

## DEMO PREPARATION

- Presentation proceeds the demo
- Pre-load:

<https://webdev.dk.ucsd.edu/demo/?id=491>

- Create new session/url (DO NOT WORRY ABOUT THE NEW LINK)
- Verify 3D volume is created and visible (DK55\_7N\_R1 tab)

COMPLETED ALL STEPS [AT END] (FOR REFERENCE):

<https://webdev.dk.ucsd.edu/preview/?id=492> (no missing contours, all correct)

## PRESENTATION

Brainsharer Platform:

Here we introduce the Brainsharer platform, which combines storage of multi-resolution brain images, a database and a browser-based front-end interface.

Neuroglancer was originally developed at Google for visualization of electro microscopy data. We have extended the original software to include functionality such as contour drawing tool and 3D volume creation I will outline shortly.


The combined software and infrastructure in this innovative platform, we call Brainsharer, will facilitate:

- **Creation:** There are differences in brains (**anatomical variance**) and how anatomists perform the annotation function (**inter-rater reliability variance**)
- **Collaboration:** As the entire platform is cloud-based, researchers may share annotated brains with other users or collaborate live
- **Convergence:** Each brain annotation can be added to the active brain atlas where machine learning is used for the transformation of individual brains to the atlas. The atlas will hold the average shape and relative spatial position of brain structures for all brains added.


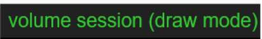


This novel approach minimizes the variance introduced during the creation function (especially that introduced by annotators).

START OF DEMO










High-level functionality with volume creation, editing and propagation of 7N\_R (facial nucleus - right) on DK55


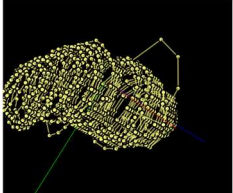
Step	Script	Notes
1. Load foundation brain (DK55 w/ 7N_R) <a href="#">LOAD DK55 + 7N_R</a>	As a demo of our Neuroglancer tool, today I will load a mouse brain. That is a brain stained by Neurotrace blue, a dye that stains the soma of the neuron.	
2. Click “New” to create new url for demo session	<p>I will create a new session for this demo. The session will retain all information related to loaded/visible brain and related annotations</p> <p>Initially Neuroglancer shows a 4-panel layout on the screen. Clockwise we have sagittal, horizontal, coronal and 3D views.</p> <p>For UCSD, the sagittal view is the raw image – or projection - due to how we section our brains. Horizontal and coronal views are virtual.</p> <p>Our modified tools allow us to show a 3D view as we annotation brain structures.</p> <p><b>HIGHLIGHT</b> : I can see some sectional annotations of concern (which I will address shortly).</p> <p>In this view, I have 4 tabs however actual tabs present will depend on filter selections from the Brainsharer portal. Starting on the left I have:</p> <ul style="list-style-type: none"> <li>- <b>C1</b> (brain image)</li> <li>- <b>7NR</b> (annotation of structure)</li> </ul> <p>The others I will discuss later.</p> <ul style="list-style-type: none"> <li>- <b>DK55_7N_R</b> (3D volume pre-generated from annotations)</li> </ul>	(optional) Lines displayed in 3D panel are guides to orient us in 3D space
3. Zoom into sagittal view (click on box in upper right corner of top left panel) until reaching ~200µm	Notice the scale bar in lower left-hand window of the sagittal panel. I will zoom in to view the additional details of this high-resolution image, where we can start to define annotations	
<p>4A. Toggle visibility of 7N_R layer by clicking the X on 7NR tab -&gt; make sure z ~ 330 section</p> <p>4B. Click on sagittal view zoom button</p>	<p>Showing or hiding layers may be toggled by clicking the ‘X’ on each tab. I start by showing the annotation layer.</p> <p>Notice in the upper part of the screen the x, y, z coordinates. The ‘z’ value correlates to the section.</p> <p>I’ll also change from the 4-panel view to the sagittal view only.</p>	<p>Current x, y, z (layer) section is in upper left-hand corner of screen</p> 

START OF DRAW

Step	Script	Notes
<p>A. Scroll through sections (z) toward section 320</p> <p>Stop at section 320</p>	<p>Now I will continue to scroll through additional sections to review for completeness.</p> <p>I notice for section 320, an annotation is missing but we have tissue at the base of the brain stem, where the facial nucleus is located. For this scenario, I can demo the draw tool.</p> <p>The active brain atlas is based on cytoarchitecture and our completed annotations will contribute to this effort.</p> <p>As you are likely aware, the cells of the facial nucleus can be distinguished from the surrounding cells by their size and density.</p> <p>Since Neuroglancer allows people to see full-resolution images, which give the morphological detail of the cell, anatomists can annotate individual brain structures (where there is visible tissue).</p> <p>This resolution shows cellular features so fine we can use to distinguish features from the surrounding area.</p>	 <p>PAUSE ON SAGITTAL VIEW AND GIVE AUDIENCE TIME TO VISUALIZE THE CELLS WE WILL CAPTURE IN CONTOURS</p>
<p>B. Hold &lt;CTRL&gt; and ‘Z’</p>	<p>Here I will add an annotation from scratch</p> <p>Toggling between edit and draw mode will change the status indicator in the top of the screen</p>	<p>&lt;CTRL&gt; + ‘Z’</p> 
<p>C. Left click on image to begin drawing</p>	<p>Clicking on image in this mode (draw) will allow us to go around the cells, adding points as we go.</p> <p>I will proceed to create a contour around the higher-density (more closely packed) and larger cells that distinguish this structure.</p> <p>After I have outlined the cells that form the facial nucleus in this section (using as many points as I need), the points auto connect with the exception of the last point.</p>	
<p>D. Right click on image for last point to auto-close structure</p>	<p>With the final point created, Neuroglancer auto-closes the contour.</p> <p>At this point, I can review the result, comparing cells inside and outside the contour.</p> <p>If I’m happy with the contour drawn on this section, I’ll move on, comparing to previous and next sections.</p>	

