Datathon MAPcore Documentation Release 1.0

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Aug 22, 2019

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The SPARC Portal provides interactive access to a growing collection of data, maps, and computational studies that focus on the role of the autonomic nervous system in controlling organ function. These resources are made available to the public with the intent of advancing bioelectronic medicine towards more precise treatment of diseases and conditions.

Here, we provide instructions on how to use the various map visualization and interaction tools available on the SPARC Portal, as well as detailed instructions guiding users of the portal through specific exemplar use cases. These specific use cases highlight various types of data and visualizations that are available.

A collection of introductory videos are available on the MAP-Core YouTube channel.

Map visualization interface



Fig. 1: The initial user interface for the map visualization interface. (A) shows the listing of exemplary use cases, selecting one will display further details and allow access to the appropriate viewers for that use case. (B) can be used to directly enter terms to query the knowledgebase for relevant data. (C) will, by default, show the human flatmap viewer, but will have tabs added with the appropriate viewers, as requested by the user.



Contents:	
• Overview	
• Usage	
- Interactive map layers	

- Querying a map's features
- Map interaction

1.1.1 Overview

The flatmap viewer tool available on the SPARC Data Portal is used to navigate a flatmap – a zoomable map showing representing anatomical features – in order to easily search for knowledge about features on the map.

A map consists of a number of image and vector tiles at different resolutions stored on a server. These are displayed in the web-browser using similar technology to that used by interactive geographical maps.

1.1.2 Usage

Interactive map layers

A map is made up of one or more interactive layers, and is initially displayed with a number of these layers active.

When there is more than one interactive layer, the layer-switcher control, represented by the \blacksquare icon at the top-left corner, can be used to manage active layers.

Querying a map's features

Some features in a layer are annotated as modelling one or more anatomical entities. These features show a tooltip when the mouse pointer hovers over them, and knowledge about the feature can can be searched for by clicking on the highlighted feature.

Some layers, such as the neural layer, have been configured to allow queries to also be made against the displayed nodes. There are two types of such node queries:

- 1. Find all edges that belong to the node, that is edges that start, stop, or pass through the node.
- 2. Find all other nodes connected by some edge to the queried node. This query also results in knowledge searches being made for those found nodes that model an anatomical entity.

Queryable nodes are highlighted when the mouse pointer is over them – they will only show a tooltip if they have an anatomical identifier.

Node queries are made using the right-click context menu.

Map interaction

Besides zoom and pan, using standard mouse or touchpad controls, a left-click will query for knowledge about the current anatomical entity, and a right-click will show a context menu, allowing the different node connectivity queries to be made.



A module of the data portal designed for viewing and exporting Ephys and Genome data.



1.2.1 Overview

This document describes how to use the data plotting viewer tool available on the SPARC Data Portal. Examples of this tool in action are available at https://data-viewer-demo.netlify.com/.

This module has the ability to:

- Plot electrophysiological CSV datasets in the knowledgbase or Blackfynn.
- Plot genome and other static CSV datasests.
- Navigate large datasets via the user interface.
- Add and remove channels from a plot and export them.
- Export selected channels as CSV for use in Excel or OpenCOR.

1.2.2 Viewer Configuration

The viewer has two modes, for small and large datasests.

Small Datasets

This mode is used for smaller datasets and has more control over exports. (All checked channels will be exported.)



Large Datasets

This mode is used to navigate larger datasets. It has search capability to plot the desired channels.



DATA VIEWER

1.2.3 Interactive Graphics Controls

You can refine the view by dragging over a region of interest.

You can also add or remove data by clicking on its label.

The table below describes the effect of different user actions in the flatmap being displayed.

Mouse action	Result
left-click	Zoom in via box selection
middle-click	Zoom in via box selection
double-click	Reset the view







1.2.4 CSV (Comma-Separated Values) Exports

The selected data traces plotted are exported to a CSV file for use in Excel, OpenCOR or any CSV-capable software.

