User guide to the

INSECT BRAIN DATABASE

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Contents

A. Menus

1) Neuron Search

Starts the neuron search interface (for details see section Schematic Search). On this page the user can choose between single species search and multispecies search. Once one of these options is chosen and species are selected, the *schematic search interface* is automatically loaded as default. Clicking on neuropil models will display all neurons that innervate this neuropil as dynamically drawn schematic paths. Clicking on neurons will display the profile page of that cell type. To return to search results, click the cross in the top right corner of the screen.

Optionally, one can search the *semi-schematic* display option (only for single species mode) by selecting the tab in the center of the screen. This loads an automatically generated cross section of the 3D reconstruction of the selected species and allows to search for neurons using this interface. Clicking on neuropils will highlight all connected neuropils and load the all found neurons into the list view of search results.

The 3D option in the central tab allows to display results, but does not function as search interface. Users can freely switch between the three display options once search results are present.

Alternatively, at the bottom of the screen, the *expert search function* can be started by selecting the 'Expert search' tab (see section Expert Search).

List view of results: At the bottom left of the screen a tab 'Search Results' shows the number of found neurons. Clicking on this tab opens a detailed list view of the search results.

2) Brain Region Search

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i)   Schematic

This option loads the interface to search for brain region data using the identical schematic brain models as the single species neuron search. First a species must be chosen to display the corresponding brain model. Then, selecting brain regions will display the profile page of the selected neuropil. By right-clicking on a region, the user can select information about higher level areas to be displayed (e.g. right-click on the protocerebral bridge allows to show the profile page of the central complex).

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ii)   Semi-schematic

Identical to the schematic search, but uses cross-sections of 3D models for search input. right-click also allows to select higher level regions.

3) 3D Brain Visualization

This option loads the built-in 3D viewer. After selecting a species and a sex (if available for a species) the 3D brain models are downloaded and displayed. The left-hand menu provides numerous tools to modify the appearance of the shown brain. Screenshots can be made by clicking the camera symbol on the bottom right. For details of the 3D viewer, see section 3D viewer.

4) Lists

i) Neurons

The list of all available neurons is loaded. It can be sorted according to various parameters by clicking the headers of the different displayed neuron parameters (species, name, neuron ID).

ii) Species

The list of all available species is loaded.

iii) Brain Structures

A hierarchical tree-view of all brain structures in the IBdb is loaded. By clicking on a brain region name, the profile images of this region is shown for each species possessing this region. Via the also displayed link, the species-specific profile page for this region can be reached.

iv) Experiments

The list of all available experiments is loaded.

5) Submit

i) Neuron

This initiates the submission process for a new neuron. The initially loaded page will ask for basic information about the neuron (name, species, owner, etc.). After this information is entered, the neuron will be assigned a unique neuron ID (NIN) for internal use of the database. At this stage the neuron will not receive a persistent handle and can accordingly still be deleted and freely modified.

Once this is achieved, the profile page of the neuron is being created automatically and all remaining information can be added incrementally by the user. To be searchable, the neuron's arborization regions must be annotated by clicking 'edit' next to 'Arborization region'. This loads a graphical user interface for selecting innervated brain regions.

Finally, to generate a schematic neuron diagram for displaying the neuron as part of the schematic search result, the branch editor has to be used. This will open a graphical user interface to interconnect the innervated brain regions in the correct way, resembling the wiring logic of the cell. See section 'Creating a Neuron' for details.

All remaining information, i.e. images, bibliography, keywords, representative functional data, transmitter content, and textual descriptions, can be added to the profile page at any time prior to publication.

Note: The IBdb can be used to house data that have been obtained by classical methods, e.g. camera lucida drawings of Golgi impregnated neurons. While no 3D information is available in those cases, the scanned drawings can be uploaded as images and annotation of the neuron's morphology (arborization regions) can be performed as described.

ii) Species

This button initiates the process of submitting a new species. The process follows an identical procedure as for neurons. First, provide all basic information. Then a species profile page is created that can be populated with data.

The most essential step is to create a schematic brain representation using the brain designer (see next point). This will create the brain region entries for the new species and automatically generate a profile page for each of these regions.

