

GridCAT Threshold Comparison

C Newton

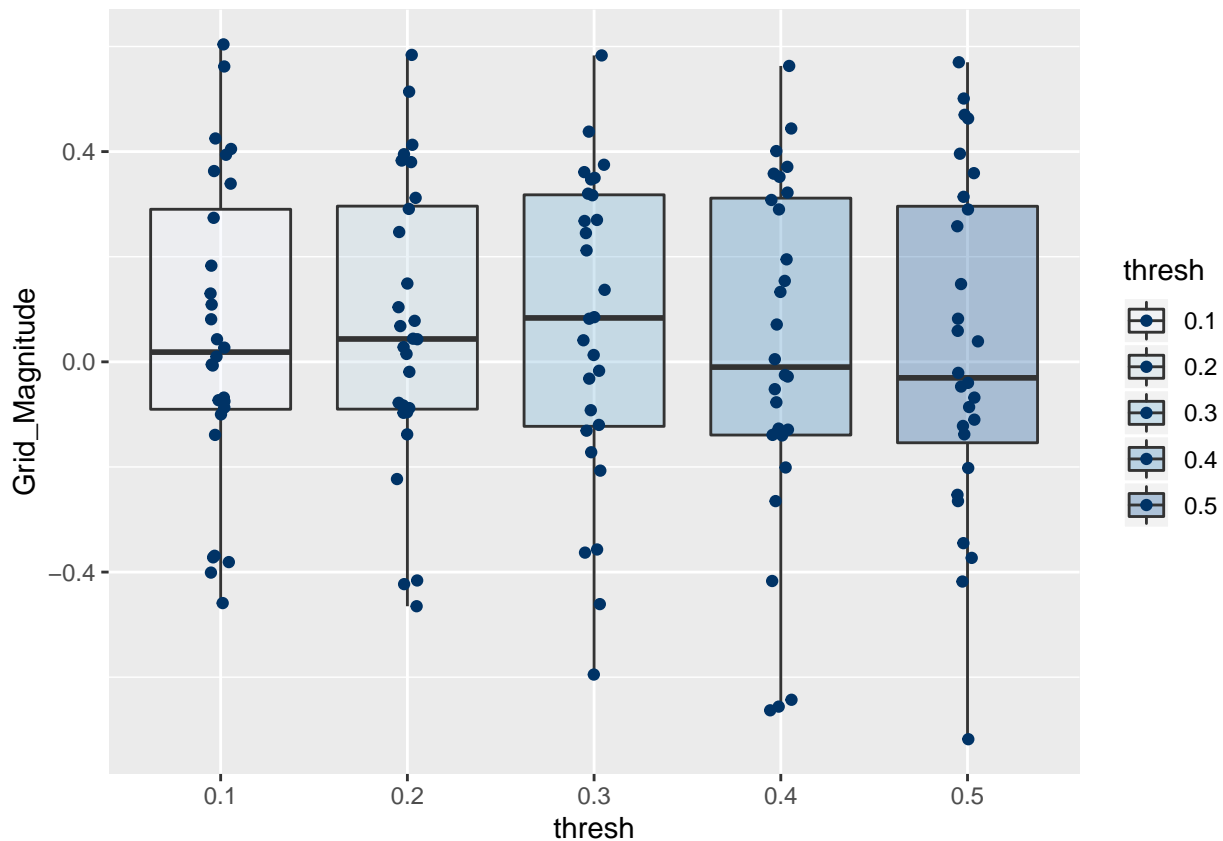
3/11/2021

Analysis of effect of SPM thresholds on gridCAT

Looking at 0.1,0.2,0.3,0.4,0.5 levels of amplitude threshold in SPM fMRI estimation models

