2018-10-19 11:23:28

Now that we have a bit better testing framework, let's repeat the within-modality assessment of datasets and see which ones fare best.

DTI

```
job_name=withinDTI_DL;
mydir=/data/NCR_SBRB/baseline_prediction/;
swarm_file=swarm.automl_${job_name};
rm -rf $swarm_file;
for f in dti_ALL_voxelwise_n223_09212018.RData.gz
dti_ALL_voxelwise_n272_09212018.RData.gz \
    dti_fa_voxelwise_n223_09212018.RData.gz
dti_fa_voxelwise_n272_09212018.RData.gz \
    dti_ad_voxelwise_n223_09212018.RData.gz
dti_ad_voxelwise_n272_09212018.RData.gz \
    dti_rd_voxelwise_n223_09212018.RData.gz
dti_rd_voxelwise_n272_09212018.RData.gz \
    dti_tracts_n223_10042018.RData.gz dti_tracts_n272_10042018.RData.gz;
do
    for target in nvVSper nvVSrem perVSrem nvVSadhd; do
        for i in {1..100}; do
            echo "Rscript --vanilla
~/research_code/automl/uni_test_autoValidation_DL.R ${mydir}/$f
${mydir}/long_clin_0918.csv ${target} ${mydir}/models_within_DL/${USER}
$RANDOM" >> $swarm_file;
        done;
    done;
done
sed -i -e "s/^/unset http_proxy; /g" $swarm_file;
split -l 1000 $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 $f -g 60 -t 16 --time 3:00:00 --partition norm --logdir
trash_${job_name} --job-name ${job_name} -m R --gres=lscratch:10 2>
swarm_wait_${USER};
        if grep -q ERROR swarm_wait_${USER}; then
            echo -e "\tError, sleeping..."
            sleep 10m;
        fi;
    done;
done
```

Structural

```
job_name=withinStruct_DL;
mydir=/data/NCR_SBRB/baseline_prediction/;
swarm_file=swarm.automl_${job_name};
rm -rf $swarm_file;
for f in struct_thickness_09192018_260timeDiff12mo.RData.gz \
    struct_area_09192018_260timeDiff12mo.RData.gz \
    struct_volume_09192018_260timeDiff12mo.RData.gz \
    struct_rois_09192018_260timeDiff12mo.RData.gz;  do
    for target in nvVSper nvVSrem perVSrem nvVSadhd; do
        for i in {1..100}; do
            echo "Rscript --vanilla
~/research_code/automl/uni_test_autoValidation_DL.R ${mydir}/$f
${mydir}/long_clin_0918.csv ${target} ${mydir}/models_within_DL/${USER}
$RANDOM" >> $swarm_file;
        done;
    done;
done
sed -i -e "s/^/unset http_proxy; /g" $swarm_file;
split -l 1000 $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 $f -g 60 -t 16 --time 3:00:00 --partition norm --logdir
trash_${job_name} --job-name ${job_name} -m R --gres=lscratch:10 2>
swarm_wait_${USER};
        if grep -q ERROR swarm_wait_${USER}; then
            echo -e "\tError, sleeping..."
            sleep 10m;
        fi;
    done;
done
```

rsFMRI

```
job_name=withinResting_DL;
mydir=/data/NCR_SBRB/baseline_prediction/;
swarm_file=swarm.automl_${job_name};
rm -rf $swarm_file;
for f in aparc.a2009s_n215_09182018.RData.gz \
    aparc.a2009s_trimmed_n215_09182018.RData.gz \
    aparc_n215_09182018.RData.gz \
    aparc_trimmed__n215_09182018.RData.gz;  do
    for target in nvVSper nvVSrem perVSrem nvVSadhd; do
        for i in {1..100}; do
            echo "Rscript --vanilla
~/research_code/automl/uni_test_autoValidation_DL.R ${mydir}/$f
${mydir}/long_clin_0918.csv ${target} ${mydir}/models_within_DL/${USER}
$RANDOM" >> $swarm_file;
        done;
    done;
done
sed -i -e "s/^/unset http_proxy; /g" $swarm_file;
split -l 1000 $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 $f -g 60 -t 16 --time 3:00:00 --partition norm --logdir trash_${job_name} --job-name ${job_name} -m R --gres=lscratch:10 2> swarm_wait_${USER};
        if grep -q ERROR swarm_wait_${USER}; then
            echo -e "\tError, sleeping..."
            sleep 10m;
        fi;
    done;
done
```

genetics

```
job_name=withinSNPs_DL;
mydir=/data/NCR_SBRB/baseline_prediction/;
swarm_file=swarm.automl_${job_name};
rm -rf $swarm_file;
for f in geno3_snps1e04_09192018.RData.gz geno3_snps1e05_09192018.RData.gz \
    geno3_snps1e05_09192018.RData.gz geno3_snps1e07_09192018.RData.gz \
    geno3_prs_09192018.RData.gz;  do
    for target in nvVSper nvVSrem perVSrem nvVSadhd; do
        for i in {1..100}; do
            echo "Rscript --vanilla ~/research_code/automl/uni_test_autoValidation_DL.R ${mydir}/$f ${mydir}/long_clin_0918.csv ${target} ${mydir}/models_within_DL/${USER} $RANDOM" >> $swarm_file;
        done;
    done;
done
sed -i -e "s/^/unset http_proxy; /g" $swarm_file;
split -l 1000 $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 $f -g 60 -t 16 --time 3:00:00 --partition norm --logdir trash_${job_name} --job-name ${job_name} -m R --gres=lscratch:10 2> swarm_wait_${USER};
        if grep -q ERROR swarm_wait_${USER}; then
            echo -e "\tError, sleeping..."
            sleep 10m;
        fi;
    done;
done
```

2018-10-22 09:23:25

And now we need to grab the results:

```
echo "target,pheno,var,seed,nfeat,model,auc,f1,acc,spec,sens,prec,ratio" > withinDomainAutoframeDL_summary.csv;
for dir in DTI_DL Resting_DL SNPs_DL Struct_DL; do
    echo $dir
    for f in `ls trash_within${dir}/*o`; do
        phen=`head -n 2 $f | tail -1 | awk '{FS=" "; print $7}' | cut -d"/" -f 5`;
        target=`head -n 2 $f | tail -1 | awk '{FS=" "; print $8}'`;
        seed=`head -n 2 $f | tail -1 | awk '{FS=" "; print $10}'`;
        var=`head -n 2 $f | tail -1 | awk '{FS=" "; print $5}' | cut -d"/" -f 4 | sed -e "s/\.R//g"`;
        model=`grep -A 1 model_id $f | tail -1 | awk '{FS=" "; print $2}' | cut -d"_" -f 1`;
        auc=`grep -A 1 model_id $f | tail -1 | awk '{FS=" "; print $3}'`;
        nfeat=`grep "Running model on" $f | awk '{FS=" "; print $5}'`;
        ratio=`grep -A 1 "Class distribution" $f | tail -1 | awk '{FS=" "; {for (i=2; i<=NF; i++) printf $i ";"}}'`;
        f1=`grep -A 2 "Maximum Metrics:" $f | tail -1 | awk '{FS=" "; print $5}'`;
        acc=`grep -A 5 "Maximum Metrics:" $f | tail -1 | awk '{FS=" "; print $5}'`;
        spec=`grep -A 8 "Maximum Metrics:" $f | tail -1 | awk '{FS=" "; print $5}'`;
        sens=`grep -A 7 "Maximum Metrics:" $f | tail -1 | awk '{FS=" "; print $5}'`;
        prec=`grep -A 6 "Maximum Metrics:" $f | tail -1 | awk '{FS=" "; print $5}'`
        echo $target,$phen,$var,$seed,$nfeat,$model,$auc,$f1,$acc,$spec,$sens,$prec,$ratio >> withinDomainAutoframeDL_summary.csv;
    done;
done
```

2018-10-25 11:50:35

Now that I know things are not doing so hot for PCA compared to raw, and while I play with ICA and AE on the side, let's check what's really the best phenotype within modality using raw, so that we can start to combine them and see if anything comes up that way.

```
job_name=withinDTI_rawDL;
mydir=/data/NCR_SBRB/baseline_prediction/;
swarm_file=swarm.automl_${job_name};
rm -rf $swarm_file;
for f in dti_ALL_voxelwise_n223_09212018.RData.gz
dti_ALL_voxelwise_n272_09212018.RData.gz \
    dti_fa_voxelwise_n223_09212018.RData.gz
dti_fa_voxelwise_n272_09212018.RData.gz \
    dti_ad_voxelwise_n223_09212018.RData.gz
dti_ad_voxelwise_n272_09212018.RData.gz \
    dti_rd_voxelwise_n223_09212018.RData.gz
dti_rd_voxelwise_n272_09212018.RData.gz \
    dti_tracts_n223_10042018.RData.gz dti_tracts_n272_10042018.RData.gz;
do
    for target in nvVSper nvVSrem perVSrem nvVSadhd; do
        for i in {1..100}; do
            echo "Rscript --vanilla
~/research_code/automl/raw_autoValidation_DL.R ${mydir}/$f
${mydir}/long_clin_0918.csv ${target}
${mydir}/models_raw_within_DL/${USER} $RANDOM" >> $swarm_file;
        done;
    done;
done
for f in dti_ALL_voxelwise_n223_09212018.RData.gz
dti_ALL_voxelwise_n272_09212018.RData.gz \
    dti_rd_voxelwise_n223_09212018.RData.gz
dti_rd_voxelwise_n272_09212018.RData.gz \
    dti_tracts_n223_10042018.RData.gz dti_tracts_n272_10042018.RData.gz;
do
    for target in nvVSper nvVSrem perVSrem nvVSadhd; do
        for i in {1..100}; do
            echo "Rscript --vanilla
~/research_code/automl/raw_autoValidation_DL.R ${mydir}/$f
${mydir}/long_clin_0918.csv ${target}
${mydir}/models_raw_within_DL/${USER} -$RANDOM" >> $swarm_file;
        done;
    done;
done
sed -i -e "s/^/unset http_proxy; /g" $swarm_file;
split -l 1000 $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 $f -g 60 -t 16 --time 3:00:00 --partition norm --logdir
trash_${job_name} --job-name ${job_name} -m R --gres=lscratch:10 2>
swarm_wait_${USER};
        if grep -q ERROR swarm_wait_${USER}; then
            echo -e "\tError, sleeping..."
            sleep 10m;
        fi;
    done;
done
```

```
job_name=withinStruct_rawDL;
mydir=/data/NCR_SBRB/baseline_prediction/;
swarm_file=swarm.automl_${job_name};
rm -rf $swarm_file;
for f in struct_thickness_09192018_260timeDiff12mo.RData.gz \
    struct_area_09192018_260timeDiff12mo.RData.gz \
    struct_volume_09192018_260timeDiff12mo.RData.gz \
    struct_rois_09192018_260timeDiff12mo.RData.gz; do
    for target in nvVSper nvVSrem perVSrem nvVSadhd; do
        for i in {1..100}; do
            echo "Rscript --vanilla
~/research_code/automl/raw_autoValidation_DL.R ${mydir}/$f
${mydir}/long_clin_0918.csv ${target}
${mydir}/models_raw_within_DL/${USER} $RANDOM" >> $swarm_file;
        done;
    done;
done
for f in struct_volume_09192018_260timeDiff12mo.RData.gz \
    struct_rois_09192018_260timeDiff12mo.RData.gz018.RData.gz; do
    for target in nvVSper nvVSrem perVSrem nvVSadhd; do
        for i in {1..100}; do
            echo "Rscript --vanilla
~/research_code/automl/raw_autoValidation_DL.R ${mydir}/$f
${mydir}/long_clin_0918.csv ${target}
${mydir}/models_raw_within_DL/${USER} -$RANDOM" >> $swarm_file;
        done;
    done;
done
sed -i -e "s/^/unset http_proxy; /g" $swarm_file;
split -l 1000 $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 $f -g 60 -t 16 --time 3:00:00 --partition norm --logdir
trash_${job_name} --job-name ${job_name} -m R --gres=lscratch:10 2>
swarm_wait_${USER};
        if grep -q ERROR swarm_wait_${USER}; then
            echo -e "\tError, sleeping..."
            sleep 10m;
        fi;
    done;
done
```

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

```
for f in aparc.a2009s_n215_10252018.RData.gz \
    aparc.a2009s_trimmed_n215_10252018.RData.gz \
    aparc_n215_10252018.RData.gz \
    aparc_trimmed_n215_10252018.RData.gz; do
    for target in nvVSper nvVSrem perVSrem nvVSadhd; do
        for i in {1..100}; do
            echo "Rscript --vanilla
~/research_code/automl/raw_autoValidation_DL.R ${mydir}/$f
${mydir}/long_clin_0918.csv ${target}
${mydir}/models_raw_within_DL/${USER} $RANDOM" >> $swarm_file;
        done;
    done;
done
for f in aparc.a2009s_n215_10252018.RData.gz aparc_n215_10252018.RData.gz;
do
    for target in nvVSper nvVSrem perVSrem nvVSadhd; do
        for i in {1..100}; do
            echo "Rscript --vanilla
~/research_code/automl/raw_autoValidation_DL.R ${mydir}/$f
${mydir}/long_clin_0918.csv ${target}
${mydir}/models_raw_within_DL/${USER} -$RANDOM" >> $swarm_file;
        done;
    done;
done
sed -i -e "s/^/unset http_proxy; /g" $swarm_file;
split -l 1000 $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 $f -g 60 -t 16 --time 3:00:00 --partition norm --logdir
trash_${job_name} --job-name ${job_name} -m R --gres=lscratch:10 2>
swarm_wait_${USER};
        if grep -q ERROR swarm_wait_${USER}; then
            echo -e "\tError, sleeping..."
            sleep 10m;
        fi;
    done;
done
```

```
job_name=withinSNP_rawDL;
mydir=/data/NCR_SBRB/baseline_prediction/;
swarm_file=swarm.automl_${job_name};
rm -rf $swarm_file;
for f in geno3_snps1e04_09192018.RData.gz geno3_snps1e05_09192018.RData.gz
\
    geno3_snps1e05_09192018.RData.gz geno3_snps1e07_09192018.RData.gz \
    geno3_snps1e08_09192018.RData.gz geno3_snps1e09_09192018.RData.gz \
    geno3_prs_09192018.RData.gz; do
    for target in nvVSper nvVSrem perVSrem nvVSadhd; do
        for i in {1..100}; do
```

```
            echo "Rscript --vanilla
~/research_code/automl/raw_autoValidation_DL.R ${mydir}/$f
${mydir}/long_clin_0918.csv ${target}
${mydir}/models_raw_within_DL/${USER} $RANDOM" >> $swarm_file;
        done;
    done;
done
for f in geno3_snps1e04_09192018.RData.gz geno3_snps1e05_09192018.RData.gz
\
    geno3_snps1e05_09192018.RData.gz geno3_snps1e07_09192018.RData.gz \
    geno3_snps1e08_09192018.RData.gz geno3_snps1e09_09192018.RData.gz \
    geno3_prs_09192018.RData.gz; do
    for target in nvVSper nvVSrem perVSrem nvVSadhd; do
        for i in {1..100}; do
            echo "Rscript --vanilla
~/research_code/automl/raw_autoValidation_DL.R ${mydir}/$f
${mydir}/long_clin_0918.csv ${target}
${mydir}/models_raw_within_DL/${USER} -$RANDOM" >> $swarm_file;
        done;
    done;
done
sed -i -e "s/^/unset http_proxy; /g" $swarm_file;
split -l 1000 $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 $f -g 60 -t 16 --time 3:00:00 --partition norm --logdir
trash_${job_name} --job-name ${job_name} -m R --gres=lscratch:10 2>
swarm_wait_${USER};
        if grep -q ERROR swarm_wait_${USER}; then
            echo -e "\tError, sleeping..."
            sleep 10m;
        fi;
    done;
done
```

2018-10-26 14:50:56

DTI is the only one that is still running. So, we can go ahead and evaluate the other ones:

```

dir=withinSNP_rawDL;
echo "target,pheno,var,seed,nfeat,model,auc,f1,acc,ratio" >
${dir}_summary.csv;
for f in `ls -1 trash_${dir}/*o`; do
    phen=`head -n 2 $f | tail -1 | awk '{FS=" "; print $6}' | cut -d"/" -f
6`;
    target=`head -n 2 $f | tail -1 | awk '{FS=" "; print $8}'`;
    seed=`head -n 2 $f | tail -1 | awk '{FS=" "; print $10}'`;
    var=`head -n 2 $f | tail -1 | awk '{FS=" "; print $5}' | cut -d"/" -f
```

```
4 | sed -e "s/\.R//g"`;
    model=`grep -A 1 model_id $f | tail -1 | awk '{FS=" "; print $2}' | cut -d"_" -f 1`;
    auc=`grep -A 1 model_id $f | tail -1 | awk '{FS=" "; print $3}'`;
    nfeat=`grep "Running model on" $f | awk '{FS=" "; print $5}'`;
    ratio=`grep -A 1 "Class distribution" $f | tail -1 | awk '{FS=" "; {for (i=2; i<=NF; i++) printf $i ";"}}'`;
    f1=`grep -A 2 "Maximum Metrics:" $f | tail -1 | awk '{FS=" "; print $5}'`;
    acc=`grep -A 5 "Maximum Metrics:" $f | tail -1 | awk '{FS=" "; print $5}'`;
    echo $target,$phen,$var,$seed,$nfeat,$model,$auc,$f1,$acc,$ratio >> ${dir}_summary.csv;
done;
```

Rerunning one of the fMRI trimmed results because of a typo. Also had to re-run all struct voxelwise because we ran out of memory.

