

README

04/13/2024

Experiments with simulated W and π_i 's

```
# please specify the path
path="~/Dropbox/research/decals/DECALS/"
source(paste0(path, "code/DECALS.R"))
load(file=paste0(path, "data/sim1/cp_decals.RData"))
load(file=paste0(path, "data/sim1/cp_ols.RData"))
load(file=paste0(path, "data/sim1/cp_mead.RData"))
# These data are generated by 'simulation1.R'.
```

```
## Loading required package: sm
```

```
## Package 'sm', version 2.2-5.7: type help(sm) for summary information
```

```
## Loading required package: zoo
```

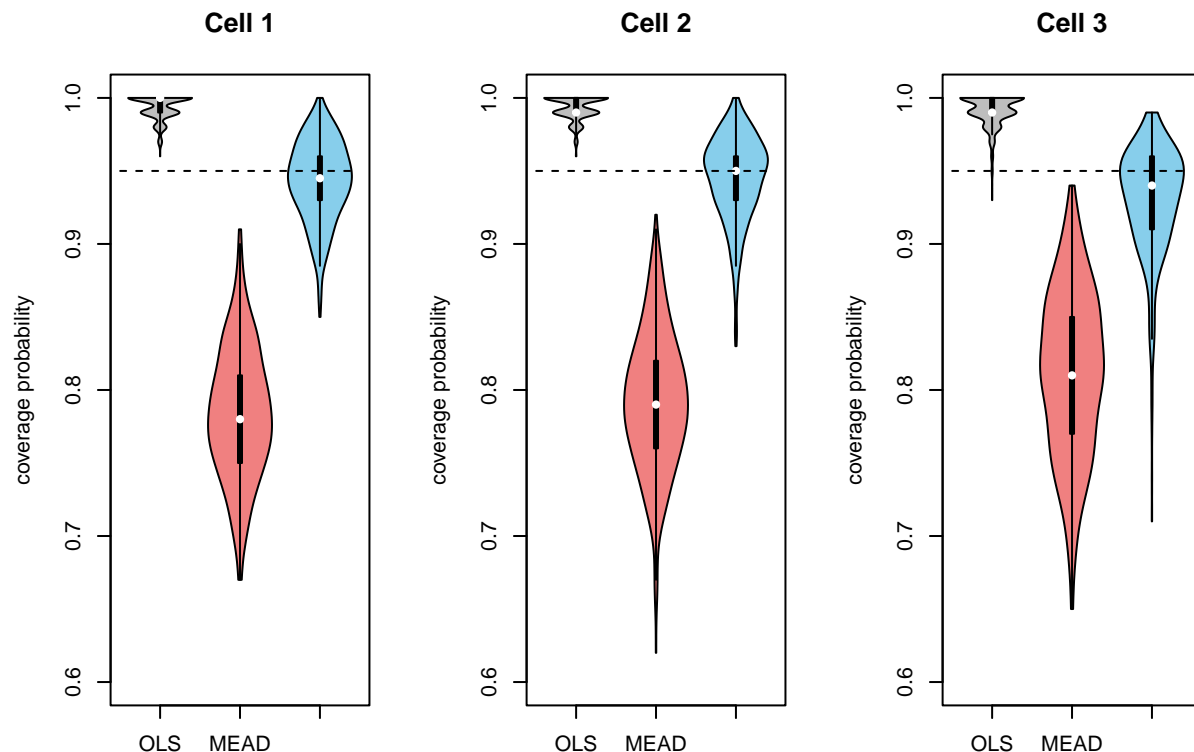
```
##
```

```
## Attaching package: 'zoo'
```

