```
[1]
"inatt,dummy,~/Downloads/gf impute based dti 165.csv,10,10,0.575597,0.0004
70"
source('~/research code/baseline prediction/nonstacked slope dataImpute du
mmy R')
[1]
"hi,dummy,~/Downloads/gf impute based dti 165.csv,10,10,0.021220,0.005598"
"hi,dummy,~/Downloads/gf impute based dti 165.csv,10,10,0.473793,0.000312"
source('~/research code/baseline prediction/nonstacked slope dataImpute du
mmy R')
[1]
"inatt,dummy,~/Downloads/qf impute based anatomy 272.csv,10,10,0.016953,0.
008076"
[1]
"inatt,dummy,~/Downloads/gf impute based anatomy 272.csv,10,10,0.641928,0.
source('~/research_code/baseline_prediction/nonstacked_slope_dataImpute_du
mmy R')
[1]
"hi,dummy,~/Downloads/gf_impute_based_anatomy_272.csv,10,10,0.009601,0.003
542"
[1]
"hi,dummy,~/Downloads/gf_impute_based_anatomy_272.csv,10,10,0.545485,0.000
228"
```

2020-03-20 15:32:28

I created a distribution using multiple reps there, so now we can access p-values for our results. But let's also check the best way of maximize the results:

```
res =
read.csv('~/data/baseline_prediction/prs_start/residsFixed_slope_impInter.
csv', header=F)
colnames(res) = c('sx', 'model', 'fname', 'nfolds', 'nreps', 'meanRMSE',
'sdRMSE')
res[which.min(res$meanRMSE),]
```

Our best RMSE result is for hi, using the dti data:

```
> res[which.min(res$meanRMSE),]
    sx     model
537 hi blassoAveraged
fname
```

```
537
/home/sudregp/data/baseline_prediction/prs_start/gf_impute_based_dti_165.c
    nfolds nreps meanRMSE sdRMSE
537
              10 0.459838
        10
                       0verall
                         100.00
striatumR 165
0FCR_165
                          89.81
unc_adR
                          86.02
amygdalaR_165
                          66.71
thalamusR_165
                          66.37
ADHD_PRS0.050000.origR
                         57.52
slf_rdR
                          55.67
ilf adR
                         43.52
ADHD_PRS0.100000.origR
                         42.60
slf_adR
                          35.79
                         34.90
cingulateR 165
ADHD PRS0.200000.origR
                         34.64
CC rd R
                          34.03
cing rdR
                         32.92
ADHD PRS0.300000.origR
                         30.89
CST rdR
                         29.96
unc_rdR
                          29.88
VMI.beery_RAW_IR
                          28.70
PS_RAW_IR_165
                          28.56
CC_ad_R
                          27.51
[1]
"hi,blassoAveraged,/home/sudregp/data/baseline_prediction/prs_start/gf_imp
ute_based_dti_165.csv,10,10,0.459838,NA"
```

The inatt result for that model is:

```
SX
                   model
533 inatt blassoAveraged
fname
533
/home/sudregp/data/baseline_prediction/prs_start/gf_impute_based_dti_165.c
SV
    nfolds nreps meanRMSE sdRMSE
533
        10
              10 0.562877
                              NA
                       0verall
FSIQ IR 165
                        100.00
PS_RAW_IR_165
                         71.41
cerebellumR_165
                         64.31
striatumR_165
                         61.78
                         56.15
unc_adR
                         53.69
ADHD_PRS0.400000.origR
ADHD_PRS0.500000.origR
                         49.13
ADHD_PRS0.005000.origR
                         46.43
```

```
amygdalaR_165
                          46.16
0FCR 165
                          44.94
                          41.58
lateral_PFCR_165
CC_ad_R
                          41.45
slf rdR
                          41.05
ADHD_PRS0.010000.origR
                          39.29
cing_adR
                          38.55
ilf adR
                          38.44
ADHD PRS0.300000.origR
                          36.67
CC_rd_R
                          35.80
unc_rdR
                          33.27
SS_RAW_IR_165
                          32.81
[1]
"inatt,blassoAveraged,/home/sudregp/data/baseline_prediction/prs_start/gf_
impute_based_dti_165.csv,10,10,0.562877,NA"
```

