2018-12-10 10:51:50

BAsed on my latest thoughts from robust_descriptives.md last Friday, let's include ADHD_NOS in our analysis, and re-run some of the results.

```
job_name=NOSstruct;
mydir=/data/NCR_SBRB/baseline_prediction/;
swarm_file=swarm.desc_${job_name};
rm -rf $swarm_file;
for f in `/bin/ls struct_*_11142018_260timeDiff12mo.RData.gz`; do
    for nn in nonew_ ''; do
        for pp in None subjScale; do
            for target in OLS_inatt_slope OLS_HI_slope; do
                echo "Rscript --vanilla
~/research_code/baseline_prediction/descriptives/structural.R
${mydir}/${f} ${mydir}/long_clin_11302018.csv ADHDNOS_${nn}${target} 42
winsorize_$pp" >> $swarm_file;
                for i in {1..250}; do
                    echo "Rscript --vanilla
~/research_code/baseline_prediction/descriptives/structural.R
${mydir}/${f} ${mydir}/long_clin_11302018.csv ADHDNOS_${nn}${target}
-${RANDOM} winsorize_$pp" >> $swarm_file;
                done;
            done;
        done;
    done;
done
split -l 3000 $swarm_file ${job_name}_split;
for f in `/bin/ls ${job_name}_split??`; do
    echo "ERROR" > swarm_wait_${USER}
    while grep -q ERROR swarm_wait_${USER}; do
        echo "Trying $f"
        swarm -f $f -g 4 -t 2 --time 30:00 --partition norm --logdir
trash_desc_${job_name} --job-name ${job_name} -m R,afni --gres=lscratch:2
2> swarm_wait_${USER};
        if grep -q ERROR swarm_wait_${USER}; then
            echo -e "\tError, sleeping..."
            sleep 10m;
        fi;
    done;
done
```

And let's see if this brings up some more DTI results as well:

```
job_name=NOSdti;
mydir=/data/NCR_SBRB/baseline_prediction/;
swarm_file=swarm.desc_${job_name};
rm -rf $swarm_file;
```

```
for f in `/bin/ls dti_??_voxelwise_n2??_09212018.RData.gz`; do
    for nn in nonew_ ''; do
        for pp in None subjScale; do
            for target in OLS_inatt_slope OLS_HI_slope; do
                echo "Rscript --vanilla
~/research_code/baseline_prediction/descriptives/dti.R ${mydir}/${f}
${mydir}/long_clin_11302018.csv ADHDNOS_${nn}${target} 42 winsorize_$pp"
>> $swarm_file;
                for i in {1..250}; do
                    echo "Rscript --vanilla
~/research_code/baseline_prediction/descriptives/dti.R ${mydir}/${f}
${mydir}/long_clin_11302018.csv ADHDNOS_${nn}${target} -${RANDOM}
winsorize_$pp" >> $swarm_file;
                done;
            done;
        done;
    done;
done
split -l 3000 $swarm_file ${job_name}_split;
for f in `/bin/ls ${job_name}_split??`; do
    echo "ERROR" > swarm_wait_${USER}
    while grep -q ERROR swarm_wait_${USER}; do
        echo "Trying $f"
        swarm -f $f -g 4 -t 2 --time 30:00 --partition norm --logdir
trash_desc_${job_name} --job-name ${job_name} -m R,afni --gres=lscratch:2
2> swarm_wait_${USER};
        if grep -q ERROR swarm_wait_${USER}; then
            echo -e "\tError, sleeping..."
            sleep 10m;
        fi;
    done;
done
```

And because we had so many results in fMRI, we should definitely play there too:

```
job_name=NOSmelodic;
mydir=/data/NCR_SBRB/baseline_prediction/;
swarm_file=swarm.desc_${job_name};
rm -rf $swarm_file;
for f in `/bin/ls melodic_fancy_IC*12142018.RData.gz
melodic_inter_IC*12142018.RData.gz`; do
    for nn in nonew_ ''; do
        for pp in None subjScale; do
            for target in OLS_inatt_slope OLS_HI_slope; do
                echo "Rscript --vanilla
~/research_code/baseline_prediction/descriptives/melodic.R ${mydir}/${f}
${mydir}/long_clin_11302018.csv ADHDNOS_${nn}${target} 42 winsorize_$pp"
>> $swarm_file;
                for i in {1..250}; do
                    echo "Rscript --vanilla
~/research_code/baseline_prediction/descriptives/melodic.R ${mydir}/${f}
${mydir}/long_clin_11302018.csv ADHDNOS_${nn}${target} -${RANDOM}
```

```
winsorize_$pp" >> $swarm_file;
                done;
            done;
        done;
    done;
done
split -l 3000 ${swarm_file} ${job_name}_split;
for f in `/bin/ls ${job_name}_split??`; do
    echo "ERROR" > swarm_wait_${USER}
    while grep -q ERROR swarm_wait_${USER}; do
        echo "Trying $f"
        swarm -f $f -g 8 -t 2 --time 5:00:00 --partition norm --logdir
trash_desc_${job_name} --job-name ${job_name} -m R,afni 2>
swarm_wait_${USER};
        if grep -q ERROR swarm_wait_${USER}; then
            echo -e "\tError, sleeping..."
            sleep 10m;
        fi;
    done;
done
```

Compiling results

structural

```
myfile=struct_NOSdescriptives.txt
rm $myfile; touch $myfile;
for f in `/bin/ls
/data/NCR_SBRB/tmp/struct_*_11142018_260timeDiff12mo/ADHDNOS*_42_?
h_ClstTable_e1_a1.0.1D`; do
    if ! grep -q 'rnd' $f; then
        echo $f >> $myfile;
        grep -v \# $f | head -n 5 >> $myfile;
    fi
done
```

```
/bin/ls -1
/data/NCR_SBRB/tmp/struct_*_11142018_260timeDiff12mo/ADHDNOS*_42_?
h_ClstTable_e1_a1.0.1D | grep -v rnd > result_files.txt;
sed -i -e 's/_42_lh_ClstTable_e1_a1.0.1D//g' result_files.txt;
sed -i -e 's/_42_rh_ClstTable_e1_a1.0.1D//g' result_files.txt;
for root_file in `cat result_files.txt`; do
    collect_name_lh=${root_file}_lh_top_rnd_clusters.txt;
    collect_name_rh=${root_file}_rh_top_rnd_clusters.txt;
    echo $collect_name_lh;
    echo $collect_name_rh;
    if [ -e $collect_name_lh ]; then
        rm $collect_name_lh $collect_name_rh;
    fi;
```

```
    for f in `ls ${root_file}_rnd*lh_ClstTable_e1_a1.0.1D`; do
        grep -v \# $f | head -n 1 >> $collect_name_lh;
    done
    for f in `ls ${root_file}_rnd*rh_ClstTable_e1_a1.0.1D`; do
        grep -v \# $f | head -n 1 >> $collect_name_rh;
    done
done
tar -zcvf struct_ADHDNOS_top_rnd_clusters.tar.gz
struct_*_11142018_260timeDiff12mo/ADHDNOS*top_rnd_clusters.txt
```

```
res_fname = '~/tmp/struct_NOSdescriptives.txt'
out_file = '~/tmp/pvals_NOSstruct.txt'
res_lines = readLines(res_fname)
for (line in res_lines) {
  # starting new file summary
  if (grepl(pattern='data', line)) {
    root_fname = strsplit(line, '/')[[1]]
    dir_name = root_fname[length(root_fname)-1]
    root_fname = strsplit(root_fname[length(root_fname)], '_')[[1]]
    root_fname = paste0(root_fname[1:(length(root_fname)-5)], sep='',
collapse='_')
    if (grepl(pattern='lh', line)) {
      rnd_fname = sprintf('~/tmp/%s/%s_lh_top_rnd_clusters.txt', dir_name,
root_fname)
    } else {
      rnd_fname = sprintf('~/tmp/%s/%s_rh_top_rnd_clusters.txt', dir_name,
root_fname)
    }
    if (file.exists(rnd_fname)) {
        rnd_results = read.table(rnd_fname)[, 3]
        nperms = length(rnd_results)
    } else {
        rnd_results = NA
        nperms = NA
    }
    if (grepl(pattern='lh', line)) {
      cat(sprintf('%s (LH): %s (%d perms)\n', dir_name, root_fname,
nperms),
          file=out_file, append=T)
    } else {
      cat(sprintf('%s (RH): %s (%d perms)\n', dir_name, root_fname,
nperms),
          file=out_file, append=T)
    }
  }
  else {
    parsed = strsplit(line, ' +')
    clus_size = as.numeric(parsed[[1]][4])
    pval = sum(rnd_results >= clus_size) / nperms
    cat(sprintf('Cluster size: %.2f, p<%.3f', clus_size, pval),
        file=out_file, append=T)
```

```
    if ( !is.na(pval) && pval < .05) {
      cat(' *', file=out_file, append=T)
    }
    if ( !is.na(pval) && pval < .01) {
      cat('*', file=out_file, append=T)
    }
    cat('\n', file=out_file, append=T)
  }
}
```

```
sudregp@HG-02070684-DM2:~/tmp$ grep -B 1 "*" pvals_NOSstruct.txt
struct_area_11142018_260timeDiff12mo (RH):
ADHDNOS_nonew_OLS_HI_slope_winsorize_None (249 perms)
Cluster size: 1015.21, p<0.008 **
--
struct_area_11142018_260timeDiff12mo (RH):
ADHDNOS_nonew_OLS_HI_slope_winsorize_subjScale (249 perms)
Cluster size: 751.57, p<0.008 **
--
struct_area_11142018_260timeDiff12mo (LH):
ADHDNOS_OLS_inatt_slope_winsorize_None (248 perms)
Cluster size: 1098.04, p<0.016 *
Cluster size: 825.97, p<0.040 *
--
struct_thickness_11142018_260timeDiff12mo (LH):
ADHDNOS_OLS_inatt_slope_winsorize_None (249 perms)
Cluster size: 306.69, p<0.032 *
--
struct_thickness_11142018_260timeDiff12mo (LH):
ADHDNOS_OLS_inatt_slope_winsorize_subjScale (250 perms)
Cluster size: 372.06, p<0.020 *
--
struct_volume_11142018_260timeDiff12mo (RH):
ADHDNOS_nonew_OLS_HI_slope_winsorize_None (250 perms)
Cluster size: 885.11, p<0.000 **
--
struct_volume_11142018_260timeDiff12mo (LH):
ADHDNOS_nonew_OLS_inatt_slope_winsorize_None (250 perms)
Cluster size: 574.77, p<0.000 **
--
struct_volume_11142018_260timeDiff12mo (RH):
ADHDNOS_nonew_OLS_inatt_slope_winsorize_None (250 perms)
Cluster size: 489.02, p<0.016 *
--
struct_volume_11142018_260timeDiff12mo (LH):
ADHDNOS_nonew_OLS_inatt_slope_winsorize_subjScale (248 perms)
Cluster size: 387.28, p<0.012 *
--
struct_volume_11142018_260timeDiff12mo (RH):
ADHDNOS_nonew_OLS_inatt_slope_winsorize_subjScale (248 perms)
Cluster size: 246.19, p<0.044 *
```

```
--
struct_volume_11142018_260timeDiff12mo (RH):
ADHDNOS_OLS_HI_slope_winsorize_None (249 perms)
Cluster size: 604.57, p<0.008 **
--
struct_volume_11142018_260timeDiff12mo (RH):
ADHDNOS_OLS_HI_slope_winsorize_subjScale (240 perms)
Cluster size: 447.18, p<0.037 *
--
struct_volume_11142018_260timeDiff12mo (LH):
ADHDNOS_OLS_inatt_slope_winsorize_None (248 perms)
Cluster size: 911.02, p<0.000 **
--
struct_volume_11142018_260timeDiff12mo (RH):
ADHDNOS_OLS_inatt_slope_winsorize_None (248 perms)
Cluster size: 804.45, p<0.000 **
--
struct_volume_11142018_260timeDiff12mo (LH):
ADHDNOS_OLS_inatt_slope_winsorize_subjScale (248 perms)
Cluster size: 489.78, p<0.008 **
```

Like before, the none results were much better, but we need to be careful we're not being fooled by outliers. So, let's filter them a bit:

```
sudregp@HG-02070684-DM2:~/tmp$ grep -B 1 "*" pvals_NOSstruct.txt | grep
None
struct_area_11142018_260timeDiff12mo (RH):
ADHDNOS_nonew_OLS_HI_slope_winsorize_None (249 perms)
struct_area_11142018_260timeDiff12mo (LH):
ADHDNOS_OLS_inatt_slope_winsorize_None (248 perms)
struct_thickness_11142018_260timeDiff12mo (LH):
ADHDNOS_OLS_inatt_slope_winsorize_None (249 perms)
struct_volume_11142018_260timeDiff12mo (RH):
ADHDNOS_nonew_OLS_HI_slope_winsorize_None (250 perms)
struct_volume_11142018_260timeDiff12mo (LH):
ADHDNOS_nonew_OLS_inatt_slope_winsorize_None (250 perms)
struct_volume_11142018_260timeDiff12mo (RH):
ADHDNOS_nonew_OLS_inatt_slope_winsorize_None (250 perms)
struct_volume_11142018_260timeDiff12mo (RH):
ADHDNOS_OLS_HI_slope_winsorize_None (249 perms)
struct_volume_11142018_260timeDiff12mo (LH):
ADHDNOS_OLS_inatt_slope_winsorize_None (248 perms)
struct_volume_11142018_260timeDiff12mo (RH):
ADHDNOS_OLS_inatt_slope_winsorize_None (248 perms)
```

So it looks like nonew is not making much difference here. We should probably use the scatterplots and the other imaging modalities to see if we should go with nonew or the entire ADHD dataset.

