Neuroinformatics Platform Documentation

User Manual

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User Manual

Web Applications

Intended audience

This manual is intended at end users of either the Neuroinformatics Platform website or APIs. If you are looking for neuroscientific data, use Search client application and explore available data by their metadata.

Search client

Purpose

The Search client is an information retrieval system design to help neuroscientists, students, and users to find and download data registered in the NeuroInformatics Platform (NIP) through free text and semantic tags queries.

The Search client is a front end application to the KSearch REST API and directly uses features it provides, albeit in a simplified and non-exhaustive way.

Features

Quick filters
The landing page of the Search client offers **2 levels of quick filters** to narrow down your search to the relevant subset of data: by species / order and then brain region. If you select a species with few datasets registered, you will not see the 2nd level of quick filters (brain region).
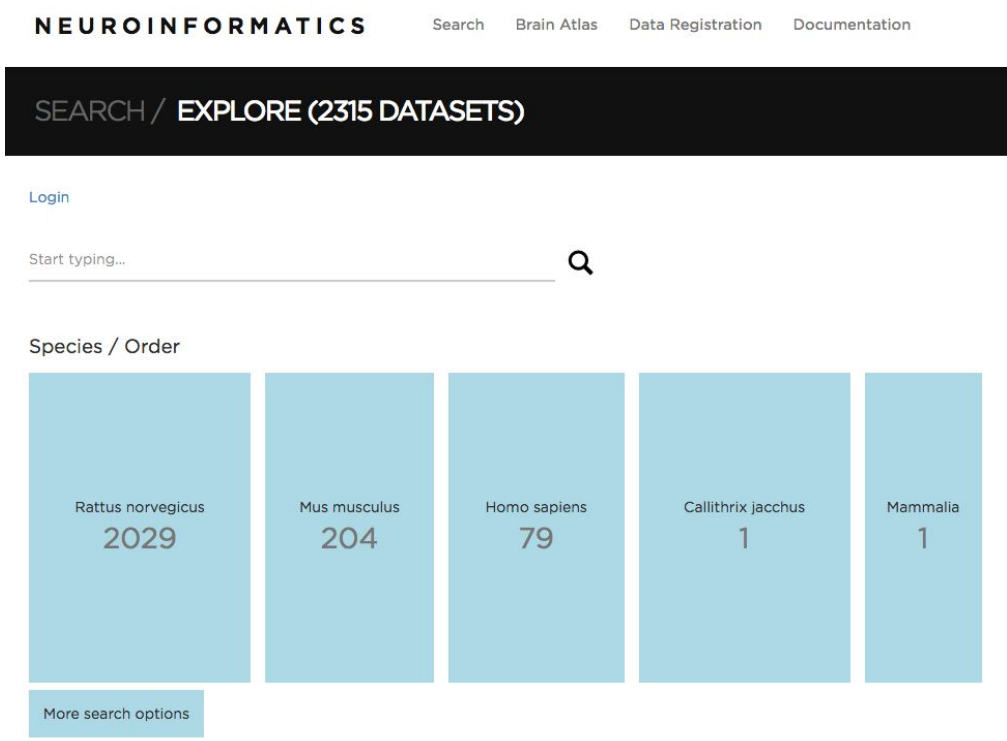
Fig. Landing page view

And selecting 'Rattus Norvegicus' we get the following screen:
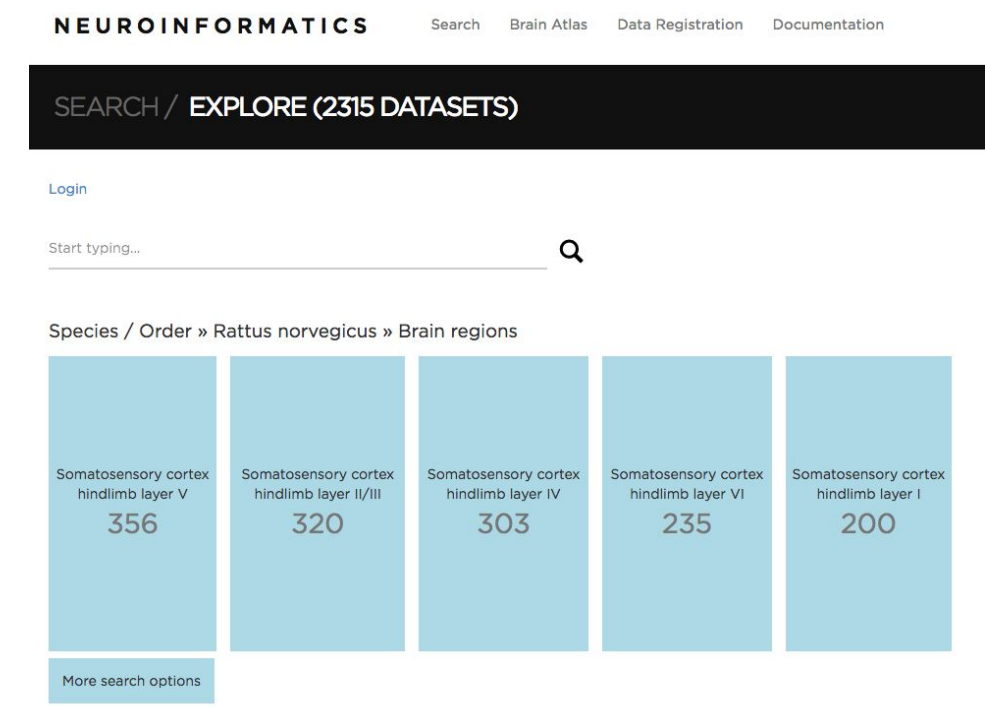
If you want to **bypass the quick filters**, you can click on the "More search options" button to show all datasets. The button is shown below.

More search options

You can also enter a free form text query to directly land to the search results for the query.

Free form text query
At any time, you can **type a free form text query in the input field at the top of the page**, and press the Enter key or click on the looking glass icon to apply the query. Please note that all existing filters will be kept.

thalamus

Paginated list of results
The main screen consists in a list of paginated search results (**10 results per page**) with a list of filters on the left.

Adding / removing filters
Filters are ordered by category. You can **add a filter** by clicking on it in the left sidebar. It will refresh the list of results and list of available filters. The active filters and categories are moved to the top of the sidebar. By clicking on the cross icon next to one of them, you can **disable the filter**.

Detailed info

To see detailed info about a given result, click on it. It will display more metadata along with a download link if relevant.

You can put the cursor over a contributor's name to **see the contributor's affiliations**.

Download dataset

Dataset **download is restricted to HBP members**. If you're not logged in yet, you will be prompted to do so. You can **login** at any time through the link at the top left of the page.

Atlas Viewer

Purpose

The [Multiresolution Atlas Viewer](#) allows you to easily visualize brain imaging datasets coming from several species, and mapped to several brain atlases spaces. This interactive context allows you to specifically target a region of the brain in the 3 axes (sagittal, coronal and axial) rapidly.

The Multiresolution Atlas Viewer sits upon the KSearch and Image Service REST APIs to discover and display the brain imaging datasets currently registered in the NIP.

Features

Visualizing brain slice
Most of the screen is taken up by the currently displayed brain slice. By default the Waxholm Space Rat brain atlas dataset will be selected, displaying the middle slice in the sagittal orientation.
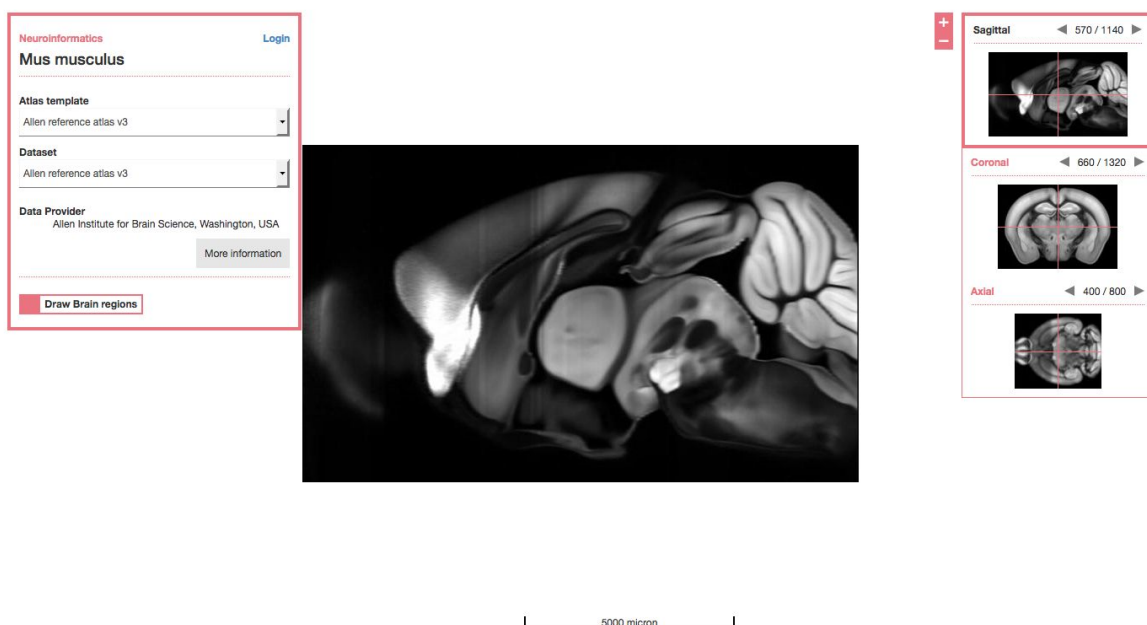
Dataset information
The left pane displays information about the currently selected dataset. By default it displays only a summary of the metadata. By clicking on the "More information" button, you will be able to see **detailed information**.

Previews

The right pane displays your current position in the dataset in all 3 orientations.
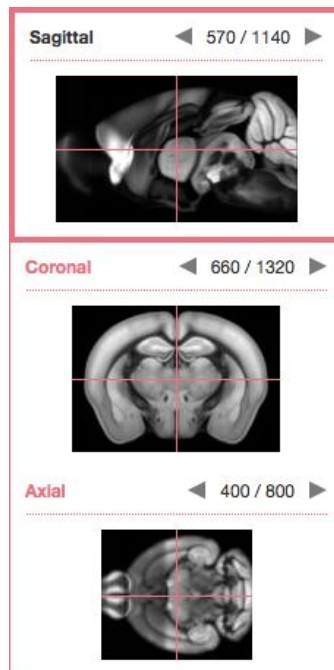
Clicking on the arrows next to the current orientation will **browse to the previous / next slice** in the preview, and change the main slice if you did it for the current orientation.

Previews have crosshairs on top of them that are showing your current position in the atlas space. By clicking anywhere on these preview images, it will cause the 2 other orientations to **quickly jump to the slice** matching the crosshairs position.
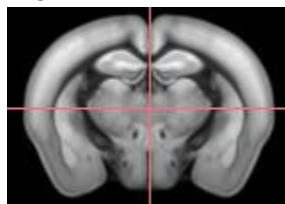
By clicking on the orientation name in the right pane, you will **switch the current dataset orientation** between sagittal, coronal and axial.
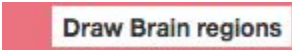
Pan and zoom

You can navigate through the current slice like in Google Maps and similar services: click and hold while moving the cursor to **pan**, scroll or click on the "+" and "-" buttons to **zoom in / zoom out**.

Overlayed annotations

On most datasets, a checkbox in the left pane allows you to **enable / disable the overlay** of brain regions on top of the current slice.

Placing the cursor hover a region on the overlay will **display the region name at the top of the screen**.

On selected datasets such as Allen Mouse Brain Atlas v3, clicking on a region will furthermore **display a popup** with links to related data fetched from KnowledgeSpace and our KnowledgeGraph.
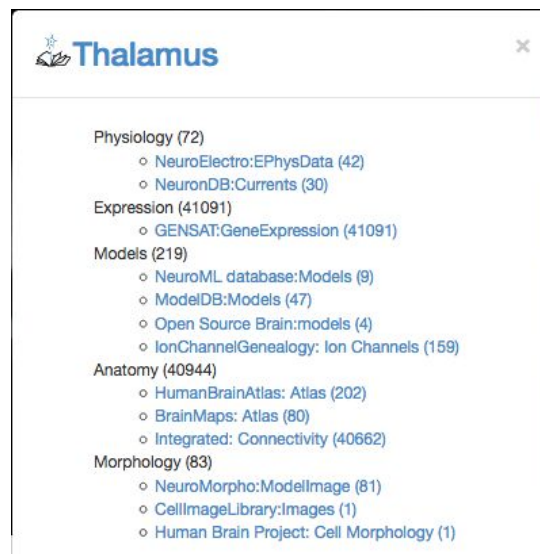
Clicking on the title of the popup will lead you to the corresponding page on KnowledgeSpace with **full information about the brain region**.
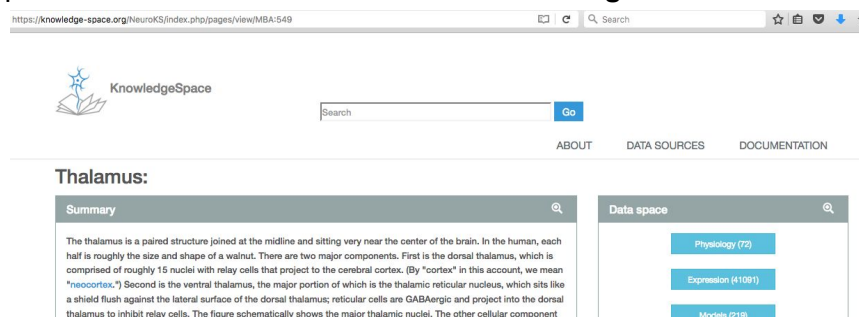
Clicking on one of the links will lead you to a **page with the list of resources**.

