FAKULTÄT
FÜR !NFORMATIK

Faculty of Informatics

Research on Graphical Interfaces to Perform Anatomical Queries on Large Collections of Gene Expression Images

BACHELORARBEIT

zur Erlangung des akademischen Grades

Bachelor of Science

im Rahmen des Studiums

Medieninformatik und Visual Computing

eingereicht von

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Mitwirkung: Dipl.-Math. Dr. Katja Bühler

Wien, 6. April 2018

Yan Cai	Eduard Gröller

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Research on Graphical Interfaces to Perform Anatomical Queries on Large Collections of Gene Expression Images

BACHELOR'S THESIS

submitted in partial fulfillment of the requirements for the degree of

Bachelor of Science

in

Media Informatics and Visual Computing

by

Yan Cai
Registration Number 1425123

to the Faculty of Informatics

at the TU Wien

Advisor: Ao.Univ.Prof. Dipl.-Ing. Dr.techn. Eduard Gröller
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Vienna, 6th April, 2018

	Yan Cai	Eduard Gröller

Acknowledgements

I express my deep sense of gratitude to my supervisor Ao.Univ.Prof. Dipl.-Ing. Dr.techn. Eduard Gröller (Vienna University of Technology, Vienna Austria) and Dipl.-Math. Dr. Katja Bühler (VRVis Research Center, Vienna Austria) for their support and patient guidance from beginning to the end.

I sincerely thank Florian Schulze, Florian Ganglberger, Nicolas Swoboda and Markus Töpfer, team members of the Biomedical Visualization Group at VRVis, for their encouragement and suggestion.

Without their support, this work would not have been possible. I appreciate all the people I mentioned above for all their effort, motivation, and support.

Abstract

As image information is increasing sharply, searching and presenting interesting images in large databases have become more and more important in image management. In this paper, an optimizing graphical query interface was designed for anatomical search to present more valuable information from the large neuro-anatomical image collections of Drosophila (fruit fly) brains. In order to achieve the goal, the relevant websites of “Fly Circuit”, “Fly Light” and “Allen Mouse Brain Atlas”, and the image management software of PivotViewer and Zegami were investigated firstly. Then, analysis and comparison for the mentioned tools using different perspectives were conducted to define the guidelines for best practices out of them. Based on the findings, several redesigns are proposed for neuro-anatomical query interfaces and part of them were implemented.

Contents

CHAPTER 1

Introduction

1.1 Motivation

The human brain contains about 100 billion neurons [NAS]. It is considered very large given current technological capabilities. Compared with the human brain, the Drosophila brain only has 135,000 neurons [ACC^{+}12]. Moreover, Drosophila exhibits many complex behaviors, such as feeding, mating, and learning [IB10]. Therefore, it is a suitable model for studying neural connections.

Brainbase [Braa] is a large database of confocal microscopy images of the Drosophila nervous system. BrainBaseWeb is the user interface of BrainBase, in which users can search and browse the confocal microscopy images and related anatomical data. In order to help neurobiologists gain better insight with these images, we want to propose a redesign concept for an important component of the BrainBaseWeb: the anatomical search interface. The anatomical search is a graphical interface to perform anatomical queries on large collections of gene expression images. It allows users to retrieve images with a certain staining expression. Staining is a genetic mark of gene expression. Currently over 12000 images are publically available and over 50000 images are used internally by our collaboration partners. How to search the right image out of tens of thousands and what is the most useful and relevant information we should provide for the users are the major questions. To be addressed in this context, we discuss them and try to solve these issues in the following sections.

1.2 Image Retrieval Techniques

Searching for images in large databases is the main problem which we want to solve in our research. There has been a wealth of papers, articles and books proposing different techniques. Overall, these techniques can be divided into two categories: description-based image retrieval and context-based image retrieval (CBIR).

1.2.1 Description-based Image Retrieval

With using description-based image retrieval, users are allowed to search images by keywords, tags, labels, subject heading, caption or descriptions associated with the image [CR99]. However, it requires users to annotate the images manually. If the image database is very large, it becomes unfeasible.

1.2.2 Content-based Image Retrieval

Content-based image retrieval allows users to search images based on their content and features, such as intensities, shapes, textures, and structure [EGF99]. Traditional content-based image retrieval is based on the idea of Query-by-Example and requires users to upload images. Interesting features of the image will be extracted, compared with other images in the database and similar images will be shown as result. Nakazato et al. [NMH02] present an advanced interface, which allows users to search, annotate, and organize digital images by group (Query-by-Group). Users can drag and group images on the interface and create groups of queries. The result will be shown on another pane beside the query pane, so that users can see the result interactively. Besides of grouping images, users can also combine simple algorithms to create a query. An approach introduced by Eidenberger [Eid00] combines several simple algorithms and groups them into query models in order to retrieve images. Query-by-Memory is another often-used concept in CBIR. Unlike Query-by-Example, Query-by-Memory uses a set of image features (color, shape, texture, spatial attributes) as query. A color-selection interface developed by Egon L. van den Broek et al. [vdBKV04] is based on the concept of Query-by-Memory.

1.3 Related Work in Research and Commerce

There are several databases on resources of neuro-anatomical data available that also provide extensive query possibilities. Examples further investigated in this context are: FlyCircuit [Flyc], FlyLight [Flyd], Allen Mouse Brain Atlas [All], FlyBase [Flya] and Virtual Fly Brain [Vir]. These websites are all interfaces for neurobiologists to explore the nervous system, for instance the connectivity and expression of neurons. Different image management tools, which are used to explore image collections such as Zegami [Zega] and PivotViewer [Piv], are also very popular in this field.

1.4 Problem Statement

There are large numbers of techniques that have been developed to retrieve images. However, it is still difficult to search the related images. Based on our research, there are mainly two reasons: one is the enormous amount of images and the other is the complexity of images. Images always carry a wealth of messages, including intensities, shapes, textures, structures, and specific meaning that pertain to a particular context. For instance, the sparsity of gene expression patterns in neuropils is an important criterion of neuro-anatomical images for the query. Moreover, for other types of images, shapes or intensities might be major criteria for retrieving. Different kinds of images require different search criteria. It also requires specialized knowledge to specify the search types and search parameters. Furthermore, an intuitive and user-friendly interface seems to be lacking. Due to the information overload, it is hard for the designers to figure out what different users want to accomplish. Although, sometimes a function was designed by the designer, which was intended to improve the convenience and understanding, it is not intuitive and complicated to employ at all for some users.

According to the "Eight Golden Rules of Interface Design" [Shn97] from Ben Shneiderman, there are several principles that the designer has to follow for an effective user interface. For instance, the interface should be designed consistently, with using similar icons, colors, and sequences of actions which help users learn more quickly to employ the website. In addition, according to Don Norman and his user-centered design, visibility, feedback, constraints, mapping, consistency, and affordance are promoted as the main interface design principles [Nor02, PRS01].

1.5 Structure of the Work

In order to get some inspirations and ideas, similar websites, which also provide a large collection of anatomical data sets of brains (See Chapter 2), are investigated firstly. Then the content, the data provided, and different functions of each website are analysed – for example, how users interact with these websites and which components are used for the interaction. Different image management applications are investigated with respect to how these applications are designed to manage large collections of different kinds of images and how images can be searched, filtered, grouped, and combined with associated metadata. Their advantages and disadvantages are analysed and best practices are defined in our work, which are used for redesigning the functionalities in BrainBaseWeb. Based on the findings, a redesign of the anatomical search of BrainBaseWeb is proposed (see Chapter 3) and after that part of it is implemented (see Chapter 4).

CHAPTER 2

Comparative Analysis of Relevant Websites

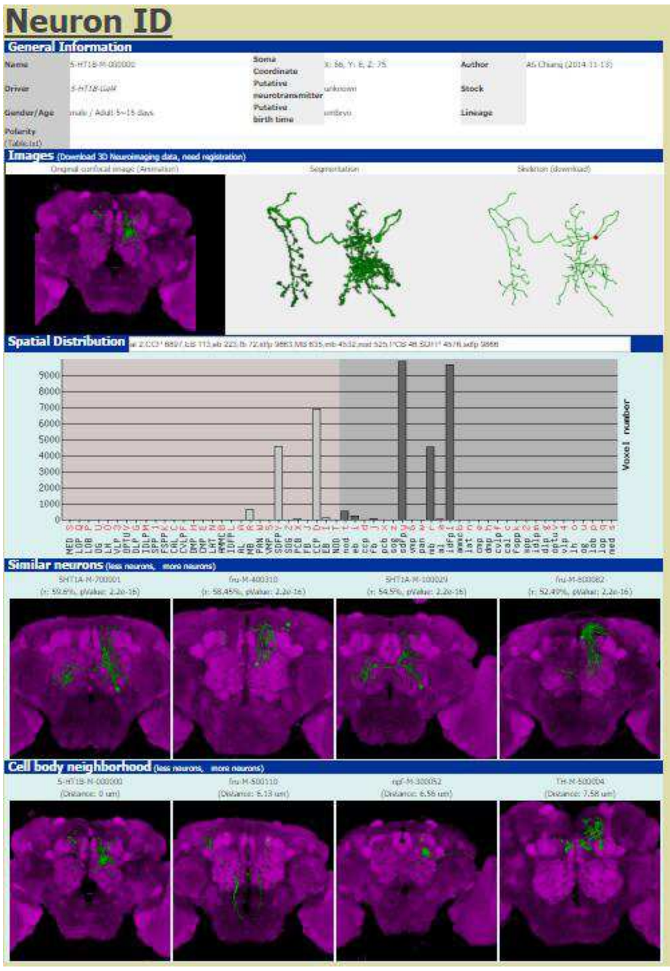
This chapter compares query interfaces for neuro-anatomical images of 3D neuron collections: Fly Circuit, Fly Light, Allen Mouse Brain Atlas, Fly Base, Virtual Fly Brain and Brain Base and also image management tools such as Zegami and PivotViewer. We will investigate the data and functions provided by the websites and tools and the advantages and disadvantages we found while using them.

2.1 Overview of the Relevant Websites

2.1.1 FlyCircuit

The first website we investigate is a Taiwanese Database of Drosophila Brains [Flyc]. This website provides functions such as basic browsing and searching, and also online archiving, data analysis, and 3D visualization.There are 23583 images of single neurons that are accessible and searchable via this website. Users can select single neurons and browse their general information (such as name, driver, gender, and age), images (confocal image, segmentation, skeleton), spatial distribution, similar neurons, and their neighbor neurons (see Figure 2.1). Furthermore, users can select several neuron images and collocate them to create a 3D visualization.

Two different search features are provided. Users are allowed to use Image-based search or Text-based search to retrieve the neurons they want. To apply Image-based search (see Figure 2.2), users just simply click on the image to select neurons in the neuropil. A neuropil is a region in the brain, which is related to a functional area. To apply Text-based search, users have to enter search terms in the appropriate boxes or select options from the drop-down lists (such as name list, driver, annotation, and innervation).



Neuron ID

General Information

Name	5-HT1B-M-000000	Soma Coordinate	X: 56, Y: 6, Z: 75	Author	AS Chiang (2014-11-13)
Driver	5-HT1B-GaW	Putative neurotransmitter	unknown	Stock	
Gender/Age	male / Adult 5~15 days	Putative birth time	embryo	Lineage	
Polarity (Table.txt)					

Images (Download 3D Neuroimaging data, need registration)

Original confocal image (Animation) | Segmentation | Skeleton (download)

Spatial Distribution al 2.CCP 6897.EB 113.eb 225.fb 72.sdfp 9883.MB 635.mb 4532.nod 525.PCB 48.SDFP 4576.sdfp 5868

9000
8000
7000
6000
5000
4000
3000
2000
1000
0
Voxel number
MED LOP LOB OG LH VLP OPTU DFTU DLP IDLP SPP FSPP CAL CVLP DMP DNP LHT AMMC IDFP AL MB PAN VMP SDFP SOG PCB FB CCP EB NOD nod eb ccp fb pcb sog sdfp vmp pan mb al idfp ammc lat dmp dmp cvlp cal fspp spp idlp dlp optu vlp lh og lob lop med

Similar neurons (less neurons, more neurons)

5HT1A-M-700001	fru-M-400310	5HT1A-M-100029	fru-M-800082
(r: 59.6%, pValue: 2.2e-16)	(r: 58.45%, pValue: 2.2e-16)	(r: 54.5%, pValue: 2.2e-16)	(r: 52.49%, pValue: 2.2e-16)

Cell body neighborhood (less neurons, more neurons)

5-HT1B-M-000000	fru-M-500110	npf-M-300052	TH-M-500004
(Distance: 0 um)	(Distance: 6.13 um)	(Distance: 6.56 um)	(Distance: 7.58 um)

Figure 2.1: Browsing Window (FlyCircuit) [Flyc]