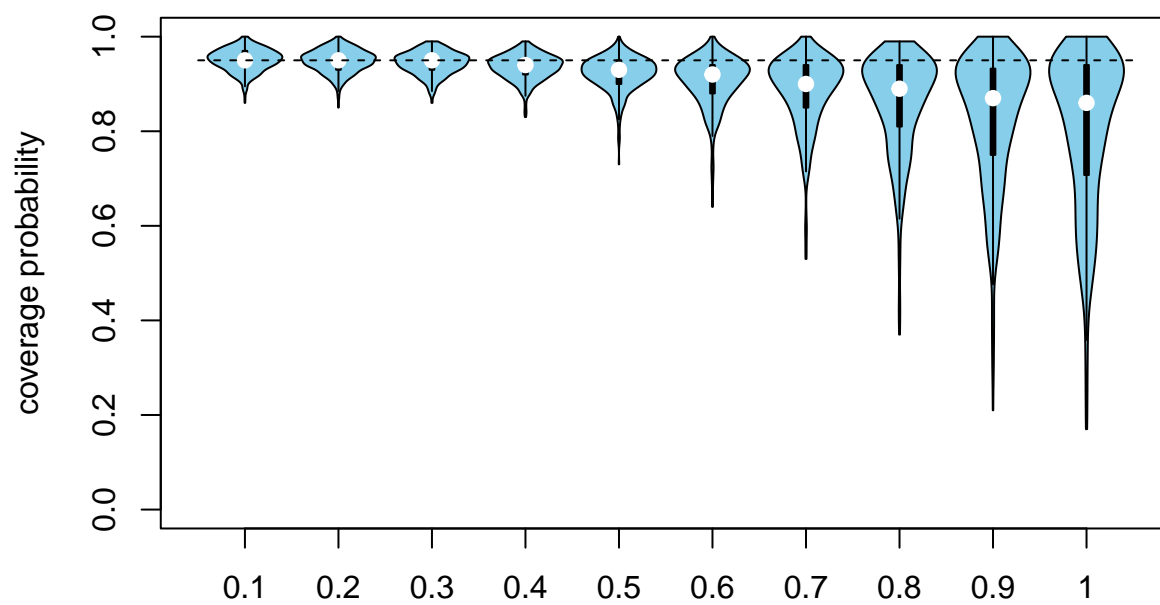
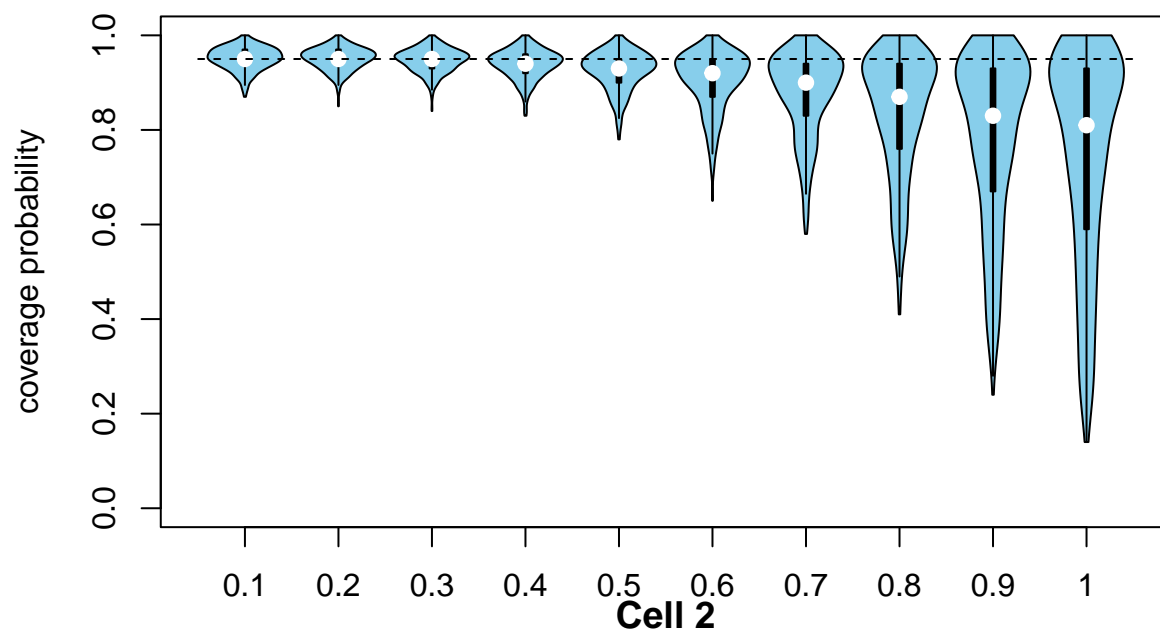
```
## The following objects are masked from 'package:base':
```

