

Obtain orientation via „get orientation via 3point selection „

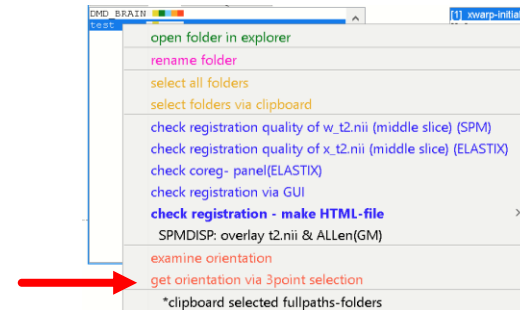
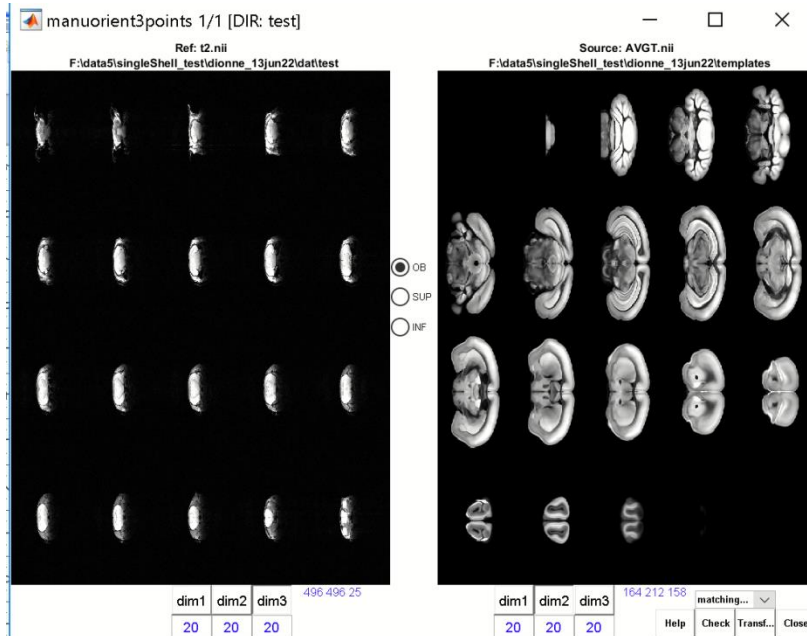
- use this method if the method „**examine orientation**“ from animal’s listbox does not work!
For example if the „t2.nii“ image is too small to examine the best orientation type via „examine orientation“

The orientation type has to be examined and checked before performing the registration to standard-space!

Hopefully all animals of the same study are roughly oriented in the same way...

In this case the definition of the orientType has to be done only once per study!

- Select **one** animal from the left animal listbox
- click right context-menu: select: **get orientation via 3point selection**

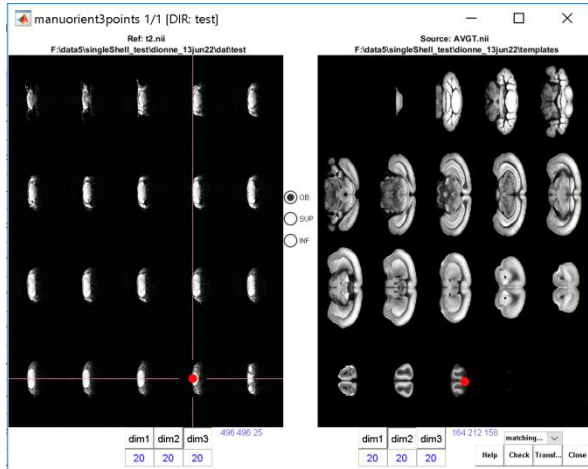


- use [dim1/2/3]-buttons of reference and source-image to obtain the coronal view of **both** images

Set pairwise points

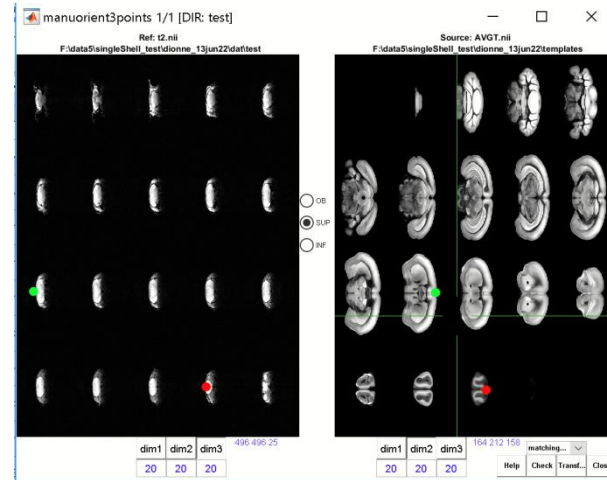
1) select the **radio-[OB]**

-click to mark the upper/anterior olfact location or a frontal brain location in both images (close to the brain-boundary) (**red dot**)