The issue with structural raw is in converting to h2o... not sure what's going on:

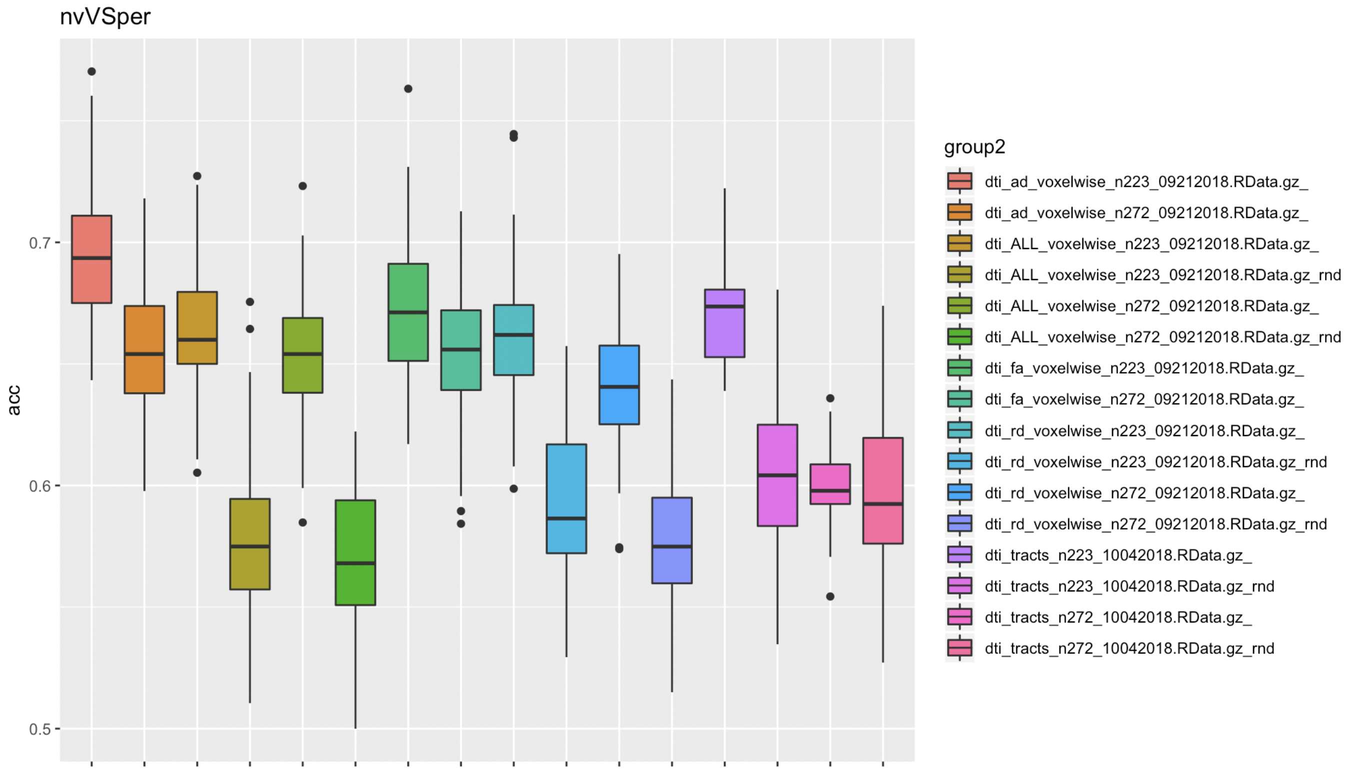
```
dtrain = as.h2o(df[, x])
Error in h2o.parseSetup(data, pattern = "", destination_frame, header,  :
  length of col.names must equal to the number of columns in dataset
```

need to look more into it...

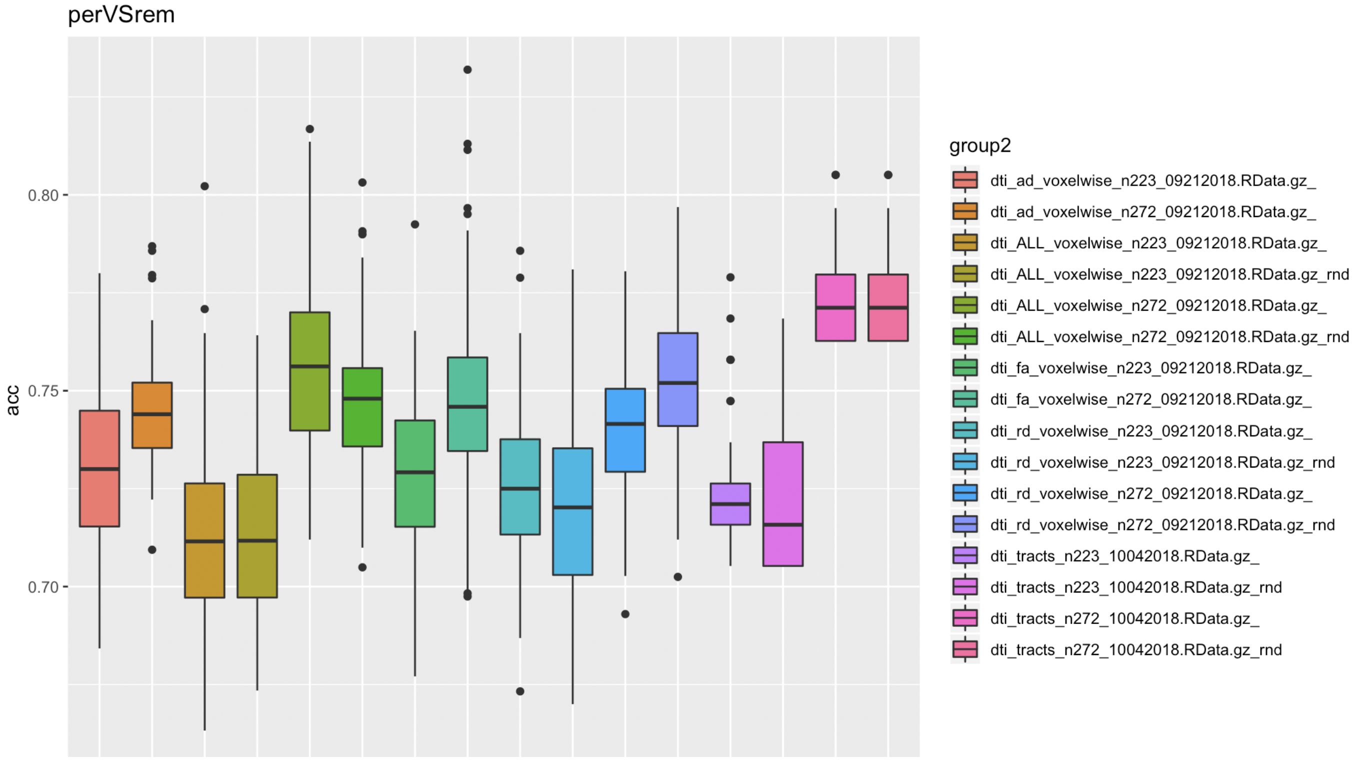
2018-10-29 10:17:03

```
for dir in withinDTI_rawDL withinResting_rawDL withinSNP_rawDL; do
    echo $dir;
    echo "target,pheno,var,seed,nfeat,model,auc,f1,acc,ratio" > ${dir}_summary.csv;
    for f in `ls -1 trash_${dir}/*o`; do
        phen=`head -n 2 $f | tail -1 | awk '{FS=" "; print $6}' | cut -d"/" -f 6`;
        target=`head -n 2 $f | tail -1 | awk '{FS=" "; print $8}'`;
        seed=`head -n 2 $f | tail -1 | awk '{FS=" "; print $10}'`;
        var=`head -n 2 $f | tail -1 | awk '{FS=" "; print $5}' | cut -d"/" -f 4 | sed -e "s/\.R//g"`;
        model=`grep -A 1 model_id $f | tail -1 | awk '{FS=" "; print $2}' | cut -d"_" -f 1`;
        auc=`grep -A 1 model_id $f | tail -1 | awk '{FS=" "; print $3}'`;
        nfeat=`grep "Running model on" $f | awk '{FS=" "; print $5}'`;
        ratio=`grep -A 1 "Class distribution" $f | tail -1 | awk '{FS=" "; {for (i=2; i<=NF; i++) printf $i ";"}}'`;
        f1=`grep -A 2 "Maximum Metrics:" $f | tail -1 | awk '{FS=" "; print $5}'`;
        acc=`grep -A 5 "Maximum Metrics:" $f | tail -1 | awk '{FS=" ";
print $5}'`;
        echo $target,$phen,$var,$seed,$nfeat,$model,$auc,$f1,$acc,$ratio
>> ${dir}_summary.csv;
    done;
done;
```

So, apparently DTI_AD_n223 is still the best, and it does perform much better tha random... the actual results is just not as exciting.



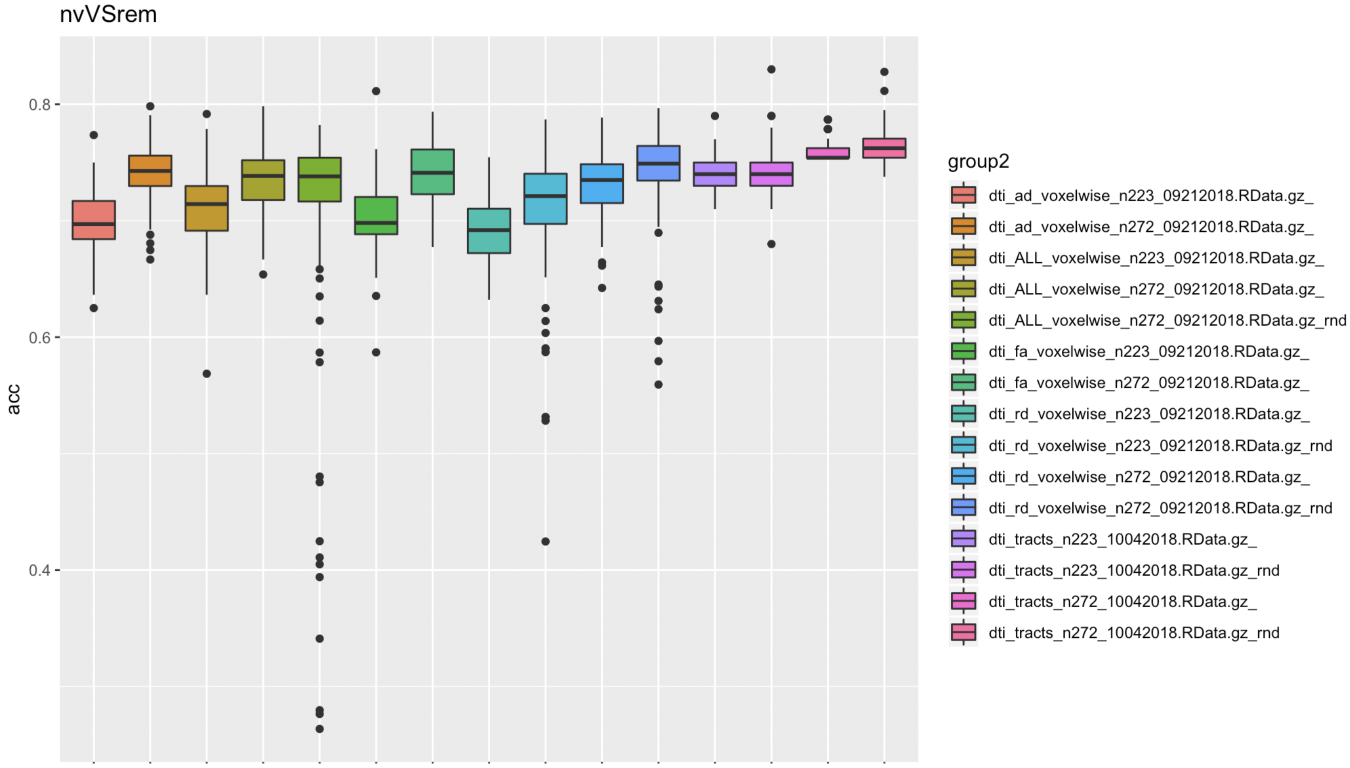
It doesn't reallt help with perVSrem though.

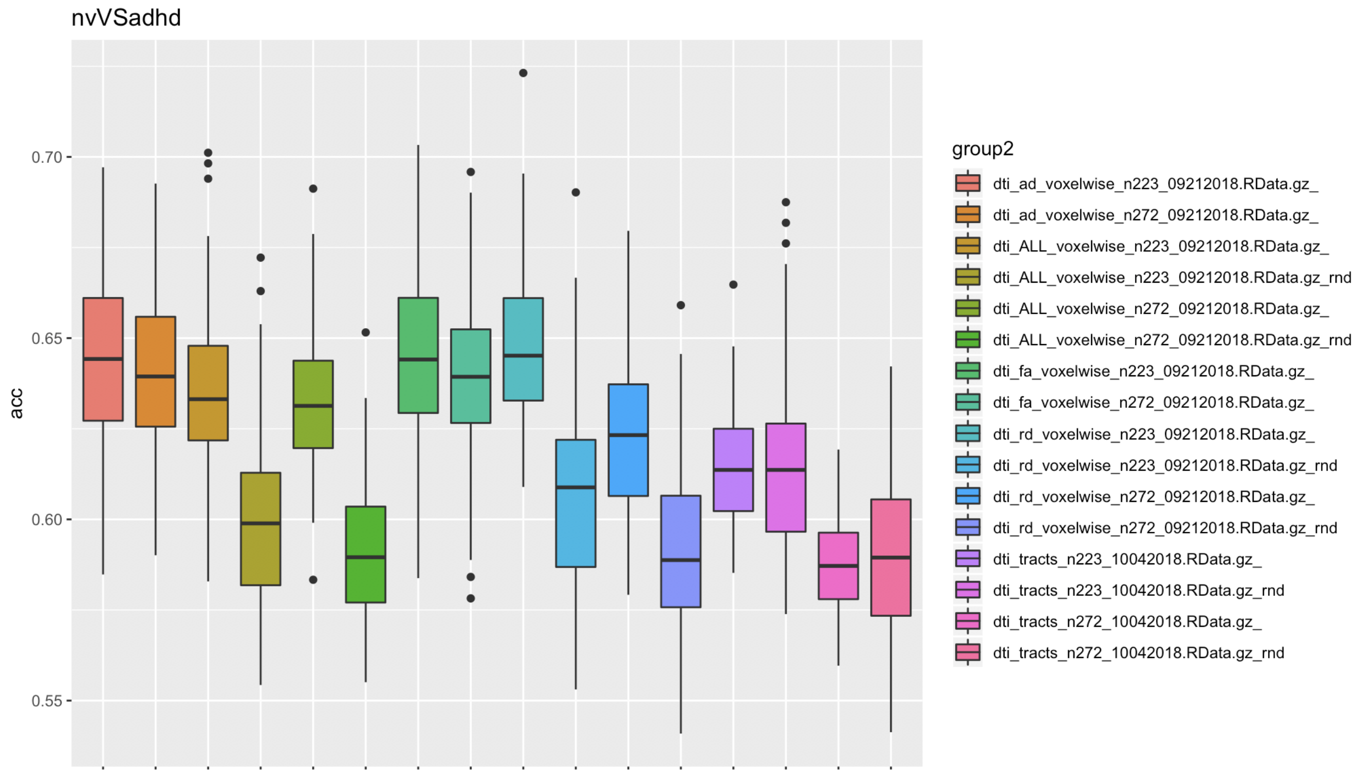


This is what I'm running to plot, btw:

```
data$group = ''
data[data$seed<0,]$group = 'rnd'
data$group2 = sapply(1:nrow(data), function(x) { sprintf('%s_%s',
data$pheno[x], data$group[x])} )
# then, for each target
target='nvVSper'
p1<-ggplot(data[data$target == target,], aes(x=group2, y=acc,
fill=group2))
print(p1+geom_boxplot() + ggtitle(target))
```

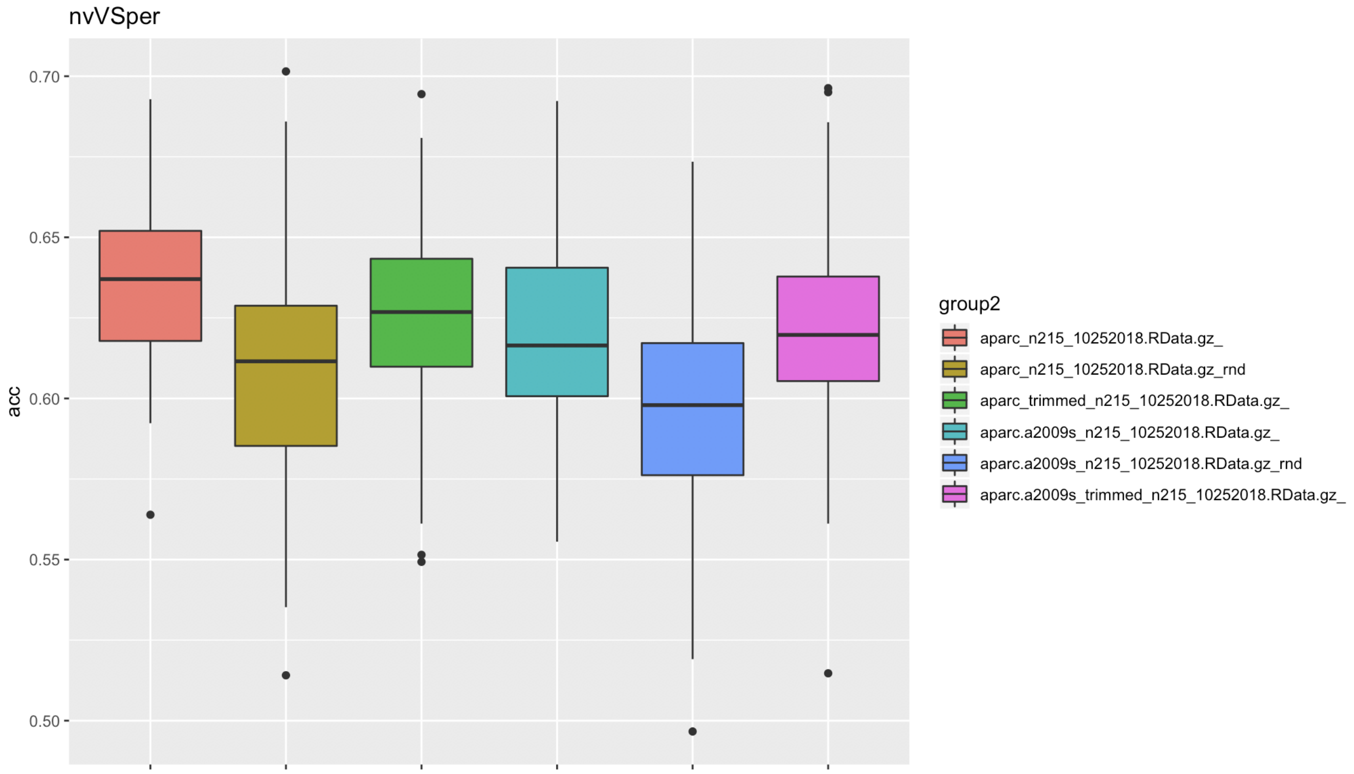
The other two plots, just for giggles:

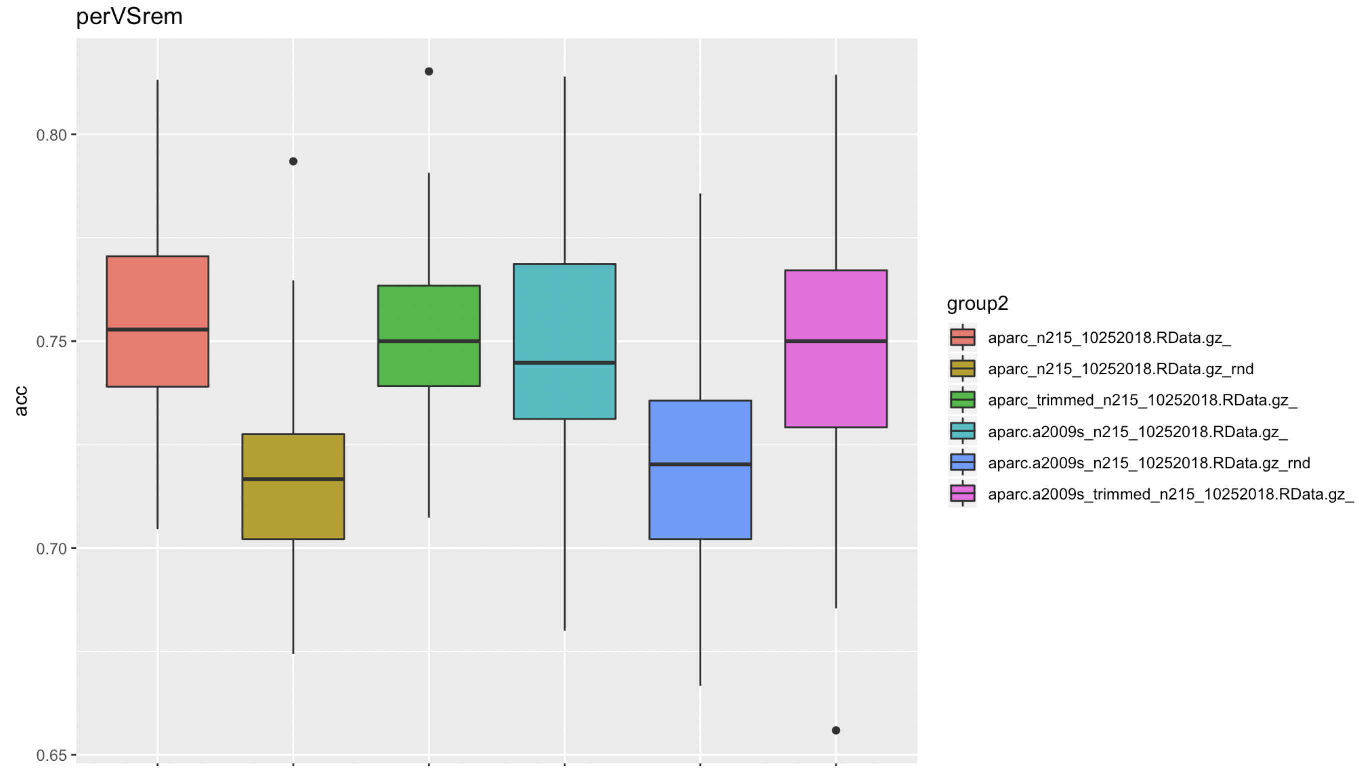




Plotting other metrics doesn't make that much difference either.

