```r
opts_chunk$set (warning = FALSE, message = FALSE, tidy=TRUE, echo=TRUE)
options(warn = -1)

rm(list=ls())

library(survival)
library(knitr)
library(kableExtra)

library(glmnet)
```

```
## Loading required package:  Matrix
## Loaded glmnet 4.1-7
```

```r
library(ggplot2)

# Following loaded in "forest_search_v0.R"
suppressMessages(library(randomForest))
#library(SPlit)

library(grf)
library(policytree)
library(DiagrammeR)

#library(cowplot)

library(data.table)
library(plyr)
library(aVirtualTwins)

suppressMessages(library(gridExtra))

# Location where code is stored
# Modified for MAC
codepath<-c("/Users/larryleon/Documents/GitHub/Forest-Search//R/")
source(paste0(codepath,"source_forestsearch_v0.R"))
source_fs_functions(file_loc=codepath)
```

```r
t.start.all <- proc.time()[3]
# GRF analysis To guide selection of binary cutpoints
df.analysis <- gbsg
df.analysis <- within(df.analysis, {
    id <- as.numeric(c(1:nrow(df.analysis)))
    # time to months
    time_months <- rfstime/30.4375
})

confounders.name <- c("age", "meno", "size", "grade", "nodes", "pgr", "er")

outcome.name <- c("time_months")
event.name <- c("status")
id.name <- c("id")
treat.name <- c("hormon")

n.min <- 60
```

```r
dmin.grf <- 12
frac.tau <- 0.6

grf.est <- grf.subg.harm.survival(data = df.analysis, confounders.name = confounders.name,
    outcome.name = outcome.name, event.name = event.name, id.name = id.name, treat.name = treat.name,
    n.min = n.min, dmin.grf = dmin.grf, frac.tau = frac.tau, details = TRUE)
```

```
## tau= 46.75811
##    leaf.node control.mean control.size control.se treated.mean treated.size
## 1          2     6.309228    82.000000   3.319779    -6.309228    82.000000
## 2          3    -4.212263   604.000000   1.052519     4.212263   604.000000
## 11         4    -8.261494   112.000000   2.790820     8.261494   112.000000
## 21         5     3.718584   177.000000   1.864177    -3.718584   177.000000
## 4          7    -5.913829   356.000000   1.326896     5.913829   356.000000
## 3         10   -11.844388    83.000000   3.140024    11.844388    83.000000
## 41        11     4.557372    97.000000   2.350344    -4.557372    97.000000
## 6         13    -5.936213   324.000000   1.322102     5.936213   324.000000
## 7         14    -7.673589    69.000000   3.693926     7.673589    69.000000
##    treated.se       diff depth
## 1    3.319779  12.618456     1
## 2    1.052519  -8.424527     1
## 11   2.790820 -16.522988     2
## 21   1.864177   7.437168     2
## 4    1.326896 -11.827658     2
## 3    3.140024 -23.688776     3
## 41   2.350344   9.114744     3
## 6    1.322102 -11.872427     3
## 7    3.693926 -15.347178     3
##    leaf.node control.mean control.size control.se treated.mean treated.size
## 1          2     6.309228    82.000000   3.319779    -6.309228    82.000000
##    treated.se      diff depth
## 1    3.319779 12.61846     1
```

