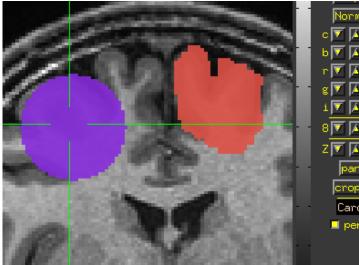


Didactics and Demonstrations

Regions of Interest (ROIs) Tools - Doing things with ROIs

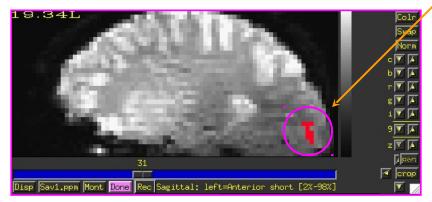


<u>3dmaskave</u>

This ROI program computes the average of voxels (usually from a functional or timeseries dataset), that are selected from an ROI mask

Class Example:

```
3dmaskave -mask anat_roi_resam+orig -q \
    rall_vr+orig > epi_avg.1D
```



The above command takes the voxels that fall within the ROI mask, and computes a mean for every time point/volume.

In this example, there are 450 time-points in this dataset, so the output will be a column of 450 means.

<u>-q</u>: Suppresses the voxel-count output (e.g., "[9 voxels] make up the ROI mask") from appearing next to each mean.

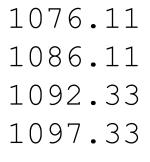
Alternatively, instead of having the results of 3dmaskave spewed into the shell, you can redirect (>) the results into a text file (epi_avg.1D) and save them for later use.

-2-

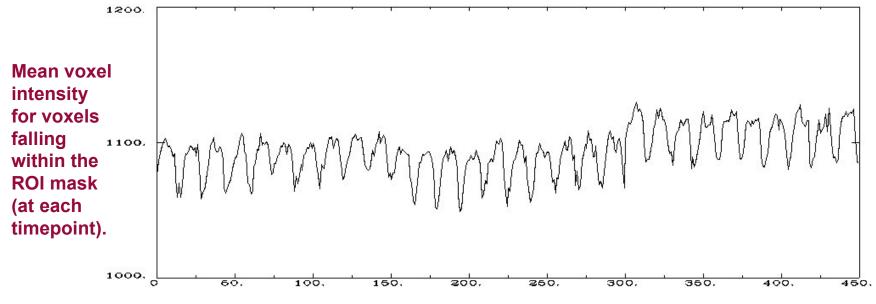
Output will look like this (450 means in the column):

```
less epi_avg.1D
Data can also be plotted out using 1dplot:
```

```
1dplot epi_avg.1D Or...
1dplot -yaxis 1000:1200:2:1 epi_avg.1D
```



... 1084.76



3 concatenated EPI runs, Timepoints (0-449)

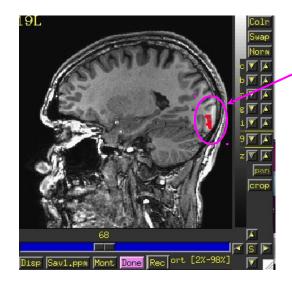
-3-

Program that dumps out all voxel values in a dataset inside the mask ROI

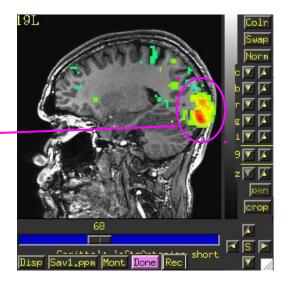
Class example:

```
3dmaskdump -noijk -mask anat_roi_resam+orig \
    'func_slim+orig[2]' > Vrel-tstats.txt
```

The output appears in the shell (unless you redirect it '>' into a text file). This example shows one column of numbers, representing the voxel values for functional sub-brick #2 ('Visual-reliable' t-values) that fall within the ROI mask:



Dump out the voxel values from the functional dataset, subbrick #2, but only for those voxels that fall within the ROI mask.



3dUndump can do the opposite – take a text file (ijk/xyz and values) to make a dataset

3dROIstats

Program to compute separate statistics for each ROI in a dataset

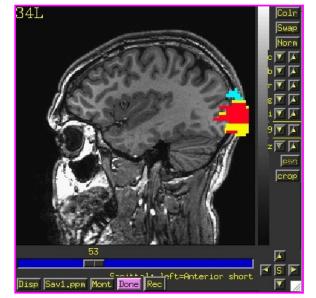
Means, medians, std. devs., ... can be computed separately for *multiple* ROIs in the same dataset

Example:

3dROIstats -mask 3rois+orig func_slim+orig'[0]'

Output shown in the shell (use > command to save into to a text file):

File	Sub-brick	Mean1	Mean_1	Mean_2
<pre>func_slim+orig[0]</pre>	0[Full_Fsta]	10.805717	69.336539	71.333655

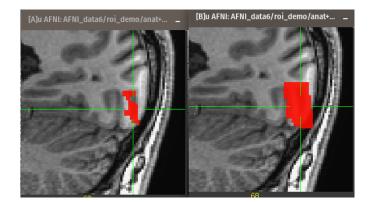


3rois+orig

-5-

More tools for ROIs

3dmask_tool -prefix mask_dil3 -dilate_result 3 \
 -inputs anat_roi+orig



3dAutomask -prefix anat_am anat+orig



- whereami can provide the user with more detailed information regarding the output of 3dClusterize
 - * For instance, say you want more information regarding the center of mass voxels from each cluster (from the 3dclust output). I.e., where do they fall approximately within the atlases?

