fMRI/DTI analysis using Dynasuite

(revised 8/23/23)

Contents:

- 1 Logging in
- 2 Finding a patient session
- 3 The screen layout and general image viewing tips
- 4 Dynasuite automated preprocessing
- 5 Checking brain segmentation and image registration
- 6 Seeing fMRI results and adjusting thresholds
- 7 Saving fMRI results
- 8 Seeing and saving DTI color map results
- 9 DTI Fiber tracking
- 10 Logging off

1 Logging in

Log-in to the Dynasuite workstation using your DHE username and password. There is a workstation in the Neuro Reading room in the Cancer Center and in the DMP MRI suite. There are 2 other workstations in offices (Petrella & Voyvodic).

All images and results are stored in the Dynasuite server, a centralized computer server located in the DUHS data processing center (somewhere in RTP I think). The Dynasuite workstations let you view and manipulate data stored on that central server.

Note: only one workstation can access any patient study at a time, so when you finish processing a patient be sure to close that study (see step 11 below).

Run the DynaSuite software by double <u>clicking the</u> "Dynasuite" icon on the desktop.



This will bring up InVivo's login window for Dynasuite.

Leave the Workspace as "dynasuite"

User name: [your Duke NETID]

Password: [your Duke password]

If successful this will start Dynasuite, which will fill your screen

Note: Only NETID's that have been entered as Dynasuite users will be recognized, so if you can't log in contact a Dynasuite administrator (e.g. Jim Voyvodic, or Carlos Cabeza).

2 Finding a patient session

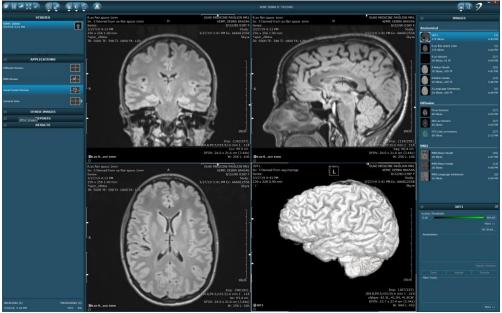
Scan sessions are organized in Dynasuite by scanner manufacturer, or you can find any session by selecting "All Studies" in the navigation pane (upper left side of screen).

Double-click the study you want to examine (loading may take a minute).

Studies are usually sorted by date (most recent first) – you can change/check the sort order by right-clicking in the navigation pane and selecting the Sorting option.

3 The screen layout and general image viewing tips

Once you enter a study you should see:



Left side of screen:

Applications: Use "Smart fusion" for most fMRI/DTI analysis
Other Images: Original images imported to Dynasuite (e.g. from scanners)
Reports: Text documents (e.g. from Neuroquant)
Results: User-generated DICOM image results made in Dynasuite

The rest of this section assumes you are running the "Smart Fusion" application

Right side, top of screen has a list of Dynasuite preprocessed images (see section 4) Anatomical

Original images recognized as suitable for processing

The most important of these is "3DT1" – it is the reference for all others FLAIR and Post-contrast T1 images

Ax tensor images - the EPI images acquired for creating DTI results

fMRI task images – the EPI images acquired for creating fMRI maps Diffusion

Map results of DTI analysis (processed "DTI" images in Anatomical list) fMRI

Activation map results of fMRI analysis (recognized tasks from Anatomical list)

Right side, bottom of screen – this changes depending on which Image data set is active. This section includes adjustment icons to let you check or change image properties.

Middle of screen - main image viewing panes

Image viewing region: This has 3 orthogonal image planes plus a 3D recon window.

- By default this window will show the 3DT1 reference data set. You can change the base image by dragging another data set to lower-left corner of any of the 3-plane views and replacing the current view
- Click the brightness icon at the top of the screen to be able to adjust image contrast.
- You can overlay other images onto the base image by dragging a data set onto an image pane, or onto the table in the lower-left corner and adding it as another view
- Within each orthogonal viewing pane you can manipulate the slice location in the other panes by dragging the crosshair.

Right-clicking the mouse will bring up a control wheel.

