

Display Forest Tree

set up libraries

```
suppressPackageStartupMessages({  
  library("tidyverse")  
  library("randomForestSRC")  
})
```

Define the directories

```
root_dir <- rprojroot::find_root(rprojroot::has_dir(".git"))  
analysis_dir <- file.path(root_dir, "relative_importance")  
  
results_dir <- file.path(analysis_dir, "results", "rfsrc")  
if(!dir.exists(results_dir)){  
  dir.create(results_dir, recursive=TRUE)  
}
```

Find the cancer groups

```
### Find the CG list  
cg_list <- c("HGG", "LGG", "EPN", "Medullo")  
  
### Now draw representative trees  
for (i in 1:length(cg_list)){  
  # find the cancer group of interest  
  x <- cg_list[i]  
  
  # find the CG group  
  results_dir_cg <- file.path(results_dir, x)  
  # get the model output  
  rfsrc_pbc_lrs_rf <-  
    readRDS(file.path(results_dir_cg, "rfsrc_optimal_lrs_output_full_data.RDS"))  
  
  # print out the figures  
  for (j in 1:10){  
    print(plot(get.tree(rfsrc_pbc_lrs_rf, j)))  
  }  
  
  # get the model output  
  rfsrc_pbc_brier_rf <-  
    readRDS(file.path(results_dir_cg, "rfsrc_optimal_brier_output_full_data.RDS"))
```

```
# print out the figures
for (m in 1:10 ){
  print(plot(get.tree(rfsrc_pbc_brier_rf,j)))
}

}
```