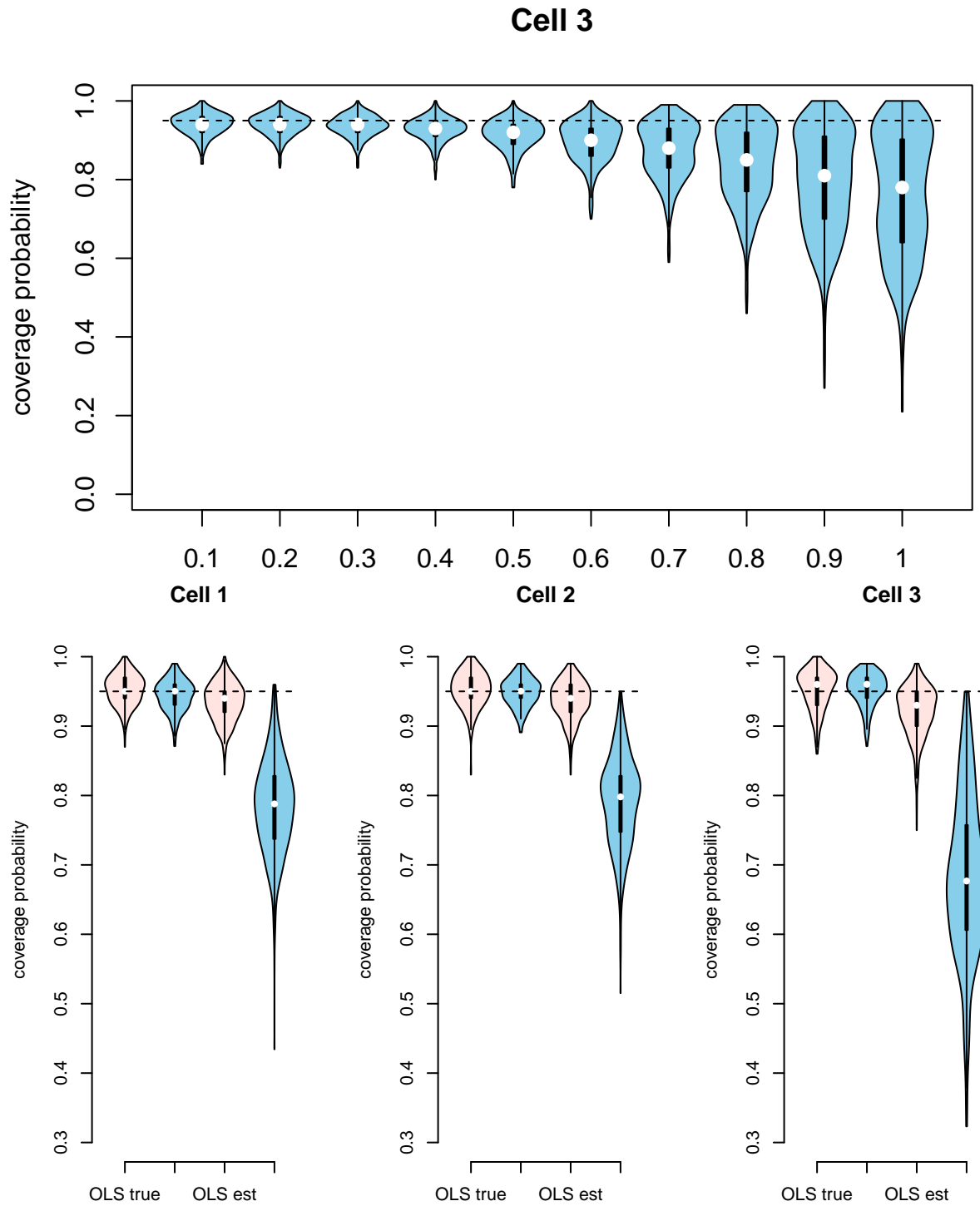
```
##
```

```
## as.Date, as.Date.numeric
```