2018-12-11 10:27:56

Let me run the other networks Philip requested in MELODIC while I compile the other results.

```
job_name=NOSmelodic;
mydir=/data/NCR_SBRB/baseline_prediction/;
swarm_file=swarm.desc_${job_name};
rm -rf $swarm_file;
for f in `/bin/ls melodic_*_IC*_12102018.RData.gz`; do
    for nn in nonew_ ''; do
        for pp in None subjScale; do
            for target in OLS_inatt_slope OLS_HI_slope; do
                echo "Rscript --vanilla
~/research_code/baseline_prediction/descriptives/dti.R ${mydir}/${f}
${mydir}/long_clin_11302018.csv ADHDNOS_${nn}${target} 42 winsorize_$pp"
>> $swarm_file;
                for i in {1..250}; do
                    echo "Rscript --vanilla
~/research_code/baseline_prediction/descriptives/dti.R ${mydir}/${f}
${mydir}/long_clin_11302018.csv ADHDNOS_${nn}${target} -${RANDOM}
winsorize_$pp" >> $swarm_file;
                done;
            done;
        done;
    done;
done
grep -v union $swarm_file > ${swarm_file}2;
split -l 3000 ${swarm_file}2 ${job_name}_split;
for f in `/bin/ls ${job_name}_split??`; do
    echo "ERROR" > swarm_wait_${USER}
    while grep -q ERROR swarm_wait_${USER}; do
        echo "Trying $f"
        swarm -f $f -g 8 -t 2 --time 5:00:00 --partition norm --logdir
trash_desc_${job_name} --job-name ${job_name} -m R,afni 2>
swarm_wait_${USER};
        if grep -q ERROR swarm_wait_${USER}; then
            echo -e "\tError, sleeping..."
            sleep 10m;
        fi;
    done;
done
```

Alright, now we're back to compiling results. struct is above, so let's look at DTI, and then we can take the first peek at MELODIC when the last ICs finish running so we don't have to repeat it.

##DTI

```
myfile=dti_NOSdescriptives.txt
rm $myfile; touch $myfile;
for f in `/bin/ls \
    /data/NCR_SBRB/tmp/dti_??_voxelwise_n2??
_09212018/ADHDNOS*_42_clusters.txt`; do
```

```
    echo $f >> $myfile;
    grep -v \# $f | head -n 5 >> $myfile;
done
```

```
/bin/ls -1 /data/NCR_SBRB/tmp/dti_??_voxelwise_n2??
_09212018/ADHDNOS*_42_clusters.txt > result_files.txt;
for root_file in `cat result_files.txt | sed -e 's/_42_clusters.txt//g'`;
do
    collect_name=${root_file}_top_rnd_clusters.txt;
    echo $collect_name;
    if [ -e $collect_name ]; then
        rm $collect_name;
    fi;
    for f in `ls ${root_file}*rnd*clusters.txt`; do
        grep -v \# $f | head -n 1 >> $collect_name;
    done
done
tar -zcvf dti_ADHDNOS_top_rnd_clusters.tar.gz dti_??_voxelwise_n2??
_09212018/ADHDNOS*top_rnd_clusters.txt
```

```
res_fname = '~/tmp/dti_NOSdescriptives.txt'
out_file = '~/tmp/pvals_NOSdti.txt'
res_lines = readLines(res_fname)
for (line in res_lines) {
  # starting new file summary
  if (grepl(pattern='clusters', line)) {
    root_fname = strsplit(line, '/')[[1]]
    dir_name = root_fname[length(root_fname)-1]
    root_fname = strsplit(root_fname[length(root_fname)], '_')[[1]]
    root_fname = paste0(root_fname[1:(length(root_fname)-2)], sep='',
collapse='_')
    rnd_fname = sprintf('~/tmp/%s/%s_top_rnd_clusters.txt', dir_name,
root_fname)
    if (file.exists(rnd_fname)) {
        rnd_results = read.table(rnd_fname)[, 1]
        nperms = length(rnd_results)
    } else {
        rnd_results = NA
        nperms = NA
    }
    cat(sprintf('%s: %s (%d perms)\n', dir_name, root_fname, nperms),
        file=out_file, append=T)
  }
  else {
    parsed = strsplit(line, ' +')
    clus_size = as.numeric(parsed[[1]][2])
    pval = sum(rnd_results >= clus_size) / nperms
    cat(sprintf('Cluster size: %d, p<%.3f', clus_size, pval),
        file=out_file, append=T)
```

```
    if (!is.na(pval) && pval < .05) {
      cat(' *', file=out_file, append=T)
    }
    if (!is.na(pval) && pval < .01) {
      cat('*', file=out_file, append=T)
    }
    cat('\n', file=out_file, append=T)
  }
}
```

```
hg-02127244-lw0:tmp sudregp$ grep -B 1 "*" pvals_NOSdti.txt
dti_ad_voxelwise_n272_09212018:
ADHDNOS_nonew_OLS_inatt_slope_winsorize_None (248 perms)
Cluster size: 41, p<0.012 *
Cluster size: 31, p<0.044 *
--
dti_ad_voxelwise_n272_09212018: ADHDNOS_OLS_inatt_slope_winsorize_None
(250 perms)
Cluster size: 38, p<0.036 *
--
dti_rd_voxelwise_n272_09212018: ADHDNOS_nonew_OLS_HI_slope_winsorize_None
(249 perms)
Cluster size: 92, p<0.004 **
--
dti_rd_voxelwise_n272_09212018: ADHDNOS_OLS_HI_slope_winsorize_None (249
perms)
Cluster size: 87, p<0.012 *
```

It looks like the nonew results are stronger. Let's start doing scatterplots of those results then, both in structural and DTI results, while we wait for MELODIC.

```
3dclust -NN1 1 -orient LPI -savemask mycluster.nii
/data/NCR_SBRB/tmp/dti_ad_voxelwise_n272_09212018/ADHDNOS_nonew_OLS_inatt_
slope_winsorize_None_42+orig
3dmaskdump -mask
/data/NCR_SBRB/baseline_prediction/mean_272_fa_skeleton_mask.nii.gz
mycluster.nii > out.txt
```

```
winsorize = function(x, cut = 0.01){
  cut_point_top <- quantile(x, 1 - cut, na.rm = T)
  cut_point_bottom <- quantile(x, cut, na.rm = T)
  i = which(x >= cut_point_top)
  x[i] = cut_point_top
  j = which(x <= cut_point_bottom)
  x[j] = cut_point_bottom
  return(x)
}
```

```
load('/data/NCR_SBRB/baseline_prediction/dti_ad_voxelwise_n272_09212018.RD
ata.gz')
a = read.table('~/tmp/out.txt')[,4]
idx = which(a==1)
clin =
read.csv('/data/NCR_SBRB/baseline_prediction/long_clin_11302018.csv')
df = merge(clin, data, by='MRN')
x = colnames(df)[grepl(pattern = '^v', colnames(df))]
idx2 = df$diag_group != 'new_onset' & df$DX != 'NV'
tgt = winsorize(df[idx2,]$OLS_inatt_slope)
plot(tgt, rowMeans(df[idx2, x[idx]]))
b = cor.test(tgt, rowMeans(df[idx2, x[idx]]))
title(sprintf('ADHDNOS nonew AD272 inatt, r=%.2f, p<%.2f', b$estimate,
b$p.value))
```

It's hard to say if those are truly outliers. Out of curiosity, even though the clusters are not as big, let's see how the scatterplots look when including the new_onset cases:

Not much difference. Might as well stick with nonew for now.

```
3dclust -NN1 1 -orient LPI -savemask mycluster.nii -overwrite
/data/NCR_SBRB/tmp/dti_ad_voxelwise_n272_09212018/ADHDNOS_nonew_OLS_inatt_
slope_winsorize_None_42+orig
3dcalc -a mycluster.nii -prefix myres.nii -overwrite -expr "amongst(a, 1)"
flirt -in myres.nii -ref
/usr/local/apps/fsl/6.0.0/data/standard/MNI152_T1_1mm.nii.gz -out
myres_inMNI152.nii.gz -applyxfm -init ~/data/aging_to_MNI152.mat -interp
nearestneighbour
# just to get the COM for labeling
3dclust -NN1 1 -orient LPI myres_inMNI152.nii.gz
```

inattention (AD):

HI (RD):

struct

We'll focus on volume, which has the most results and combine area and thickness. For convenience, these are the nonew results:

```
struct_volume_11142018_260timeDiff12mo (RH):
ADHDNOS_nonew_OLS_HI_slope_winsorize_None (250 perms)
struct_volume_11142018_260timeDiff12mo (LH):
ADHDNOS_nonew_OLS_inatt_slope_winsorize_None (250 perms)
```

```
struct_volume_11142018_260timeDiff12mo (RH):
ADHDNOS_nonew_OLS_inatt_slope_winsorize_None (250 perms)
```

```
awk 'NR>=13 && NR<2575'
/data/NCR_SBRB/tmp/struct_volume_11142018_260timeDiff12mo/ADHDNOS_nonew_OL
S_HI_slope_winsorize_None_42_rh_ClstMsk_e1_a1.0.niml.dset >
~/tmp/clusters.txt
```

```
winsorize = function(x, cut = 0.01){
  cut_point_top <- quantile(x, 1 - cut, na.rm = T)
  cut_point_bottom <- quantile(x, cut, na.rm = T)
  i = which(x >= cut_point_top)
  x[i] = cut_point_top
  j = which(x <= cut_point_bottom)
  x[j] = cut_point_bottom
  return(x)
}
clin =
read.csv('/data/NCR_SBRB/baseline_prediction/long_clin_11302018.csv')
load('/data/NCR_SBRB/baseline_prediction/struct_volume_11142018_260timeDif
f12mo.RData.gz')
df = merge(clin, data, by='MRN')
x = colnames(df)[grepl(pattern = '^v_rh', colnames(df))]
a = read.table('~/tmp/clusters.txt')[,1]
idx = which(a==1)
idx2 = df$diag_group != 'new_onset' & df$DX != 'NV'
tgt = winsorize(df[idx2,]$OLS_HI_slope)
plot(tgt, rowMeans(df[idx2, x[idx]]))
b = cor.test(tgt, rowMeans(df[idx2, x[idx]]))
title(sprintf('ADHDNOS nonew volume RH HI, r=%.2f, p<%.2f', b$estimate,
b$p.value))
```

This second one is clearly moved by outliers...

```
awk 'NR>=13 && NR<2575'
~/tmp/struct_volume_11142018_260timeDiff12mo/ADHDNOS_nonew_OLS_HI_slope_wi
nsorize_None_42_rh_ClstMsk_e1_a1.0.niml.dset > ~/tmp/clusters.txt
# single out the one region
awk '{ if ($1 != 1 ) print 0; else print 1 }' ~/tmp/clusters.txt >
rh_HI.txt
awk 'NR>=13 && NR<2575'
~/tmp/struct_volume_11142018_260timeDiff12mo/ADHDNOS_nonew_OLS_inatt_slope
_winsorize_None_42_lh_ClstMsk_e1_a1.0.niml.dset > ~/tmp/clusters.txt
```

```
awk '{ if ($1 != 1 ) print 0; else print 1 }' ~/tmp/clusters.txt >
lh_inatt.txt
suma -i_fs
/Volumes/Shaw/freesurfer5.3_subjects/fsaverage4/SUMA/lh.pial.asc
```

2018-12-13 13:11:17

Let's run some crappy domain descriptives.

```
mydir=~/data/baseline_prediction/;
for f in cog_all_09242018.RData.gz geno3_prs_09192018.RData.gz \
    social_09262018.RData.gz clinics_binary_sx_baseline_10022018.RData.gz
\
    adhd200_10042018.RData.gz; do
    for target in OLS_inatt_slope OLS_HI_slope; do
        echo ==== $f $target ====;
        Rscript --vanilla
~/research_code/baseline_prediction/descriptives/generic.R ${mydir}/${f}
${mydir}/long_clin_11302018.csv ADHDNOS_nonew_${target} 42 winsorize_None;
    done;
done
```

Note that I'm only running that for the nonew subset, conforming to the previous results. I used script to output the results, and here are the main findings:

```
==== cog_all_09242018.RData.gz OLS_HI_slope ====
[1] "Variables at p<.05: 2 / 25"
[1] "v_Raw_SS_total" "v_Raw_SSB"
==== geno3_prs_09192018.RData.gz OLS_inatt_slope ====
[1] "Variables at p<.05: 2 / 13"
[1] "v_PROFILES.0.0001.profile" "v_PROFILES.0.0005.profile"
==== geno3_prs_09192018.RData.gz OLS_HI_slope ====
[1] "Variables at p<.05: 1 / 13"
[1] "v_PROFILES.0.00001.profile"
==== social_09262018.RData.gz OLS_HI_slope ====
[1] "Variables at p<.05: 1 / 18"
[1] "v_Priv_School"
==== clinics_binary_sx_baseline_10022018.RData.gz OLS_inatt_slope ====
[1] "Variables at p<.05: 8 / 8"
[1] "v_SX_inatt"          "v_SX_HI"             "vCateg_diff.organ"
[4] "vCateg_avoids"       "vCateg_loses"        "vCateg_easily.distr"
[7] "vCateg_forgetful"    "vCateg_waiting.turn"
==== clinics_binary_sx_baseline_10022018.RData.gz OLS_HI_slope ====
[1] "Variables at p<.05: 3 / 11"
[1] "v_SX_HI"             "vCateg_fidgety"      "vCateg_waiting.turn"
[1] "Variables at q<.05: 2 / 11"
```

```
[1] "v_SX_HI"             "vCateg_waiting.turn"
==== adhd200_10042018.RData.gz OLS_inatt_slope ====
[1] "Variables at p<.05: 1 / 3"
[1] "v_Age"
[1] "Variables at q<.05: 1 / 3"
[1] "v_Age"
```

I decided to report only the nominal p-values because I didn't want to restrict the number of variables we're using for FDR or Meff. If they're crappy in the end, the ML algorithm will likely throw it away. The results not listed did not have any nominal results. Also, I think we could probably get rid of the socioeconomic variables for now.

