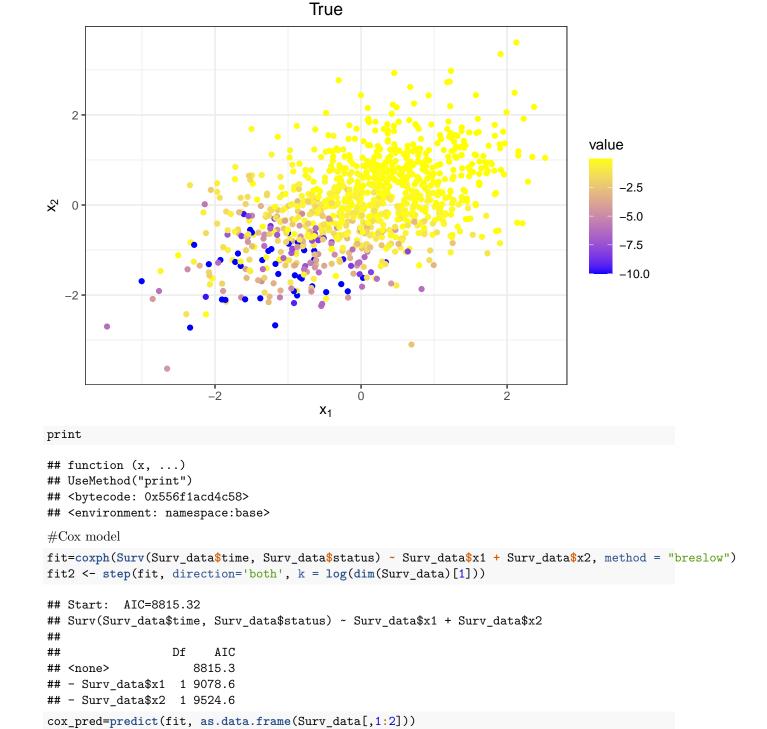
MKL Cox (MKCox)

We will be mimicking example 1, two factors with linear relationship with the hazard function $h(X) = (X_1 + 2 * X_2)$, from 'Fenchel duality of Cox partial likelihood and its application in survival kernel learning' Wilson et. al (2020). Here is quick example of how to run the code. The concordance for Random survival forest, gradient boosting, and MKCox are printed and note that they are compatible. All of the machine learning methods are able to capture the linear relationship between the features and hazard function as shown in the scatterplots.

Loading data and plotting data

```
library(RMKL)
library(ggplot2)
library(survival)
library(gbm)
## Loaded gbm 2.1.5
library(randomForestSRC)
##
##
   randomForestSRC 2.9.3
##
##
   Type rfsrc.news() to see new features, changes, and bug fixes.
##
library(kernlab)
## Attaching package: 'kernlab'
## The following object is masked from 'package:ggplot2':
##
##
       alpha
data(Surv_data)
head(Surv_data)
##
                                   time status
## 1 0.70152066 0.8990872 0.040041376
                                          TRUE
## 2 -0.21223395 -0.6490695 1.230534188
                                          TRUE
## 3 -0.08404824 1.4702301 0.005509966
                                          TRUE
## 4 0.86906459 0.4015776 0.437023163
                                          TRUE
## 5 -1.88954937 -1.9095317 4.220627369
                                          TRUE
## 6 -0.58108709 0.1864732 0.138348879
                                          TRUE
ggplot(Surv_data, aes(x = x1, y = x2, color = -time)) + geom_point() + scale_color_gradient(low = 'blue
labs(color = 'value', title = 'True', x = expression(x[1]), y = expression(x[2])) + theme_bw() + theme(p
```



ggplot(Surv_data, aes(x = x1, y = x2, color = Cox)) + geom_point() + scale_color_gradient(low = 'blue',