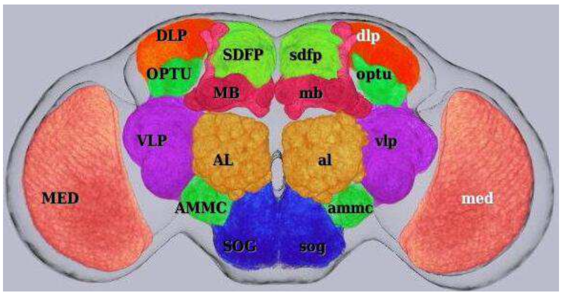
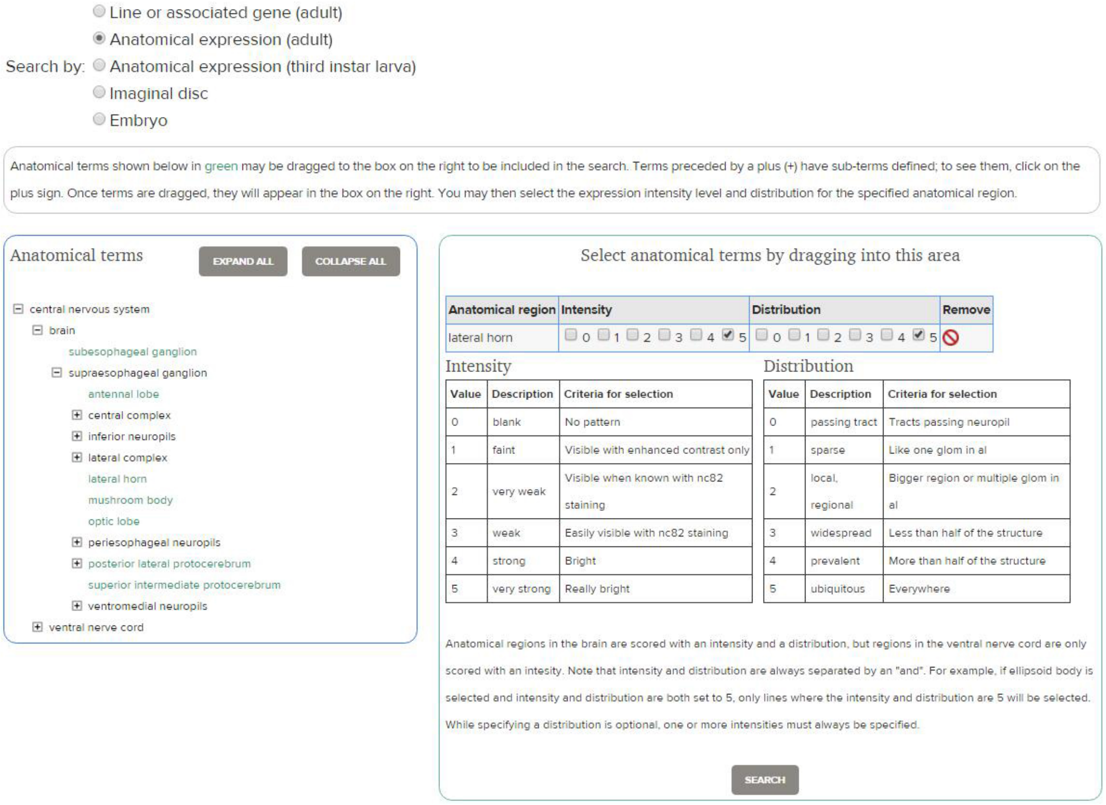


Figure 2.2: Image-based Search (FlyCircuit) [Flyc]

Besides all the functionality we mentioned above, FlyCircuit also allows users to analyze the connectivity and similarity of the neurons. Users can search neurons with similar structure by cell body neighborhood and neuron morphology, find tracts between neuropils and find wiring diagram to neuropils.

2.1.2 FlyLight



○ Line or associated gene (adult)
● Anatomical expression (adult)
Search by: ○ Anatomical expression (third instar larva)
○ Imaginal disc
○ Embryo

Anatomical terms shown below in green may be dragged to the box on the right to be included in the search. Terms preceded by a plus (+) have sub-terms defined; to see them, click on the plus sign. Once terms are dragged, they will appear in the box on the right. You may then select the expression intensity level and distribution for the specified anatomical region.

Anatomical terms

⊟ central nervous system
  ⊟ brain
    subesophageal ganglion
    ⊟ supraesophageal ganglion
      antennal lobe
      ⊞ central complex
      ⊞ inferior neuropils
      ⊞ lateral complex
      lateral horn
      mushroom body
      optic lobe
      ⊞ periesophageal neuropils
      ⊞ posterior lateral protocerebrum
      superior intermediate protocerebrum
      ⊞ ventromedial neuropils
  ⊞ ventral nerve cord

Select anatomical terms by dragging into this area

Anatomical region	Intensity	Distribution	Remove
lateral horn	□ 0 □ 1 □ 2 □ 3 □ 4 ☑ 5	□ 0 □ 1 □ 2 □ 3 □ 4 ☑ 5	⃠

Intensity

Value	Description	Criteria for selection
0	blank	No pattern
1	faint	Visible with enhanced contrast only
2	very weak	Visible when known with nc82 staining
3	weak	Easily visible with nc82 staining
4	strong	Bright
5	very strong	Really bright

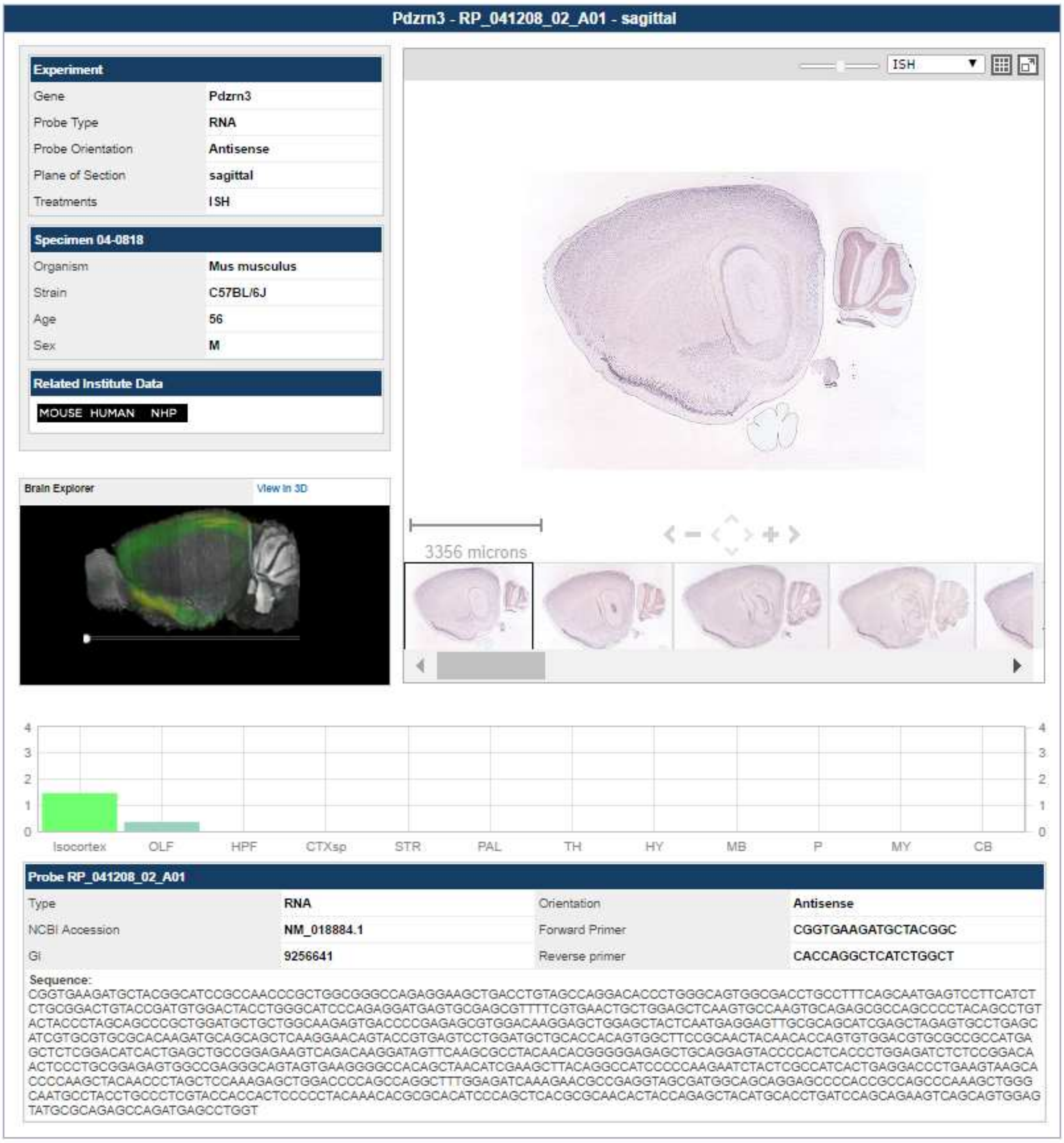
Distribution

Value	Description	Criteria for selection
0	passing tract	Tracts passing neuropil
1	sparse	Like one glom in al
2	local, regional	Bigger region or multiple glom in al
3	widespread	Less than half of the structure
4	prevalent	More than half of the structure
5	ubiquitous	Everywhere

Anatomical regions in the brain are scored with an intensity and a distribution, but regions in the ventral nerve cord are only scored with an intesity. Note that intensity and distribution are always separated by an "and". For example, if ellipsoid body is selected and intensity and distribution are both set to 5, only lines where the intensity and distribution are 5 will be selected. While specifying a distribution is optional, one or more intensities must always be specified.

Figure 2.3: Anatomical Search (FlyLight) [Flyd]

FlyLight is a database for GAL4 line and LexA line images [Flyd]. When browsing different GAL4 and LexA driver lines, general information of this line is provided. Users can also browse information such as projection, translation movie, or substack of the lines. This website provides several Text-based search features, such as search by line or associated gene and search by anatomical expression. In this paper we focus on the search by anatomical expression. In the anatomical user interface, users can select neuropils by dragging them from the anatomical term list on the left into the pane on the right side. After doing this, they can specify the intensity and distribution with two quantifiers (from “0” to “5”, with “0” meaning no pattern or tracts passing neuropil, “5” meaning very strong presence of tracts or they are everywhere) in order to retrieve images (See Figure 2.3).



Pdzrn3 - RP_041208_02_A01 - sagittal

Experiment	
Gene	Pdzrn3
Probe Type	RNA
Probe Orientation	Antisense
Plane of Section	sagittal
Treatments	ISH

Specimen 04-0818	
Organism	Mus musculus
Strain	C57BL/6J
Age	56
Sex	M

Related Institute Data

Probe RP_041208_02_A01			
Type	RNA	Orientation	Antisense
NCBI Accession	NM_018884.1	Forward Primer	CGGTGAAGATGCTACGGC
GI	9256641	Reverse primer	CACCAGGCTCATCTGGCT

Sequence:

```
CGGTGAAGATGCTACGGCATCCGCCAACCCGCTGGCGGGCCAGAGGAAGCTGACCTGTAGCCAGGACACCCTGGGCAGTGGCGACCTGCCTTTCAGCAATGAGTCCTTCATCT
CTGCGGACTGTACCGATGTGGACTACCTGGGCATCCCAGAGGATGAGTGCGAGCGTTTTCGTGAACTGCTGGAGCTCAAGTGCCAAGTGCAGAGCGCCAGCCCCTACAGCCTGT
ACTACCCTAGCAGCCCGCTGGATGCTGCTGGCAAGAGTGACCCCGAGAGCGTGGACAAGGAGCTGGAGCTACTCAATGAGGAGTTGCGCAGCATCGAGCTAGAGTGCCTGAGC
ATCGTGCGTGCGCACAAGATGCAGCAGCTCAAGGAACAGTACCGTGAGTCCTGGATGCTGCACCACAGTGGCTTCCGCAACTACAACACCAGTGTGGACGTGCGCCGCCATGA
GCTCTCGGACATCACTGAGCTGCCGGAGAAGTCAGACAAGGATAGTTCAAGCGCCTACAACACGGGGGAGAGCTGCAGGAGTACCCCACTCACCCTGGAGATCTCTCCGGACA
ACTCCCTGCGGAGAGTGGCCGAGGGCAGTAGTGAAGGGGCCACAGCTAACATCGAAGCTTACAGGCCATCCCCCAAGAATCTACTCGCCATCACTGAGGACCCTGAAGTAAGCA
CCCCAAGCTACAACCCTAGCTCCAAAGAGCTGGACCCCAGCCAGGCTTTGGAGATCAAAGAACGCCGAGGTAGCGATGGCAGCAGGAGCCCCACCGCCAGCCCAAAGCTGGG
CAATGCCTACCTGCCCTCGTACCACCACTCCCCCTACAAACACGCGCACATCCCAGCTCACGCGCAACACTACCAGAGCTACATGCACCTGATCCAGCAGAAGTCAGCAGTGGAG
TATGCGCAGAGCCAGATGAGCCTGGT
```

Figure 2.4: Browsing Window (Allen Mouse Brain) [All]

2.1.3 Allen Mouse Brain Atlas

The Allen Mouse Brain Atlas provides large anatomical data sets of adult mice brain with powerful browsing and search features (such as gene searches, ISH image viewer, microarray and RNA sequencing data, Brain Explorer software for 3D visualization and atlas viewer) [SNL$^+$12, All]. It supports a large number of functionalities to browse and explore gene expressions. First of all, the browsing page (see Figure 2.4) of an individual gene includes experiment details as well as general information of the gene,