The baseline SX results are interesting, especially the individual binary symptoms. The baseline SX makes sense, as one cannot have negative OLS at zero, not positive at 9, so that makes the distribution somewhat diagonal, creating a correlation. One could also argue that the more symptoms at baseline, the more one has to lose, so there's your correlation.

Now, it's a matter of putting those variables together in a model, to combine with the neural cluster averages.

2018-12-14 09:37:15

##melodic

```
myfile=melodic_NOSdescriptives.txt
rm $myfile; touch $myfile;
for f in `/bin/ls \
    /data/NCR_SBRB/tmp/melodic_*IC*/ADHDNOS*_42_clusters.txt`; do
    echo $f >> $myfile;
    grep -v \# $f | head -n 5 >> $myfile;
done
```

```
/bin/ls -1 /data/NCR_SBRB/tmp/melodic_*_IC*/ADHDNOS*_42_clusters.txt >
result_files.txt;
for root_file in `cat result_files.txt | sed -e 's/_42_clusters.txt//g'`;
do
    collect_name=${root_file}_top_rnd_clusters.txt;
    echo $collect_name;
    if [ -e $collect_name ]; then
        rm $collect_name;
    fi;
    for f in `ls ${root_file}*rnd*clusters.txt`; do
        grep -v \# $f | head -n 1 >> $collect_name;
    done
done
tar -zcvf melodic_ADHDNOS_top_rnd_clusters.tar.gz
melodic_*_IC*/ADHDNOS*top_rnd_clusters.txt
```

```
res_fname = '~/tmp/melodic_NOSdescriptives.txt'
out_file = '~/tmp/pvals_NOSmelodic.txt'
res_lines = readLines(res_fname)
for (line in res_lines) {
  # starting new file summary
  if (grepl(pattern='clusters', line)) {
    root_fname = strsplit(line, '/')[[1]]
    dir_name = root_fname[length(root_fname)-1]
    root_fname = strsplit(root_fname[length(root_fname)], '_')[[1]]
    root_fname = paste0(root_fname[1:(length(root_fname)-2)], sep='',
collapse='_')
    rnd_fname = sprintf('~/tmp/%s/%s_top_rnd_clusters.txt', dir_name,
root_fname)
    if (file.exists(rnd_fname)) {
        rnd_results = read.table(rnd_fname)[, 1]
        nperms = length(rnd_results)
    } else {
        rnd_results = NA
        nperms = NA
    }
    cat(sprintf('%s: %s (%d perms)\n', dir_name, root_fname, nperms),
        file=out_file, append=T)
  }
  else {
    parsed = strsplit(line, ' +')
    clus_size = as.numeric(parsed[[1]][2])
    pval = sum(rnd_results >= clus_size) / nperms
    cat(sprintf('Cluster size: %d, p<%.3f', clus_size, pval),
        file=out_file, append=T)
    if (!is.na(pval) && pval < .05) {
      cat(' *', file=out_file, append=T)
    }
    if (!is.na(pval) && pval < .01) {
      cat('*', file=out_file, append=T)
    }
    cat('\n', file=out_file, append=T)
  }
}
```

Overall, every time there was a subjScale and None results, the subjScale clusters were bigger, but the actual p-value for None was smaller. So, let's focus on those for now.

But there might be something odd here, as all results are either ADHDNOS_nonew_OLS_HI with 40 voxels, or ADHDNOS_OLS_inatt for 56 voxels. Across all 7 ICs in fancy, but nothing in inter.

```
hg-02127244-lw0:tmp sudregp$ grep -B 1 "*" pvals_NOSmelodic.txt
dti_ad_voxelwise_n272_09212018:
ADHDNOS_nonew_OLS_inatt_slope_winsorize_None (248 perms)
Cluster size: 41, p<0.012 *
```

```
Cluster size: 31, p<0.044 *
--
dti_ad_voxelwise_n272_09212018: ADHDNOS_OLS_inatt_slope_winsorize_None
(250 perms)
Cluster size: 38, p<0.036 *
--
dti_rd_voxelwise_n272_09212018: ADHDNOS_nonew_OLS_HI_slope_winsorize_None
(249 perms)
Cluster size: 92, p<0.004 **
--
dti_rd_voxelwise_n272_09212018: ADHDNOS_OLS_HI_slope_winsorize_None (249
perms)
Cluster size: 87, p<0.012 *
```

It looks like the nonew results are stronger. Let's start doing scatterplots of those results then, both in structural and DTI results, while we wait for MELODIC.

```
3dclust -NN1 1 -orient LPI -savemask mycluster.nii
/data/NCR_SBRB/tmp/dti_ad_voxelwise_n272_09212018/ADHDNOS_nonew_OLS_inatt_
slope_winsorize_None_42+orig
3dmaskdump -mask
/data/NCR_SBRB/baseline_prediction/mean_272_fa_skeleton_mask.nii.gz
mycluster.nii > out.txt
```

```
winsorize = function(x, cut = 0.01){
  cut_point_top <- quantile(x, 1 - cut, na.rm = T)
  cut_point_bottom <- quantile(x, cut, na.rm = T)
  i = which(x >= cut_point_top)
  x[i] = cut_point_top
  j = which(x <= cut_point_bottom)
  x[j] = cut_point_bottom
  return(x)
}
load('/data/NCR_SBRB/baseline_prediction/dti_ad_voxelwise_n272_09212018.RD
ata.gz')
a = read.table('~/tmp/out.txt')[,4]
idx = which(a==1)
clin =
read.csv('/data/NCR_SBRB/baseline_prediction/long_clin_11302018.csv')
df = merge(clin, data, by='MRN')
x = colnames(df)[grepl(pattern = '^v', colnames(df))]
idx2 = df$diag_group != 'new_onset' & df$DX != 'NV'
tgt = winsorize(df[idx2,]$OLS_inatt_slope)
plot(tgt, rowMeans(df[idx2, x[idx]]))
b = cor.test(tgt, rowMeans(df[idx2, x[idx]]))
title(sprintf('ADHDNOS nonew AD272 inatt, r=%.2f, p<%.2f', b$estimate,
b$p.value))
```

2018-12-17 15:14:56

##melodic

```
myfile=melodic_NOSdescriptives.txt
rm $myfile; touch $myfile;
for f in `/bin/ls \
    /data/NCR_SBRB/tmp/melodic_*_IC*12142018/ADHDNOS*_42_clusters.txt`; do
    echo $f >> $myfile;
    grep -v \# $f | head -n 5 >> $myfile;
done
```

```
/bin/ls -1
/data/NCR_SBRB/tmp/melodic_*_IC*_12142018/ADHDNOS*_42_clusters.txt >
result_files.txt;
for root_file in `cat result_files.txt | sed -e 's/_42_clusters.txt//g'`;
do
    collect_name=${root_file}_top_rnd_clusters.txt;
    echo $collect_name;
    if [ -e $collect_name ]; then
        rm $collect_name;
    fi;
    for f in `ls ${root_file}*rnd*clusters.txt`; do
        grep -v \# $f | head -n 1 >> $collect_name;
    done
done
tar -zcvf melodic_ADHDNOS_top_rnd_clusters.tar.gz
melodic_*_IC*_12142018/ADHDNOS*top_rnd_clusters.txt
```

```
res_fname = '~/tmp/melodic_NOSdescriptives.txt'
out_file = '~/tmp/pvals_NOSmelodic.txt'
res_lines = readLines(res_fname)
for (line in res_lines) {
  # starting new file summary
  if (grepl(pattern='clusters', line)) {
    root_fname = strsplit(line, '/')[[1]]
    dir_name = root_fname[length(root_fname)-1]
    root_fname = strsplit(root_fname[length(root_fname)], '_')[[1]]
    root_fname = paste0(root_fname[1:(length(root_fname)-2)], sep='',
collapse='_')
    rnd_fname = sprintf('~/tmp/%s/%s_top_rnd_clusters.txt', dir_name,
root_fname)
    if (file.exists(rnd_fname)) {
        rnd_results = read.table(rnd_fname)[, 1]
        nperms = length(rnd_results)
    } else {
        rnd_results = NA
```

```
        nperms = NA
    }
    cat(sprintf('%s: %s (%d perms)\n', dir_name, root_fname, nperms),
        file=out_file, append=T)
  }
  else {
    parsed = strsplit(line, ' +')
    clus_size = as.numeric(parsed[[1]][2])
    pval = sum(rnd_results >= clus_size) / nperms
    cat(sprintf('Cluster size: %d, p<%.3f', clus_size, pval),
        file=out_file, append=T)
    if (!is.na(pval) && pval < .05) {
      cat(' *', file=out_file, append=T)
    }
    if (!is.na(pval) && pval < .01) {
      cat('*', file=out_file, append=T)
    }
    cat('\n', file=out_file, append=T)
  }
}
```

For melodic our results using subjScale were actually better.

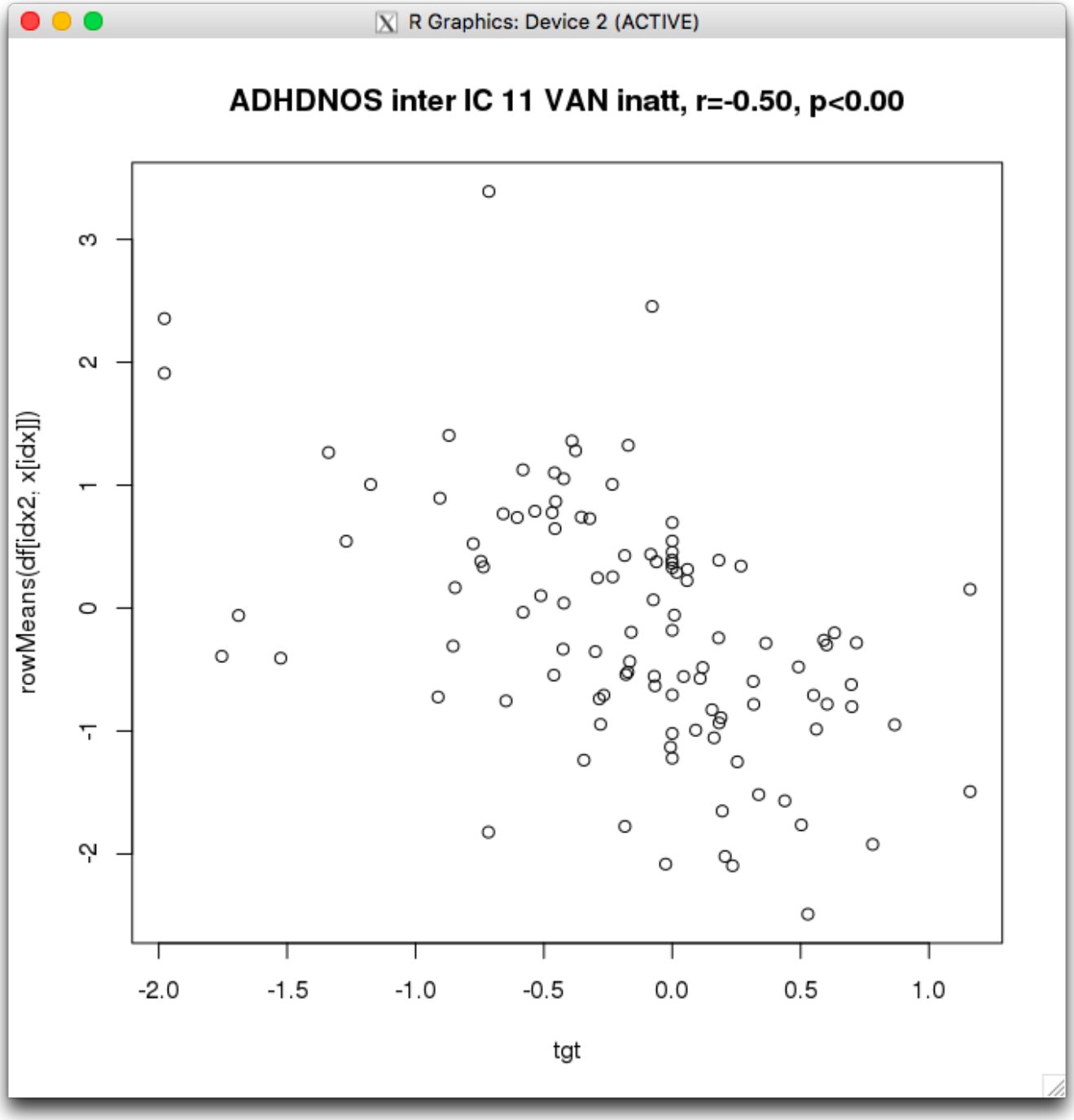
```
hg-02127244-lw0:tmp sudregp$ grep -B 1 "*" pvals_NOSmelodic.txt | grep
nonew
melodic_fancy_IC37_12142018:
ADHDNOS_nonew_OLS_inatt_slope_winsorize_subjScale (249 perms)
melodic_fancy_IC57_12142018: ADHDNOS_nonew_OLS_HI_slope_winsorize_None
(250 perms)
melodic_inter_IC11_12142018:
ADHDNOS_nonew_OLS_inatt_slope_winsorize_subjScale (249 perms)
melodic_inter_IC2_12142018:
ADHDNOS_nonew_OLS_inatt_slope_winsorize_subjScale (248 perms)
melodic_inter_IC31_12142018:
ADHDNOS_nonew_OLS_inatt_slope_winsorize_subjScale (250 perms)
```