If we restrict it to the best inatt results in DTI, we get:

```
614 inatt blackboost
fname
614
/home/sudregp/data/baseline_prediction/prs_start/gf_impute_based_dti_165.c
SV
    nfolds nreps meanRMSE sdRMSE
        10
              10 0.562351
614
  only 20 most important variables shown (out of 40)
                        0verall
FSIQ_IR_165
                         100.00
PS RAW IR 165
                          71.41
cerebellumR_165
                          64.31
striatumR_165
                          61.78
                          56.15
unc_adR
ADHD_PRS0.400000.origR
                          53.69
ADHD_PRS0.500000.origR
                          49.13
ADHD_PRS0.005000.origR
                          46.43
amygdalaR_165
                          46.16
0FCR_165
                          44.94
lateral_PFCR_165
                          41.58
CC_ad_R
                          41.45
slf_rdR
                          41.05
ADHD_PRS0.010000.origR
                          39.29
                          38.55
cing_adR
ilf_adR
                          38.44
ADHD_PRS0.300000.origR
                          36.67
CC_rd_R
                          35.80
                          33.27
unc_rdR
SS_RAW_IR_165
                          32.81
[1]
```

"inatt,blackboost,/home/sudregp/data/baseline_prediction/prs_start/gf_impute_based_dti_165.csv,10,10,0.562351,0.000000"

and the HI correspondent is:

```
model
615 hi blackboost
fname
615
/home/sudregp/data/baseline_prediction/prs_start/gf_impute_based_dti_165.c
    nfolds nreps meanRMSE sdRMSE
615
        10 10 0.460291
  only 20 most important variables shown (out of 40)
                       0verall
striatumR 165
                        100.00
0FCR 165
                         89.81
                         86.02
unc_adR
amygdalaR 165
                         66.71
                         66.37
thalamusR_165
ADHD_PRS0.050000.origR
                         57.52
slf rdR
                         55.67
ilf_adR
                         43.52
ADHD_PRS0.100000.origR
                         42.60
slf_adR
                         35.79
                         34.90
cingulateR_165
                         34.64
ADHD_PRS0.200000.origR
CC_rd_R
                         34.03
                         32.92
cing_rdR
ADHD_PRS0.300000.origR
                         30.89
CST_rdR
                         29.96
unc rdR
                         29.88
                         28.70
VMI.beery_RAW_IR
PS_RAW_IR_165
                         28.56
                         27.51
CC_ad_R
[1]
"hi,blackboost,/home/sudregp/data/baseline_prediction/prs_start/gf_impute_
based_dti_165.csv,10,10,0.460291,0.000000"
```

Switching now to the anatomy data, which is always worse than the DTI results, we check the best model:

```
sx model
513 hi svmLinear
fname
513
```

```
/home/sudregp/data/baseline_prediction/prs_start/gf_impute_based_anatomy_2
    nfolds nreps meanRMSE sdRMSE
513
        10
              10 0.522771
                               NA
                                0verall
OFCR
                                 100.00
amygdalaR
                                  93.35
striatumR
                                  91.60
ADHD_PRS0.000050.origR
                                  74.13
VMI.beery_RAW_IR
                                  46.85
ADHD_PRS0.000100.origR
                                  38.24
                                  34.17
cinqulateR
thalamusR
                                  30.30
PS_RAW_IR
                                  30.14
                                  29.04
DS RAW IR
lateral PFCR
                                  26.17
cerebellumR
                                  19.51
FSIQ IR
                                  17.57
EstimatedTotalIntraCranialVolR
                                  17.34
                                  15.35
ADHD PRS0.000500.origR
ADHD_PRS0.001000.origR
                                  15.28
ADHD PRS0.100000.origR
                                  14.84
ADHD_PRS0.500000.origR
                                  14.39
ADHD_PRS0.200000.origR
                                  13.59
ADHD_PRS0.050000.origR
                                  12.09
[1]
"hi,svmLinear,/home/sudregp/data/baseline_prediction/prs_start/gf_impute_b
ased_anatomy_272.csv,10,10,0.522771,NA"
```