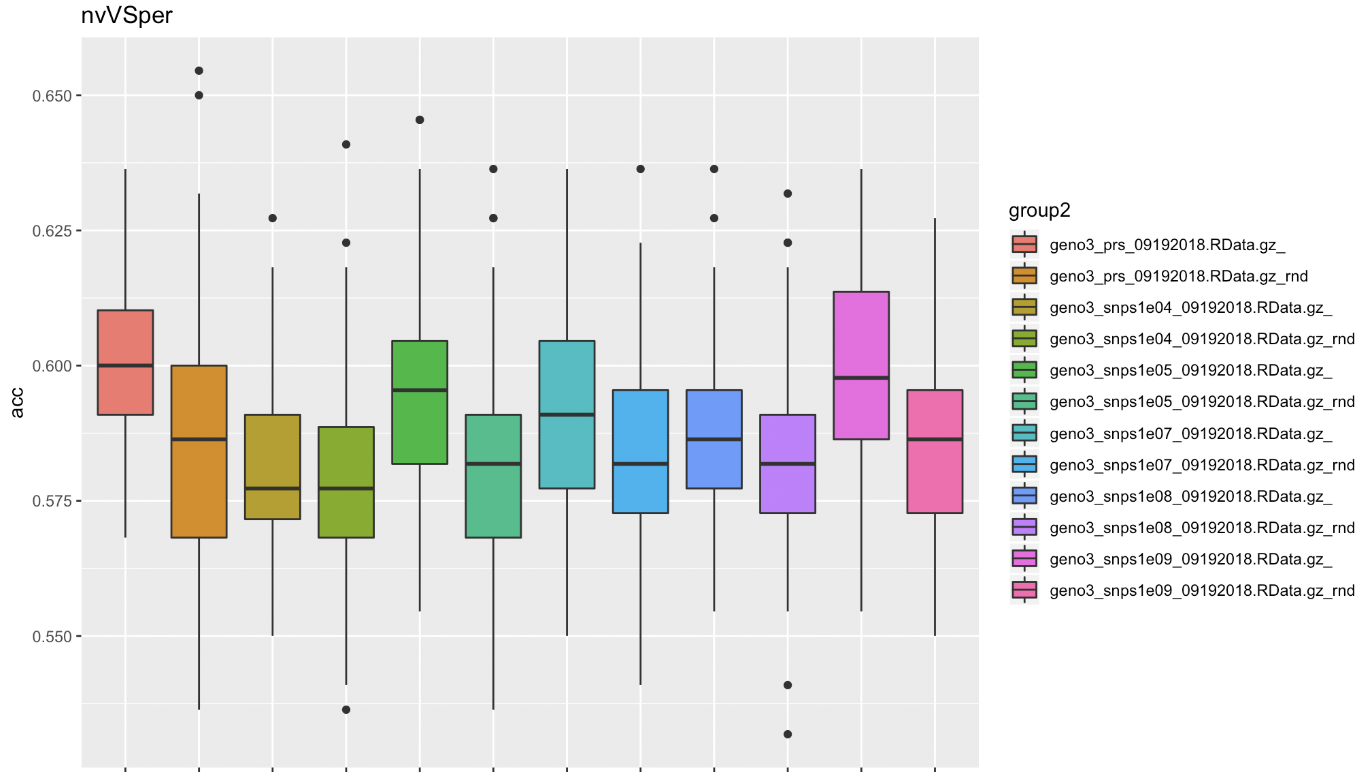
How about fMRI?

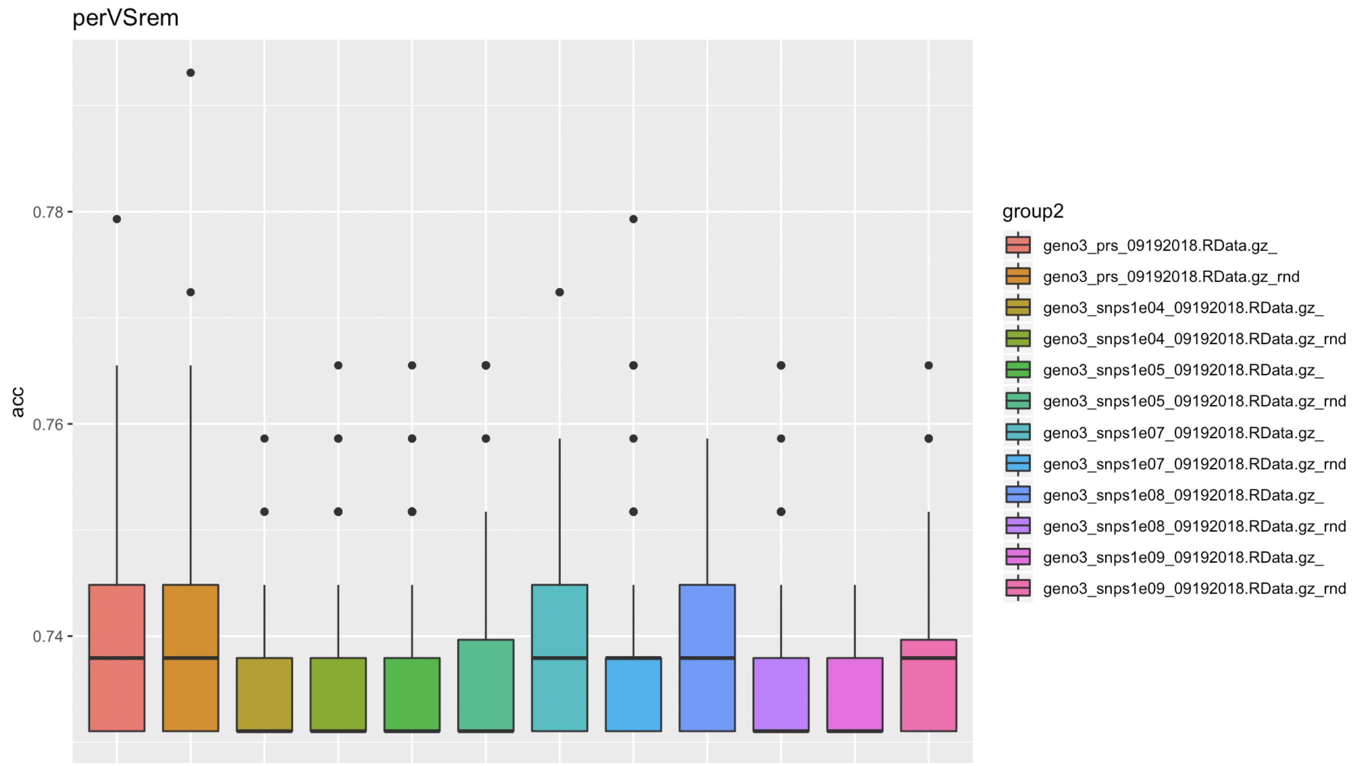




So, again, there is some signal there, a bit better than chance, but still nothing impressive.

Finally, SNPs.





As expected, barely better than chance.

BTW, it looks like it works to have the raw MR data firs tsaved to a tmp .csv and then read in with importFile. So, let's change the raw function to do that in those cases!

2018-10-30 07:54:01

I was looking at some old notes, and even if I manage to load the structural data in the raw script, it will fail during computations due to lack of memory, even in 120Gb machines. I could use a large memory node, but this might be overkill. Let's invest some time in the same space idea and see what we get.

2018-11-01 16:39:03

Going to fire up the within-domain tests using the spatial filter and test set approach, using 90-10 split. This only applies to DTI and spatial, but it's still worth trying out.

```
job_name=withinDTI_spatialTestDL;
mydir=/data/NCR_SBRB/baseline_prediction/;
swarm_file=swarm.automl_${job_name};
rm -rf $swarm_file;
for f in dti_fa_voxelwise_n223_09212018.RData.gz
dti_fa_voxelwise_n272_09212018.RData.gz \
    dti_ad_voxelwise_n223_09212018.RData.gz
dti_ad_voxelwise_n272_09212018.RData.gz \
    dti_rd_voxelwise_n223_09212018.RData.gz
dti_rd_voxelwise_n272_09212018.RData.gz; do
    for target in nvVSper nvVSrem perVSrem nvVSadhd; do
        for i in {1..100}; do
```

```
            echo "Rscript --vanilla
~/research_code/automl/uni_spatial_test_autoValidation_DL.R ${mydir}/$f
${mydir}/long_clin_0918.csv ${target}
${mydir}/models_spatial_within_DL/${USER} $RANDOM 8" >> $swarm_file;
        done;
    done;
done
sed -i -e "s/^/unset http_proxy; /g" $swarm_file;
split -l 1000 $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 $f -g 40 -t 16 --time 3:00:00 --partition norm --logdir
trash_${job_name} --job-name ${job_name} -m R,afni --gres=lscratch:10 2>
swarm_wait_${USER};
        if grep -q ERROR swarm_wait_${USER}; then
            echo -e "\tError, sleeping..."
            sleep 10m;
        fi;
    done;
done
```

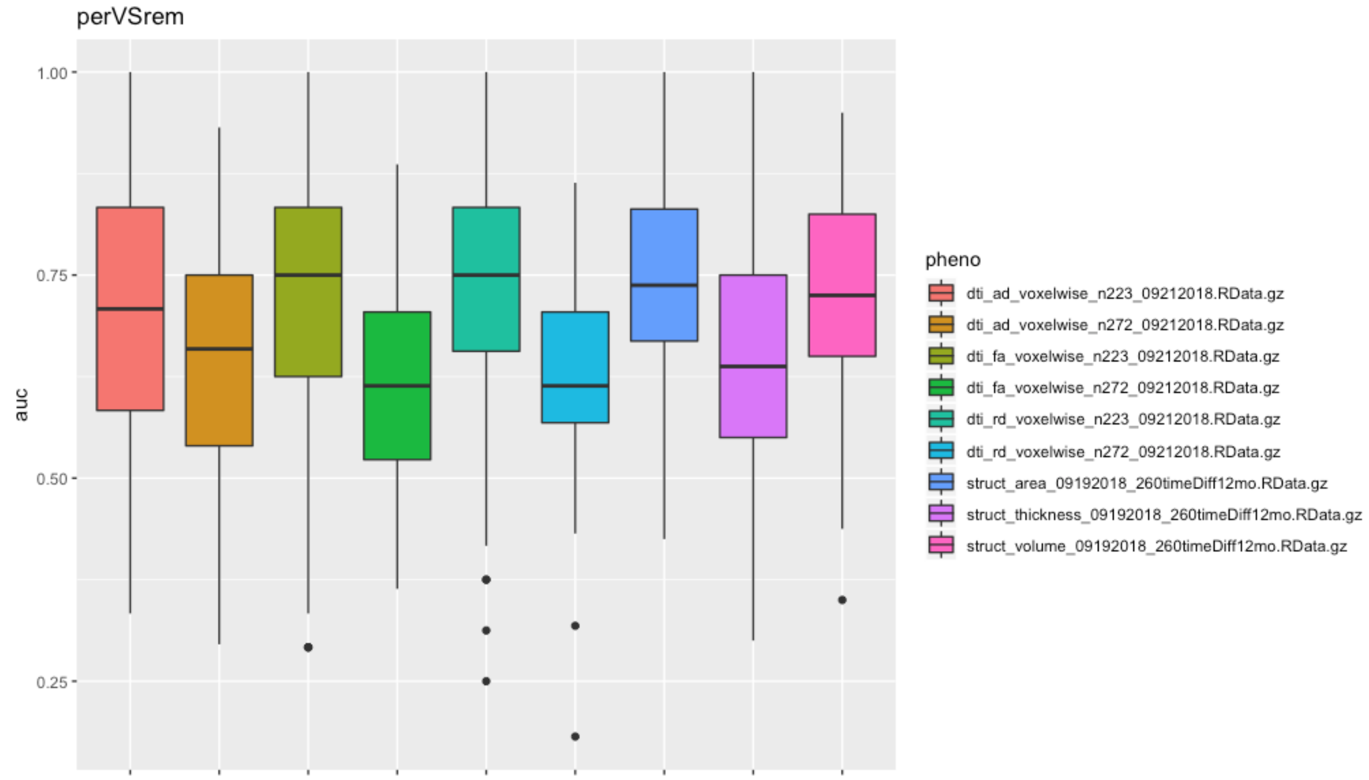
```
job_name=withinStruct_spatialTestDL;
mydir=/data/NCR_SBRB/baseline_prediction/;
swarm_file=swarm.automl_${job_name};
rm -rf $swarm_file;
for f in struct_thickness_09192018_260timeDiff12mo.RData.gz \
    struct_area_09192018_260timeDiff12mo.RData.gz \
    struct_volume_09192018_260timeDiff12mo.RData.gz; do
    for target in nvVSper nvVSrem perVSrem nvVSadhd; do
        for i in {1..100}; do
            echo "Rscript --vanilla
~/research_code/automl/uni_spatial_test_autoValidation_DL.R ${mydir}/$f
${mydir}/long_clin_0918.csv ${target}
${mydir}/models_spatial_within_DL/${USER} $RANDOM 35" >> $swarm_file;
        done;
    done;
done
sed -i -e "s/^/unset http_proxy; /g" $swarm_file;
split -l 1000 $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 $f -g 60 -t 16 --time 3:00:00 --partition norm --logdir
trash_${job_name} --job-name ${job_name} -m R,afni --gres=lscratch:10 2>
swarm_wait_${USER};
        if grep -q ERROR swarm_wait_${USER}; then
            echo -e "\tError, sleeping..."
            sleep 10m;
        fi;
    done;
done
```