Switch dataset

The two select lists in the left pane allow you to **switch between atlases and datasets**. An atlas may have one or more datasets mapped to it.
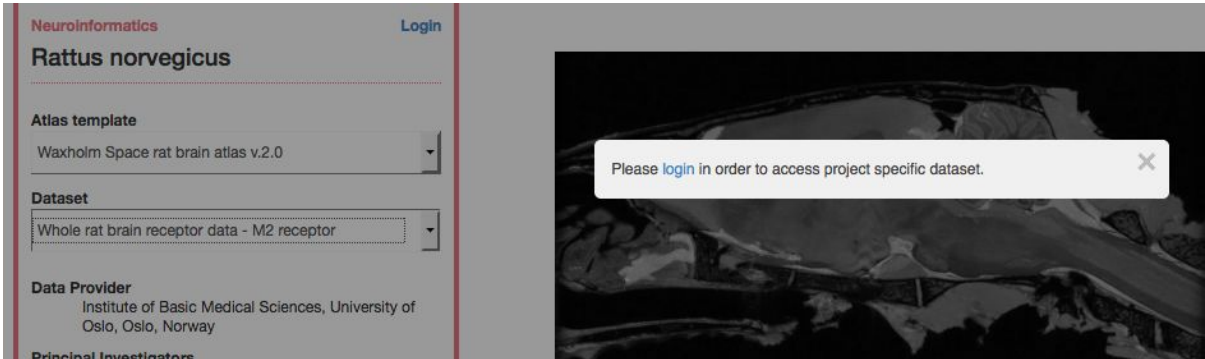
Access to some datasets is **restricted to HBP members**, and you will be prompted to **log in** in order to view them.

Direct link to dataset
You can share a direct link to a given dataset by copy-pasting the URL and sending it to someone else. The URL will be something like
https://nip.humanbrainproject.eu/atlas/#/?dataset=5954630a-ec21-11e4-a5f8-6003088da632

Use case

Christian is interested in finding information related to the Thalamus in the mouse brain.

He browses to the Multiresolution Atlas Viewer and **switch dataset** to the Allen Reference Atlas v3 for the mouse by using the select list.
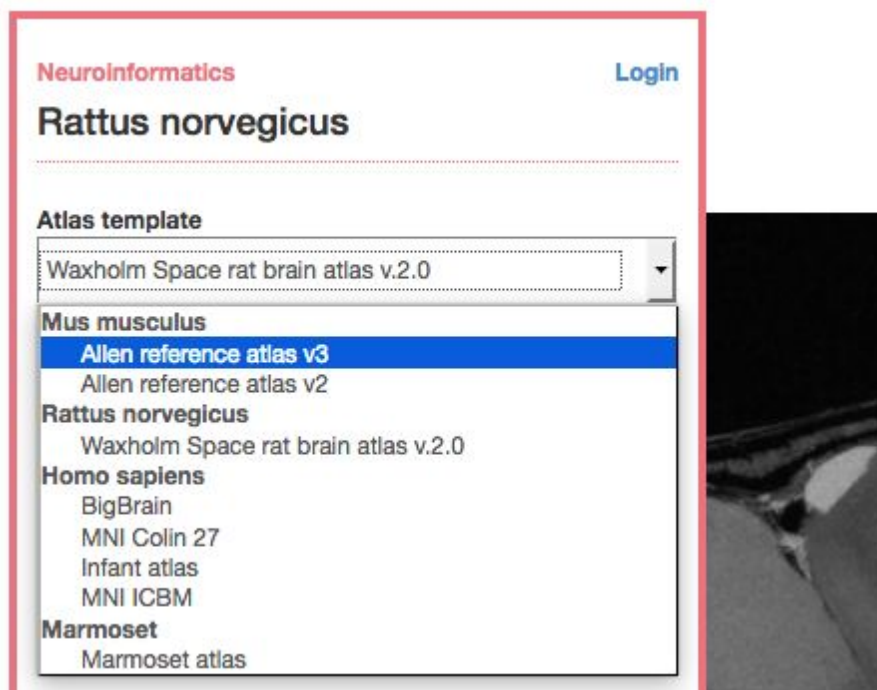
He clicks on the "Draw brain regions" checkbox to **enable the overlaid annotations**.
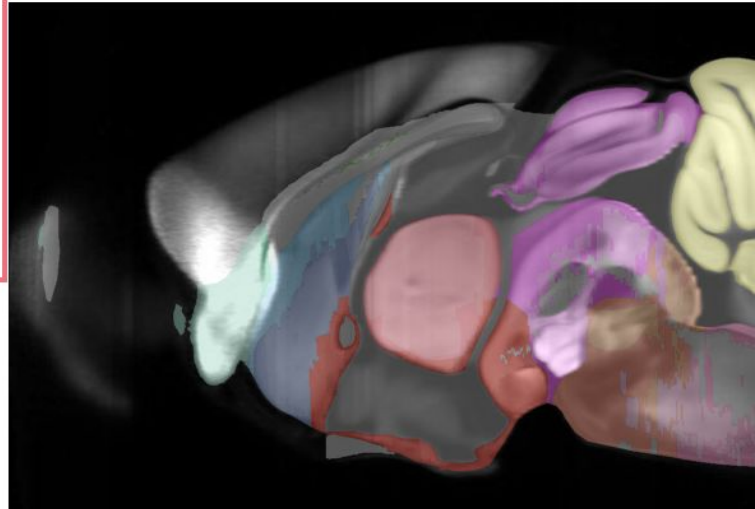
He uses the mouse scroll wheel to **zoom in** a bit to focus on the relevant part of the brain slice, then he puts the mouse cursor over the overlay regions to find the Thalamus, as he can **see the brain region name at the top of the screen**.
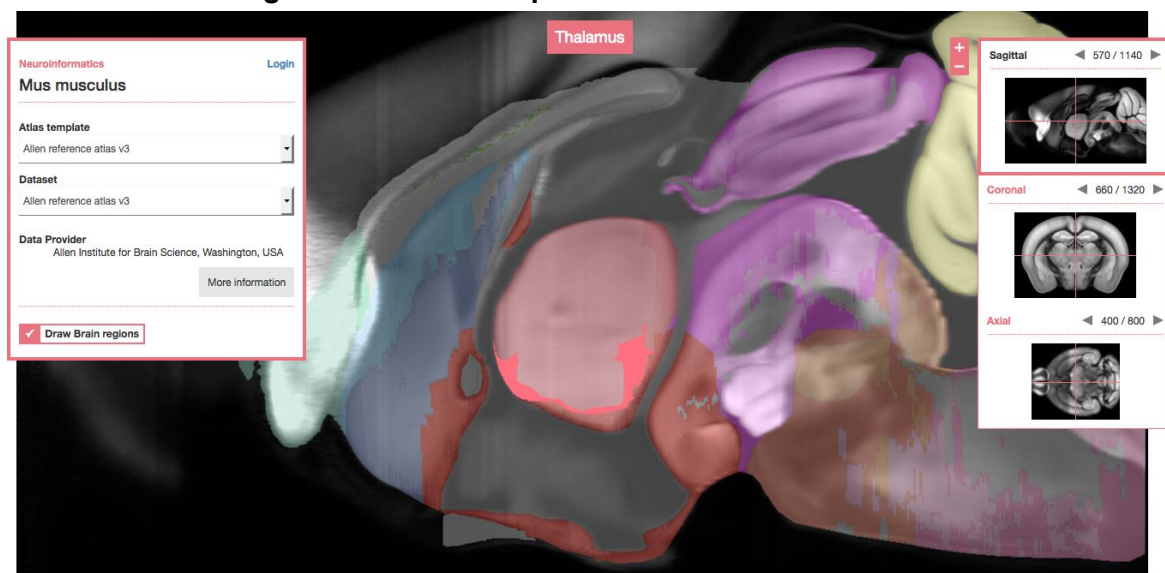
He clicks on the Thalamus region, which **opens a popup with a list of thematic resources** about the brain region.
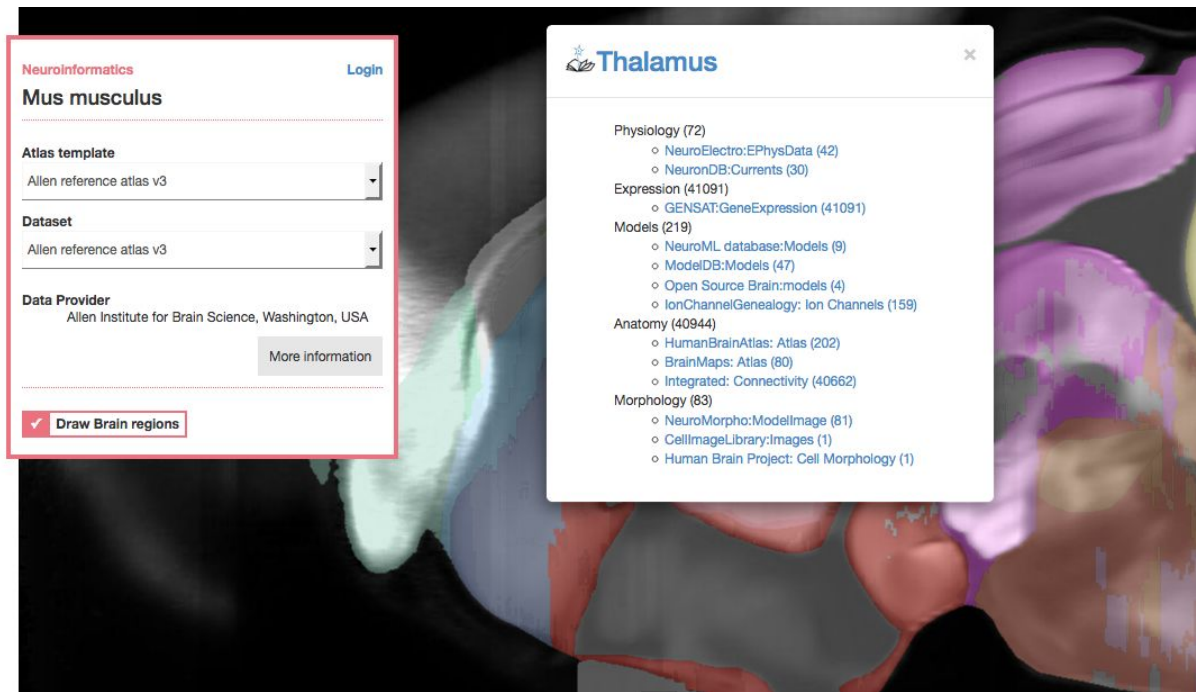
He can see there are 81 morphology results in NeuroMorpho, and clicks on the NeuroMorpho link. He **lands on a KnowledgeSpace page** with the links to all individual NeuroMorpho results for the Thalamus.

Since Christian is mostly interested in the Allen v3 dataset, he **bookmarks a direct link** to it in his browser.

Ontology Viewer

Purpose

The ontology viewer allows to visualize ontologies available in the NIP Platform, the ontology terms (concepts) they define as well as how those terms are related each other through relations. Descriptions of ontologies and ontology terms can be retrieved.

Features

The application consists on the search bar and the tree viewer and provides the following features:

Navigate the taxonomic graph of an ontology
The viewer support both ontologies where the main relationship is subClassOf and those where the main relationship is part of (partonomy).
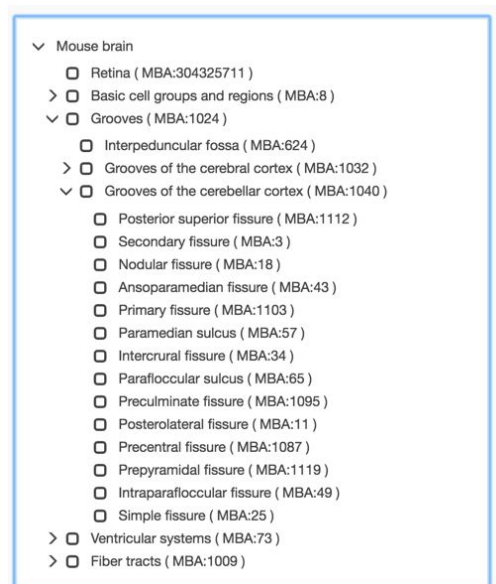
Fig. An example of a partonomy is the [Allen mouse brain atlas v3 ontology](#).