That is for hi, and its counterpart in inatt is:

```
model
       SX
508 inatt svmLinear
fname
508
/home/sudregp/data/baseline_prediction/prs_start/gf_impute_based_anatomy_2
72.csv
    nfolds nreps meanRMSE sdRMSE
        10
508
              10 0.64174
                               NA
                                 100.00
FSIQ_IR
striatumR
                                  50.63
amygdalaR
                                  50.43
                                  44.79
PS RAW IR
0FCR
                                  41.07
ADHD_PRS0.000100.origR
                                  36.09
ADHD_PRS0.000050.origR
                                  35.40
                                  29.34
ADHD_PRS0.500000.origR
ADHD_PRS0.001000.origR
                                  28.15
ADHD_PRS0.005000.origR
                                  27.78
ADHD_PRS0.400000.origR
                                  27.50
```

```
EstimatedTotalIntraCranialVolR
                                 26.43
VMI.beery_RAW_IR
                                 23.84
thalamusR
                                 23.63
SS RAW IR
                                 23.04
lateral PFCR
                                 21.53
ADHD PRS0.300000.origR
                                 19.91
cingulateR
                                 17.69
ADHD PRS0.100000.origR
                                 17.38
ADHD PRS0.000500.origR
                                 17.10
"inatt,svmLinear,/home/sudregp/data/baseline_prediction/prs_start/gf_imput
e_based_anatomy_272.csv,10,10,0.641740,NA"
```

Conversely, the best inatt for is:

```
model
       SX
541 inatt cforest
fname
541
/home/sudregp/data/baseline_prediction/prs_start/gf_impute_based_anatomy_2
    nfolds nreps meanRMSE
                            sdRMSE
541
              10 0.619933 0.000505
                       0verall
FSIQ_IR
                       100.000
sex_numeric
                        47.797
ADHD_PRS0.000100.origR 46.733
                        46.726
PS_RAW_IR
ADHD_PRS0.001000.origR 28.726
ADHD_PRS0.005000.origR 25.707
striatumR
                        20.324
ADHD_PRS0.400000.origR 18.904
thalamusR
                        18.021
DS_RAW_IR
                        15.366
ADHD_PRS0.200000.origR 15.126
ADHD_PRS0.300000.origR 14.252
VMI.beery_RAW_IR
                        14.008
ADHD_PRS0.500000.origR 10.230
lateral_PFCR
                        7.659
ADHD_PRS0.010000.origR 7.592
amygdalaR
                         7.002
SES_group3
                         6.229
ADHD PRS0.050000.origR
                         5.844
ADHD_PRS0.000500.origR
                         5.699
"inatt,cforest,/home/sudregp/data/baseline_prediction/prs_start/gf_impute_
based_anatomy_272.csv,10,10,0.619933,0.000505"
```

and it's counterpart in hi is:

```
model
    SX
545 hi cforest
fname
545
/home/sudregp/data/baseline_prediction/prs_start/gf_impute_based_anatomy_2
    nfolds nreps meanRMSE
                            sdRMSE
545
        10
              10 0.52578 0.000603
                       0verall
striatumR
                        100.00
OFCR
                         96.78
                         93.80
amygdalaR
                         72.56
VMI.beery_RAW_IR
ADHD_PRS0.000050.origR
                         38.74
SES_group3
                         33.22
FSIQ IR
                         32.10
ADHD PRS0.100000.origR
                         25.31
ADHD_PRS0.400000.origR
                         25.18
lateral PFCR
                         24.98
ADHD_PRS0.050000.origR
                         22.02
ADHD_PRS0.000100.origR 19.93
                         18.85
ADHD_PRS0.500000.origR
ADHD_PRS0.300000.origR
                         18.32
SS_RAW_IR
                         18.27
sex_numeric
                         17.91
ADHD_PRS0.001000.origR
                         17.51
                         16.92
DS_RAW_IR
ADHD_PRS0.200000.origR
                         16.57
cerebellumR
                         16.03
[1]
"hi,cforest,/home/sudregp/data/baseline_prediction/prs_start/gf_impute_bas
ed_anatomy_272.csv,10,10,0.525780,0.000603"
```

Now, let's redo everything for R2. First, DTI dataset:

Best hi:

```
sx model
510 hi rvmLinear

fname
510
/home/sudregp/data/baseline_prediction/prs_start/gf_impute_based_dti_165.c
sv
    nfolds nreps    meanR2 sdR2
510    10    10 0.102126    NA
```

```
0verall
striatumR_165
                         100.00
0FCR_165
                          89.81
unc adR
                          86.02
amygdalaR 165
                          66.71
thalamusR_165
                          66.37
ADHD PRS0.050000.origR
                          57.52
slf rdR
                          55.67
ilf_adR
                          43.52
ADHD_PRS0.100000.origR
                          42.60
                          35.79
slf_adR
cingulateR_165
                          34.90
ADHD_PRS0.200000.origR
                          34.64
CC_rd_R
                          34.03
cing_rdR
                          32.92
ADHD_PRS0.300000.origR
                          30.89
                          29.96
CST rdR
unc rdR
                          29.88
                          28.70
VMI.beery_RAW_IR
PS_RAW_IR_165
                          28.56
CC_ad_R
                          27.51
[1]
"hi,rvmLinear,/home/sudregp/data/baseline_prediction/prs_start/gf_impute_b
ased_dti_165.csv,10,10,0.102126,NA"
```

Counterpart inatt:

```
0verall
FSIQ_IR_165
                         100.00
PS_RAW_IR_165
                          71.41
                          64.31
cerebellumR_165
striatumR_165
                          61.78
unc_adR
                          56.15
ADHD_PRS0.400000.origR
                          53.69
ADHD_PRS0.500000.origR
                          49.13
ADHD_PRS0.005000.origR
                          46.43
amygdalaR_165
                          46.16
0FCR_165
                          44.94
lateral_PFCR_165
                          41.58
CC_ad_R
                          41.45
slf rdR
                          41.05
ADHD_PRS0.010000.origR
                          39.29
cing_adR
                          38.55
ilf adR
                          38.44
ADHD_PRS0.300000.origR
                          36.67
CC_rd_R
                          35.80
unc_rdR
                          33.27
SS_RAW_IR_165
                          32.81
"inatt,rvmLinear,/home/sudregp/data/baseline_prediction/prs_start/gf_imput
e_based_dti_165.csv,10,10,0.067602,NA"
```

Best inatt:

```
model
       SX
312 inatt kernelpls
fname
312
/home/sudregp/data/baseline_prediction/prs_start/gf_impute_based_dti_165.c
SV
    nfolds nreps
                   meanR2
                               sdR2
312
        10
              10 0.081295 0.012537
                                    Overall
PS_RAW_IR_165
                                     100.00
                                      69.32
sex_numeric
SS_RAW_IR_165
                                      50.62
0FCR_165
                                      49.91
CC ad R
                                      47.37
ADHD_PRS0.050000.origR
                                      43.59
ilf_adR
                                      42.87
cerebellumR 165
                                      42.25
                                      41.56
FSIQ_IR_165
CC_rd_R
                                      40.01
                                      36.62
cing_adR
                                      36.59
ADHD_PRS0.000100.origR
ADHD_PRS0.000050.origR
                                      31.97
ilf_rdR
                                      31.26
DS_RAW_IR_165
                                      26.80
ADHD_PRS0.010000.origR
                                      25.71
                                      25.53
cingulateR_165
slf_rdR
                                      24.12
EstimatedTotalIntraCranialVolR_165
                                      22.72
lateral_PFCR_165
                                      22.65
[1]
"inatt, kernelpls, ~/Downloads/gf_impute_based_dti_165.csv,10,10,0.081295,0.
012537"
```

Counterpart hi:

```
sx model
329 hi kernelpls

fname
329
/home/sudregp/data/baseline_prediction/prs_start/gf_impute_based_dti_165.c
sv
    nfolds nreps meanR2 sdR2
329 10 10 0.094364 0.011303
```

```
0verall
unc_adR
                                      100.00
striatumR_165
                                      95.38
amygdalaR 165
                                      87.43
VMI.beery RAW IR
                                      83.69
cingulateR_165
                                      79.42
                                      72.98
slf adR
slf rdR
                                      68.00
SES_group3_165
                                      55.47
ilf_adR
                                      44.27
ADHD_PRS0.050000.origR
                                      44.16
0FCR_165
                                      41.28
ADHD_PRS0.000500.origR
                                      40.54
cerebellumR 165
                                      38.57
EstimatedTotalIntraCranialVolR_165
                                      38.20
ilf rdR
                                      36.74
ADHD PRS0.100000.origR
                                      34.85
DS RAW IR 165
                                      34.81
ADHD_PRS0.000100.origR
                                      33.01
ADHD_PRS0.500000.origR
                                      29.77
thalamusR 165
                                      29.49
[1]
"hi, kernelpls, ~/Downloads/gf_impute_based_dti_165.csv, 10, 10, 0.094364, 0.011
```