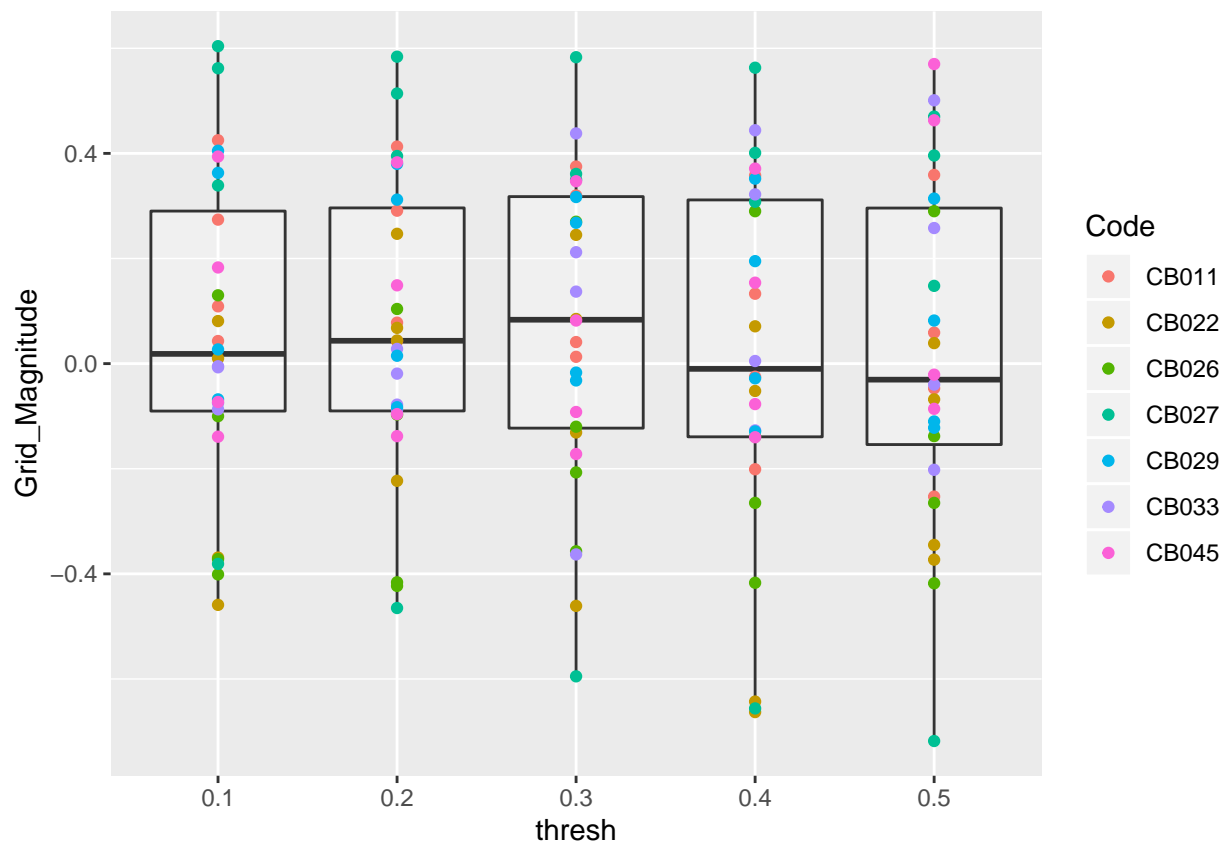
Effect of SPM threshold on grid magnitude for right pmEC xFold model

```
ggplot(data=GC.pmRight.mag,aes(thresh,Grid_Magnitude)) +  
  geom_boxplot(aes(fill=thresh),alpha=0.3) +  
  geom_point(aes(colour=thresh),position=position_jitterdodge()) +  
  scale_colour_manual(values=c("#003366","#003366","#003366","#003366","#003366")) +  
  scale_fill_brewer(palette = "Blues")
```



On a subject level basis (shows runs1-3 and allRuns average per subject)

```
ggplot(data=GC.pmRight.mag,aes(thresh,Grid_Magnitude)) +  
  geom_boxplot(alpha=0.3) +  
  geom_point(aes(colour=Code))
```

