# CS463/516F01 202305 VOLUMETRIC IMAGE ANALYSIS AND VISUALIZATION

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# Code: Dataset 1

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~	Name	^	Date Modified	Size	Kind
	ref.nii.gz		Yesterday at 10:19 AM	3.4 MB	gzip co…archiv€
	> <b>=</b> sub1		Today at 9:19 PM		Folder
	> == sub2		Today at 9:22 PM		Folder
	> <b>=</b> sub3		Today at 9:23 PM		Folder
	> <b>=</b> sub4		Today at 9:24 PM		Folder
	> <u>sub5</u>		Today at 9:24 PM		Folder
	> <b>=</b> sub6		Today at 9:25 PM		Folder
	> <b>=</b> sub7		Today at 9:26 PM		Folder
	> <b>=</b> sub8		Today at 9:27 PM		Folder
	> <b>=</b> sub9		Today at 9:28 PM		Folder
	> == sub10		Today at 9:20 PM		Folder
	> == sub11		Today at 9:20 PM		Folder
sity	> == sub12		Today at 9:22 PM		Folder

subs=\$(ls -d sub\*)

This command is used to create a list of directory names that start with "sub" in the current directory and store them in the variable subs.

```
echo $subs
```

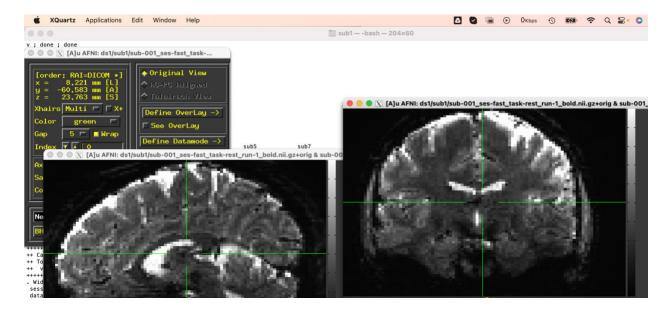
```
for sub in $subs ; do cd /Volumes/md/ds/ds1/${sub} ; echo
$sub ; ls ; done

for sub in $subs ; do cd /Volumes/md/ds/ds1/${sub} ;
gzs=$(ls *gz) ; for gz in $gzs ; do echo $gzs ; done ; done
```

The script loops through each value in the \$subs variable, changes the current working directory to a specific location based on the value, prints the value, lists the directory's contents, and then moves on to the next iteration. The purpose of this script might be to perform operations on each subdirectory specified in the \$subs variable, such as listing its contents. The purpose of this script is to list files with the "gz" extension in subdirectories specified by \$subs.

#### Motion Correction:

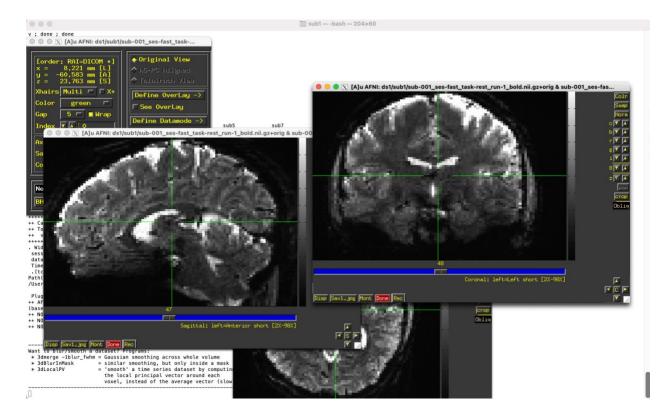
for sub in \$subs ; do cd /Volumes/md/ds/ds1/\${sub} ;
gzs=\$(ls \*gz) ; for gz in \$gzs ; do 3dvolreg -prefix \$gz overwrite \$gz ; done ; done



this script snippet iterates through each value in the \$subs variable, changes the working directory based on that value, lists all files ending with "gz" in the directory, and for each of those files, it performs a volume registration operation using the 3dvolreg command from AFNI. The volume registration result is saved with the same filename, but with the specified prefix. The purpose of this script is to perform volume registration on files with the "gz" extension in subdirectories specified by \$subs.