Then, anatomy dataset:

Best hi:

```
model
    SX
571 hi bagEarth
fname
571
/home/sudregp/data/baseline_prediction/prs_start/gf_impute_based_anatomy_2
72.csv
    nfolds nreps meanR2
                             sdR2
571
              10 0.09305 0.004943
       10
  only 20 most important variables shown (out of 28)
                                0verall
0FCR
                                100.000
striatumR
                                84.676
ADHD_PRS0.000100.origR
                                74.440
VMI.beery_RAW_IR
                                62.347
cingulateR
                                51.312
DS_RAW_IR
                                38.942
ADHD_PRS0.100000.origR
                                25.506
ADHD_PRS0.400000.origR
                                14.003
lateral PFCR
                                 8.521
```

```
thalamusR
                                  2.293
ADHD PRS0.050000.origR
                                  0.000
ADHD_PRS0.001000.origR
                                  0.000
PS RAW IR
                                  0.000
ADHD PRS0.010000.origR
                                  0.000
ADHD PRS0.200000.origR
                                  0.000
EstimatedTotalIntraCranialVolR
                                  0.000
amygdalaR
                                  0.000
ADHD_PRS0.005000.origR
                                  0.000
cerebellumR
                                  0.000
sex_numeric
                                  0.000
[1]
"hi,bagEarth,/home/sudregp/data/baseline_prediction/prs_start/gf_impute_ba
sed_anatomy_272.csv,10,10,0.093050,0.004943"
```

Counterpart inatt:

```
573 inatt bagEarth
fname
573
/home/sudregp/data/baseline_prediction/prs_start/gf_impute_based_anatomy_2
    nfolds nreps
                   meanR2
                               sdR2
573
              10 0.060669 0.011501
        10
  only 20 most important variables shown (out of 28)
                                0verall
                                    100
VMI.beery_RAW_IR
                                      0
ADHD_PRS0.000100.origR
                                      0
population_self2
ADHD_PRS0.300000.origR
                                      0
striatumR
                                      0
SS_RAW_IR
                                      0
                                      0
SES_group3
ADHD_PRS0.000500.origR
                                      0
thalamusR
                                      0
ADHD_PRS0.100000.origR
                                      0
0FCR
                                      0
                                      0
cingulateR
EstimatedTotalIntraCranialVolR
                                      0
lateral PFCR
                                      0
ADHD_PRS0.050000.origR
                                      0
PS_RAW_IR
                                      0
ADHD PRS0.000050.origR
                                      0
ADHD_PRS0.400000.origR
                                      0
FSIQ_IR
ADHD_PRS0.500000.origR
                                      0
[1]
"inatt,bagEarth,/home/sudregp/data/baseline_prediction/prs_start/gf_impute
_based_anatomy_272.csv,10,10,0.060669,0.011501"
```

Best inatt:

```
sx model
572 inatt evtree
fname
572
/home/sudregp/data/baseline_prediction/prs_start/gf_impute_based_anatomy_2
    nfolds nreps
                   meanR2
                               sdR2
572
      10 10 0.067843 0.000728
                                0verall
FSIQ_IR
                                 100.00
striatumR
                                  50.63
                                  50.43
amygdalaR
PS_RAW_IR
                                  44.79
OFCR
                                  41.07
ADHD PRS0.000100.origR
                                  36.09
ADHD PRS0.000050.origR
                                  35.40
ADHD_PRS0.500000.origR
                                  29.34
ADHD PRS0.001000.origR
                                  28.15
ADHD PRS0.005000.origR
                                  27.78
ADHD PRS0.400000.origR
                                  27.50
EstimatedTotalIntraCranialVolR
                                  26.43
VMI.beery_RAW_IR
                                  23.84
thalamusR
                                  23.63
SS_RAW_IR
                                  23.04
lateral_PFCR
                                  21.53
                                  19.91
ADHD_PRS0.300000.origR
                                  17.69
cingulateR
ADHD_PRS0.100000.origR
                                  17.38
ADHD_PRS0.000500.origR
                                  17.10
[1]
"inatt, evtree, /home/sudregp/data/baseline_prediction/prs_start/gf_impute_b
ased_anatomy_272.csv,10,10,0.067843,0.000728"
```