Using the viewer, it's possible to pick different ontologies:
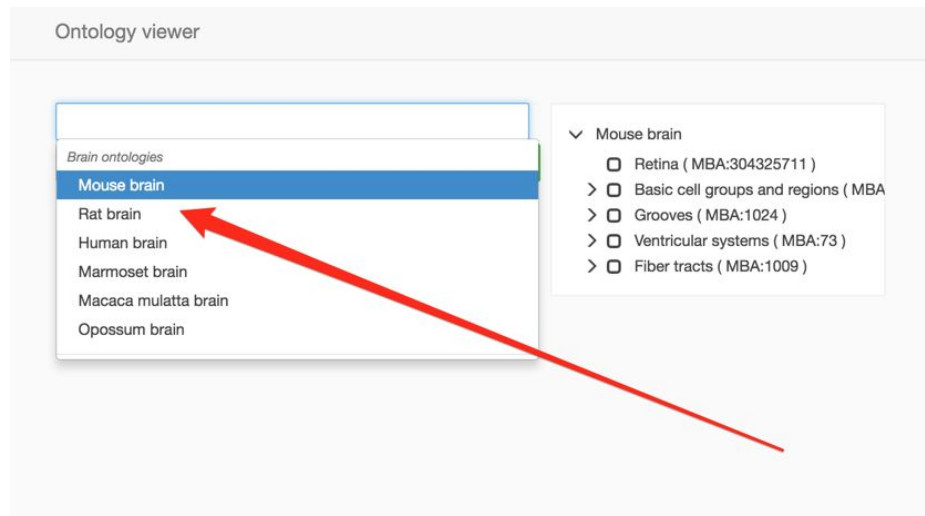
Search for an ontology term

It's possible to search for a term using the search bar. Suggestions of terms gradually appear right below the search bar as the user is typing. The suggestions can be filtered by the picked ontology, as shown in the screenshot below:
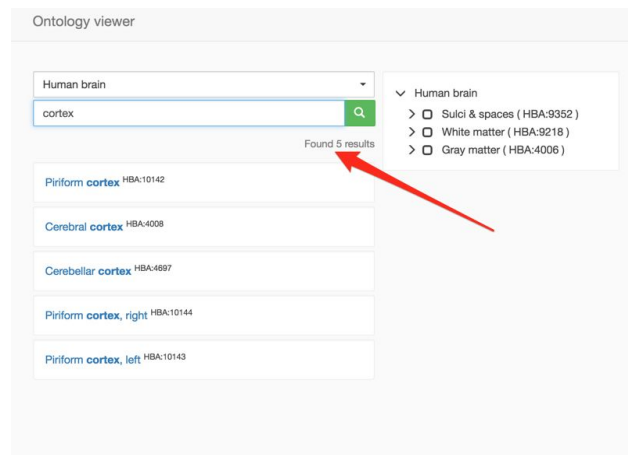
Spelling correction

In case of wrong spelling of an ontology term, corrections are suggested in a 'Did you mean section' right below the search bar:
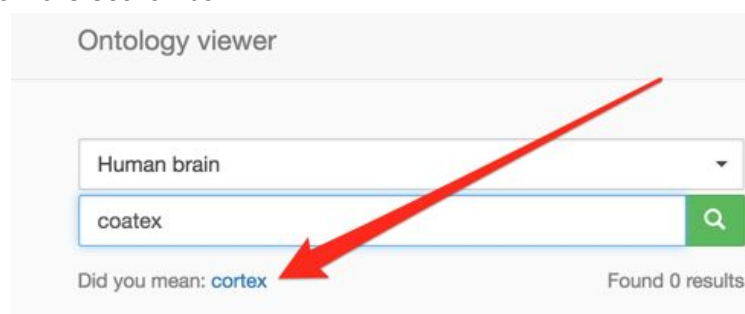
Identify the place of a retrieved term in the ontological structure

From the search results it's possible to click on any term and see its place in the ontological structure: its parents and immediate children are shown:
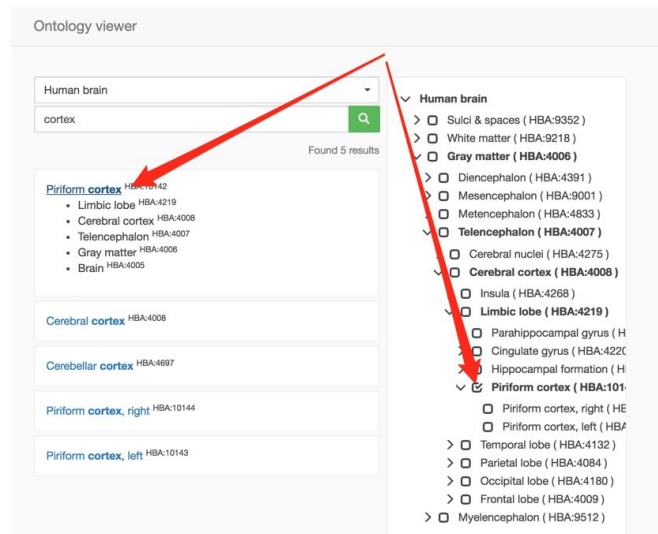
Link to the term and the search results

In order to facilitate the communication, it's possible to share a link to any given ontology or ontological term.

Use case

The main use case of the ontology viewer is during the communications of the data curator and data provider.

- Data provider has the data related to the brain region X.
- He enters the name of the brain region to the search and finds the region.
- He looks at the parents of the region using the partonomic tree view, looks at the description of the term and ensures that it is indeed the region he means
- He then copies the identifier (URI) of the brain region and gives it to the Data curator.
- The data curator proceeds with formalizing the metadata knowing that the ambiguity of the brain regions is resolved.

Registration App

Purpose

The registration app is a web application allowing an authenticated user to submit experimental data (datasets and their corresponding metadata) to the Neuroinformatics Platform (NIP). The main metadata to provide for any data submission are defined in Minimal Information for Neuroscience Datasets (MINDS).

General dataset metadata

- Dataset title: information describing the dataset such as type of data, brain region, cell type, version. A good title is important in order to search and find a dataset using Ksearch. Some examples of dataset titles: 'P40 mouse hippocampus oligodendrocyte single-cell transcriptomics', 'Subcellular signalling kinetic model of the striatal medium spiny neuron (MSNs),
- Dataset description: more detailed information about the data submitted including type of data, brain region, cell type, if the data was annotated with a brain template or any other important information. This description can be used to find the dataset as well,
- publications: PubMed and/or DOI identifiers of the publication that describes the generation of the dataset,
- Production date: the date by which the production of the dataset has been finished.
- License: the license of the dataset,
- Data categories: the broad categories (modalities) of the data, like electrophysiological data or simulation data. It's possible to pick more than one category.

Metadata about the sample
It's possible to fill the following metadata regarding the sample: sex and age of the specimen used for the experiment, list of brain regions, comments.

Contributors
Information about agents that contribute to data generation can be provided along with their roles.

Methods and protocol used to generate the data
The app allows to describe dataset generation protocols and to list the measurement and analytical methods used.

User manual

In order to register the data within the NIP, the following steps should be taken:

Go to the main page of the Registration App

Fig. Main page of the Registration App.

Agreement with the Terms of Service

Read carefully our Terms of Service and accept them

Fig. Terms and Condition page.

Register the Metadata related to the dataset

For a given dataset the metadata would typically record the following
- Specimen: age, sex, species, strain
- Classification properties, such as cell type
- Brain location using the ontological term
- Contributors and their affiliations
- Methods and protocols used to generate the data
- Access to the data and its format.

Fig. The metadata page of the app

"Data categories" and "Methods" fields have "Browse" buttons that will allow to choose the terms from the respective ontologies:

Fig. Ontology visualisation for the Categories ontology

Fill in the contributors information

This information will define acknowledgements as well as contact information for a specific dataset. It consists of the following:

- Organisations involved
- Contributors informations specifically the email of the institution they are affiliated to.

Fig. "Add contributor" modal window.

Save the metadata

Click save button to save the metadata. It will be possible to return to the editing of the metadata later.

Publish Dataset

After the file you uploaded is processed by neuroinformatics system, the Publish button will become active. Clicking it will result of the dataset to be published and the metadata will be fixed.

To be noticed:

- The submitted data is published as-is (ie. not curated).
- The register dataset is final. Once published it's not possible to change it,
- The metadata associated to the dataset can't be modified.

Do not close your browser window until the dataset is completely uploaded.

Follow the NIP registration process

Shortly after submitting your data, on the MyUploads page you can check the status of the submitted dataset.

Fig. Status of the dataset.

For any information, question or help, we suggest to contact the team.

Security

All people that have a Collaboratory account can access the app. To get an access the user should first request a HBP Collaboratory account.

Licenses

During the process of the registration a choice between 2 licenses will be required depending on the commercial potential use of your Dataset.

We strongly recommend to carefully read the information related to the following licenses in our ToS:

- Creative Commons Attribution-ShareAlike 4.0 International (CC BY-SA 4.0)
- Creative Commons Attribution-NonCommercial-ShareAlike 4.0 International (CC BY-NC-SA 4.0)

KnowledgeSpace

Purpose

The KnowledgeSpace is a community encyclopedia linking brain research concepts to data, models, and literature. It provides ontologies as defined by the Neuroscience Information Framework (NIF). The Neuroinformatics platform relies on some of these ontologies to describe the scientific concepts describing the data we integrate in the platform.

Numerous data sources are integrated, such as:
- Neurolex.org

- Allen Brain Institute cell-types

- Blue Brain Project

- Neuromorpho.org

- Neuroelectro.org

- Cell Image Library

- NIF Integrated Connectivity

- Channelpedia.net

- Ion Channel Genealogy

- ModelDB

- OpenSourceBrain

- GenSat

- Pubmed

The KnowledgeSpace develops SciGraph, an ontology service that the Neuroinformatics Platform uses to integrate and make available our ontologies.
Where appropriate, the Neuroinformatics Platform provide deeper integration with the KnowledgeSpace, for instance, when browsing Brain Atlases, a user can search for known datasets related to a given brain parcel.

Programmatic Interfaces

Intended Audience: this part of the documentation is intended mainly at developers wishing to interface with the Neuroinformatics platform through a programmatic interface.

KSearch

Purpose

Ksearch is the search component of the Neuroinformatics Platform (NIP). It is a REST API allowing searching curated datasets using different filters that are mainly taken from MINDS.

Features

Ksearch allows searching datasets shared in NIP. There are five main features:

- Full text search:
  - free text search on all dataset fields: all datasets fields will be searched,
  - field free text search: specific dataset fields can be targeted when search for a term,
- Boolean search:
  - Boolean operator (AND, OR,...) can be specified between the keywords of a text
- Filtering: a set of filters are available to narrow down search results

- Query expansion through term synonyms and specialisation: for example a search for "Rodentia" will be able to retrieve datasets annotated with "Rattus Norvegicus" because "Rattus Norvegicus" is a rodent

- Documents aggregation: Ksearch results can be grouped by data modality, brain regions by other metadata available in MINDS. This feature enables document exploration and faceted navigation.

Details of how the previous Ksearch features are implemented in term of endpoints are described as follow.

Ksearch endpoints

The following endpoints are exposed by Ksearch. As shown in the figure below, only read access (GET http verb) to data is allowed. An interactive documentation of Ksearch API is available here.

datasets Show/Hide | List Operations | Expand Operations

GET	/datasets/filters	List of dataset filters
GET	/datasets/storage/types	List of dataset storage types
GET	/datasets/{id}	Get a dataset by id

search Show/Hide | List Operations | Expand Operations

GET	/search	Search for datasets (the default vertical)
GET	/search/{verticalName}	Search for documents of type the given vertical name: dataset,...
GET	/search/{verticalName}/{filter_field}	Search for documents of type the given vertical name and filtered by the given field

verticals Show/Hide | List Operations | Expand Operations

| GET | /verticals | List of available document types: dataset (the default type), ... |

Verticals

Verticals are the types of documents exposed for search in Ksearch. This means a call to one of the **/search** endpoints will always return documents whose type is one of the verticals. The list of available verticals can be obtained by calling:

```
curl -X GET https://nip.humanbrainproject.eu/api/ksearch/verticals
```

A sample response is:

```
[
  {
    "name": "dataset",
    "schema_path":
"https://schema.humanbrainproject.eu/neuroinformatics/search/search-datase
t-schema-v1.0.json",
    "filters": [
      {
        "name": "species",
        "field": "specimen.species.term.raw_term",
        "description": "Species",
        "type": "String"
      },
      {
        "name": "methods",
        "field": "methods.term.raw_term",
        "description": "Methods",
        "type": "String"
      },
      {
        "name": "protocols",
        "field": "protocols.title.raw_term",
```

```
        "description": "Protocols",
        "type": "String"
      },
      {
        "name": "classifications",
        "field": "classifications.term.raw_term",
        "description": "Cell types",
        "type": "String"
      },
      {
        "name": "data_modalities",
        "field": "data_modalities.term.raw_term",
        "description": "Data Modalities",
        "type": "String"
      },
      {
        "name": "full_name",
        "field": "",
        "description": "Contributing organisations",
        "type": "String"
      },
      {
        "name": "affiliations",
        "field": "contributors.affiliations.raw_affiliations",
        "description": "Contributor's affiliations",
        "type": "String"
      },
      {
        "name": "brain_regions",
        "field": "brain_regions.term.raw_term",
        "description": "Brain Regions",
        "type": "String"
      }
    ]
  }
]
```

For each vertical, the following fields are retrieved:

Field	Description
name	*A vertical name which is a document type: **dataset** for example*
schema_path	*The URI of the schema the vertical instances (the documents) are consistent with*

filters	*Available filters that can be used to narrow down results having the current vertical as type*

The term 'document' will be used below to name Ksearch results.

Response format

A call to a Ksearch endpoint will return search results in json format.

All Ksearch results are wrapped in the following json document ([which is consistent with this json schema](#)):

```
{
  "took" : 26,
  "total" : 2126,
  "max_score" : 1.0,
  "hits" : [ ],
  "aggregations":[]
}
```

Field	Description	Data type	Default
took	*The query execution duration in milliseconds*	*long*	*0.0*
total	*the total number of results*	*integer*	*0*
max_score	*The highest result score*	*float*	*1.0*
hits	*The array of the results*	*array*	*empty*
aggregations	*a list of buckets/facets that group results*	*array*	*empty*

An element of the "hits" array is a result wrapping a document (a dataset for example) that matches the user query:

```
{
    "id" : "05b4691e-ee47-11e4-8074-6003088da632",
    "score" : 1.0,
    "source" : { },
    "schema" : ""
}
```

The corresponding json schema of the previous result is available here.

Field	Description	Data type	Default
id	*The identifier of the result*	*String*	*NA*
score	*A number measuring how much a document matches the user query.*	*float*	*1.0*
source	*The actual document*	*object*	*NA*
schema	*The schema with which the result (in source field) is consistent*	*String*	*empty*

Results Pagination

Large number of datasets can be potentially retrieved from Ksearch when making a call. In that case, it will be useful to have results paginated.