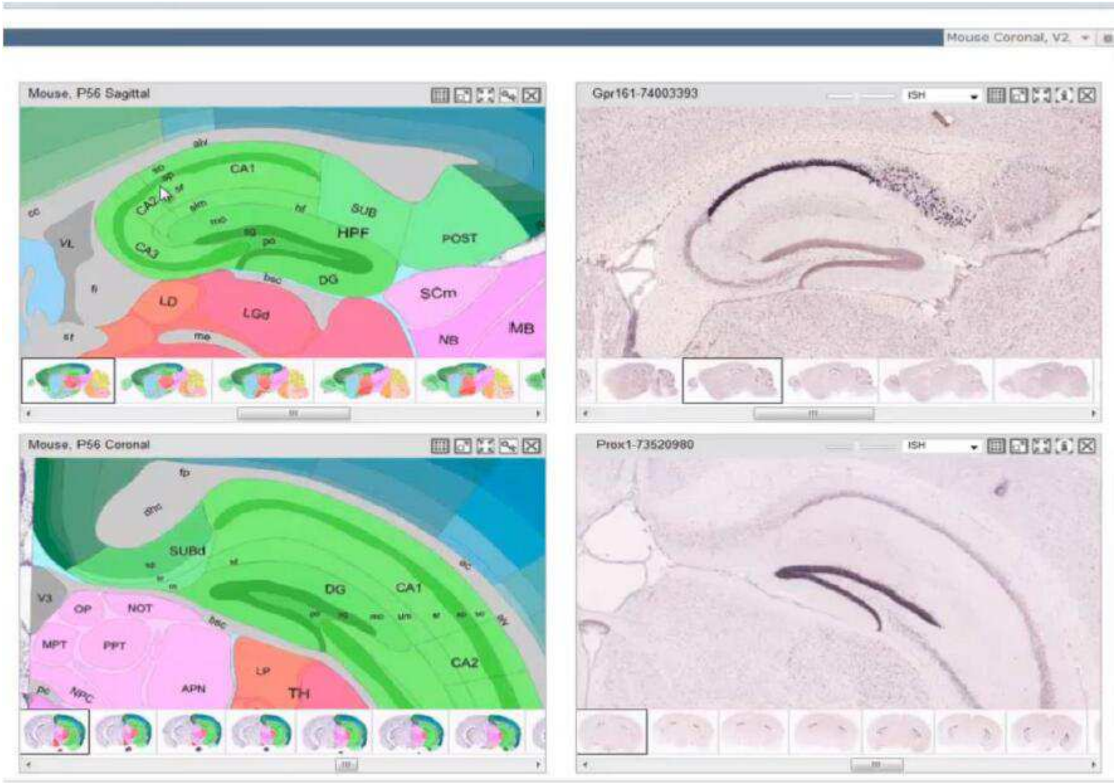
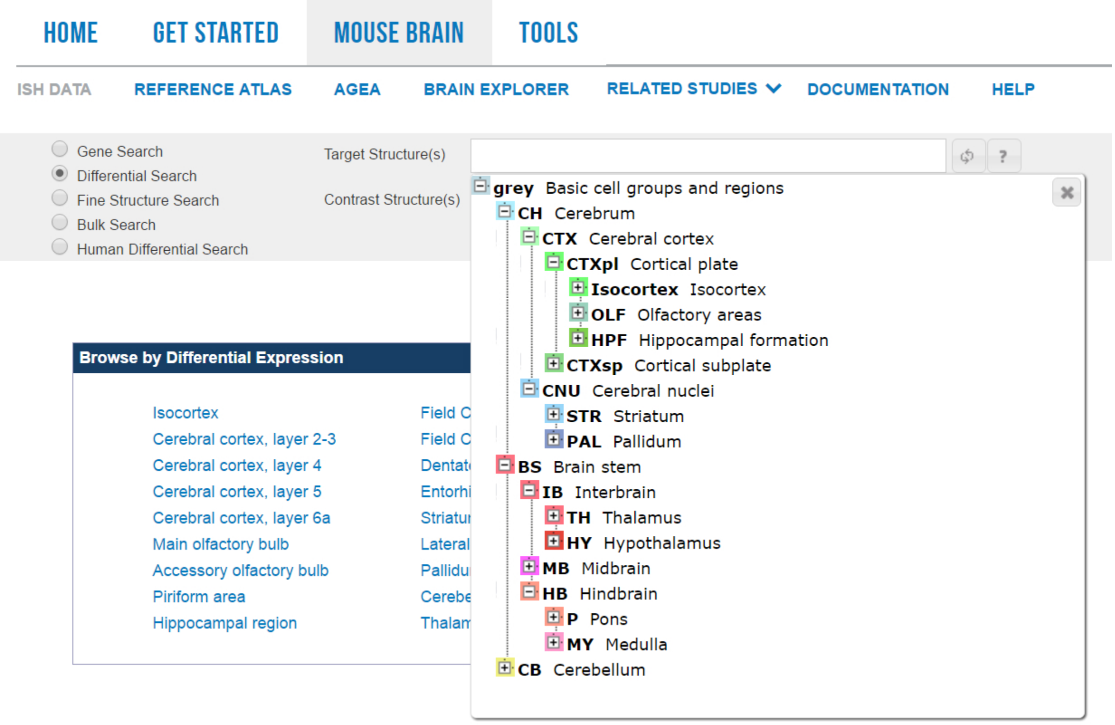


Figure 2.5: Left: Reference Atlases, Right: two different expression patterns (Allen Mouse Brain) [All]

a 3D thumbnail view expression, and an ISH image viewer. With using the ISH image viewer, users are allowed to zoom and pan the gene expression images in different slices. At the bottom of the browsing page, a histogram is shown, which provides a quantitation of a gene expression. Twelve large structures are represented in the histogram. When the users move the mouse over the structure, gene expression values will be indicated. A powerful tool called Reference Atlas Viewer is available on the website. It provides users a reference when exploring and analyzing gene expression images. Furthermore, users can explore several genes at the same time, add Reference Atlases which we mentioned above and synchronize all the expression patterns (see Figure 2.5). In addition, a 3D viewer called Brain Explorer is also provided. It is an extension of the Reference Atlas Viewer. Users can view 3D visualized data with an associated Reference Atlases and metadata.

Allen Mouse Brain provides mainly two different search features: gene search and anatomical search. Gene search allows users to search gene expressions using gene symbols and gene names. Anatomical search allows users to select certain anatomical terms from a drop-down list, in order to retrieve gene expressions in a particular brain structure (see Figure 2.6). Beside gene search and anatomical search, a correlate gene search is also provided. Users can find other genes with similar expressions, accomplished



○ Gene Search
● Differential Search
○ Fine Structure Search
○ Bulk Search
○ Human Differential Search

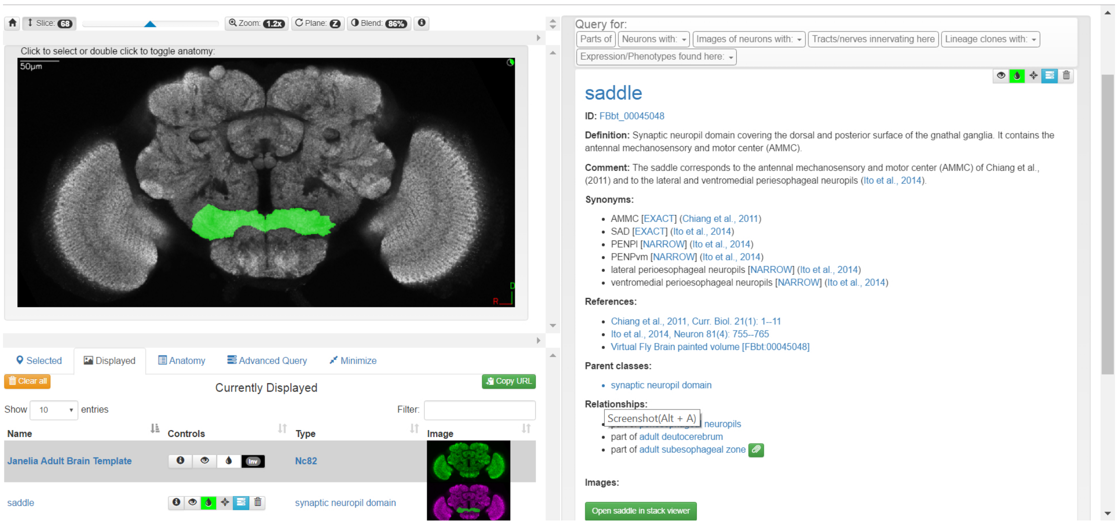
Figure 2.6: Anatomical Search (Allen Mouse Brain) [All]

using the NeuroBlast Search. Once a gene has been selected and the query has been applied, a list of genes matching the selection criteria with similar expression profiles will be returned.

2.1.4 FlyBase

FlyBase is the database most frequently used by Drosophila researchers. It provides the most complete amount of information, such as information of expression data, stocks, mutants, researchers, publications, references and more [Flya, Flyb]. However, FlyBase does not host large image collections, but only links to other collections. When browsing different gene expressions in FlyBase, general information, genomic location, families, domain and molecular function, and gene ontology are available for users to view.

According to search features, FlyBase provides also different search tools. QuickSearch, QueryBuilder and TermLink are the main tools for searching. The search features are mainly text-based. Users can select options from drop-down lists, enter search terms, and have check boxes or option buttons available to specify queries.



Click to select or double click to toggle anatomy:

Currently Displayed

Show 10 entries Filter:

Name	Controls	Type	Image
Janelia Adult Brain Template		Nc82	
saddle		synaptic neuropil domain	

saddle

ID: FBbt_00045048

Definition: Synaptic neuropil domain covering the dorsal and posterior surface of the gnathal ganglia. It contains the antennal mechanosensory and motor center (AMMC).

Comment: The saddle corresponds to the antennal mechanosensory and motor center (AMMC) of Chiang et al., (2011) and to the lateral and ventromedial periesophageal neuropils (Ito et al., 2014).

Synonyms:

- AMMC [EXACT] (Chiang et al., 2011)
- SAD [EXACT] (Ito et al., 2014)
- PENPI [NARROW] (Ito et al., 2014)
- PENPvm [NARROW] (Ito et al., 2014)
- lateral perioesophageal neuropils [NARROW] (Ito et al., 2014)
- ventromedial perioesophageal neuropils [NARROW] (Ito et al., 2014)

References:

- Chiang et al., 2011, Curr. Biol. 21(1): 1--11
- Ito et al., 2014, Neuron 81(4): 755--765
- Virtual Fly Brain painted volume [FBbt:00045048]

Parent classes:

- synaptic neuropil domain

Relationships:

- neuropils
- part of adult deutocerebrum
- part of adult subesophageal zone

Images:

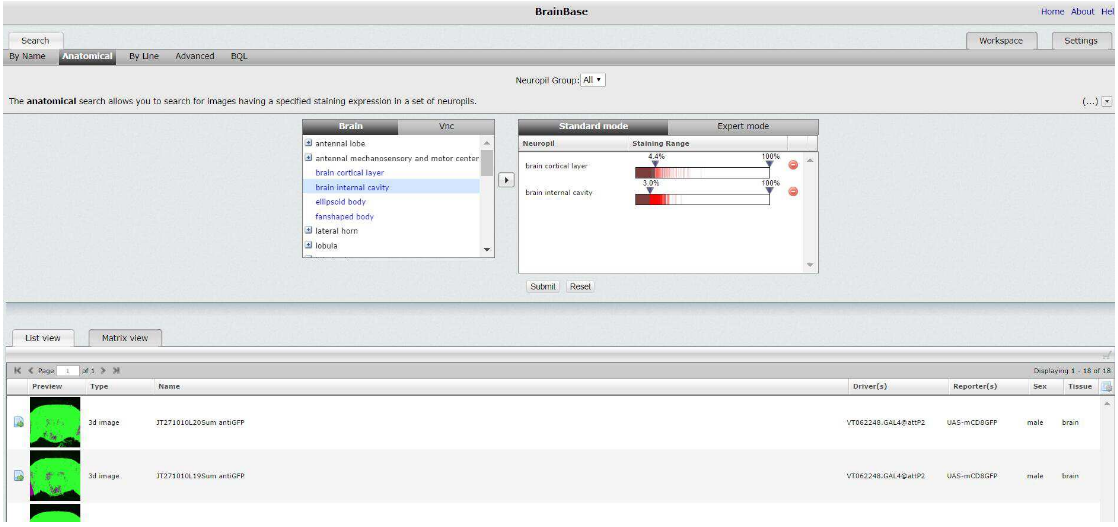
Figure 2.7: Browsing Window (Virtual Fly Brain) [Vir]

2.1.5 Virtual Fly Brain

Virtual Fly Brain is another interactive tool to explore the nervous system of Drosophila, such as its connectivity, anatomy, and expressions [Vir]. Image datasets are integrated into three different brain templates, in order to determine the position of the expression and to find similar neurons or neuropils. The Browsing window of Virtual Fly Brain is divided into three parts: Stack Viewer (upper left), Info Window (right) and Viewer Menu (bottom left) (see Figure 2.7). Stack Viewer is a slice browser: users can view the neuropils in different slices and also zoom and pan the slices. With clicking on the image, the name of the selected neuropil will be shown on the Stack Viewer, and the general information about this neuropil will be shown on the right side in the Info Window. In the Viewer Menu (buttom left), users can modify the selected neuropils, they can choose if they want to show the neuropil in the Stack Viewer, and they can delete or add a neuropil to the Viewer Menu. Users can also switch to an anatomy view to select specific anatomical terms to add. Furthermore, users can apply queries for a particular neuropil, by clicking the “Query for” menu bar above the Info Window. The “Query for” menu bar is context dependent. It includes query options such as “search neurons with some part here”, “search tracts/nerves innervating here”.

In addition to these, Virtual Fly Brain provides analysis features, such as “One against all search”, “Pairwise comparison”, “Upload tracing” and “GAL4 Search”. “One against all search” allows users to compare one neuron against all other neurons stored in the Virtual Fly Brain, in order to find the nearest neighbor and same type of neurons. “Pairwise comparison” makes it possible to compare two different neurons, to know if they are related. “Upload tracing” and “GAL4 Search” request users to upload a tracing or enter a neuron to compare against all cluster example or neuropil based staining patterns of GAL4 lines stored in the Virtual Fly Brain. All the results and neurons found will be listed and shown in a 3D view. Users can interact with the 3D model and download the information of the neurons.

2.1.6 BrainBaseWeb



Neuropil Group: All

The **anatomical** search allows you to search for images having a specified staining expression in a set of neuropils.