Remaining information, such as 3D reference brain, image stacks, profile picture, text descriptions, and bibliography can be added incrementally at any time before publication.

iii) Brain Designer

This button loads the brain designer tool. This tool is used to generate and modify the schematic brain model that is used as the basis for the graphical search interface. First, the user selects a reference brain from the menu on the left. This will draw an outline of each brain region in the reference brain on the canvas. Ideally, a closely related species of the one to be added should be selected. Then, regions to be added to the new species are selected from the menu on the left. The boxes must be resized and moved to the correct position on the canvas. Ensure to correctly place right and left brain regions. Right and left are seem from the insect's point of view (the viewer's right side is the insect's left side).

Finally, tracts for fiber bundles and invisible bridges are placed on the canvas. Tracts provide guidance for schematic neurons that are tagged as innervating this tract. Bridges allow passage of schematic neurons across neuropils in certain places to avoid highly convoluted neuron paths in the schematic search results.

6) Applications

i) API-reference

Logged in users can view the details of the API documentation. This allows to gain software based queries to the content of the database the user has access to.

Additionally, users can request API based read and write access. These will be granted to users that aim at contributing large amounts of data and will be decided on an individual basis.

7) Forum

Loads the user forum and displays the list of available topics. New topics can be created with the 'New Topic' button. Clicking on a topic name will load the history of comments and will allow to respond with own comments.

8) About

i) Who we are

Contains a brief mission statement of the IBdb.

ii) Supporters

This is a list of the informal consortium that initiated and supported the work on the IBdb during its construction starting in 2014.

iii) Terms of use

Specifies the licenses and usage terms for the content of the database.

iv) Privacy

Specifies details about which information we collect from users and how we handle cookies.

v) Contacts

Provides the contact details of the scientific and technical administrators.

9) Bottom menus right (click on user name)

i) User Group

This button opens the list of user groups the user is associated with, and allows to create new groups. These groups allow sharing of unpublished, private datasets between any users of the database (e.g. lab members, collaborators).

When editing a group, the user can first specify the members of the group. Each member has identical access rights to the content that has been committed to the group. Each member can not only view content, but also commit own data to the group. Committed content will be either neurons, species, or experiments. The basic unit for sharing are the profile pages in each of these categories. Neurons can be committed either as individuals or by their associated species (e.g. all neurons from the honeybee).

Once a user has been added to a user group, they will be notified within the database (banner at the bottom of the screen).

ii) Neuron Datasets

From this menu, users can create datasets containing arbitrary groups of neurons. These neurons must be either public or pre-public. Each dataset can be identified via a unique link. Every person with this link can view all neurons in the dataset, irrespective of being logged into the database. This is ideal to share prepublished neuron data with editors and reviewers (by sharing the unique link).

Sets of neuron that are part of a single publication can be combined using this function. When several neuron datasets have been created by a user, all of them are listed here. They can be edited by clicking on the edit icon next to the name of the dataset.

iii) Account Administration

Opens user account administration page. On this page, the user can modify personal information, reset the password, etc. Curators can view their pending assignments on this page, e.g. neurons and species waiting for approval.

iv) Logout

Logs the user out of the database. Only content freely available to the public will be visible and no content can be generated or downloaded.

10)　　Bottom menus left (Public/Private Mode)

When clicking on the 'Public/Private Mode' button on the bottom left, a menu will appear that allows to choose the mode of the database. One can choose either Private, Private/Public, and Public.

Private mode allows to only see the unpublished data one has access to, essentially turning the database into a data management tool.

Public mode allows to only view and download all published content.

Public/Private mode allows to see all content, enabling to compare unpublished data with published data.

B. The 3D viewer - general instructions

Mouse gestures: Left click-and-hold will rotate the brain into the direction of movement. Right click-and-hold will pan the field of view. Scrolling will zoom in and out of the brain.

Screenshot: Click on the camera icon in the bottom left of the screen.

Download source data: Click on the download icon next to the camera icon to download the .obj files shown in the viewer.

Source information: The DOI in the bottom right corner of the screen links to the publication containing the displayed 3D brain and that must be cited when using images of this brain generated with the IBdb. If not published, the names of the owners/creators of the 3D brain are shown (must be credited when using image data).

