to introduce the first comparisons between functional organisation and connectivity.
- Task 2.4.1 to provide a reference and comparison when performing high-resolution local acquisitions and comparison across species.
- Task 2.5.1 to compare *in vivo* and *post-mortem* parcellations of the brain.
- Task 2.6.1 to develop novel deformation models for intersubject registration that take as input richer information than traditional anatomical contrasts, which will ultimately enable human atlas data to be projected onto new scans from the clinic, making parcellations, maps, and quantitative data from *post-mortem* and large cohort studies available for work in the medical informatics platform. This is a goal beyond SGA1 that SP2 pursues in close cooperation with SP8 (J. ASHBURNER).
- They will be used in the new CDP3 to provide the functional location for brain features.
- They will be considered in the SP3 projects that consider human data acquisitions, as they provide a natural reference to map cognitive parameters to brain activity.
- Finally, the introduction of brain atlases to represent brain activity and connectivity is a request from SP8 that will be handled with the IBC data.

3.1.1.8 Are the data considered final?

Not yet. The data will be further processed and quality checked. A fix release will occur within one year for the data acquired in the initial phase of IBC.

3.1.1.9 Publications connected to the gathered data

Journal publications have not yet been produced. We need to complete a first set of analyses. For the moment, we start with three conference and workshop publications to introduce the concept and methods:

- A.L. Grilo Pinho and B. Thirion, High resolution encoding of cognitive information within the IBC project News 2016 workshop, Jan 2016.
- A.L. Grilo Pinho and B. Thirion, Individual Brain Charting: high-resolution normative fMRI database OHBM 2016 conference, June 2016.
- A.L. Grilo Pinho and B. Thirion, Individual Brain Charting: a comprehensive neuroimaging database towards a macroscopic representation of the human brain FENS 2016 conference, June 2016.

3.1.2 Provenance

SP2

WP2.1

Task 2.1.1

3.2 Quantification of the Diameter and Number of Axons in Each Major Tract in Adult Human Brains

3.2.1 Data Description

3.2.1.1 Task(s)/group(s) responsible for generating data

Neurospin's group is in charge of contributing quantification of the axon density and geometry in major tracts of the human brain.

3.2.1.2 Data, tools and methodologies storage location(s)

The Ramp-Up Phase targets methodological development (diffusion MRI sequence parameter tuning and algorithmic development to interpret images), and experiments providing first estimations for major tracts corresponding to the first atlas released by the same group during the Ramp-Up. The quantifications will be refined during SGA1 and extended to a wider set of tracts. For each tract of the atlas, the deliverable is a series of measurements of axon density and diameter computed along the tract. These measurements will be embedded into the HBP bundle atlas. All image analyses have been performed using Connectomist, the software developed by C. POUPON at Neurospin to analyse diffusion MRI data.

3.2.1.3 Description of data

The delivered data come from averaging estimations computed from ten subjects from dedicated acquisitions performed in the context of a collaboration between CEA (C. POUPON), the University of Manchester (G. PARKER), University College London (D. ALEXANDER) and the University of Concepción, Chile (P. GUEVARA). These acquisitions were performed using the 3T of Manchester University, which is equipped with an 80m Tesla gradient field, one of the most efficient in Europe at that time. The ten selected subjects belong to the ARCHI cohort of 79 subjects already delivered to the HBP (4h of MRI

acquisitions per subject). The delivered quantifications are at the scale of large tracts connecting brain regions.

3.2.1.4 Completeness of data

The delivered dataset agrees with the anticipated version. The next stage of work has already been triggered. A new series of acquisition focused on corpus callosum has been performed with ten new subjects on the 7T magnet of Neurospin equipped with a 50mT gradient. This experiment has shown that increasing the number of shells in the QA-space and the sampling of the diffusion time of diffusion-weighted images allows large improvement of the quantification accuracy, which has been proven by comparison with information obtained from *post-mortem* autopsy. Note that traditional *post-mortem* strategy is limited to the few specific white matter areas like corpus callosum that can be visualised during dissection. This explains the attractiveness of the diffusion-based strategy, which can directly be compared with 3D-Polarized Light Imaging as obtained in SP2 (see below).

3.2.1.5 Current data set versus a projected full data set to be generated by the research community

The success of the corpus callosum experiment is now leading us to begin a new acquisition campaign that will aggregate five MRI sessions for each subject, in order to obtain reliable quantification of all the bundles of the next generation of atlas. This campaign will rely on the last generation of 3T MRI with an 80mT/m gradient recently installed in Neurospin in October 2015.

A prototype of the second generation of atlas to be delivered to the HBP during SGA1 includes more than 100 stable U-fiber bundles. This second generation relies on the ARCHI database already hosted by HBP. The third generation will rely on the Human Connectome Dataset at disposal of the community. This third generation is likely to stem from a distributed effort of the community to identify bundles that are stable across the population. The current stage of the field shares some similarities with the early times of genomics when the number of genes in the human genome was unknown. Hence, it is difficult to forecast how many U-fiber bundles are stable across the population, but the outstanding HCP data will probably lead to several hundred.

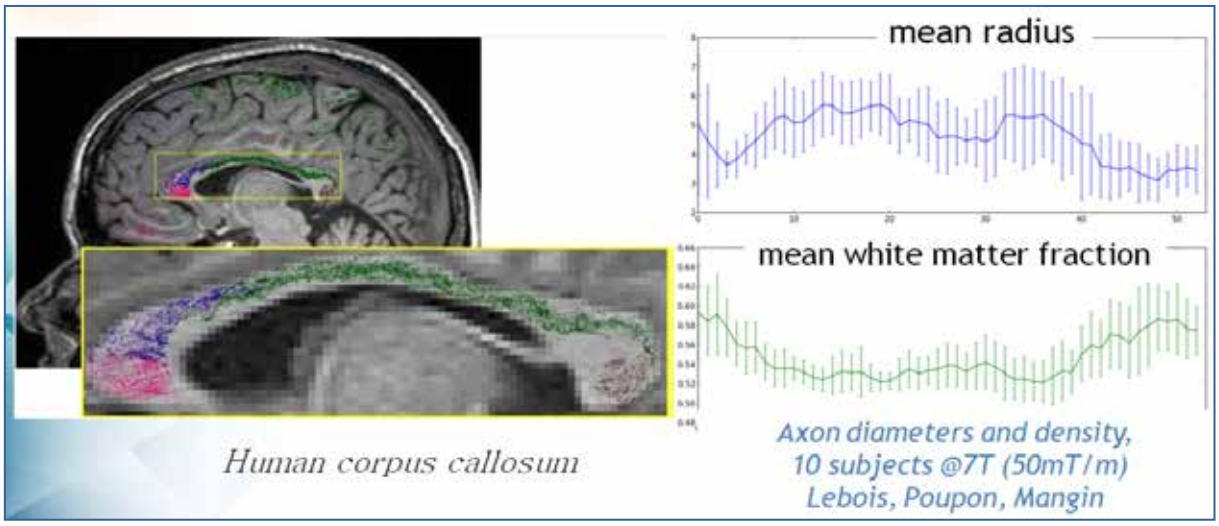

Figure 3: Analysis of axon radius and diameter in the human corpus callosum (data averaged over ten subjects).