Neuropil	Staining Range
brain cortical layer	4.4% – 100%
brain internal cavity	3.0% – 100%

Page 1 of 1 Displaying 1 - 18 of 18

Preview	Type	Name	Driver(s)	Reporter(s)	Sex	Tissue
	3d image	JT271010L20Sum antiGFP	VT062248.GAL4@attP2	UAS-mCD8GFP	male	brain
	3d image	JT271010L19Sum antiGFP	VT062248.GAL4@attP2	UAS-mCD8GFP	male	brain

Figure 2.8: Anatomical Search (BrainBaseWeb) [Braa]

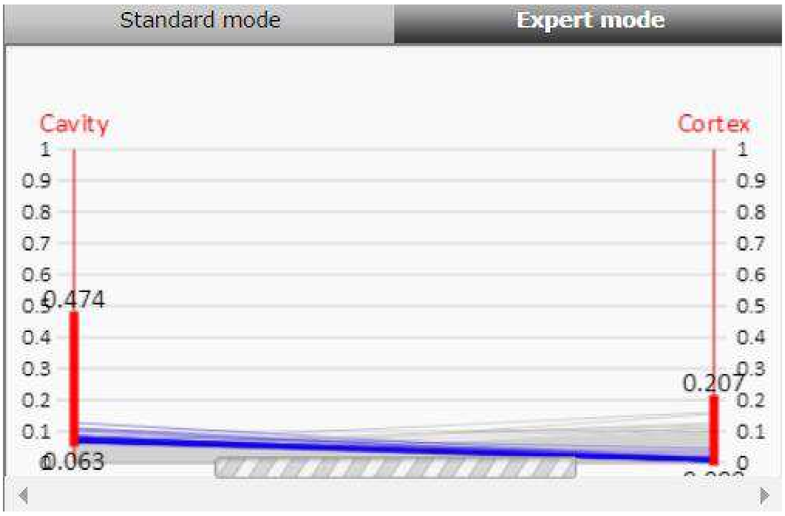


Figure 2.9: Parallel Coordinates (BrainBaseWeb) [Braa]

BrainBase is a large database of confocal microscopy images of the Drosophila nervous system. BrainBaseWeb is the user interface of BrainBase [Braa, Brab]. The anatomical search of BrainBaseWeb allows users to retrieve images, which have a certain staining expression. The search interface is divided into three parts: available anatomical terms, which can be selected, are positioned at the upper left, standard mode and export mode used for searching are at the upper right, list view and matrix view used to view the results are at the bottom (see Figure 2.8). To apply a query, users can simply select neuropils and add them to the search mode area. There are two different search modes. In the standard mode, each selected neuropil is shown as a slider in the search mode area. Users can employ the slider to specify a staining expression range within a neuropil. In the expert mode, the selected neuropils are shown as vertical lines. Users can employ the parallel coordinate widget to specify complex staining patterns over several neuropils (see Figure 2.9). One advantage of the parallel coordinate widget is that the users get immediate feedback on the number of images corresponding to the defined pattern while defining the expression range for each neuropil. If no result is found, all the lines will be gray; otherwise, the result lines will be drawn in blue. If users employ the standard mode, the results cannot be explored simultaneously. Therefore, it could happen that users cannot find any results with the expression range they specified.

2.2 Investigation of Image Management Applications

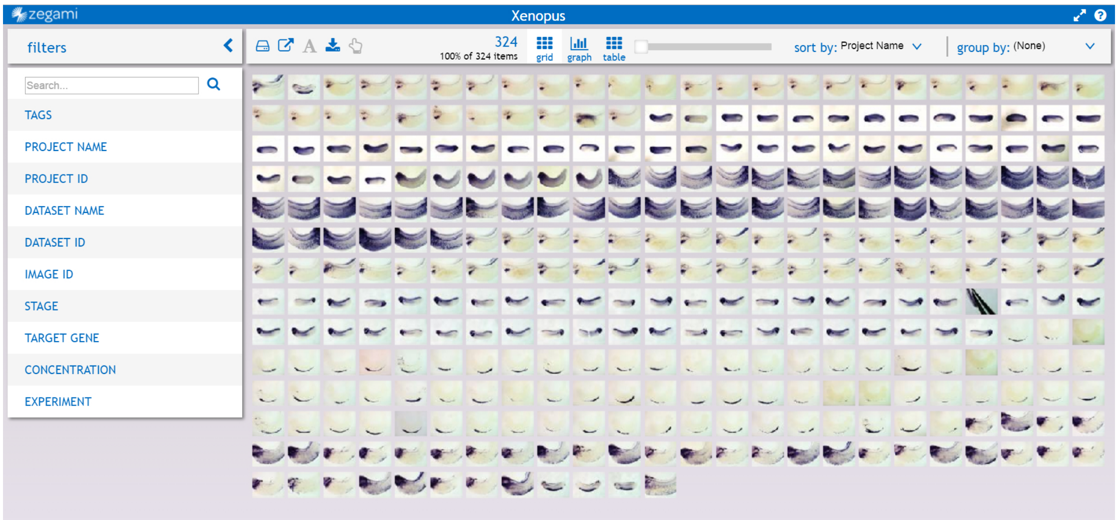


Figure 2.10: Grid View (Zegami) [Zega]

Zegami and PivotViewer are two image management tools, helping users to search, sort, filter, and group their images and associate the images with metadata [Zega, Piv]. While using Zegami and PivotViewer, users are allowed to explore and manage tens of thousands of images at once. Zegami is the extension of PivotViewer. In Zegami, more features are integrated, and more images can be manipulated and managed than in the PivotViewer. So we only introduce the functionalities and interface design of Zegami in this section.

The browsing window of Zegami is divided into three parts: filter panel, toolbar and view (see Figure 2.10). In the toolbar, users can switch between three different views:

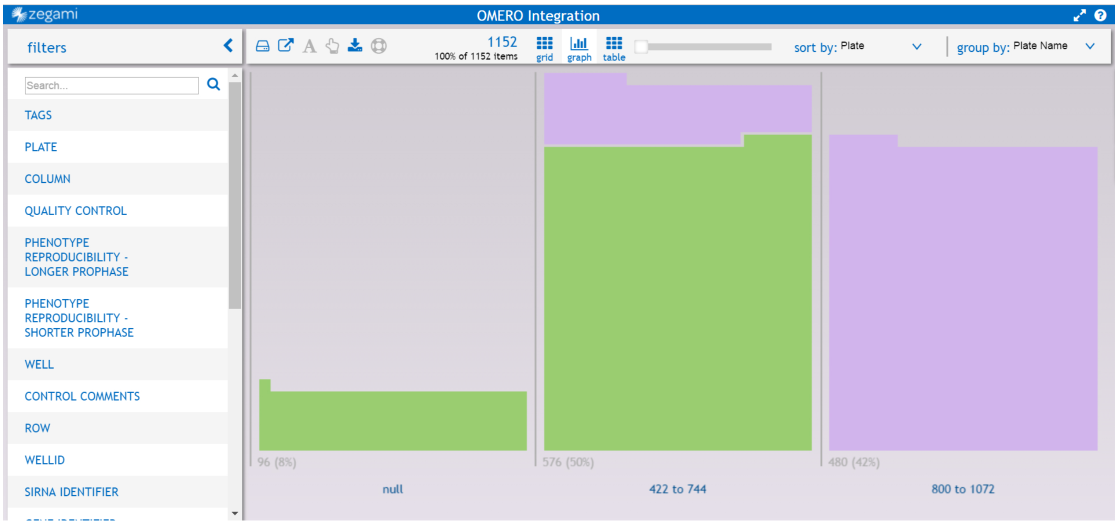
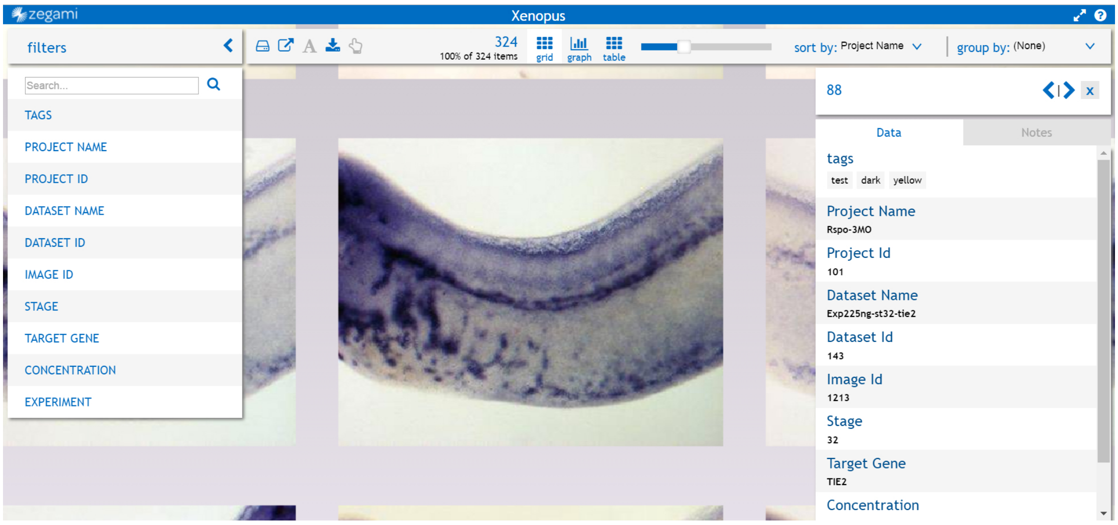


Figure 2.11: Graph View (Zegami) [Zegb]



88

tags
test dark yellow

Project Name
Rspo-3MO

Project Id
101

Dataset Name
Exp225ng-st32-tie2

Dataset Id
143

Image Id
1213

Stage
32

Target Gene
TIE2

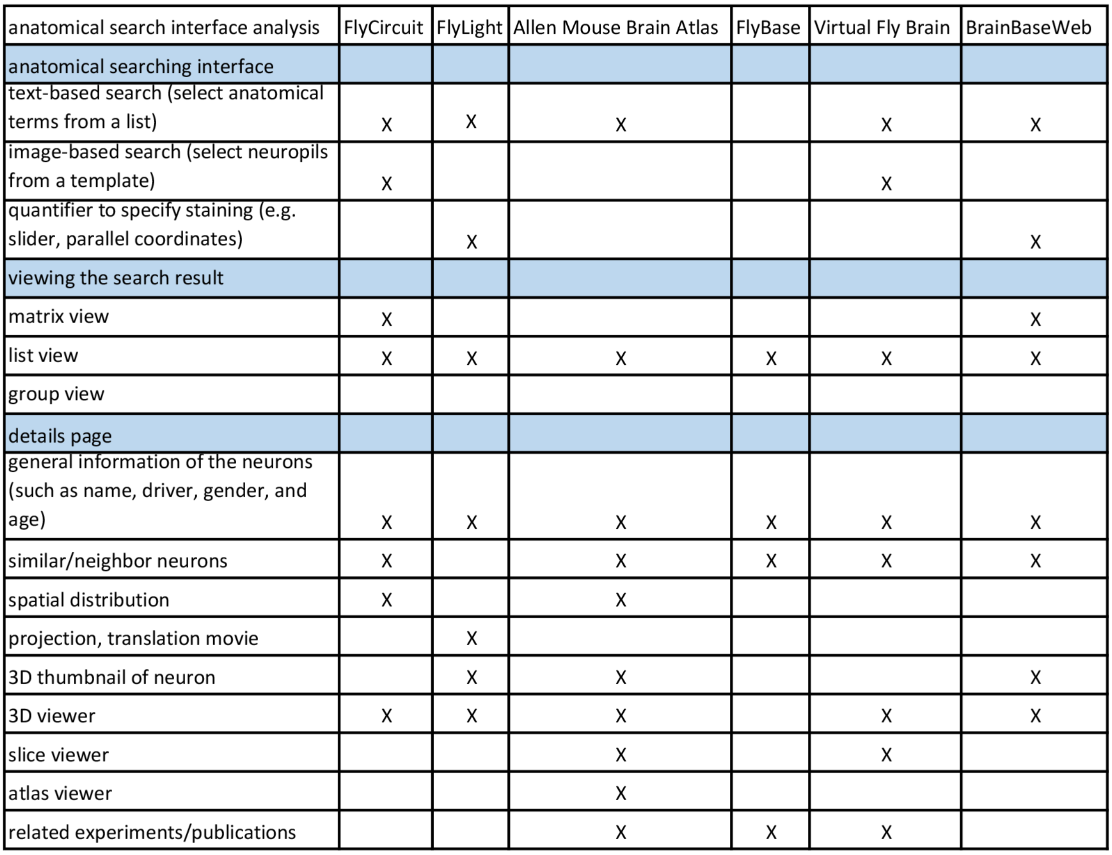
Concentration

Figure 2.12: Detail of the selected image (Zegami) [Zegb]

grid view, graph view, table view, or map view. In the grid view, the previews of images are shown as a matrix. In the graph view (Figure 2.11), images are sorted and grouped according to several criteria, and shown as histograms in different columns. In the table view, all information of a neuron will be shown in a list. In the map view, labels showing the number of the images taken in this region are displayed. Besides different views, users can also use the “sort by” and “group by” drop-down lists to sort and group the images with different criteria. In addition to this, users can employ the filter options in the filter panel to filter the images. In Figure 2.10, possible filters are tags, path, project name, dataset ID and so on. For different datasets, different filter, group, and sort criteria should be used. If the user clicks on the image, the details of the selected image will be displayed on the right side. With selecting “find 10 similar” users can employ image similarity search to find images similar to the selected image(Figure 2.12).

2.3 Comparison and Analysis

Based on the investigation of different graphical query interfaces, we found out that, in order to apply a query, three steps are needed: Firstly, use the search interface to search. Secondly, view the search result and choose the image the users want to view. Lastly, users click on the image and open the details page to view further information. In the following text, the design of these three steps in different interfaces will be analyzed and compared.



anatomical search interface analysis	FlyCircuit	FlyLight	Allen Mouse Brain Atlas	FlyBase	Virtual Fly Brain	BrainBaseWeb
anatomical searching interface						
text-based search (select anatomical terms from a list)	X	X	X		X	X
image-based search (select neuropils from a template)	X				X	
quantifier to specify staining (e.g. slider, parallel coordinates)		X				X
viewing the search result						
matrix view	X					X
list view	X	X	X	X	X	X
group view						
details page						
general information of the neurons (such as name, driver, gender, and age)	X	X	X	X	X	X
similar/neighbor neurons	X		X	X	X	X
spatial distribution	X		X			
projection, translation movie		X				
3D thumbnail of neuron		X	X			X
3D viewer	X	X	X		X	X
slice viewer			X		X	
atlas viewer			X			
related experiments/publications			X	X	X	

Figure 2.13: Anatomical search interface analysis

2.3.1 Similarity of Relevant Websites

Anatomical searching interface:

As shown in Figure 2.13, most of the interfaces only provide Text-based search. Users enter search terms in the search box or select options from the drop-down lists (for instance by selecting anatomical terms from a list of particular brain areas) or select checkboxes.

Viewing the search result:

Most of the interfaces only provide a list view.

Details page of the neuron:

Most of the interfaces provide general information of the neurons (such as name, driver, gender, and age), publications, experiments, and references associated with the neurons. Some of them also provide information about similar neurons and their neighbor neurons. Almost all of the relevant interfaces also provide a 3D viewer, so that the users can view a neuron in 3D and rotate the model in different perspectives.