```r
cat("Truncation point for RMST:", c(grf.est$tau.rmst), "\n")
```

```
## Truncation point for RMST: 46.75811
```

```r
df0.grf <- subset(grf.est$data, treat.recommend == 0)
df1.grf <- subset(grf.est$data, treat.recommend == 1)

# Terminal leaf corresponding to selected SG
cat("Terminal leaf:", c(grf.est$sg.harm.id), "\n")
```

```
## Terminal leaf: er <= 0
```

```r
# action=1 --> recommend control

# plot(grf.est£tree) plot(grf.est£tree2) plot(grf.est£tree3)

cat("GRF variables in selected tree", "\n")
```

```
## GRF variables in selected tree
```

```r
print(grf.est$tree.names)
```

```
## [1] "er"
```

```r
cat("GRF cuts wrt selected tree:", "\n")
```

```
## GRF cuts wrt selected tree:

print(grf.est$tree.cuts)

## [1] "er <= 0"

# Tree 2
cat("GRF variables in selected tree 2", "\n")

## GRF variables in selected tree 2

print(grf.est$tree2.names)

## [1] "age" "er"

cat("GRF cuts wrt selected tree 2:", "\n")

## GRF cuts wrt selected tree 2:

print(grf.est$tree2.cuts)

## [1] "age <= 50" "age <= 43" "er <= 0"

# Tree 3
cat("GRF variables in selected tree 3", "\n")

## GRF variables in selected tree 3

print(grf.est$tree3.names)

## [1] "age"  "pgr"  "size" "er"

cat("GRF cuts wrt selected tree 3:", "\n")

## GRF cuts wrt selected tree 3:

print(grf.est$tree3.cuts)

## [1] "age <= 48"  "pgr <= 8"   "size <= 36" "age <= 33"  "age <= 43"
## [6] "er <= 0"    "er <= 107"

check <- subset(df.analysis, er <= 0)
print(dim(check))

## [1] 82 13

print(dim(df0.grf))

## [1] 82 18

check <- subset(df.analysis, er > 0)
print(dim(check))

## [1] 604  13

print(dim(df1.grf))

## [1] 604  18

# Second candidate with delta=4.6 2nd node for tree=3
check <- subset(df.analysis, age <= 48 & pgr > 8 & age > 43)
print(dim(check))
```

```
## [1] 97 13

# Examining Tree3, the next sg in favor of control Split: Age<=48, Pgr>8,
# Age>43 (43 < Age <=48) & (Pgr>8)

# Second candidate Not quite 6-month?

df0.grfB <- subset(df.analysis, age <= 48 & pgr > 8 & age > 43)
df1.grfB <- subset(grf.est$data, age > 48 | pgr <= 8 | age <= 43)

layout(matrix(c(1, 2, 3, 4), 2, 2, byrow = TRUE))
plot.subgroup(sub1 = df0.grf, sub1C = df1.grf, tte.name = "time_months", event.name = "status",
    treat.name = "hormon", fix.rows = FALSE, byrisk = 6, show.med = FALSE)
plot.subgroup(sub1 = df0.grfB, sub1C = df1.grfB, tte.name = "time_months", event.name = "status",
    treat.name = "hormon", fix.rows = FALSE, byrisk = 6, show.med = FALSE)
```
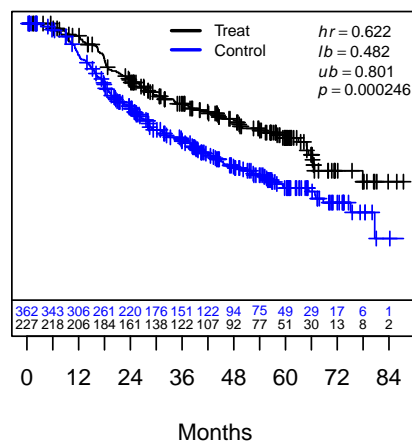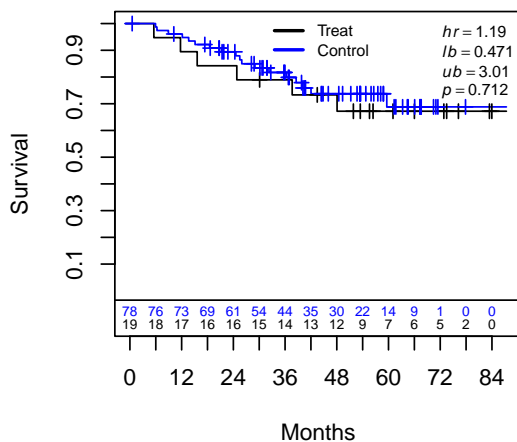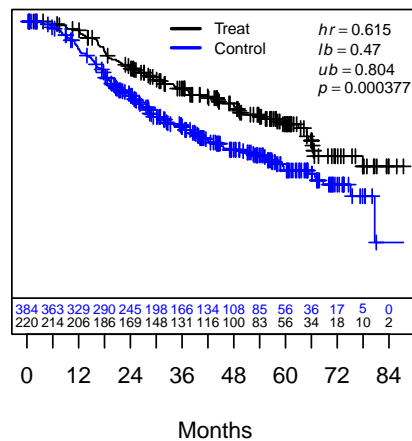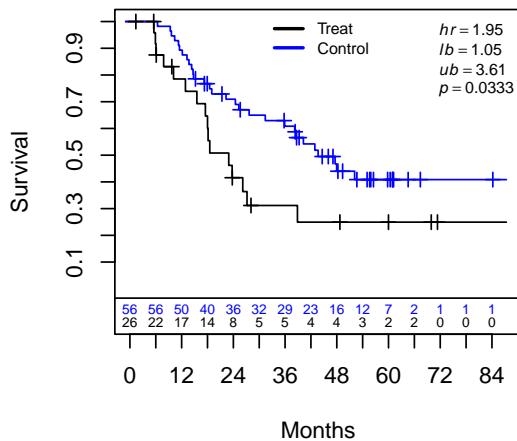
```