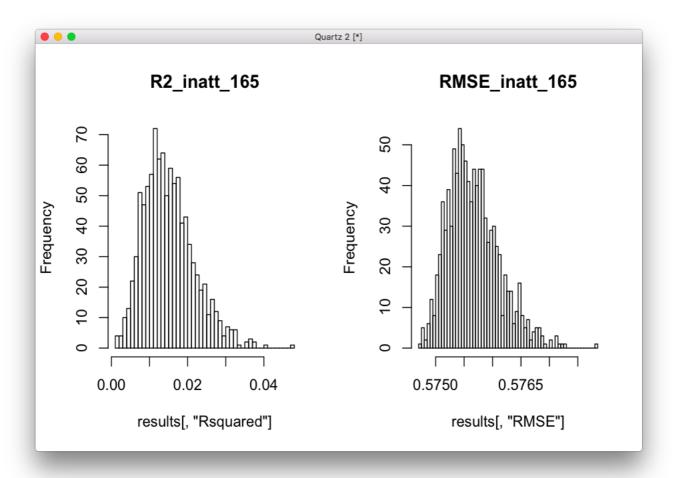
Counterpart hi:

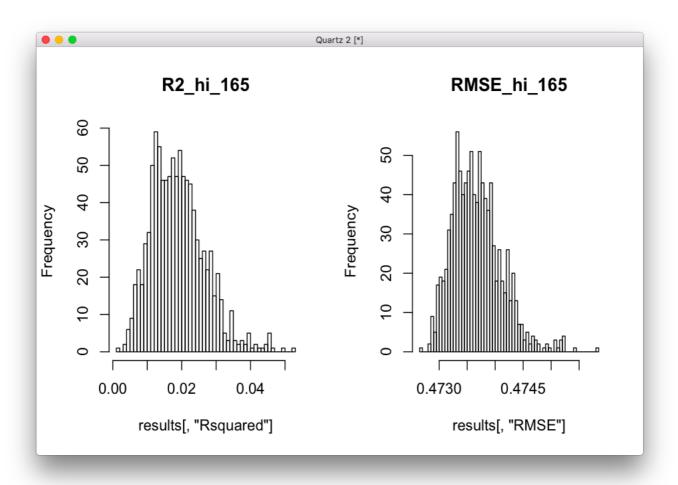
```
OFCR
                                 100.00
amygdalaR
                                  93.35
striatumR
                                  91.60
ADHD_PRS0.000050.origR
                                  74.13
VMI.beery RAW IR
                                  46.85
ADHD PRS0.000100.origR
                                  38.24
                                  34.17
cinqulateR
thalamusR
                                  30.30
PS RAW IR
                                  30.14
                                  29.04
DS RAW IR
lateral_PFCR
                                  26.17
cerebellumR
                                  19.51
FSIQ_IR
                                  17.57
EstimatedTotalIntraCranialVolR
                                  17.34
ADHD PRS0.000500.origR
                                  15.35
ADHD_PRS0.001000.origR
                                  15.28
ADHD_PRS0.100000.origR
                                  14.84
                                  14.39
ADHD PRS0.500000.origR
ADHD PRS0.200000.origR
                                  13.59
ADHD_PRS0.050000.origR
                                  12.09
[1]
"hi,evtree,/home/sudregp/data/baseline_prediction/prs_start/gf_impute_base
d_anatomy_272.csv,10,10,0.063882,0.000685"
```

