Viewer

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First Steps

Learning by doing is most of the times the best option. So, try out the demos on

https://www.nora-imaging.org/

to get an inital experience. Note that there is also a non-web version of the viewer (packed in electron) to allow local non-internet usage of the viewer (download also here)

NORA's desktop

NORA's basic working screen is like that: image-1602508371722.png
NORA's imaging data is organized in projects. Each projects contains a set of subjects/studies, which appear in the left table of the desktop.

Loading data for viewing happens in most of the cases per **drag&drop.** You can drag images from the subject/study table (see here for more about the table) into the viewports on the right. By **double-clicking** a file its content is loaded and placed into next available viewport. You can also **drag&drop files from your local computer** into the viewports for visulization (note that the data is not uploaded, it stays on your local machine).

Depending on the file type different drop options appear in the viewports. For example, if you want to overlay one image onto another just drop on "drop as overlay". Hence, each viewport can contain multiple items: a background, overlays, masks, fibers and surfaces (in 3D) etc.. Corresponding to each item a **viewbar** appears in the upper right corner of the viewport. The viewbar controls the appearence of the associated object/contrast. Most properties (colormapping, outlines, etc.) are set for all instances of the object in all viewports. If you want to choose the same object to have different appearence properties in different viewports use the shift key while selecting the property.

The viewbar of the "background" image is organzed as follows

image-1601650455715.png

Central Toolbar

image-1601633873571.png

Viewports and Viewer Layout

To control the layout of the viewports use the layout selector located at the central toolbar. Note that for the horizontal viewports at the bottom a mosaic view is default.

image-1601633656873.png

Mouse

Mouse wheel	change slice
Ctrl + Mouse wheel	zoom
Right mouse button (hold down)	pan
Left mouse buttom click	change position of crosshair (world position)
Middle mouse button	Change windowing
Ctrl + Left Mouse button hold	Reformatting MPR (rotation/translation) , see Navigation Tool

Keyboard Shortcuts

1-6,0	shortcuts to standard CT windowings
Space	toggle ROI edit, see ROI tool
s	open settings window
x,y	decrease/increase scroll speed
arrow up/down	change subject (when using autoloader)
(shift) Ctrl-Z	Undo/Redo ROI drawing

ROI-Tool

image-1600462098461.png The

ROI-Tool

The term Region of Interest (ROI) is used throughout the tutorial as a synonym for a "Mask", "Binary Mask", "Segmentation" or "Volume of Interest". Technically, it is a binary 3D volumetric image matrix, which is quite similar to **3D image** apart from the fact that voxel values are binary (on or off). Thus, a ROI has also the same properties as image (like resolution and matrix size). ROIs can also be just 2D, however, one has to be remember that the 2D slice has also a position in 3D space, which can sometimes be confusing.
ROIs are close to what is represented by DICOM SEG objects.

To open the **ROI-tool** just go via the toolbox menu of the vertical iconbar or use the shortcut via the "pen" icon:

image-1600354205749.png image-1600354220857.png

This opens the following toolbox window, which contains the access to all functionalities of the ROI-tool

image-1600354300543.png

On the right you have list of currently opened ROIs togeter with information about matrix size and patientID/studyID. There is also information about the size of ROI and several tool icons:

image-1600356837328.png	focuses the position of the viewer to the center of gravity of the current ROI
image-1600356743419.png	turns the ROI to be the "current ROI" on which currently is drawn on
image-1600356769770.png	toggles the visiblity of the ROI in all viewports
image-1600356803683.png	open several options to modfiy ROIs (see below: ROI operations)

image-1600356868723.png	save the ROI (upload to server)
image-1600356897331.png	downloads the ROI to your local computer
image-1600356924459.png	erases/clears all on voxels of the ROI
image-1600356948798.png	deletes the ROI from workspace

Drawing and Pens

Generally, the **left mouse button turns voxels on,** while **right mouse button eraśes** voxels. Drawing happens always on the ROI which is currently selected for drawing. You can select a ROI for drawing by highlighting the pencil icon in the viewbar, or in the ROItool

image-1601631951727.png   image-1601631990561.png

A shortcut for switching drawing on/off you cane use the **spacebar**. You can also **hold shift pressed** while being in drawing mode to disable mouse drawning features.