save(grf.est, file = "output/grf-Nsg_analysis.Rdata")
```

```
t.done <- proc.time()[3]
t.min <- (t.done - t.start.all)/60
cat("Minutes and hours for GRF estimation", c(t.min, t.min/60), "\n")
```

```
## Minutes and hours for GRF estimation 0.1703333 0.002838889
```

```
par(mfrow = c(1, 2))
plot.subgroup(sub1 = df0.grf, sub1C = df1.grf, tte.name = "time_months", event.name = "status",
    treat.name = "hormon", fix.rows = FALSE, byrisk = 9, show.med = FALSE)
```
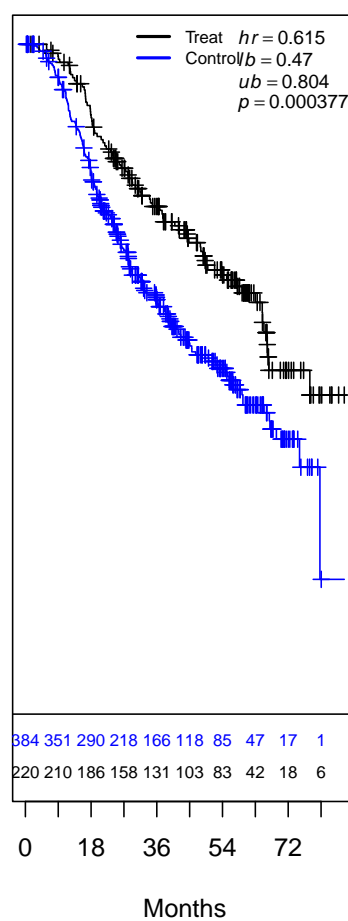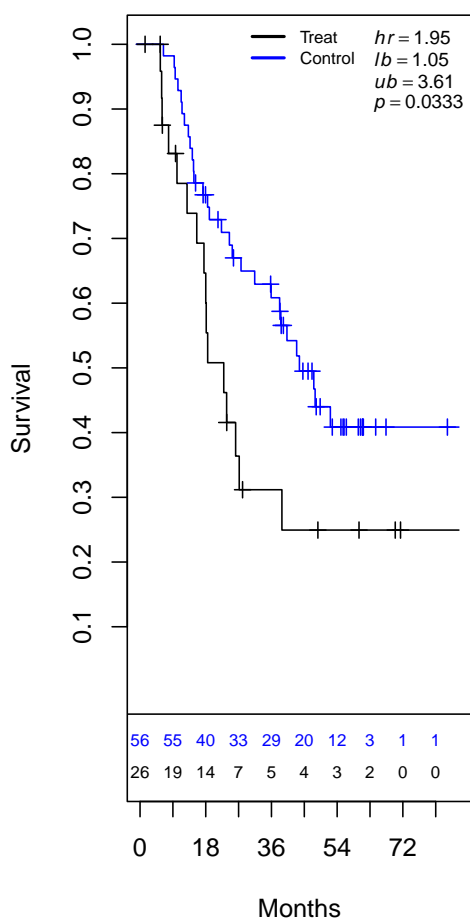


```
# Recall, GRF splits
```

```
t.start <- proc.time()[3]
```

```
cat("GRF variables in selected tree", "\n")
```

```r
## GRF variables in selected tree

print(grf.est$tree.names)

## [1] "er"

cat("GRF cuts wrt selected tree:", "\n")

## GRF cuts wrt selected tree:

print(grf.est$tree.cuts)

## [1] "er <= 0"

# Tree 2
cat("GRF variables in selected tree 2", "\n")

## GRF variables in selected tree 2

print(grf.est$tree2.names)

## [1] "age" "er"

cat("GRF cuts wrt selected tree 2:", "\n")

## GRF cuts wrt selected tree 2:

print(grf.est$tree2.cuts)

## [1] "age <= 50" "age <= 43" "er <= 0"

# Tree 3
cat("GRF variables in selected tree 3", "\n")

## GRF variables in selected tree 3

print(grf.est$tree3.names)

## [1] "age"  "pgr"  "size" "er"

cat("GRF cuts wrt selected tree 3:", "\n")

## GRF cuts wrt selected tree 3:

print(grf.est$tree3.cuts)

## [1] "age <= 48"  "pgr <= 8"   "size <= 36" "age <= 33"  "age <= 43"
## [6] "er <= 0"    "er <= 107"

df.analysis <- gbsg
df.analysis <- within(df.analysis, {
    id <- as.numeric(c(1:nrow(df.analysis)))
    # time to months
    time_months <- rfstime/30.4375
    z1a <- ifelse(er <= 0, 1, 0)
    z1b <- ifelse(er <= 107, 1, 0)

    z2a <- ifelse(pgr <= 8, 1, 0)
    z2b <- ifelse(pgr <= 74, 1, 0)
```

```r
    z3a <- ifelse(age <= 33, 1, 0)
    z3b <- ifelse(age <= 43, 1, 0)
    z3c <- ifelse(age <= 48, 1, 0)
    z3d <- ifelse(age <= 50, 1, 0)   # Close to median=53

    z4 <- ifelse(meno == 0, 1, 0)

    z5 <- ifelse(nodes <= quantile(nodes, c(0.5)), 1, 0)

    z6 <- ifelse(size <= 36, 1, 0)

    z7a <- ifelse(grade == 1, 1, 0)
    z7b <- ifelse(grade == 3, 1, 0)

    # As factors
    v1a <- as.factor(z1a)
    v1b <- as.factor(z1b)

    v2a <- as.factor(z2a)
    v2b <- as.factor(z2b)

    v3a <- as.factor(z3a)
    v3b <- as.factor(z3b)
    v3c <- as.factor(z3c)
    v3d <- as.factor(z3d)

    v4 <- as.factor(z4)
    v5 <- as.factor(z5)
    v6 <- as.factor(z6)

    v7a <- as.factor(z7a)
    v7b <- as.factor(z7b)
})


confounders.name <- c("v1a", "v1b", "v2a", "v2b", "v3a", "v3b", "v3c", "v3d", "v4",
    "v5", "v6", "v7a", "v7b")

# Note, can try smaller subset to check initial code run
# confounders.name<-c('v1a','v1b','v1c',
#'v2a','v2b','v2c',