Around the edge of the wheel are display control options; these let you select what the left mouse button controls (e.g. brightness, position, zoom, rotation, etc).Inside each display control there is an arrow; these give you more control options.The arrow at the top of the wheel allows you to change various display settings.The camera icon in the upper-left part of the wheel lets you save a snapshot of the current image, or if you choose its arrow you can save a whole series of images

- for that pane.
- At the lower-left of each viewing pane there is an arrow and legend. Clicking a legend icon selects that portion of the display (i.e. base image or overlay); for example, if an overlay is active then the display adjustments will be applied to the overlay.
- Clicking the arrow in the lower-left corner shows what is currently being displayed in that pane. You can turn on and off different components by clicking the 'eye' icon for each.
- To change the image series being displayed, drag the new series you want to see from the Image list on the right of the screen and drop it on the current base image in the image legend (e.g. 3DT1). Only one image series will be shown in full grayscale at a time.
- To add another image series as a color overlay on top of the base images, drag that series from the Image list and hover over the legend; you will then be able to either drop it on top of an existing series name (replacing that series), or drop it in an empty legend slot to add it as another overlay.
- In the 3D reconstruction pane, the lower-left arrow also lets you manipulate transparency of different components of the 3D scene, and it allows you to select different cutting planes for looking within the reconstructed brain.
- If you want, you can turn off the large crosshairs. Turning this off makes no difference in the saved images, but I find those lines distracting. To do so, right click in any slice image, select the top arrow, and then "Displayed Information", then the "Show/hide Cutlines" option.

4 Dynasuite automated preprocessing

When Dynasuite receives images (seen in the "Other images" list on the left side of the screen), it attempts to identify each series based on descriptors contained in the DICOM image headers. When a series has descriptors matching one of its preprocessing "rules" it

will automatically apply that rule's algorithm to generate new image results, which will appear in the "Images" list in the upper-right section of the screen.

Dynasuite uses a whole-brain T1 scan (3DT1) as its reference for all processing. When it finds that "T1-ref" it will automatically attempt to generate a 3D brain segmentation mask that separates brain tissue from the rest of the T1 images. It uses that segmentation mask to create the 3D brain reconstruction and to register fMRI and DTI images.

fMRI scans are identified as EPI images with more than 50 timepoints. The type of task can be specified in the series descriptor, but by default our system assumes all clinical tasks are alternating 15 second blocks of rest and active task. Preprocessing includes automated registration to the T1 image (which is rarely good enough), motion detection, some smoothing, and then statistical analysis using a standard general-linear-model approach. Activation maps are thresholded at p<0.05.

DTI scans are identified as EPI images with at diffusion gradients. If the scanner type (GE/Siemens) and number of gradient directions matches its internal tables it will automatically calculate diffusion tensors, diffusion, and color-coded fractional anisotropy maps. (Not clear how many diffusion tensors it has tables for – 6, 15, 25, and 30 at least).

Note 1: If Dynasuite does not recognize any scan as a T1-ref (T1-weighted with more than 50 slices) it will not do any automated processing.

Note 2: Occasionally Dynasuite will fail to recognize or process a series properly. In that case you can find the series in the "Other images" list on the left side of the screen, then right-click that series to see a list of image descriptors that dynasuite has detected as "matching" and if necessary you can modify that list of matching descriptors. Then you can "force" it to apply the preprocessing rule for the new descriptors.

Note 3: Dynasuite expects all images to arrive before it does preprocessing. If it preprocesses some images and then receives new images later, it will delete all processed images (and any registrations or adjustments you have made) and then reprocess everything. (This stupid design flaw has cost me a lot of extra work.)

5 Checking brain segmentation and image registration

<u>Proper registration of fMRI and DTI images to anatomical images is very important!</u> Dynasuite's automatic preprocessing is fairly good but always needs to be checked and almost always needs manual corrections to register fMRI and DTI results to T1 images.

To check/modify the T1 brain segmentation:

Select the 3DT1 image set by clicking on it in the Anatomical Images list (upper right) Click on the "3D check" option in the 3DT1 panel in the lower right of the screen. This should change the middle windows to display the segmentation mask as a brown overlay on the 3DT1 images

Move through the display by dragging the crosshair in any view

To remove non-brain regions from the mask click on that region (this will usually remove a portion of the mask)

- To add brain regions not included in the mask, click on that region (this should add some tissue to the mask)
- This should (eventually) let you get a reasonable segmented brain (it doesn't need to be perfect)
- Click "Save" in the lower right corner if you have made changes.
- Click "Done" (lower right corner) when finished.

Checking image registration

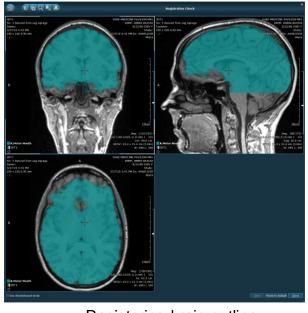
You must verify that all image series (FLAIR, DTI, fMRI, and post-contrast if present) are properly registered to the 3DT1 images.

Note: you should register the "Anatomical" images in the upper right section, not the DTI or fMRI map images. Changing anatomical images will automatically change the maps.