Left-hand menus:
- Species: choose species
- Sex: choose male or female (if available); if not defined, 'unknown' is displayed.
- Brain regions, settings: clicking the cogwheel icon opens general display properties for brain regions.
- Brain regions, appearance: visibility of each region can be individually switched on and off by clicking the eye icon; appearance can be switched between greyscale and color by clicking on the color palette icon; opacity can be changed by clicking on the drop icon and adjusting the opacity value with the slider.
- Settings: clicking the cogwheel icon next to 'Settings' will open general display settings of the viewer. Adjustable are background color, camera mode (orthographic/perspective), rotation mode (free orbit/fixed rotation), and lighting (high contrast/diffuse).

Additional menus when neurons are displayed:
- Display neurons: color is adjustable for each neuron by clicking the color square in front of the neuron name; visibility can be toggled on and off by clicking the eye icon in front of each neuron name.
- Neuron display options: clicking the cogwheel icon reveals the neuron drawing mode option; low detail = skeleton view only; high detail = skeleton view plus diameter and shading.
- Brain region options: 'Smooth' button will smoothen brain region surfaces, which are loaded without smoothening for faster load (when neurons are shown).
- Opacity slider for 'innervated neuropils': Allows to simultaneously adjust opacity for all neuropils innervated by the displayed set of neurons.

C. Navigating neuron profile pages

The Neuron profile pages are organized as a continuous scroll page. Users simply scroll to the desired section to view or download the desired material. From top to bottom, the following sections are displayed: Version, general information, morphology, 3D reconstruction, image stacks, functional data, experiments (linked), bibliography, keywords and other information.

At the top of the page, the version of the displayed neuron profile can be selected. Each republishing will create a new handle, which in turn generates a new entry in the list of version to choose from. The viewer can thus go back in time to select, e.g., a version referenced in a publication. The owner of the dataset also sees the current version, i.e. the private and editable profile page. This version is only viewable by the owner and users that were granted explicit permission to view or edit the profile page.

Viewing of content is allowed for every user, irrespective of whether one is logged in or not. For download, users need to be logged into their personal account. For profile pictures and image stacks, more than one image or stack can be present on the page. For images, this is indicated by small thumbnails on the right of the default image. For image stacks, a dropdown menu will appear when clicking the name of the current stack. Other stacks can be chosen from this menu.

For image stacks and 3D reconstructions, a full screen mode is available for viewing. This can be reached via the full screen icon (bottom right) near the data preview. 3D reconstructions are loaded as a preview when viewing the page and for speed reasons, the actual reconstruction is only loaded when clicking the preview. Image stacks are loaded in a low quality preview, which can be changed to high quality by clicking either the full screen option, or the 'high quality' option.

Editing of content (if users have the appropriate rights) can be done by clicking on the edit icon next to each section header.

Data owners and curators have additional display items: The list of users that are allowed to edit the page are listed below the displayed version. This allows to identify potentially unwanted permissions that were accidentally granted by applying a permission rule. Also owners and curators have the option of posting comments on each profile page. These are only viewable by the owner and curator and serve to resolve potential issues in the way of the approval of the dataset. New comments posted will lead to a notification of the owner/curator(s) of this page.

Finally, the owner will have a list of publishing options available. For completely private neurons, owners can either 'Prepublish' or 'Publish' their profile page. Prepublishing does not notify the curator and does not make the neuron appear in any lists or search interfaces. With a direct link to the handle, the neuron can be viewed, e.g. by reviewers and editors of journals.

Publishing will also create a persistent handle for the neuron (i.e. lock the page) and will notify the species' curator to check and approve the neuron page. The curator will now see an 'Approve' button on his/her version of the page. By making a neuron page public, the owner must explicitly agree to the licenses that will be attached to their data.

D. Neuron Search

Schematic search

When loading the neuron search page the user can choose between single species search and multispecies search. Once one of these options is chosen and species are selected, the *schematic search interface* is automatically loaded as default. Clicking on neuropil models will display all neurons that innervate this neuropil as dynamically drawn schematic paths. These illustrate the overall morphology of the neuron as defined by the owner upon upload. Somata are not displayed to focus on information flow between neuropils. When hovering over schematic paths, single neurons are highlighted. Clicking on neurons will display the profile page of that cell type. to return to search results, click the cross in the top right corner of the screen.

Optionally, one can also select the *semi-schematic* display option (only for single species mode) by selecting the tab in the center of the screen. This loads an automatically generated cross section of the 3D reconstruction of the selected species and allows to search for neurons using this interface. Clicking on neuropils will highlight all connected neuropils and load the all found neurons into the list view of search results.