On the left panel of the ROI-tool the current type of pen mode (pen type) and the size of the pen can be set. You can turn on "**live preview**" to see what the current pen would draw. Displayed **opacity** of the ROI can be determined and whether **outlines** are drawn. The available pen types are as follows:

image-1600428072743.png	**Thresholding based pen**.
	Depending on the threshold (either choose clImL/R or an actual number) the pen turns voxels ON, which are above ("Higher") or below ("Lower") the threshold. Additional you can select "Higher RGrow"/"Lower RGrow" to enforce the ON voxels to be connected to the central voxel.
	image-1600432433860.png
image-1600428113719.png	**Magic pen (unconnected)**.
	Turns voxel ON, which have a 1) similar contrast compared to the central voxel, 2) are within pen's radius. The similarity depends on the color limits chosen for the current contrasts.
	image-1600432118373.png

image-1600428149703.png	**Magic pen (connected)**. Turns voxel ON, which have a 1) similar contrast compared to the central voxel, 2) are within pen's radius. and 3) are connected to central voxel via a **region growing approach.** The similarity depends on the color limits chosen for the current contrasts. image-1600432170357.png
image-1600428181303.png	**Unconstrained 3D region Growing.** Select a pixel by keeping left mouse button pressed. By moving the mouse left/right (while mouse pressed) the similarity threshold can be changed. image-1601375047324.png image-1601374884021.png move the mouse left/right to adapt size
image-1600428224875.png	**Polygontool** Use the polygon tool to determine a ROI by its outline. You can either create the outline by holding the mouse button down, or click by click. You can also move points of the outline manually after creation. Use trashcan to delete outline, use the pencil to render the polygon into the current ROI enabled for drawing. image-1601375520249.png image-1601375544409.png

Creating a ROI

To create you always have to give a reference on which basis the underlying geometry the ROI is created. There are several ways to do this:

1. Take an existing onto ROI-tool by dragging the hand-icon
    image-1600368649317.png
    from the viewbar of the image (or the file from patienttable) and decide on the type of creation
    image-1600368594193.png
    The threshold for creation is the lower limit of the current windowing of the contrast

2. Or use the cog-wheel item of the viewbar to do the same thing.
   image-1600368375832.png
   Image not found or type unknown

3. Or just use the "New ROI" button in ROI-tool itself.

image-1600356803683.png ROI operations
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- **Morphological Operations:** NORA provides the typical 4 operations (erosion, dilation, opening and closing) using a 6-neighborhood in the slicing of the ROI matrix, i.e. the size of the neighborhood varies depending on the underlying matrix size.
- **Set Operations:** NORA provides intersection, union and set difference. Select
- **Remove Salt:** Does a connected component analysis and removes components than the given threshold.

ROI statistics

Open the ROIstats window by clicking on the menubar in the ROI-tool

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The ROI statitics table appears which computes for all possible combinations of contrasts and ROIs currently present in the viewer the following statistics:

- median of contrast (percentile 50%)
- iqr1/iqr2 - inter quartile ranges (percentile 25% and 75%)
- mean/std - mean and standrad deviation
- volume (in mL)
- area (in cm2, makes only sense when ROI is 2D, or a single slice in the matrix)

image-1601631457986.png
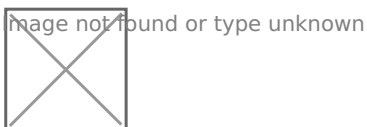Image not found or type unknown

Fiber Viewer

NORA includes fiberviewer based on webGL and Babylon.js. The main features are:

- Supports TCK (mrtrix) and TRK (TrackVis) formats
- Fiber Manipulations
  - Interactive selection by variable sized spheres
  - Interactive deletion by variable sized sphere
  - Selection and Deletion of tracts by ROIs
  - Selection by sphere sets, (annotation type: poinset)
  - Selection by waypoints (annotation type: freeline)
  - Selection by DBS electrodes
- Rendering
  - Vistmaps (fiber densities)
  - Terminalmaps
  - LIveupdate of visit/terminal maps
- Tracking
  - a simplistic fibertracking algorithm based on tensor/orientationl fields is provided

Starting the fiber viewer

Choose an appropriate background image (like a T1w) and simply drop a tck or trk file into a viewport and the viewer will automatically switch to 3D mode a displays the fibers. An additional viewbar appears, which is associated with the loaded tracts. The viewbars allows you manipulate the streamlines, select subsets, etc. Here a short overview:

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Fiber Selection

- **Manually:**
  Hold **Shift key** pressed, a yellow sphere appears when hovering with mouse over the tracking, click to select all fibers going through the
- **By ROI:**
- **By Annotation:**

Cropping Selections and iterative selections.