2.3.2 Difference of Relevant Websites

Anatomical searching interface:

FlyLight developed a quantifier (from “0” to “5”, with “0” meaning no pattern or tracts passing neuropil, “5” meaning very strong presence of tracts or they are everywhere) for intensity and distribution in the anatomical search. Some of the websites also developed an Image-based search. For example, in FlyCircuit and Virtual Fly Brain, users can simply click on the template of neuropils to retrieve neurons or neuropils in a certain brain region (see Figure 2.2 and Figure 2.7).

Viewing the search result:

Most of the interfaces only provide a list view. Only some of them provide a matrix view.

Details page of the neuron:

Only a few interfaces provide projection and movies of neurons. As mentioned before, a 3D viewer is provided in almost all the interfaces. However, some interfaces also provide other views, which have different functions. For instance, Allen Mouse Brain Atlas provides a slice viewer and an atlas viewer. With using the slice viewer, users are allowed to zoom and pan the gene expression images in different slices. Atlas viewer is a legend viewer. It provides users an atlas map while exploring gene expression images (see Figure 2.5). Some websites provide a small 3D thumbnail, which is a small 3D model of the neuron. Some websites provide a more advanced tool such as Brain Explorer from the Allen Mouse Brain, which integrates the Reference Atlases we mentioned before with 3D visualized data and metadata. 3D visualization helps users better explore the neurons and increase the interactivity, we also use it in our redesign.

2.3.3 General Guidelines for Designing a Graphical Query Interface

Based on our research, there are several general guidelines to follow when designing a graphical query interface.

Easily understandable

The interface should be simple and all the features should be easy to understand how to use them.

Eliminating the unimportant

It is important to eliminate the unimportant information to make the important thing stand out more.

Offer new insight

For instance, in Virtual Fly Brain, when users open the details page, they do not only see information about the single neuron but also relevant information of similar neurons or neighborhoods (see Figure 2.7). The websites should not only show the basic information of the neuron, but also relevant information of them.

Provide data visualization

The Allen Mouse Brain Atlas encodes the gene expression distribution into a bar chart. It is a good example of data mapping. The data is mapped into a graph, which is intuitive and easier to gain a better understanding of the gene expression distribution (see Figure 2.4).

Divide information into modules and link them

Almost all interfaces are divided into different modules, so that the information is structured and organized.

Show the search result in different views

The search result is shown in a list view in the most of the interfaces, and in only few of the interfaces the search result is shown in a matrix view. We want to introduce a group view in our redesign. The group view allows users to group the images with different criteria, which will be further presented in our redesign.

Often used design components and color

User experience and interaction design components, frequently used for searching, are: a) Textfield b) Checkbox c) Option Buttons d) Drop-down list e) Radio box. According to the style of the investigated websites, most of the websites are designed pretty simple. Green, blue, orange, and yellow are often used colors on these websites.

CHAPTER 3

Redesign of Anatomical Search

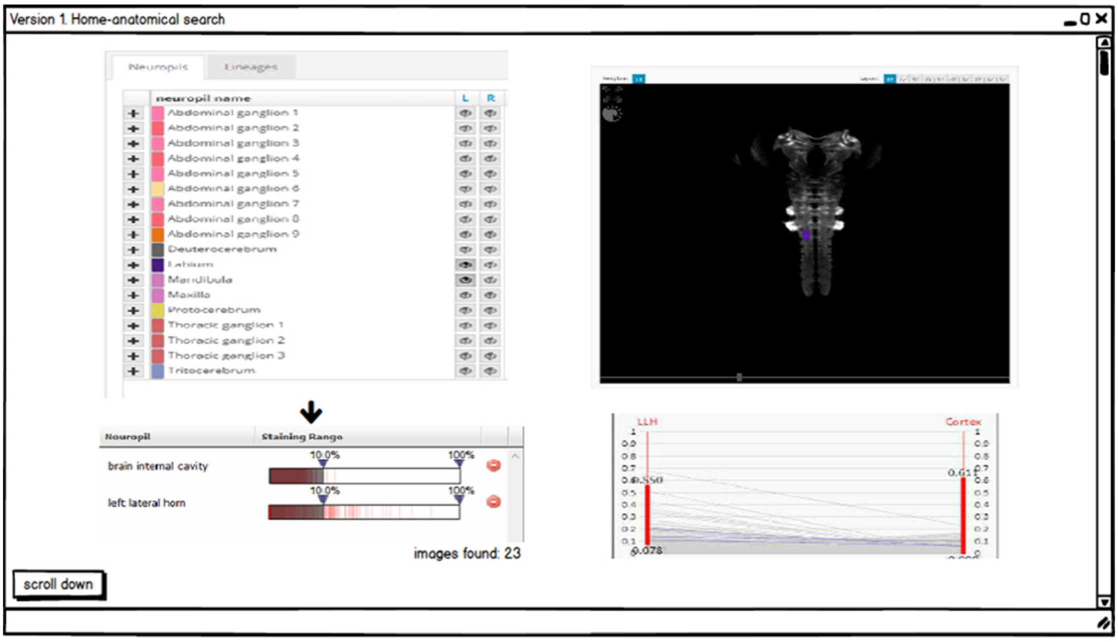
In this chapter, the redesign of the neuro-anatomical search for BrainBaseWeb is presented. The anatomical search function of BrainBaseWeb allows users to retrieve images using a certain staining expression. In the following section, the original interface of BrainBaseWeb and the redesigned version in this study will be shown and compared. Then, the advantages of the redesigned user interface and the modifications including anatomical search user interface, views, and details page will also be introduced.

3.1 Anatomical Search User Interface

3.1.1 Original Anatomical Search User Interface

The original anatomical search interface can be divided into three parts: available anatomical terms, search modes, and the result views (see Figure 2.8). The available anatomical terms, which can be used for the selections of neuropils, are positioned at the upper left. When a query was conducted, users can select interesting neuropils and add them to the search mode area. The search modes, which contain the standard mode and expert mode, are at the upper right of the interface. The difference is that, in the standard mode, each selected neuropil is listed as a slider in the search mode area, while the selected neuropils are shown as vertical lines in the expert mode. As the parallel coordinate widget was used in the expert mode to specify complex staining patterns over several neuropils (see Figure 2.9), the users can get immediate feedback on the number of images corresponding to the defined pattern while defining the expression range for each neuropil. If no result is found, all the lines will be gray; otherwise, the result lines will be drawn in blue. However, the results cannot be explored simultaneously in the standard mode. Therefore, it may happen that users cannot find any results with the expression range they specified. The result views, including list view and matrix view, are placed at the bottom. Users can find the result in this part.

3.1.2 Redesigned Anatomical Search User Interface



Version 1. Home-anatomical search

Neuropils | Lineages

		neuropil name	L	R
+	🟥	Abdominal ganglion 1	👁	👁
+	🟥	Abdominal ganglion 2	👁	👁
+	🟥	Abdominal ganglion 3	👁	👁
+	🟥	Abdominal ganglion 4	👁	👁
+	🟥	Abdominal ganglion 5	👁	👁
+	🟨	Abdominal ganglion 6	👁	👁
+	🟥	Abdominal ganglion 7	👁	👁
+	🟥	Abdominal ganglion 8	👁	👁
+	🟧	Abdominal ganglion 9	👁	👁
+	⬛	Deuterocerebrum	👁	👁
+	🟪	Labium	👁	👁
+	🟪	Mandibula	👁	👁
+	🟪	Maxilla	👁	👁
+	🟨	Protocerebrum	👁	👁
+	🟥	Thoracic ganglion 1	👁	👁
+	🟥	Thoracic ganglion 2	👁	👁
+	🟥	Thoracic ganglion 3	👁	👁
+	🟦	Tritocerebrum	👁	👁

Neuropil	Staining Range
brain internal cavity	10.0% – 100%
left lateral horn	10.0% – 100%

images found: 23

scroll down

Figure 3.1: Redesign: Anatomical Search User Interface

The redesigned search interface is divided into four parts: available anatomical terms, which can be selected, are placed at the upper left, slider widget and parallel coordinates used for searching are located separately at the lower left and lower right, and a 3D larval template is positioned on the upper right.

Compared with the original interface, there are two parts of modifications in the redesigned anatomical search user interface. One is that both of the search modes are shown in the interface (Figure 3.1). The reason for this modification is that, at first sight, parallel coordinates seem difficult to use. In the redesigned anatomical search user interface, when the users specifie a range in parallel coordinates, the result will also be synchronized and shown in the slider widget. It helps the users to gain a better understanding of how parallel coordinates work.

In addition to this, the selected neuropils or axon tracts will be highlighted in a 3D larval template on the right side. If the users drag the slider control to reduce the staining percentage, the highlighted region will be darker, if the users increase the staining percentage, the highlighted region will be brighter.

The slider widget, parallel coordinates, and 3D larval template are synchronized and linked with each other. It gives the users the possibility to search images intuitively in different aspects.

3.2 Three Search Result Views

3.2.1 Original Search Result Views

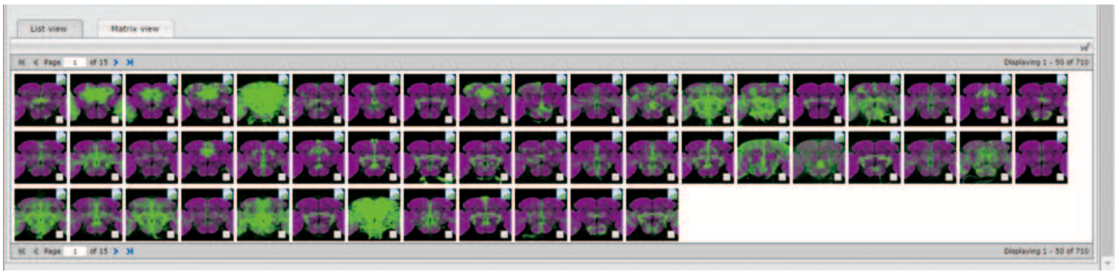
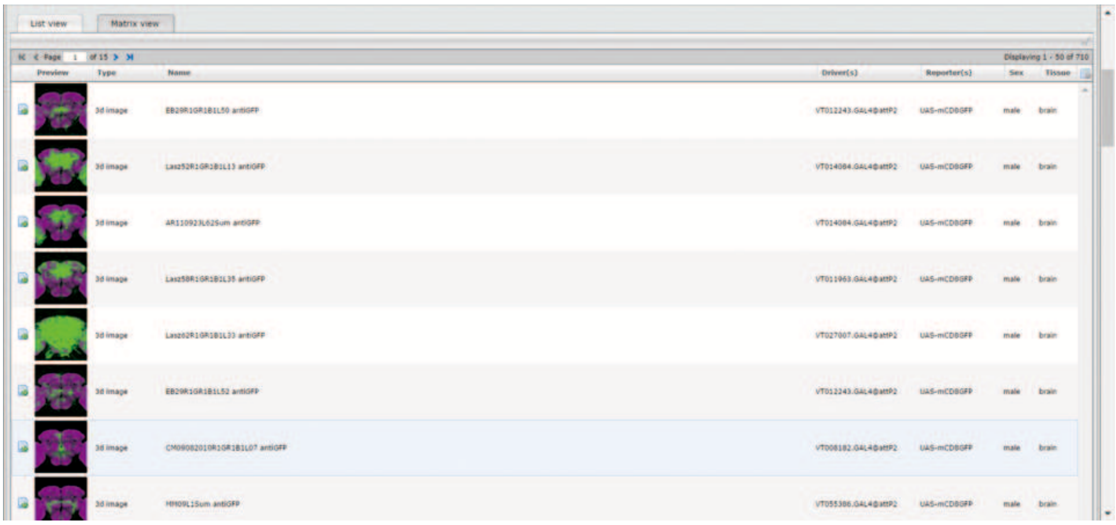


Figure 3.2: Original: Anatomical Search User Interface



Preview	Type	Name	Driver(s)	Reporter(s)	Sex	Tissue
	3d image	EB29R1GR1B1L50 antiGFP	VT012243.GAL4@attP2	UAS-mCD8GFP	male	brain
	3d image	Lasz52R1GR1B1L13 antiGFP	VT014084.GAL4@attP2	UAS-mCD8GFP	male	brain
	3d image	AR110923L62Sum antiGFP	VT014084.GAL4@attP2	UAS-mCD8GFP	male	brain
	3d image	Lasz58R1GR1B1L35 antiGFP	VT011963.GAL4@attP2	UAS-mCD8GFP	male	brain
	3d image	Lasz62R1GR1B1L33 antiGFP	VT027007.GAL4@attP2	UAS-mCD8GFP	male	brain
	3d image	EB29R1GR1B1L52 antiGFP	VT012243.GAL4@attP2	UAS-mCD8GFP	male	brain
	3d image	CM09082010R1GR1B1L07 antiGFP	VT008182.GAL4@attP2	UAS-mCD8GFP	male	brain
	3d image	HM09L15um antiGFP	VT055386.GAL4@attP2	UAS-mCD8GFP	male	brain

Figure 3.3: Original: Anatomical Search User Interface

After the users have applied a query, the search results could be shown in different views. In the original interface, only a list view and a matrix view are provided (see Figure 3.2 and Figure 3.3).

3.2.2 Redesigned Search Result Views

In the redesigned interface, users are able to view the results with three different views: matrix, group, and list views. Moreover, some filter criteria, sort criteria, and group criteria were also added for better interaction. Using the "sort" and "group" drop-down list and the "filters" in the Filter Panel, users can sort, group, and filter the images. For instance, to filter the images, criteria such as name, template, sex, drivers, reporters, slide name, sample number, stain score, symmetry score, genotype, tissue, tag, creator, and creation date will be implemented. To sort the image, criteria such as staining range, genotype, creation date, similarity, and sparsity will be implemented. To group the images, we employ criteria such as similarity, sparsity, template, sex, drivers, reporters, and creator. Moreover, the interface also provides an in-depth look at the results and the selected images. Once an image is selected, the general information of the image will be displayed on the right side. Users can tag and annotate the image. By double clicking the image, the details of the image will be shown in another window.