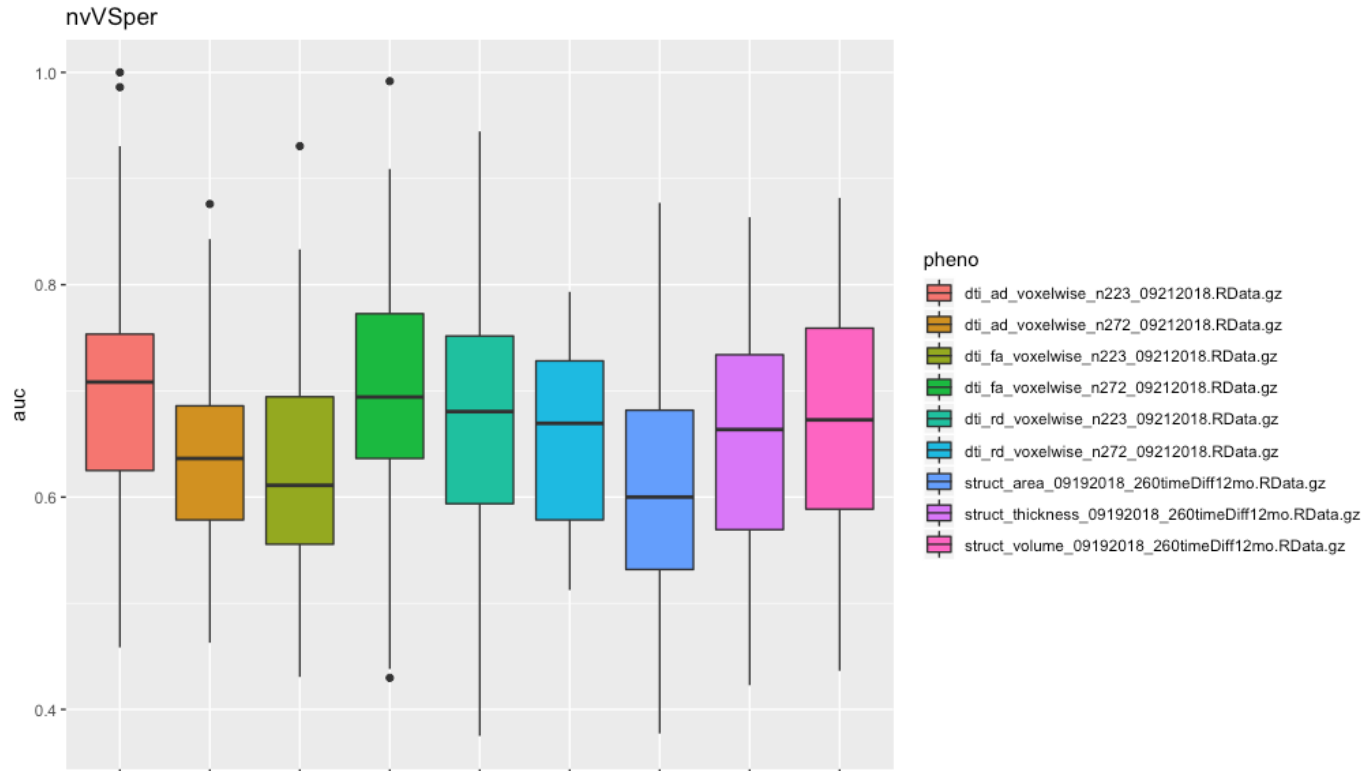
2018-11-02 09:36:57

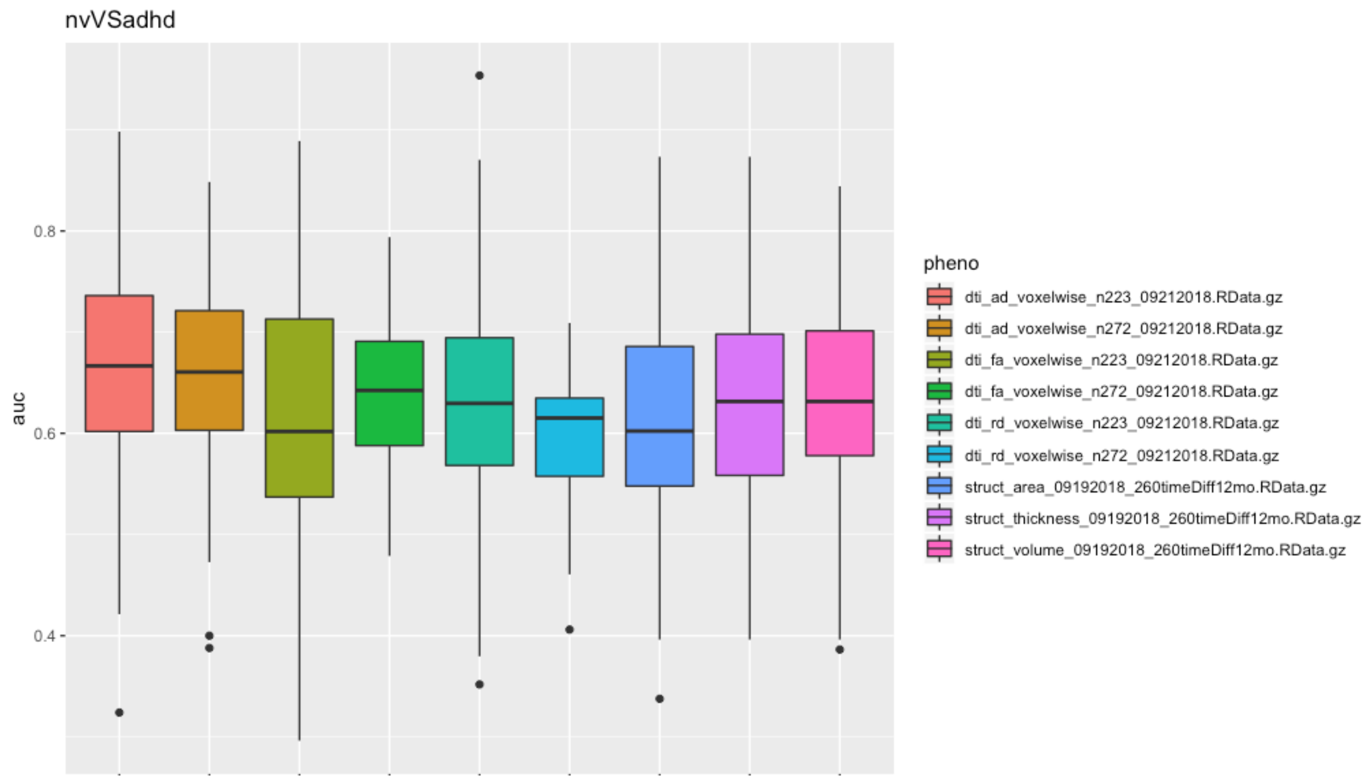
Time to grab the results again:

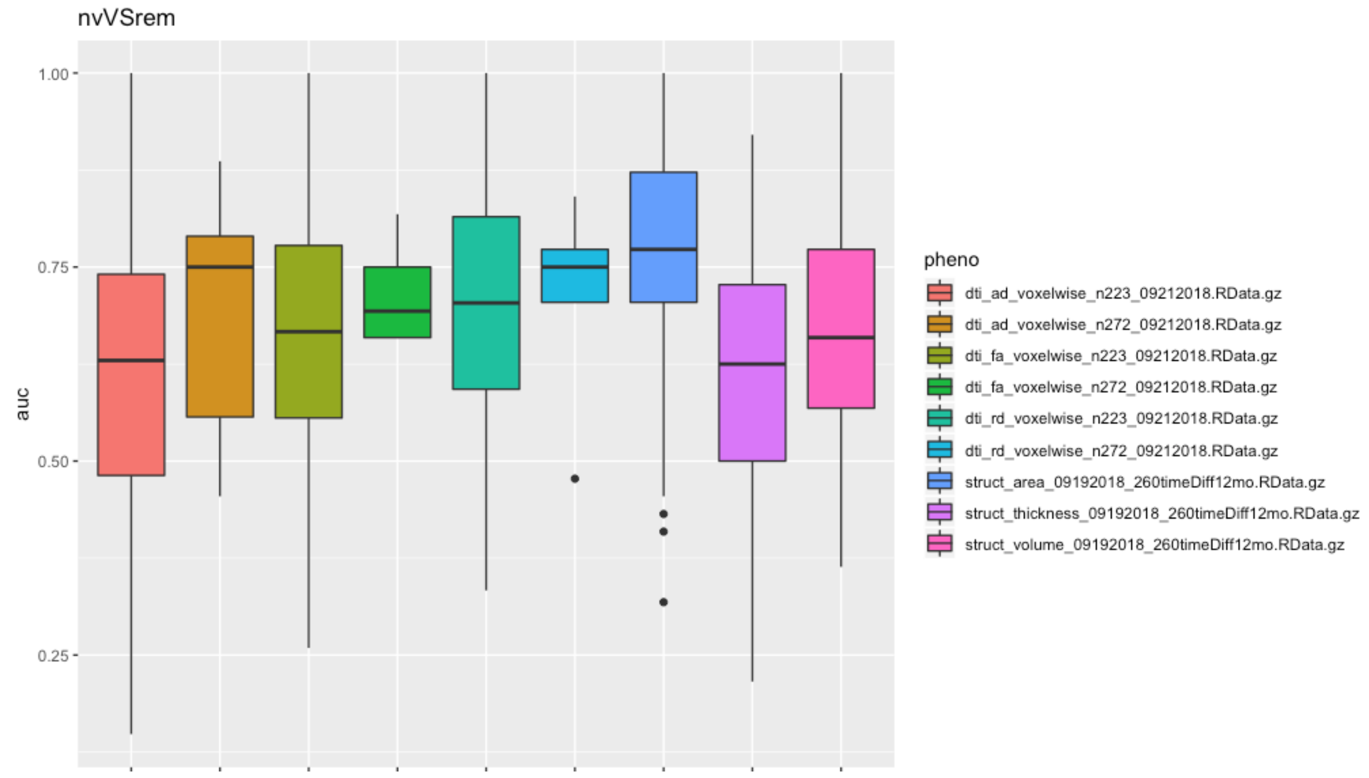
```
echo "target,pheno,var,seed,nfeat,model,auc,f1,acc,ratio" > spatialTest_summary.csv;
for dir in withinDTI_spatialTestDL withinStruct_spatialTestDL; do
    echo $dir;
    for f in `ls -1 trash_${dir}/*o`; do
        phen=`head -n 2 $f | tail -1 | awk '{FS=" "; print $6}' | cut -d"/" -f 6`;
        target=`head -n 2 $f | tail -1 | awk '{FS=" "; print $8}'`;
        seed=`head -n 2 $f | tail -1 | awk '{FS=" "; print $10}'`;
        var=`head -n 2 $f | tail -1 | awk '{FS=" "; print $5}' | cut -d"/" -f 4 | sed -e "s/\.R//g"`;
        model=`grep -A 1 model_id $f | tail -1 | awk '{FS=" "; print $2}' | cut -d"_" -f 1`;
        auc=`grep -A 1 model_id $f | tail -1 | awk '{FS=" "; print $3}'`;
        nfeat=`grep "Running model on" $f | awk '{FS=" "; print $5}'`;
        ratio=`grep -A 1 "Class distribution" $f | tail -1 | awk '{FS=" "; {for (i=2; i<=NF; i++) printf $i ";"}}'`;
        f1=`grep -A 2 "Maximum Metrics:" $f | tail -1 | awk '{FS=" "; print $5}'`;
        acc=`grep -A 5 "Maximum Metrics:" $f | tail -1 | awk '{FS=" "; print $5}'`;
        echo $target,$phen,$var,$seed,$nfeat,$model,$auc,$f1,$acc,$ratio >> spatialTest_summary.csv;
    done;
done;
```

I'm plotting AUC because it's easier to see the differences there. But it looks like the n223 DTI is indeed better. For struct, area and volume are better!

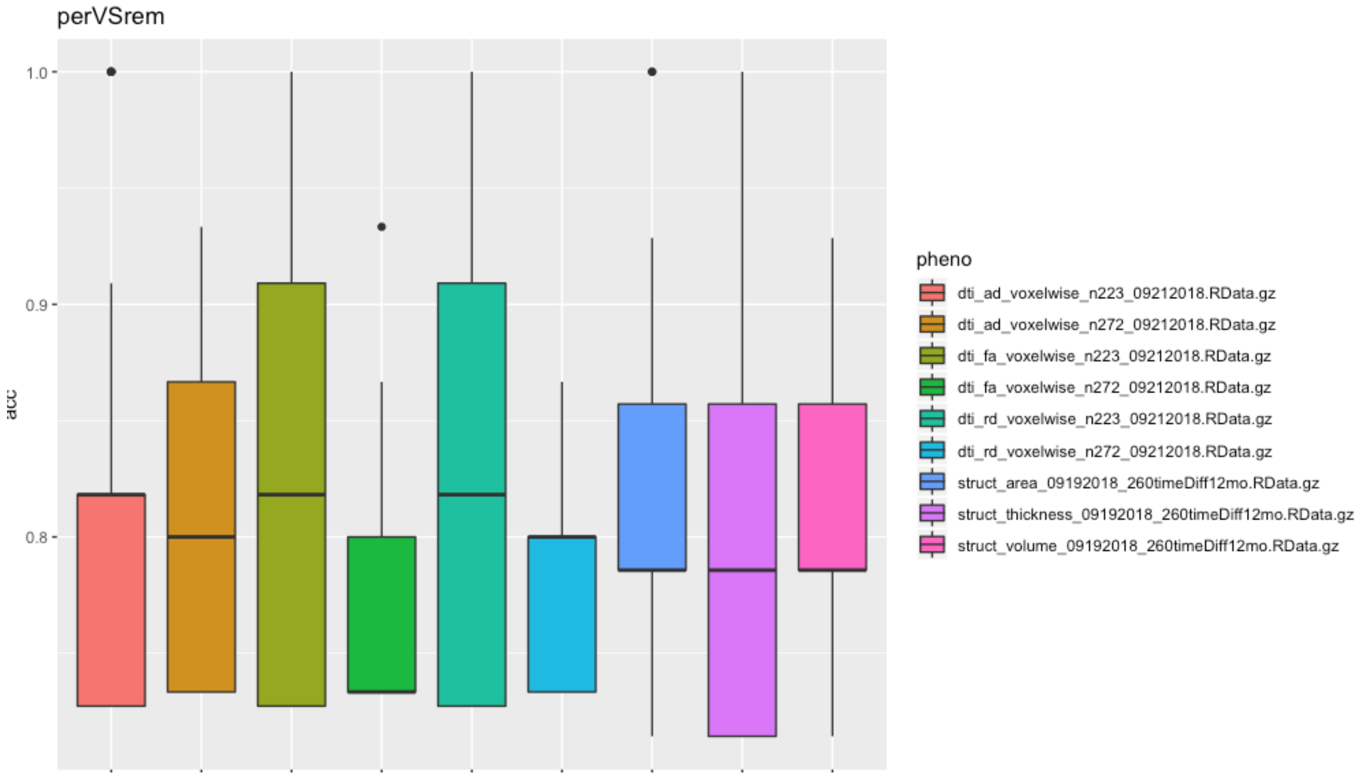

perVSrem
auc
1.00
0.75
0.50
0.25
pheno
dti_ad_voxelwise_n223_09212018.RData.gz
dti_ad_voxelwise_n272_09212018.RData.gz
dti_fa_voxelwise_n223_09212018.RData.gz
dti_fa_voxelwise_n272_09212018.RData.gz
dti_rd_voxelwise_n223_09212018.RData.gz
dti_rd_voxelwise_n272_09212018.RData.gz
struct_area_09192018_260timeDiff12mo.RData.gz
struct_thickness_09192018_260timeDiff12mo.RData.gz
struct_volume_09192018_260timeDiff12mo.RData.gz

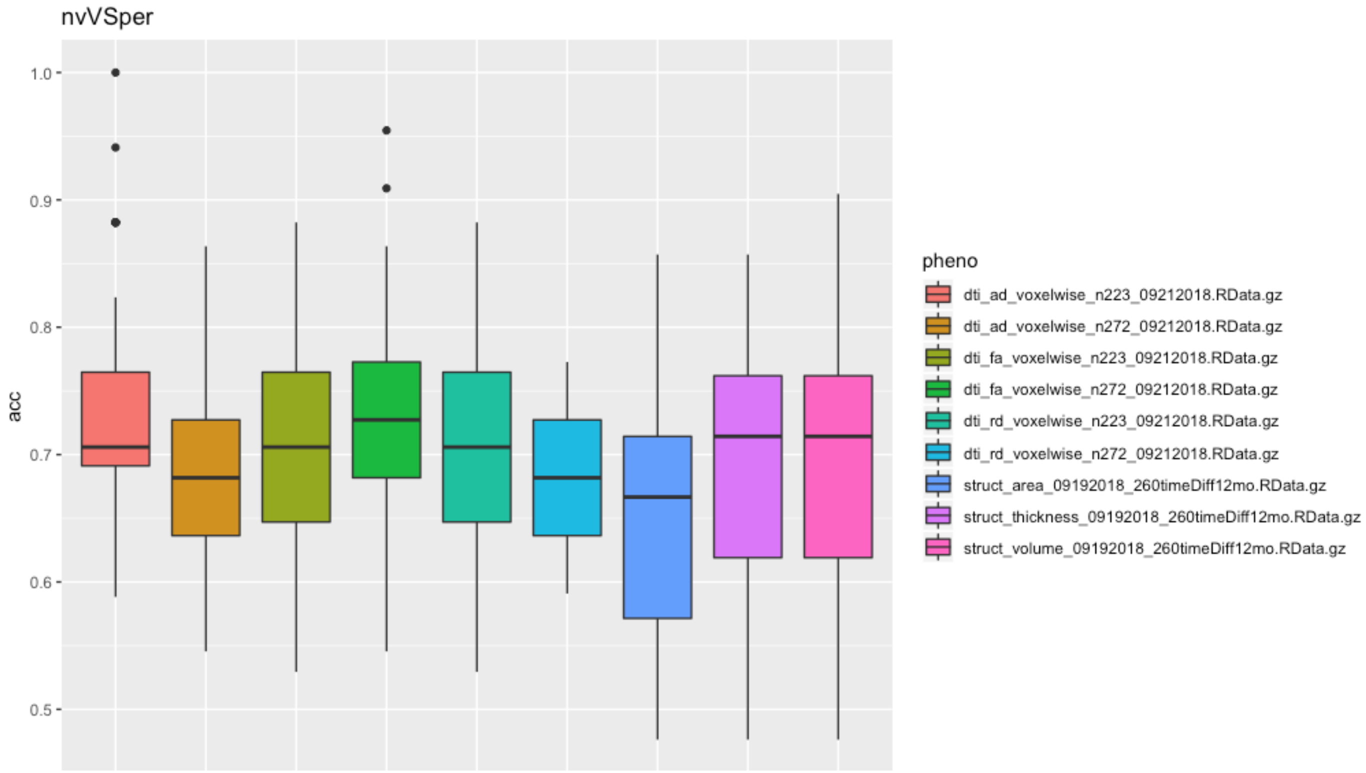

nvVSper
auc
1.0
0.8
0.6
0.4
pheno
dti_ad_voxelwise_n223_09212018.RData.gz
dti_ad_voxelwise_n272_09212018.RData.gz
dti_fa_voxelwise_n223_09212018.RData.gz
dti_fa_voxelwise_n272_09212018.RData.gz
dti_rd_voxelwise_n223_09212018.RData.gz
dti_rd_voxelwise_n272_09212018.RData.gz
struct_area_09192018_260timeDiff12mo.RData.gz
struct_thickness_09192018_260timeDiff12mo.RData.gz
struct_volume_09192018_260timeDiff12mo.RData.gz