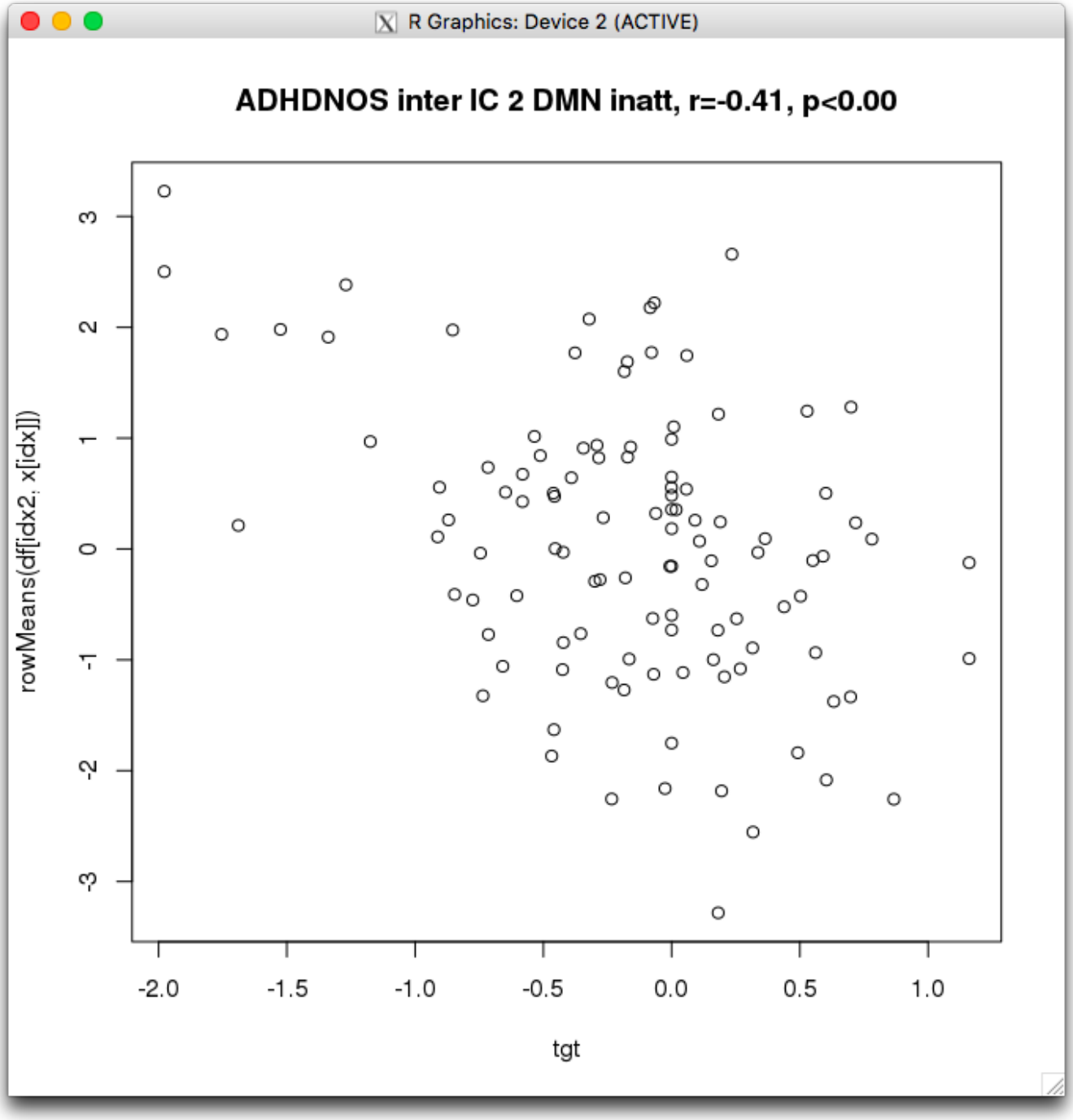
Those networks are VAN, limbic, and DMN. Let's make the usual scatterplots.

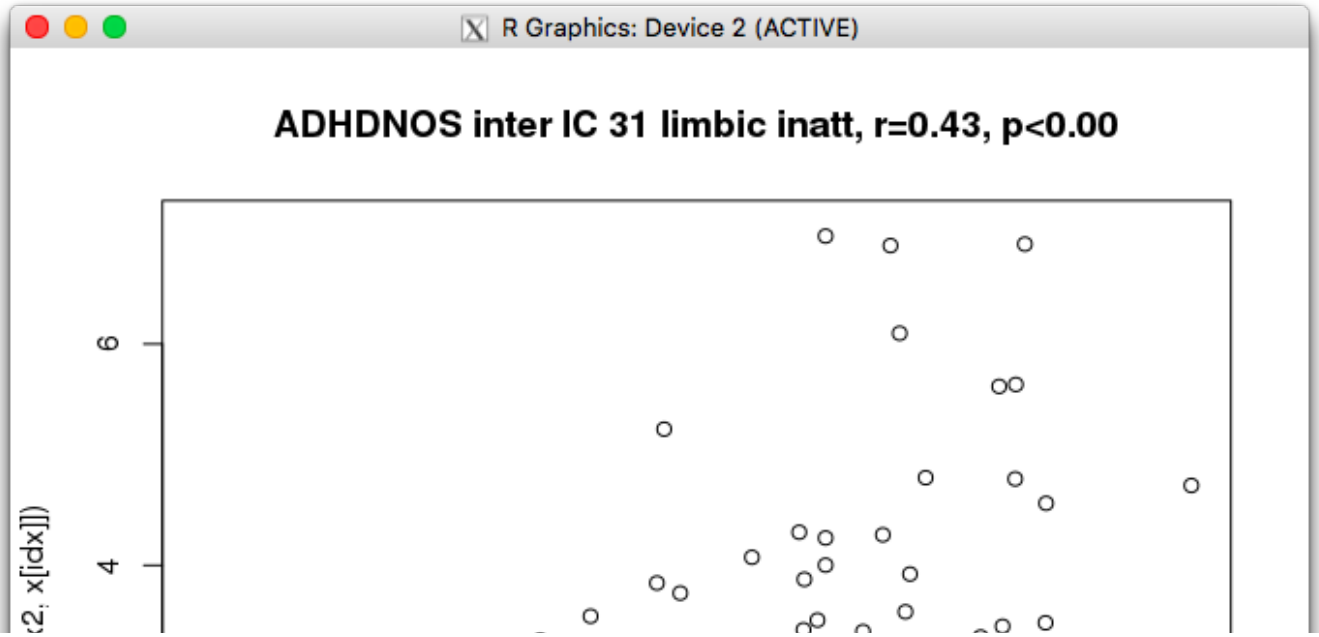
```
3dclust -NN1 1 -orient LPI -savemask mycluster.nii -overwrite
/data/NCR_SBRB/tmp/melodic_inter_IC31_12142018/ADHDNOS_nonew_OLS_inatt_slo
pe_winsorize_subjScale_42+tlrc
3dmaskdump -mask
~/data/baseline_prediction/same_space/epi/group_epi_mask_inter.nii
mycluster.nii > out.txt
```

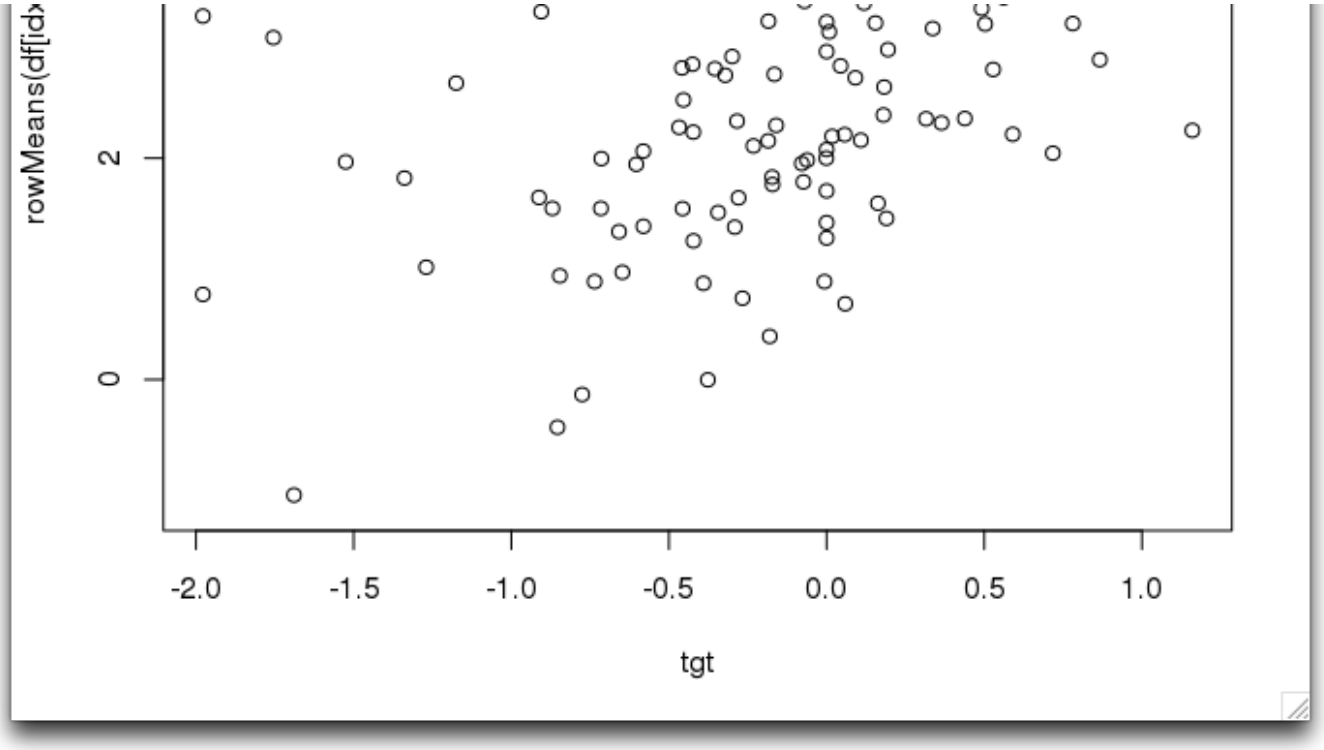
```
winsorize = function(x, cut = 0.01){
  cut_point_top <- quantile(x, 1 - cut, na.rm = T)
```

```
  cut_point_bottom <- quantile(x, cut, na.rm = T)
  i = which(x >= cut_point_top)
  x[i] = cut_point_top
  j = which(x <= cut_point_bottom)
  x[j] = cut_point_bottom
  return(x)
}
load('/data/NCR_SBRB/baseline_prediction/melodic_inter_IC31_12142018.RData
.gz')
a = read.table('~/tmp/out.txt')[,4]
idx = which(a==1)
clin =
read.csv('/data/NCR_SBRB/baseline_prediction/long_clin_11302018.csv')
df = merge(clin, data, by='MRN')
x = colnames(df)[grepl(pattern = '^v', colnames(df))]
idx2 = df$diag_group != 'new_onset' & df$DX != 'NV'
tgt = winsorize(df[idx2,]$OLS_inatt_slope)
plot(tgt, rowMeans(df[idx2, x[idx]]))
b = cor.test(tgt, rowMeans(df[idx2, x[idx]]))
title(sprintf('ADHDNOS inter IC 31 limbic inatt, r=%.2f, p<%.2f',
b$estimate, b$p.value))
```