To check registration of a series:

- 1. Select the series from the "Anatomical" section of the Images list (upper right).
- 2. Click the "Registration Check" option in the series-dependent panel (middle right).
- 3. This should result in a blue overlay of that image series on top of the 3DT1 images.
- 4. Adjust intensity of the 3DT1 and blue overlays to have contrast in both (see below) You can either adjust blue intensities to see gyri (left) or whole brain outline (right)
- 5. Move through the display by dragging the crosshair in any view.
- 6. If necessary, translate the overlay images to improve registration.
- 7. You may also need to adjust rotation (especially in the sagittal view).
- 8. Repeat steps 5-7 until you get good registration (especially near lesion)
- 9. Click "Save" in the lower right corner if you have made changes.
- 10. Click "Done" (lower right corner) when finished.





Registering gyri (preferred

Registering brain outline

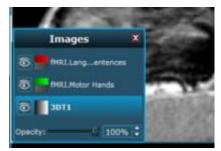
Each series needs to be registered independently. Once you register an Anatomical image series, the changes you made will be automatically applied to the associated Diffusion and fMRI result images as well.

Image registration is tiresome but essential!

6 Seeing fMRI results and adjusting thresholds

To overlay an fMRI activation map on top of anatomical images, select the map from the "fMRI" results list (right panel), and drag it onto any of the 3 orthogonal image panes in the central viewing region.

If multiple fMRI maps are overlaid they should each appear as a different color. The colors and series names appear in the display legend in the lower left of each view.



Overlays are color-coded and thresholded according to the parameter settings in the series-dependent section of the right panel.

Note: positive activation signals (BOLD signal increased with task) are assigned bright colors with each task result displayed in a different color, whereas negative activations (BOLD increased during rest) are all overlaid as gray. Dynasuite does not allow you to set different thresholds for positive and negative activations. Gray overlays should in general be ignored as their meaning is not well defined.

To change the color for an fMRI map, click on the map and then in its adjustment window (lower right of screen), click the "More" option. This will bring up the color adjuster:

fMRI.Language Sentences	
t-value: ()	
p(Bonf) <	0.000001
🗌 Enable Outline Mode	
Color Selection: +	
min. Cluster Size:	3
	Reset
	Less <<
	Motion Check
	Registration Check

To change color from red to green, for example, you first click the bright red region of the color selector, then select bright green when the color palette appears, and save. Then click the dark red part of the color selector, and then select dark green from the color palette. (I usually use red for language, blue for hand motor, and green for a third).

Note: Dynasuite provides a separate fMRI application (upper left) to enable closer inspection of fMRI results than is provided using the Smart Fusion application. The fMRI tool allows viewing time series plots for signal fluctuations for individual active regions. I never use this, however, because the software just lets you inspect the time series but provides no way to fix problems. (I created a web-based tool so the MR techs can inspect fMRI results during scanning, which is more helpful than Dynasuite's tool.)

Adjusting fMRI activation threshold levels

Adjusting the threshold for fMRI activations can make a big difference in map results. At Duke, we use the AMPLE approach to get consistent activation maps. AMPLE simply involves setting the threshold at approximately half the maximum signal value for the activation region of interest. This works well for robust activations (i.e., peaks over t-value of 10); for weak signals the threshold should probably not go below t-value of 4 to avoid lots of false-positive blobs.

So, for each fMRI map, center your crosshair on the region you are most interested in (e.g. motor area ipsilateral to the lesion, or expressive/receptive language areas) and raise the threshold slider until all that activation just disappears. Note that maximum t-value, then move the slider down to half that value.

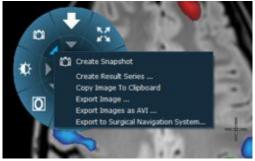
Activations adjusted using the AMPLE threshold approach have been shown to be reproducible and to correspond to expected functional anatomical areas (Voyvodic 2006, Voyvodic et al 2009, Voyvodic et al 2012).

7 Saving fMRI results

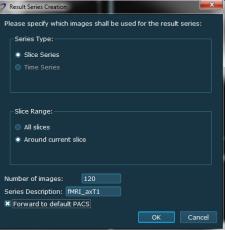
Save a series of overlaid images

To save a whole series of images of different slices, you should first decide how many slices you want to save, and then identify which is the middle slice of that series.

To do so, scroll through slices until that middle slice is on the screen. Then right-click on the image, select the arrow under the camera icon, and select "Create Result Series".