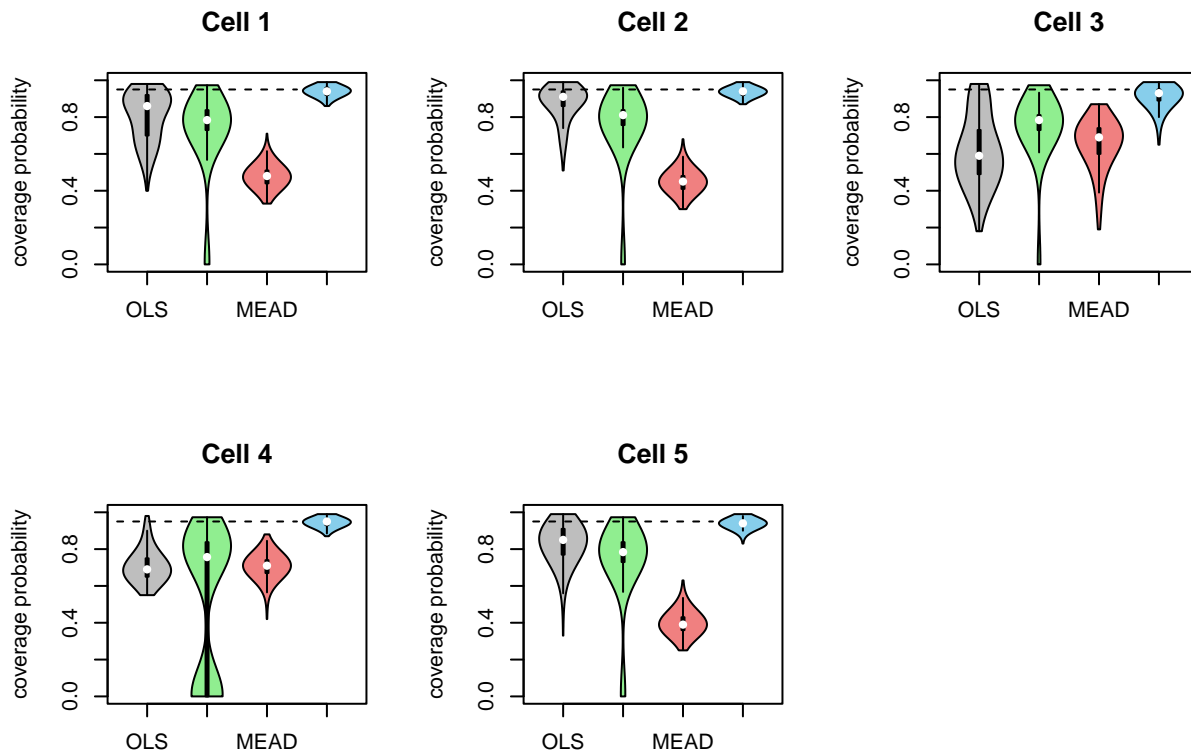
Cell 1



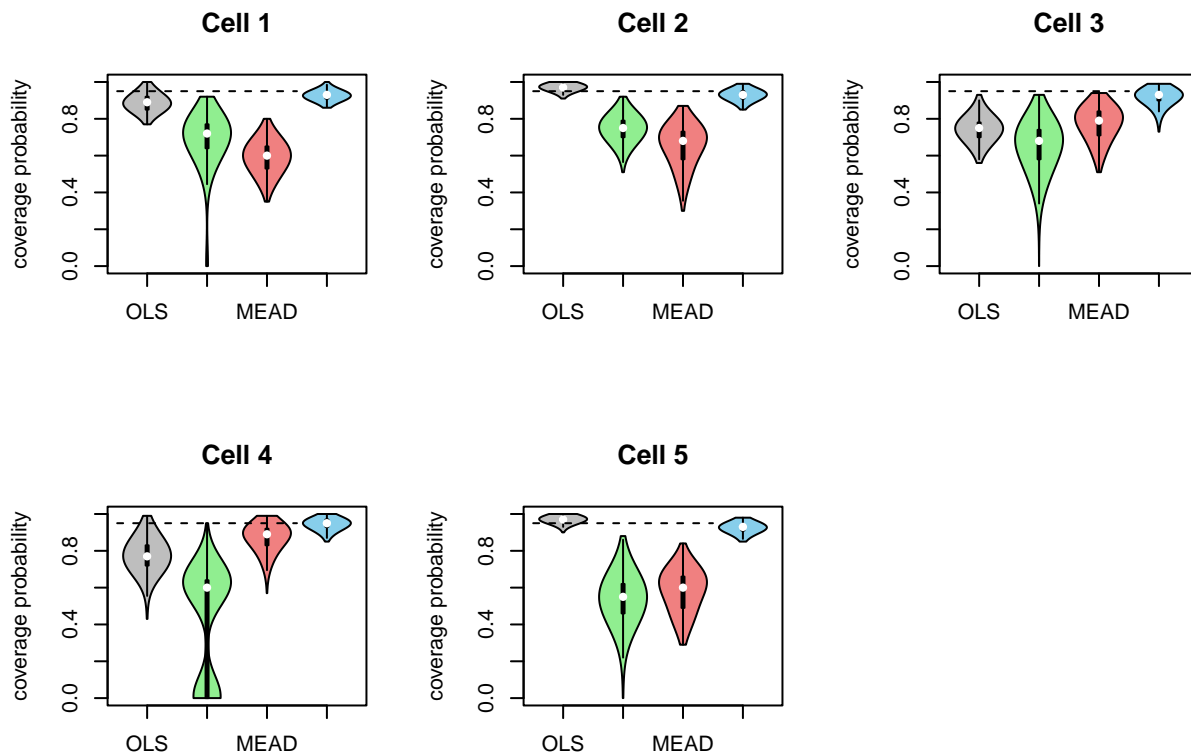


Experiments with W and π_i 's inferred from real data

```
load(file=paste0(path,"data/sim2/cp_decals.RData"))
load(file=paste0(path,"data/sim2/cp_ols.RData"))
load(file=paste0(path,"data/sim2/cp_mead.RData"))
load(file=paste0(path,"data/sim2/cp_rna_sieve.RData"))
# These data are generated by 'simulation2.R'.
```



```
load(file=paste0(path,"data/sim2/gaussian/cp_decals.RData"))
load(file=paste0(path,"data/sim2/gaussian/cp_ols.RData"))
load(file=paste0(path,"data/sim2/gaussian/cp_mead.RData"))