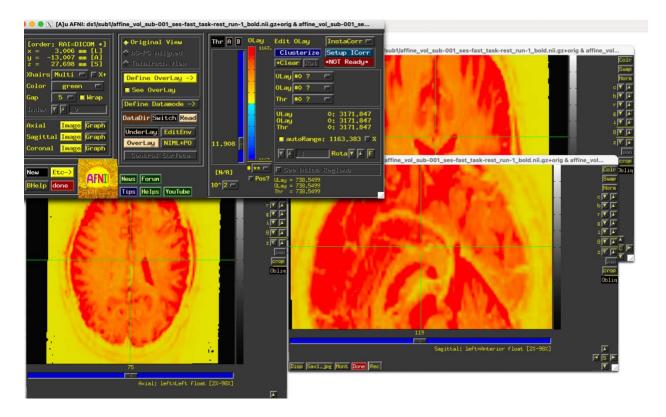
#### Extract:

```
for sub in $subs ; do cd /Volumes/md/ds/ds1/${sub} ;
gzs=$(ls *gz) ; for gz in $gzs ; do 3dTcat -prefix vol_${gz}
${gz}[0] ; done ; done
```



this script snippet iterates through each value in the \$subs variable, changes the working directory based on that value, lists all files ending with "gz" in the directory, and for each of those files, it takes the first volume (timepoint) from the 4D dataset represented by that file using the 3dTcat command. The result is saved with a filename prefix "vol\_" followed by the original filename. The purpose of this script might be to extract the first volume from 4D datasets (time series data) with the "gz" extension in subdirectories specified by \$subs.

# AntsRegistration:



Through each value in the \$subs variable, changes the working directory based on that value, lists files starting with "vol" in the directory, and for each of those files, it performs an image registration using the ANTs antsRegistration command. The registration process aims to align the current volume with a reference volume using an affine transformation. The output transformation and affine matrix filenames are generated based on the current volume's filename. The purpose of this script might is to perform volume registration and alignment on volumes in subdirectories specified by \$subs using the ANTs software.

#### BANDPASS FILTERING:

```
for file in $all ; do cd /Volumes/md/ds/ds1/${file} ;
gzs=$(ls *gz) ; for gz in $gzs ; do 3dTproject -input $gz
-prefix bp ${gz} -passband 0.01 0.1 ; done ; done
```

In the \$all variable, changes the working directory based on that value, lists all files ending with "gz" in the directory, and for each of those files, it performs temporal filtering using the 3dTproject command. The filtered result is saved with a filename prefix "bp" followed by the original filename. The purpose of this script might be to

apply bandpass filtering to 4D datasets (time series data) with the "gz" extension in subdirectories specified by \$all using the AFNI software.

#### REHO:

```
for file in $all ; do cd /Volumes/md/ds/ds1/${file} ;
bps=$(ls bp*gz) ; for bp in $bps ; do 3dReho -prefix
reho ${bp} -inset $bp ; done ; done
```

This script snippet iterates through each value in the \$all variable, changes the working directory based on that value, lists files starting with "bp" and ending with "gz" in the directory, and for each of those files, it performs the calculation of regional homogeneity (ReHo) using the 3dReho command from AFNI. The ReHo results are saved with a filename prefix "reho\_" followed by the original filename. The purpose of this script is to calculate and analyze the ReHo of bandpass-filtered volumes in subdirectories specified by \$all using the AFNI software.

```
for file in $all ; do cd /Volumes/md/ds/ds1/$file ;
rehos=$(ls reho*gz) ; for reho in $rehos ; do
matname=${reho/reho_bp_/to_vol_} ;
matname=${matname/.nii.gz/0GenericAffine.mat};
antsApplyTransforms -d 3 -e 0 -i $reho -r ../ref.nii.gz -o
inref_${reho} -t $matname ; done ; done
```

This script snippet iterates through each value in the \$all variable, changes the working directory based on that value, lists files starting with "reho" and ending with "gz" in the directory, and for each of those files, it applies an affine transformation using the antsApplyTransforms command from ANTs. The transformation matrix used for registration is determined by the filename manipulations in the script. The transformed results are saved with the "inref\_" prefix added to the original ReHo filename. The purpose of this script might be to apply a previously calculated affine transformation to ReHo volumes and generate transformed images in reference to a common image.