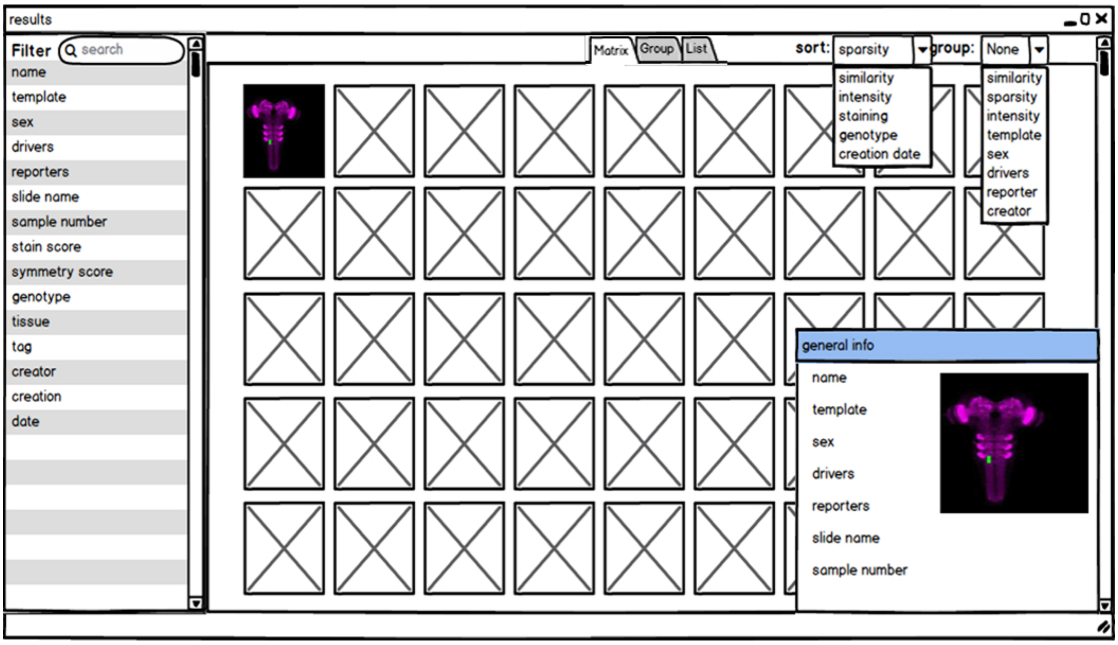
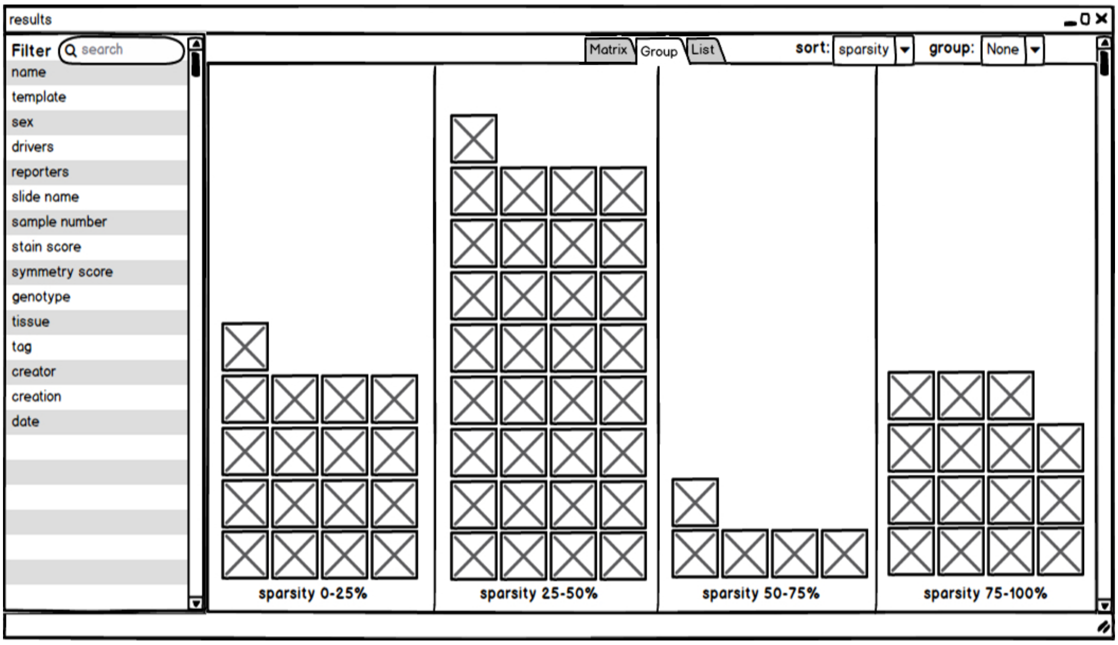


Figure 3.4: Redesign: Matrix View

In the matrix view (see Figure 3.4), only previews of the images are shown. The advantage of this view is that the users can get a quick overview of all the images and only view the most important information of the neuropils. If a neuropil is interesting for them, they could open the details page to read further information.

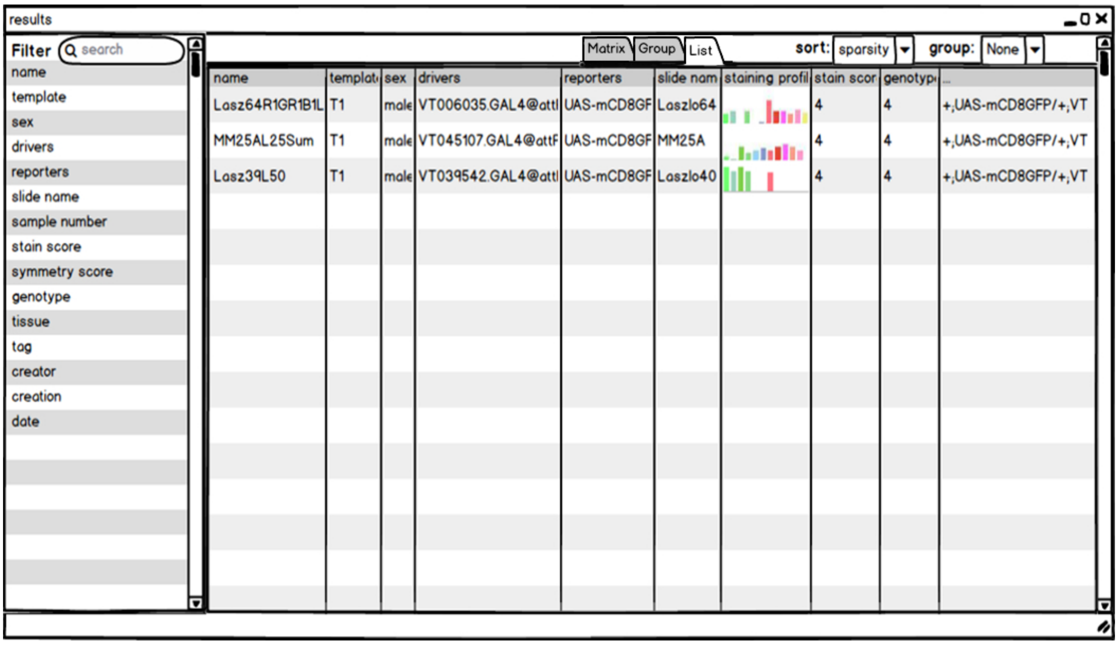
The group view (see Figure 3.5) is an extended version of the matrix view. Beyond sort and filter functions, the group view also provides image grouping. The users can select neuropils from the drop-down list named “group”, in order to search images having a specified staining expression. For example in Figure 3.5, the images are grouped into four different categories. The first group of images has a sparsity from 0% to 25%, the second group has a sparsity from 25% to 50%, the third group has a sparsity from 50% to 75%, and the last group has a sparsity from 75% to 100%. This group view helps users to refine the search results into more specific categories.

The last view, which is provided in the redesigned interface is the list view (see Figure 3.6). In this list view, important information such as name, template, sex, drivers, reporters, slide name, preview of the staining profiles are listed in a table, where staining profiles is a bar chart with the quantitation of staining expressions. Users can always switch



sort: sparsity
group: None

Figure 3.5: Redesign: Group View - images are classified into different categories, in this example, images are classified into different categories based on sparsity.



sort: sparsity
group: None

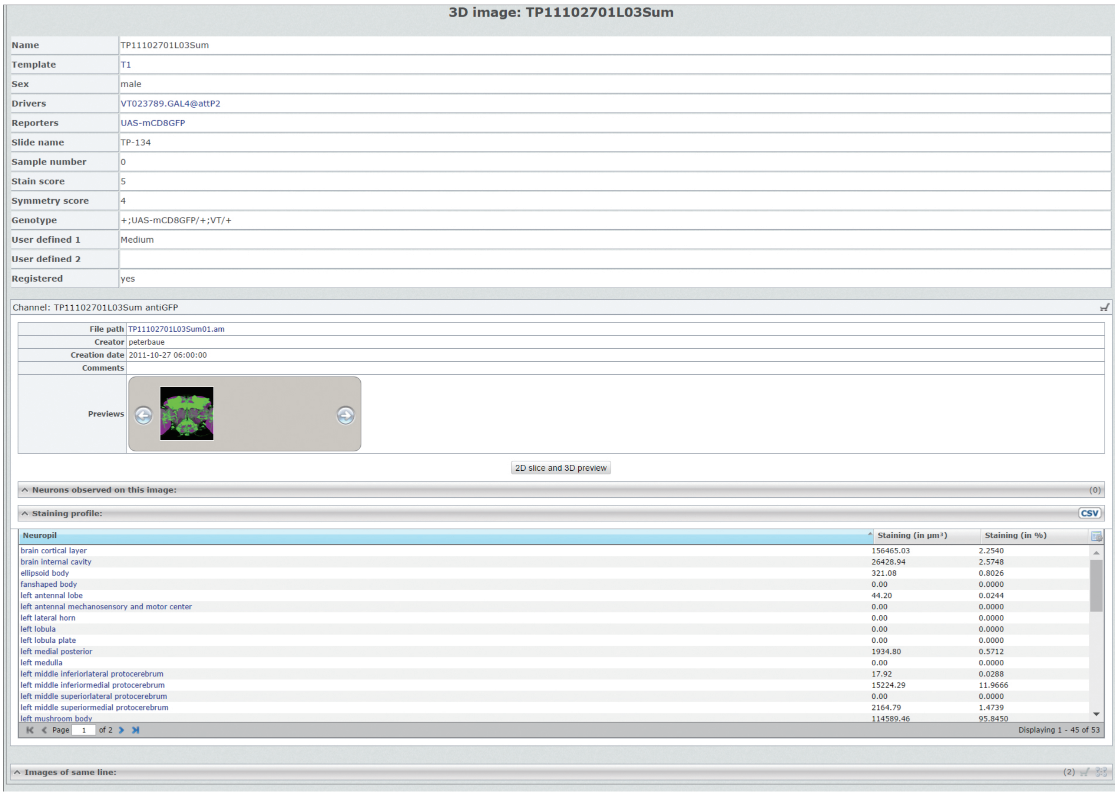
name	templat	sex	drivers	reporters	slide nam	staining profil	stain scor	genotyp	...
Lasz64R1GR1B1L	T1	male	VT006035.GAL4@attl	UAS-mCD8GF	Laszlo64		4	4	+;UAS-mCD8GFP/+;VT
MM25AL25Sum	T1	male	VT045107.GAL4@attF	UAS-mCD8GF	MM25A		4	4	+;UAS-mCD8GFP/+;VT
Lasz39L50	T1	male	VT039542.GAL4@attl	UAS-mCD8GF	Laszlo40		4	4	+;UAS-mCD8GFP/+;VT

Figure 3.6: Redesign: List View - all information of a neuron will be shown in a list.

between matrix, group, and List view depending on their needs, whether they want to browse the neuropils with images, with text or to categorize them.

3.3 Details Page

3.3.1 Original Details Page



3D image: TP11102701L03Sum

Name	TP11102701L03Sum
Template	T1
Sex	male
Drivers	VT023789.GAL4@attP2
Reporters	UAS-mCD8GFP
Slide name	TP-134
Sample number	0
Stain score	5
Symmetry score	4
Genotype	+;UAS-mCD8GFP/+;VT/+
User defined 1	Medium
User defined 2	
Registered	yes

Channel: TP11102701L03Sum antiGFP

File path	TP11102701L03Sum01.am
Creator	peterbaue
Creation date	2011-10-27 06:00:00
Comments	
Previews	

Neurons observed on this image: (0)

Staining profile:

Neuropil	Staining (in μm³)	Staining (in %)
brain cortical layer	156465.03	2.2540
brain internal cavity	26428.94	2.5748
ellipsoid body	321.08	0.8026
fanshaped body	0.00	0.0000
left antennal lobe	44.20	0.0244
left antennal mechanosensory and motor center	0.00	0.0000
left lateral horn	0.00	0.0000
left lobula	0.00	0.0000
left lobula plate	0.00	0.0000
left medial posterior	1934.80	0.5712
left medulla	0.00	0.0000
left middle inferiorlateral protocerebrum	17.92	0.0288
left middle inferiormedial protocerebrum	15224.29	11.9666
left middle superiorlateral protocerebrum	0.00	0.0000
left middle superiormedial protocerebrum	2164.79	1.4739
left mushroom body	114589.46	95.8450

Displaying 1 - 45 of 53

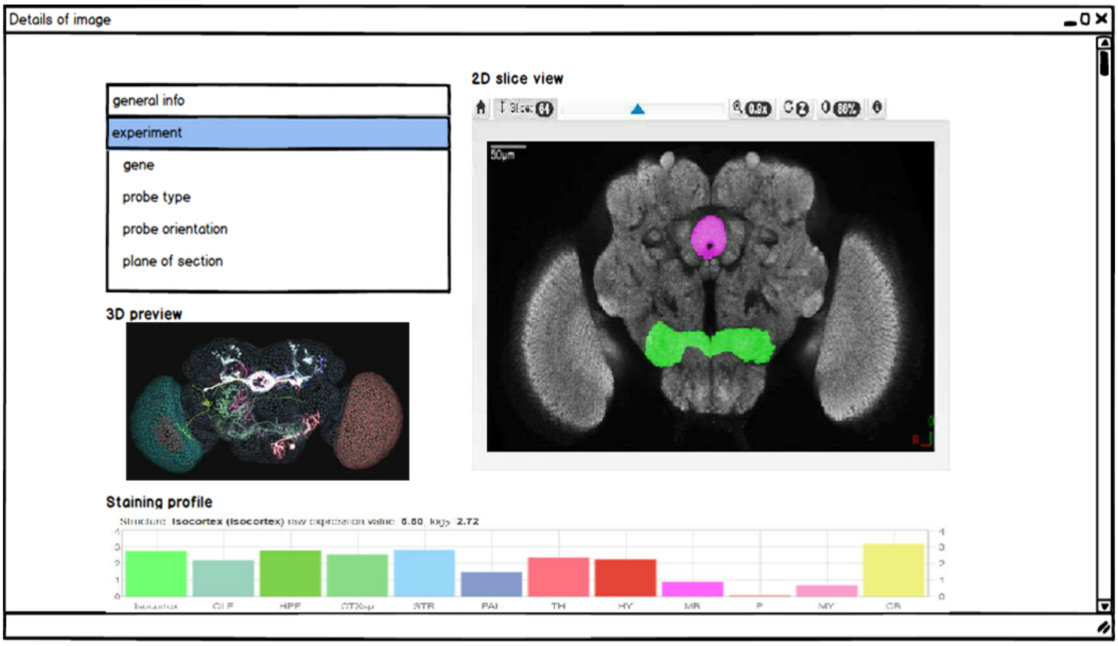
Images of same line: (2)

Figure 3.7: Original Details Page

When users click on the images, which are shown on the views, a details page of the neuron will be shown. Information such as name, template, sex, drivers, and reporters will be shown on the details page. In addition to this, staining profiles, neurons observed on this image, and images of the same line are also presented. Furthermore, data of staining profiles will be listed in a table (see Figure 3.7).