Most of the methodological efforts of the community on this topic have been targeting the corpus callosum because of its rather simple geometry, at least in the mid-line region. Hence, the quantifications delivered by this task are at the cutting edge of the field, but will probably have to evolve rapidly following the research programme of SGA1. The Neurospin group (C. POUPON) now has a formal collaboration with Tours University (France, Christophe DESTRIEUX) and the Martinos Center for Biomedical Imaging (Harvard, B. FISCHL) to validate some of the results using MRI of *post-mortem* brains (https://sites.google.com/site/fibratlas/). Note that the Martinos hosts the strongest gradient (300mT/m) for whole brain imaging, and is one of the top centres for structural and functional imaging.

In addition, in the context of the HBP, a very accurate comparison between MRI and Polarized Light Imaging (Jülich) is in progress. A scan of a human temporal lobe has been acquired in Neurospin at 11.7 T and a 700mT gradient, leading to diameter estimations at a spatial resolution of 300 microns. The same specimen is now in Jülich for PLI imaging, which will lead to complementary quantification and validation with outstanding resolutions (50 to 1.5 microns). These high-resolution MRI and PLI data will allow the mapping of bundles beyond reach for the HCP data, like the inner connectivity of hippocampus fields. They will lead to the quantification of white matter geometry at the meso- and microscale.

3.2.1.6 Data Quality and Value

Axon diameter quantification is currently difficult to validate, but PLI provides an independent method to check on reliability. While PLI will be considered as the "ground truth", MRI will contribute an evaluation of intersubject variability. Further verification is planned, with electromicroscopic data during SGA1 for a few, small regions of interest.

Quantification of the microstructure of white matter bundle will have direct applications for simulations, leading for instance to the correct number of axons in each bundle, and for biomarker research in brains of patients with neurological or psychiatric diseases by providing the estimation of the mean and normal range of variability.

3.2.1.7 Data usage to date

SP5: a) T5.5.2 integration in human SP5 atlas b) T5.3.2, SP4: T4.4.1.

3.2.1.8 Are the data considered final?

No, this is an iterative process.

3.2.1.9 Publications connected to the gathered data

- M. Guevara, C. Roman, J. Houenou, D. Duclap, C. Poupon, J. F. Mangin, P. Guevara, A whole brain multi-subject short association bundle atlas, submitted to Neuroimage
- N. Labra, P. Guevara, D. Duclap, J. Houenou, C. Poupon, J.-F. Mangin, M. Figueroa, Fast automatic segmentation of white matter fibers based on a multi-subject bundle atlas, submitted to Neuroinformatics
- P Guevara, D Duclap, C Poupon, L Marrakchi-Kacem, P Fillard, D Lebihan, M Leboyer, J Houenou, J-F Mangin, Automatic fiber bundle segmentation in massive tractography datasets using a multi-subject bundle atlas, NeuroImage, 61(4):1083-99, 2012

3.2.2 Provenance

SP2

WP1

Task 2.1.2

3.3 Additional data

3.3.1 Homologies between humans and other primates (T2.1.7 Vanduffel/Goebel)

3.3.1.1 Data Description

Task(s)/group(s) responsible for generating data

T2.1.7 Rainer GOEBEL and Elia FORMISANO from the University of Maastricht, Netherlands, and Wim VANDUFFEL from the KU Leuven, Belgium.

Data, tools and methodologies storage location(s)

fMRI data comes from healthy human subjects and nonhuman primates. Human fMRI data comes from scanning at 7T, while the monkey data came from 3T; the use of contrast agents and phased-array receive coils embedded in the headpost of the animals improved the sensitivity by a factor of five. Data analysis includes a combination of analytical tools: BrainVoyager, SPM, Freesurfer, FSL and in-house tools tailored to perform interspecies comparisons. Data are stored locally in two different locations: local server as well as off-line hard disks. Pre-processed data have been uploaded on the Jülich server (JADE system). However, For the human visual 7T study, the data is enormous: zipped raw Dicom data 280 GB, analysed data several TB (volumes, meshes etc.), and we therefore decided to provide the link to these data, and not to move them physically at this point.

Description of data

- Monkey data: *Macaca mulatta*, 6-10 animals in total, male and female subjects are included.
- Scale: entire brain (monkey data), at least occipital and ventral visual cortex (human data).
- Human Data: Homo sapiens, 8 participants scanned in 3 sessions, 2 participants excluded due to excessive head motion, i.e. 6 full data sets.

Completeness of data

For two experiments (visual and auditory comparative experiment) we acquired the full data set in human and monkey. We may have to acquire data from a third animal for the comparative auditory study.

Current data set versus a projected full data set to be generated by the research community

N/A

A short review of data generated by the community over the past 30 months, and how these data validate the data gathered by the HBP Task, and/or complement it.

N/A

3.3.1.2 Data Quality and Value

The data are amongst highest resolution data currently available from awake monkeys. Long-term use of contrast agents in monkeys has somewhat a negative effect on data quality; hence we aim to collect new data in monkeys that have not been scanned much.

Some of the data are of exceedingly high quality, some other data could have been better (mainly due to susceptibility artefacts induced by long term use of contrast agent).

Data usage to date

So far, analyses have been performed by the groups of GOEBEL/VANDUFFEL (visual comparative experiment) and FORMISANO/VANDUFFEL (auditory comparative experiments.

a) Ramp-Up Phase T2.1.7: Homologies between humans and other primates

b) SGA1: T2.4.1: Multi-scale processing in space, time and frequency, T2.4.2: Separation of activity in different cortical layers, T2.4.3: The role of attention in perception and learning, T2.4.4: Development of an empirically-derived brain atlas on sensorimotor integration (CDP-4), T3.1.1: Deep learning network constraint to human brain imaging.

Are the data considered final?