#### Stack

```
3dTcat -prefix all_fast.nii.gz sub1/inref_reho_bp_sub-001_ses-fast_task-rest_run-1_bold.nii.gz sub2/inref_reho_bp_sub-002_ses-fast_task-rest_run-1_bold.nii.gz sub3/inref_reho_bp_sub-005_ses-fast_task-rest_run-1_bold.nii.gz
```

In summary, the 3dTcat command is concatenating three input 3D volumes from different subjects and sessions into a single 4D dataset. The resulting dataset will have the filename "all\_fast.nii.gz".

## 3Dttest:

'ispositive(a+2)'

neg fast vs std threshmap.nii.gz

```
3dttest++
           -setA all fast.nii.gz[0] all fast.nii.gz[1]
all fast.nii.gz[2]
                          -setB
                                       all std.nii.gz[0]
all std.nii.gz[1] all std.nii.gz[2] -overwrite -paired -
prefix ttest reho fast vs std.nii.gz
3dcalc
                ttest reho fast vs std.nii.gz[1]
          -a
                                                    -expr
'isnegetive(a+2)'
                                                  -prefix
neg fast vs std threshmap.nii.gz
              ttest reho fast vs std.nii.gz[1]
                                                    -expr
3dcalc
```

-prefix

In summary, these commands are used to perform t-tests on two groups of 4D datasets, generate thresholded maps based on the t-test results, and create binary masks where voxels are classified as either negative or positive based on certain mathematical criteria. The purpose is likely to analyze the statistical differences between "fast" and "std" groups and create thresholded maps to visualize these differences. The negative thresholded map might indicate regions where the "fast" group has lower values than the "std" group, while the positive thresholded map might indicate regions with higher values in the "fast" group compared to the "std" group.

```
Dataset 2:
subs=$(ls -d sub*)
echo $subs

for sub in $subs ; do cd /Volumes/md/ds/ds2/${sub} ; echo
$sub ; ls ; done

for sub in $subs ; do cd /Volumes/md/ds/ds2/${sub} ;
niis=$(ls *nii) ; for nii in $niis ; do echo $niis ; done
; done
```

The script loops through each value in the \$subs variable, change the current working directory to a specific location based on the value, prints the value, lists the contents of that directory, and then moves on to the next iteration. The purpose of this script might be to perform operations on each subdirectory specified in the \$subs variable, such as listing its contents. The purpose of this script might be to list files with the "gz" extension in subdirectories specified by \$subs.

#### Motion Correction:

```
for sub in $subs ; do cd /Volumes/md/ds/ds2/${sub} ;
niis=$(ls *nii) ; for nii in $niis ; do 3dvolreg -prefix
$nii -overwrite $nii ; done ; done
```

this script snippet iterates through each value in the \$subs variable, changes the working directory based on that value, lists all files ending with "gz" in the directory, and for each of those files, it performs a volume registration operation using the 3dvolreg command from AFNI. The volume registration result is saved with the same filename, but with the specified prefix. The purpose of this script is to perform volume registration on files with the "gz" extension in subdirectories specified by \$subs.

#### Extract

```
for sub in $subs ; do cd /Volumes/md/ds/ds1/${sub} ;
gzs=$(ls *gz) ; for gz in $gzs ; do 3dTcat -prefix vol_${gz}
${gz}[0] ; done ; done
```

this script snippet iterates through each value in the \$subs variable, changes the working directory based on that value, lists all files ending with "gz" in the directory, and for each of those files, it takes the first volume (timepoint) from the 4D dataset represented by that file using the 3dTcat command. The result is saved with a filename prefix "vol\_" followed by the original filename. The purpose of this script might be to extract the first volume from 4D datasets (time series data) with the "gz" extension in subdirectories specified by \$subs.