In the dialog window, choose "Around current slice", then enter the number of slices, give the series a descriptive name (eg "fMRI_axT1"), and select "Forward to default PACS". That will create a whole series of screenshot images and send them directly to PACS.



I usually create DICOM images overlaid on T1 images only in the axial view (120 slices). I create DICOM overlays on FLAIR images in axial (120 slices), coronal (130 slices), and sagittal (140 slices) views.

Creating a Results folder

To keep your result images organized you should create a different Results folder whenever you change the anatomical underlay images.

To create a new Results folder, right-click the "Results" section header and select "create new folder".

If you do not create a new folder, all new images will be added to the same folder by default. All images in the same Results folder appear in PACS as a single image series. If you send results to PACS and they never seem to arrive it is usually because they have been tacked onto the end of the previous series.

Saving single screenshots

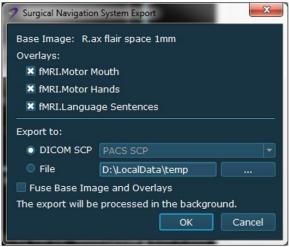
To generate a screenshot of any viewing pane you can right-click on that pane and select the camera icon. That will save a single image.

To send single screenshots to PACS you will need to export it explicitly, either by right clicking that single Result image and export, or by right-clicking the folder title and exporting the whole folder.

<u>Send images and overlays to PACS for surgical navigation (i.e., Brainlab/Synaptive)</u> We always send a copy of the fMRI statistical activation maps to PACS so they are available if the neurosurgeons want to import them into surgical navigation systems.

Note: the surgical navigation fMRI results are not color overlays, they are grayscale-coded statistical values, with positive and negative activations stored in separate series files for each task scan. The fMRI activations and their underlying anatomical image are all stored with the same voxel orientation/resolution so they can be recombined by any software.

To create such files, right click in the axial view image, then click the arrow under the camera icon, then select "Export to neuronavigation system" from the option list. When the export window appears, select the "DICOM SCP" option (see image) and then "OK".



Whole brain series of all images and overlays will be sent to PACS. This is done in the background so you don't need to wait for it.

Temp files for making montages (optional)

If you have access to other software, such as fScan, to make 2-D multislice montage images (neurosurgeons' preferred format), you can send copies of the fMRI overlay images to the local filesystem.

To export to files, repeat the steps above for sending to PACS, except instead of selecting "DICOM SCP" as the target you should select "File", which will then send DICOM images to the folder specified.

Overlay fMRI maps on FLAIR or post-contrast images

After saving fMRI maps on T1 images, you should replace the T1 images with FLAIR images (or with post-contrast T1 images if you prefer).

Drag the FLAIR images from the upper right box and drop them on top of the T1 image name. Note you want to replace the T1 underlay images with the FLAIRs; if the FLAIRs appear as a colored overlay on top of the T1s, right-click on the FLAIR in the images overlay list and "delete". Then drag and drop on the T1 again to change the underlay.

When you change the underlay remember to create a new Results folder, by right clicking in the "Results" bar on the left side of the screen.

With FLAIR as the underlay images you should repeat step 4 above to send images to PACS.

If you sent activation maps to local files you should also repeat that process for the FLAIR images. However, this time you should uncheck the overlay boxes at the top to avoid sending duplicate copies of all the activation maps. Unchecking those boxes will cause a warning message to appear when you click OK, but just say OK again. There is no need to send FLAIR images to PACS for neuronavigation.

The process is the same if you want to save overlays on post-contrast images.

8 Seeing and saving DTI color map results

To create color DTI overlay images replace the fMRI activation map overlays by selecting the color FA map from the list of Diffusion images in the upper right side of the screen, and dragging that map to the overlay box in the lower left corner of any brain image view. You should also delete (by right-clicking the overlay name) any fMRI map overlays.

Adjust the intensity/contrast of the FA map colors a bit (generally I just raise the intensity slightly), then save "Result series" in all 3 view windows (axial, coronal, and sagittal) as you did for fMRI series in step 7.

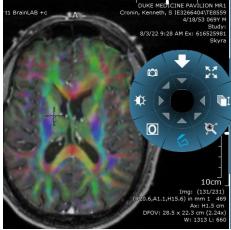
9 DTI Fiber tracking

DTI fiber-tracking is an interactive process in Dynasuite. It involves first finding an image that contains a cross-section of the nerve bundle you want to track, manually drawing an ROI around that bundle, then telling Dynasuite to follow as many paths as it can that pass through that ROI. If too many tracks are found (pathways you don't want) you can edit

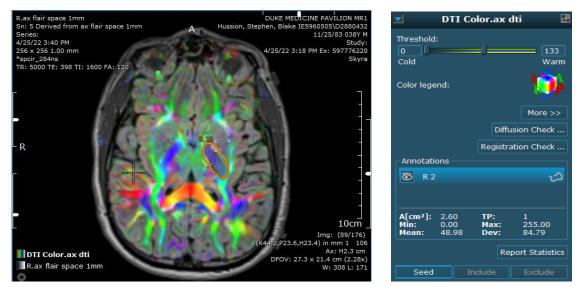
those out; if tracking is incomplete you can draw additional ROIs and track more. Once tracking is complete you have to decide how best to view the pathways and then save screenshots to send to PACS.