3.3.2 Redesigned Details Page

In Figure 3.8, the redesign of the details page is shown. In order to organize and structure the information, the details page is divided into four different parts. On the left side is the general information, such as details on the experiment and related papers of the image. Below is a 3D preview of the neuropils, users can rotate the model to view the neuropil in different perspectives. On the right side is a 2D slice view, where users can change



Details of image

general info

experiment

gene

probe type

probe orientation

plane of section

3D preview

2D slice view

Staining profile

Structure: Isocortex (Isocortex) raw expression value: 6.60 log2 2.72

Figure 3.8: Redesign: Details and associated metadata of the image

slices, zoom, and the background color. Different neuropils will be colored differently in this 2D slice view. In comparison with the original interface, staining profiles in the redesigned interface will be shown as bar chart instead of a table. The bar chart provides a quantization of staining values. Staining is a genetic mark of gene expression. Neuropils are represented as bars in the bar chart, and when the users hover over a bar, the value of staining and the percentage of the staining are indicated there.

CHAPTER 4

Implementation

In this chapter, the implementation of part of the redesign is presented. Firstly, the technology used in the web application BrainBaseWeb will be introduced. Then, data used in this study and the structure of the application will be presented. After that, the implementation of two different views will be described in detail.

4.1 Technology

The redesign is implemented using the React user interface library of JavaScript [reaa]. Redux [red] is used for managing the application state.

4.1.1 React

React [reaa] is a JavaScript library for implementing interactive user interfaces. React is component-based. The components are independent of each other and manage their own state. They can be composed together to build complex user interfaces. When the data changes, React will update and render the appropriate components. “this.props” and “this.state” are two important concepts in React. “this.props” is the input data of a component. “this.state” is the internal state data; it is private and can only be controlled by the component. When a component’s state data changes, React will automatically update the component [reaa].

4.1.2 Redux

Redux [red] is a state management library for JavaScript applications. There are three important concepts in Redux: state, action, and reducer. The whole state of the application is stored in an object tree within a store. The only way to change the state is to emit an action, which describes what happened. Reducer specifies how the state is transformed by an action to the next state. Therefore, the behavior of the application is completely predictable [red].

4.2 Data

We use 3767 confocal microscopy images of the larval Drosophila. The highlighted part of the larval images is the staining expression.

4.3 Structure of the Application

The application BrainBaseWeb is divided into different modules, such as actions, components, containers, stores, api, util, images and lib. Each module has different functions. For example, actions are used to represent what happened and send data to stores. Components are used to describe the appearance of the application (markup, styles). Containers are used to define data fetching and state updates[reab]. Stores contain reducers that update states according to the actions. Api contains interfaces such as “Table.js”, “Search.js”. “Table.js” defines how to store and access data in a table. “Search.js” defines different search types and parameters of Ajax-requests.

In Figure 4.1, the basic structure of the application BrainBaseWeb is shown. It presents the classes, which are used to implement group view, matrix view, and list view. GroupViewTable, MatrixViewTable, DataTable are components, which used to define the appearance of the group view, matrix view and list view respectively. The component TabPanel used here is to separate different views into different tabs, so that the users can switch between different views through the tabs. The SearchResultViews in container is only used to transfer data to DataTable. DataTable is the real container to fetch data and update states. The SearchResultViews has three subclasses: SearchResultGroup, SearchResultMatrix, and SearchResultTable. They define the parameters of the table for group view, matrix view, and list view. Parameters of the table include data of the table, width, height, name of the columns and data type. The parameters will be transferred to the containers of different views separately (GroupViewContainer, MatrixViewContainer, DataTableContainer).

4.4 Matrix View

In order to implement the matrix view, a container called MatrixViewContainer to define data fetching and state updates is needed. Furthermore, a component MatrixViewTable to define the markups and styles of the matrix view is also needed.

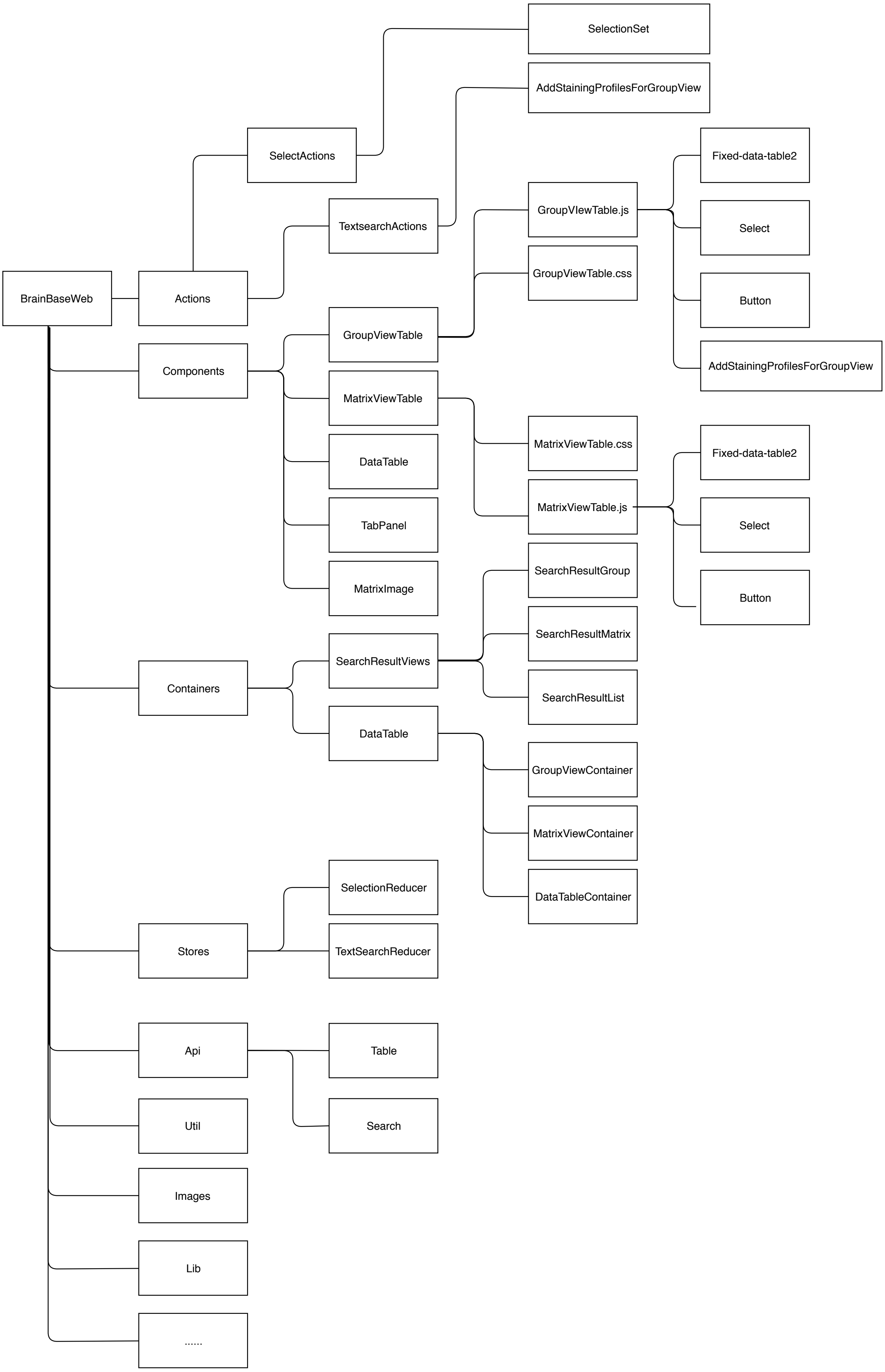


Figure 4.1: Structure of the application

4.4.1 MatrixViewTable

A component MatrixViewTable consists of a JavaScript file “MatrixViewTable.js” and a “MatrixViewTable.css”. “MatrixViewTable.js” is used to describe the interactive elements of the application. “MatrixViewTable.css” is used for the design of the application, where to place the elements and how they look like.

“MatrixViewTable.js" again consists of three components: Fixed-data-table2 (render the table), Select (render the drop-down-list), and Button (render clickable buttons).

Render the Table in MatrixViewTable

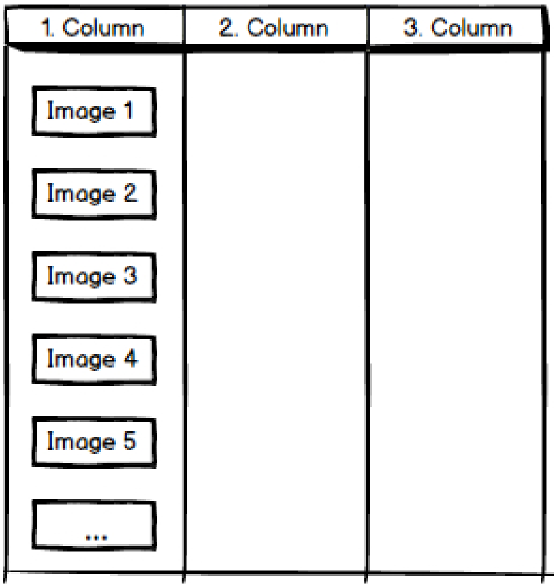


Figure 4.2: Fixed-data-table2 [fix] stores data according to columns.

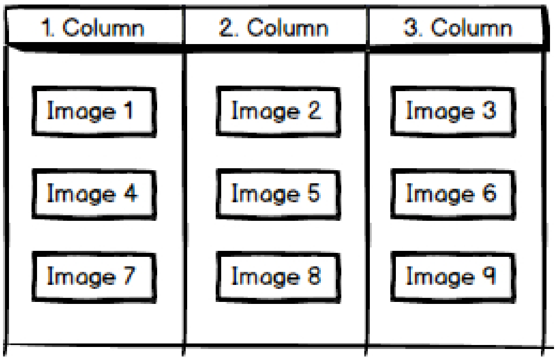


Figure 4.3: The formula is used to calculate which image to be shown.

Fixed-data-table2 [fix] is a component which provides features such as fixed headers and footer, columns, rows, column resizing and fixed and scrollable columns, was used to implement the matrix view .

However, it is only possible to define the way, where the data is displayed for each column in the table (see Figure 4.2), we cannot define the data according to rows. Therefore, we have to calculate which image will be shown one after another in a row. We use the following formula to calculate, which image should be shown in the table:

indexOfImage = indexOfcolumn + rowIndex * imagePerRow

For example, in the first column, second row, the image to be shown is 0 + 1*3 = 3, i.e., the image with index three (index starts with 0) (see Figure 4.3).

Filtering and sorting in MatrixViewTable

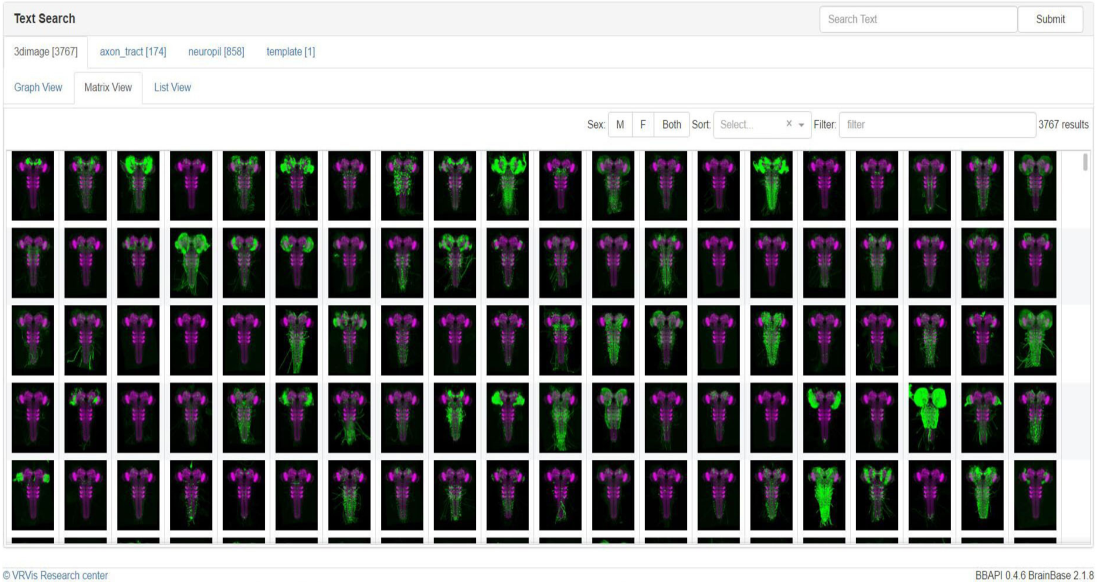


Figure 4.4: Implementation: Matrix View

Filter and sort functions are also provided in the matrix view (see Figure 4.4). In the matrix view, the users can select whether they want to show images from male or female Drosophila or type text in the filter search field in the top-right corner. Furthermore, they can also sort the images based on names. The number of images, which meet the filter and sort requirements, is indicated beside the filter search field.