The 3D option in the central tab allows to display results, but does not function as search interface. Users can freely switch between the three display options once search results are present.

Alternatively, at the bottom of the screen, the *expert search function* can be started by selecting the 'Expert search' tab (see section expert search).

Schematic search extras:

- Shift-click schematic neuron path: add neuron to database internal **neuron clipboard**
- Shift-click neuropil schematics: Add neuropils to **complex search** to search for neurons that innervate 'all' or 'any' of the added regions. Click on the minus icon to remove neuropils from selection.
- Right-click neuropil schematics (as well as semi-schematic neuropils): **Select higher level regions** as search input (bilateral)
- **Apply filters** to search results in the left-hand menu: restrict search results by e.g. input/output or sensory modality

List view of results: At the bottom left of the screen a tab 'Search Results' shows the number of found neurons. Clicking on this tab opens a detailed list view of the search results, from where neurons can be added to the database clipboard or profile pages can be displayed. This list also includes neurons that cannot be displayed as schematic neuron paths (e.g. if paths were not correctly defined by the owner).

'Clear Selection' button: Removes search results from display, but keeps database clipboard intact.

Camera icon, bottom right: Downloads screenshot of current search display.

Full screen icon: Restores full field of view.

Mouse scrolling: Zooms in and out of display.

Mouse click-and-hold (right or left) on background: Pans field of view.

Expert search

Next to the 'Search Results' list view on the bottom left of the search screen, there is the 'Expert Search' tab. Selecting this tab will reveal a text based search function at the bottom half of the search screen.

This function allows to search for any neuron based information in the database and will display a list of neuron IDs and experiment IDs (which are connected to the found neurons) as a result. The neuron results can be sent to the schematic display (click on 'Draw results in schematic display') or directly to the neuron clipboard (click on the + icon in the first column of search results).

To search, the user adds a search field to constrain the search and presses 'Search'. Every part of a neuron profile page can be queried, including all free text fields. Several fields are automatically combined by an AND connection, i.e. the search results have to match *all* constraints. Individual fields can be used to exclude results obtained by this aspect of the query (AND NOT connection) by selecting the 'exclude' option.

If several search fields of the same category are chosen (e.g. species) they are linked by an OR relation.

A more complex search can be performed for arborization regions. Here any inputs can be linked by logical AND or OR links, which are then combined with any additional constraints.

Individual constraints can be removed by clicking on the *x* icon next to the search field.

If the option 'Include experiments' is selected, experiments linked to the neuron search results are also displayed.

To clear search results, click 'Clear'.

E. Built-in applications - Comparing neurons

Neurons that are sent to the **neuron clipboard** can be used for applications built into the database. The neuron clipboard is found on the left side of the neuron search screen. Neurons can be removed by clicking on the minus icon to their right. All neurons can be sent to the schematic viewer, the 3D viewer, or compared with each other.

The clipboard is maintained until the search page is closed or refreshed in the browser.

Comparing neurons

Up to four arbitrary neurons can be chosen from the neuron clipboard at the same time and compared side by side on screen. To do that, choose the neurons by selecting the tick boxes to their left and click 'Compare Neurons'.

When clicking on compare neurons, the profile pictures of the selected neurons will be displayed in the main viewer. This display can be changed for the 3D view or the confocal image stack of the neurons (if available). Each of the four viewers on the screen is a fully functional 3D viewer, allowing to take screenshots and manipulate the view.

This function is ideally suited for comparing homologous neurons from different species.

To return to the search interface, click on 'Exit multi-view'.

Constructing circuit visualizations

If all neurons in the neuron clipboard are from the same species, they can be sent to the 3D viewer by clicking 'View Shared 3D'.

This allows to display an arbitrary collection of 3D neurons from any one species and thereby construct visualizations of neural circuits. In practice, we recommend to search for the desired neurons in consecutive searches (in any of the available search modules), moving the neurons into the clipboard after each search, and then displaying the accumulated collection.

Basic information

After clicking 'submit species' menu, the user has to provide basic information. This includes Scientific name of the species, common name, host laboratory, and a free text description of the species. Only the scientific name is mandatory.

After clicking 'Submit' the species profile page will be created and the user can now start to populate this page with information. A species ID will be created (SIN) at the same time. The species will be private until it is actively published via the 'Create Persistent Record' button. Click this button only once the species entry is complete. This will send an approval request to the database administrator. Once approved, the species will be publicly available.