Not yet

Publications connected to the gathered data

We are currently working on three manuscripts. We are building novel analytical tools to assess functional correspondences across species.

There are conference publications (posters) available for the human auditory and visual experiments.

3.3.1.1 Provenance

All data (T2.1.7) are collected at the KU Leuven and University of Maastricht. The data are collected with the appropriate approval from the local ethical committees. The data are stored locally and at the JADE server in Jülich. As soon as the first publications are in press, the data will become available for everyone. Meanwhile, researchers from HBP can request to use the current data.

3.3.2 Revealing the activity and function of cortical layers (T2.1.8 Goebel/Roelfsema)

3.3.2.1 Data Description

Task(s)/group(s) responsible for generating data

T2.1.8 The ROELFSEMA group provides electrophysiological data (Multi-unit activity and current-source density) from the different layers of V1 of macaque monkey during a figure-ground segregation task. The GOEBEL group provides high-field strength MRI data on a similar task in humans.

Data, tools and methodologies storage location(s)

Monkey data: The data consist of 46 electrode penetrations. The data are provided as trial-based multi-unit activity and current source density plus a look-up table giving the trial conditions and a timebase. The data is stored on the JADE server.

Description of data

Monkey data: *Macaca mulatta*, 2 monkeys, male, age 8 and 10 years. Recordings made with laminar electrodes from the operculum of V1. Data is at the level of multi-unit activity and current flow in different layers of V1.

Human data: Human V1 laminar profile of Figure Ground Segmentation, fMRI BOLD imaging at 9.4T.

Completeness of data

Monkey data: The dataset is complete and was recorded prior to the Ramp-Up Phase.

Human data: Due to delays with the functioning of the 9.4T scanner (such a high-field scanner is technically still highly challenging, and its usage is not yet in routine stage), this data set is not yet available. Scans will be performed from March 2016.

Data Quality and Value

Monkey Data: The data comprise a very high quality set of recordings across the different layers of V1. Signal-to-noise ratios were very high and the consistency of the data is very high across penetrations. The data from the superficial layers of Monkey S is of slightly poorer quality due to damage caused by electrode penetrations, the data from Monkey E is of outstanding quality throughout all layers.

Data usage to date

SGA1: T2.4.2: Separation of activity in different cortical layers, T2.4.3: The role of attention in perception and learning, T2.4.4: Development of an empirically-derived brain atlas on sensorimotor integration (CDP-4), T3.1.1: Deep learning network constraint to human brain imaging

Are the data considered final?

The monkey data is final (recorded prior to the Ramp-Up Phase). The human data is not final due to delays in operation of the 9.4T human MRI scanner. The data will be acquired in March including preliminary data analysis.

Publications connected to the gathered data

- The monkey data has been published.
- Self, M. W., van Kerkoerle, T., Supèr, H. & Roelfsema, P. R. Distinct Roles of the Cortical Layers of Area V1 in Figure-Ground Segregation. Current Biology 23, 2121–2129 (2013). Full description of data and methodology.
- We have defined clear hypotheses about the outcome of the human data. We plan to publish the results of the human data and the monkey-human comparison later this year.

3.3.2.2 Provenance

The monkey data was recorded prior to the Ramp-Up Phase in Amsterdam and the full description of the data has been published. The data were collected with appropriate approval from the local ethics committee. The data has been uploaded onto the JADE server in Jülich.

The human data is currently recorded at the 9.4T scanner. The data are collected with the appropriate approval from the local ethical committees. The data will be stored locally

and at the JADE server in Jülich. As soon as the first publications are in press, the data will become available for everyone. Meanwhile, researchers from HBP can request to use the current data.

3.3.3 Human Intracranial Database (T2.1.9/T2.2.3 Lachaux/Kahane)

3.3.3.1 Data Description

Task(s)/group(s) responsible for generating data

T2.1.9 - Human Intracranial Database – Lyon, Grenoble – LACHAUX, KAHANE

Data, tools and methodologies storage location(s)

Intracranial EEG (iEEG: meso- micro-recordings), fMRI, DTI, CCEP (Cortico-cortical Evoked Potentials)

Description of data

Humans, male/female, age >18, 30 patients, spatial resolution of iEEG ranges between .1 to 1 mm, recorded in >100 cortical sites in each patient (electrophysiological recordings, ms temporal resolution), distributed in the entire cortical mantle, including superficial and deep structures. fMRI data collected at 1.5T.

Completeness of data

- The number of patients provided at M30 will match or exceed the figures announced at the beginning of the project. Single-unit activity difficult to extract from micro-recordings. iEEG data quality during simultaneous fMRI acquisition largely exceeds expected quality.
- The notion of "full dataset" has no real meaning in this case, as each data set collected in a new patient brings more information about the global and local dynamics of the human brain at work. A potential full data set would therefore include an infinite number of patients.
- iEEG data are collected during cognitive tasks in a dozens of epilepsy centers throughout the world. The originality of the present dataset is two-fold: a) it includes the systematic collection of iEEG data in eight different cognitive paradigms covering major human brain functions and b) it includes simultaneous recordings of fMRI and iEEG data, which is, to our knowledge, only performed in London (L. LEMIEUX) otherwise.

Data Quality and Value

Subjective analysis of the value of the data for the users: extremely high for iEEG data. fMRI data collected simultaneously with iEEG have low signal-to-noise ratio at the precise location of the electrodes, but this can be worked around and will be an interesting challenge for methodologists.

Data usage to date

Simultaneous iEEG/fMRI data have been used for a publication (under review) on the feasibility and interest of such simultaneous recordings. iEEG data collected in cognitive tasks will be published as part of a series of papers on the global brain dynamics underlying the perception of complex visual and auditory objects, verbal and visuo-spatial working memory, visual attention and reading

Are the data considered final?

Yes, regarding the present dataset, but it is planned that it will be completed by a second set of iEEG recordings in at the least the same number of patients (next phase, as part of the Human Brain Atlas CDP, T5.3.2).

Publications connected to the gathered data

See above (data usage to date). Raw data are processed through standard analysis pipeline of our group to extract task-related High-Frequency Activity [50-150 Hz].