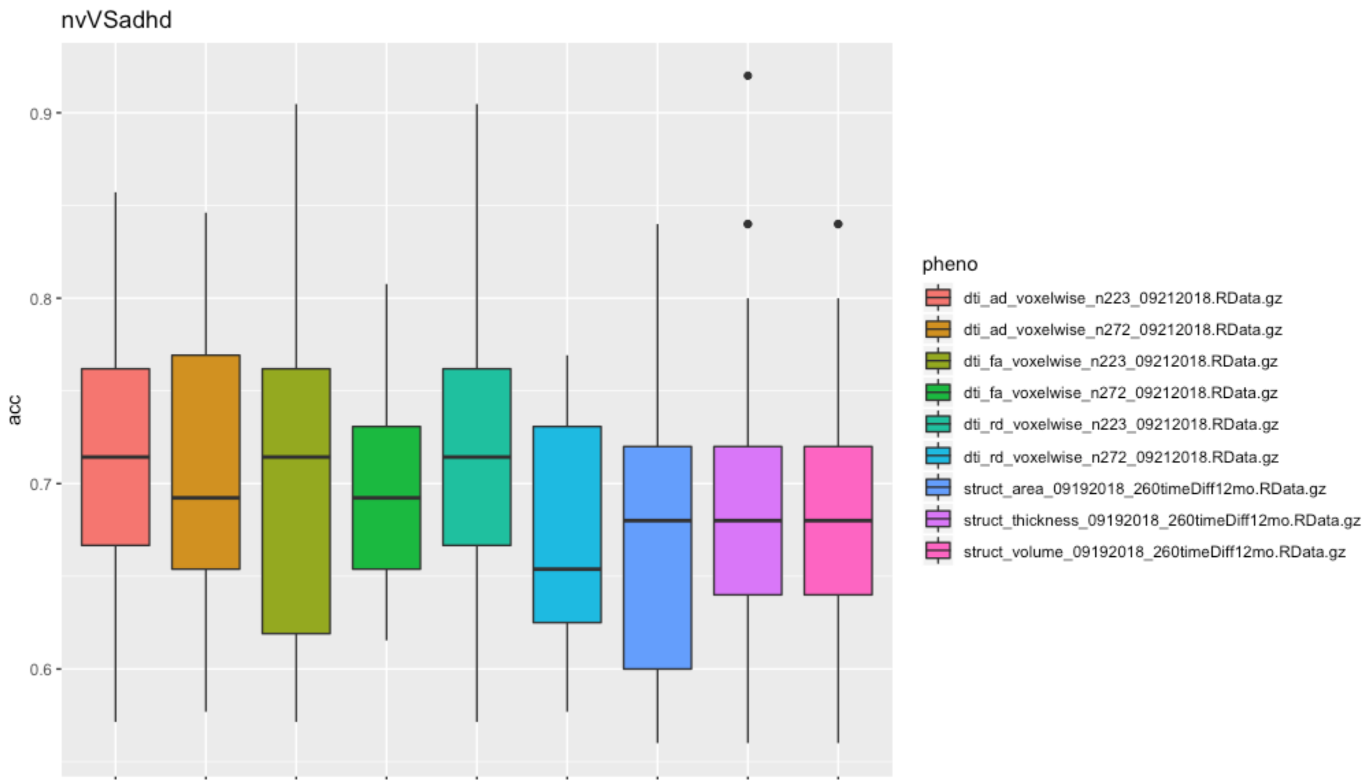


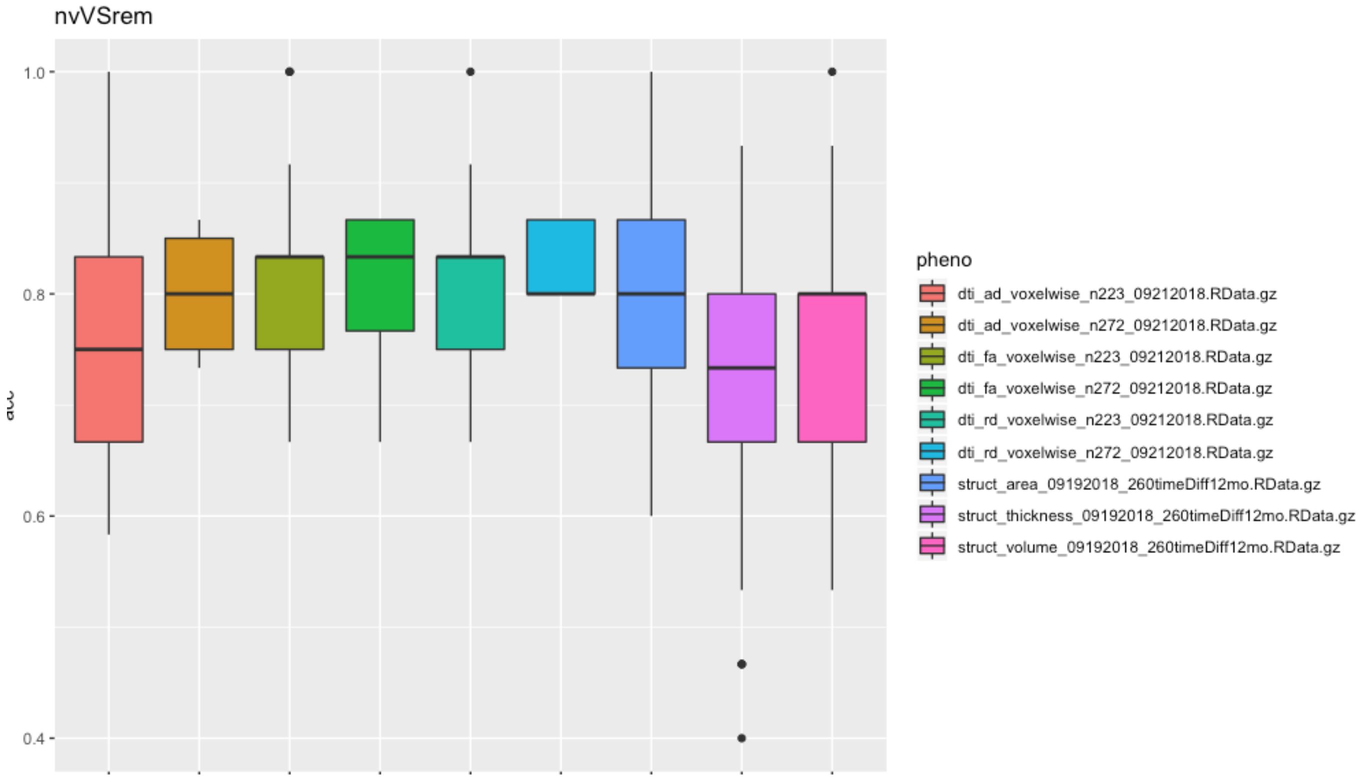


But let's also plot accuracy, in case it helps with decisions:


perVSrem
acc
1.0
0.9
0.8
pheno
dti_ad_voxelwise_n223_09212018.RData.gz
dti_ad_voxelwise_n272_09212018.RData.gz
dti_fa_voxelwise_n223_09212018.RData.gz
dti_fa_voxelwise_n272_09212018.RData.gz
dti_rd_voxelwise_n223_09212018.RData.gz
dti_rd_voxelwise_n272_09212018.RData.gz
struct_area_09192018_260timeDiff12mo.RData.gz
struct_thickness_09192018_260timeDiff12mo.RData.gz
struct_volume_09192018_260timeDiff12mo.RData.gz


nvVSper
acc
1.0
0.9
0.8
0.7
0.6
0.5
pheno
dti_ad_voxelwise_n223_09212018.RData.gz
dti_ad_voxelwise_n272_09212018.RData.gz
dti_fa_voxelwise_n223_09212018.RData.gz
dti_fa_voxelwise_n272_09212018.RData.gz
dti_rd_voxelwise_n223_09212018.RData.gz
dti_rd_voxelwise_n272_09212018.RData.gz
struct_area_09192018_260timeDiff12mo.RData.gz
struct_thickness_09192018_260timeDiff12mo.RData.gz
struct_volume_09192018_260timeDiff12mo.RData.gz





2018-11-07 12:10:47

Today I thought about averaging the voxels inside a cluster, because that would reduce the number of features and sqaush any concerns about overfitting others might have. So, let's re-run the different DTI scenarios that way, and then run structural as well when the code is ready.

```
job_name=withinDTI_spatialAvgTestDL;
mydir=/data/NCR_SBRB/baseline_prediction/;
```

```
swarm_file=swarm.automl_${job_name};
rm -rf $swarm_file;
for f in dti_fa_voxelwise_n223_09212018.RData.gz
dti_fa_voxelwise_n272_09212018.RData.gz \
    dti_ad_voxelwise_n223_09212018.RData.gz
dti_ad_voxelwise_n272_09212018.RData.gz \
    dti_rd_voxelwise_n223_09212018.RData.gz
dti_rd_voxelwise_n272_09212018.RData.gz; do
    for target in nvVSper nvVSrem perVSrem nvVSadhd; do
        for i in {1..100}; do
            echo "Rscript --vanilla
~/research_code/automl/uni_spatialAverage_test_autoValidation_DL.R
${mydir}/$f ${mydir}/long_clin_0918.csv ${target}
${mydir}/models_spatial_within_DL/${USER} $RANDOM 8" >> $swarm_file;
        done;
    done;
done
sed -i -e "s/^/unset http_proxy; /g" $swarm_file;
split -l 1000 $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 $f -g 40 -t 16 --time 3:00:00 --partition norm --logdir
trash_${job_name} --job-name ${job_name} -m R,afni --gres=lscratch:10 2>
swarm_wait_${USER};
        if grep -q ERROR swarm_wait_${USER}; then
            echo -e "\tError, sleeping..."
            sleep 10m;
        fi;
    done;
done
```

```
job_name=withinStruct_spatialAvgTestDL;
mydir=/data/NCR_SBRB/baseline_prediction/;
swarm_file=swarm.automl_${job_name};
rm -rf $swarm_file;
for f in struct_thickness_09192018_260timeDiff12mo.RData.gz \
    struct_area_09192018_260timeDiff12mo.RData.gz \
    struct_volume_09192018_260timeDiff12mo.RData.gz; do
    for target in nvVSper nvVSrem perVSrem nvVSadhd; do
        for i in {1..100}; do
            echo "Rscript --vanilla
~/research_code/automl/uni_spatialAverage_test_autoValidation_DL.R
${mydir}/$f ${mydir}/long_clin_0918.csv ${target}
${mydir}/models_spatial_within_DL/${USER} $RANDOM 35" >> $swarm_file;
        done;
    done;
done
sed -i -e "s/^/unset http_proxy; /g" $swarm_file;
split -l 1000 $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 $f -g 40 -t 16 --time 3:00:00 --partition norm --logdir
trash_${job_name} --job-name ${job_name} -m R,afni --gres=lscratch:10 2>
swarm_wait_${USER};
        if grep -q ERROR swarm_wait_${USER}; then
            echo -e "\tError, sleeping..."
            sleep 10m;
        fi;
    done;
done
```

2018-11-08 17:01:02

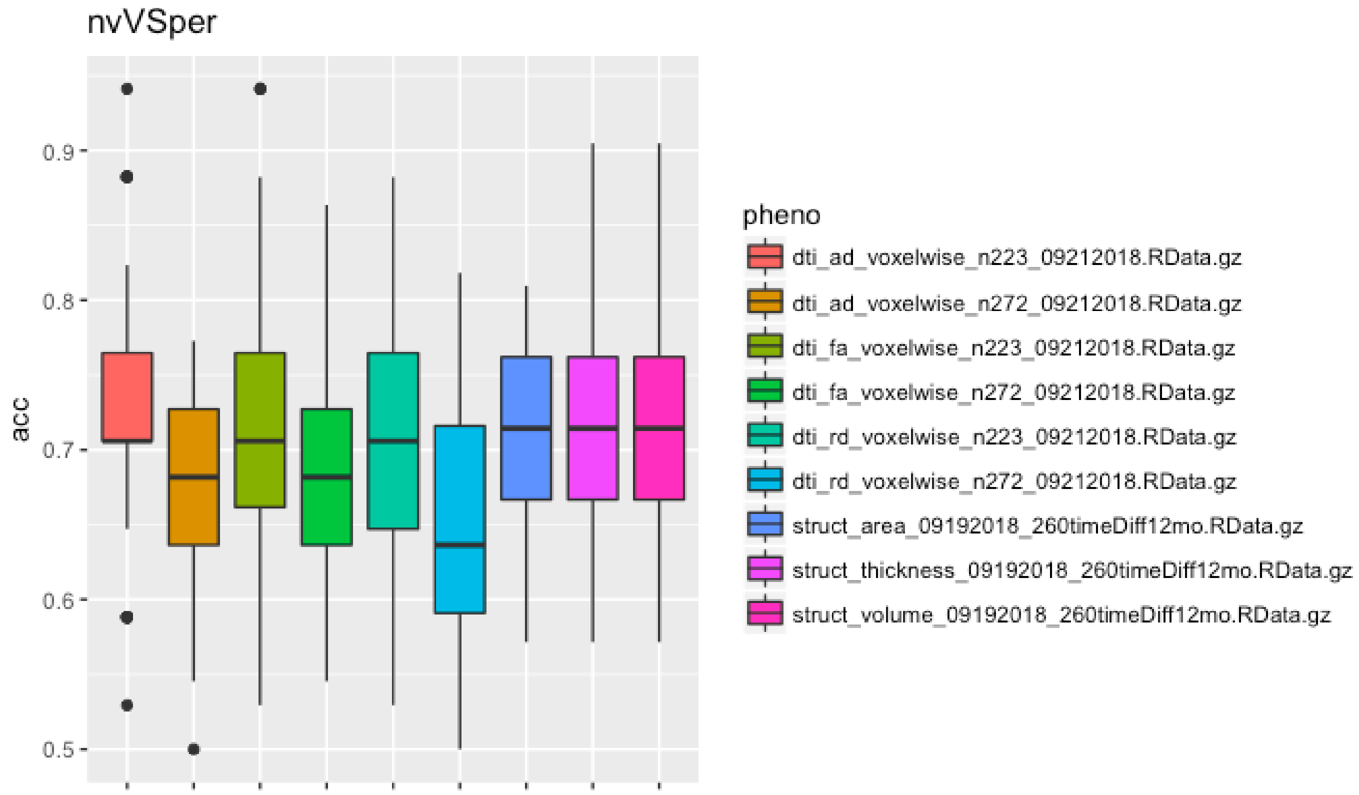
Let's put together the results for the spatialAverage pipeline:

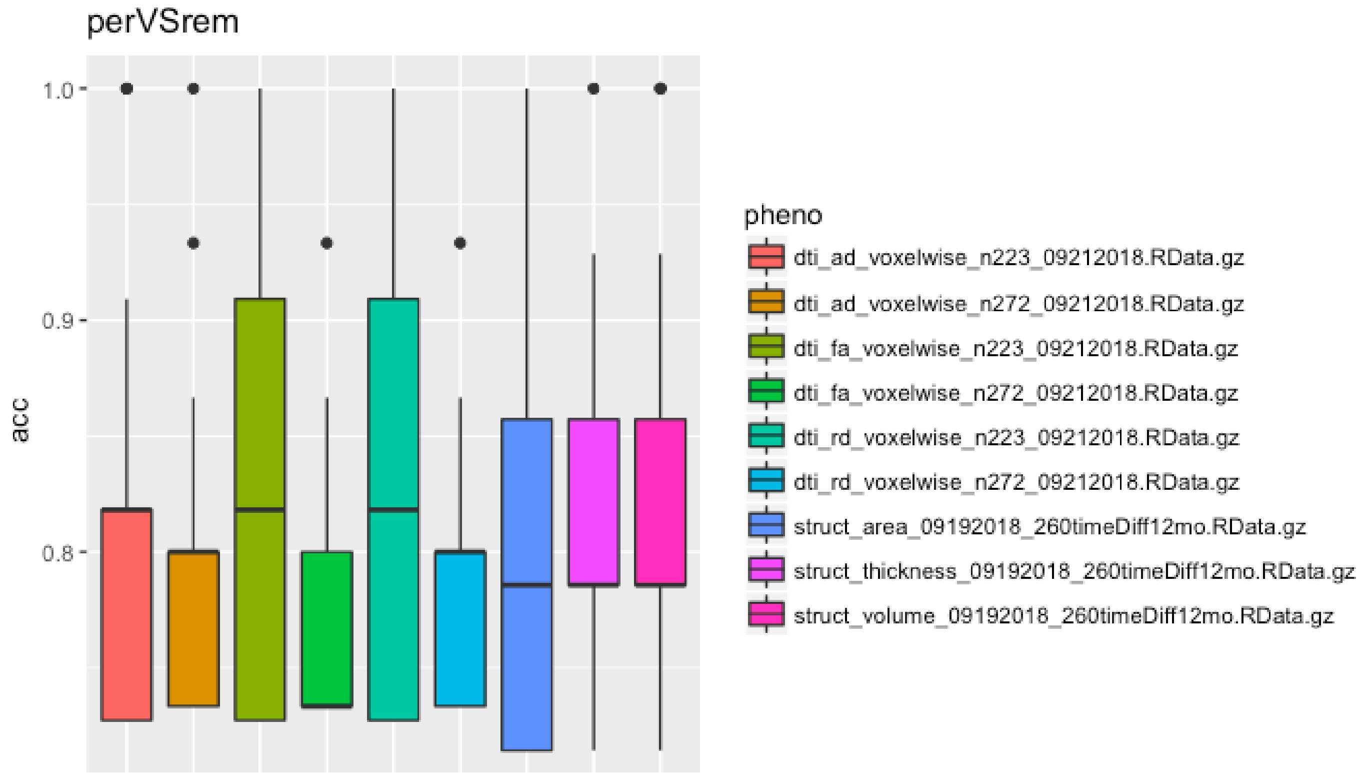
```
echo "target,pheno,var,seed,nfeat,model,auc,f1,acc,ratio" >
spatialAverageTest_summary.csv;
for dir in withinDTI_spatialAvgTestDL withinStruct_spatialAvgTestDL; do
    echo $dir;
    for f in `ls -1 trash_${dir}/*o`; do
        phen=`head -n 2 $f | tail -1 | awk '{FS=" "; print $6}' | cut -
d"/" -f 6`;
        target=`head -n 2 $f | tail -1 | awk '{FS=" "; print $8}'`;
        seed=`head -n 2 $f | tail -1 | awk '{FS=" "; print $10}'`;
        var=`head -n 2 $f | tail -1 | awk '{FS=" "; print $5}' | cut -d"/"
-f 4 | sed -e "s/\.R//g"`;
        model=`grep -A 1 model_id $f | tail -1 | awk '{FS=" "; print $2}'
| cut -d"_" -f 1`;
        auc=`grep -A 1 model_id $f | tail -1 | awk '{FS=" "; print $3}'`;
        nfeat=`grep "Running model on" $f | awk '{FS=" "; print $5}'`;
        ratio=`grep -A 1 "Class distribution" $f | tail -1 | awk '{FS=" ";
{for (i=2; i<=NF; i++) printf $i ";"}}'`;
        f1=`grep -A 2 "Maximum Metrics:" $f | tail -1 | awk '{FS=" ";
print $5}'`;
        acc=`grep -A 5 "Maximum Metrics:" $f | tail -1 | awk '{FS=" ";
print $5}'`;
        echo $target,$phen,$var,$seed,$nfeat,$model,$auc,$f1,$acc,$ratio
>> spatialAverageTest_summary.csv;
    done;
done;
```