3dClusterize -clust_nvox 200 -bisided -8.0 8.0 -ithr 2 -idat 1 - NN 1 -inset func_slim+origquiet > visual_clusters.1D						
<pre>whereami -coord_file clusts.1D'[1,2,3] ++ Input coordinates orientation set by default rules to RAI +++++++ nearby Atlas structures +++++++ Original input data coordinates in TLRC space Focus point (LPI) Coord.Space -3 mm [L], -83 mm [P], 2 mm [S] {TLRC} -3 mm [L], -86 mm [P], -3 mm [I] {MNI} -3 mm [L], -90 mm [P], 2 mm [S] {MNI_ANAT}</pre>	' -tab less Center of mass output, columns 1,2,3, from 3dClusterize, Clusterize plugin or 3dclust reports. <u>Shown</u> : Cluster #1's coordinates according to various atlases					
AtlasWithinLabelTT_Daemon0.0LeftLingual GyrusTT_Daemon0.0LeftBrodmann area 18TT_Daemon1.0LeftBrodmann area 17TT_Daemon4.0LeftCuneusTT_Daemon4.0RightLingual GyrusTT_Daemon4.0RightBrodmann area 18TT_Daemon4.0RightBrodmann area 18TT_Daemon5.0RightBrodmann area 17TT_Daemon7.0RightCuneusCA_ML_18_MNIA0.0LeftCalcarineCA_ML_18_MNIA3.0LeftLingual GyrusCA_MPM_18_MNIA0.0Area 17CA_MPM_18_MNIA1.0Area 18	Prob.CodeMPM232MPM295MPM294MPM240MPM32MPM95MPM94MPM40434748181240					

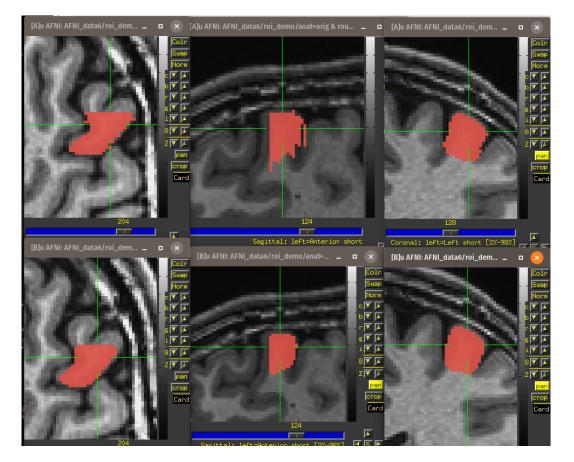
whereami can report on the overlap of ROIs with atlas-defined regions

whereami -omask anat roi+tlrc

```
++ Input coordinates orientation set by default rules to RAI
++ Input coordinates space set by default rules to TLRC
++ In ordered mode ....
++ Have 2 unique values of:
   0 1
++ Skipping unique value of 0
++ Processing unique value of 1
     195 voxels in ROI
++
++
     195 voxels in atlas-resampled mask
Intersection of ROI (valued 1) with atlas TT_Daemon (sb0):
   89.2 % overlap with Middle Occipital Gyrus, code 33
  6.7 % overlap with Middle Temporal Gyrus, code 35
  95.9 % of cluster accounted for.
Intersection of ROI (valued 1) with atlas TT_Daemon (sb1):
  19.5 % overlap with Brodmann area 37, code 113
  1.5 % overlap with Brodmann area 19, code 96
  21.0 % of cluster accounted for.
      195 voxels in atlas-resampled mask
++
Intersection of ROI (valued 1) with atlas CA_N27_MPM (sb0):
  1.5 % overlap with hOC5 (V5 / MT+), code 110
  1.5 % of cluster accounted for.
      195 voxels in atlas-resampled mask
++
Intersection of ROI (valued 1) with atlas CA_N27_ML (sb0):
   61.0 % overlap with Right Middle Occipital Gyrus, code 52
   20.0 % overlap with Right Middle Temporal Gyrus, code 86
   81.0 % of cluster accounted for.
```

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ROI irregularities - Modal smoothing