R Graphics: Device 2 (ACTIVE)
ADHDNOS inter IC 11 VAN inatt, r=-0.50, p<0.00
rowMeans(df[idx2, x[idx]])
3
2
1
0
-1
-2
-2.0
-1.5
-1.0
-0.5
0.0
0.5
1.0
tgt

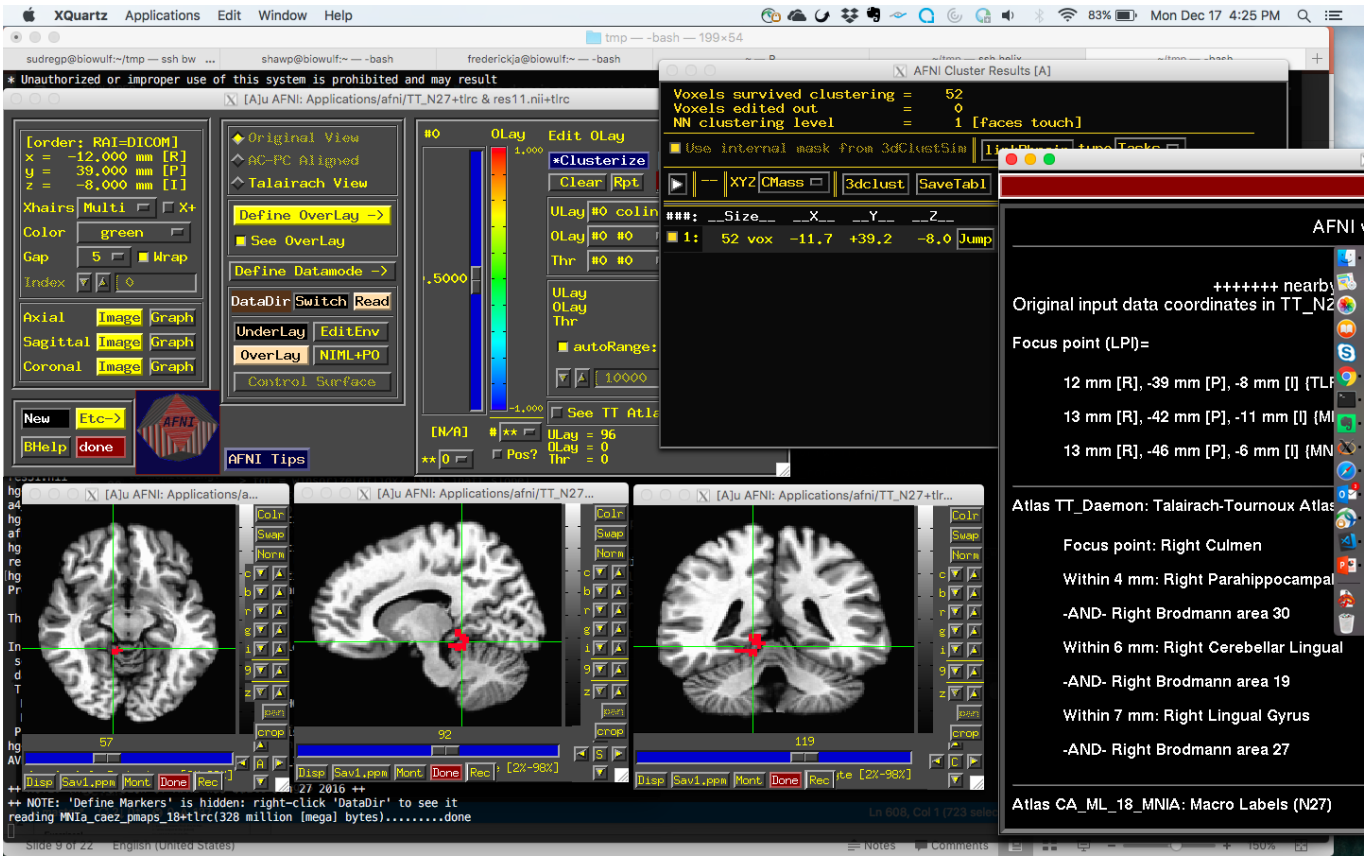

R Graphics: Device 2 (ACTIVE)
ADHDNOS inter IC 2 DMN inatt, r=-0.41, p<0.00
rowMeans(df[idx2, x[idx]])
tgt
-2.0
-1.5
-1.0
-0.5
0.0
0.5
1.0
3
2
1
0
-1
-2
-3

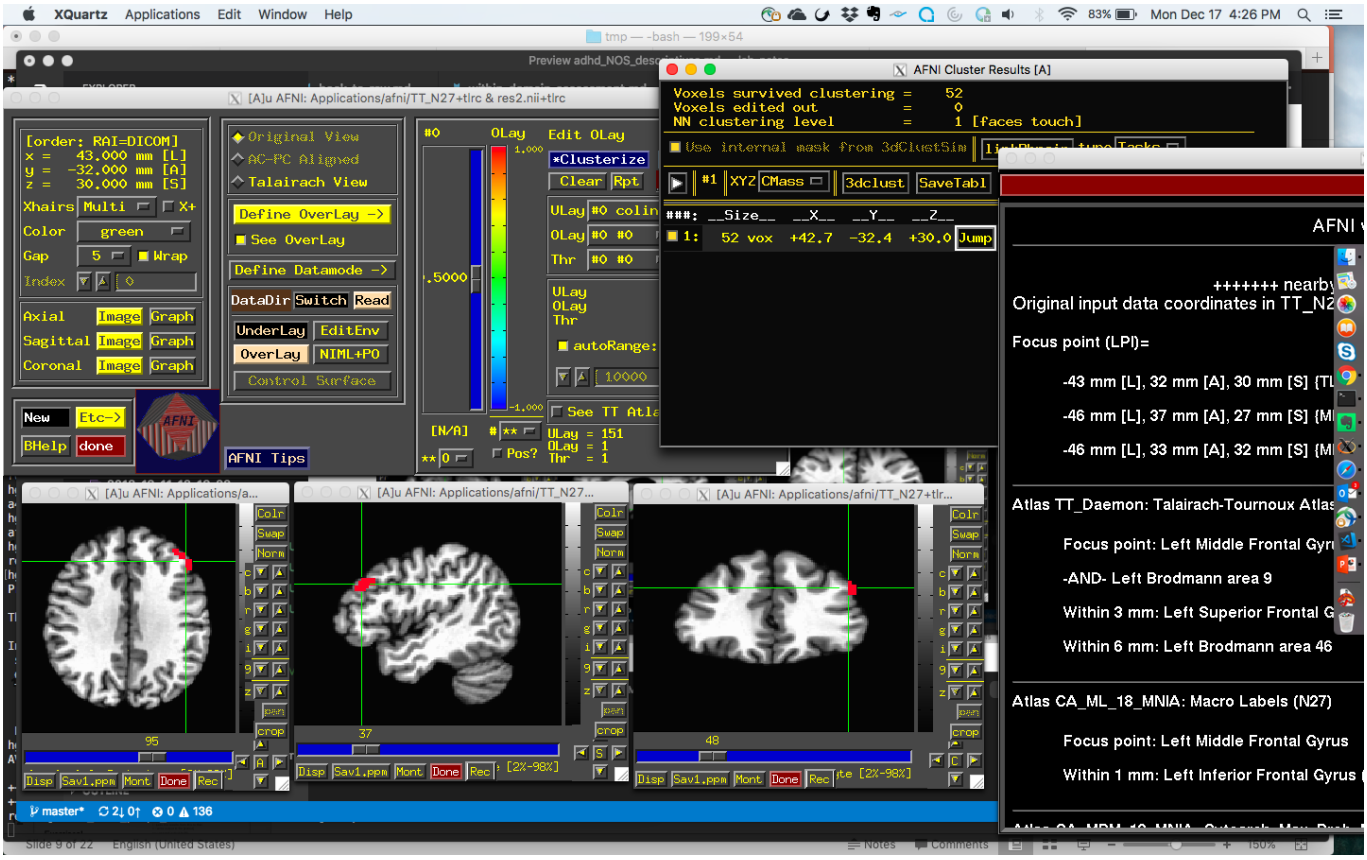

R Graphics: Device 2 (ACTIVE)
ADHDNOS inter IC 31 limbic inatt, r=0.43, p<0.00
6
4

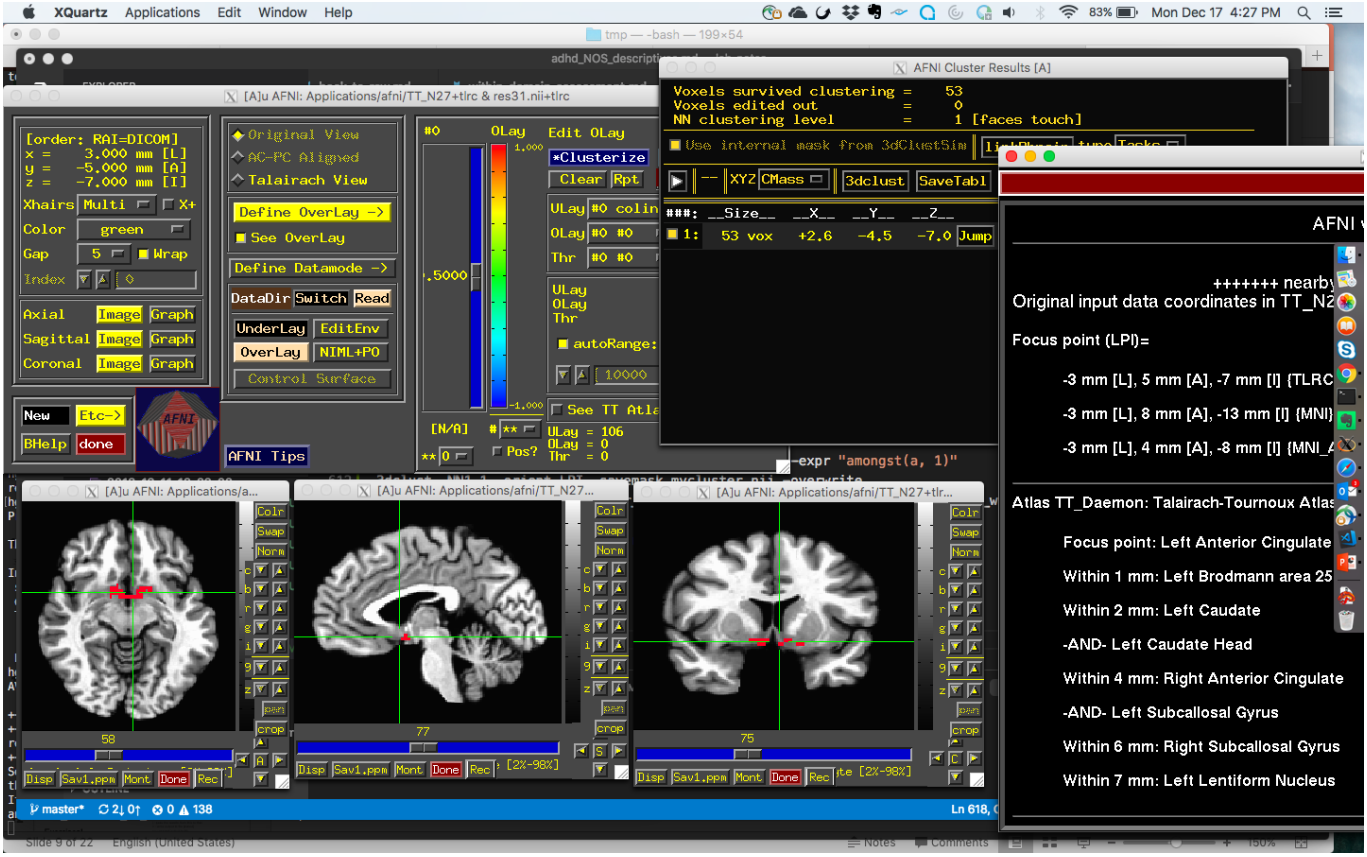


And we should probably check out where in the brain they are, before setting them up for classification. I'm not going to make the 95 percentile masks we used in the paper for now, but we can have an idea of where the cluster is base don the pictures, and then compare to the actual networks in the Yeo paper to see if they make sense.

```
3dclust -NN1 1 -orient LPI -savemask mycluster.nii -overwrite
/data/NCR_SBRB/tmp/melodic_inter_IC31_12142018/ADHDNOS_nonew_OLS_inatt_slo
pe_winsorize_subjScale_42+tlrc
3dcalc -a mycluster.nii -prefix res31.nii -overwrite -expr "amongst(a, 1)"
3dclust -NN1 1 -orient LPI -savemask mycluster.nii -overwrite
/data/NCR_SBRB/tmp/melodic_inter_IC2_12142018/ADHDNOS_nonew_OLS_inatt_slop
e_winsorize_subjScale_42+tlrc
3dcalc -a mycluster.nii -prefix res2.nii -overwrite -expr "amongst(a, 1)"
3dclust -NN1 1 -orient LPI -savemask mycluster.nii -overwrite
/data/NCR_SBRB/tmp/melodic_inter_IC11_12142018/ADHDNOS_nonew_OLS_inatt_slo
pe_winsorize_subjScale_42+tlrc
3dcalc -a mycluster.nii -prefix res11.nii -overwrite -expr "amongst(a, 1)"
```