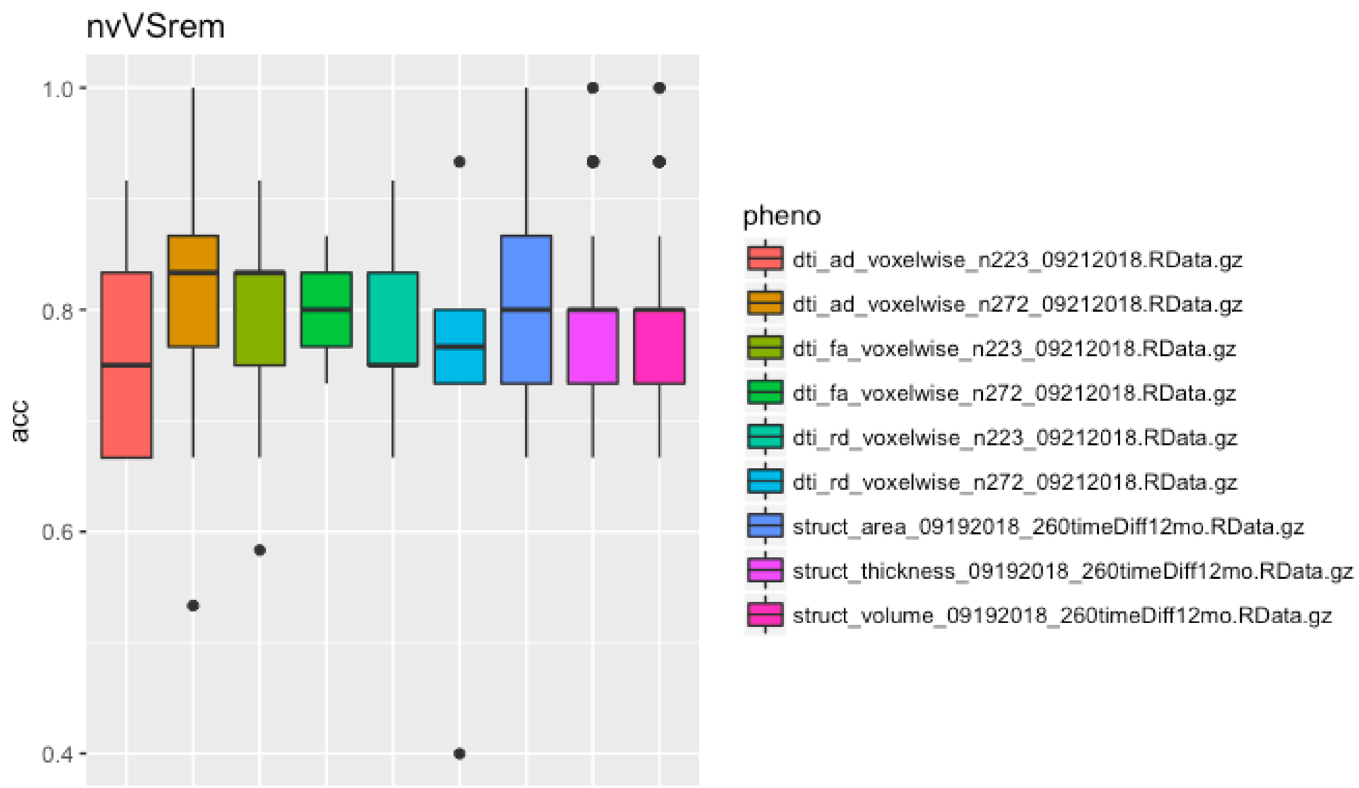
And for plotting:

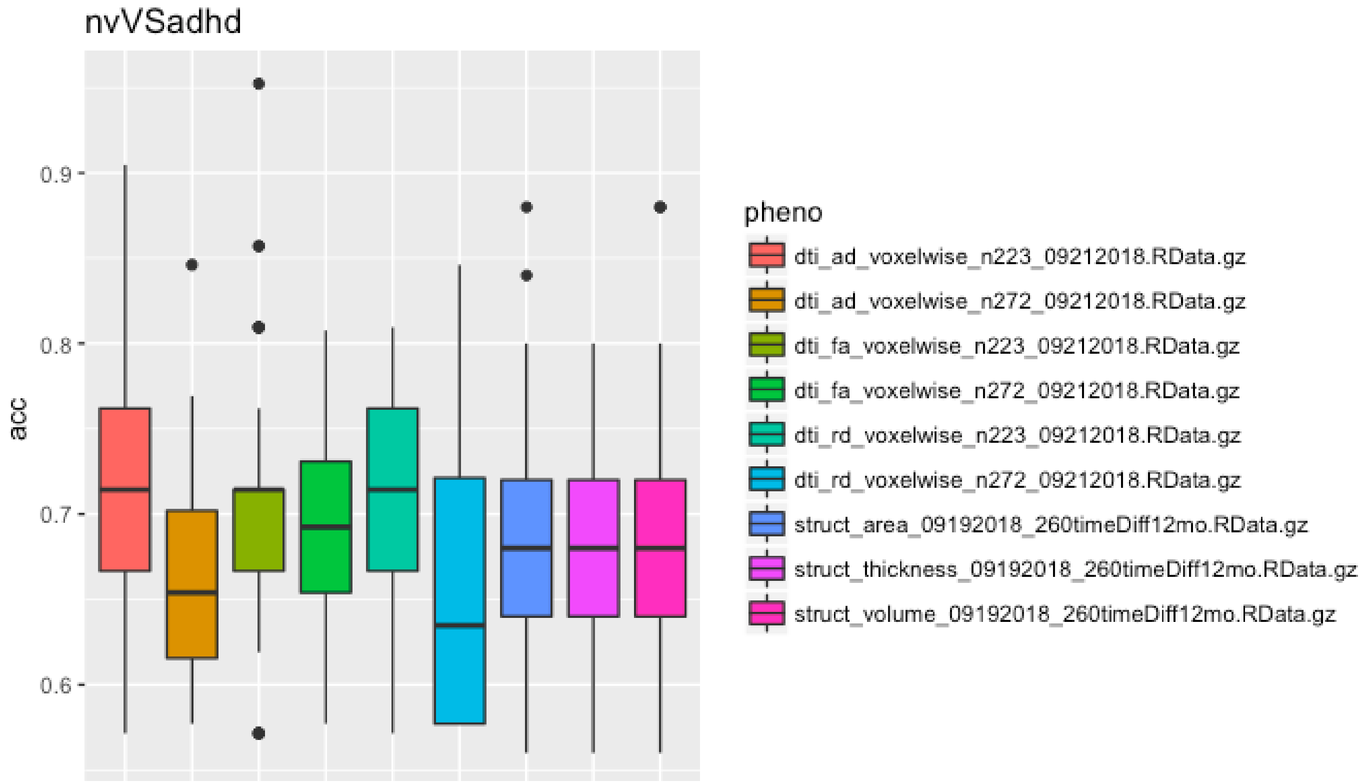
```
data = read.csv('~/tmp/spatialAverageTest_summary.csv')
target='nvVSper'
```

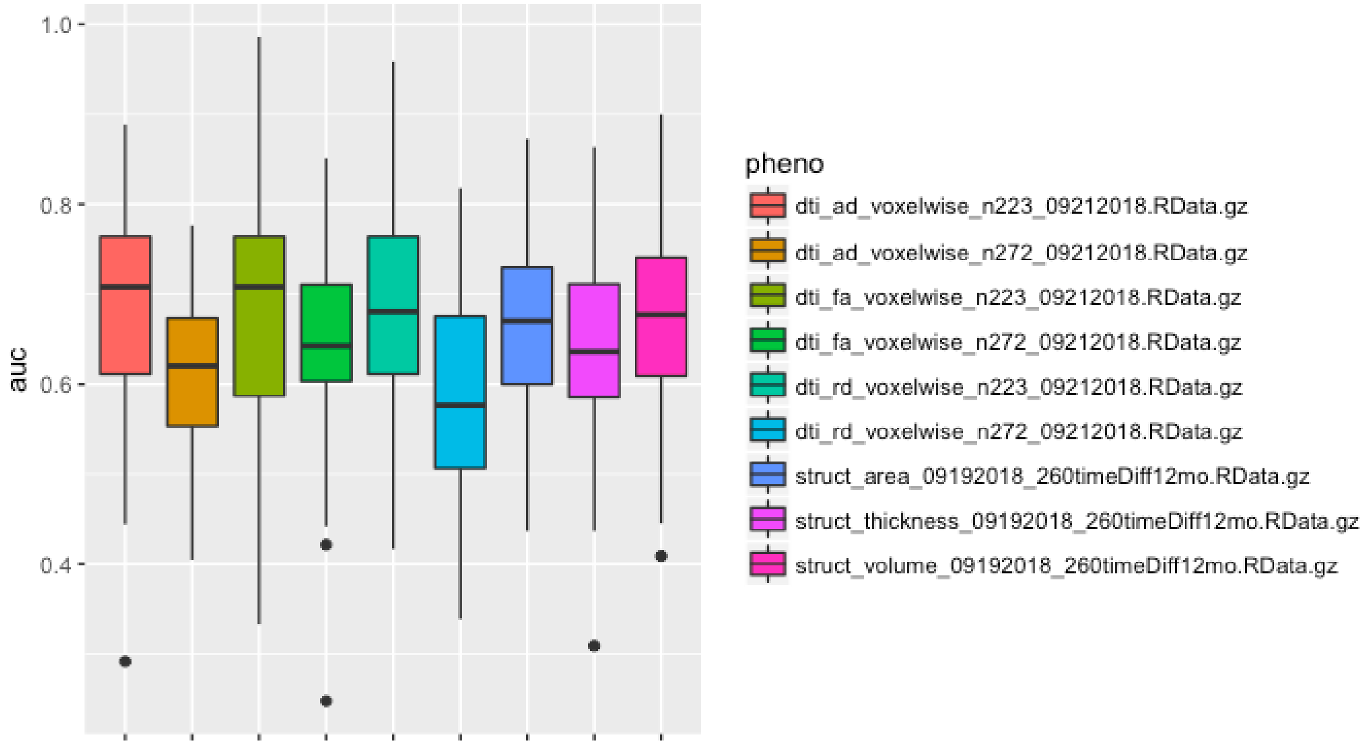
```
p1<-ggplot(data[data$target == target,], aes(x=pheno, y=acc, fill=pheno))
print(p1+geom_boxplot() + ggtitle(target))
```



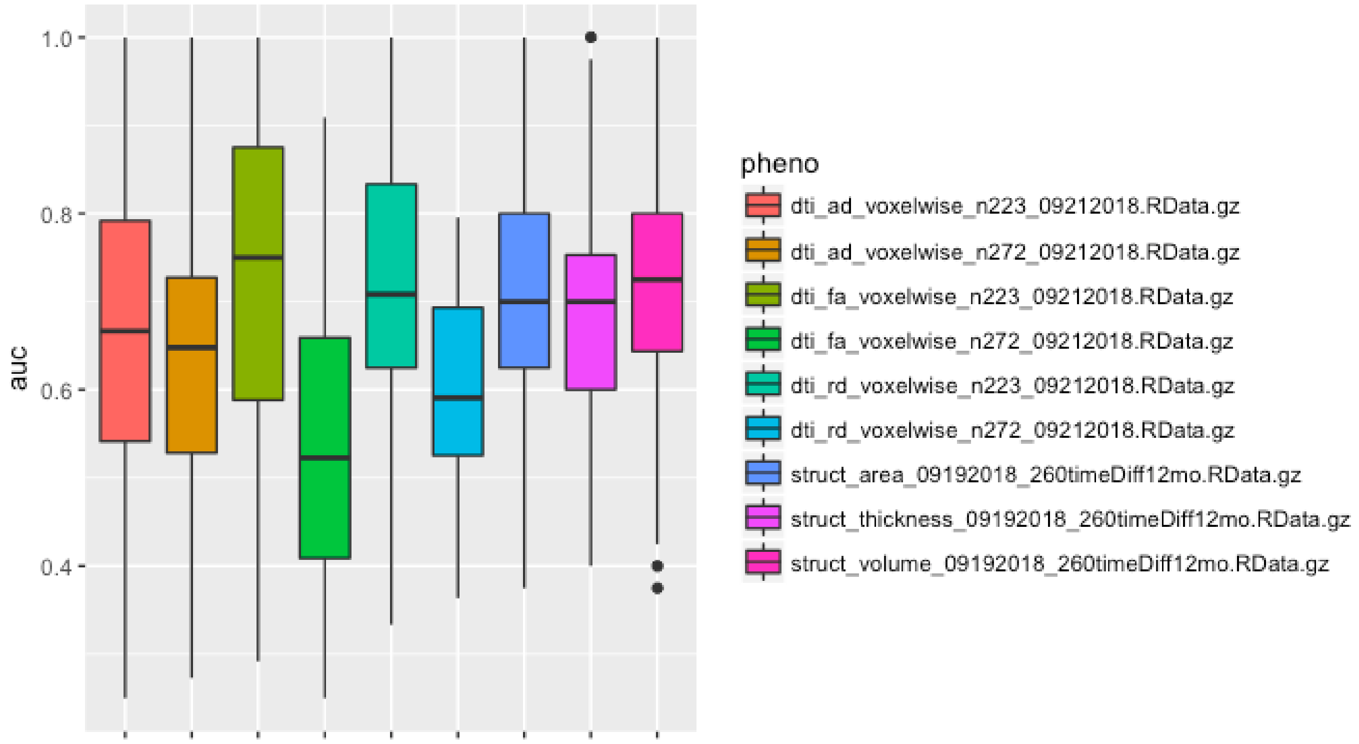



nvVSrem
acc
1.0
0.8
0.6
0.4
pheno
dti_ad_voxelwise_n223_09212018.RData.gz
dti_ad_voxelwise_n272_09212018.RData.gz
dti_fa_voxelwise_n223_09212018.RData.gz
dti_fa_voxelwise_n272_09212018.RData.gz
dti_rd_voxelwise_n223_09212018.RData.gz
dti_rd_voxelwise_n272_09212018.RData.gz
struct_area_09192018_260timeDiff12mo.RData.gz
struct_thickness_09192018_260timeDiff12mo.RData.gz
struct_volume_09192018_260timeDiff12mo.RData.gz

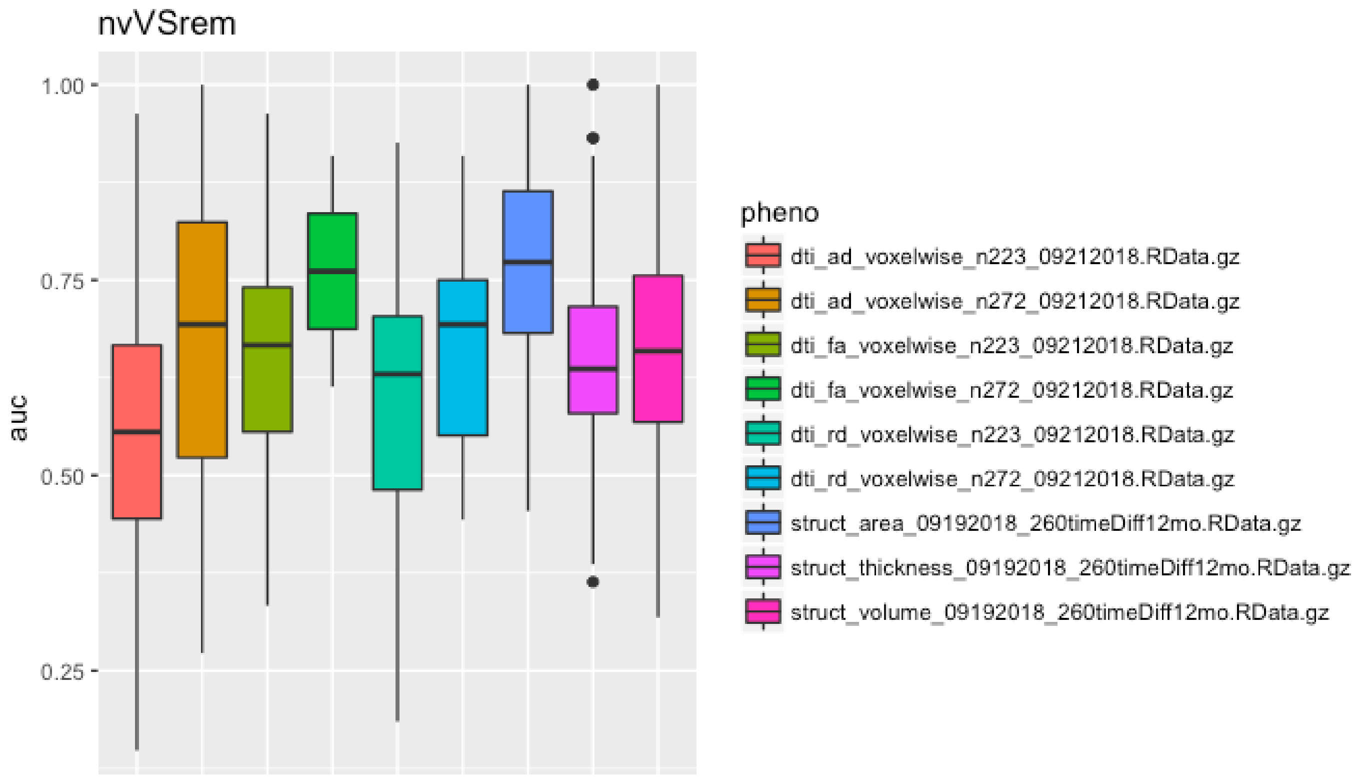

nvVSadhd
acc
0.9
0.8
0.7
0.6
pheno
dti_ad_voxelwise_n223_09212018.RData.gz
dti_ad_voxelwise_n272_09212018.RData.gz
dti_fa_voxelwise_n223_09212018.RData.gz
dti_fa_voxelwise_n272_09212018.RData.gz
dti_rd_voxelwise_n223_09212018.RData.gz
dti_rd_voxelwise_n272_09212018.RData.gz
struct_area_09192018_260timeDiff12mo.RData.gz
struct_thickness_09192018_260timeDiff12mo.RData.gz
struct_volume_09192018_260timeDiff12mo.RData.gz

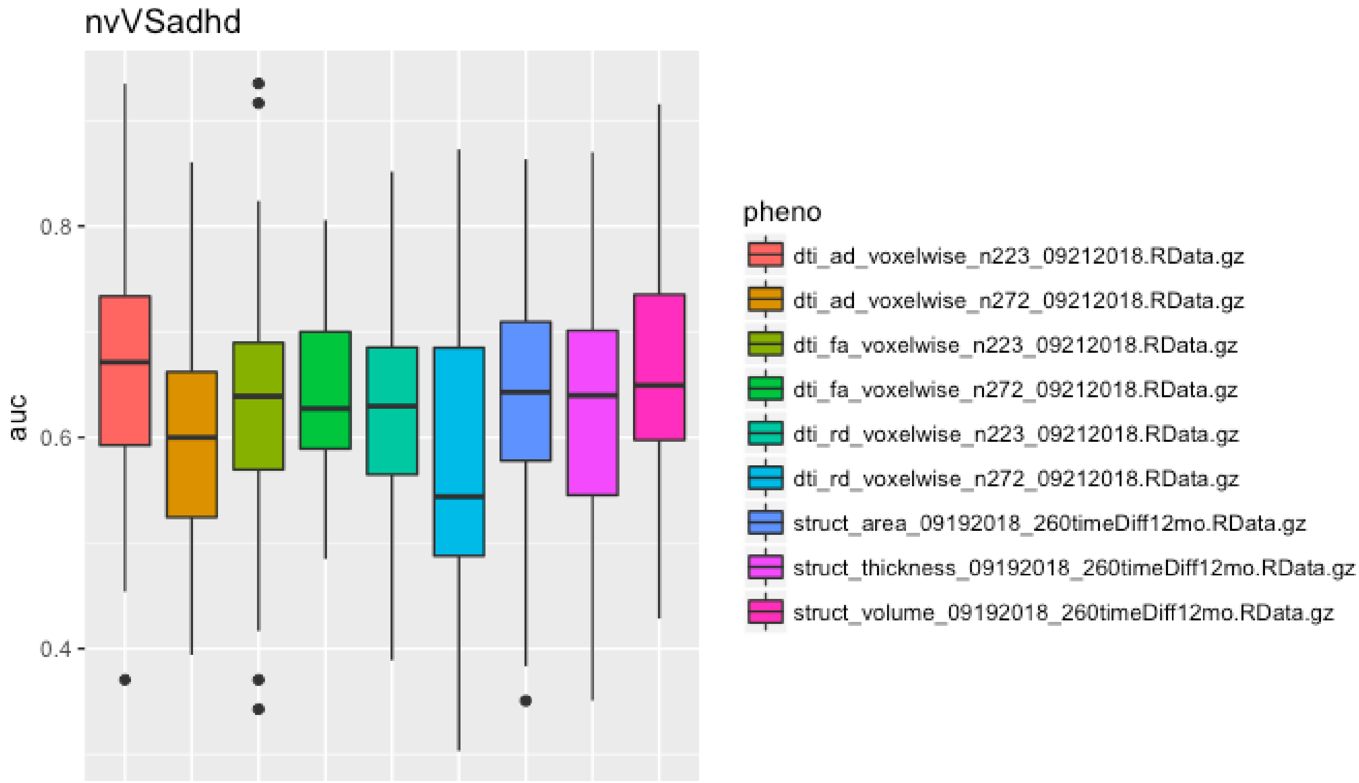


nvVSper



perVSrem





The results are honestly not that different. It might make a difference later when we start combining datasets and the number of variables might make some difference.