# AntsRegistration:

Through each value in the \$subs variable, changes the working directory based on that value, lists files starting with "vol" in the directory, and for each of those files, it performs an image registration using the ANTs antsRegistration command. The registration process aims to align the current volume with a reference volume using an affine transformation. The output transformation and affine matrix filenames are generated based on the current volume's filename. The purpose of this script might is to perform volume registration and alignment on volumes in subdirectories specified by \$subs using the ANTs software

## BANDPASS FILTERING:

```
for file in $all ; do cd /Volumes/md/ds/ds2/${sub} ;
niis=$(ls *nii) ; for nii in $niis ; do 3dTproject -input
$nii -prefix bp ${nii} -passband 0.01 0.1 ; done ; done
```

In the \$all variable, changes the working directory based on that value, lists all files ending with "gz" in the directory, and performs temporal filtering using the 3dTproject

command for each of those files. The filtered result is saved with a filename prefix "bp\_" followed by the original filename. The purpose of this script might be to apply bandpass filtering to 4D datasets (time series data) with the "gz" extension in subdirectories specified by \$all using the AFNI software.

### REHO:

```
for file in $all ; do cd /Volumes/md/ds/ds2/${file} ;
bps=$(ls bp*nii) ; for bp in $bps ; do 3dReho -prefix
reho ${bp} -inset $bp ; done ; done
```

This script snippet iterates through each value in the \$all variable, changes the working directory based on that value, lists files starting with "bp" and ending with "gz" in the directory, and for each of those files, it performs the calculation of regional homogeneity (ReHo) using the 3dReho command from AFNI. The ReHo results are saved with a filename prefix "reho\_" followed by the original filename. The purpose of this script is to calculate and analyze the ReHo of bandpass-filtered volumes in subdirectories specified by \$all using the AFNI software.

This script snippet iterates through each value in the \$all variable, changes the working directory based on that value, lists files starting with "reho" and ending with "gz" in the directory, and for each of those files, it applies an affine transformation using the antsApplyTransforms command from ANTs. The transformation matrix used for registration is determined by the filename manipulations in the script. The transformed results are saved with the "inref\_" prefix added to the original ReHo filename. The purpose of this script might be to apply a previously calculated affine transformation to ReHo volumes and generate transformed images in reference to a common image.

#### STACK:

```
3dTcat -prefix all_fast.nii sub1/inref_reho_bp_sub-001_ses-fast_task-rest_run-1_bold.nii
```

```
sub2/inref_reho_bp_sub-002_ses-fast_task-rest_run-
1_bold.nii sub3/inref_reho_bp_sub-005_ses-fast_task-
rest_run-1_bold.nii
```

In summary, the 3dTcat command is concatenating three input 3D volumes from different subjects and sessions into a single 4D dataset. The resulting dataset will have the filename "all\_fast.nii.gz".

## T-VALUE MAPS:

```
3dttest++ -setA all_fast.nii[0] all_fast.nii[1]
all_fast.nii[2] -setB all_std.nii[0] all_std.nii[1]
all_std.nii[2] -overwrite -paired -prefix
ttest_reho_fast_vs_std.nii

3dcalc -a ttest_reho_fast_vs_std.nii[1] -expr
'isnegetive(a+2)' -prefix neg_fast__vs_std_threshmap.nii
3dcalc -a ttest_reho_fast_vs_std.nii[1] -expr
'ispositive(a+2)' -prefix neg_fast_ vs_std_threshmap.nii
```

In summary, these commands are used to perform t-tests on two groups of 4D datasets, generate thresholded maps based on the t-test results, and create binary masks where voxels are classified as either negative or positive based on certain mathematical criteria. The purpose is likely to analyze the statistical differences between "fast" and "std" groups and create thresholded maps to visualize these differences. The negative thresholded map might indicate regions where the "fast" group has lower values than the "std" group, while the positive thresholded map might indicate regions with higher values in the "fast" group compared to the "std" group.