- Vidal JR *et al.* (2015) Intracranial spectral amplitude dynamics of perceptual suppression in fronto-insular, occipito-temporal, and primary visual cortex. Front. Psychol., http://dx.doi.org/10.3389/fpsyg.2014.01545

3.3.3.2 Provenance

SP2

WP1

Task 2.1.9

2. How Can Platform Developers Provide You With Feedback on The Data?

Section 3.2.1: Bertrand THIRION, (bertrand.thirion@inria.fr)

Section 3.2.2: Cyril POUPON (cyril.poupon@cea.fr)

Section 3.3.3.1: Rainer GOEBEL (R.Goebel@Psychology.Unimaas.Nl), Wim VANDUFFEL (wim.vanduffel@med.kuleuven.be)

Section 3.3.3.2: Rainer GOEBEL (R.Goebel@Psychology.Unimaas.Nl), Pieter ROELFSEMA (p.roelfsema@nin.knaw.nl)

Section 3.3.3.3: Jean-Philippe LACHAUX (jphlachaux@me.com)

What types of feedback are most helpful/constructive?

We are interested in any information about the usage of the data, e.g.

1) How often has the data been viewed? How long has it been viewed? How did the user interact with the data
2) How often has the data been downloaded
3) How has the data been found (knowledge graph query, direct link, crosslink from other views/datasets)?
4) From where has the data ben accessed (country, etc.)
5) What is the user's feedback on the data (if applicable)

We are also interested in technical information, e.g. how long did it take on average to load and render individual datasets?

What collaborations are you looking for?

We are looking for further cooperations with neuroscientists working in simulation and modelling of the human brain, to discuss their requirements for human brain data and atlas tools. We also want to continue and deepen our close collaboration with HPC centres to build analytics workflows for datasets, and co-design HPC architectures for such analysis of image datasets.

Annex A: Dataset Information Cards

Task	Partner	Data / model name	DIC name	DIC registered	Link
2.1.1	INRIA	High-resolution Anatomical, Diffusion and Functional MRI Images from Subjects Selected for Massive Mapping	Individual Brain charting and meta-analysis	yes	https://jade01.zam.kfa-juelich.de:2880/INM1/HBP-SP2/ibc/
2.1.2	INRIA	Quantification of the Diameter and Number of Axons in Each Major Tract in Adult Human Brains	Functional mapping of the brain (ARCHI database)	yes	https://jade01.zam.kfa-juelich.de:2880/INM1/Neurospin/archi_fmri/release_01/
2.1.2	JUELICH	Wistar rat brain fibre orientation model	Wistar rat brain fibre orientation model	yes	https://jade01.zam.kfa-juelich.de:2880/INM1/HBP-SP2/wistar-fom
2.1.2	CEA	In vivo fibre tract scans and diffusion-based data on major and U-shaped tracts	In vivo fibre tract scans and diffusion-based data on major and U-shaped tracts	yes	https://jade01.zam.kfa-juelich.de:2880/INM1/Neurospin/CONNECT_ARCHI/RELEASE-01/
2.1.3	UPM	Numbers and Distributions of Neurons and Glia	Numbers and Distributions of Neurons and Glia	yes	https://jade01.zam.kfa-juelich.de:2880/INM1/HBP-SP2/interneuron-maps/
2.1.4	VU	Morphologies of neurons in different brain regions	Morphologies of selected neurons	yes	https://jade01.zam.kfa-juelich.de:2880/INM1/HBP-SP2/neuron-morphologies/
2.1.5	JUELICH	Quantitative Receptor data in different, cytoarchitectonically defined brain regions	Quantitative Receptor data	yes	https://jade01.zam.kfa-juelich.de:2880/INM1/HBP-SP2/receptors/
2.1.5	JUELICH	Quantitative Whole Brain Receptor Data	Whole rat brain receptor data	yes	https://jade01.zam.kfa-juelich.de:2880/INM1/HBP-SP2/wistar-receptor
2.1.6	CEA	Infant atlas	Infant atlas and major tracts in infant brains	yes	https://jade01.zam.kfa-juelich.de:2880/INM1/HBP-SP2/infant-template

2.1.7	KUL	Homologies between human and monkey	Monkey visual/ auditory	yes	visual data: https://jade01.zam.kfa-juelich.de:2880/INM1/HBP-SP2/Monkey-visual and auditory data: https://jade01.zam.kfa-juelich.de:2880/jade/INM1/HBP-SP2/Monkey-auditory
2.1.7	UM	Homologies between humans and other primates	Human visual/ auditory	yes	file path Universiteit Maastricht (internal): smb://fpnisi001.fpn.isilon/projects/36020092e
2.1.8	KNAW	Revealing the activity and function of cortical layers, monkey	Neuronal activity profile across the cortical layers during figure-ground perception	yes	https://jade01.zam.kfa-juelich.de:2880/INM1/HBP-SP2/monkey-laminar/
2.1.8	UM	Revealing the activity and function of cortical layers, human	Human V1 laminar profile of Figure Ground Segmentation	yes	Due to delays with the functioning of the 9.4 Tesla scanner, this data set is NOT yet available. Scans will be performed in the next couple of weeks (start: March 2016).
2.1.9/ 2.2.3	UCBL	Human Intracranial database	Human Intracranial database	yes	tbd
2.2.1	CEA	A cross modality alignment toolbox based on sulci	A cross modality alignment toolbox based on sulci	yes	http://brainvisa.info
2.2.2	JUELICH	Big Brain	High resolution whole brain volumetric data; BigBrain (Release 2015)	yes	ftp://bigbrain.loris.ca/BigBrainRelease.2015
2.2.2	JUELICH	Whole Human Brain Cytoarchitectonic and Maximum Probability Maps	Whole Human Brain Cytoarchitectonic and Maximum Probability Maps	yes	https://jade01.zam.kfa-juelich.de:2880/INM1/HBP-SP2/Anatomy-v22c/
2.2.2	JUELICH	SPM Anatomy Toolboox	SPM Anatomy Toolbox	yes	http://www.fz-juelich.de/SharedDocs/Downloads/INM/INM-1/DE/Toolbox/Toolbox_22c.html;jsessionid=ECE6C7FA1182485F102B8849C12381F1?nn=1090980