Export as CSV



Data in Excel

1.3 Scaffold Viewer

Contents:

- Overview
- Interaction and Viewing
- Viewer Configuration

1.3.1 Overview

Some datasets in the SPARC knowledgebase search results are registered to an *anatomical scaffold*: a 3D model of the anatomy of interest. This is indicated by the 3D box icon shown at the top of this page. To click on the icon in the search results opens a *Scaffold Viewer* tab in which the scaffold and embedded data can be viewed and interacted with in 3D. The following image of the Scaffold Viewer tab shows a fitted rat stomach scaffold with neurite data from Powley *et al.*

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7 HB_60A	_4	-1.6683192	227														
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1.3.2 Interaction and Viewing

Moving the mouse pointer over the scaffold or embedded data highlights and overlays a label for what is under it. With an entity highlighted, to click the left button performs a search for the label terms in the SPARC knowledgebase. The search can bring up related datasets for the study, allowing further viewer tabs to be opened.

Interactively rotating, zooming and panning the view gives a greater understanding of the 3D structure. Hold down one of the mouse buttons and drag to change the view. The following table lists the controls.

Mouse action	Result
left-click	Search knowledgebase for highlighted entity
Left-drag	Rotate
Middle-drag, wheel	Zoom
right-click	Pan

On some systems, e.g. macOS, modifier keys Ctrl, Alt, etc. may be used in place of different buttons.

Some Scaffold views may contain time-varying or multi-state data. In these cases, a slider control is shown to change the time or state, and a play button enables animation between states. These controls are shown in the above rat stomach Scaffold viewer.

1.3.3 Viewer Configuration

The *icon at the top-left corner of the window brings up a menu of additional viewing controls:*

- Reset View Restore the initial view of the scaffold to the default state.
- *View All* Zoom in/out to see all of the scaffold in its current orientation.
- Visibility Controls Checkboxes controlling the visibility of each entity.

To click on the \blacksquare icon closes this menu.

Cell Body Segmentation and Electrophysiology Data: Stellate Ganglion

Contents:

- Overview
- Step-by-step instructions

2.1 Overview

Mouse stellate ganglion neuronal cell shape data from the Shivkumar/Tompkins group are displayed in a 3D stellate scaffold. 15 neurons, including their cell bodies, axons and dendrites, are displayed on five cross-sections of the stellate with the high resolution image displayed as a texture map. Electrophysiological data from these cells can be visualized by clicking on the cell. *Note* that the scaffold in this example is a geometrically simple shape designed to register the images in the appropriate anatomical location. The shape of the scaffold will be improved once more data are available to define the stellate boundaries.

This document guides a user of the SPARC Data Portal through the steps required to discover a collection of segmented cell bodies from the stellate ganglion which have been mapped to a common coordinate framework for visualization purposes. The user is able to discover any electrophysiological data that has been recorded for each of the cell bodies.

2.2 Step-by-step instructions

Follow these step-by-step instructions to familiarise yourself with the flow of the web interface.

Step 1. Perform a search using keywords stellate or stellate ganglion and click on $\underbrace{\forall}$ icon.

Step 1. The default **Result** column displays the use cases available on the portal. Click on the *Cell Body Segmentation and Electrophysiology Data: Stellate Ganglion* box.



Step 2. A new tab called Scaffold Viewer will open to display the anatomical organ scaffold of the stellate. The current scaffold is a rectangular cube with slots to contain the stellate image stacks using texture mapping techniques within the scaffold elements. Segmented cells (soma) with associated axon and dendrites have been mapped and embedded in the image-scaffold structure. Each cell will have electrophysiological data properly registered.

Find SPARC maps Investigate interactive maps of the	autonomic nervous system,	Â
	stellate Search H	lelp
*	NCBITaxon:9606(Flatmap) x UBERON:0002440(Scaffold) x	
X Mouse Stellate Ganglion Data from the Shivkumar/Tompkins group displayed in a 3D stellate scaffold. 		

Step 3. Click on *icon* on the search result to visualise the electrophysiological data associated with the samples.