AFNI Cluster Results [A]
Voxels survived clustering = 52
Voxels edited out = 0
NN clustering level = 1 [faces touch]
Original input data coordinates in TT_N2
Focus point (LPI)=
12 mm [R], -39 mm [P], -8 mm [I]
13 mm [R], -42 mm [P], -11 mm [I]
13 mm [R], -46 mm [P], -6 mm [I]
Atlas TT_Daemon: Talairach-Tournoux Atlas
Focus point: Right Culmen
Within 4 mm: Right Parahippocampal
-AND- Right Brodmann area 30
Within 6 mm: Right Cerebellar Lingual
-AND- Right Brodmann area 19
Within 7 mm: Right Lingual Gyrus
-AND- Right Brodmann area 27
Atlas CA_ML_18_MNIA: Macro Labels (N27)


AFNI Cluster Results [A]
Voxels survived clustering = 52
Voxels edited out = 0
NN clustering level = 1 [faces touch]
Original input data coordinates in TT_N2
Focus point (LPI)=
-43 mm [L], 32 mm [A], 30 mm [S]
-46 mm [L], 37 mm [A], 27 mm [S]
-46 mm [L], 33 mm [A], 32 mm [S]
Atlas TT_Daemon: Talairach-Tournoux Atlas
Focus point: Left Middle Frontal Gyr
-AND- Left Brodmann area 9
Within 3 mm: Left Superior Frontal G
Within 6 mm: Left Brodmann area 46
Atlas CA_ML_18_MNIA: Macro Labels (N27)
Focus point: Left Middle Frontal Gyrus
Within 1 mm: Left Inferior Frontal Gyrus



We got a couple hard hits there. For DMN (IC2), we got LMFG, which is neat. But limbic (IC31) we got left ACC, quite inferior, and VAN (IC11) we got cerebellum. We coudl restrict it to DMN, so we'll see.

2018-12-19 14:39:43

Philip asked me to re-run the results, but this time keeping the new_onset folks and also plotting NVs in the scatterplots. Let's do it

DTI

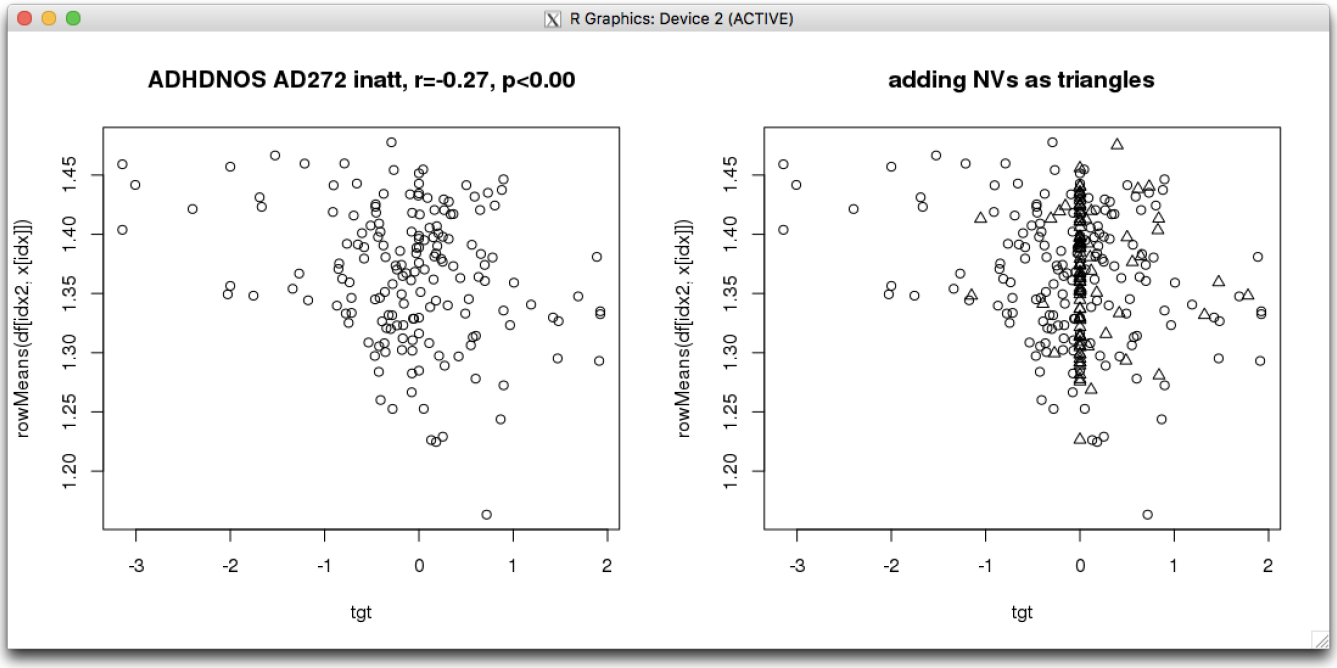
```
sudregp@HG-02070684-DM2:~/tmp$ grep -B 1 "*" pvals_NOSdti.txt | grep S_O -
A 1
dti_ad_voxelwise_n272_09212018: ADHDNOS_OLS_inatt_slope_winsorize_None
(250 perms)
dti_rd_voxelwise_n272_09212018: ADHDNOS_OLS_HI_slope_winsorize_None (249
perms)
```

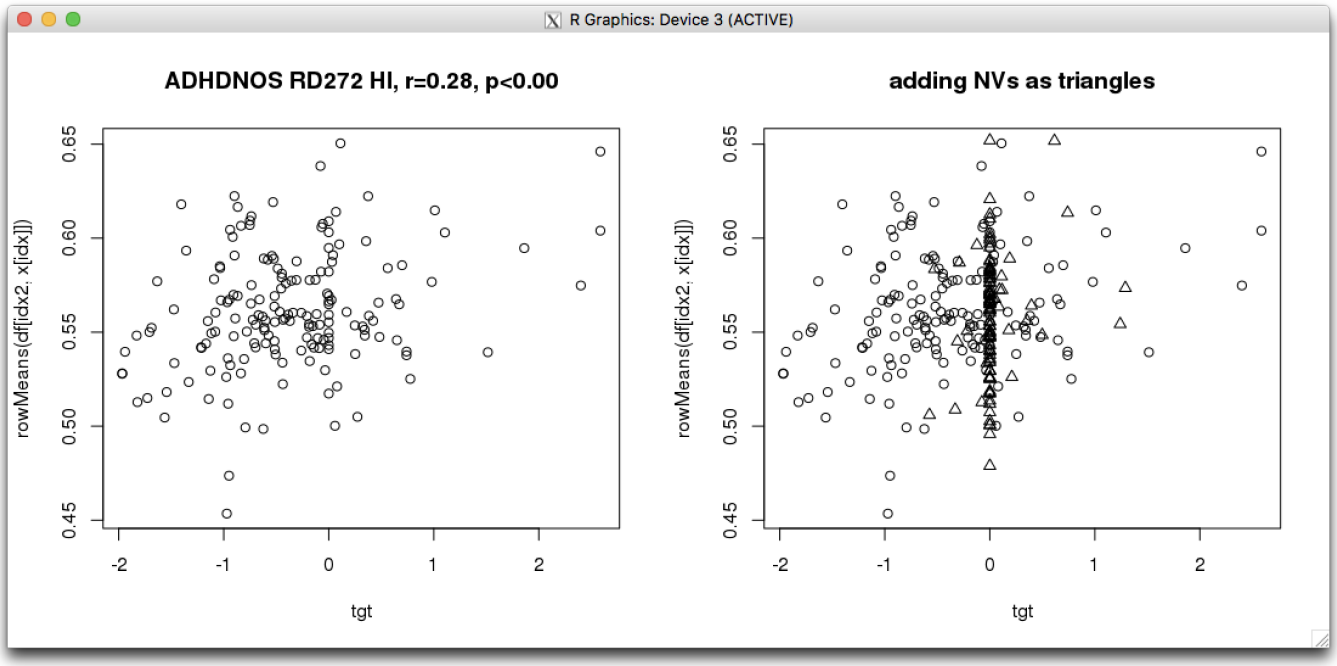
```
3dclust -NN1 1 -orient LPI -savemask mycluster.nii -overwrite
/data/NCR_SBRB/tmp/dti_ad_voxelwise_n272_09212018/ADHDNOS_OLS_inatt_slope_
winsorize_None_42+orig
3dmaskdump -mask
/data/NCR_SBRB/baseline_prediction/mean_272_fa_skeleton_mask.nii.gz
mycluster.nii > out_AD_inatt.txt
3dclust -NN1 1 -orient LPI -savemask mycluster.nii -overwrite
/data/NCR_SBRB/tmp/dti_rd_voxelwise_n272_09212018/ADHDNOS_OLS_HI_slope_win
```

```
sorize_None_42+orig
3dmaskdump -mask
/data/NCR_SBRB/baseline_prediction/mean_272_fa_skeleton_mask.nii.gz
mycluster.nii > out_RD_HI.txt
```

```
winsorize = function(x, cut = 0.01){
  cut_point_top <- quantile(x, 1 - cut, na.rm = T)
  cut_point_bottom <- quantile(x, cut, na.rm = T)
  i = which(x >= cut_point_top)
  x[i] = cut_point_top
  j = which(x <= cut_point_bottom)
  x[j] = cut_point_bottom
  return(x)
}
clin =
read.csv('/data/NCR_SBRB/baseline_prediction/long_clin_11302018.csv')
load('/data/NCR_SBRB/baseline_prediction/dti_ad_voxelwise_n272_09212018.RD
ata.gz')
a = read.table('~/tmp/out_AD_inatt.txt')[,4]
idx = which(a==1)
df = merge(clin, data, by='MRN')
x = colnames(df)[grepl(pattern = '^v', colnames(df))]
idx2 = df$DX != 'NV'
tgt = winsorize(df[idx2,]$OLS_inatt_slope)
par(mfrow=c(1,2))
plot(tgt, rowMeans(df[idx2, x[idx]]))
b = cor.test(tgt, rowMeans(df[idx2, x[idx]]))
title(sprintf('ADHDNOS AD272 inatt, r=%.2f, p<%.2f', b$estimate,
b$p.value))
plot(tgt, rowMeans(df[idx2, x[idx]]))
idx3 = df$DX == 'NV'
points(df[idx3,]$OLS_inatt_slope, rowMeans(df[idx3, x[idx]]), pch=2)
title('adding NVs as triangles')

dev.new()
load('/data/NCR_SBRB/baseline_prediction/dti_rd_voxelwise_n272_09212018.RD
ata.gz')
a = read.table('~/tmp/out_RD_HI.txt')[,4]
idx = which(a==1)
df = merge(clin, data, by='MRN')
x = colnames(df)[grepl(pattern = '^v', colnames(df))]
idx2 = df$DX != 'NV'
tgt = winsorize(df[idx2,]$OLS_HI_slope)
par(mfrow=c(1,2))
plot(tgt, rowMeans(df[idx2, x[idx]]))
b = cor.test(tgt, rowMeans(df[idx2, x[idx]]))
title(sprintf('ADHDNOS RD272 HI, r=%.2f, p<%.2f', b$estimate, b$p.value))
plot(tgt, rowMeans(df[idx2, x[idx]]))
idx3 = df$DX == 'NV'
points(df[idx3,]$OLS_HI_slope, rowMeans(df[idx3, x[idx]]), pch=2)
title('adding NVs as triangles')
```