#'v3a','v3b','v3c')

outcome.name <- c("time_months")
event.name <- c("status")
id.name <- c("id")
treat.name <- c("hormon")

df.confounders <- df.analysis[, confounders.name]
df.confounders <- dummy(df.confounders)

hr.threshold <- 1.5   # Initital candidates
hr.consistency <- 1.25   # Candidates for many splits

# For Nsg set to 95%
```

```r
pconsistency.threshold <- 0.95
maxk <- 4
# Limit timing for forestsearch
max.minutes <- 60
nmin.fs <- 60
# stop.threshold<-0.60 # If any sg meets this, then choose this (stop here);
m1.threshold <- Inf   # Turning this off (Default)
stop.threshold <- 1
# =1 will run through all sg's meeting HR criteria
fs.splits <- 1000   # How many times to split for consistency
# vi is % factor is selected in cross-validation --> higher more important
vi.grf.min <- 0.2
# Null, turns off grf screening

d.min <- 10   # Min number of events for both arms (d0.min=d1.min=d.min)
# default=5


sg_focus <- "Nsg"


# Default FS implementation (Max consistency with harm) sg_focus<-'Nsg' largest
# SG with at least pconsistency.threshold

# The FS algorithm orders subgroups by largest hazard ratios and then cycles
# through each SG candidate (HR>1.5) to calculate consistency.  Note: there is
# a pstop_futile input which is default at 0.5, meaning that once a subgroup
# with consistency less than 50% the algorithm will stop searching: Since
# meeting 90% consistency for SG's with even lower HR's seems unlikely Setting
# pstop_futile=0 will cycle through all candidates (HR>1.5)

fs.est <- forestsearch(df = df.analysis, confounders.name = confounders.name, df.predict = df.analysis,
    details = TRUE, sg_focus = sg_focus, outcome.name = outcome.name, treat.name = treat.name,
    event.name = event.name, id.name = id.name, n.min = nmin.fs, hr.threshold = hr.threshold,
    hr.consistency = hr.consistency, fs.splits = fs.splits, stop.threshold = stop.threshold,
    d0.min = d.min, d1.min = d.min, pconsistency.threshold = pconsistency.threshold,
    max.minutes = max.minutes, maxk = maxk, plot.sg = FALSE, vi.grf.min = vi.grf.min)
```

```
## Confounders per grf screening v1a v2b v2a v3d v7b v1b v5 v6 v3b v4 v3c
## Number of possible subgroups= 4194303
## Number of possible subgroups (in millions)= 4.194303
## # of subgroups based on # variables > k.max and excluded 4185195
## k.max= 4
## Events criteria for control,exp= 10 10
## # of subgroups with events less than criteria: control, experimental 5569 6949
## # of subgroups meeting all criteria = 1268
## # of subgroups fitted (Cox model estimable) = 1268
## Minutes= 0.3040833
## Number of criteria not met for subgroup evaluation
## crit.failure
##        0        1        2        3        4
## 4186463      964     4735      911     1230
## Number of subgroups meeting HR threshold 62
## Subgroups (1st 10) meeting overall screening thresholds (HR, m1) sorted by focus: (m1,sg_focus)= Inf
##      K   n  E d1    m1     m0   HR L(HR) U(HR) v1a.0 v1a.1 v2b.0 v2b.1 v2a.0
##   1: 2 177 55 18 66.20    Inf 1.53  0.87  2.69     0     0     0     0     0
```