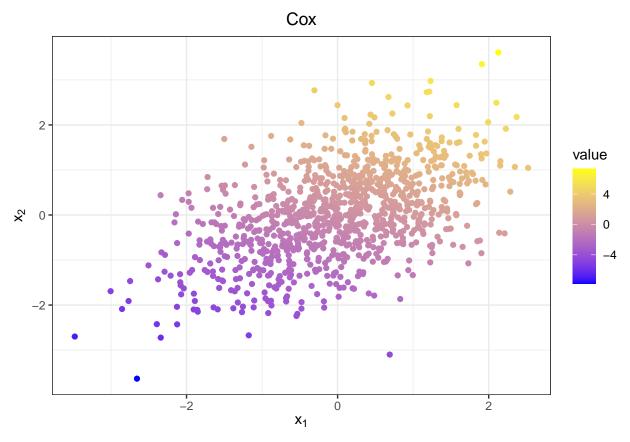
summary(fit)\$concordance[1]

C

Surv_data\$Cox = cox_pred

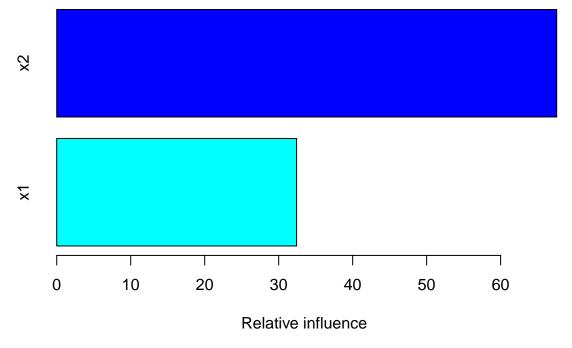
##

0.831493



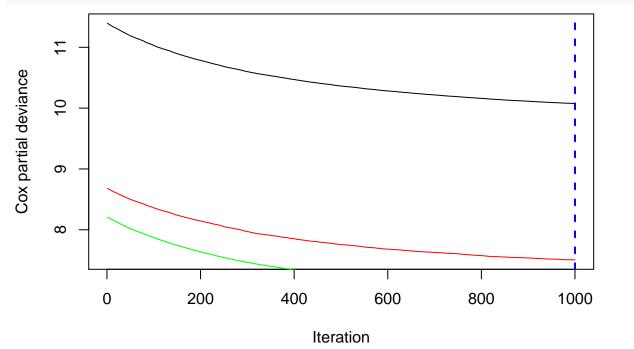
#Gradient Boosting

```
gbm1 <- gbm(Surv(time, status) ~ x1 + x2,</pre>
                                                 # formula
              data=Surv_data,
                                               # dataset
              distribution="coxph",
              n.trees=1000,
                                         # number of trees
              shrinkage=0.005,
                                         # shrinkage or learning rate, 0.001 to 0.1 usually work
                                         # 1: additive model, 2: two-way interactions, etc
              interaction.depth=1,
                                        # subsampling fraction, 0.5 is probably best
              bag.fraction = 0.5,
              train.fraction = 0.8,
                                         \# fraction of data for training, first train.fraction*N used f
              cv.folds = 5,
                                         \# do 5-fold cross-validation
              verbose = F)
                                     # print progress
summary(gbm1)
```