These filtering and sorting functions are implemented in MatrixViewTable. To filter female or male Drosophila images, the selected button “M” or “F” will be first transformed to a string (female or male information is stored as string in database) and then the string will be searched in the table column named “sex”. Images found will be shown.

To filter the images using the search text from the filter search field, the filter criterion will be split up firstly, if there are spaces between the search texts. Then, all the words will be transformed into lower case to make the filtering case insensitive. After that, all search words will be searched in the table. Only images meeting the search text will be shown.

To sort the images by name, the column “name” will be selected and the “Table.js” from api will be used. The name of each image will be compared and a reordered table will be created and returned. Then, the reordered images will be shown.

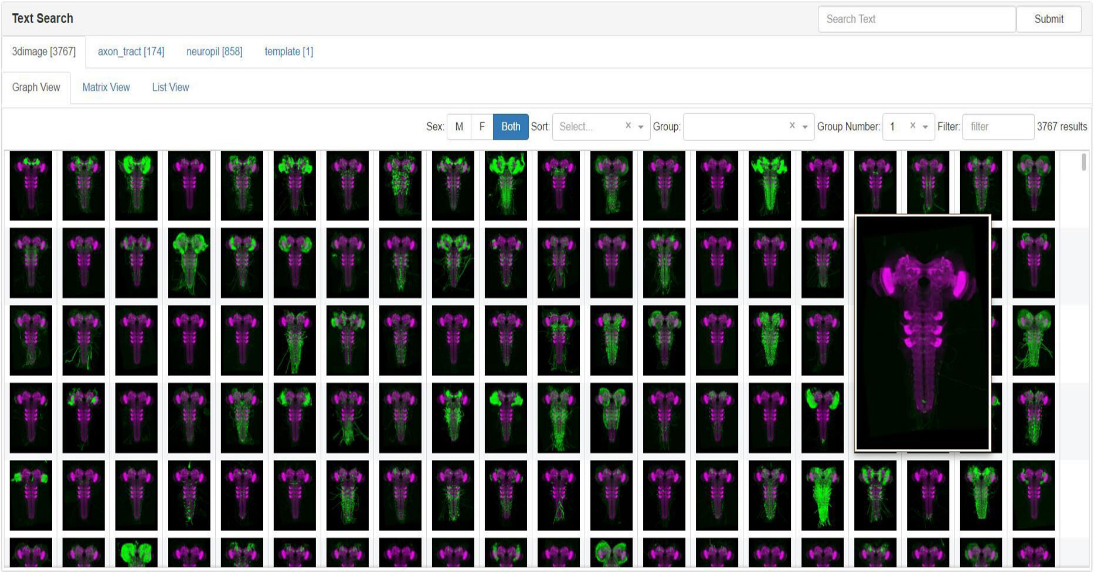
4.4.2 MatrixViewContainer

As mentioned above, data is transformed from SearchResultMatrix to MatrixViewContainer. MatrixViewContainer contains the component MatrixViewTable which is used to describe how the table looks like. Besides MatrixViewTable, MatrixViewContainer also contains the component MatrixImage. MatrixImage is used to create the preview of the images. If the users hover his mouse over the image, a preview will be shown.

By clicking the image, the function SelectionSet from SelectActions in actions will be called. Then SelectionReducer will be called and it specifies how the state changes in response to SelectionSet sent to the store. A new window will be opened and a detail page will be shown.

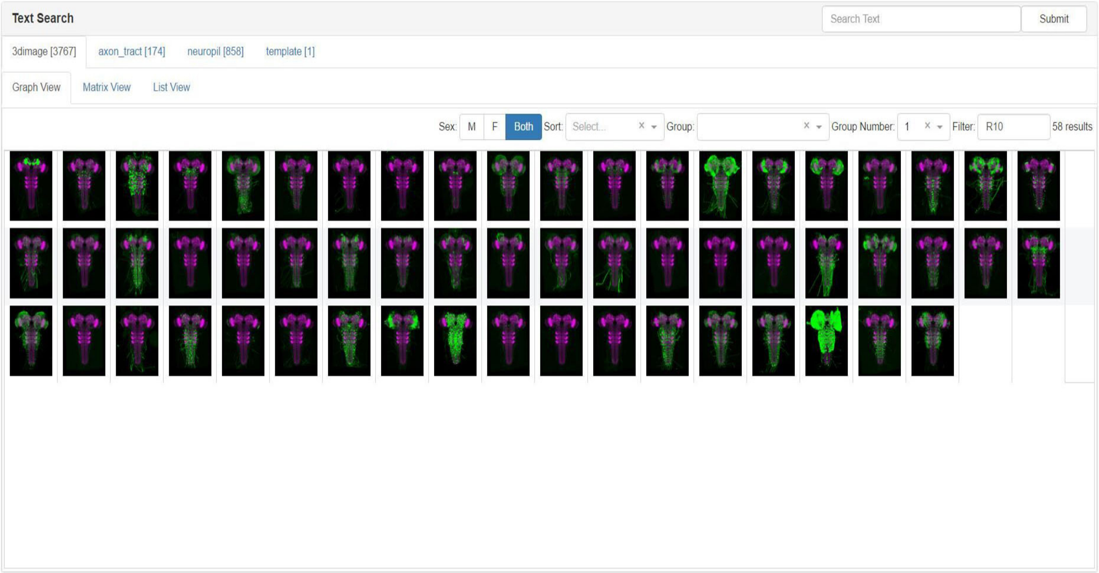
4.5 Group View

The the group view is an extended version of the matrix view (See Figure 4.5 and Figure 4.6). Besides sort and filter functions, the group view also provides image grouping. Users can select neuropils from the drop-down list called "Group” in order to search images having a specified staining expression. In addition to this, users can also group images into different categories and define the group number. Based on the percentage of the staining expression which the images have, they are separated into different groups. In Figure 4.7, “MD” (an abbreviate of a neuropil) is selected and “Group Number 5” is also selected. It means that images with neuropil MD will be shown in the table. Furthermore, they are separated into five different groups with an interval of 20%.



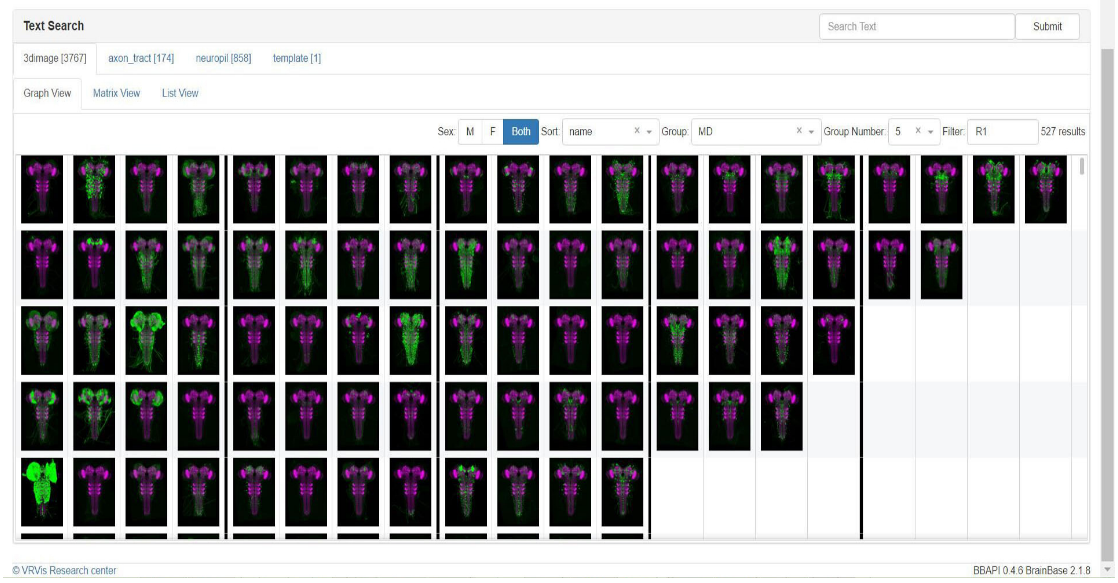
Sex: Both Sort: Select... Group: Group Number: 1 Filter: filter 3767 results

Figure 4.5: Implementation: Group View - wenn the users hover over an image, the larger version of the image will be shown



Sex: Both Sort: Select... Group: Group Number: 1 Filter: R10 58 results

Figure 4.6: Implementation: Group View - with using the search text "R10"



Sex: Both Sort: name Group: MD Group Number: 5 Filter: R1 527 results

Figure 4.7: Implementation: Group View - images are classified into different categories. In this example, images are classified into different categories based on sparsity.

4.5.1 GroupViewTable and GroupViewContainer

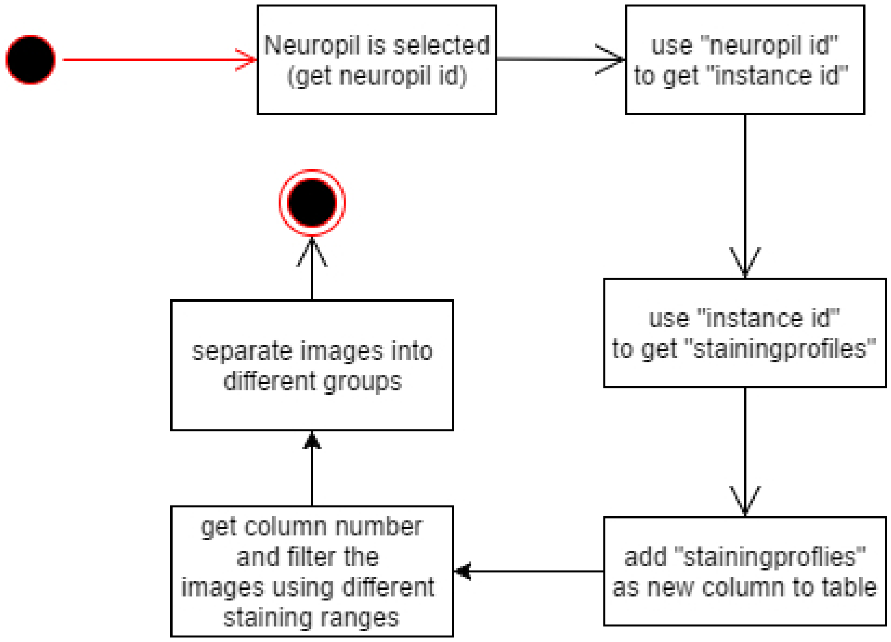

Neuropil is selected (get neuropil id)
use "neuropil id" to get "instance id"
use "instance id" to get "stainingprofiles"
add "stainingproflies" as new column to table
get column number and filter the images using different staining ranges
separate images into different groups

Figure 4.8: Activity diagram of applying a group search query

In order to implement the group view, firstly, an asynchronous function is needed in GroupViewTable to get all neuropil ids and abbreviations of the neuropils' names. The names will be loaded in the drop-down list. If users select a name from the drop-down list, the function selectNeuropil in GroupViewContainer will be called to get instance id using neuropil id (stainingprofiles is only accessible through instance id). Then, the function AddStainingProfilesForGroupView in TextSearchAction will be called. In the function AddStainingProfilesForGroupView the function Search.stainingprofile in api will be called to get the stainingprofiles. After getting the stainingprofiles, the instance id is needed again to get the stainingprofiles for a certain neuropil. An additional column stainingprofiles will be added to the table, it contains the staining of this neuropil (which has been selected).

According to the group number, images per group will be calculated. For example, the images are divided into 5 groups, the maximum number of images per row is 20, therefore each row of each group can contain 4 images. A line is added before each group to separate the groups visually. The progress of applying a group search query is visualized in Figure 4.8

CHAPTER 5

Conclusions and Future Work

5.1 Conclusions

After the investigation and studies of the websites and image management tools, some redesign of the web frontend of the anatomical research platform BrainBaseWeb was proposed. To improve the search features, slider widgets, parallel coordinates, and 3D templates were used to specify the staining expression range and synchronize them. Furthermore, a matrix, group and a list view were added to show the images more intuitively and different “filter”, “group”, and “sort” criteria are added in order to manage the images.

5.2 Future Work

Parts of our redesign (the Anatomical Search) were implemented, we will finish implementing other features. After all the features are implemented, the interface will be evaluated. The evaluation consists of the following steps: user testing, expert evaluation and performing questionnaire [Min07]. Neurobiologists will be invited to participate different user tests.

Different testing methods such as A/B test, Eye-Tracking will be used. A/B test is a user test in which both the original and the redesigned interface are shown to the user, and the user can decide which one he prefers and give also his reasons. In Eye-Tracking, eye movement of the users will be analysed to find out which features attract the users attention most. Based on the test results, the interface will be adjusted and the usability could be evaluated.

The redesigned interface will be then evaluated by experts. Heuristic evaluation, which has been introduced by Jakob Nielsen [JR90], is often used by experts to examine the visibility, consistency, efficiency, and aesthetics of an interface. Ten general guidelines to evaluate interfaces are [JR90]:

- Visibility of system status
- Match between system and the real world
- User control and freedom
- Consistency and standards
- Error prevention
- Recognition rather than recall
- Flexibility and efficiency of use
- Aesthetic and minimalist design
- Help users recognize, diagnose, and recover from errors
- Help and documentation

The last step of our evaluation is based on a questionnaire. They will be applied after the interface has been into service for some time. However, it would not be part of this thesis.

List of Figures

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