Annex B: Summary Table

Basis				Biological data							Metadata				Integration			
task id	partner	contact	short name	species	region(s)	cell type	detection method	captured features, data domain	data information card (DIC)	URL (DIC)	template space alignment	data standard, format	number of planned datasets	number of datasets (actual)	downstream consumer task ids (Ramp-Up)	data used for maps, model etc. integration, please specify	downstream consumer task ids (SGA1)	publications
2.1.1	INRIA	Bertrand Thirion	Functional mapping of the brain (ARCHI database)	homo sapiens	whole brain	—	functional MRI, on 80 subjects (20 functional contrasts)	human brain functional circuits	Functional mapping of the brain (ARCHI database)	https://jade01.zam.kfa-juelich.de:2880/IM1/Neurospin/archi_fmri/release_01/	MNI	nifti, gifti, csv, json	79 subjects scanned in 4 tasks	79 subjects scanned (2000 files)	5.5.2	SP5 3d atlas	Tasks 2.1, 2.3, 2.4, 2.5, 5.3.2, (CDP3)	D. Bzdok, M. Eickenberg, O. Grisel, B. Thirion, G. Varoquaux. Semi-Supervised Factored Logistic Regression for High-Dimensional Neuroimaging Data. Neural Information Processing Systems, 2015
2.1.1	INRIA	Bertrand Thirion	Individual Brain charting and meta-analysis	homo sapiens	whole brain	—	High-resolution anatomical, diffusion and functional MRI	human brain functional circuits	Individual Brain charting and meta-analysis	https://jade01.zam.kfa-juelich.de:2880/IM1/HBP-SP2/ibc/	MNI	nifti, gifti, csv, json	12 subjects scanned in 10 conditions	8 subjects scanned in 43 conditions (2000 files)	5.5.2	SP5 3d atlas	Tasks 2.1, 2.3, 2.4, 2.5, 5.3.2, (CDP3)	Not yet published. Workshop publications: A.L. Grilo Pinho and B. Thirion, High resolution encoding of cognitive information within the IBC project News 2016 workshop, Jan 2016; A.L. Grilo Pinho and B. Thirion, Individual Brain Charting: high-resolution normative fMRI database OHBM 2016 conference, June 2016; A.L. Grilo Pinho and B. Thirion, Individual Brain Charting: a comprehensive neuroimaging database towards a macroscopic representation of the human brain FENS 2016 conference, June 2016
2.1.2	JUELICH	Markus Axer	Wistar rat brain fibre orientation model	rattus norvegicus	whole brain	—	3D PLI	fiber orientations	Wistar rat brain fibre orientation model	https://jade01.zam.kfa-juelich.de:2880/IM1/HBP-SP2/wistar-fom	Waxholm space	nifti	not part of HBP deliverable	4	5.5.1	SP5 2d atlas SP5 3d atlas	5.3.2, WP5.2	Not yet published. Publication describing method: Axer M. et al. (2011) A novel approach to the human connectome: ultra-high resolution mapping of fiber tracts in the brain. NeuroImage 54:1091-1101 and Axer M. et al. (2011) High-resolution fiber tract reconstruction in the human brain by means of three-dimensional polarized light imaging. Frontiers in

																		Neuroinformatics 5:34.
2.1.2	CEA	Jeff Mangin	In vivo fibre tract scans and diffusion-based data on major and U-shaped tracts	homo sapiens	whole brain	—	structural, functional and diffusion MRI	deep white matter fibre bundles	In vivo fibre tract scans and diffusion-based data on major and U-shaped tracts	https://jade01.zam.kfa-juelich.de:2880/INM1/Neurospin/CONNECT_ARCHI/RELEASE-01/	Native space MNI Colin 27	nifti	79 subjects	individual data from 79 subjects, probabilistic maps for each bundle	5.5.2	SP5 2d atlas SP5 3d atlas	5.3.2, 4.4.1	M. Guevara, C. Roman, J. Houenou, D. Duclap, C. Poupon, J. F. Mangin, P. Guevara, A whole brain multi-subject short association bundle atlas, submitted to Neuroimage; N. Labra, P. Guevara, D. Duclap, J. Houenou, C. Poupon, J.-F. Mangin, M. Figueroa, Fast automatic segmentation of white matter fibers based on a multi-subject bundle atlas, submitted to Neuroinformatics; P Guevara, D Duclap, C Poupon, L Marrakchi-Kacem, P Fillard, D Lebihan, M Leboyer, J Houenou, J-F Mangin, Automatic fiber bundle segmentation in massive tractography datasets using a multi-subject bundle atlas, NeuroImage, 61(4):1083-99, 2012
2.1.3	UPM	Javier DeFelipe	Numbers and Distributions of Neurons and Glia	homo sapiens	Brodmann's cytoarchitectonic subdivisions of the cortex: 1, 3b, 4, 6, 9, 10, 11, 12, 13, 14, 17, 18, 20, 21, 22, 24, 32, 38, 45, 46, 47	different types of cells (NeuN, PV, CR, CB, TH neurons) and axon terminal specializations (chandelier and Double bouquet cell axon terminals and	immunocytochemistry	cell densities	Numbers and Distributions of Neurons and Glia	https://jade01.zam.kfa-juelich.de:2880/INM1/HBP-SP2/interneuron-maps/	none	xlsx	was not specified	350	5.5.2	SP5 2d atlas	5.3.2	Data are considered to be a robust draft of the neuronal population density maps that we are generating, and constitute the body of a manuscript that is currently in preparation.

						Complex Basquet)												
2.1.4	VU	Huibert Mansvelder	Morphologies of neurons in different brain regions	homo sapiens	temporal cortex	Adult human pyramidal neurons	neural recordings	digitally reconstructed neurons with matching physiological data	Morphologies of selected neurons	https://jade01.zam.kfa-juelich.de:2880/INM1/HBP-SP2/neuron-morphologies/	none	ascii	was not specified	100 files	4.1.1, 6.1.3	model of single neuron properties	T4.1.1, T4.1.2, T6.2.1	Eyal G, Mansvelder HD, de Kock CP, Segev I. (2014), Dendrites impact the encoding capa-bilities of the axon. J Neurosci. Jun 11; 34(24): 8063-71. doi:10.1523/JNEUROSCI.5431-13.2014. PMID: 24920612
2.1.5	JUELICH	Karl Zilles	Quantitative Receptor data in different, cytoarchitectonically defined brain regions	homo sapiens	three primary sensory, the primary motor, 11 higher associative cortical areas, putamen, globus pallidus and two thalamic nuclei.	—	histology, receptor autoradiography	receptor densities of AMPA, NMDA, kainate, mGluR 2/3, GABAA, GABAA associated benzodiazepine binding sites, GABAB, muscarinic M1, M2 and M3, nicotinic a4/b2, a1, a2, 5-HT1A, 5-HT2A, D1, D2, A1, A2	Quantitative Receptor data	https://jade01.zam.kfa-juelich.de:2880/INM1/HBP-SP2/receptors/	none	csv	was not specified	1 file (densities of 15 receptor of 38 regions)	5.5.2	Human Brain Atlas	5.3.2	Zilles, K. et al. (2015) Common molecular basis of the sentence comprehension network revealed by neurotrans-mitter receptor fingerprints. Cortex 63: 79-8, Zilles, K. et al. (2002). Quantitative analysis of cyto- and receptorarchitecture of the human brain, pp. 573-602. In: Brain Mapping: The Methods, 2nd edition (A.W. Toga and J.C. Mazziotta, eds.). San Diego, Academic Press.
2.1.5	JUE	Karl	Quantitat	rattu	whole	—	histology,	recepto	Whole	https://jade01.zam	Waxhol	nifti	was not	5 files	5.5.1	SP5 2d	5.3.2	Huynh A.-M., Kirlangic M.E.,