The Ksearch endpoints supporting results pagination are:

When using the above search endpoints, the size of a page and the start point (offset) of the page can be controlled respectively with "size" and "from" parameters:

Name	Description	Data type	Default
from	*the index (within results set) of the first result you want to get*	*integer*	*0*
size	*the total number of results you want to get.*	*integer*	*20*

To go through the results page by page, set the size value to S and start from 0:

- get the S first results
- the **n**th page will start from (**n-1**) x S (**n starting by 2**) while the size stays the same.
- If from+size >= total result set size, then all result pages have been visited.

Filtering syntax
Filtering allows retrieving documents that match exact values for specified fields. It is the base of faceted/aggregated search. Two things are then needed to build a filter query: fields and their corresponding exact values.
Note that only **/search** endpoints allow documents filtering.

The syntax of a filter parameter in Ksearch is as follows:

```
filters={"field_1":["value1_1","value1_2",...],"field_2":["value2_1"]}
```

As an example, let retrieve datasets that fall into "**Single cell morphology reconstruction**" data modality:

```
curl -g -X GET
"https://nip.humanbrainproject.eu/api/ksearch/search?q=*&filters={%22data_
modalities.term.raw_term%22:[%22Single%20cell%20morphology%20reconstructio
n%22]}"
```

Only an **AND** filtering strategy is currently implemented. With the above syntax, it means that **only documents** with value1_1 **and** value1_2 as field_1 values **and** with value2_1 as field_2 value, will be retrieved.

Sorting syntax
Results can be sorted in an ascendant or descending way and by fields using the following syntax:

```
sort={"field_1":"asc","field_2":"desc"}
```

For example, the following query will ordered documents by title:

```
curl -g -X GET
"https://nip.humanbrainproject.eu/api/ksearch/search?q=*&sort={%22title%22
:%22desc%22}"
```

Note that by default Ksearch results are sorted by score.

Field selection
A user can specify which document fields to retrieve when using Ksearch or the fields he want to exclude.

The syntax of field selection is:

```
retrieve={"field_1":["subfield"],"field_2":["subfield"]}"
```

For example, instead of retrieving all dataset fields defined in MINDS, a user can choose to only retrieve dataset id, title and the affiliations of its contributors:

```
curl -g -X GET
"https://nip.humanbrainproject.eu/api/ksearch/search?q=*&retrieve={%22id%2
2:[%22%22],%22title%22:[%22%22],%22contributors%22:[%22affiliations%22]}"
```

Let exclude the field "specimen" of datasets:

```
curl -g -X GET
"https://nip.humanbrainproject.eu/api/ksearch/search?q=*&exclude={%22speci
men%22:[%22%22]}"
```

The "retrieve" and "exclude" parameters can be mixed. In that case, the "exclude" parameter takes precedence over the "retrieve" one: an excluded field will never be retrieved.

Full text search
With the following query, only documents having the keywords rat **AND** morphologies as values of at least one field will be retrieved:

```
curl -X GET
"https://nip.humanbrainproject.eu/api/ksearch/search?q=rat%20morphologies"
```

To consider "rat morphologies" as a phrase and not as two tokens, double quotes can be used:

```
curl -X GET
"https://nip.humanbrainproject.eu/api/ksearch/search?q=%22rat%20morphologi
es%22"
```

So by default, the full text search is a conjunctive boolean query between user keywords. However, the keywords can be searched in specific fields. Let search for documents with "rat" or "morphologies" in their "title":

```
curl -X GET
"https://nip.humanbrainproject.eu/api/ksearch/search?q=title:rat%20OR%20ti
tle:morphologies"
```

The possible boolean operators are: AND, OR and NOT

Aggregation
By default, a call to a Ksearch search endpoint will retrieve a results list (hits) and groups of results which are retrieved under the "aggregations" array.
To disable the aggregations, the parameter "aggreg" can be set to "false":

```
curl -X GET
"https://nip.humanbrainproject.eu/api/ksearch/search?q=*&aggreg=false"
```

To only retrieve aggregations (not the hit list), the "size" parameter can be set to 0:

```
curl -X GET
"https://nip.humanbrainproject.eu/api/ksearch/search?q=*&size=0"
```

Let now see how to use aggregations to narrow down Ksearch results. An aggregation is a json object with at least the following fields (the complete schema is available here):

```
"aggregations" : [ {
      "buckets" : [ {
    "key" : "Untufted pyramidal cell",
    "doc_count" : 49
  }, {
    "key" : "Tufted pyramidal cell towards layer IV",
    "doc_count" : 15
  }, {
    "key" : "Tufted pyramidal cell towards layer I",
    "doc_count" : 17
  }],
  "name" : "Cell Types",
  "field" : "classifications.term.raw_term"
}]
```

Field	Description
name	*The name of the aggregation*

field	The field to use for document filtering (see *filter syntax*)
buckets	The list of document groups: groups of a number of "aggregations[*].buckets[*].doc_count" documents with "aggregations[*].buckets[*].key" value for the field "aggregations[*].field".

The value of aggregations[*].field can be used as filter field and the value of aggregations[*].buckets[*].key can be used as filter value.

How to download a dataset

Dataset metadata can be retrieved by full text search or by id. The metadata of the dataset with id "b9cab473-9f32-4260-9a73-cc7d714ec791" can be obtained using the following call:

```
curl -X GET
"https://nip-dev.humanbrainproject.eu/api/ksearch/datasets/b9cab473-9f32-4
260-9a73-cc7d714ec791"
```

A sample response is:

```
{
  "title" : "Electrophysiology [Action potential dependent sIPSCs from a
3-4 months old C57BL/6J X SJL female mice hippocampus CA1 pyramidal cell
(B1)]",
  "uuid" : "b9cab473-9f32-4260-9a73-cc7d714ec791",
  "data_modalities" : [ {
    "id" : "HBP_DAMO:0000008",
    "term" : "Electrophysiology"
```

```
    } ],
    "specimen" : [ {
      "uuid" : "e0b9fa0f-e217-4cf4-84cc-af82f58e273e",
      "species" : {
        "id" : "obo:NCBITaxon_10090",
        "term" : "Mus musculus"
      },
      "strain" : {
        "id" : "HBP_TAX:0000015",
        "term" : "C57BL/6J X SJL"
      },
      "sex" : "female",
      "age" : "Post-natal 90.0"
    } ],
    "contributors" : [ ... ],
    "representations" : [ {
      "access" : "https://zenodo.org/record/XXX/files/expYYYY.txt",
      "datatype" : {
        "id" : "HBP_DATT:0000077",
        "term" : "application/vnd.ebri.traces.txt;version=0"
      },
      "storagetype" : {
        "id" : "HBP_STO:0000007",
        "term" : "Zenodo",
        "term_suggest" : {
          "output" : "Zenodo [null]",
          "input" : [ "Zenodo" ]
        }
      },
      "uuid" : "0a588da8-8cde-44af-abed-eb88790f7fc6"
    } ],
    "protocols" : [...],
    "classifications" : [ {
      "id" : "HBP_CELL:0000145",
      "term" : "Hippocampus CA1 pyramidal cell"
    } ],
    "brain_regions" : [ {
      "id" : "MBA:382",
      "term" : "Field CA1"
    } ]
}
```

The "representations" field of the above dataset holds the necessary download information:

```
curl -g -X GET
"https://nip.humanbrainproject.eu/api/ksearch/datasets/b9cab473-9f32-4260-
9a73-cc7d714ec791?retrieve={%22representations%22:[%22%22]}}"
```

A sample response is:

```
{
  "representations" : [ {
    "access" : "https://zenodo.org/record/XXX/files/expYYYY.txt",
    "datatype" : {
      "id" : "HBP_DATT:0000077",
      "term" : "application/vnd.ebri.traces.txt;version=0"
    },
    "storagetype" : {
      "id" : "HBP_STO:0000007",
      "term" : "Zenodo"
    },
    "uuid" : "0a588da8-8cde-44af-abed-eb88790f7fc6"
  } ]
}
```

For each dataset, the **'representations'** array holds the following fields:

Field	Description
storagetype	The storage where the raw registered data are stored.
access	An id or a URL that can be used (with the storage type) to download the data: • If storagetype.term="Zenodo" then "access" is the url of the raw data (access="https://zenodo.org/record/XXX/files/expYYYY.txt" in the example above) • If storagetype.term="HBP Document Service" then the value of "access" is a UUID to be used with HBP internal storage (not available from outside)
datatype	The type of data: "Neurolucida ASC" for example

The list of available storage types can be retrieved from Ksearch using the following call:

```
curl -X GET
"https://nip.humanbrainproject.eu/api/ksearch/datasets/storage/types"
```

A sample response is:

```
[ {
  "description" : "Zenodo builds and operates a service that enables
researchers to share and preserve research results.",
  "curie" : "HBP_STO:0000007",
  "name" : "Zenodo"
}, {
  "description" : "Repository maintained by Human Brain Project.",
  "curie" : "HBP_STO:0000008",
  "name" : "HBP Document service"
} ]
```

Scigraph can be used to see more details about the above storage type ontology terms.

Demo

A demo of the Ksearch API is available here.

Scigraph: a graph-based ontology service

Purpose

Scigraph is the Neuroinformatics platform (NIP) ontology service and is [implemented](#) as a REST API. As such, it provides access to neuroscience related ontologies (brain regions, cell types, species, measurement methods,...) .

As a REST API, Scigraph is best suited for programmatic usage and can be involved in most data integration pipelines whenever ontology data access is needed. There is a [web-based client](#) available for a more user friendly view or browse of ontologies available in the NIP platform.

It is not possible to use scigraph to import/load any ontologies into the NIP platform. To achieve that, please see the [ontology page in the curation section](#) or contact data.nip@humanbrainproject.eu.

Features

Scigraph provides read access to the ontologies used in the NIP platform. To simplify, the following entity types can be retrieved from scigraph:

- ontology terms: in Allen human brain atlas v2 ontology, "gray matter" with http://api.brain-map.org/api/v2/data/Structure/4006 as identifier is an ontology term.
- properties/attributes: an ontology term can have properties or attributes that clarifies its meaning.
- relations: ontology terms are linked by the mean of relations.

All the previous ontology elements will be referred to as ontology entities below.

Using Scigraph, a client can:
  A. Get the list of available ontologies
  B. Get the list of ontology entities that are defined in a specific ontology
  C. Get a specific ontology entity along with it's properties or attributes:
      ○ Labels
      ○ definitions
      ○ synonyms
      ○ acronyms
      ○ abbreviations
  D. Traverse the ontology graph: retrieve terms that in relation with a specific ontology term.
  E. Search for ontology entities by its properties
  F. Get ontology entity suggestions from a text query
  G. Autocomplete a text query (useful to implement a did you mean functionality)

Ontology entities are referred to with their identifiers in Scigraph. Because those identifiers can take different forms and thus be confusing, the next section will introduce them.

Ontology entity identifiers in Scigraph

An ontology as well as an ontology entity has a URI as identifier. For example, the URI of the Allen human brain atlas ontology (as integrated in NIP) is http://api.brain-map.org/api/v2/data/Structure, while the URI of the specific term "gray matter" is http://api.brain-map.org/api/v2/data/Structure/4006. The previous two URIs can have a short form which is called prefix (a stable string) for the ontology and CURIE for the ontology entities. Let take again the previous example. The prefix name of (the short form of) "http://api.brain-map.org/api/v2/data/Structure " can be 'HBA' while the curie of the term "grey matter" is 'HBA:4006'. Given the curie 'HBA:4006', 'HBA' is the prefix name and '4006' is the fragment.

Scigraph REST API endpoints

An interactive documentation of the Scigraph API is available here as well as a wiki page with more details. The next points describe how Scigraph endpoints can be used to benefit from the previous features in the context of NIP.

Scigraph REST API data formats

All Scigraph responses are in json format as described here.

Vocabulary endpoint

An overview of the vocabulary endpoints:

Fig. Scigraph vocabulary endpoints

- list available ontology prefix names useful as filter to narrow down ontology entities results (feature A):

```
curl -X GET
"https://nip.humanbrainproject.eu/api/scigraph/vocabulary/prefixes"
```

A sample response is:

```
{
  "list": [
    "MESH",
    "HBP_REC",
    "obo",
    "efo",
    "nifstd",
    "MBA",
    "HBP_ACT",
    "HBP_CELL",
    "HBP_DAMO",
    "HBP_DATT",
    "HBP_HBA",
    "HBA",
    "HBP_ROLE",
    "HBP_SCL",
    "HBP_SEX",
    "HBP_STO",
    "HBP_LICENSE",
    "cc",
    "HBP_TAX",
    "HBP_MEM",
    "HBP_DTAT",
    "JHBA",
    "HBP_WHS_SD",
    "HBP_BATT"
  ]
}
```

Only ontology prefix names are obtained from the API by the previous GET call.