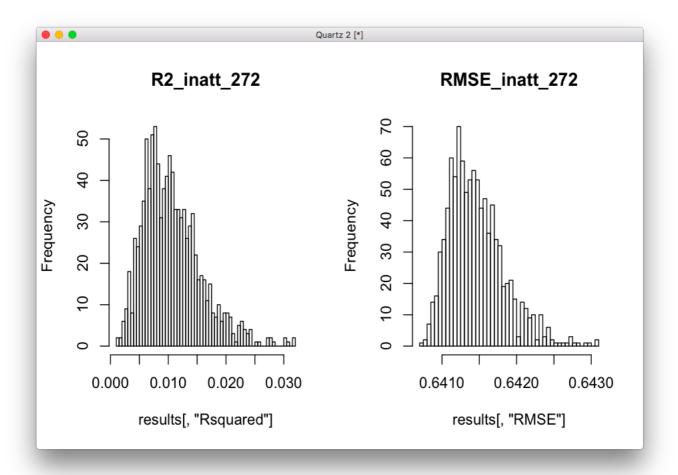
Not much preference here... best to visualize it in Excel. I'll also add p-values there.

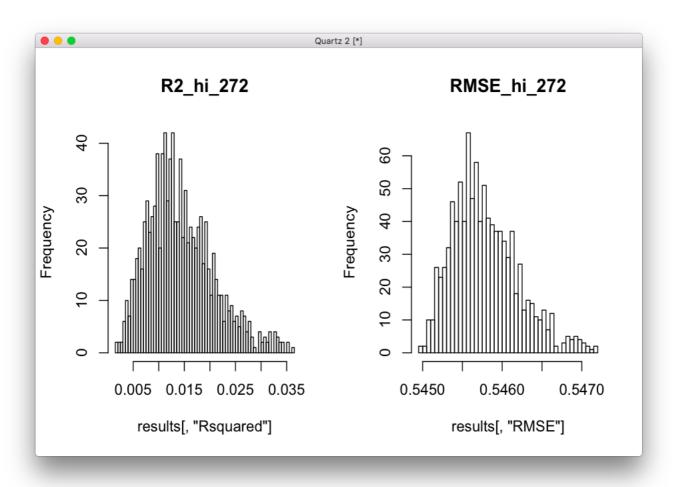
SX	model	metric	value	pval	dataset	notes
inatt	blassoAveraged	RMSE	0.562877	p<.001	DTI	counterpart to best RMSE
hi	blassoAveraged	RMSE	0.459838	p<.001	DTI	best RMSE
inatt	blackboost	RMSE	0.562351	p<.001	DTI	best inatt RMSE; also best average sx results
hi	blackboost	RMSE	0.460291	p<.001	DTI	counterpart to best inatt RMSE
inatt	svmLinear	RMSE	0.64174	p = 0.7987	79! anatomy	counterpart to best RMSE within anatomy
hi	svmLinear	RMSE	0.522771	p<.001	anatomy	best RMSE within anatomy
inatt	cforest	RMSE	0.619933	p<.001	anatomy	best inatt RMSE within anatomy; also best average sx result within anatomy
hi	cforest	RMSE	0.52578	p<.001	anatomy	counterpart to best inatt RMSE within anatomy
inatt	rvmLinear	R2	0.067602	p<.001	DTI	counterpart to best R2
hi	rvmLinear	R2	0.102126	p<.001	DTI	best R2
inatt	kernelpls	R2	0.081295	p<.001	DTI	best inatt R2; also best average sx results
hi	kernelpls	R2	0.094364	p<.001	DTI	counterpart to best inatt R2
inatt	evtree	R2	0.067843	p<.001	anatomy	best inatt R2 within anatomy (best HI didn't work for inatt based on varimp)
hi	evtree	R2	0.063882	p<.001	anatomy	counterpart to best inatt R2 within anatomy

I used 1000 perms there (well, 999), but the null distributions are quite tight, so it makes sense that the results are quite significant.









I think it makes sense to go with the blackboost results in the DTI set. They're quite significant and the variable distribution looks interesting.

If maximizing R2, then the kernelpls results would be the ones to use. The R2 is not too impressive though.

If the goal is to maximize subject instead, and go with the anatomical dataset, we could only use the conditional forest results because symLinear isnot significant for inatt. And the R2 results, although significant, are quite pathetic.