load(file=paste0(path,"data/sim2/gaussian/cp_rna_sieve.RData"))
# These data are generated by the Gaussian part of 'simulation2.R'.
```

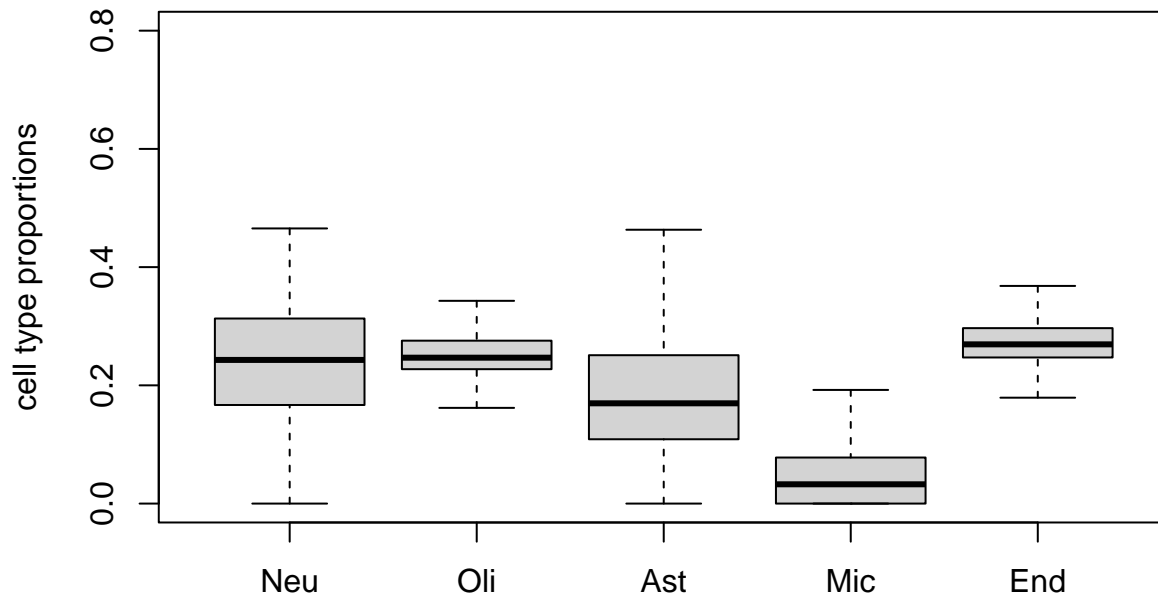


ROSMAP Data

```
load(file=paste0(path,"data/rosmap/bulk.RData"))
load(file=paste0(path,"data/rosmap/sig.RData"))
CTS_proportion=constraint_ols(sig=sig,bulk=bulk)
dim(CTS_proportion) # samples * CTS_proportions
```

```
## [1] 541    5
```

```
# These data are generated by 'rosmap.R'.
# The result for bMIND analysis is given in "data/rosmap".
# The analysis for DE genes are given in 'rosmap.R'.
```