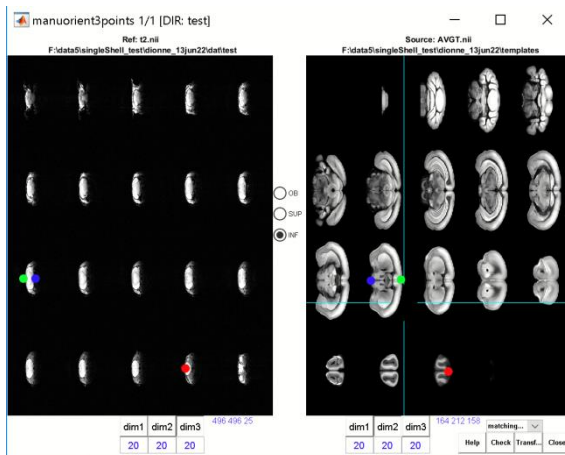
2) select the **radio-[SUP]**

- click to mark the upper/superior brain location in one of the midbrain slices (close to the brain-boundary) in both images (**green dot**)



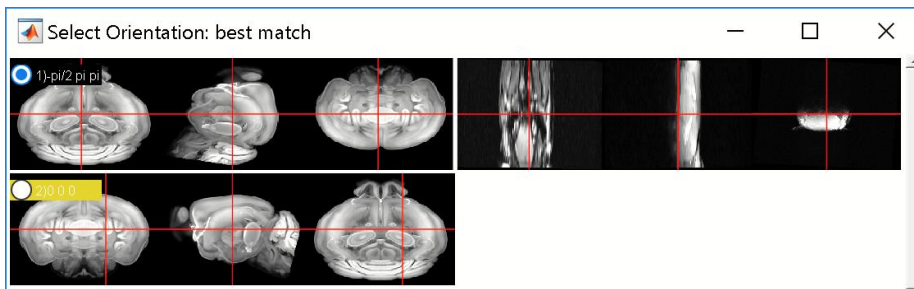
3) select the **radio-[INF]**

- click to mark the inferior brain location in the same slice as used for SUP, (close to the brain-boundary) in both images (**blue dot**)



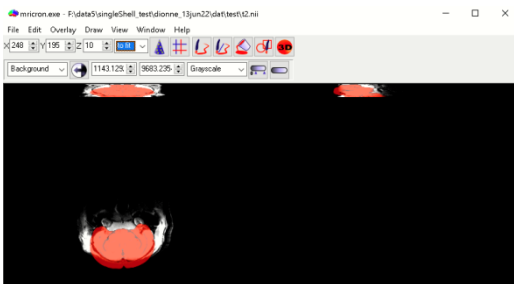
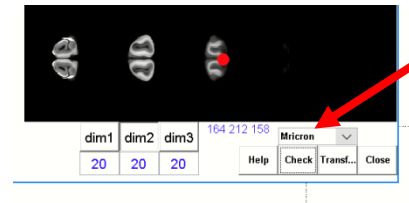
Now we have defined 3 pairwise points and the idea is to estimate the rotations to bring the locations A & A', B & B' and C and C' of the reference and source image as close as possible

Hit [[check](#)]-button



The first panel will show the rough match (left: template; right: t2.nii) when considering the rotations defined by the three pairwise locations

- The lower panel shows the unrotated reference image
- If the visualization is suboptimal to inspect (low resolution) select „**MRicron**“-from dropdown list and hit the [[check](#)]-button again.




MRicron: overlay of the two images when considering the three rotations

- note that we are only interested in a **rough** orientation, thus approximate rotations are sufficient!
- when hitting the [[check](#)]-button, the rotations are displayed in the CMD-window:

```
>>
>>
ROTATIONS:  -1.5708  -1.2246e-16  -1.2246e-16
TRANSLATIONS: -1.2633  -5.4028  1.3811
fx >>
<
Busy
```

Note that the 2nd & 3rd rotations are close to zero

Hit [[Close](#)]-button to close UI

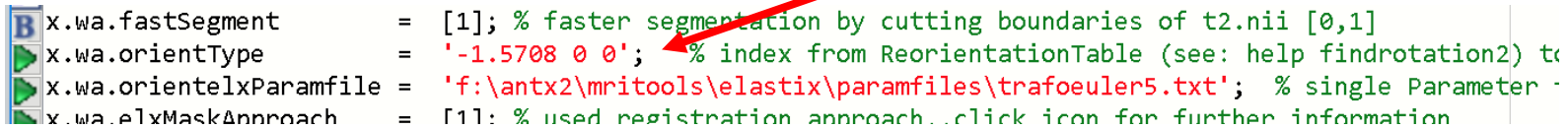
- copy the rotation paramters from the CMD-window to clipboard
- open the parameter settings via [[settings](#)]-button → gear-icon 

For „[x.wa.orientType](#)“ we now insert the rotation as **string**.

Note that the 2nd & 3rd rotation angles are close to zero ...thus we use zeros there:

`x.wa.orientType = '-1.5708 0 0'; % index ...`

Define here as string!



```

x.wa.fastSegment      = [1]; % faster segmentation by cutting boundaries of t2.nii [0,1]
x.wa.orientType       = '-1.5708 0 0'; % index from ReorientationTable (see: help findrotation2) to
x.wa.orientelxParamfile = 'f:\antx2\mrtools\elastix\paramfiles\trafoeuler5.txt'; % single Parameter -
x.wa.elxMaskApproach  = [1]; % used registration approach..click icon for further information
  
```

- Hit [[OK](#)] and overwrite this setting (proj-file)

Now the orientation is defined for this animal.

Hopefully all animals of the same study are roughly oriented in same the way...

In this case the definition of the orientType has to be done only once per study!

Now, we can register the „t2.nii“-image of this animal or all other animals to standard-space!