- Get all entities defined in a given ontology identified by it's prefix name (feature B)

Let retrieve all entities defined in HBA (Allen human brain atlas ontology v2):

```
curl -X GET
"https://nip.humanbrainproject.eu/api/scigraph/vocabulary/search/*?prefix=
HBA"
```

A sample response is:

```
{
  "concepts": [
    {
      "uri": "http://api.brain-map.org/api/v2/data/4006",
      "labels": [
```

```
      "gray matter"
    ],
    "fragment": "4006",
    "curie": "HBA:4006",
    "synonyms": [
      "GM"
    ],
    "acronyms": [],
    "abbreviations": [],
    "deprecated": false,
    "definitions": []
  },
    …
}
```

For each ontology entity retrieved from the vocabulary endpoints, the following fields are available:

Field	Description
URI	The identifier of the ontology entity.
labels	An array of the ontology entity names
fragment	The last part of the URI after the last separator character (mainly after / or #)
curie	The short form of the ontology entity URI
synonyms	An array of the ontology entity synonyms
acronyms	An array of the ontology entity acronyms
abbreviations	An array of the ontology entity abbreviations
deprecated	A flag to indicate whether the ontology entity is deprecated (true) or not (false)
definitions	An array of the ontology entity definitions

- Search for a specific ontology entity (feature E):
  - by id

The entity identifier can be either a curie or a fragment. Let search for the entity with the curie HBA:4006:

```
curl -X GET
"https://nip.humanbrainproject.eu/api/scigraph/vocabulary/id/HBA:4006"
```

The response is:

```
{
  "concepts": [
    {
      "uri": "http://api.brain-map.org/api/v2/data/4006",
      "labels": [
        "gray matter"
      ],
      "fragment": "4006",
      "curie": "HBA:4006",
      "synonyms": [
        "GM"
      ],
      "acronyms": [],
      "abbreviations": [],
      "deprecated": false,
      "definitions": []
    }
  ]
}
```

○ by labels: let search for "gray matter":

```
curl -X GET
"https://nip.humanbrainproject.eu/api/scigraph/vocabulary/term/gray
matter"
```

When search for a multi-token term ("gray matter" for example), ontology entities that match an individual token ("gray" or "matter") will be retrieved. There is thus no guarantee to only retrieve one result with the previous query.

Also a targeted ontology prefix name can be specified when searching by label for any ontology entity. In such case, only entities defined in the specified ontology will be retrieved.

```
curl -X GET
"https://nip.humanbrainproject.eu/api/scigraph/vocabulary/term/gray
matter?prefix=HBA"
```

○ by synonyms: search by synonyms can enable by setting the parameter "searchSynonyms" to true:

```
curl -X GET
"https://nip.humanbrainproject.eu/api/scigraph/vocabulary/term/gray
matter?searchSynonyms=true"
```

- suggest ontology entity by label (useful to implement did you mean feature and spell checking features):

```
curl -X GET
"https://nip.humanbrainproject.eu/api/scigraph/vocabulary/suggestions/grey
mtter?limit=1"
```

A sample response is:

```
{
  "list": [
    "gray matter"
  ]
}
```

- autocomplete query (feature G):

```
curl -X GET
"https://nip.humanbrainproject.eu/api/scigraph/vocabulary/autocomplete/inf
erior occipital?limit=1
```

A sample response is:

```
{
  "list": [
    {
      "completion": "gray matter",
      "type": "label",
      "concept": {
        "uri": "http://api.brain-map.org/api/v2/data/4006",
        "labels": [
          "gray matter"
        ],
        "fragment": "4006",
        "curie": "HBA:4006",
        "categories": [],
        "synonyms": [
          "GM"
        ],
         "acronyms": [],
        "abbreviations": [],
        "deprecated": false
      }
    }
  ]
}
```

The vocabulary endpoints doesn't allow to navigate between ontology entities. For example, it's not possible to know which brain parcels "gray matter" is sub-region of. The graph endpoints described in the following paragraph can answer to that question.

Graph endpoint

An overview of the graph endpoints:

Fig. Scigraph graph endpoints

It allows to:

- get a specific ontology entity by curie or fragment (feature C)

```
curl -X GET "https://nip.humanbrainproject.eu/api/scigraph/graph/HBA:4006"
```

A sample response is:

```
{
  "nodes": [
    {
      "id": "HBA:4006",
      "lbl": "gray matter",
      "meta": {
        "fragment": [
          "4006"
        ],
        "synonym": [
          "GM"
        ],
        "types": [
          "Class"
        ],
        "http://www.w3.org/2000/01/rdf-schema#label": [
          "gray matter"
        ],
        "http://www.FIXME.org/nsupper#synonym": [
          "GM"
        ]
      }
    }
```

```
  ],
  "edges": []
}
```

Note the vocabulary switch between vocabulary endpoints and graph endpoints responses. In vocabulary endpoints, "**concepts**" is used as container of retrieved entities while "**nodes**" and "**edges**" are used in graph endpoints. The navigation between ontology entities is done by following edges.

- get the available relationship types between ontology entities:

```
curl -X GET
"https://nip.humanbrainproject.eu/api/scigraph/graph/relationship_types"
```

A sample response is:

```
[
  "equivalentClass",
  "filler",
  "has_domain_aspect",
  "has_rank",
  "isDefinedBy",
  "is_smaller_than",
  "legalcode",
  "part_of",
  "property",
  "seeAlso",
  "subClassOf"
]
```

- get the ontology terms that are in relation with (in the neighbor of) a specific one identified by an id (curie or fragment) and through a specific relation (part_of is used in the example below) taken from the above relationship types (feature D):

```
curl -X GET
"https://nip.humanbrainproject.eu/api/scigraph/graph/neighbors/HBA:4006?de
pth=1&relationshipType=part_of&direction=OUTGOING"
```

The direction of the relation can be specified through the "direction" parameter.The possible values are "OUTGOING", "INCOMING" AND "BOTH".

A sample response is:

```
{
  "nodes": [
    …,
    {
      "id": "HBA:4005",
      "lbl": "brain",
      ...
    },
    {
      "id": "HBA:4006",
      "lbl": "gray matter",
      ...
    }
  ],
  "edges": [
    {
      "sub": "HBA:4006",
      "obj": "HBA:4005",
      "pred": "part_of",
      "meta": {}
    },
    …
  ]
}
```

The 'edges' array in the graph endpoints responses has the following fields:

Field	Description
sub (for subject)	is the curie or URI of entity under interest. HBA:4006 in the example above.
obj (for object)	is the curie or URI of a neighbor of the term referenced in sub
pred (for predicate)	a relation (curie, uri or fragment) linking sub and obj

Navigation through ontology terms is possible by getting the neighbors of the entity having the value of "obj" as id.
Use case

An iPython notebook demonstration is available here.

Voxel Brain

Purpose

This REST service provides access to volumetric brain atlas and their annotation layers in the form of voxels.

Endpoints

HTTP Method	Endpoint	Usage
GET	https://nip.humanbrainproject.eu/api/analytics/atlas/metadata	List metadata available for a given atlas. It provides a description for each metadata item.
GET	https://nip.humanbrainproject.eu/api/analytics/atlas/filters	List all parameters users can leverage to filter when looking for atlases.
GET	https://nip.humanbrainproject.eu/api/analytics/atlas/releases	List all available atlases, filters can be specified to restrict results. Note that the 'id' field for each atlas is subsequently used to refer to a given atlas. We show it as [ID] in subsequent API calls
GET	https://nip.humanbrainproject.eu/api/analytics/atlas/releases/[ID]	Lookup an atlas by its identifier. **Parameters** [ID] denotes the atlas we search in.
GET	https://nip.humanbrainproject.eu/api/analytics/atlas/releases/[ID]/data	Lists all annotation layers available for that atlas. Each layer is an independent data file in NRRD format. **Parameters** [ID] denotes the atlas we search in.
GET	https://nip.humanbrainproject.eu/api/analytics/atlas/releases/[ID]/filters/brain_region/search/[TERM]	Search brain regions by name in a given atlas parcellation scheme. The given query can match either the name or acronym of ontological terms. **Parameters** [ID] denotes the atlas we search in. [TERM] denotes the ontology term name or acronym (not case sensitive, substring matching).
GET	http://nip.humanbrainproject.eu/api/analytics/atlas/download?uri=[LAYER URI]	Typically, this API call is not built by the developer but given by the output of the API call: /api/analytics/atlas/releases/[ID]/data

		Download an Annotation Layer (referred to by URI) associated to a given Atlas (referred to by identifier). The data format returned is [NRRD](#). **Parameters** [LAYER URI] is the uri of the NRRD representation of the layer.

An interactive version of this endpoint documentation is available [here](#).

Use Case Illustration: Build a virtual brain

Description
To build a virtual brain for the purpose of running a software simulation,
a user needs to get access to data positioned in a brain template in the form of voxels.
The data required for this exercise need to be aligned in a brain template, e.g. the Allen mouse CCFv2 with voxel size of 25 micron.
The following information need to be made available for each voxels in the accessed data:
    a. brain region id
    b. Boolean value or probabilistic distribution indicating if cells are located in a given voxel
    c. Intensity values of given image modalities
The template is annotated using brain regions. These brain regions are represented in a hierarchical structure, i.e. a region can have sub-regions.This brain region hierarchy is specific to the given brain template.
The user needs the ability to filter target voxels by a given brain region.
If the given brain region has sub-regions, all voxels annotated with either the parent regions or sub-regions should be selected.
The user should have the ability to search for a brain region by its name or acronym (non case sensitive search)
For a given brain region id, the user should be able to retrieve the hierarchy of its children.

How to use the API to execute this use case

1. The user looks up for all existing releases available

API call:

```
GET /atlas/releases
```

returns

```
[
  {
    "id": "6C4F0E89-6D2A-46D4-B4D5-B2BE4840F87D",
    "name": "Mouse 25 micron CCFv2",
    "species": "mouse",
```

```
      "resolution": "25",
      "template_source": "Allen mouse brain CCFv2",
      "hbp_release": "2016-01-12",
      "data_types": [
        "nissl",
        "gray_levels",
        "brain_regions"
      ]
    },
    {
      "id": "1192CEAC-17C5-4A74-B88C-48065C048678",
      "name": "Mouse 25 micron CCFv3",
      "species": "mouse",
      "resolution": "25",
      "template_source": "Allen mouse brain CCFv3",
      "hbp_release": "2016-01-12",
      "data_types": [
        "nissl",
        "gray_levels",
        "brain_regions"
      ]
    }
  ]
```

The user selects the above release and keep notes of its id:
6C4F0E89-6D2A-46D4-B4D5-B2BE4840F87D

2. The user lookup filters available in the system

API call:

```
GET /atlas/filters
```

returns

```
[
  {
    "filter": "data_type",
    "description": "The data modality",
    "type": "string",
    "values": [
      "gray_levels",
      "brain_regions"
    ]
  },
  {
    "filter": "brain_region",
    "description": "The region of the brain a voxel is located into",
    "type": "string",
    "values": [
      "cortex",
      "hypocampus"
    ]
```

```
    }
]
```

Here we can see that there are two filters available:
- data_type
- brain_region

3. The user searches in this release for brain regions by name: 'hippocamp'

API call:

```
GET
/atlas/releases/6C4F0E89-6D2A-46D4-B4D5-B2BE4840F87D/filters/brain_region/s
earch/hippocamp
```

returns:

```
[
  [
    "1089",
    "Hippocampal formation",
    "HPF"
  ],
  [
    "1080",
    "Hippocampal region",
    "HIP"
  ],
  [
    "822",
    "Retrohippocampal region",
    "RHP"
  ],
  [
    "333",
    "Septohippocampal nucleus",
    "SH"
  ],
  [
    "618",
    "hippocampal commissures",
    "hc"
  ],
  [
    "443",
    "dorsal hippocampal commissure",
    "dhc"
  ],
  [
    "449",
    "ventral hippocampal commissure",
    "vhc"
```

```
    ],
    [
      "1063",
      "hippocampal fissure",
      "hf"
    ]
]
```

The user inspects the returned list above, and select the term 'hippocampal region' for which the ID is **1080**.

4. the user now searches for all children terms of this term by ID

API call:

```
GET
/atlas/releases/6C4F0E89-6D2A-46D4-B4D5-B2BE4840F87D/filters/brain_region/1
080
```