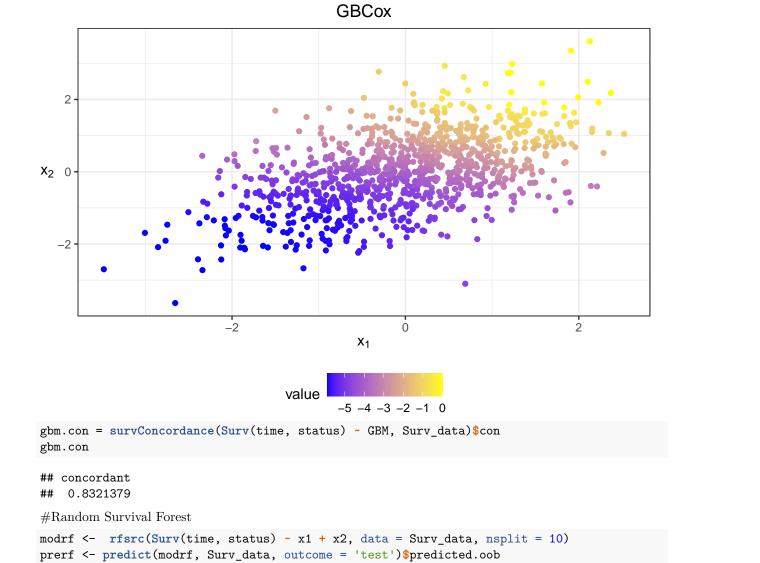


var rel.inf ## x2 x2 67.57844 ## x1 x1 32.42156

best.iter <- gbm.perf(gbm1,method = "cv")</pre>

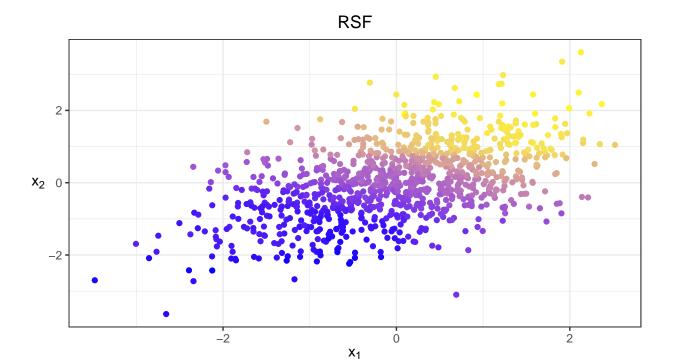


gpred2=predict(gbm1,Surv_data,best.iter)
Surv_data\$GBM = gpred2
ggplot(Surv_data, aes(x = x1, y = x2, color = GBM)) + geom_point() + scale_color_gradient(low = 'blue',



ggplot(Surv_data, aes(x = x1, y = x2, color = RSF)) + geom_point() + scale_color_gradient(low = 'blue',

Surv_data\$RSF = prerf



value
500 100015002000

RSF.con = survConcordance(Surv(time, status) ~ RSF, Surv_data)\$con

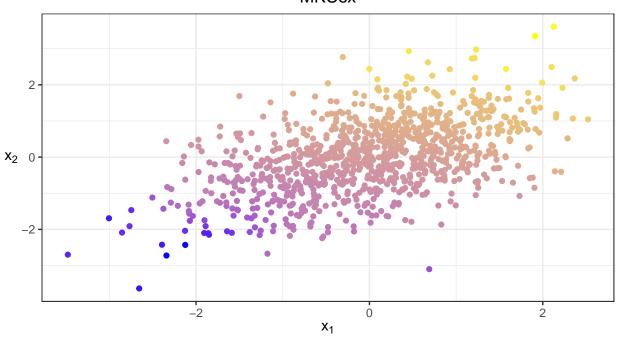
```
## concordant
## 0.8204752
```

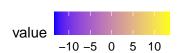
RSF.con

```
#MKCox
#Getting survival times in ascending order
ordtr <- order(Surv_data$time)</pre>
Surv_data_ordered = Surv_data[ordtr,]
xx = Surv_data_ordered[,1:2]
del = Surv_data_ordered$status
yy = Surv_data_ordered$time
if (!del[1]) {
  first1 <- which(del)[1]</pre>
  xx <- xx[-(1:(first1 - 1)),]
  yy <- yy[-(1:(first1 - 1))]</pre>
  del <- del[-(1:(first1 - 1))]</pre>
  nn <- dim(Surv_data)[1] - first1 + 1
} else {
  nn <- dim(Surv_data)[1]</pre>
rho0 <- .001*(Surv_data$status - seq(0, 10, length.out = dim(Surv_data)[1]))
klist <- list(kernelMatrix(rbfdot(1), as.matrix(xx)),</pre>
              kernelMatrix(vanilladot(), as.matrix(xx)))
ktlist <- list(kernelMatrix(rbfdot(1), as.matrix(xx), as.matrix(Surv_data[,1:2])),</pre>
```

```
kernelMatrix(vanilladot(), as.matrix(xx), as.matrix(Surv_data[,1:2])))
kk <- simplify2array(klist)
kkk <- simplify2array(ktlist)
modmkl <- SurvMKL(y = Surv_data$time, del = Surv_data$status, K = kk, rho = rho0, C = 0.005, lambda = mkl = predict_Surv(modmkl, kkk)
Surv_data$MKCox = mkl
ggplot(Surv_data, aes(x = x1, y = x2, color = MKCox)) + geom_point() + scale_color_gradient(low = 'blue</pre>
```

MKCox





MKCox.con = survConcordance(Surv(time, status) ~ MKCox, Surv_data)\$con
MKCox.con

concordant ## 0.8329882