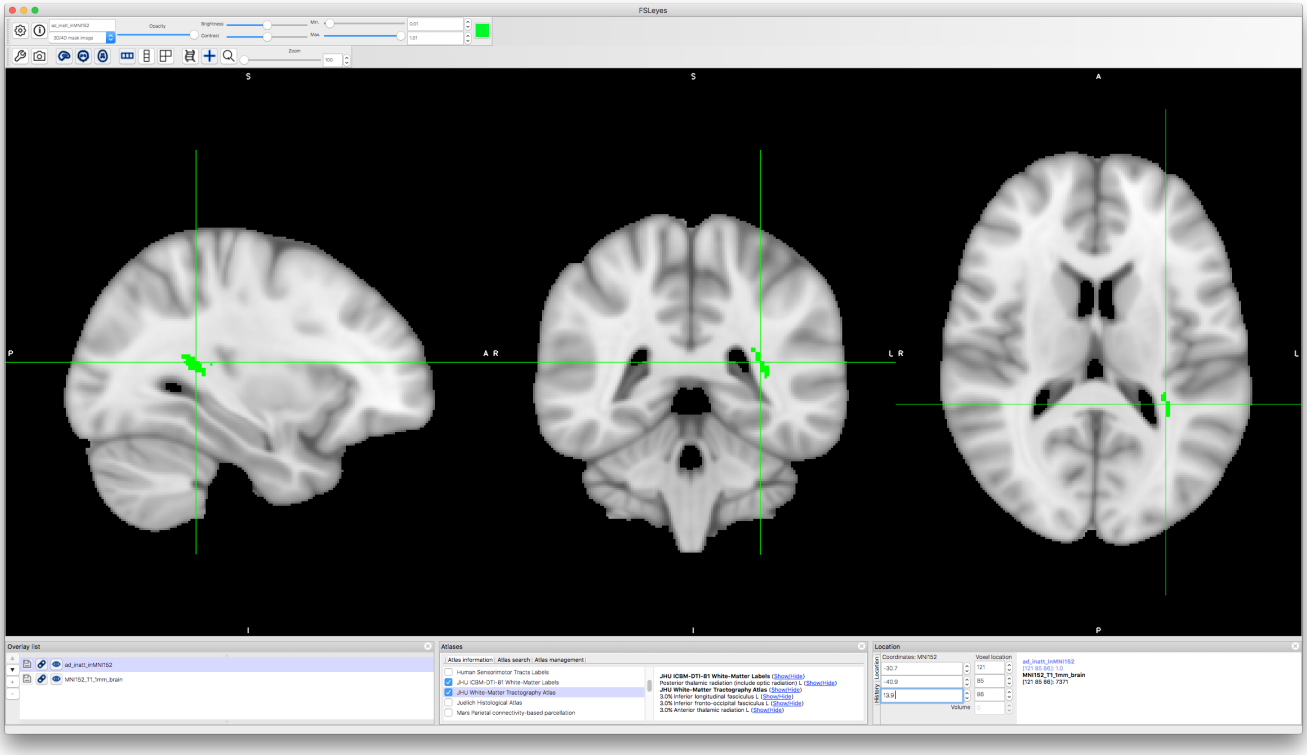



```
3dclust -NN1 1 -orient LPI -savemask mycluster.nii -overwrite
/data/NCR_SBRB/tmp/dti_ad_voxelwise_n272_09212018/ADHDNOS_OLS_inatt_slope_
winsorize_None_42+orig
3dcalc -a mycluster.nii -prefix myres.nii -overwrite -expr "amongst(a, 1)"
flirt -in myres.nii -ref
/usr/local/apps/fsl/6.0.0/data/standard/MNI152_T1_1mm.nii.gz -out
ad_inatt_inMNI152.nii.gz -applyxfm -init ~/data/aging_to_MNI152.mat -
interp nearestneighbour
3dclust -NN1 1 -orient LPI -savemask mycluster.nii -overwrite
/data/NCR_SBRB/tmp/dti_rd_voxelwise_n272_09212018/ADHDNOS_OLS_HI_slope_win
sorize_None_42+orig
3dcalc -a mycluster.nii -prefix myres.nii -overwrite -expr "amongst(a, 1)"
flirt -in myres.nii -ref
```

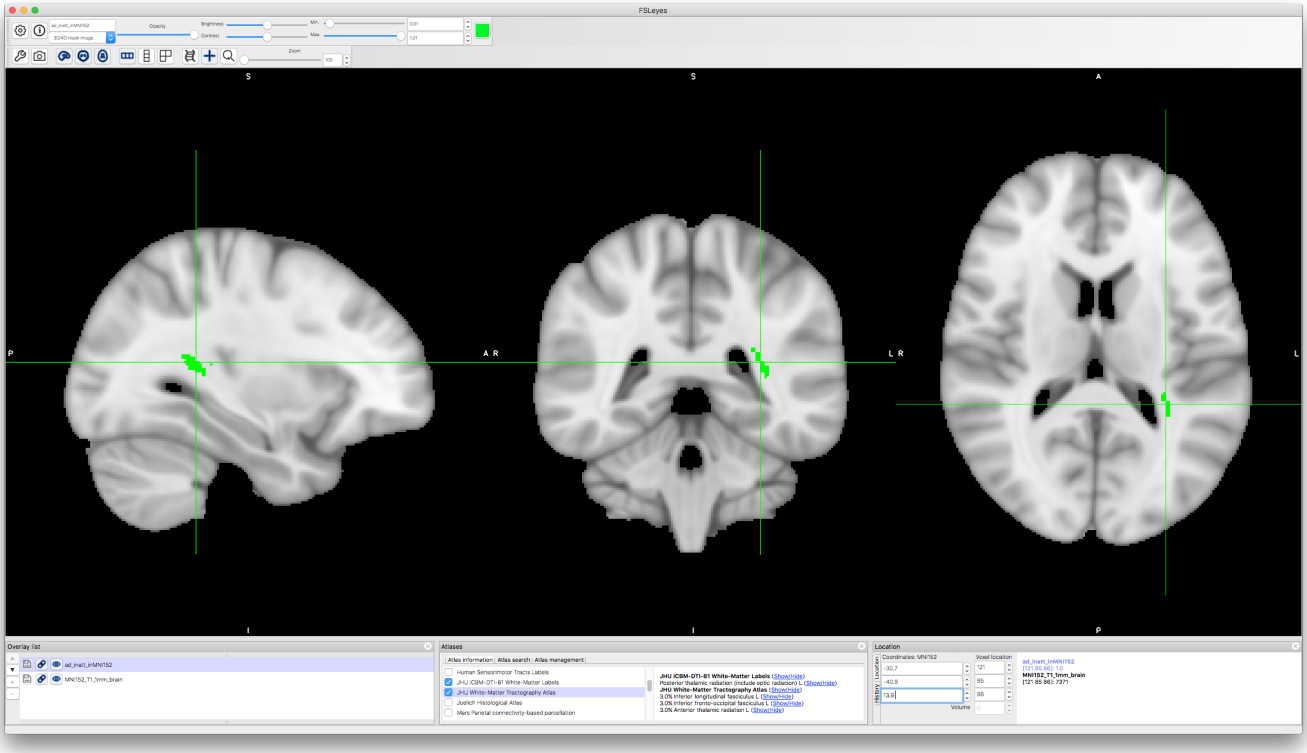
```
/usr/local/apps/fsl/6.0.0/data/standard/MNI152_T1_1mm.nii.gz -out
rd_HI_inMNI152.nii.gz -applyxfm -init ~/data/aging_to_MNI152.mat -interp
nearestneighbour

# just to get the COM for labeling
3dclust -NN1 1 -orient LPI ad_inatt_inMNI152.nii.gz
3dclust -NN1 1 -orient LPI rd_HI_inMNI152.nii.gz
```

inattention (AD):



HI (RD):



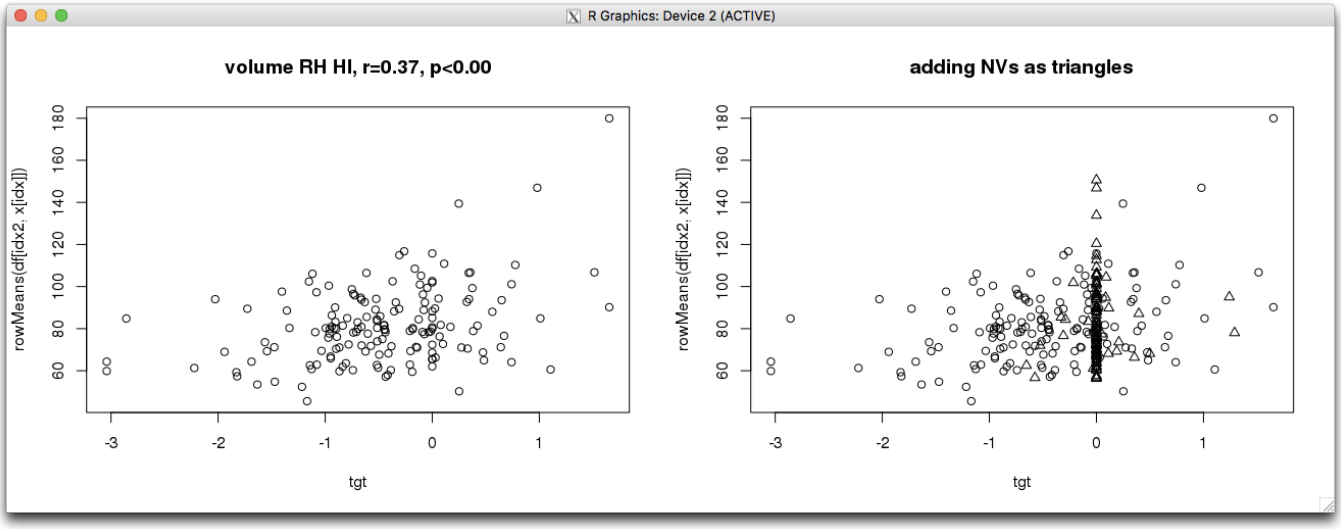
structural

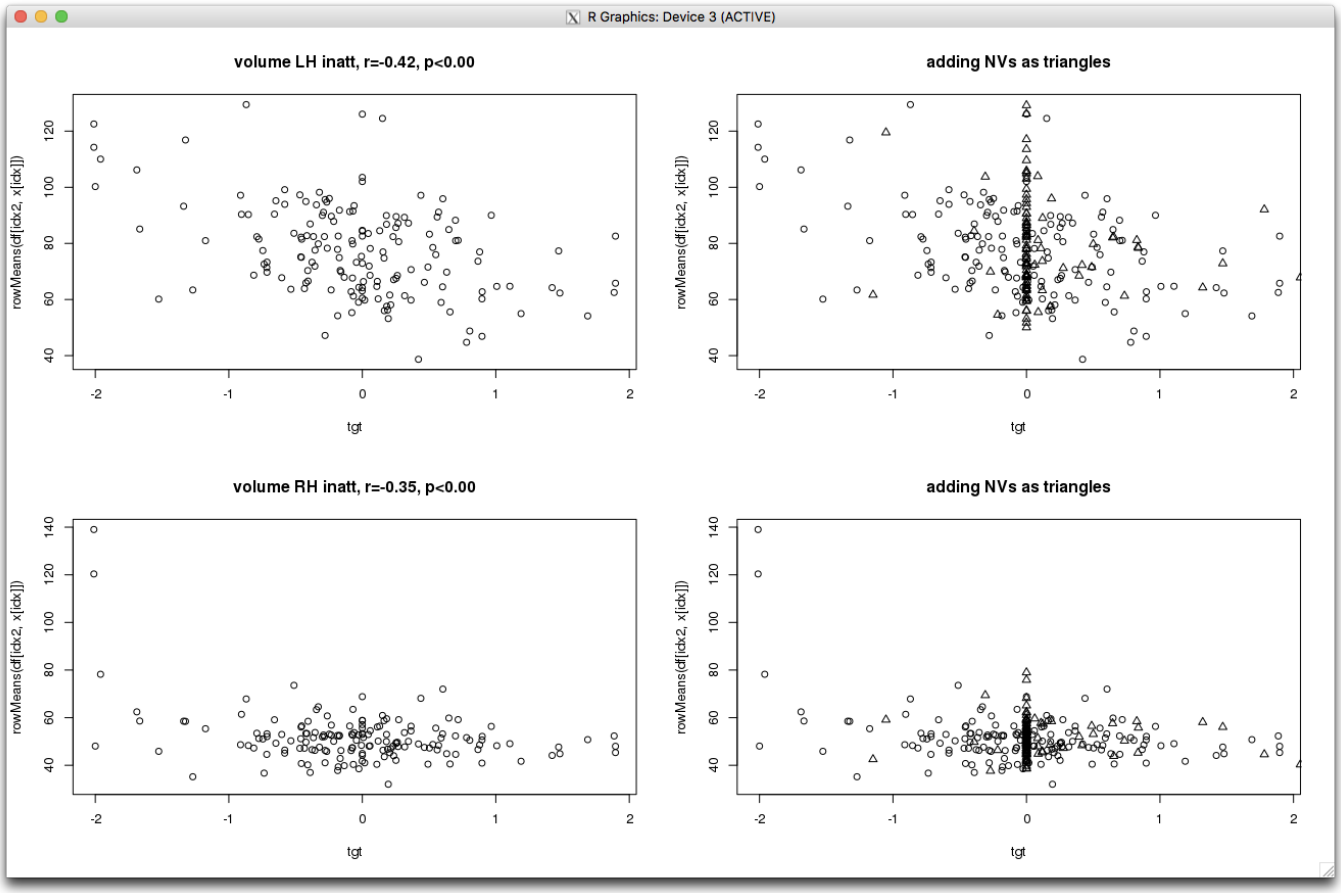
```
sudregp@HG-02070684-DM2:~/tmp$ grep -B 1 "*" pvals_NOSstruct.txt | grep
S_0 | grep None
struct_area_11142018_260timeDiff12mo (LH):
ADHDNOS_OLS_inatt_slope_winsorize_None (248 perms)
struct_thickness_11142018_260timeDiff12mo (LH):
ADHDNOS_OLS_inatt_slope_winsorize_None (249 perms)
struct_volume_11142018_260timeDiff12mo (RH):
ADHDNOS_OLS_HI_slope_winsorize_None (249 perms)
struct_volume_11142018_260timeDiff12mo (LH):
ADHDNOS_OLS_inatt_slope_winsorize_None (248 perms)
struct_volume_11142018_260timeDiff12mo (RH):
ADHDNOS_OLS_inatt_slope_winsorize_None (248 perms)
```