The species profile page will become automatically linked to every brain region that is generated for the species, which will be displayed as a brain structure hierarchy.

Additionally, all experiments linked to the species (on the species level) will be linked to this page as well (e.g. behavioral experiments, ecological studies, etc.).

The brain designer tool

The most important step to complete the species entry in the database is to create a schematic brain layout for this species. This will generate the schematic search interface for neurons and brain regions, but also generate the brain region entries linked to this species. These are required to upload 3D information, to generate the brain region pages and to link neurons with their arborization regions.

To generate the schematic brain, go to the main menu 'Submit' and then to 'Brain Designer'. A new graphical interface will appear, in which the schematic brain can be drawn. This tool allows to either create new schematic brains or to modify existing models. To create a new model, click 'Add Schematic' in the top left of the screen. Now you can select your species as well as choose an initial state of the brain model. If a related species is already in the database, you can choose this species as starting point and simply copy it. To do that select this species as your initial state. Otherwise, choose 'generic brain' as your starting point. In some cases it might also make sense to start with a blank canvas.

For orientation, a template brain can be chosen to be drawn in the background of the canvas. This makes it easy to draw brain outlines of new regions not included in the initial state, but potentially present in other species.

It is generally important to not deviate more than absolutely necessary from the generic brain outline, as highly divergent brains will be difficult to process when generating a multispecies schematic representation.

To modify existing neuropil models, they can be selected by clicking on the rectangles that represent them and their size and location on the canvas can be adjusted at will. To add objects, select the type of object and click 'Add structure'.

Available objects: Structures (super-regions, neuropils, subregions), fiber bundles and invisible bridges.

Rules:

- Super-regions cannot be displayed at the same time as neuropils that comprise them. Either choose to display a part of the brain on the level of super-region, or on the level of neuropil.
- Neuropils cannot be displayed at the same time as the subregions that comprise them.
- Invisible bridges should link regions on either side of a large neuropil, allowing schematic neurons to cross brain regions at that point (avoiding convoluted paths of these cells, which otherwise cannot cross brain regions)
- Ensure that right and left regions are located on the correct side of the canvas. Right and left is defined from the animal's point of view.
- To remove a region, select is on the canvas and click 'remove' on the left side.
- If a super-region is going to be replaced by its components (as new anatomical insights are made), remove the super-region model and then add each component one by one.
- 'Clear Selection' deselects all brain structures.

Additional rules for central complex: The regular layout of the central complex consisting of layers and columns (strata and slices) require a special way to generate the numerous individual arborization domains resulting from this regular array structure:
- After creating the neuropil (e.g. the PB), select it on the canvas and click 'Add slice/stratum' on the left side.
- The new interface will now allow to specify the number of strata and slices to be added to the selected structure.
- Each stratum and slice can be named by using names from a list immediately left of strata and above slices. If the provided names are not sufficient, new names can be added via the menus below the neuropil illustration.
- The default for columns is 16 slices, counting eight slices from medial to lateral on each hemisphere. If nine slices are needed on either side, we suggest to add a slice R0 and L0 next to the midline. This will allow slices containing homologous neurons be named identically.
- In principle, strata and slices can be added to any neuropil that is organized as a regular array of subregions that can be reliably identified.

All changes are automatically saved. To continue to another part of the database, simply navigate to the desired function.

Images, Curator, Bibliography
To allow easy identification of the species, one or several photographs or other illustrations of the species should be uploaded by clicking on the 'edit' icon next to the 'Images heading. If several images are provided, one has to be chosen as default. Note that there should be no copy-rights attached to any images used that are incompatible with the CC-BY-NC 4.0 license that will be attached to the profile page content once made public.

Curators for the species can be chosen by clicking on the 'edit' icon next to the 'Curator' heading. Normally, the creator of the species (or the affiliated research group leader) will be most suited for this task. Note that there can be several curators for one species.

Publications linked to the species can be added by clicking on the 'edit' icon next to 'Publications' at the bottom of the page. Most simply, provide the DOI of a publication that should be added and check the found information for completeness. Once approved, click 'yes, looks good'. Otherwise, click one of the remaining options to manually correct the entry. If DOI is not available, users can also search by title or manually create a new publication.