START OF EDIT

Step	Script	Notes
A. Scroll through sections (z) toward section 319	As I scroll through the sections, I notice this next section, 319, is incorrect	
B. Hold <CTRL> and ‘X’	I need to toggle back to edit mode to make the required changes.  The volume tool status will change to ‘edit mode’ and the icon will be highlighted.	<CTRL> + ‘C’   
C. Left click (and hold) on point and drag into place  Release mouse button to stop	Once in the correct mode, I can select an individual point and drag it to the correct position.  The connecting segments will snap into place and auto-connect after each point is moved to the correct location.	
D. <CTRL> <ALT> Left-click	If I need to add extra vertices (points) to outline all the cells, I can use the defined key combination to accomplish this task.  I add the points and drag them into place with the same auto-connect functionality as before.	<CTRL> + <ALT> + 
E. <CTRL> <ALT> Right-click	Removing unnecessary points (overfitting) is also available by selecting a point and using a similar key combination	<CTRL> + <ALT> + 
F. Scroll back to section 318 and forward to section 320	Once all vertices are in place, I can review visually within this section and also by looking at the previous and next sections	
G. Left click on volume annotation tool ‘v’	Once we’re finished annotating the facial nucleus, we’re ready to preview the 3D shape.  First we stop the annotation session. I click on the volume annotation icon, which brings up the session menu.  Here we select ‘Close current active session’ on the menu.  The volume has been fully annotated and we can preview what these section look like when viewed section-to-section (or stacked up).	- START OF PREVIEW   Icon WILL be highlighted  <b>Volume session</b> Description: <input type="text" value="Select landmark"/> <span>▼</span> Color: <input type="text" value="Yellow"/> <input type="button" value="Start a new volume"/> <input type="button" value="Edit selected volume"/> <input type="button" value="Close current active session"/> <input type="button" value="Segment selected volume"/>
H. Switch to 4 panel layout	I’ll switch to the 4-panel layout to access the 3D view.	

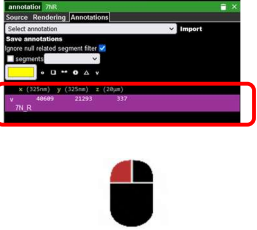
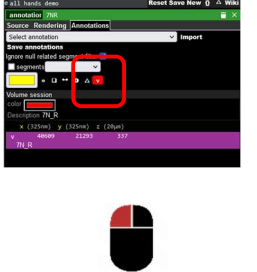
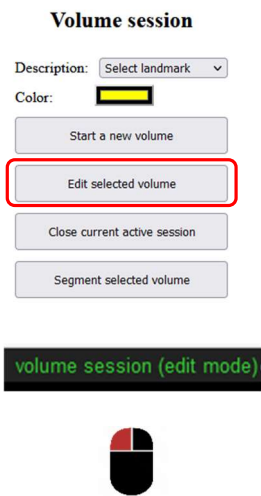
Step	Script	Notes
I. Expand 3D view	Clicking on the shortcut in the top-right corner of the 3D panel will expand that view to the entire viewing area.	
J. Click on 3D structure and rotate	We can then click and drag the 3D structure to see it from different angles.	Screen similar to: 

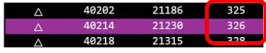

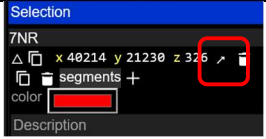


**IF NOT DEMONSTRATING 'PROPOGATION TOOL', SKIP TO 3D CONTOUR CREATION**

(TRANSITION SCRIPT)




If we're happy with the 3D version of the annotated contours, we can now "fill in the blanks" and smooth it out, making a complete 3D volume.