The None results were stronger overall. Like before, we focus on volume. So, we do:

```
awk 'NR>=13 && NR<2575'
/data/NCR_SBRB/tmp/struct_volume_11142018_260timeDiff12mo/ADHDNOS_OLS_HI_s
lope_winsorize_None_42_rh_ClstMsk_e1_a1.0.niml.dset > vol_HI_rh.txt
awk 'NR>=13 && NR<2575'
/data/NCR_SBRB/tmp/struct_volume_11142018_260timeDiff12mo/ADHDNOS_OLS_inat
t_slope_winsorize_None_42_lh_ClstMsk_e1_a1.0.niml.dset > vol_inatt_lh.txt
awk 'NR>=13 && NR<2575'
/data/NCR_SBRB/tmp/struct_volume_11142018_260timeDiff12mo/ADHDNOS_OLS_inat
t_slope_winsorize_None_42_rh_ClstMsk_e1_a1.0.niml.dset > vol_inatt_rh.txt
```

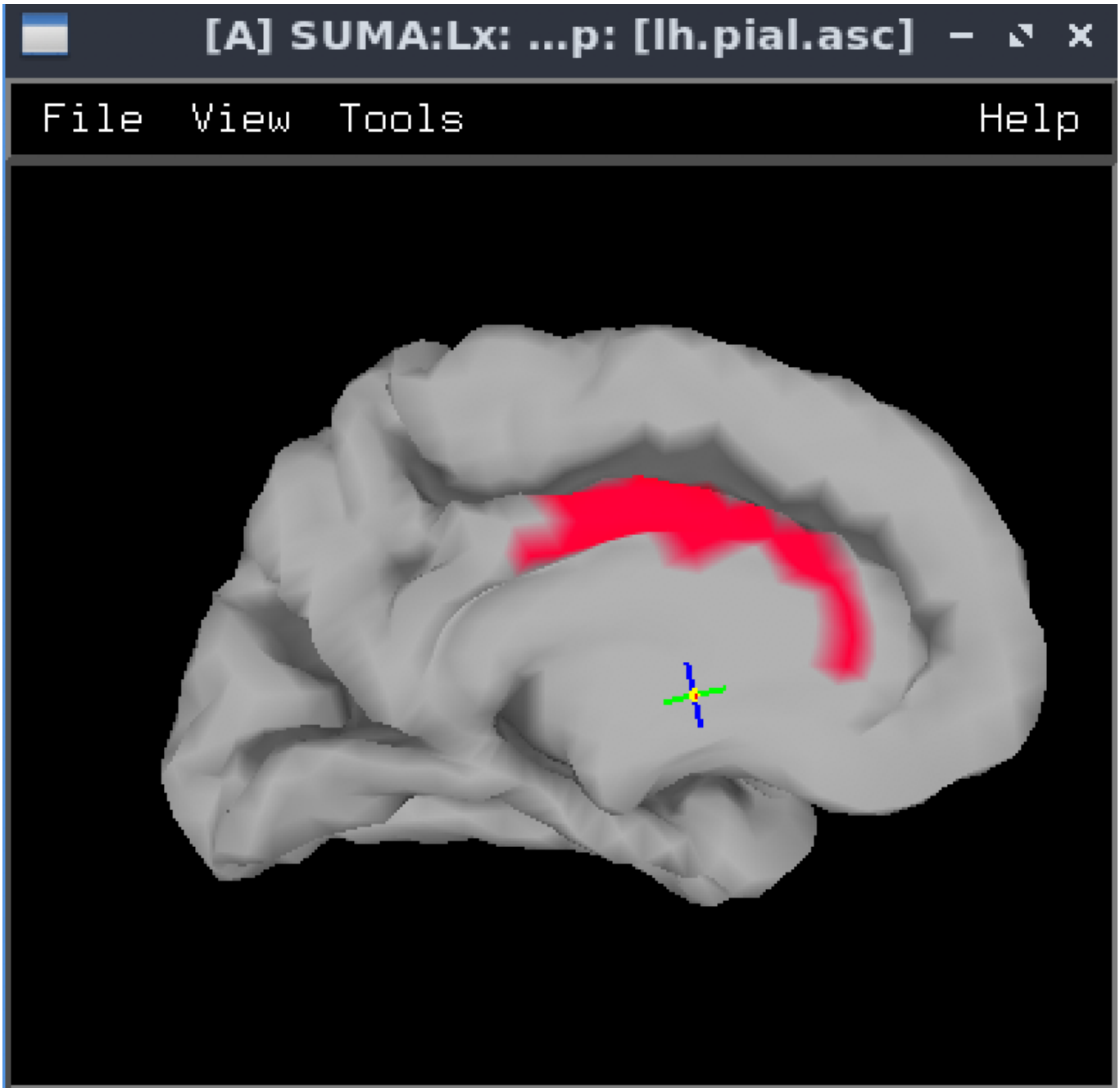
```
winsorize = function(x, cut = 0.01){
  cut_point_top <- quantile(x, 1 - cut, na.rm = T)
  cut_point_bottom <- quantile(x, cut, na.rm = T)
  i = which(x >= cut_point_top)
  x[i] = cut_point_top
  j = which(x <= cut_point_bottom)
  x[j] = cut_point_bottom
  return(x)
}
clin =
read.csv('/data/NCR_SBRB/baseline_prediction/long_clin_11302018.csv')
load('/data/NCR_SBRB/baseline_prediction/struct_volume_11142018_260timeDif
f12mo.RData.gz')
df = merge(clin, data, by='MRN')
x = colnames(df)[grepl(pattern = '^v_rh', colnames(df))]
a = read.table('~/tmp/vol_HI_rh.txt')[,1]
idx = which(a==1)
idx2 = df$DX != 'NV'
tgt = winsorize(df[idx2,]$OLS_HI_slope)
par(mfrow=c(1,2))
plot(tgt, rowMeans(df[idx2, x[idx]]))
b = cor.test(tgt, rowMeans(df[idx2, x[idx]]))
title(sprintf('volume RH HI, r=%.2f, p<%.2f', b$estimate, b$p.value))
plot(tgt, rowMeans(df[idx2, x[idx]]))
idx3 = df$DX == 'NV'
points(df[idx3,]$OLS_HI_slope, rowMeans(df[idx3, x[idx]]), pch=2)
title('adding NVs as triangles')
dev.new()
x = colnames(df)[grepl(pattern = '^v_lh', colnames(df))]
a = read.table('~/tmp/vol_inatt_lh.txt')[,1]
idx = which(a==1)
idx2 = df$DX != 'NV'
tgt = winsorize(df[idx2,]$OLS_inatt_slope)
par(mfrow=c(2,2))
plot(tgt, rowMeans(df[idx2, x[idx]]))
b = cor.test(tgt, rowMeans(df[idx2, x[idx]]))
title(sprintf('volume LH inatt, r=%.2f, p<%.2f', b$estimate, b$p.value))
plot(tgt, rowMeans(df[idx2, x[idx]]))
idx3 = df$DX == 'NV'
points(df[idx3,]$OLS_inatt_slope, rowMeans(df[idx3, x[idx]]), pch=2)
title('adding NVs as triangles')
x = colnames(df)[grepl(pattern = '^v_rh', colnames(df))]
a = read.table('~/tmp/vol_inatt_rh.txt')[,1]
idx = which(a==1)
plot(tgt, rowMeans(df[idx2, x[idx]]))
b = cor.test(tgt, rowMeans(df[idx2, x[idx]]))
title(sprintf('volume RH inatt, r=%.2f, p<%.2f', b$estimate, b$p.value))
plot(tgt, rowMeans(df[idx2, x[idx]]))
idx3 = df$DX == 'NV'
points(df[idx3,]$OLS_inatt_slope, rowMeans(df[idx3, x[idx]]), pch=2)
title('adding NVs as triangles')
```

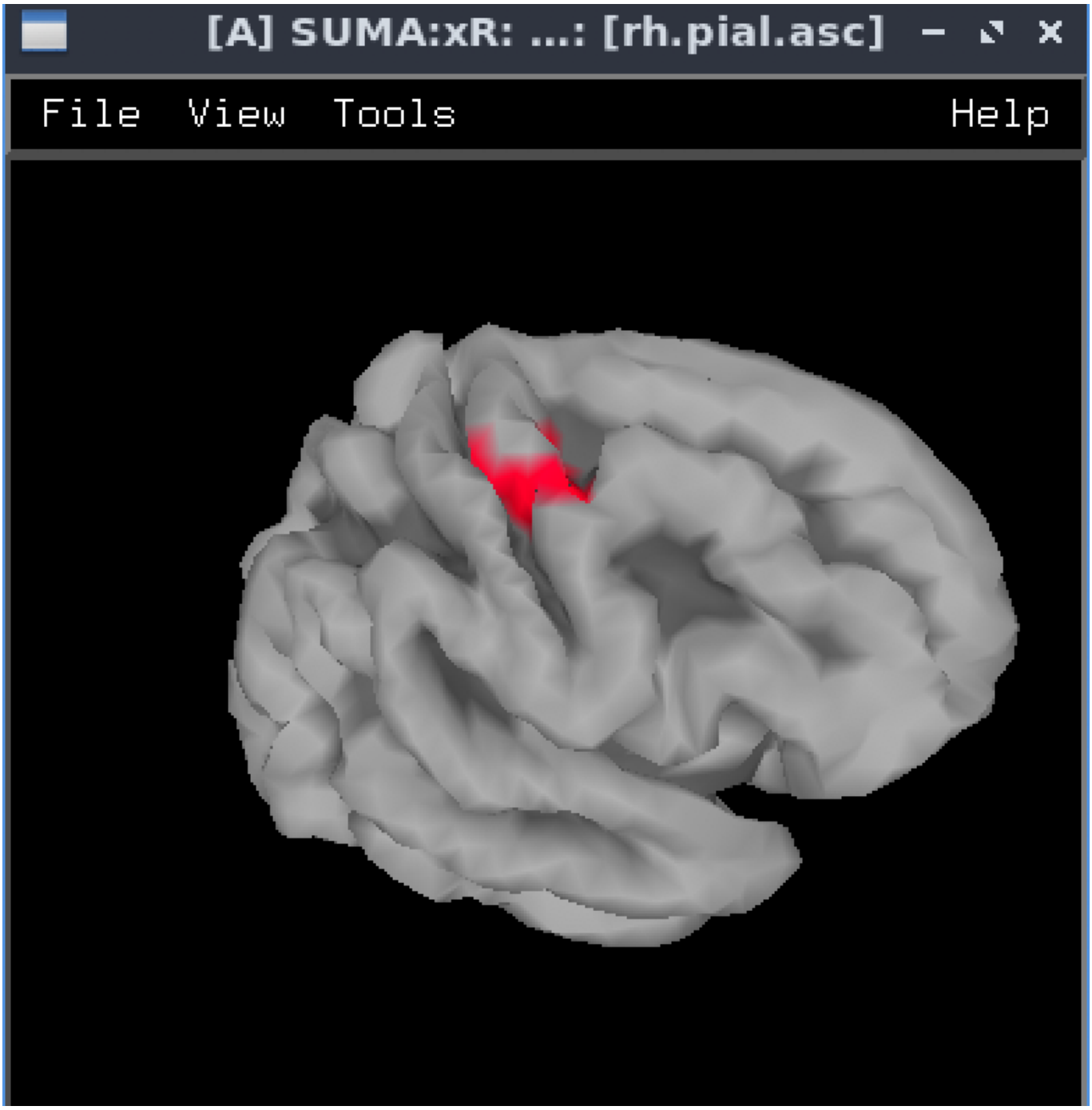




The RH inatt result is clearly driven by outliers, so let's not go through with it.

```
awk '{ if ($1 != 1 ) print 0; else print 1 }' ~/tmp/vol_HI_rh.txt >
rh_HI.txt
awk '{ if ($1 != 1 ) print 0; else print 1 }' ~/tmp/vol_inatt_lh.txt >
lh_inatt.txt
suma -i_fs
/Volumes/Shaw/freesurfer5.3_subjects/fsaverage4/SUMA/lh.pial.asc
```


[A] SUMA:Lx: ...p: [lh.pial.asc]
File View Tools Help



MELODIC

```
sudregp@HG-02070684-DM2:~/tmp$ grep -B 1 "*" pvals_NOSmelodic.txt | grep
1214 | grep S_O | grep subjS
melodic_fancy_IC24_12142018: ADHDNOS_OLS_inatt_slope_winsorize_subjScale
(250 perms)
melodic_fancy_IC37_12142018: ADHDNOS_OLS_inatt_slope_winsorize_subjScale
(248 perms)
melodic_fancy_IC54_12142018: ADHDNOS_OLS_inatt_slope_winsorize_subjScale
(250 perms)
melodic_inter_IC31_12142018: ADHDNOS_OLS_inatt_slope_winsorize_subjScale
(250 perms)
```

The subjScale results were stronger overall. Now I'm getting 3 networks with the fancy mask: 24 (somatomotor), 37 (visual), and 54 (limbic). Not great... The None results also didn't have any DMN in it. The only way to get it is excluding new_onset...

TODO

- plot resting state/melodic results even though they're in crappy networks?