Step 4. Click on \blacksquare to open the control panel. You can select different sweep or channel data for that cell in this tab to visualise both simultaneously. You can also export the data as a CSV format file.



Find SPARC maps Investigate interactive maps of the	autonomic nervous system.	
	Stellate Search	Help
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Mapping Cardiac Electromechanics in the Pig

Contents:

- Overview
- Step-by-step instructions
- Scaffold Generation
- Future Steps

3.1 Overview

Pig heart electromechanical data from the Shivkumar/Ardell group is displayed on a 3D pig heart scaffold. The deforming geometry of the pig heart is fitted through the cardiac cycle with the pig heart scaffold. Electrophysiological measurements from two 64-electrode patches, one on the left ventricle (LV) and one on the right ventricle (RV), are fitted as time-varying fields via scaffold parameters and shown on the LV and RV epicardial surfaces, respectively, of the beating heart model. *Note* that these electromechanical data, fitted to the 3D scaffold, are from the same pig heart and include both physiological normal contracting heart beats and the whole heart response to stellate stimulation. This use-case demonstrates the use of the scaffold to merge two types of data set (one mechanical and one electrophysiological) and begins to illustrate the connection between stimulation of the peripheral nervous system and the response at the whole heart level.

This document guides a user of the SPARC Data Portal through the steps required to discover some data looking at autonomic control of the heart.

3.2 Step-by-step instructions

Follow these step-by-step instructions to familiarise yourself with the flow of the web interface.

Step 1: The default **Result** column displays some of the use cases available on the portal. Click on the *Mapping Cardiac Electromechanics in the Pig* box.

Maps Interactive maps reveal spatial dynamics, connec	he anatomy and functional relationships of the autonomic nerves and the organs that they innervate. 2D and 3D r tivity, and physiology across a range of species and nerve-organ systems.	naps render
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Mapping the Mouse Heart Neurites from Imag Mouse heart immunohistochemical mapping		
Showing results 1 - 5 of 9		+

Step 2: Click on the V to open the **Scaffold Viewer** tab to visualise the heart scaffold.

Step 3: In the **Scaffold Viewer** tab, a 3D pig heart scaffold has been fitted to the 2D video data. In addition a 64-electrode patch mesh has been constructed from the original electrode patch on the surface of the left ventricular epicardium. Electro-physiological data recorded from this patch has been registered on the mesh and a field is displayed on the surface of this mesh. This mesh is then *embedded* on the corresponding surface of the scaffold.

Press play to see the video.

Step 4: By clicking on **E** you can control visibility of each of the graphical objects in the scene.

3.3 Scaffold Generation

The following Figure depicts the workflow for the generation of the 3D scaffold.









3.4 Future Steps

In the current version, the scaffold has only been fitted to the video data through anisotropic scaling and some shear. This was a limitation as only one view angle was available. In future, a stereo camera system will be installed to reconstruct a 3D view of the beating heart in order to accurately fit the scaffold and capture the deformation of cardiac tissue.

Mapping the Mouse Heart Neurites from Image to Scaffold

Contents:

- Overview
- Step-by-step instructions
- Scaffold Generation

4.1 Overview

Immunohistochemical mapping of neural pathways in cleared heart (sham heart 4) stained with PGP9.5 (glycoprotein surface axonal antibody labelling) from the Shivkumar/Pradeep group is displayed in a 3D mouse heart scaffold that has been fitted to the segmented heart surface data from Sham Heart 44, which provides a more extensive geometric dataset. Future experiments are likely to provide much better quality mouse data for both the heart's anatomy and its embedded neurons.

4.2 Step-by-step instructions

Follow these step-by-step instructions to familiarise yourself with the flow of the web interface.

Step 1. The default **Result** column displays the use cases available on the portal. Click on the *Mapping the Mouse Heart Neurites from Image to Scaffold* box.

Step 2 Click on the 🖅 to open the **Scaffold Viewer** tab to visualise the heart scaffold.