	LICH	Zilles	ive Whole Brain Receptor Data	s norvegicus	brain		receptor autoradiography	r densities of AMPA, NMDA, kainate, mGluR 2/3, GABAA, GABAA associated benzodiazepine binding sites, GABAB, muscarinic M1, M2 and M3, nicotinic a4/b2, a1, a2, 5-HT1A, 5-HT2A, D1, D2, A1, A2	rat brain receptor data	.kfa-juelich.de:2880/INM1/HBP-SP2/wistar-receptor	m space		specified			atlas SP5 3d atlas		Schubert N., Schober M., Amunts K., Zilles K., Axer M. (2015) Reconstructing a Series of Auto-Radiographic Images in Rat Brains. Procs. BVM, 167-172; Schober M., Schlömer P., Cremer M., Mohlberg H., Huynh A.-M., Schubert N., Kirlangic M.E., Amunts K., Axer M. (2015) Reference Volume Generation for Subsequent 3D-Reconstruction of Histological Sections. Procs BVM, 143-148; Schubert N., Kirlangic M.E., Schober M., Huynh A.-M., Amunts K., Zilles K., Axer M. (2015) 3D Reconstruction of Histological Rat Brain Images. Procs BVM, 149-154; Zilles, K., Schleicher, A., Palomero-Gallagher, N., Amunts, K. (2002) Quantitative analysis of cytoand receptorarchitecture of the human brain, pp. 573-602. In: Brain Mapping: The Methods, 2nd edition (A.W. Toga and J.C. Mazziotta, eds.). Academic Press.
2.1.6	CEA	Ghislaine Dehaene-Lambertz	Infant atlas	homo sapiens	whole brain	—	DTI	MR volume, surface mesh, atlas parcellation	Infant atlas and major tracts in infant brains	https://jade01.zam.kfa-juelich.de:2880/INM1/HBP-SP2/infant-template	no alignment (serves as a template)	nifti, Brainvisa Mesh, gifti	0	1	5.5.2	SP5 2d atlas SP5 3d atlas	5.3.2	Kabdebon, C., Leroy, F., Simmonet, H., Perrot, M., Dubois, J., & Dehaene-Lambertz, G. (2014). Anatomical correlations of the international 10-20 sensor placement system in infants. Neuroimage, 99, 342–356. http://doi.org/10.1016/j.neuroimage.2014.05.046; Kulikova S, Hertz-Pannier L, Dehaene-Lambertz G, Buzmakov A, Poupon C, Dubois J. Multi-parametric evaluation of the white matter

																		maturation. Brain Struct Funct. 2015 Nov;220(6):3657-72. doi: 10.1007/s00429-014-0881-y. Epub 2014 Sep 3. PubMed PMID: 25183543; PubMed Central PMCID: PMC4575699; Dubois J et al. (2015) Exploring the Early Organization and Maturation of Linguistic Pathways in the Human Infant Brain. Cereb. Cortex, doi: 10.1093/cercor/bhv082;
2.1.7	KUL	Wim Vanduffel	Homologies between human and monkey	Macaca Mulata	whole brain	—	fMRI	Activation patterns in visual and auditory cortex	Monkey visual/ auditory	visual data: https://jade01.zam.kfa-juelich.de:2880/INM1/HBP-SP2/Monkey-visual and auditory data: https://jade01.zam.kfa-juelich.de:2880/jade/INM1/HBP-SP2/Monkey-auditory	1 subject of the individual expts	nifti	3	2	T2.1.7	monkey atlas	possible input to /interactions with 1.3.4, 1.4.1, 1.4.2, 2.2.1, 2.2.3, 2.2.4, 2.3.1, 2.3.2, 2.4.1, 2.4.2, 2.4.3, 2.4.4, 2.5.1, 2.5.2, 2.5.3, 2.6.2, 2.6.4, 3.1.1, 3.1.2, 4.2.1, 4.4.1, 4.4.2, 4.4.5, 5.1.5, 5.5.2, 7.3.1, 7.3.2, 10.1.2, 10.2.1, 10.2.3	publications in preparation
2.1.7	UM	Rainer	Homologies	homo	ventral visual	—	High-resolution	Activation	Human visual/	file path Universiteit	ACPC / MNI	DICOM	Human visual	Human visual	T2.1.7	Human Brain Atlas	possible input to	Not yet published. Budnik U, Qi Z, Vanduffel W, Goebel R