3D reconstruction
To add a 3D reconstruction to the species, navigate to the species profile page and click the edit icon next to the 'Reconstruction' heading. On the edit page, click 'Add Reconstruction' to

create a new 3D data entry. You can choose between male, female and undefined as sex (e.g. if sex was not known, or an average brain including both sexes is uploaded, chose 'undefined').

Generally, the 3D brain can be either a representative individual brain or an average brain (standard brain) generated by an appropriate averaging procedure. *Note:* If the 3D brain shall serve as reference for neuron registration, it should be carefully chosen, *as changing it at a later stage, while possible, will require re-registration of all existing neurons* either based on the original raw data or via an appropriate bridging registration transferring the data from the old to the new template. If multiple users contribute data to that species, this will require substantial coordination between users.

Each reconstruction has to be tagged with a source publication DOI. This is the publication that should be cited when images are created in the database that use these data. If the data are not published, add the name of the owner here.

In principle, files can be uploaded individually for each brain region that was created in the schematic brain. The files will have to be formatted as obj-files and will be displayed online. These are called the 'VIEWER FILES'.

Additionally, 'Source Files' can be provided in any format that should be available for download to users (called: 'Original Label Field Data'). Each file is tagged with a creator and can be made available for download.

Note: As 3D segmentation often lags behind anatomical understanding of a species' brain, several brain structures can be assigned to a single surface model. This is important for regions that are separate entities in the schematic brain (e.g. superior protocerebrum and inferior protocerebrum), but the exact border of these regions has not yet been worked out. These regions can be reconstructed as one combined model and then associated with both identities.

Adding viewer files:
- Click 'Add viewer file' and chose the file to upload from your local computer (obj file!)
- From the menus on the right, chose the correct brain region is should be associated with, as well as the correct hemisphere. Choose the most detailed category appropriate (either super-region, neuropil or subregion).
- More than one region can be chosen if the 3D file corresponds to several schematic brain regions (holding CTRL or CMD). Click the 'Add Structure' button.
- Color is selected by default and cannot be changes
- Choose the depth ordering value for correct 3D display. This option generates a loading sequence for the 3D brain regions in the 3D viewer, so that regions in the foreground are loaded last and are thus transparent when viewed from the front. Small numbers should be attached to regions in the background and larger numbers to regions in the foreground. This can be adjusted at any time.
- Click the 'Update' button.
- To view a preview, click 'show preview' at the bottom of the screen.

When finished, return to the species page by clicking on the species name on the top of the screen.

Semi-schematic view

The scrollable 2D sections of the 3D brain are automatically generated from the provided 3D brain and can be viewed by clicking on the 'View Semi-Schematic' link.

Image stacks

To add an image stack of the species, click on the edit icon next to the Image Stack heading. On the edit page, click 'Add confocal stack' to add an image stack. Note that the images do not have to result from confocal imaging, but can also be obtained by e.g. micro-CT, or classic histology methods.

When adding an image stack entry, users should add a short description of the stack, which will be used to populate the drop down menu for selecting one of multiple stacks on the species page.

Two sets of files have to be uploaded, the 'Source files' and the 'viewer files'. Source files are displayed as a link and can only be downloaded. Viewer files are used to view the image stack online. To limit their size and optimize loading speed of the profile page, only jpg files are allowed as viewer files.

To upload, select the list of files on your local computer and click 'Upload File'. Data is automatically saved. When finished, return to the species profile page by clicking on the name of the species on the top of the screen.

G. Creating a neuron

When submitting a neuron, an empty profile page is generated after basic information about the neuron is provided. This profile page has to be populated with data and is located in the private section of the owner's account until it is published.

Basic information

- *full name*: please adhere to the naming scheme and put a species denominator as first part of the neuron, e.g. **am**-Pe1 for honeybee Pe-1 cell, or **dp**-CPU1-R4 for Monarch butterfly CPU1 cell in column R4
- *short name*: a simplified name without the species prefix
- *alternative names*: specify any additional names that have been used for this neuron
- *species*
- *sex: male, female, or unspecified*

Profile image

Select an image of the neuron by clicking 'add neuron image'. This is the 'profile picture' of the neuron and can be a composite image, a drawing, a 3D projection, etc. It should capture the most important characteristics of the cell at a single glance. The staining type can be specified here as well and a caption should be included. Several images can be uploaded to create a gallery of representative images (e.g. the neuron from different angles). Select 'default' for the image that should be the primary profile image.
Select 'available for download', if users should be able to download the image in full resolution.