```
##  2: 3 151 49 17 64.95  Inf 1.78 0.98 3.21  0  0  0  0  0
##  3: 3 150 41 15 66.20  Inf 1.55 0.82 2.94  1  0  0  0  0
##  4: 3 144 69 16 27.17 52.21 1.55 0.89 2.73  0  0  0  1  0
##  5: 4 144 69 16 27.17 52.21 1.55 0.89 2.73  0  0  0  1  0
##  6: 3 134 41 14 66.20  Inf 1.80 0.94 3.44  0  0  0  0  0
##  7: 2 130 40 13 64.95  Inf 1.78 0.92 3.46  0  0  0  0  0
##  8: 3 130 40 13 64.95  Inf 1.78 0.92 3.46  0  0  0  0  0
##  9: 4 127 42 13 64.95  Inf 1.77 0.91 3.45  0  0  0  0  0
## 10: 4 124 35 14 66.20  Inf 1.85 0.94 3.65  1  0  0  0  0
##     v2a.1 v3d.0 v3d.1 v7b.0 v7b.1 v1b.0 v1b.1 v5.0 v5.1 v6.0 v6.1 v3b.0 v3b.1
##  1:     0     0     1     0     0     0     0    0    0    0    0     1     0
##  2:     0     0     1     0     0     0     1    0    0    0    0     1     0
##  3:     0     0     1     0     0     0     0    0    0    0    0     1     0
##  4:     0     0     0     0     0     0     1    0    0    0    0     0     0
##  5:     0     0     1     0     0     0     1    0    0    0    0     0     0
##  6:     0     0     1     0     0     0     0    0    0    0    1     1     0
##  7:     0     0     0     0     0     0     0    0    0    0    0     1     0
##  8:     0     0     1     0     0     0     0    0    0    0    0     1     0
##  9:     0     0     1     0     0     0     1    0    0    0    0     1     0
## 10:     0     0     1     0     0     0     1    0    0    0    0     1     0
##     v4.0 v4.1 v3c.0 v3c.1
##  1:    0    0     0     0
##  2:    0    0     0     0
##  3:    0    0     0     0
##  4:    0    0     0     1
##  5:    0    0     0     1
##  6:    0    0     0     0
##  7:    0    0     0     1
##  8:    0    0     0     1
##  9:    0    1     0     0
## 10:    0    0     0     0
## Consistency 0.04
## Consistency 0.154
## Consistency 0.047
## Consistency 0.064
## Consistency 0.064
## Consistency 0.11
## Consistency 0.103
## Consistency 0.103
## Consistency 0.097
## Consistency 0.123
## Consistency 0.045
## Consistency 0.065
## Consistency 0.045
## Consistency 0.337
## Consistency 0.217
## Consistency 0.217
## Consistency 0.091
## Consistency 0.091
## Consistency 0.059
## Consistency 0.048
## Consistency 0.048
## Consistency 0.053
## Consistency 0.033
## Consistency 0.976
```

```