The details of this process are as follows, using corticospinal tracts (CST) as an example: First overlay the DTI color FA map on an anatomical series as described in step 8.

Right-click the image and select the ROI drawing tool at the bottom of the wheel.

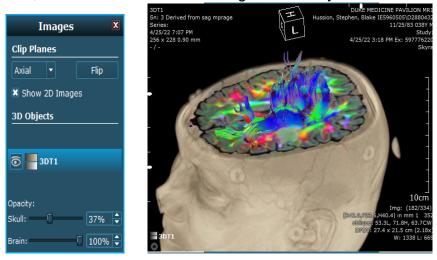


- Find an axial slice in which you can see a good cross-section of the pathway in blue at about the level of the basal ganglia and posterior limb of the internal capsule..Then draw an ROI around the blue nerve bundle. Choosing where and how big to draw the ROI depends on what aspect of tracks you want to highlight. In general, it's best to slightly overestimate the girth of the CST.
- Once you have the ROI drawn, click the "Seed" button in the lower right corner of the screen (may need to scroll down in the DTI section to see the buttons).

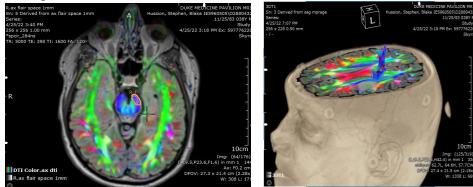


Seeding causes Dynasuite to look for any high-FA fiber streams that pass through a voxel anywhere in the ROI and create a track both inferior and superior, stopping when the FA value is too low or the track has too sharp a bend.

Visualizing tracks is best done in the 3D brain window. To highlight the fiber tracks, open the skull by adding a clip plane; click the arrow at the lower-left corner of the 3D reconstruction pane then choose Axial clip plane. You can also adjust Skull and Brain opacities, and rotate the 3D model to get the view you like.



To isolate specific sub-pathways, you can choose different target ROIs and you can draw and seed multiple ROIs. You can also draw ROIs around portions of fiber tracks you don't want, and then click the "Exclude" button to remove those tracks. Keep in mind that the fastest way to trim a track after the initial seeding is to draw another target ROI and hit the "Include" button. This will isolate only fiberstreams passing though both the seed and target ROI's.



- Drawing 3D fiber tracks is an art, best learned from experienced neuroradiologists and then a lot of practice. The main tracts we are concerned with are the CSTs. Use a seed in the posterior limb of the internal capsule on the axial images to create a large track bundle. We can isolate the "hand" fibers by using a target ROI in the hand portion of the motor strip, the "omega". Use similar technique for the "foot fibers". The seed ROI for the optic radiations is created on coronal images starting at the junction of Meyer's loop and the optic radiations. Find that on the axial images and triangulate to the location on the coronal images. Draw an oval seed ROI, then move to the occipital lobes lateral to the lateral ventricles and draw a broad target ROI.
- If the fiber tracks become too sparse, delete the target ROI and draw a larger one. You can select different tracks in the lower right hand corner if you want to re-edit them.

You can also hide or display more than one track by clicking on boxes in the lower right-hand corner of the screen.

Once you have the 3D view of the fiber tracks you like you can create screenshots. First right-click on the "Results" bar and Create a new Results folder, then save sequential screenshots while stepping through different axial slices (e.g. advance 2-3 slices between screenshots). This will result in a dynamic view of both the tracts and lesion. Right click the Result folder name, rename it appropriately, then right click again and then Export the folder to send all the screenshots to PACS as a single image series. The only way to have separate named series in PACS for different tracks is to create new Results folders for each track and rename them prior to exporting.

10 Logging off Dynasuite

To close a patient study, click the check mark icon near the upper left corner of the screen This will then ask you whether you want to "Defer" or "Complete" the study. Always select "Defer" – this allows someone else to return to that study later.

To log off, click the "X" in the upper right corner to close the Dynasuite display. This will then ask you if you want to log out of Dynasuite - say yes.