		Goebel	between human and monkey	sapiens	cortex or auditory cortex in human study		fMRI	patterns in visual and auditory cortex	auditory	Maastricht (internal): smb://fpnisi001.fpn.isilon/projects/36020092e			cortex 7T study: 8 participants	cortex 7T study: 6 participants, 2-4 scanning sessions			/interactions with 1.3.4, 1.4.1, 1.4.2, 2.2.1, 2.2.3, 2.2.4, 2.3.1, 2.3.2, 2.4.1, 2.4.2, 2.4.3, 2.4.4, 2.5.1, 2.5.2, 2.5.3, 2.6.2,	(2015). Is Species-Specific Visual Input Processing Different in Humans and Monkeys? A 7T fMRI Mapping Study. Poster #4057, OHBM meeting, June 2015
2.1.8	UM, KNAW	Pieter Roelfsema	Activity and function of cortical layers	Macaca Mulata	V1	—	MUA/SUA, CSD	activity in the different cortical layers in monkey V1 during the segregation of figure from ground in a texture-segregation task	Neuronal activity profile across the cortical layers during figure-ground perception	https://jade01.zam.kfa-juelich.de:2880/INM1/HBP-SP2/monkey-laminar/	none (semantic location: V1)	nifti	was not specified	50	T2.1.8	Comparison with human MRI data, Human Brain Atlas	T2.4.2, T2.4.3, T2.4.4, T3.1.1	Self, M.W., van Kerkoerle, T., Supèr, H. & Roelfsema, P.R. (2013) Distinct roles of the cortical layers of area V1 in figure-ground segregation, Curr. Biol., 23, 2121-2129.; Self, M.W., van Kerkoerle, T., Supèr, H. & Roelfsema, P.R. (2013) Distinct roles of the cortical layers of area V1 in figure-ground segregation, Curr. Biol., 23, 2121-2129.
2.1.8	UM, KNAW	Rainer Goebel	Activity and function of cortical layers	homo sapiens	V1	—	fMRI BOLD imaging at 7T and 9.4T	laminar profile of Figure Ground Segmentation processes	Human V1 laminar profile of Figure Ground Segmentation	Due to delays with the functioning of the 9.4 Tesla scanner, this data set is NOT yet available. Scans will be performed in the next couple of weeks (start: March 2016).	Individual brain space	not specified	Human 9.4 Tesla: 3	Human 9.4 Tesla: 0	—	Comparison with monkey MRI data, Human Brain Atlas	T2.4.2, T2.4.3, T2.4.4, T3.1.1	no publications
2.1.9/ 2.2.3	UCBL	Jean-	Human intracrani	homo	whole brain	—	iEEG, fMRI,	human brain	Human Intracra	tbd	MNI	nifti, eeg (ELAN	30 patients	iEEG data from 30	5.3.1	SP5 electrophysi	5.3.2	Vidal JR et al. (2015) Intracranial spectral

		Phillippe Lachaux	al database	sapiens			DTI/CCEP	functional circuits	nial database			dataformat http://elan.lyon.inserm.fr)		patients (8 localisers), iEEG and MRI from 8 of those patients, 6 structural connectivity DTI/CCEP		ology, population analysis		amplitude dynamics of perceptual suppression in fronto-insular, occipito-temporal, and primary visual cortex. Front. Psychol., http://dx.doi.org/10.3389/fpsyg.2014.01545
2.2.1	CEA	Jeff Mangin	A cross modality alignment toolbox based on sulci	homo sapiens	whole brain	—	T1 MRI, histological whole brain data	sulci	A cross modality alignment toolbox based on sulci	http://brainvisa.info	MNI Colin 27, MNI 152	nifti	not specified	>10.000 files	5.5.2	SP5 3d atlas	5.3.4	Mangin J.-F. et al. (2015) Sulcus Identification and Labeling. In: Arthur W. Toga, editor. Brain Mapping: An Encyclopedic Reference, vol. 1, pp. 365-371. Academic Press: Elsevier, Mangin J.-F. et al. (2015) Sulci as Landmarks. In: Arthur W. Toga, editor. Brain Mapping: An Encyclopedic Reference, vol. 2, pp. 45-52. Academic Press: Elsevier
2.2.2	JUELICH	Katrin Amunts	Big Brain	homo sapiens	whole brain	—	Cell body staining	Cytoarchitecture	High resolution whole brain volumetric data; BigBrain (Release 2015)	ftp://bigbrain.loris.ca/BigBrainRelease.2015	no alignment (serves as a template)	minc, png	first Big Brain	2D, 3D reconstruction of the BigBrain (50000 files)	5.5.2	SP5 2d atlas SP5 3d atlas	5.3.2	Amunts et al. (2013) Big Brain: An Ultrahigh-resolution 3D Human Brain Model. Science Vol. 340, Issue 6139, pp. 1472-1475
2.2.2	JUELICH	Katrin Amunts	Whole Human Brain Cytoarchitectonic and Maximum Probability Maps	homo sapiens	cortical and subcortical areas	—	cell body staining, 3D reconstruction	probabilistic atlas parcellation	Whole Human Brain Cytoarchitectonic and Maximum Probability Maps	https://jade01.zam.kfa-juelich.de:2880/INM1/HBP-SP2/Anatomy-v22c/	MNI Colin 27	nifti	not specified	134 probabilistic maps	5.5.2	SP5 2d atlas SP5 3d atlas	5.3.2	Amunts K., Schleicher A., Bürgel U., Mohlberg H., Uylings H.B.M., Zilles K. (1999). Broca's region revisited: Cytoarchitecture and intersubject variability. The Journal of Comparative Neurology 412(2): 319-341; Amunts K., Weiss P.H., Mohlberg H., Pieperhoff P., Eickhoff S., Gurd J., Shah J.N., Marshall J.C., Fink G.R., Zilles K (2004) Analysis of the neural mechanisms underlying verbal fluency in cytoarchitectonically defined stereotactic space – The role of Brodmann's areas 44 and

																		45. NeuroImage 22(1): 42-56; Eickhoff S, Stephan KE, Mohlberg H, Grefkes C, Fink GR, Amunts K, Zilles K (2005):A new SPM toolbox for combining probabilistic cytoarchitectonic maps and functional imaging data. NeuroImage 25(4), 1325-1335; Eickhoff, S. B.; Heim, S.; Zilles, K.; Amunts, K. (2006): Testing anatomically specified hypotheses in functional imaging using cytoarchitectonic maps. NeuroImage 32(2), 570-582; Eickhoff SB, Paus T, Caspers S, Grosbras MH, Evans A, Zilles K, Amunts K (2007) Assignment of functional activations to probabilistic cytoarchitectonic areas revisited. NeuroImage 36(3), 511-521; Schleicher, A.; Palomero-Gallagher, N.; Morosan, P.; Schleicher, S.B.; Kowalski, T.; de Vos, K.; Amunts, K.; Zilles, K. (2005) Quantitative architectural analysis: a new approach to cortical mapping. Anat Embryol 210: 373-386; Zilles, K., Schleicher, A., Palomero-Gallagher, N., Amunts, K. (2002) Quantitative analysis of cytoand receptorarchitecture of the human brain, pp. 573-602. In: Brain Mapping: The Methods, 2nd edition (A.W. Toga and J.C. Mazziotta, eds.). Academic Press.
2.2.2	JUELICH	Simon Eickhoff	SPM Anatomy Toolboox	homo sapiens	cortical and subcortical areas	—	cell body staining, 3D reconstruction	probabilistic atlas	SPM Anatomy Toolbox	http://www.fz-juelich.de/SharedDocs/Downloads/INM/INM-1/DE/Toolbox/Tool	MNI Colin 27	nifti	not specified	Toolbox including 134 probabilistic maps	5.5.2	SP5 2d atlas SP5 3d atlas	5.3.2, 5.1.4	Eickhoff S et al. (2005) A new SPM toolbox for combining probabilistic cytoarchitectonic maps and functional imaging data.