Step 3. In the Scaffold Viewer tab, click on = to open the control panel. There are three objects visible: 1) fitted heart scaffold, 2) sham heart 44 neurite tracing, 3) sham heart 4 neurite tracing.









Step 4. Turn off Sham 4 neurons to only visualise the scaffold and Sham 44 neurons.

Step 5. Turn Sham 4 neurons back on and now turn off Sham 44 neurons to visualise the registered neurons on the scaffold surface.



Step 6. To visualise only the neurons, turn off the scaffold.

4.3 Scaffold Generation

The following figure illustrates an overview of the workflow for the generation of the 3D scaffold.

Below is an introductory video which explains the mapping of the mouse heart neurites from image to scaffold.



Mapping Cellular Gene Expression in the Rat Heart from Image to Scaffold

Contents:

- Overview
- Step-by-step instructions
- Scaffold Generation

5.1 Overview

Rat heart geometric 3Scan data for both ventricles and both atria from the Schwaber/Vadigepalli/Cheng group has been fitted with a 3D rat heart scaffold. The location of a cluster of 151 intrinsic cardiac neuron (ICN) samples, which have been lifted for RNA-Seq analysis (molecular cell body transcript data) from a region of the left atrium (from a different animal), are indicated on the 3D scaffold. To click on one of these tissue locations displays the RNA message level for the 154 genes examined. To visualize the spatial distribution of the RNA message, the 151 samples have been fitted with a continuous field description using scaffold nodal parameters. Any one of the 154 genes can be selected to show the spatial variation of that transcript as a heat map. Rat heart neural pathway data showing the efferent connectome linking ICN cells in the left atrium and the SA node cells on the right atrium are visualized in the next iteration of this use case.

5.2 Step-by-step instructions

Follow these step-by-step instructions to familiarize yourself with the flow of the Web interface.

Step 1. The default **Result** column displays the use cases available on the portal. Click on the *Mapping Cellular Gene Expression in the Rat Heart from Image to Scaffold* box, then click on icon.



The Scaffold Viewer tab opens and the fitted heart scaffold can be visualized. A number of lifted neuronal cells have been mapped and registered on the scaffold (purple spheres).

Step 2. Click on the *icon to pop up the drop-down menu. Visibility can be turned on or off for each item.*

Step 3. Hover on the different regions to highlight the chambers separately.

Each cell has been lifted and assayed for the expression of 154 genes selected as associated with neuromodulation and cardiac function using qPCR or RNASeq. These have been mapped on the registered cells on the scaffold. Each cell has a unique ID.

Step 4. Now, click on the icon.

The Data Viewer tab opens to view the gene expression data. At this point, the data can only viewed using a bar chart. However, additional visualization capabilities, such as heatmap and clustering, will be available in the future.

Step 5. Add more genes to the bar chart by expanding the drop-down menu.

The bar chart will show the expression of each gene using a unique color for all the registered cells on the scaffold.

5.3 Scaffold Generation

The following Figure depicts the workflow for the generation of the 3D scaffold.

The treatment process needed to extract the cells for RNA-Seq analysis left that rat heart in a very distorted state and was therefore not fitted with a scaffold. Instead, corresponding locations of the ICN cells in the much less distorted 3Scan-processed heart were identified by eye and the cell information was transferred to that heart.



















Mapping Gene Expression in the Mouse Lungs from Images to Scaffold

Contents:

- Overview
- Step-by-step instructions
- Scaffold Generation

6.1 Overview

A 3D scaffold of the mouse thoracic cavity created using segmentation of longitudinal microCT scans from the SIMBA VIA (Vision and Image Analysis) public database is visualized. The trachea and main bronchi are also shown as rings of segmented points. Confocal stained images from Taylor-Clark group for mouse lungs are embedded into the scaffold. The confocal images were obtained from the right middle lobe (RML). The scaffold was registered to ensure alignment with the airway branch visible on the confocal. This use-case is one of many that link an organ systems with the brainstem.

6.2 Step-by-step instructions

Follow these step-by-step instructions to familiarise yourself with the flow of the web interface.