## Splitting method, # of splits= Random 1000
## Model, % Consistency Met= v2b.1 v3d.1 v3b.0 0.976
## Number of subgroups meeting consistency criteria= 1
##    p.consistency Nsg group.id m.index K   M.1   M.2   M.3 M.4
## 1:         0.976 102       26     24 3 v2b.1 v3d.1 v3b.0
##    p.consistency Nsg group.id m.index K   M.1   M.2   M.3 M.4
## 1:         0.976 102       26     24 3 v2b.1 v3d.1 v3b.0
```

```r
# plot.sg=TRUE will plot the estimated subgroups but this is plotted below

# These are the frequency each factor appears in a SG combination

xx <- fs.est$find.grps$out.found$hr.subgroups
covs.found <- xx[, -c(1:10)]
covs.most <- apply(covs.found, 2, sum)
covs.most <- covs.most[covs.most > 0]
print(covs.most)
```

```
## v1a.0 v1a.1 v2b.1 v2a.0 v2a.1 v3d.1 v7b.0 v7b.1 v1b.1  v5.0  v6.0  v6.1 v3b.0
##    10     4    27     1    13    31     7     4    18     1     1    10    41
##  v4.1 v3c.1
##    13    26
```

```r
print(fs.est$grp.consistency$result)
```

```
##    p.consistency Nsg group.id m.index K   M.1   M.2   M.3 M.4
## 1:         0.976 102       26     24 3 v2b.1 v3d.1 v3b.0
```

```r
df0.fs <- subset(fs.est$df.pred, treat.recommend == 0)
df1.fs <- subset(fs.est$df.pred, treat.recommend == 1)


save(fs.est, df.analysis, confounders.name, file = "output/fs-Nsg_gbsg_final.Rdata")
```

```r
t.done <- proc.time()[3]
t.min <- (t.done - t.start)/60
cat("Minutes and hours for FS estimation", c(t.min, t.min/60), "\n")
```

```
## Minutes and hours for FS estimation 0.4525833 0.007543056
```

```r
t.start <- proc.time()[3]

library(doParallel)
registerDoParallel(parallel::detectCores(logical = FALSE))

cox.formula.boot <- as.formula(paste("Surv(time_months,status)~hormon"))
split_method <- "Random"
est.loghr <- TRUE

stop.threshold <- 1
# Can probably set to 0.95 or 0.99, but we set the same as above to mimic the
# estimation algorithm
fs.splits <- 1000
max.minutes <- 6
```

```
# Compare with GRF
layout(matrix(c(1, 2, 3, 4), 2, 2, byrow = TRUE))
plot.subgroup(sub1 = df0.grf, sub1C = df1.grf, tte.name = "time_months", event.name = "status",
    treat.name = "hormon", fix.rows = FALSE, byrisk = 9, show.med = FALSE)
plot.subgroup(sub1 = df0.fs, sub1C = df1.fs, tte.name = "time_months", event.name = "status",
    treat.name = "hormon", fix.rows = FALSE, byrisk = 9, show.med = FALSE)
```
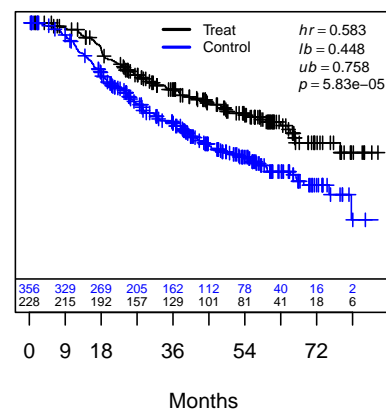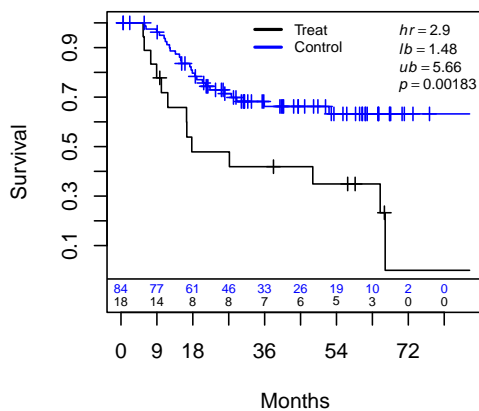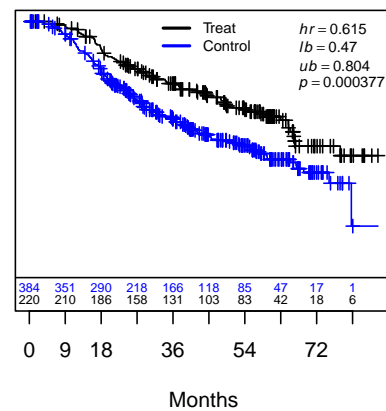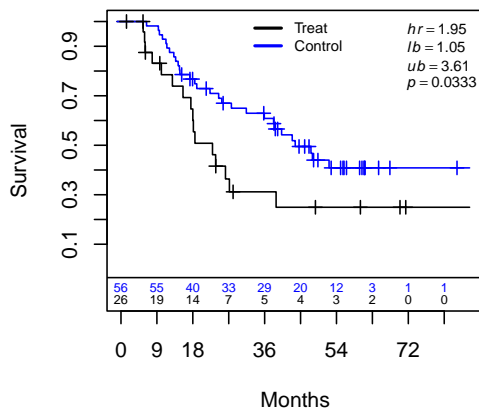


```
NB <- 2000

df_temp <- fs.est$df.pred[, c("id", "treat.recommend")]
dfa <- merge(df.analysis, df_temp, by = "id")
df_boot_analysis <- dfa

fitH <- get_Cox_sg(df_sg = subset(df_boot_analysis, treat.recommend == 0), cox.formula = cox.formula.bo
    est.loghr = est.loghr)
H_obs <- fitH$est_obs   # log(hr) scale
seH_obs <- fitH$se_obs
# Hc observed estimates
```

```
fitHc <- get_Cox_sg(df_sg = subset(df_boot_analysis, treat.recommend == 1), cox.formula = cox.formula.bo