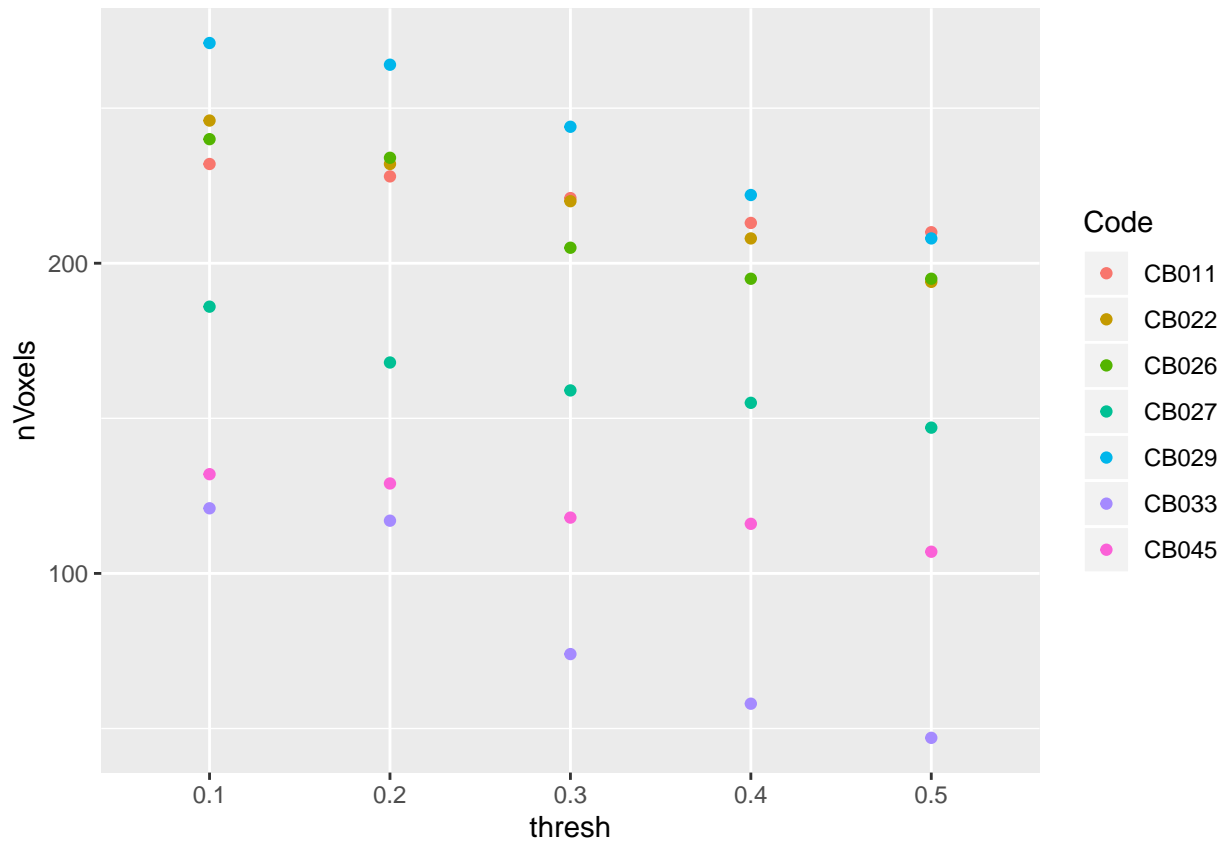


```
#scale_colour_manual(values=c("#003366", "#003366", "#003366", "#003366", "#003366")) +
#scale_fill_brewer(palette = "Blues")
```