Step 1. The default Result column displays the use cases available on the portal. Click on the Mapping Gene

Expression in the Mouse Lungs from Images to Scaffold box, then on \checkmark icon.

Step 2. Allow model to load.

Step 3. To view only the confocal image in the right middle lobe (RML), select only RML10x007 checkbox after clicking on \equiv icon for drop-down menu.



Find SPARC maps Investigate interactive maps of the	utonomic nervous system.	
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Data for Mouse Lungs Data from Tom Taylor-Clark visualised on a 3D scaffold with electrophysiclogical data.		

Find SPARC maps Investigate interactive maps of th	utonomic nervous system.		
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6.3 Scaffold Generation

A diagram and video are below, detailing the workflow for the generation of an anatomically-based 3D thoracic shape of the lungs.



3D Mapping and Visualization of 2D Experimental Data Stomach Afferents and Efferents

Contents:

- Overview
- Step-by-step instructions
- Scaffold Generation
- Future Steps

7.1 Overview

A 3D scaffold of the rat stomach created using segmented microCT data from the Powley group is shown. The neurites including nerve endings (both intraganglionic laminar endings (IGLEs) and longitudinal intramuscular arrays (IMAs) are displayed on the 3D scaffold. The scaffold can be cut and opened out flat to match the experimental whole-mount preparation, and to then display the experimental data. Note that 152 neurite maps (from 152 different rats) were each registered to a fitted scaffold for each rat and then morphed into the average flat mount scaffold. At specific locations on the scaffold, the corresponding microscopy image of the neurite can be seen via Biolucida. This use-case demonstrates both the application of neural pathway data to the stomach and the use of a transformation between the normal 3D stomach anatomy and the 2D whole-mount preparation.

7.2 Step-by-step instructions

Follow these step-by-step instructions to familiarise yourself with the flow of the web interface.

Step 1. The default Result column displays the use cases available on the portal. Click on the 3D Mapping and

Visualization of 2D Experimental Data Stomach Afferents and Efferents box. Click on the scaffold icon (



Step 2. Allow a few seconds for the scaffold to load. Navigate between the 3D scaffold and layers view using the slider. Click on the play button to automate toggle between the configurations.



Step 3. Under unexpanded view, right-click and drag to rotate the scaffold. On the longitudinal ventral surface, locate 3 yellow spheres, which represent distinct neurites.

Step 4. Click on a yellow sphere. In the left panel inset, a link to a light microscopy image of the neurites in the corresponding location on the fitted scaffold is visible.

7.3 Scaffold Generation

A statistically representative and anatomically-based 3D scaffold of the rat stomach was created to map nerve ending pathways. Micro-CT image data of 11 animals were used to construct this 3D scaffold. Imaging and data segmentation was performed at the Powley laboratory using Neurolucida (MBF Bioscience). An approximate surface was generated for each case using gross morphometric measurements of the organ. These surfaces were then fitted to the segmented data (Fig. 1). The fitted scaffolds surfaces were combined to form an average stomach surface of representative thickness to generate the 3D scaffold, which was subsequently split into three anatomically-distinct tissue layers.

230 neurite pathways imaged and segmented from whole mounts of 68 different rats were then mapped into the multilayered 3D scaffold. Each neurite was first deformed in the X-Y plane to match its standard contour using a free-form deformation technique (Fig 6(a)). The standard contour was then transformed with its contents to its 3D counterpart (b).







Fig. 1 (a) Micro-CT of rat stomach (b) Segmented data (c) Fitted scaffold surface



Fig. 6 Mapping 2D experimentally determined nerve ending to representative 3D scaffold (a) Actual 2D ventral contour with neurite tracing (b) Deformed to match standard 2D ventral contour (c) Transformed to 3D ventral scaffold

The neurites consisted of three types of afferents- IMAs, IGLEs and circular IMAs; efferents were mapped from their standard 2D contour to the 3D scaffold. The afferent IGLEs and efferents were placed between smooth muscle layers (myenteric plexus layer) while IMAs were included between respective smooth muscle layers (Fig. 7).