    est.loghr = est.loghr)
Hc_obs <- fitHc$est_obs
seHc_obs <- fitHc$se_obs
rm("fitH", "fitHc")

Ystar_mat <- bootYstar({
    ystar <- get_Ystar(boot)
}, boots = NB, seed = 8316951, counter = "boot", export = fun_arg_list_boot)
# Check dimension
if (dim(Ystar_mat)[1] != NB | dim(Ystar_mat)[2] != nrow(df_boot_analysis)) stop("Dimension of Ystar_mat

tB.start <- proc.time()[3]
# Bootstraps
resB <- bootPar({
    ans <- fsboot_forparallel(boot)
}, boots = NB, seed = 8316951, counter = "boot", export = fun_arg_list_boot)
tB.now <- proc.time()[3]
tB.min <- (tB.now - tB.start)/60

doParallel::stopImplicitCluster()

cat("Minutes for Boots", c(NB, tB.min), "\n")

## Minutes for Boots 2000 95.31312

cat("Projection per 100", c(tB.min * (100/NB)), "\n")

## Projection per 100 4.765656

cat("Propn bootstrap subgroups found =", c(sum(!is.na(resB$H_biasadj_1))/NB), "\n")

## Propn bootstrap subgroups found = 0.9015

# How many timmed out
cat("Number timmed out=", c(sum(is.na(resB$H_biasadj_1) & resB$tmins_search > max.minutes)),
    "\n")

## Number timmed out= 0

H_estimates <- get_dfRes(Hobs = H_obs, seHobs = seH_obs, H1_adj = resB$H_biasadj_1,
    ystar = Ystar_mat, cov_method = "standard", cov_trim = 0.05)

Hc_estimates <- get_dfRes(Hobs = Hc_obs, seHobs = seHc_obs, H1_adj = resB$Hc_biasadj_1,
    ystar = Ystar_mat, cov_method = "standard", cov_trim = 0.05)

print(H_estimates)

##          H0       sdH0 H0_lower H0_upper       H1      sdH1 H1_lower H1_upper
## 1: 2.898823 0.9901874  1.48411 5.662097 2.017775 0.2336931 1.608011 2.531958

print(Hc_estimates)

##          H0       sdH0  H0_lower  H0_upper       H1       sdH1  H1_lower
## 1: 0.5825361 0.07831384 0.4476006 0.7581497 0.6199001 0.08131831 0.4793595
##      H1_upper
## 1: 0.8016449

save(fs.est, Ystar_mat, resB, H_estimates, Hc_estimates, df_boot_analysis, file = "output/fsBoot-Nsg_gbs
```

```r
t.done <- proc.time()[3]
t.min <- (t.done - t.start)/60
cat("Minutes and hours for FS bootstrap", c(t.min, t.min/60), "\n")

## Minutes and hours for FS bootstrap 95.33093 1.588849


df0.fs <- subset(fs.est$df.pred, treat.recommend == 0)
df1.fs <- subset(fs.est$df.pred, treat.recommend == 1)

# ITT analysis
cox_itt <- summary(coxph(Surv(time_months, status) ~ hormon, data = fs.est$df.pred))$conf.int

# ITT estimates
resITT <- c(round(cox_itt[c(1, 3, 4)], 2), nrow(fs.est$df.pred))

# Forest Search Un-adjusted
Hstat <- c(unlist(H_estimates))[c(1, 3, 4)]
resH_obs <- c(c(Hstat), nrow(df0.fs))
# Bias-corrected
Hstat <- c(unlist(H_estimates))[c(5, 7, 8)]
resH_bc <- c(c(Hstat), nrow(df0.fs))

Hstat2 <- c(unlist(H_estimates))[c(5, 7, 8)]
Hstat2 <- round(Hstat2, 2)
a <- paste0(Hstat2[1], " [")
a <- paste0(a, Hstat2[2])
a <- paste0(a, ",")
a <- paste0(a, Hstat2[3])