A small fiber viewer pptx

Projects and Subject/Studies

Projects

NORA's subject pools are called "Projects". Each user has rights to see a certain subset of projects. The subject/study table on NORA's desktop shows only the subjects/studies of the current project. Projects can differ in their nameing conventions (anonym) and way of storing the data in the backend. They can also have custom processing functions and autoexecution queues.

Subjects/Studies

image-1602517651838.png

Filterbars

Use the filter bars to select a subset of studies/subjects. All bars share the following funtionalities: multiple queries are separated by spaces and are interpreted as a "OR" concatenation. If you want to combine expressions that have to be simultanously fulfilled use an explicit "&" sign. All expression have implicity a wildcard at the end of the pattern. For example, search for all patients, whose given name start with A or B, write "A B" into the filter bar of the name column. The "file search" bar can be used to select studies that contain files which match the given file pattern. Explicit wildcards are * and _, where * represents zero or more arbitrary characters and _ represents exactly one abitrary character.

Examples for file searches:

- All studies that have a T1 from a trio: `t1_trio*/s0*.nii`
- Sometimes naming conventions are different, so use multiple queries: `t1_trio*/s0*.nii` `MPR_t1*/s*.nii`
- If you want to restrict for those which have specific study tag: `t1_tri*/s0*.nii & STAG:control`

There are special search attributes:

STAG, PTAG, FTAG, JOB, SDESC

For example, search for all studies, which have the tag "control"

`STAG:control`

Jobs can be queues (q) or running (r) or errornous (e). Find all subjects that have an errornous job

Using Tags

Subjects, studies and files can be decorated with tags. Use the context menu to assign tags. Tags help to group and label items. Files can have special tags

Autoloaders

Marker-Tool

The Marker-Tool enables other types of labels, for instance point-labels.

- To open it click on the wrench symbol an select "Marker Tool".
- To create a new pointset go to the menu of the Marker-Tool and select "new+" -> "pointset".
- The pointset can be renamed by clicking on the text in the yellow bar. To enable a list view closer to the image, select the respective list symbol from the yellow bar. To enable adding points by clicking on the image, select the pen symbol.
- Now points are added by clicking on the image. The points are renamed by selecting the text in the list. When finished the pointset must be saved by clicking on the "Save" button. The pointset is stored in a subfolder "annotations" of the current patient.

Marker-Tool-1.png type unknown	Marker-Tool-2.png type unknown	Marker-Tool-3.png type unknown
Marker-Tool-4.png type unknown		

Navigation Tool (alignment and deformations)

NORA provides the possibility to manually align volumetric images (nifits) in a rigid (affine) and deformable fashion. You can interactively **translate/rotate/scale the images by holding the Ctrl-key and using the mouse** with the yellow crosshair symbol. The deformable transformation is specified by either a set of displacements, or by two set of matching keypoints.

image-1650886820387.png

image-1650891141188.png   image-1650891235110.png

The navigation tool is organized as follows:

image-1650905242339.png

By default, all images are transformed/moving. You can also specify the "moving" images by dropping the nifti into the navigation tool. The moving images are shown in the lower box of the tool. Using the APPLY button(s) the current transformation is applied and written to the niftis defined as 'moving'.

Transformation results are only displayed when the "gridding" is defined to be on one common image matrix. Use either the "world"-image matrix by clicking on the WORLD button or use the "m" symbol on the viewbar of a specific nifti to use the image matrix of this specific nifti. The "world"-system uses a matrix with bounding box including all visible niftis and the voxel size given.

Deformable transformations (warping)

To create a warp field, press the "enable" button in the deformable transform section. By default you can add displacement markers ("correspondences") by pressing the "add" button. The size of the marker defines the extent of the displacement. You can combine multiple displacements. Each displacement is represented by a Gaussian shaped displacement field. By pressing the "dump" button, the displacements markers are rendered as a combined displacement field and markers are deleted. On top of this "dumped" displacement field you can now add again new displacements. Instead of using displacements, one can use two sets of keypoints. Therefore, choose in the "type" combo-box "pair of sets".