Fig. 7. Mapped 2D neurite pathways in 3D scaffold (230 neurites - 68 stomachs)

7.4 Future Steps

Plans are under way to acquire more detailed high-resolution images to better understand the tissue structural composition and vasculature. Once available, the 3D scaffold's tissue layers will be updated accordingly. This includes having the data and models being visualized at varying levels of stomach fills i.e. empty to full states.

Rat Superior Cervical Ganglion

Contents:

- Overview
- Step-by-step instructions

8.1 Overview

Mapping of neuroanatomical connectivity is illustrated using rat superior cervical ganglion (SCG) data from Steve Lewis' group at CWRU and rat brainstem data from Don Bolser's group at UFL. This knowledge is assimilated into the SPARC SciGraph, to demonstrate cross-domain data linkage. The Bolser and Lewis work has three major areas of physiological complementarity:

Larynx/Trachea: The sensory (Bolser) and motor (Lewis) limbs of protective mechanisms for the upper respiratory tract are captured in the connectivity model.

Carotid Body: Chemosensing for oxygen partial pressure by the Carotid Body is key to respiratory control (Bolser). The SCG (Lewis) sends effector projections to the Carotid Body that modulate its chemosensing.

Carotid Sinus: Non-intuitively, blood pressure sensing by the carotid sinus is also key to respiratory control (Bolser). The SCG (Lewis) sends effector projections to the Carotid Sinus that modulate its barosensing.

Knowledge that links the above pathways provides a key means to discover multiple datasets (usually siloed behind institutional and collaborative divides) in these diverse physiology domains.

8.2 Step-by-step instructions

Follow these step-by-step instructions to familiarise yourself with the flow of the web interface.

Step 1. Select Neural system from the drop-down menu lopen-control on the human flatmap.







Step 2. *Right-click* on pink rectangles that symbolizes portion of nerve.



For example, neuronal routes conveyed by the SLN as shown below.

Step 4. *Left-click* on 'Find nodes and edges connected to node' to find data relevant to structures connected by the selected nerve.

For example, structures connected by the SLN as shown below.





Mapping Image Data in Mouse Colon

Contents:

- Overview
- Step-by-step instructions
- Scaffold Generation

9.1 Overview

A 3D scaffold fitted to the structural data of mouse colon is visualized. Apart from its 3D configuration, the scaffold is displayed as a flat preparation which represents the state where a colon is stretched out, cut open and laid flat on a surface for imaging purposes. Segmented image data of enteric neurons and nerve fibers (Tache group) and vasculature (Howard group) of mouse tissue samples are mapped onto the flat scaffold based on the locations where the tissue samples were obtained from. This allows image and experimental data to be embedded and displayed at labelled material points on the scaffold in both its 3D and flat configuration.

9.2 Step-by-step instructions

Follow these step-by-step instructions to familiarise yourself with the flow of the web interface.

Step 1. The default Result column displays the use cases available on the portal. Click on the Mapping Image Data

in Mouse Colon box. Click on the scaffold icon (lscaffold-icon). Click on the scaffold icon (\bigcirc).

Step 2. Allow a few seconds for the scaffold to load. Navigate between the 3D and flat scaffold using the slider. Click on the **play** button to automate toggle between the two configurations.



Find SPARC maps Investigate interactive maps of the	re autonomic nervous system.	
	colon Search	Help
×	Human NCBITaxon:9606(Flatmap) × colon UBERON:0001155(Scaffold) ×	
Mouse Colon Data Data from the Howard & Tache groups where a 3D scaffold fitted to these data will be visualised on a 3D scaffold.		

9.3 Scaffold Generation



The Figure below illustrates an overview of the workflow.

Below is an introductory video which explains how the structural data of mouse colon are mapped onto a 3D scaffold.

Interactive Graphics Controls

The table below describes the effect of different mouse buttons in manipulating the view.

Mouse Button	Transformation
Left	Rotate
Middle	Zoom
Right	Pan