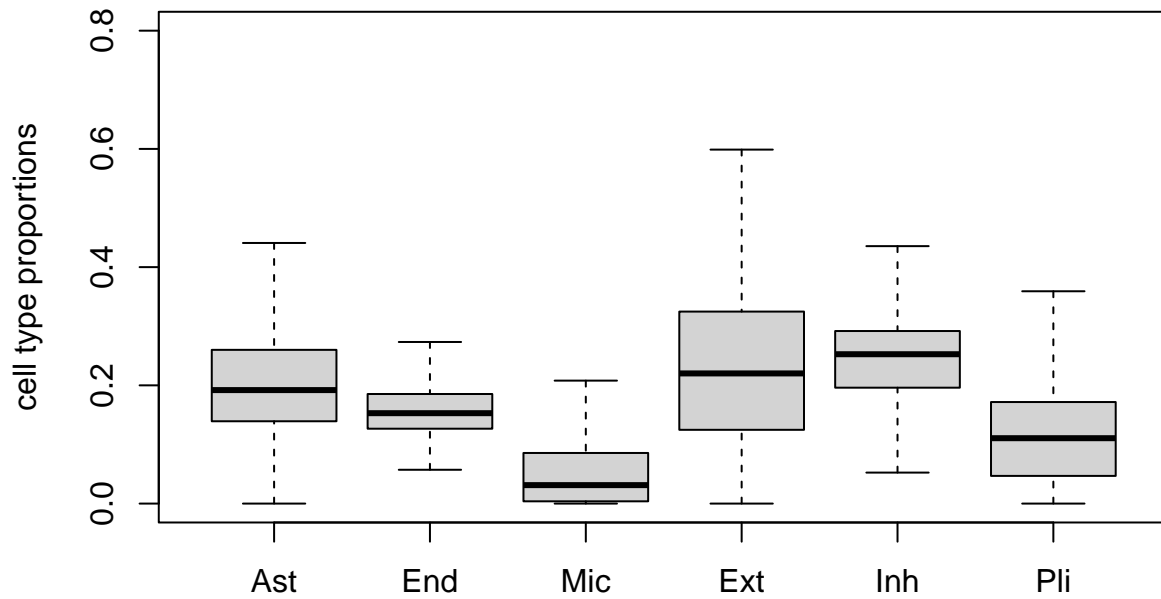


GTEX Data

```
load(file=paste0(path,"data/gtex/bulk.RData"))
load(file=paste0(path,"data/gtex/sig.RData"))
CTS_proportion=constraint_ols(sig=sig,bulk=bulk)
dim(CTS_proportion) # samples * CTS_proportions
```

```
## [1] 1671    6
```

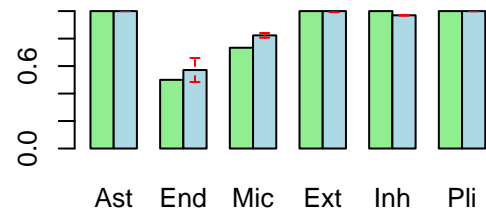
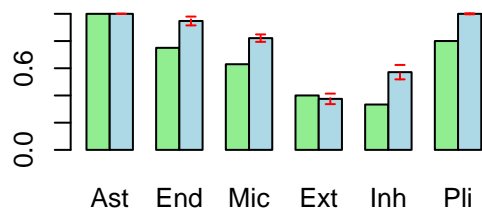
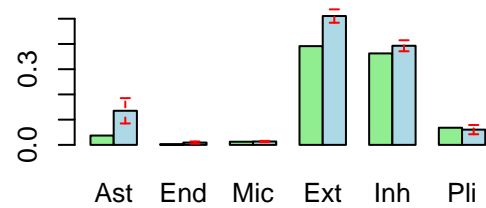
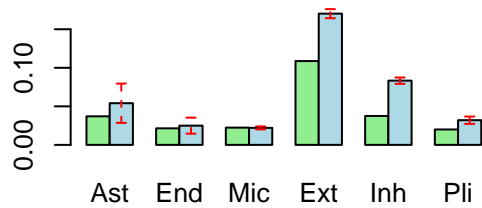
```
# These data are generated by 'gtex.R'.
# The result for bMIND analysis is given in "data/gtex".
# The analysis for DE genes are given in 'gtex.R'.
```



```
load(file=paste0(path,"data/gtex/x_genes.RData"))
load(file=paste0(path,"data/gtex/y_genes.RData"))
load(file=paste0(path,"data/gtex/CTS_chr_sd.RData"))
load(file=paste0(path,"data/gtex/x_sex.RData"))
load(file=paste0(path,"data/gtex/y_sex.RData"))
load(file=paste0(path,"data/gtex/sex_de_sd.RData"))
# These data are generated by 'rosmap.R'.
```

proportions of DE transcripts on Chromos

Ratio of DE genes in Chromosome Y



All of these can be obtained <https://github.com/BiaoCai1993/DECALS/tree/main>.