Morphology

Clicking on the edit icon next to the 'Morphology' heading will allow to deposit information about the general morphology of a neuron. This includes innervated fiber bundles (chosen from a list of available bundles), hemisphere of the soma, soma location, and a free text description.

Arborization editor

The most important morphological information needed to allow users to find neurons and to display them as search results are links to innervated brain regions. All regions innervated by a neuron must be linked from the neuron by selecting the neuron's branching areas. To facilitate this manual process, the arborization editor exists. It can be reached by clicking on the edit icon next to the Arborization Regions subheading.

A graphical user interface will appear that displays the schematic brain layout of the species the neuron belongs to. By clicking 'Add Arborization', the user is asked to add an innervated brain area and can do so by clicking on the relevant region in the schematic brain. In the dialogue appearing on the bottom right, the direction of the innervation (input, output, unknown, the hemisphere of the neuropil, and the size of arborization (small field or large field) can be selected. If the 'passes through' option is selected, the neuron does not arborize in the selected brain region, but passes through it in a way that defines this cell type (this option is rarely needed).

A list of added brain areas will appear on the left side of the screen, from where accidentally added region can also be deleted. Note that right and left versions of brain areas have to be selected separately.

Special case – central complex: If a neuron innervates the central complex (CX), a graphical user interface will appear that allows to specify the layers and columns of the innervated CX division (e.g. ellipsoid body). Note that, for technical reasons, a single arborization region can only either contain multiple columns (slices) or multiple layers (strata). If a neuron innervates multiple complete layers, several arborization regions have to be created (each one containing all slices of one innervated layer).

Branch editor

The second key piece of information needed to have a neuron appear in the search results of the graphical search interface is its branching layout, i.e. a schematic outline of how the different arborization regions are connected. This will give the drawing algorithm of the schematic results display sufficient information to dynamically draw the neuron.

To draw the neuron outline click on 'Edit Neuron Path and BranchPoints' below the 'Schematic Search Options' subheading. This will open a graphical user interface in which the neuron outline can be generated in a few simple steps.

Neurons with only two arborizations: simply click on the first brain area, then on the second one. The connection will be drawn as a straight line illustrating a direct connection. If a tract or fiber bundle is used by the neuron, click on the first brain area, then on the fiber bundle. A connection will be drawn. The click on the fiber bundle and connect it to the second brain area.

Neurons with several innervated brain areas: As each brain area can only directly be linked to one other brain area, if there are more than two regions innervated, branch points have to be created. To create a branch point, click 'ADD' on the left side of the screen. A red dot will appear in the schematic brain illustration and can be moved to the desired location. Branch points can be linked to other branch points and several brain regions. Their location should roughly resemble the location of major bifurcations of the neuron in the animal.

Neurons innervating the central complex: For arborizations inside the CX several extra rules apply. Arborization domains (intersections of slices and strata) can be chained together, so that all arborizations of one slice (e.g. column R3) can be linked to one single branch point located outside the CX. These chained connections can link arborization domains within a

column (slice) or within a stratum (layer), but cannot connect several strata and slices (reflecting the way the arborization regions are defined within the CX).

To delete connections, click on the red line illustrating the connection. To delete a branch point, click 'Remove' on the left side and then click on a branch point.

To clear the path, click 'Clear path'. To trouble-shoot an erroneous path, click 'Repair Path'.

Once changes are made, click 'Save path' to save it.

Return to either the neuron profile page, the view of the neuron in the schematic brain, or to edit arborization regions via the links provided in the top left of the screen.

Please also refer to the 'Usage tips' in the bottom left of the screen.

3D reconstruction

A 3D version of the cell can be uploaded by clicking the edit icon next to the 'Reconstruction' heading on the neuron profile page. On the edit page, clicking 'Add Reconstruction' will create a new reconstruction entry for the chosen neuron. By clicking the UUID the user can add information to the reconstruction.

Voxel size of the images used for reconstruction should be added, as well as the actual reconstruction files. A free text description is available for any comments that might be needed to describe the reconstruction or to clarify any known issues with it.