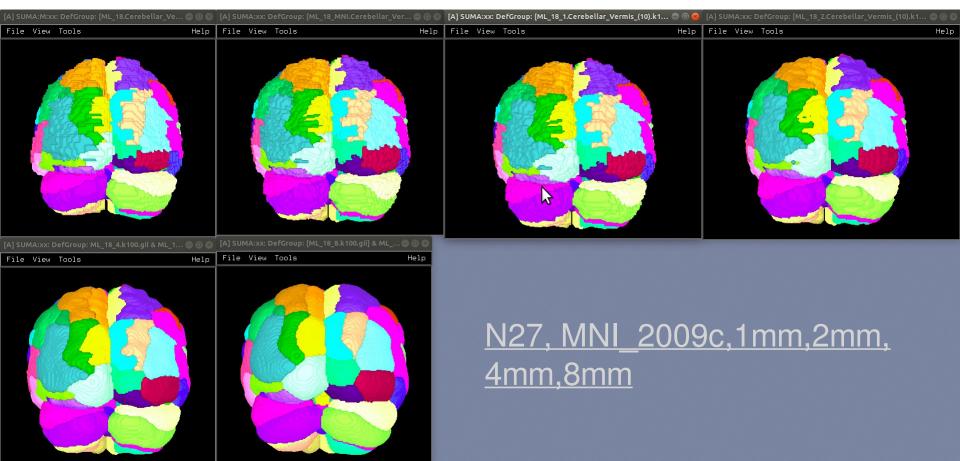


Original drawing

Smoothed

3dLocalstat -stat mode -prefix coronal_mode3 \
 -nbhd 'SPHERE(3)' roughcoronalROI+orig.
3drefit -cmap INT_CMAP coronal_mode3+orig.

MacroLabel atlas - modal smoothing example



Eickhoff-Zilles MPM 2.2 atlas - modal smoothing example

[A] SUMA:xx: DefGroup: [ML_18.Amyg_(CM) 🖨 🗊 📀	[A] SUMA:xR: DefGroup: ML_22.Amygdala 🖨 🗊 🔊 🗍	[A] SUMA:xx: DefGroup: ML_22_mode1.k 🖱 🗈 😣	[A] SUMA:xx: DefGroup: ML_22_mode2.k10 🖨 🗉 📀
File View Tools Help	File View Tools Help	File View Tools Help	File View Tools Help
[A] SUMA:xx: DefGroup: [ML_22_mode4.k102 🖨 🗉 🚳	[A] SUMA:xx: DefGroup: [ML_22_mode8.k10 🖨 🗊 🔕		
File View Tools Help	File View Tools Help		
		<u>1.8 version, 2.2 version,</u> <u>1mm,2mm,4mm,8mm</u>	

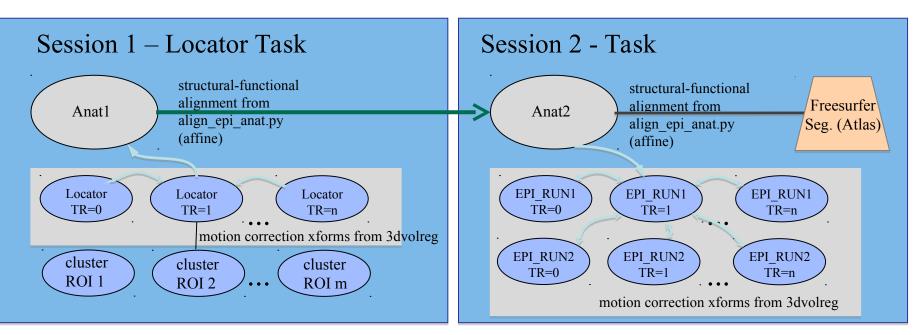
Circularity – "double dipping"

Using results from one set of data to limit the data in that same set.

- FMRI example:
- •Find largest differences with some threshold between groups A and B
- •Create ROIs from those differences
- •Show differences between ROIs for the same two groups showing that indeed A is very different from B with a p-value of 0.05. They're different because they're different.

•Solution : Use ROIs from independent data: Atlas regions, locator tasks, other subjects

-13ROIs from Locator session day 1 applied to session day 2 EPI

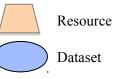


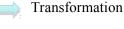
align_epi_anat a2 to e2 => a2e2.aff12.1D align_epi_anat a1 to a2 => a1a2.aff12.1D align_epi_anat L1 to a1 => L1a1.aff12.1D

cat_matvec a2e2.aff12.1D a1a2.aff12.1D L1a1.aff12.1D > L1e2.aff12.1D e2 -> a2 \Rightarrow a2 -> a1 \Rightarrow a1 -> L1 e2 -> L1

3dAllineate -1Dmatrix_apply L1e2.aff12.1D -final NN -prefix ROI1_e2 \ -base epi_run1+orig'[1]' -input ROI1+orig

Known or User-defined transformations





Same space / Identity xform

That's All for Now



That's All for Now