a <- paste0(a, "]")
H_bc2 <- c(a)

# Un-adjusted
Hcstat <- c(unlist(Hc_estimates))[c(1, 3, 4)]
resHc_obs <- c(c(Hcstat), nrow(df1.fs))
# Bias-corrected
Hcstat <- c(unlist(Hc_estimates))[c(5, 7, 8)]
resHc_bc <- c(c(Hcstat), nrow(df1.fs))


Hcstat2 <- c(unlist(Hc_estimates))[c(5, 7, 8)]
Hcstat2 <- round(Hcstat2, 2)
a <- paste0(Hcstat2[1], " [")
a <- paste0(a, Hcstat2[2])
a <- paste0(a, ",")
a <- paste0(a, Hcstat2[3])
a <- paste0(a, "]")
Hc_bc2 <- c(a)

res <- rbind(resITT, resH_obs, resH_bc, resHc_obs, resHc_bc)

resf <- as.data.frame(res)

colnames(resf) <- c("HR Estimate", "Lower", "Upper", "$\\#$ Subjects")
```

```r
rnH <- c("$\\hat{H}$", "$\\hat{H}_{bc}$")
rnHc <- c("$\\hat{H}^{c}$", "$\\hat{H}^{c}_{bc}$")
rnItt <- c("ITT")
rownames(resf) <- c(rnItt, rnH, rnHc)
```

```r
# Resolve conflict with dplyr
library(conflicted)
group_rows <- kableExtra::group_rows

options(knitr.kable.NA = ".", format = "latex")
tab_gbsg <- kbl(resf, longtable = FALSE, align = "c", format = "latex", booktabs = TRUE,
    escape = F, digits = 3, caption = "\\label{tab:gbsg} GBSG FS Analysis: Cox hazard ratio (HR) estimat
Cox model estimates are based on subgroups: H true (knowing the actual subgroup, a-priori); the estimate
the bootstrap ($B=2,000$) bias-correction to $\\hat{H}$ estimates, denoted $\\hat{H}_{bc}$.  Estimates f
The number of subjects in each population ($\\#$ Subjects) are listed.") %>%
    kable_styling(full_width = FALSE, font_size = 9, latex_options = "hold_position") %>%
    group_rows("ITT", 1, 1) %>%
    group_rows("H subgroup estimates", 2, 3) %>%
    group_rows("H-complement subgroup estimates", 4, 5)
```

Table 1:   GBSG FS Analysis: Cox hazard ratio (HR) estimates for the ITT population and subgroups H and H^c. Cox model estimates are based on subgroups: H true (knowing the actual subgroup, a-priori); the estimated subgroup $\hat{H}$; and the bootstrap ($B = 2,000$) bias-correction to $\hat{H}$ estimates, denoted $\hat{H}_{bc}$. Estimates for the complement H^c are defined analogously. The number of subjects in each population (# Subjects) are listed.

	HR Estimate	Lower	Upper	# Subjects
ITT				
ITT	0.690	0.540	0.890	686
H subgroup estimates				
$\hat{H}$	2.899	1.484	5.662	102
$\hat{H}_{bc}$	2.018	1.608	2.532	102
H-complement subgroup estimates				
$\hat{H}^c$	0.583	0.448	0.758	584
$\hat{H}^c_{bc}$	0.620	0.479	0.802	584

```r
t.done <- proc.time()[3]
t.min <- (t.done - t.start.all)/60
cat("Minutes and hours to finish", c(t.min, t.min/60), "\n")
```

```
## Minutes and hours to finish 95.95817 1.599303
```

```r
cat("Machine=", c(Sys.info()[[4]]), "\n")
```

```
## Machine= Mac-Studio-M1-Ultra-2022.local
```

```r
cat("Number of cores=", c(detectCores(logical = FALSE)), "\n")
```

```
## Number of cores= 20
```