As for file upload, a viewer file is distinguished from a source file. While the source file can be any format that the user would like to make available for download, the viewer file has to be in **swc format**. Ideally, the 3D skeleton is registered in the reference brain that is available for this species, so that the neuron can be included in the 3D display of search results. This can be specified by choosing the appropriate option in the field CFR (common frame of reference): affine registration, elastic registration, or not registered.

If not registered, 3D neuropils reconstructed from the individual preparation can also be provided, allowing to display the neuron's skeleton in combination with its surrounding brain structures in individual neuron display mode (again as viewer files in obj format, and as source files for download).

If several skeleton files are provided for a reconstruction entry, all of them are displayed at the same time, allowing to split highly complex neurons into several parts.

Any neuron can be associated with several reconstruction entries, e.g. if a new improved version becomes available. One of these must be defined as 'default' and will be the one displayed on the profile page. If a reconstruction is linked to a published neuron, it will be locked and cannot be deleted or modified. It can be replaced/updated by adding a new reconstruction with the updated files and defining the new reconstruction as default. The current version of the neuron profile will now display the updated version. The old version will remain associated with the original, published profile page to maintain data persistence.

Confocal image stack

One or several confocal image stacks can be provided to illustrate the neuron's morphology. Image stacks are uploaded both as source files (any format), and as a series of jpg-images for online display (viewer files). The procedure is identical to that used for 3D reconstructions. Different from reconstructions, several image stacks can be made available at the same time. A stack that is part of a public neuron cannot be deleted. If a stack is going to be replaced in the current version of the neuron profile, it can be archived (selecting the *archive* option on the editing page). It will then no longer appear in the current neuron profile page, but will remain available on all published version of the page.

Functional data

Add information about the function of the neuron (if known). This includes representative (consensus) information about firing rate, response categories, sensory modality, transmitter expression, role in the network (inhibitory versus excitatory) and neuromodulators. An image illustrating a typical response of the neuron can be added as well (e.g. a spike train, a tuning-graph, etc.).

Keywords and other information

Add keywords and remaining information by filling in the relevant fields. Keywords should be filled in using the autocomplete function to avoid duplicated with conflicting spelling.

H. Creating an experiment

Each experiment consists of data files and meta information. A new experiment can be added either by clicking 'Add experiment' in the experiment list, or by clicking the edit icon next to 'experiment' on neuron profile pages, species profile pages, or brain region profile pages. When adding an experiment from the list view, the entity it should be linked to has to be manually specified.

Meta-information

As basic information, the user has to provide the entry the experiment should be connected with (species, brain regions, neurons), the type of experiment (choose from list of entries), the experimenter, a brief description, the date the experiment was performed, and any additional comments.

If the experiment is included in a publication, it can be linked here as well.

Once created, the experiment will receive a unique ID (EIN) for internal database use. All experiments are private until explicitly published by the owner.

Data Files

Data files can be in any format and are available for download. Choose the file from your local computer and click 'Upload File' to upload to the database. Any number of files can be uploaded.

I. Modifying published entries

In general, modifying data works in the identical way to creating data in the first place. This is fully true for private data, and all edit functions are available. Data can also be deleted, including species and neuron entries.

To ensure persistency, data are locked and cannot be edited or deleted once published. They receive a digital handle, i.e. a unique identifier similar to a DOI, that can be used to reference the dataset in publications.

To enable datasets to evolve, the private version of the dataset (current version) exists in parallel to the published one. The private version can be fully edited and data can be freely

added. Once changes have accumulated that warrant a new public version, the dataset can be republished and will receive a new version of the handle.

As each entry that is linked to a published dataset is locked, they cannot be deleted. This applies to all images, image stacks, 3D reconstructions and experiment files.

To update these files, a new entry has to be created, in which the new data is uploaded. This new data is then defined as default (images, 3D reconstructions, confocal stacks) and will be visible on the current version of the linked profile page. The old version will still be online and linked to the public versions.

Special rules for image stacks: As many image stacks can exist in parallel in each neuron or species, they have to be archived if they are meant to disappear from the current version of the pages.

Special rules for 3D reconstructions of species: Once a species 3D brain is public, it can be modified only as a new entry. To prevent users from having to re-upload all 3D data (e.g. if only small, yet important changes were made), the edit page of the 3D species reconstructions allows to duplicate the existing entry. After duplication, this new dataset can be modified at will and defined as new default data. Once it is default, it will be displayed on the current version of the species page. It will be publicly available only after republication of the current page.