returns

```
{
  "id": 1080,
  "acronym": "HIP",
  "name": "Hippocampal region",
  "children": [
    {
      "id": 375,
      "acronym": "CA",
      "name": "Ammon's horn",
      "children": [
        {
          "id": 382,
          "acronym": "CA1",
          "name": "Field CA1",
          "children": [
            {
              "id": 391,
              "acronym": "CA1slm",
              "name": "Field CA1, stratum lacunosum-moleculare"
            },
            {
              "id": 399,
              "acronym": "CA1so",
              "name": "Field CA1, stratum oriens"
            },
            {
              "id": 407,
              "acronym": "CA1sp",
              "name": "Field CA1, pyramidal layer"
            },
            {
              "id": 415,
              "acronym": "CA1sr",
```

```json
              "name": "Field CA1, stratum radiatum"
            }
          ]
        },
        {
          "id": 423,
          "acronym": "CA2",
          "name": "Field CA2",
          "children": [
            {
              "id": 431,
              "acronym": "CA2slm",
              "name": "Field CA2, stratum lacunosum-moleculare"
            },
            {
              "id": 438,
              "acronym": "CA2so",
              "name": "Field CA2, stratum oriens"
            },
            {
              "id": 446,
              "acronym": "CA2sp",
              "name": "Field CA2, pyramidal layer"
            },
            {
              "id": 454,
              "acronym": "CA2sr",
              "name": "Field CA2, stratum radiatum"
            }
          ]
        },
        {
          "id": 463,
          "acronym": "CA3",
          "name": "Field CA3",
          "children": [
            {
              "id": 471,
              "acronym": "CA3slm",
              "name": "Field CA3, stratum lacunosum-moleculare"
            },
            {
              "id": 479,
              "acronym": "CA3slu",
              "name": "Field CA3, stratum lucidum"
            },
            {
              "id": 486,
              "acronym": "CA3so",
              "name": "Field CA3, stratum oriens"
            },
            {
              "id": 495,
              "acronym": "CA3sp",
              "name": "Field CA3, pyramidal layer"
            },
            {
```

```json
              "id": 504,
              "acronym": "CA3sr",
              "name": "Field CA3, stratum radiatum"
            }
          ]
        }
      ]
    },
    {
      "id": 726,
      "acronym": "DG",
      "name": "Dentate gyrus",
      "children": [
        {
          "id": 10703,
          "acronym": "DG-mo",
          "name": "Dentate gyrus, molecular layer"
        },
        {
          "id": 10704,
          "acronym": "DG-po",
          "name": "Dentate gyrus, polymorph layer"
        },
        {
          "id": 632,
          "acronym": "DG-sg",
          "name": "Dentate gyrus, granule cell layer"
        },
        {
          "id": 10702,
          "acronym": "DG-sgz",
          "name": "Dentate gyrus, subgranular zone"
        },
        {
          "id": 734,
          "acronym": "DGcr",
          "name": "Dentate gyrus crest",
          "children": [
            {
              "id": 742,
              "acronym": "DGcr-mo",
              "name": "Dentate gyrus crest, molecular layer"
            },
            {
              "id": 751,
              "acronym": "DGcr-po",
              "name": "Dentate gyrus crest, polymorph layer"
            },
            {
              "id": 758,
              "acronym": "DGcr-sg",
              "name": "Dentate gyrus crest, granule cell layer"
            }
          ]
        },
        {
          "id": 766,
```

```json
        "acronym": "DGlb",
        "name": "Dentate gyrus lateral blade",
        "children": [
          {
            "id": 775,
            "acronym": "DGlb-mo",
            "name": "Dentate gyrus lateral blade, molecular layer"
          },
          {
            "id": 782,
            "acronym": "DGlb-po",
            "name": "Dentate gyrus lateral blade, polymorph layer"
          },
          {
            "id": 790,
            "acronym": "DGlb-sg",
            "name": "Dentate gyrus lateral blade, granule cell layer"
          }
        ]
      },
      {
        "id": 799,
        "acronym": "DGmb",
        "name": "Dentate gyrus medial blade",
        "children": [
          {
            "id": 807,
            "acronym": "DGmb-mo",
            "name": "Dentate gyrus medial blade, molecular layer"
          },
          {
            "id": 815,
            "acronym": "DGmb-po",
            "name": "Dentate gyrus medial blade, polymorph layer"
          },
          {
            "id": 823,
            "acronym": "DGmb-sg",
            "name": "Dentate gyrus medial blade, granule cell layer"
          }
        ]
      }
    ]
  },
  {
    "id": 982,
    "acronym": "FC",
    "name": "Fasciola cinerea"
  },
  {
    "id": 19,
    "acronym": "IG",
    "name": "Induseum griseum"
  }
  ]
}
```

The user now decides to go ahead and to collect data for this region.

5. The user introspect the release to find out which data_types are available

API call:

```
GET /atlas/releases/6C4F0E89-6D2A-46D4-B4D5-B2BE4840F87D/data
```

returns

```
[
  {
    "url":
"http://nip-dev.humanbrainproject.eu:80/api/analytics/atlas/download?uri=6C
4F0E89-6D2A-46D4-B4D5-B2BE4840F87D/brain_regions/brain_regions.nrrd",
    "atlas_id": "6C4F0E89-6D2A-46D4-B4D5-B2BE4840F87D",
    "data_type": "brain_regions"
  },
  {
    "url":
"http://nip-dev.humanbrainproject.eu:80/api/analytics/atlas/download?uri=6C
4F0E89-6D2A-46D4-B4D5-B2BE4840F87D/gray_levels/gray_levels.nrrd",
    "atlas_id": "6C4F0E89-6D2A-46D4-B4D5-B2BE4840F87D",
    "data_type": "gray_levels"
  },
  {
    "url":
"http://nip-dev.humanbrainproject.eu:80/api/analytics/atlas/download?uri=6C
4F0E89-6D2A-46D4-B4D5-B2BE4840F87D/nissl/nissl.nrrd",
    "atlas_id": "6C4F0E89-6D2A-46D4-B4D5-B2BE4840F87D",
    "data_type": "nissl"
  }
]
```

Here we can see that for the selected release, there are 3 data_types available:

1. brain_regions: integer values that match the identifiers of the corresponding ontology terms
2. gray_levels: integer value of the image data of the averaged mouse template
3. nissl: numerical values of the nissl staining

The user notes that at this stage, all data_types are distributed using the NRRD data format. This is likely to change in the future in favour of an Avro based format.

6. Now the user requests the same data_types but this time filtered by the chosen region 1080 (i.e. hippocampal region)

API call:

```
GET
/atlas/releases/6C4F0E89-6D2A-46D4-B4D5-B2BE4840F87D/data?brain_region=1080
```

returns

```
[
  {
    "url":
"http://nip-dev.humanbrainproject.eu:80/api/analytics/atlas/download?uri=6C
4F0E89-6D2A-46D4-B4D5-B2BE4840F87D/brain_regions/brain_region/1080.nrrd",
    "atlas_id": "1192CEAC-17C5-4A74-B88C-48065C048678",
    "data_type": "brain_regions"
  },
  {
    "url":
"http://nip-dev.humanbrainproject.eu:80/api/analytics/atlas/download?uri=6C
4F0E89-6D2A-46D4-B4D5-B2BE4840F87D/gray_levels/brain_region/1080.nrrd",
    "atlas_id": "1192CEAC-17C5-4A74-B88C-48065C048678",
    "data_type": "gray_levels"
  },
  {
    "url":
"http://nip-dev.humanbrainproject.eu:80/api/analytics/atlas/download?uri=6C
4F0E89-6D2A-46D4-B4D5-B2BE4840F87D/nissl/brain_region/1080.nrrd",
    "atlas_id": "1192CEAC-17C5-4A74-B88C-48065C048678",
    "data_type": "nissl"
  }
]
```

The user notes that the same data_types are returned. However the content of these NRRD files are limited to the voxels that are annotated with the requested brain region (i.e. **1080**) or any of its children.

Now the user only needs to use the URL provided in each data_type to download the corresponding NRRD file.

Image Service

Purpose

Image Service provides access to image tiles through REST API operation request. Image tiles are created at different zoom levels for sagittal, coronal and/or axial orientations, in order to display two dimensional large images (captured from brain slices) of brain imaging dataset (volumetric) through browser. These tiled images become part of image pyramid. All tiles of each orientations are written into one single file as stacks in BBIC format.
Image Service also provides meta information about the brain image stack file structure and content through operation request.
The client application that consumes Image Service is currently [Multiresolution Atlas Viewer](#).

Features

We could get a single tile at certain zoom level, meta information about the image stack, and a tile after running minimum or maximum intensity projection of several slices like 64. These query requests are explained below:

Meta information query
<image-service>/bbic?mode=meta&fname=<fname>

Tile query
<image-service>/bbic?mode=ims&fname=<fname>&prog='TILE 0'stack=<n>&level=k(&slice=<m>|&slice_orig_id=<id>)&x=<x>&y=<y>&proj=<proj>&proj_d=<d>&extend_tiles=<e>

This query returns a tile image specified by BBIC filename <fname>, stack number <n>, slice number <m< or slice <id>, detail level <k>, "x" position <x>, "y" position <y> and optional parameters:
<proj> specifying projection type, <proj_d> specifying projection depth and <extend_tiles> specifying handling of last row/column/diagonal tiles, which are usually smaller than declared <tile_size>.

In the following figure, we could see image tiles at different zoom levels.
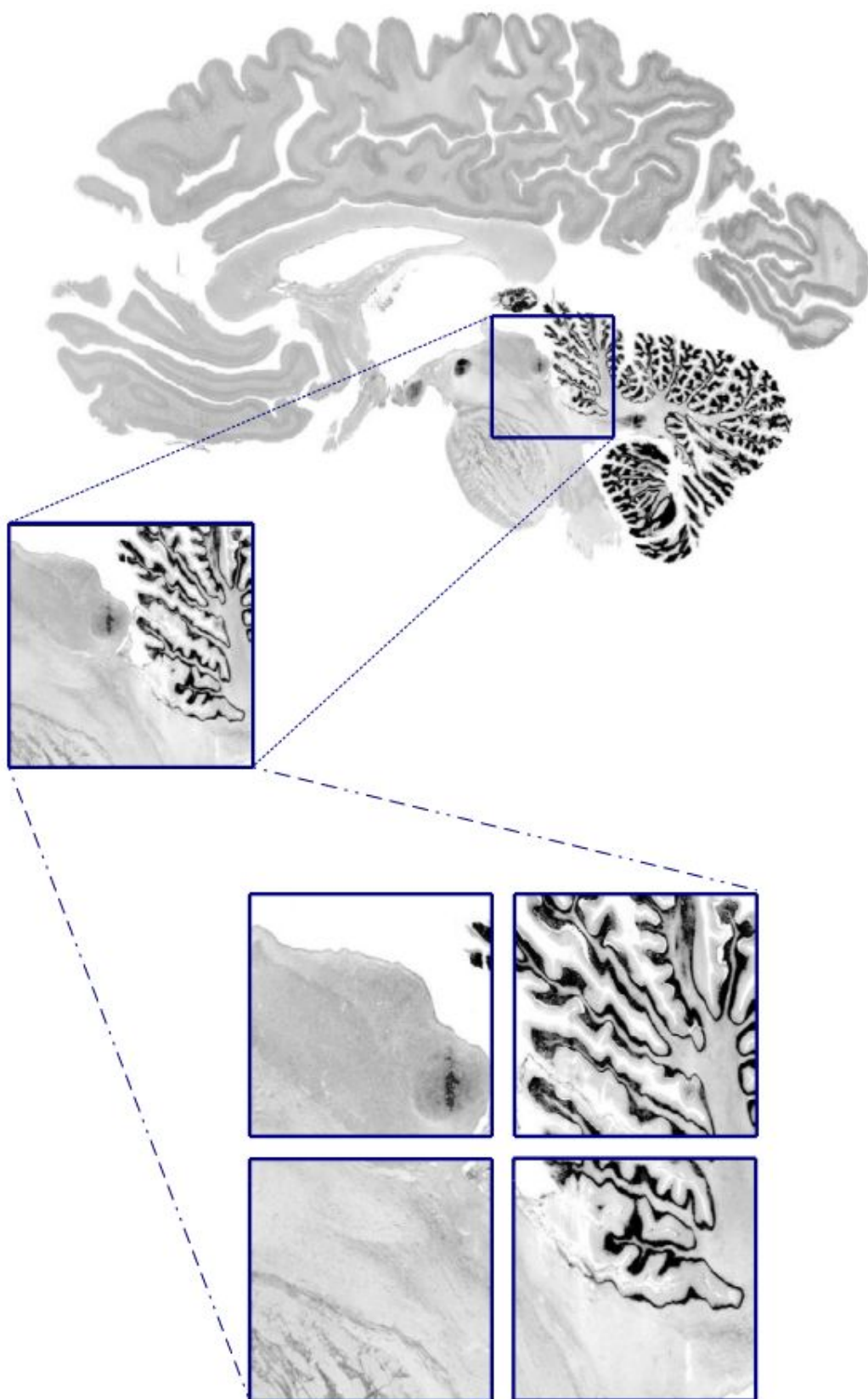
Fig. Sagittal slice of BigBrain dataset were divided into image tiles in different zoom levels.

Endpoints

HTTP Method	Endpoint	Usage	Returns
GET	https://nip.humanbrainproject.eu/api/image-service/image/v0/api/bbic?fname=/gpfs/bbp.cscs.ch/project/proj39/template/human/bigbrain/release2015/bbic/sections/bigbrain.h5&mode=ims&prog=TILE 0 2 2 3285 4 3 none 10 1	Get a tile of BigBrain without any image manipulation	Image tile (original)
GET	https://nip.humanbrainproject.eu/api/image-service/image/v0/api/bbic?fname=/gpfs/bbp.cscs.ch/project/proj39/template/rat/waxholm/v2/bbic/sections/whs.h5&mode=ims&prog=TILE 0 0 1 511 0 0 max 8 1	Get a tile of Waxholm with maximum intensity projection of 8 slices	Tile with image manipulation
GET	https://nip.humanbrainproject.eu/api/image-service/image/v0/api/bbic?fname=/gpfs/bbp.cscs.ch/project/proj39/data/golgi/Golgi_rat_sections_can/golgi_rat_sections_proj2.h5&mode=ims&prog=TILE 0 0 0 7078 60 3 min 64 1	Get a tile of Golgi stained rat with minimum intensity projection of 64 slices	Tile with image manipulation
GET	https://nip.humanbrainproject.eu/api/image-service/image/v0/api/bbic?mode=meta&fname=/gpfs/bbp.cscs.ch/project/proj39/template/human/bigbrain/release2015/bbic/sections/bigbrain.h5	Get meta data about BigBrain image stack	Meta data

HBP-PROV Validator

Purpose

This REST service provides the ability to check the correctness of an HBP-PROV file instance.

This verification is two fold:

- **Syntactic**: it verifies that the format is correct against the corresponding Json schema, this encompasses the naming and cardinality of entities as well as their attributes.
- **Semantic**: we have the ability of implemented custom validation rules that can perform neuroscience oriented verifications as well as other aspects that a JSON schema cannot enforce.

Please note that currently 3 data formats are supported in the Neuroinformatics Platform: HBP-PROV, Excel and SAM (Single Activity Metadata). However, only HBP-PROV and Excel are meant to be used externally, the SAM format is only used internally by the Neuroinformatics Platform for the purpose of the Registration App.