START OF PROPOGATION

Step	Script	Notes
<p>A. Scroll through sections (mouse wheel) to section 327 (z)</p> <p>SLOW and back-and-forth!</p>	<p>As an example, I will show annotations of the facial nucleus (7N_R). Scrolling through the sections (z) of the imaging, we will be able to view enough detail to identify brain structures of interest and subsequently create contours around them.</p> <p>I see on section 327 there is an issue. The tissue is missing from this section. Since the structure appears on the previous and next sections, I'll assume there was some tissue damage that could not be scanned. As a result, I'll demonstrate propagation of a previous section's annotation to this section.</p>	<p>Tissue is missing on section 327, will copy from previous section, 328</p>
<p>B. Left click on the volume annotation title</p>	<p>We will go directly to the specific layers where annotations have been created. I'll select the existing annotation volume in the top part of the right-hand panel.</p> <p>Although there will be a single 'volume' listing, it is actually a grouping of individual contours from each layer. Volumes a denoted by a small 'v' next to the name.</p>	
<p>&lt;ctrl&gt; RIGHT CLICK</p>	<p><b>TO SELECT POINT IN SAGITTAL VIEW (SHORTCUT TO SELECTING CONTOUR)</b></p>	
<p>C. Left click on volume annotation tool 'v'</p>	<p>After selecting the volume group, I want to go directly to the contour annotations (because I need to find the annotations on section 326 or 328). The Volume annotation tool (denoted by a 'V' above the volume listings) is used for this.</p> <p>Clicking on this tool will take us there. Clicking the 'V' icon opens a new dialog box with contextual options.</p>	
<p>D. Left click on 'Edit selected volume'</p>	<p>The Volume annotation tool menu has 4 options. Since we need to propagate an annotation from one section to another, I'll choose 'Edit selected volume'</p> <p>Selecting this option will enable 'edit mode' and show the individual sections where contours have been created. 'Edit mode' will be indicated in the top of the window.</p> <p>You will see 'volume session (edit mode)' in green at the top.</p> <p>If the constituent sections don't automatically appear, you can right click on the volume group to display the sections that make up the volume. Note, you can also toggle volume/contours sections as needed.</p>	<p><b>Volume session</b></p> <p>Description: <input type="text" value="Select landmark"/></p> <p>Color: <input type="text" value="Yellow"/></p> <p><input type="button" value="Start a new volume"/></p> <p><input type="button" value="Edit selected volume"/></p> <p><input type="button" value="Close current active session"/></p> <p><input type="button" value="Segment selected volume"/></p> <p><b>volume session (edit mode)</b></p> 

Step	Script	Notes
E. Locate section 326 and select it with left click	<p>Once I locate the previous section (326), I can click it to go directly to the section where that contour is located.</p> <p>Note, you may need to scroll through the section list until that section is visible. The section I want will highlight after the click.</p>	<p>Section 326 will be indicated in 'z' column</p>  
F. Left click on the arrow icon in lower part of annotation panel	<p>With section 326 selected (as indicated by the highlighting), I use the arrow icon in the lower part of the annotation panel to go directly to that section.</p>	 
G. Hold <CTRL> and right click on any point in the contour	<p>Clicking any point in the contour will select it. Once selected we can then propagate the entire contour "as-is" to the next section.</p> <p>The lower part of the annotation panel will display information about the individual point I selected.</p>	<p>&lt;CTRL&gt;</p> 
H. Hold <CTRL> and 'C'	<p>From here I simply do a &lt;CTRL&gt; + C combination to copy the entire contour into the next section.</p> <p>Note in addition to the propagation into the next section, the sagittal view will advance to the next section 327 so a user can review.</p>	<p>&lt;CTRL&gt; + 'C'</p>

3D CONTOUR CREATION

Step	Script	Notes
A. Left click on volume annotation tool ‘v’	To complete the annotation to 3D volume creation, there is 1 final step.  I click on the volume tool icon again (V)	- START OF 3D VOLUME CREATION –  Icon will NOT be highlighted
B. Left click on ‘Edit selected volume’	When the volume tool is select the menu reappears but this time we choose the ‘segment selected volume’ option  This will submit all the contours (contours per section) to the server that turns them into a 3D volume.  We use the contours as a means to an end. The stacked contours are used to form the 3D volumes.  As we are using a test server, this step may take a while to complete (5-20 minutes). In production, the time will depend on the structure complexity and server load.	<b>Volume session</b> Description: <input type="text" value="Select landmark"/> Color: <input type="text" value="Yellow"/> <input type="button" value="Start a new volume"/> <input type="button" value="Edit selected volume"/> <input type="button" value="Close current active session"/> <input type="button" value="Segment selected volume"/>
C. Toggle (show) DK55_7N_R visibility by clicking the X on the DK55_7N_R tab	Rather than wait for this volume to finish generating, I previously generated one based on doing these same steps.	
D. Toggle (hide) 7NR visibility by clicking the X on the 7NR tab	We are currently viewing both the annotations and 3D volume but can hide the annotations layer by clicking the ‘X’ on the 7NR tab  <b>HIGHLIGHT VOLUME:</b> FADE OUT CONTOURS	

**ADDITIONAL SCRIPT:**

With Neuroglancer contouring tool we can now define the shape of structures in new brain samples. As we accumulate annotation sets (new brains), the active atlas is refined by capturing natural anatomical variation from increase sample size.

Thank you for your time! I’ll now open the forum up to questions and answers.

<https://webdev.dk.ucsd.edu/preview/?id=492> (no missing contours, all correct)