Another thing to try is to log-transform the data (or whatever makes it more Gaussian), prior to doing the univariate analysis. I don't think many of the algorithms will care that the data is gaussian, but it's worth a try to make it look nicer. I'd probably do some more work on combining these results and fMRI, but this is transformation might be something to be tried later.

Another check we can try is check for outliers. Instead of removing the entire subject (unless it's necessary, of course), we could try setting variables to NA, as out algorithms can handle that. And, of course we could using caret's nearZero variance filter and also findCorrelation if we end up too concerned about many variables in the raw data. It might help, and still keep non-univariate features in the model.

So, I guess next thing is to write code to combine the domains, and while that is running, to play more with rsfMRI.

2018-11-14 15:45:35

Now that I have the downsampled structural data, let's run it to see how it looks under rawCV:

```
job_name=withinStructDS_rawDL;
mydir=/data/NCR_SBRB/baseline_prediction/;
swarm_file=swarm.automl_${job_name};
rm -rf $swarm_file;
for f in struct_thickness_11142018_260timeDiff12mo.RData.gz \
    struct_area_11142018_260timeDiff12mo.RData.gz \
    struct_volume_11142018_260timeDiff12mo.RData.gz; do
    for target in nvVSper nvVSrem perVSrem nvVSadhd; do
        for i in {1..100}; do
            echo "Rscript --vanilla
~/research_code/automl/raw_autoValidation_DL.R ${mydir}/$f
${mydir}/long_clin_0918.csv ${target}
${mydir}/models_raw_within_DL/${USER} $RANDOM" >> $swarm_file;
        done;
    done;
done
f=struct_volume_11142018_260timeDiff12mo.RData.gz;
for target in nvVSper nvVSrem perVSrem nvVSadhd; do
    for i in {1..100}; do
        echo "Rscript --vanilla
~/research_code/automl/raw_autoValidation_DL.R ${mydir}/$f
${mydir}/long_clin_0918.csv ${target}
${mydir}/models_raw_within_DL/${USER} -$RANDOM" >> $swarm_file;
    done;
done;
sed -i -e "s/^/unset http_proxy; /g" $swarm_file;
split -l 1000 $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 $f -g 60 -t 16 --time 3:00:00 --partition norm --logdir
trash_${job_name} --job-name ${job_name} -m R --gres=lscratch:10 2>
swarm_wait_${USER};
        if grep -q ERROR swarm_wait_${USER}; then
            echo -e "\tError, sleeping..."
            sleep 10m;
        fi;
    done;
done
```

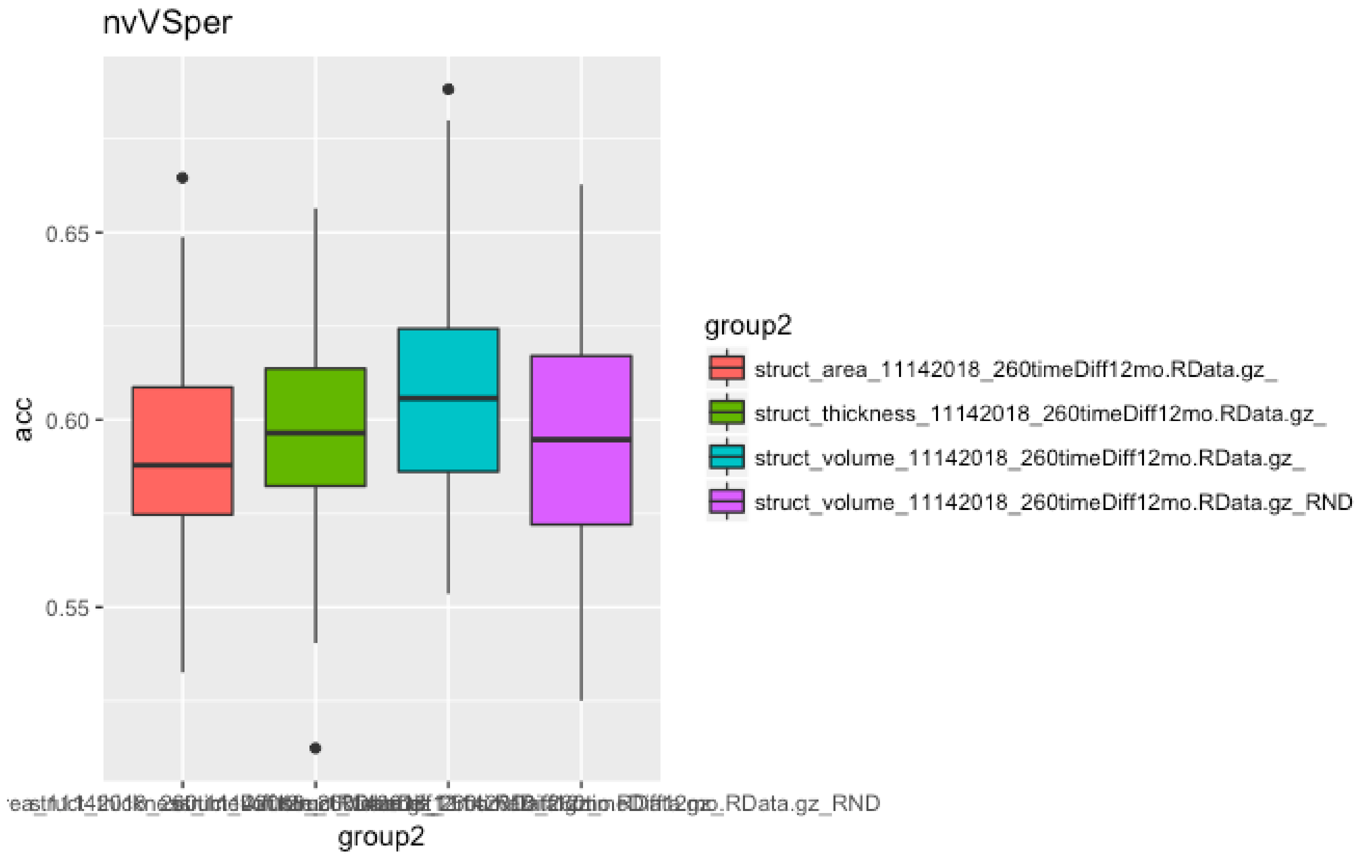
2018-11-15 10:13:36

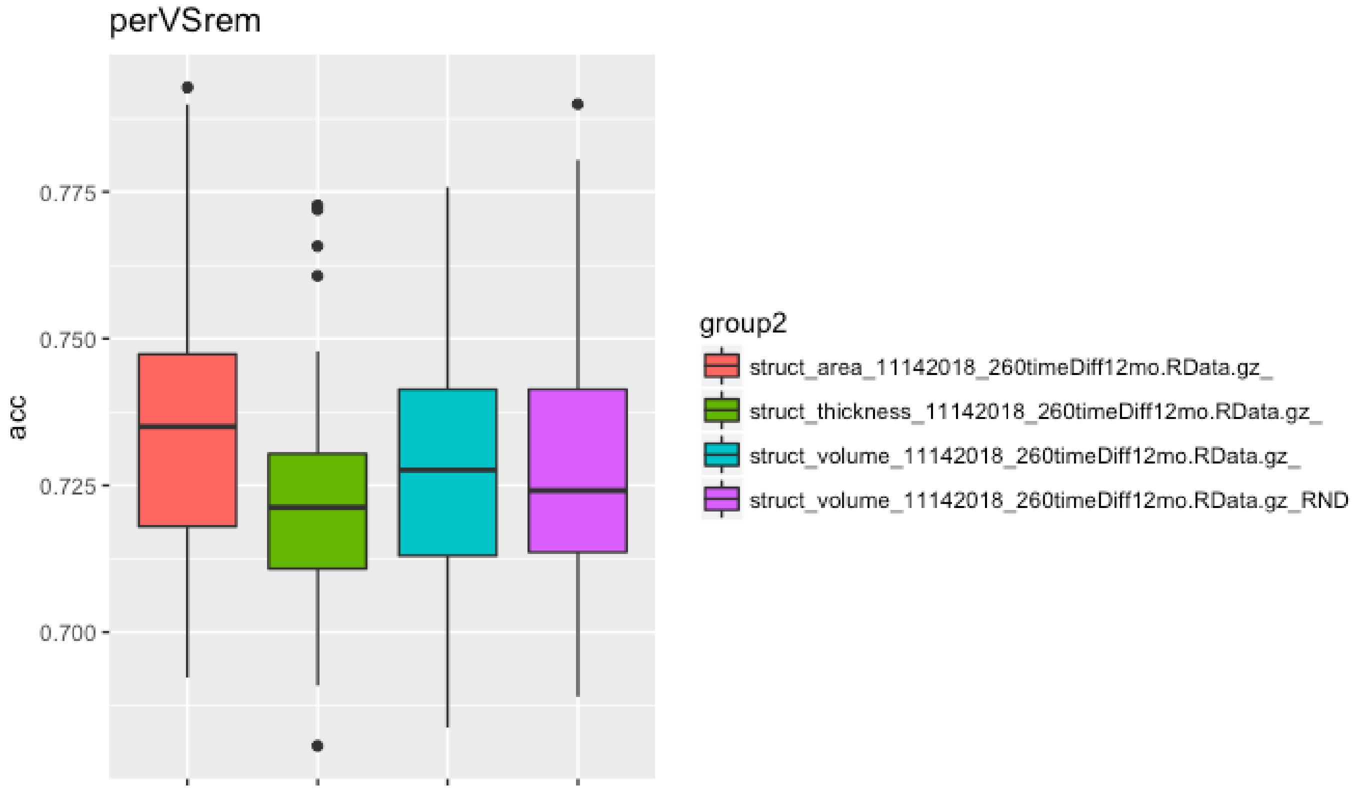
Let's compile the downsampled structural results:

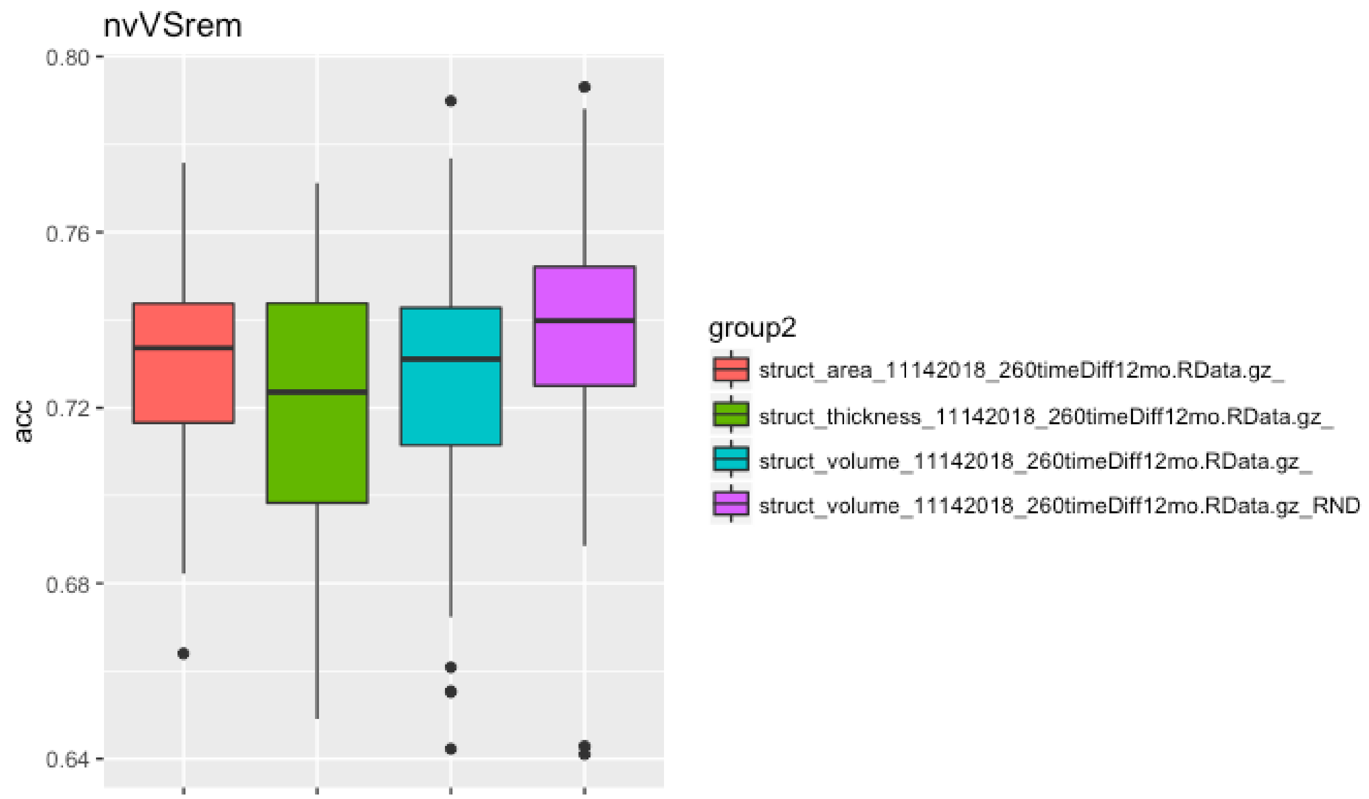
```
echo "target,pheno,var,seed,nfeat,model,auc,f1,acc,ratio" > structDSRawDL_summary.csv;
dir=withinStructDS_rawDL;
for f in `ls -1 trash_${dir}/*o`; do
    phen=`head -n 2 $f | tail -1 | awk '{FS=" "; print $7}' | cut -d"/" -f 6`;
    target=`head -n 2 $f | tail -1 | awk '{FS=" "; print $9}'`;
    seed=`head -n 2 $f | tail -1 | awk '{FS=" "; print $11}'`;
    var=`head -n 2 $f | tail -1 | awk '{FS=" "; print $6}' | cut -d"/" -f 4 | sed -e "s/\.R//g"`;
    model=`grep -A 1 model_id $f | tail -1 | awk '{FS=" "; print $2}' | cut -d"_" -f 1`;
    auc=`grep -A 1 model_id $f | tail -1 | awk '{FS=" "; print $3}'`;
    nfeat=`grep "Running model on" $f | awk '{FS=" "; print $5}'`;
    ratio=`grep -A 1 "Class distribution" $f | tail -1 | awk '{FS=" "; {for (i=2; i<=NF; i++) printf $i ";"}}'`;
    f1=`grep -A 2 "Maximum Metrics:" $f | tail -1 | awk '{FS=" "; print $5}'`;
    acc=`grep -A 5 "Maximum Metrics:" $f | tail -1 | awk '{FS=" "; print $5}'`;
    echo $target,$phen,$var,$seed,$nfeat,$model,$auc,$f1,$acc,$ratio >> structDSRawDL_summary.csv;
done;
```

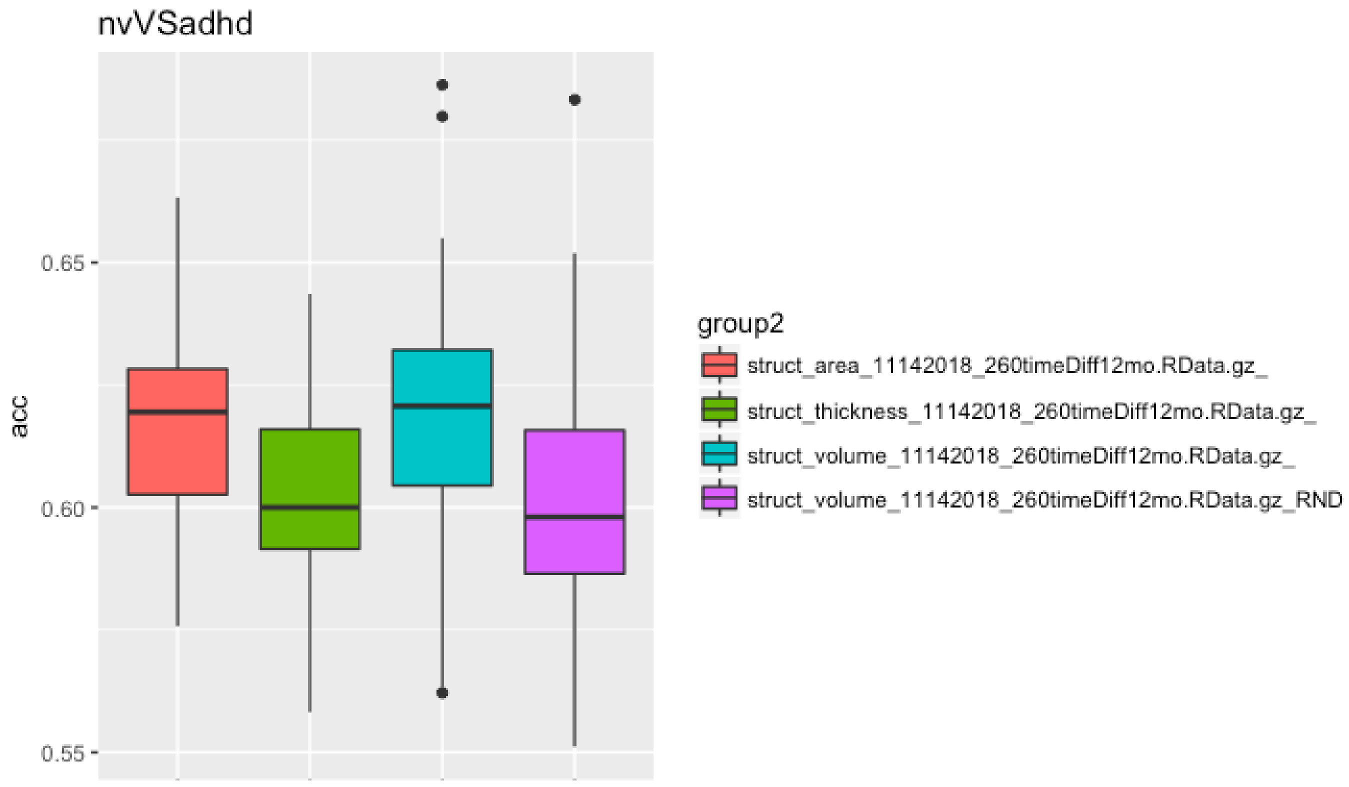
Then we plot it in R:

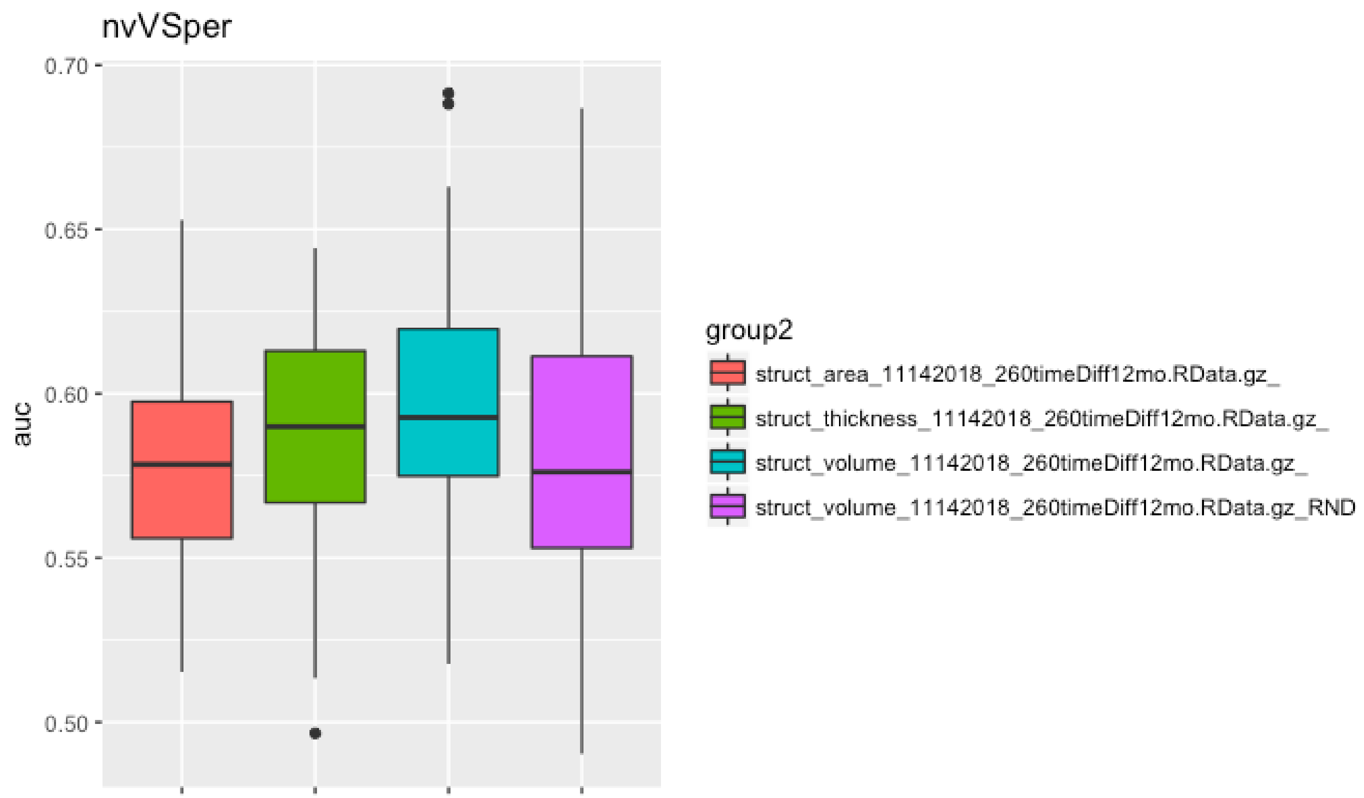
```
data = read.csv('~/tmp/structDSRawDL_summary.csv')
data$group = ''
data[data$seed<0,]$group = 'RND'
data$group2 = sapply(1:nrow(data), function(x) { sprintf('%s_%s', data$pheno[x], data$group[x])} )
# then, for each target
target='nvVSper'
p1<-ggplot(data[data$target == target,], aes(x=group2, y=acc, fill=group2))
print(p1+geom_boxplot() + ggtitle(target))
```

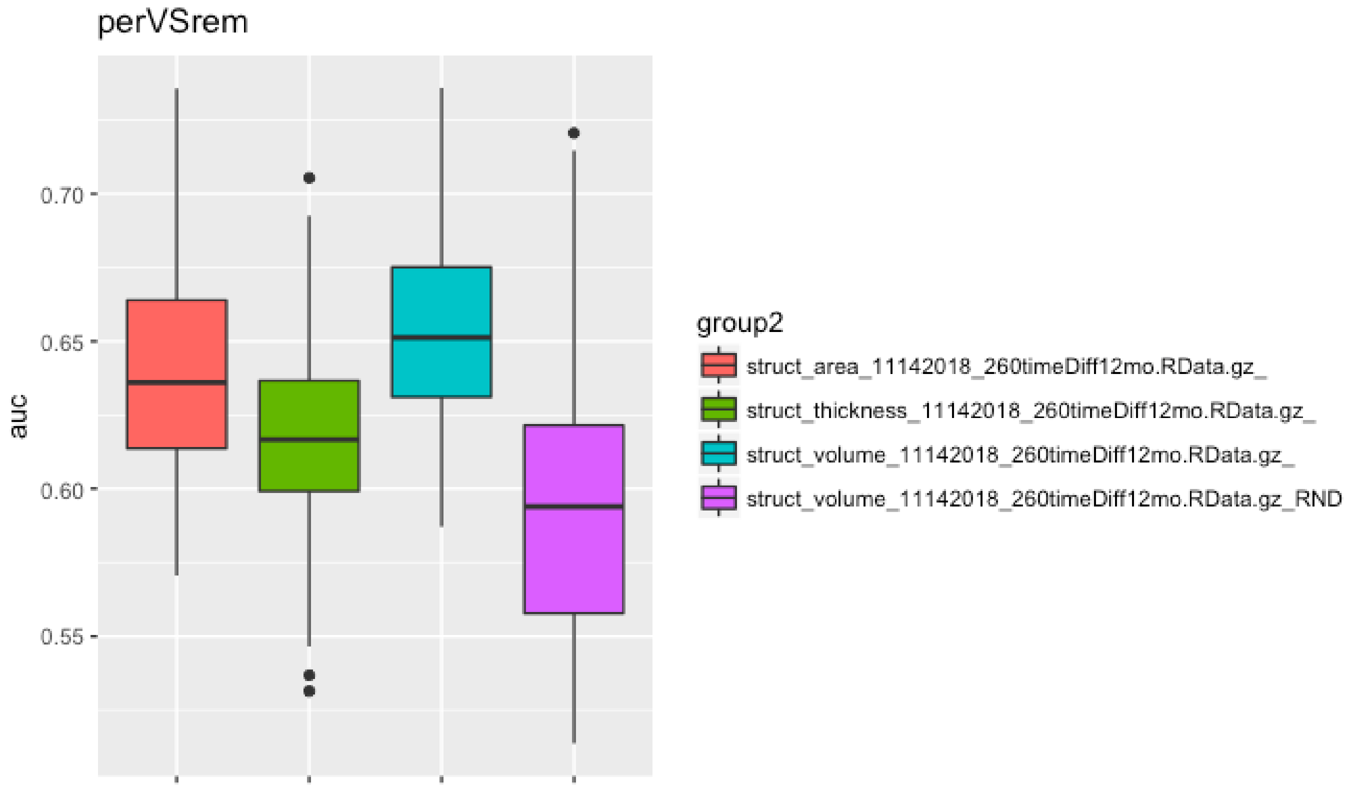

nvVSper
acc
0.65
0.60
0.55
group2
group2
struct_area_11142018_260timeDiff12mo.RData.gz_
struct_thickness_11142018_260timeDiff12mo.RData.gz_
struct_volume_11142018_260timeDiff12mo.RData.gz_
struct_volume_11142018_260timeDiff12mo.RData.gz_RND

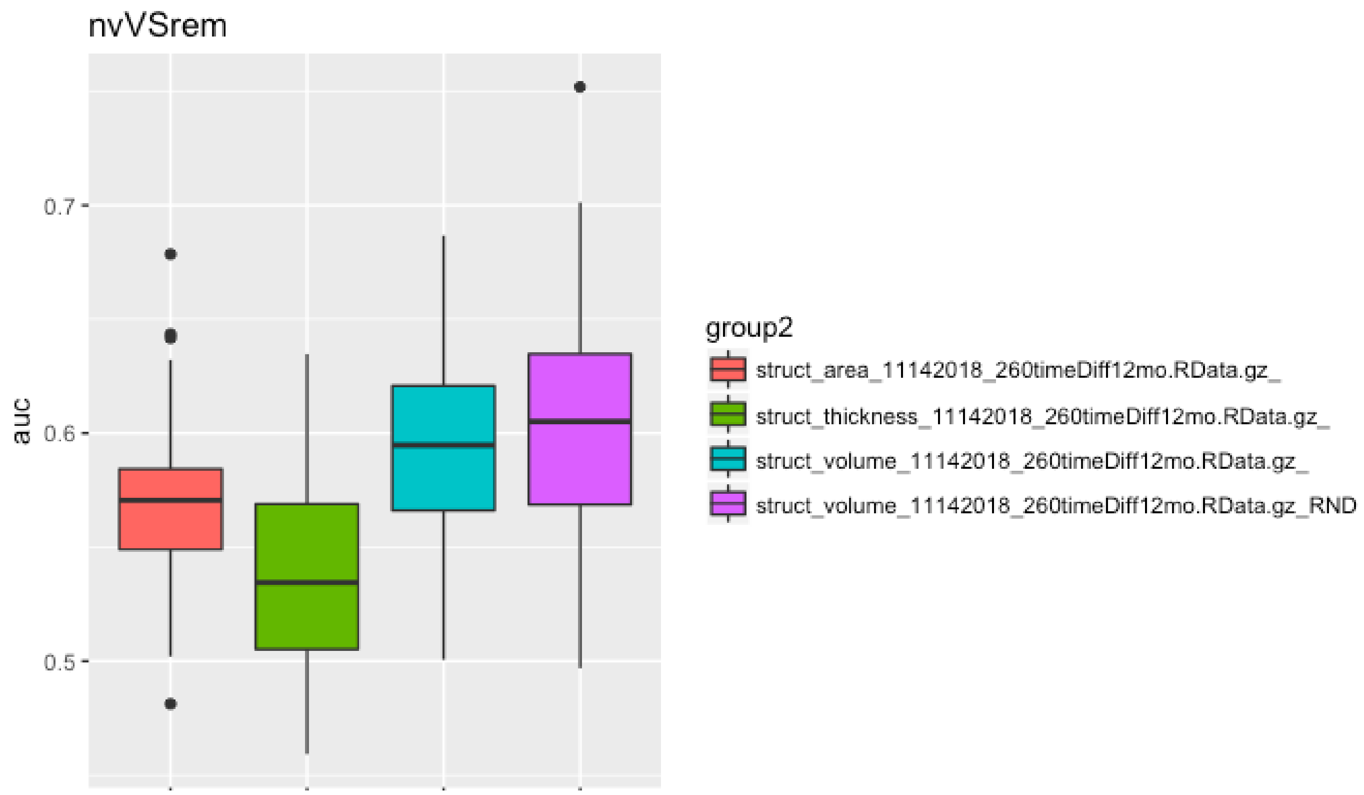

perVSrem
acc
0.775
0.750
0.725
0.700
group2
struct_area_11142018_260timeDiff12mo.RData.gz_
struct_thickness_11142018_260timeDiff12mo.RData.gz_
struct_volume_11142018_260timeDiff12mo.RData.gz_
struct_volume_11142018_260timeDiff12mo.RData.gz_RND

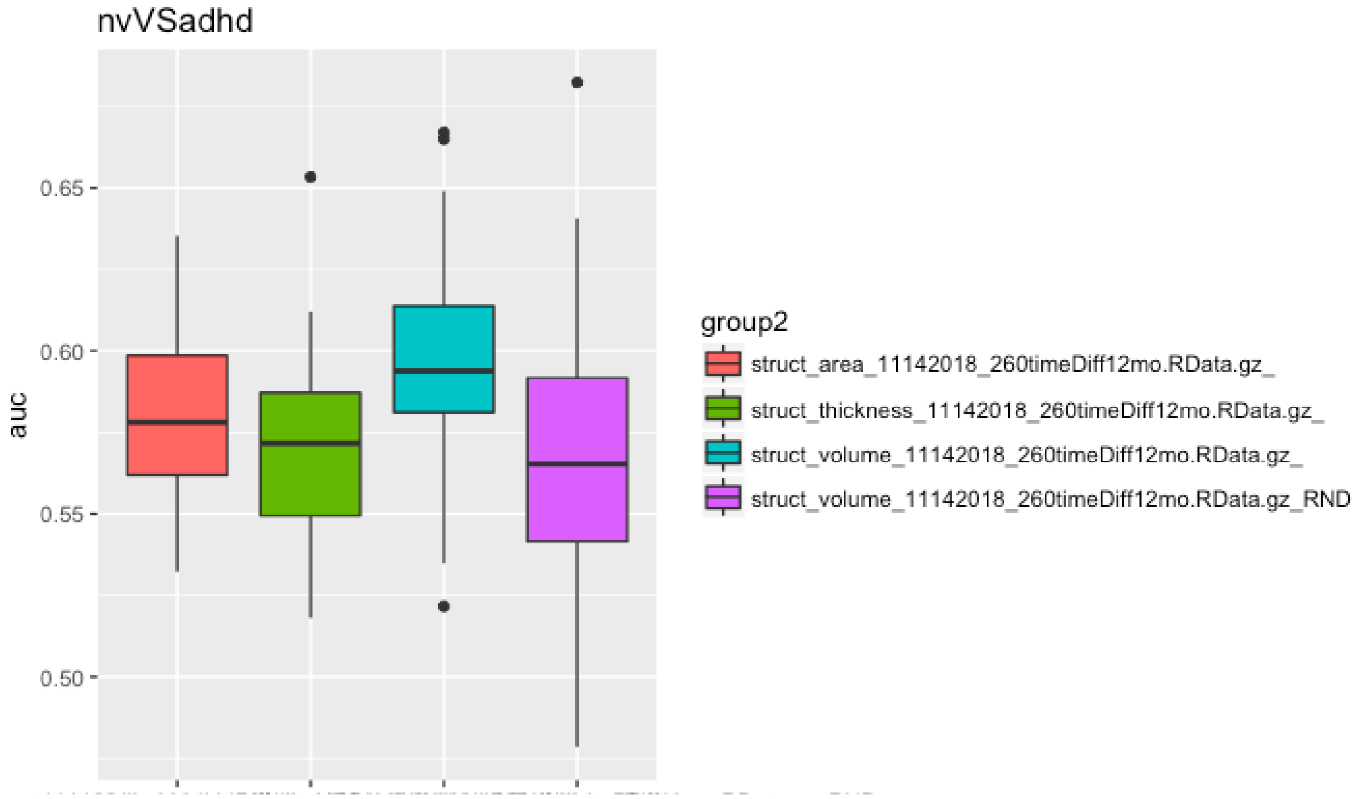

nvVSrem
acc
0.80
0.76
0.72
0.68
0.64
group2
struct_area_11142018_260timeDiff12mo.RData.gz_
struct_thickness_11142018_260timeDiff12mo.RData.gz_
struct_volume_11142018_260timeDiff12mo.RData.gz_
struct_volume_11142018_260timeDiff12mo.RData.gz_RND


nvVSadhd
acc
0.65
0.60
0.55
group2
struct_area_11142018_260timeDiff12mo.RData.gz_
struct_thickness_11142018_260timeDiff12mo.RData.gz_
struct_volume_11142018_260timeDiff12mo.RData.gz_
struct_volume_11142018_260timeDiff12mo.RData.gz_RND


nvVSper
auc
0.70
0.65
0.60
0.55
0.50
group2
struct_area_11142018_260timeDiff12mo.RData.gz_
struct_thickness_11142018_260timeDiff12mo.RData.gz_
struct_volume_11142018_260timeDiff12mo.RData.gz_
struct_volume_11142018_260timeDiff12mo.RData.gz_RND


perVSrem
auc
0.70
0.65
0.60
0.55
group2
struct_area_11142018_260timeDiff12mo.RData.gz_
struct_thickness_11142018_260timeDiff12mo.RData.gz_
struct_volume_11142018_260timeDiff12mo.RData.gz_
struct_volume_11142018_260timeDiff12mo.RData.gz_RND





Nothing terribly impressive. Maybe if we combine it with DTI?

Before we do that, let's run the combined struct dataset... it's the same as DTI_ALL, but I just didn't create one big file.

```
job_name=combinedStructDS_rawDL;
mydir=/data/NCR_SBRB/baseline_prediction/;
swarm_file=swarm.automl_${job_name};
```

```
rm -rf $swarm_file;
f="${mydir}/struct_area_11142018_260timeDiff12mo.RData.gz,${mydir}/struct_
volume_11142018_260timeDiff12mo.RData.gz,${mydir}/struct_thickness_1114201
8_260timeDiff12mo.RData.gz";
for target in nvVSper nvVSrem perVSrem nvVSadhd; do
    for i in {1..100}; do
        myseed=$RANDOM;
        echo "Rscript --vanilla
~/research_code/automl/raw_multiDomain_autoValidation_oneAlgo.R $f
${mydir}/long_clin_0918.csv ${target}
${mydir}/models_raw_within_DL/${USER}  $myseed DeepLearning" >>
$swarm_file;
        echo "Rscript --vanilla
~/research_code/automl/raw_multiDomain_autoValidation_oneAlgo.R $f
${mydir}/long_clin_0918.csv ${target}
${mydir}/models_raw_within_DL/${USER}  -$myseed DeepLearning" >>
$swarm_file;
    done;
done
sed -i -e "s/^/unset http_proxy; /g" $swarm_file;
swarm -f $swarm_file -g 60 -t 16 --time 3:00:00 --partition norm --logdir
trash_${job_name} --job-name ${job_name} -m R --gres=lscratch:10;
```