Features

HBP-PROV Semantic rules available

Rule	Description	Examples
Entity UUID references	This rule verifies that when an entity refers to an other one by its UUID, then such entity should exist in the HBP-PROV file.	**a.** if a Sample was generated by an Activity with uuid 025e58ea-8f40-4136-97b7-63a 0e13f74ee, we will check that an Activity exists in the current file with that specific UUID. **b.** if an Activity refers to a Contributor by UUID, we check that a contributor exists with that specific UUID
Ontology usage	This rule verifies that when using an Ontology term to annotate a dataset, the ontology from which the selected term comes from is appropriate.	**a.** When defining the species of a Specimen, the ontology term should originate from the NCBI taxonomy. **b.** When defining a brain parcel for a dataset originating from a mouse Specimen, the ontology

		term should originate from the [Allen Mouse Parcellation Scheme]().

This section will be updated when new rules are being added.

Validation output data format

```
{
  "success": true,
  "messages": [
    {
      "type": "SYNTAX|SEMANTIC",
      "severity": "INFO|WARNING|ERROR|FATAL",
      "message": "string",
      "location": "string"
    }
  ]
}
```

Sample validation output:

Successful validation

```
{
  "success": true,
  "messages": []
}
```

Failed syntactic validation (2 errors)

```
{
  "success": false,
  "messages": [
    {
      "type": "SYNTAX",
      "severity": "ERROR",
      "message": "object has missing required properties ([\"id\"])",
      "location": "{\"pointer\":\"/activities/0/protocol\"}"
    },
    {
      "type": "SYNTAX",
      "severity": "ERROR",
      "message": "object has missing required properties ([\"unit\"])",
      "location": "{\"pointer\":\"/specimen/0/age\"}"
    }
  ]
}
```

Failed semantic validation (1 error)

```
{
  "success": true,
  "messages": [
    {
      "type": "SEMANTIC",
      "severity": "ERROR",
      "message": "Ontology term of type 'ACTIVITY_TYPE' are expected to be
defined using 'http://www.hbp.FIXME.org/hbp_activity_ontology', instead found
term ('null', 'MBA:1063') of type 'http://www.hbp.FIXME.org/hbp_abam_ontology'",
      "location": "Activity: [id: 0e9e371e-ee47-11e4-8c8b-6003088da632]"
    }
  ]
}
```

Endpoints

HTTP Method	Endpoint	Usage	Returns
POST	https://nip.humanbrainproject.eu/api/validator/hbp-prov/v3	The HBP-PROV to validate is given in the body of the request. The given data instance is validated both syntactically and semantically and report summarises the validation status and potential errors.	Validation output defined above
POST	https://nip.humanbrainproject.eu/api/validator/single-activity-metadata	The SAM to validate is given in the body of the request. The given data instance is validated both syntactically and semantically and report summarises the validation status and potential errors.	Validation output defined above

An interactive version of this endpoint documentation is available here.

How to validate an HBP-PROV file on the command line:

```
curl -X POST https://nip.humanbrainproject.eu/api/validator/hbp-prov/v3
--header 'Content-Type: application/json' --header 'Accept:
application/json' -d '<insert json content here>'
```

REST APIs Demos

Several demos have been compiled as iPython Notebooks to illustrate the use of our APIs:

1. **Ontology API** - in this demo you will learn to query a SciGraph server and perform the following operations:
    a. Search for ontology terms by name
    b. Compare ontology terms available in two instances of SciGraph
    c. List existing relationships between ontology terms
    d. Build and render a hierarchy of ontology terms matching a given name

2. **KnowledgeGraph API** - in this demo you will learn how to run searches in the KnowledgeGraph and interpret the results, it covers the following operations:
    a. Search for a dataset by brain region in the Search web application and the same search in the Search REST API (via Swagger using curl),
    b. Find the list of available filters through the Search REST API,
    c. Find the list of available storage types through the Search REST API,
    d. Use the JSON output of a Search to print a user friendly summary of a dataset,
    e. Learn how to enable/disable search result aggregations,
    f. Learn how to customise a search output to make it return the details that you care about,
    g. Download a morphology dataset that was stored in the HBP Document Service
    h. Render a 3D view of the downloaded morphology using NeuroM

3. **Voxel Brain API** - in this demo you will learn a little about the Multiresolution Atlas Viewer web application as well as how to use the Voxel Brain API. It will take you through the following steps:
    a. Browse brain atlas in your browser using the Multiresolution Atlas Viewer web application
    b. Select a brain region in the Brain Atlas and browse brain region related datasets in the KnowledgeSpace
    c. Programmatically list all atlases available in the Voxel Brain API
    d. List all the filters one can use to restrict the atlases returned
    e. Search for brain parcels by name in a selected atlas
    f. Get the annotation layers available for a selected atlas and brain region
    g. Download an annotation layer (nissl staining) and render a 2D visualisation

General

FAQ

What is NIP ?
The Neuroinformatics Platform (NIP) will provide to the neuroscientist community with:
- An integrated multi-level, data enriched atlas of the Human and rodent brain.
- Tools to curate and spatially register datasets to standard reference atlases.
- Analytics pipeline to automatically process sub-sets of data in order to provide an integrated view of the multi-level atlases to users.
- 2D and 3D Viewers to navigate, query and annotate the atlases.
- Programmatic API to access data in the atlases.

How do I sign-up?
All you need is to become a HBP Collaboratory member, a valid institution email address and to agree to our terms of use.
Visit the [HBP webpage](#).

What are the Terms and conditions for use of NIP?
In order to access the NIP tools and Dataset, you have to agree on the following [Terms of Use](#).

How can I become a contributor ?
This documentation will guide you the [Contributor Process](#).

What information should I provide when submitting a dataset ?
For all submitted datasets into the Neuroinformatics should be accompanied with a standard set of metadata called [MINDS](#) (Minimum Information about a Neuroscience DataSet), please read this section to find out more.

What information should I provide when submitting a model ?
In order to integrate the data, curate it and assess data quality the following information is required to be specified:

1) What are the specific models (channels, cells, regions, etc) to be developed and their scientific objectives?

2) What data are needed to constrain these models? What is the number of samples required and precision of the data necessary for the models?

3) Is the data necessary coming from SP1-3 or outside of HBP? How many samples, what is the data format, what is the size of the data they are planning to deliver? How mature is the data production process?

4) What features of the data are required to constrain the parameters and to validate the models?

5) What quality level (e.g. signal-to-noise ratio, stain completeness, input resistance, etc) is required of the data to extract a sufficient number of the required features?

6) Do feature extractors (analysis tools) exist or do they need to be developed? What are the data quality requirements of the feature extractors? Has this already been tested on actual datasets? What is the maturity of the feature extraction process?

7) Do the data need to be combined or linked with other key data to be valuable? (For example do the electrophysiological recordings need to come from exactly the same cell as the morphological data?) Is this feasible?

8) What are the curation requirements to make the data searchable and accessible by the model building and validation pipelines? For example, what are the properties that a query would need to be built on?

9) What are the specific atlases required, who will be responsible for registering data to these atlases. Will the data be gathered with sufficient information/landmarks/etc to perform this registration?

10) What are the computational and storage requirements for each dataset. Which size archival data repositories are required. Which size active data repositories are required and with which services. Do the services exist yet? What is the flow of data from depositing, staging, processing and deployment?

11) Is the necessary metadata for data registration recorded with the data? These include: contributor, specimen details, methods/protocols, brain region/location, data type, data location). Is there sufficient location information or landmarks to register this data to a specific template brain atlas?

Under what licensing could I register my open access Dataset?
During the process of your open access dataset registration, a choice between 2 licenses will be required depending the commercial potential use of your Dataset. We strongly recommend you to carefully read the informations related to the following licenses in our ToS:
[Creative Commons Attribution-ShareAlike 4.0 International (CC BY-SA 4.0)](#)
or
[Creative Commons Attribution-NonCommercial-ShareAlike 4.0 International (CC BY-NC-SA 4.0)](#)

What file format can I upload ?
The NIP platform will take any format submitted but we strongly recommend you inform yourself about which standard formats are recommended in the section about [Specific Data Categories](#). In any case, all published data should respects the ethical regulation described in our [Terms of Use](#).

Who can access the file I upload ?
Depending of your restriction data policy you can select between:
- **Public** access: metadata can be viewed and data downloaded by anybody
- **HBP Only** access: metadata can be viewed by anybody but file download is restricted to HBP accredited users.

Can I modify / complete a previously download File ?
Two possibilities:
- The NIP provides a [one-click registration process](#) for open source data. Once published those data and the metadata associated are immutable.
- Using the NIP restricted registration, you will be able to change the Metadata but not the uploaded immutable Dataset.

What is the maximum size of the data I can upload ?
Regarding *Restricted access*, you can upload unlimited files but 2GB per file is our size constraint. for large dataset, please contact directly the members of the NIP

Who will use my data, for what purpose ?
Users will have to follow the NIP Terms of Use that contain the following piece of information: *Use of the Data Set is restricted to academic, research, educational, government or other charitable or humanitarian purposes that are not-for-profit. The Data User is permitted to produce and distribute derived works from this Data Set provided that those derivatives are released under the same license terms as those accompanying this Data Set. Any other uses for the Data Set or its derived products will require explicit permission from the Contributor.*

When can I see my file ?
Everybody will be able to access your newly integrated information within a few days. After hitting the submit button, the NIP team will need a few days to register and curate your metadata. Your data will become "visible" in our [Search client](#) / [Search API](#)

How can I be sure the upload was complete?
Go to your « My Uploads » page (both in the NIP dataset registration page or on relative services webpages) and the status of your documents will be register.

Tools

How to access the NeuroInformatics Platform tools?
We provide you with Structural data analysis, functional analysis as well as brain atlases tools that have been specifically developed in order to help neuroscientists to retrieve information and visualize dataset can be easily find within our NeuroInformatics Platform (https://collab.humanbrainproject.eu/#/collab/47/nav/6641).
The different tools are listed within our Neuroinformatics Platform Collaboratory section.
Here is a non exhaustive list of HBP collaboratory NIP tools available:

Structural Data Analysis Tools:

EspINA
EspINA is a user-friendly tool which performs segmentation and analysis of elements in a reconstructed 3D volume of the cerebral cortex, and greatly facilitates and accelerates these processes. It allows visualization and segmentation of large image stacks datasets, both from electron microscopy (e.g. FIB/SEM) and light microscopy.
Link: website, user manual

3DSomaMS
3DSomaMS is an R package for soma reparation, segmentation and characterization.
Link: website, user manual

Functional Analysis Tools:
Elephant
Electrophysiology Analysis Toolkit
Link: website, user manual

Brain Atlases Tools

AligNII
Web-based tool for anchoring 2D image data into 3D atlas space
Link: website, user manual

Scalable Brain Atlas
The Scalable Brain Atlas (SBA) is a fully web-based display engine for brain atlases, imaging data and topologies. It allows client websites to show brain region related data in a 3D interactive context and provides services to look up regions, generate thumbnails or download nomenclature- and delineation data.
Link: website, user manual

QuickNII
Standalone tool for anchoring 2D image data into 3D atlas space.
Link: website, user manual

Morphology Viewer
Web-based 3D neuron morphology viewer.
Link: website, user manual

Synapse Generator
SynapseGenerator is a pipeline used to predict connectivity at the synapse level.
Link: website, user manual

MeshView
Web-based mesh viewer with user-defined cut plane support
Link: website, user manual

MeshGen
Mesh generator for volumetric segmentation data.
Link: website, user manual

CutNII
Standalone viewer for volumetric atlases with custom-angle slicing support
Link: website, user manual

Acknowledgement

Get Support

Report an issues
Please do not hesitate to contact us, there are currently two ways to get in touch with the Neuroinformatics Team:
- Via email: data.nip@humanbrainproject.eu
- Via the HBP Neuroinformatics Forum where you can create a public post.

The HBP Collaboratory plans in its roadmap to integrate a Helpdesk system, we intend to start integrating with this service as soon as it become available.

Report an Ethical Issue
If you believe an ethical outreach has happened, please fill the following document

Media Contact
For any press inquiries on the HBP :
email:
EPFL ENT CBS BBP 2nd floor
Campus Biotech
Chemin des Mines 9
1202 Geneva
Tel: +41 (0)21 693 7660
Fax: +41 (0)21 693 7260

Traveling to Campus Biotech

By Train
From the Geneva airport, take the train to Geneva Cornavin (schedule here: Train connection, it takes 25 minutes trip between the airport and the Campus. From there, take bus 1 or 25 destination Jardin Botanique, stop "Mines" right in front of the main entrance, or the tram 15, stop "France" and then follow the directions to the Campus.

By Car
Follow the destination at this link.
Once on site announce yourself as a BBP guest at the reception which will contact your host and let you into the building.

Disclaimer

Platform General Terms of use

Introduction
The Terms of Service (ToS) outline the HBP minimum standards for data sharing, access, authorship, citation, and restrictions of data and apply to all users of HBP Collaboratory data. Users who register an account with the HBP agree to the Terms of Service. This includes agreement to comply with institutional rules and regulations.
If you do not accept the Terms & Conditions when applying for registration or thereafter, when using the Platform, you are not permitted to access or use the Platform or post or submit any materials on it.
HBP platforms and data are subject to European and national legislation and regulation and conform to the ethical principles of H2020. This means you may need the approval of your IRB or Ethics Committee to use the data. Different national, state and local laws may apply and be interpreted differently, so it is important that you consult with your IRB or Ethics Committee before beginning your research. If needed and upon request, the HBP collaboratory will provide a certificate stating that you have accepted the NIP Data use Terms and conditions.
Following EU principles, data funded by the EU should normally be available open access, unless there are valid reasons speaking against open access.