										box_22c.html;jsessionid=ECE6C7FA1182485F102B8849C12381F1?nn=1090980								NeuroImage 25(4), 1325-1335; Eickhoff et al. (2007) Assignment of functional activations to probabilistic cytoarchitectonic areas revisited. NeuroImage 36(3), 511-521

Annex C: Methodologies

Task	partner	contact	Methodology/Tool	Validation	Limitations	Potential for innovation and IPR
2.1.1	INRIA	Thirion	Prediction of brain activity from localizer data with principal components analysis regression	State-of-the-art prediction accuracy on the ARCHI dataset	Requires a large training dataset	The tool relies on open-source library and is meant to be used freely. See https://github.com/bthirion/fMRI_PCR
2.1.1	INRIA	Thirion	Two-layer classifier for decoding multiple concurrent cognitive labels from large-scale datasets	Successful decoding on a corpus of 30 datasets (openfMRI mostly). Decoding accuracy is higher than that of linear classifiers.	Computationally expensive	To be confirmed upon validation on larger scale experiments
2.1.1	INRIA	Thirion	Semi-supervised factored logistic regression for the concurrent analysis of task and resting-state brain activity	Experiments on the HCP dataset: improved performance and redovery	Computationally expensive	To be confirmed upon validation on larger scale experiments
2.1.1	INRIA	Thirion	Fast dictionary for large-scale datasets (matrices of size 1M*1M)	Experiments on large-scale fMRI datasets (2TB) and recommender systems	The method is asymptotically suboptimal, but this issue is never met in practical settings	Inclusion in OSS: scikit learn and Nilearn.
2.1.2	CEA	Mangin	Connectomist bundle pipeline	Applied on more than 2000 subjects	Tractography from diffusion MRI can create spurious fiber because of crossing	tool developed before HBP
2.1.2	CEA	Poupon	Connectomist microstructure pipeline	Consistency with postmortem dissection data in corpus callosum	Aggregating several acquisitions required to improve accuracy	fundamental research

2.1.2	JUELICH	Axer	HPC- and Workflow-based fiber orientation estimation from 3D-Polarized Light Imaging (3D-PLI) data	application to human hippocampus, rat and vervet monkey brains with neuroanatomists' validation and simulation comparison	few semi-automated image processing steps required	___
2.1.2	JUELICH	Axer	HPC-based generation of orientation distribution functions (ODF) in 3D-PLI data	comparison with dMRI ODFs	___	___
2.1.2	JUELICH	Axer	brain volume reconstruction from serial section images based on 3D-PLI	application to an entire rat brain including transfer into Waxholm space	registration precision not yet at a few microns level	___
2.1.2	UDUS	Eickhoff	SPM Anatomy Toolbox	In use since ~10 years	___	No IPR, the tool is being used outside of HBP under a GNU licence, we do not pay any licence fees
2.1.3	JUELICH	Amunts	JuBrain - Whole Human Brain Cytoarchitectonic and Maximum Probability maps	Methode in use since more than 10 years	time consuming: cytoarchitectonic mapping requires analysis of hundreds of brain slices	No potential for IPR.
2.1.3	UPM	DeFelipe	Immunohistochemical techniques and Stereological software tools	Currently used in many laboratories	Requires human tissue samples with sort postmortem periods and proper fixation	No potential IPR. Techniques are used by groups outside of HBP. No license fees.
2.1.4	VU	Mansvelder	Quantitative morphological reconstruction of human neurons	91 human neurons full dendritic reconstruction, 22 human neurons including axons	low thru-put	___

				(Mohan et al., 2015)		
2.1.5	JUELICH	Zilles	Receptor autoradiography	Saturation and competition studies to confirm specificity of the receptor ligands. Comparisons of receptor binding and in situ hybridization studies. Comparisons between data obtained from sections exposed to tritium-sensitive films and to FUJI-BAS plates. Intersubject variability of binding site concentrations tested.	Tissue availability; short post mortem delays; time constraints of exposition; financial load	Fundamental research; basic data for drug discovery (see CDP6)
2.1.5	JUELICH	Zilles	brain volume reconstruction from serial section images based on receptor autoradiography and histological cell body staining	application to an entire rat brain for muscarinic M2 receptor and histological images including transfer into Waxholm space	deformations caused by sectioning and mounting of the brains (e.g. tears, gaps)	___
2.1.6	CEA	Dehaene	Clustering the infant brain tissues using multi-parametric MRI	Application on a 17-infants database. Results consistent with previous studies	Results accuracy can depend on the number of classes used by the clustering algorithm	tool mainly developed before HBP
2.1.7	KUL	Vanduffel	comparative functional imaging	novel analytical tools	Computationally expensive	fundamental research

2.1.7	UM	Goebel	fMRI BOLD imaging at 7T / BrainVoyager software and custom Matlab tools	Replicate known data at lower fMRI resolution	Comparision of human and monkey data difficult	New tools for detailed human - monkey comparison
2.1.8	UM	Goebel	fMRI BOLD imaging at 7T and 9.4T / BrainVoyager software and custom Matlab tools	Comparision to expected data from electrophysiological monkey experiments	Comparision of human and monkey data difficult	New tools for detailed human - monkey comparison
2.1.8	KNAW	Roelfsema	Laminar recordings of multi-unit activity and current-source density	Laminar profiles of visual response latencies and receptive field size replicate known data from single-cell studies confirming accuracy of depth assignments.	Large electorde sizes can damage neurons in the superficial layers. Single-unit data is difficult to obtain.	No potential for IR. Technique has been independently developed by other groups outside of HBP. No license fees.
2.2.1	CEA	Mangin	Morphologist and DISCO	Morphologist validated on 10000 subjects, DISCO with 52 subjects	Can require manual correction of sulcus labelling	tool mainly developed before HBP
2.2.3/2.1.9	UCBL	Lachaux	Hibop: Human Intracranial Data Visualizer	Succesful visualizationof intracranial EEG data from 30 patients	——	tool developed within HBP
2.2.4	JUELICH	Dickscheid	Papaya webviewer with custom functionality to manage and display area-specific contextual information	Successful access to the customized version as a prototype level collaboratory app, with working functionality to retrieve receptor plots for selected	Local access to datafiles, not bound via knowledge graph.	No potential for IPR. The software core has been independently developed at UTHSCSA outside of HBP and is freely available. The new custom functionality has been implemented for HBP, and will be opensourced as well. No license fees.

				brain regions.		