Effect of nVoxels included in mask per threshold

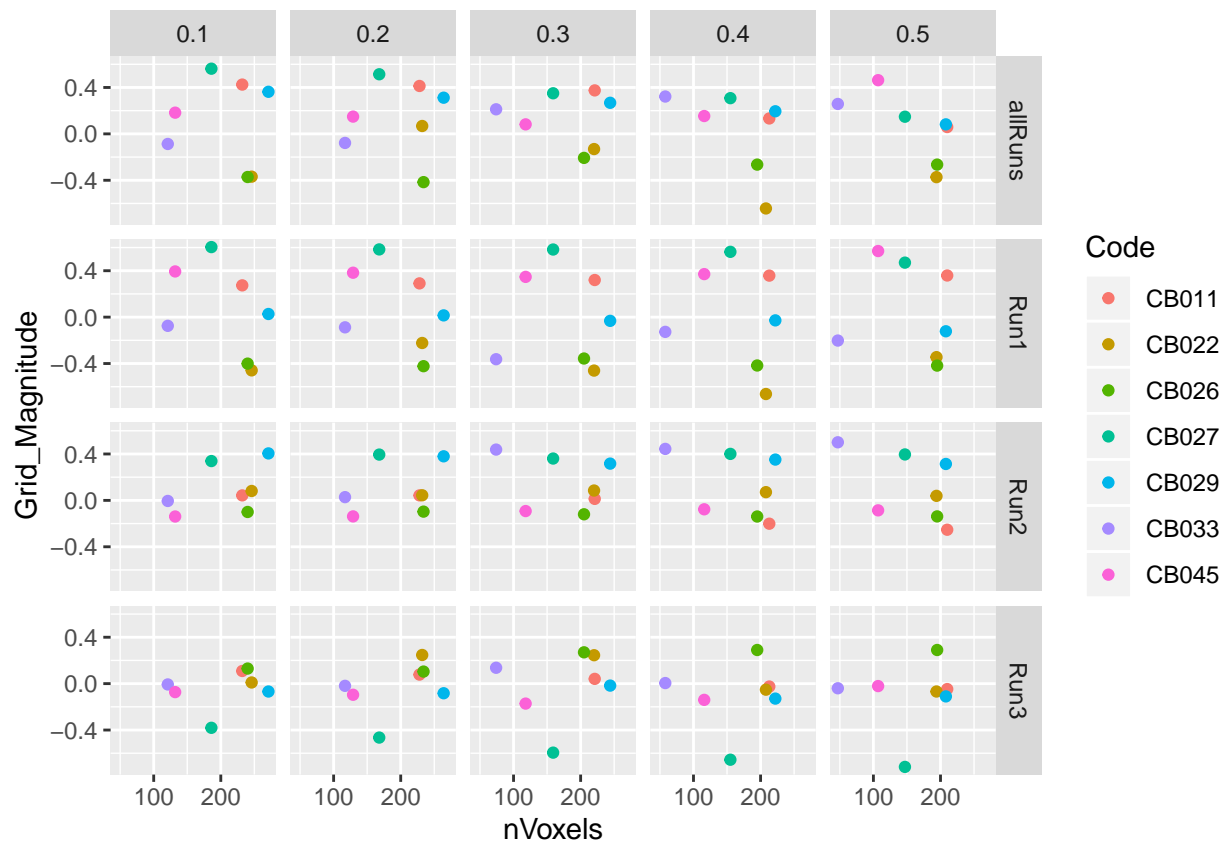
Higher threshold = fewer voxels kept in mask for estimation

```
ggplot(filter(GC.pmRight.mag, Run=="allRuns"), aes(thresh, nVoxels)) +
  geom_point(aes(colour=Code))
```



How number of voxels in mask associates with grid magnitude for each threshold and per run (so data point in each graph will change according to number of voxels and grid magnitude)

```
ggplot(GC.pmRight.mag, aes(nVoxels, Grid_Magnitude)) +  
  geom_point(aes(colour=Code)) +  
  facet_grid(Run~thresh)
```



For just all runs averaged

```
ggplot(filter(GC.pmRight.mag, Run=="allRuns"), aes(nVoxels, Grid_Magnitude)) +  
  geom_point(aes(colour=Code)) +  
  facet_wrap(~thresh)
```