Data access requirements
Access to all HBP data and services is subject to requirements set forth by these Terms and Service to enable data providers to track usage, evaluate its impact in the Neuroscientists community, and confirm users' acceptance of the terms of acceptable use. These requirements are standardized across the HBP to provide contractual exchange of data among the Contributors (defined below) within the HBP collaboratory and Data Users (defined below) that can be encoded into electronic form and exchanged between computers. This will allow direct access to data through a common portal once these requirements have been fulfilled.
The following registration information is required directly or by proxy prior to the transference of any Data Set:
- Name
- Affiliation
- Institutional Email Address
- Acceptance of the below General Data Use Agreement
- A Statement of Intended Use that is compliant with the approved use defined below. Such statements may be submitted explicitly or made implicitly via the data access portal interface.

GENERAL TERMS OF SERVICE
IMPORTANT: PLEASE READ CAREFULLY. Use of the Data Set (defined below) is subject to the Terms of Service set forth below. By clicking this box, the Data User (defined below) agrees to be bound by these Terms and Conditions and enters into a legally binding

Agreement with the Data Set Creator ("Agreement"). Users refusing to agree to the terms provided herein are not authorized to use the Data Set.

Definitions
Dataset. Digital data, either raw or derived, and its metadata provided through the data access portal interface, or through other media, including data and metadata derived from HBP monitoring protocols, field observations, collections, laboratory analysis, camera trap images, all written, recorded, graphic, audio, visual, and other materials in any media, whether or not subject to copyright protection, or the post-processing of existing data and identified by a unique identifier issued by the HBP.
All datasets provided by contributors (below v.) should have been produced following EC ethical regulation.
The HBP will not be held responsible for the data provenance.
Third Party Data Set. Digital data and its metadata provided through the data access portal interface, or through other media, not derived from HBP monitoring protocols, but provided by third party Data Set Creators.
Data Set Identifier. A unique identifier created by the information system to be included with a Data Set for the purpose of tracking and ongoing identification.
Data User. Individual to whom access to this Data Set may be granted, subject to acceptance of these Terms and Conditions by such individual and his or her immediate collaboration sphere, defined here as the institutions, partners, students and staff with whom such individual collaborates and to whom access must be granted in order to fulfill the such individual's intended use of the Data Set.
Contributor. Individual or institution that produced the dataset. The data will be accessible to the whole community. Therefore, experimental data are not permitted. Moreover, no personal information related to patients or de-anonymized data are accepted.
Dataset Contact. Party designated in the accompanying metadata of the dataset as the primary contact for the dataset.
Data Registration. a unique set of information related to one specific dataset. It includes all piece of information required by the API or service registration pages as well as all piece of information about the Contributor registration, the contributors of the dataset and data user conditions.

Specific purpose
Use of the Data Set is restricted to academic, research, educational, government or other charitable or humanitarian purposes that are not-for-profit.
The Data User is permitted to produce and distribute derived works from this Data Set provided that those derivatives are released under the same license terms as those accompanying this Data Set.
Any other uses for the Data Set or its derived products will require explicit permission from the Contributor.

Limitation of use / approved use
The Data User agrees to the following terms:
- The Data User may receive access to de-identified or aggregated data and in such cases will not attempt to establish the identity of, or attempt to contact any of the participants.

- The Data User will not further disclose these data beyond the uses outlined in this agreement.
-The Data User will require anyone on their team who utilizes these data, or anyone with whom they share these data to accept and comply with this data use agreement.
- The Data User will comply with any rules and regulations imposed by their institutions and its institutional review board in requesting these data.
- The Data User will ensure that Investigators who utilize HBP data use appropriate administrative, physical and technical safeguards to prevent use or disclosure of the data other than as provided for by this Agreement.
- The Data User will report any use or disclosure of the data not provided for by this Agreement of which they become aware within 15 days of becoming aware of such use or disclosure. Reports/disclosures should be submitted to the HBP Point of Registration at www.hbp-pore.eu.
Users may not: - download, send or disseminate data containing viruses, worms, spyware, malware or any other similar malicious programs;
- carry out any calculations, operations or transactions that may interrupt, destroy or restrict the functionality of the operation of EES or any program, computer or means of telecommunications; or
- submit any information or materials that infringe third party rights, are libellous, obscene, threatening or otherwise unlawful.

Dual Use / Misuse
The HBP services and the associated data are provided for the purposes of peacetime Neuroscience and brain research. In particular all users of the HBP services and associated data must comply with the [COUNCIL REGULATION (EC) No 428/2009](#), in particular Annex I LIST OF DUAL-USE ITEMS. Specifically all users of the HBP services and associated data confirm that any results derived from the use of these services are for the purposes of peacetime Neuroscience and brain research, are not for military use and are not in breach of said EC regulations.

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Year of Data Publication,

Title of Data Set,

Data Set Identifier

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It is the policy of the HBP to make every reasonable effort to resolve all issues or disputes that may arise under this Agreement fairly by negotiation without litigation, if practicable. Any dispute arising out of or relating to this Agreement which is not settled by agreement of the parties shall be finally settled by arbitration in accordance with the UNCITRAL Arbitration Rules in force at the time the dispute arises.

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Severability

In the event that any one or more of the provisions contained herein shall, for any reason, be held to be invalid, illegal or unenforceable in any respect, such invalidity, illegality or unenforceability shall not affect any other provisions of this Agreement, but this Agreement shall be construed as if such invalid, illegal or unenforceable provisions had never been contained herein, unless the deletion of such provision or provisions would result in such a material change so as to cause completion of the transactions contemplated herein to be unreasonable.

Waiver

HBP may specifically and expressly waive any breach of this Agreement by Data User, but no such waiver shall constitute a continuing waiver of similar or other breaches. HBP's

consent or approval of any act by Data User shall not be deemed to render unnecessary the consent to or approval of any subsequent act by Data User.

Entire agreement
This Agreement constitutes the entire understanding between the parties with respect to its subject matter hereunder, is intended as a complete and exclusive statement of the terms of their agreement, and supersedes any prior or contemporaneous agreements or understandings relating to the subject matter hereunder.

Acknowledgement /acceptance of agreement
The Data User agrees to the terms and conditions outlined in this Terms of Use Agreement ("Agreement") with respect to the HBP's site (the "Site"). This Agreement constitutes the entire and only agreement between us and you, and supersedes all prior or contemporaneous agreements, representations, warranties and understandings with respect to the Site, the content, products or services provided by or through the Site, and the subject matter of this Agreement.
The HBP may amend this Agreement at any time without specific notice to the Data User. The latest Agreement will be posted on the Site, and the Data User should review this Agreement prior to using the Site.

Changes to the Terms of Service
The HBP Platforms may, at any time, vary, add to or delete any provision of these Terms and Conditions.
Users and their organisations expressly acknowledge and agree that such new terms and conditions.
Any access to or use of the HBP shall constitute unconditional acceptance of these Terms of Service (in the then-current version).

HBP Data Registration Declaration
A specific section of or Term of Service regarding HBP Data Registration can be find here. Please, read carefully this documentation if you consider to become a contributor.

Related documents
Data protection directive - Directive 95/46/EC
European charter for access to research infrastructures
European Medical Information Framework
SAIL databank

HBP Data Registration Declaration
This is the structure of a data registration declaration that details the various aspects that a data owner would need to agree to, in order to ensure ethical compliance of the data. This declaration clarifies questions concerning the registration of data, focusing on ethics and compliance issues. For further information, and complementary agreement, please read our Disclaimers

Authorisation
- I have accepted the HBP's Terms of Service.
- I am authorised to register the data and give permission for the subsequent uses of the data for the purposes of the HBP.
- I give permission for the use of this data:
    - For internal use of the HBP only. Internal use will be covered by the Grant Agreement and the Consortium Agreement.
    - For use covered by a specific data use agreement, if so state which one.
    - For any use covered by the terms of service of the HBP.

Compliance
I confirm that the data registered with the HBP was collected in research that complied with:
- applicable international, EU and national law
- ethical principles as indicated by the [Horizon 2020 Ethics Self Assessment](#)
- IRB approval where applicable
- the Horizon 2020 Data Management Guidelines see [PDF](#)

Audit
I confirm that I have access to documents that demonstrate the ethics compliance of the data. I am willing to comply with an audit by an appropriate body and am willing to provide the above evidence to the HBP within 30 calendar days of receiving a request.

Sanctions
I am aware that failure to provide relevant evidence to an HBP audit can lead to the removal of the data from the HBP systems, the closing of my user account and/or a notification to my institution's ethics bodies concerning potentially unethical practice.

Data use
I give permission for the use of this data:
1) For internal use of the HBP only. Internal use will be covered by the Grant Agreement and the Consortium Agreement
2) For use covered by a specific data use agreement, if so state which one
3) For any use covered by the terms of service of the HBP.

License
During the process of your « open access Data registration » a choice between 2 licenses will be required depending the commercial potential use of your Dataset. We strongly

recommend you to carefully read the informations related to the following licenses in our ToS:

[Creative Commons Attribution-ShareAlike 4.0 International (CC BY-SA 4.0)](#)
or
[Creative Commons Attribution-NonCommercial-ShareAlike 4.0 International (CC BY-NC-SA 4.0)](#)

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The latest Agreement will be posted on the Site, and the Data User should review this Agreement prior to using the Site.

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Changes to the Terms of Service

The HBP Platforms may, at any time, vary, add to or delete any provision of these Terms and Conditions.

Users and their organisations expressly acknowledge and agree that such new terms and conditions.

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Related documents

Data protection directive - Directive 95/46/EC
European charter for access to research infrastructures
European Medical Information Framework
SAIL databank

Glossary

Voxel Brain annotation layer
In the context of the Voxel Brain, an annotation layer is the dataset we attach to the voxels of a data volume.
Here are a few examples:
   a. A brain region annotation layer would store an ontology term describing a given brain region or brain parcel per voxel in the atlas space.
   b. a cell density Annotation layer would store a float value to every voxel of a given atlas space.
   c. A gene expression annotation layer would store in each voxel of the atlas space a list of gene names with associated numerical expression level.

Atlas space
Atlas space refers to three-dimensional coordinate system of a given brain atlas.

Brain atlas
A brain atlas is a spatial representation of the brain that comprises ontology, parcellation, coordinate system, and multiple features/layers of the cerebral characteristics.

Brain parcel
A brain parcel is a specific brain region that is defined deterministically or probabilistically in the context of a given brain atlas.

Contributor
Individual or institution that produced the Data Set. The data will be accessible to the whole community. Therefore, experimental data are not permitted. Moreover, no personal information related to patients or de-anonymized data are accepted.

Data Registration

A unique set of information related to one specific dataset. It includes all piece of information required by the API or service registration pages as well as all piece of information about the Contributor registration, the contributors of the dataset and data user conditions.

Dataset

Digital data, either raw or derived, and its metadata provided through the data access portal interface, or through other media, including data and metadata derived from HBP monitoring protocols, field observations, collections, laboratory analysis, camera trap images, all written, recorded, graphic, audio, visual, and other materials in any media, whether or not subject to copyright protection, or the post-processing of existing data and identified by a unique identifier issued by the HBP.
All datasets provided by contributors should have been produced following EC ethical regulation.

Dataset Contact

Party designated in the accompanying metadata of the dataset as the primary contact for the dataset.

Data User

Individual to whom access to this dataset may be granted, subject to acceptance of these Terms and Conditions by such individual and his or her immediate collaboration sphere, defined here as the institutions, partners, students and staff with whom such individual collaborates and to whom access must be granted in order to fulfill the such individual's intended use of the dataset.

Human Brain Project

Human Brain Project (HBP) is a European Commission Future and Emerging Technologies Flagship that aims to achieve a multi-level, integrated understanding of brain structure and function through the development and use of information and communication technologies (ICT).

HBP-PROV

HBP-PROV is an exchange data format intended to represent how data was created, which organism was used, how it was processed - including which contributor participated, which software was used - and what dataset/files resulted from it.

KnowledgeGraph

KnowledgeGraph is a metadatabase built on a provenance data model HBP-PROV. In other words, it is a provenance graph to which data are registered for discovery, search, access and tracking. Currently, the KnowledgeGraph consists of Search API which is public and Indexer API which is private.

KnowledgeSpace

KnowledgeSpace (KS) is a community encyclopaedia that links brain research concepts with data, models and literature from around the world. It is an open project and welcomes participation and contributions from members of the global research community.

Ksearch

Ksearch is the search component of the Neuroinformatics Platform. It is a REST API allowing searching curated datasets using different filters that are mainly taken from MINDS.

MeSH

MeSH is the National Library of Medicine's controlled vocabulary thesaurus used for indexing articles for PubMed. It consists of sets of terms naming descriptors in a hierarchical structure that permits searching at various levels of specificity.

MINDS

MINDS stands for Minimum Information for Neuroscience DataSets. Data shared on the Neuroinformatic Platform are enriched with minimal metadata to provide essential information in order to ensure traceability of any data artefact.

Neuroinformatics Platform

Neuroinformatics Platform (NIP) is Sub-Project 5 of the Human Brain Project. The Neuroinformatics Platform and the Brain Atlases allow neuroscientists to collaboratively curate, analyse, share, and publish heterogeneous neuroscience data.

Parcellation

Brain parcellations define spatial or volumetric boundaries of brain region/structure. They could be represented in 2D and 3D depending on the use case.

Registration

For 2D or 3D volumetric datasets, we use different registration methods to convert one dataset from its own space to another space. Following registration methods are used: Linear registration registration is used to capture the global transformation between the subject image and the atlas image.
Landmark registration module is used in the 3D Slicer to pick corresponding landmark in both subject image and atlas image.
Deformable registration is a process consisting of establishing functional or spatial correspondences between two images.

NOTE: There are "Data registration" and "Registration App", which are separate terms.

Voxel

The etymology of the work comes from a *blend* of '*volumetric'* and '*pixel'.* A voxel is the three-dimensional analogue of a pixel in a two-dimensional space.

Voxel Brain

Voxel brain is a REST service provides access to volumetric brain atlas and their annotation layers in the form of voxels.