

# Evaluate testing data (survival) - rfsrc

*EVE W.*

*2019-09-17*

## Contents

0. Load Data . . . . .	1
1. Scores . . . . .	2
2. Important Features . . . . .	4

Label: os\_time

```
## user input
project_home <- "~/EVE/examples"
project_name <- "rfsrc_outCV_test"
```

## 0. Load Data

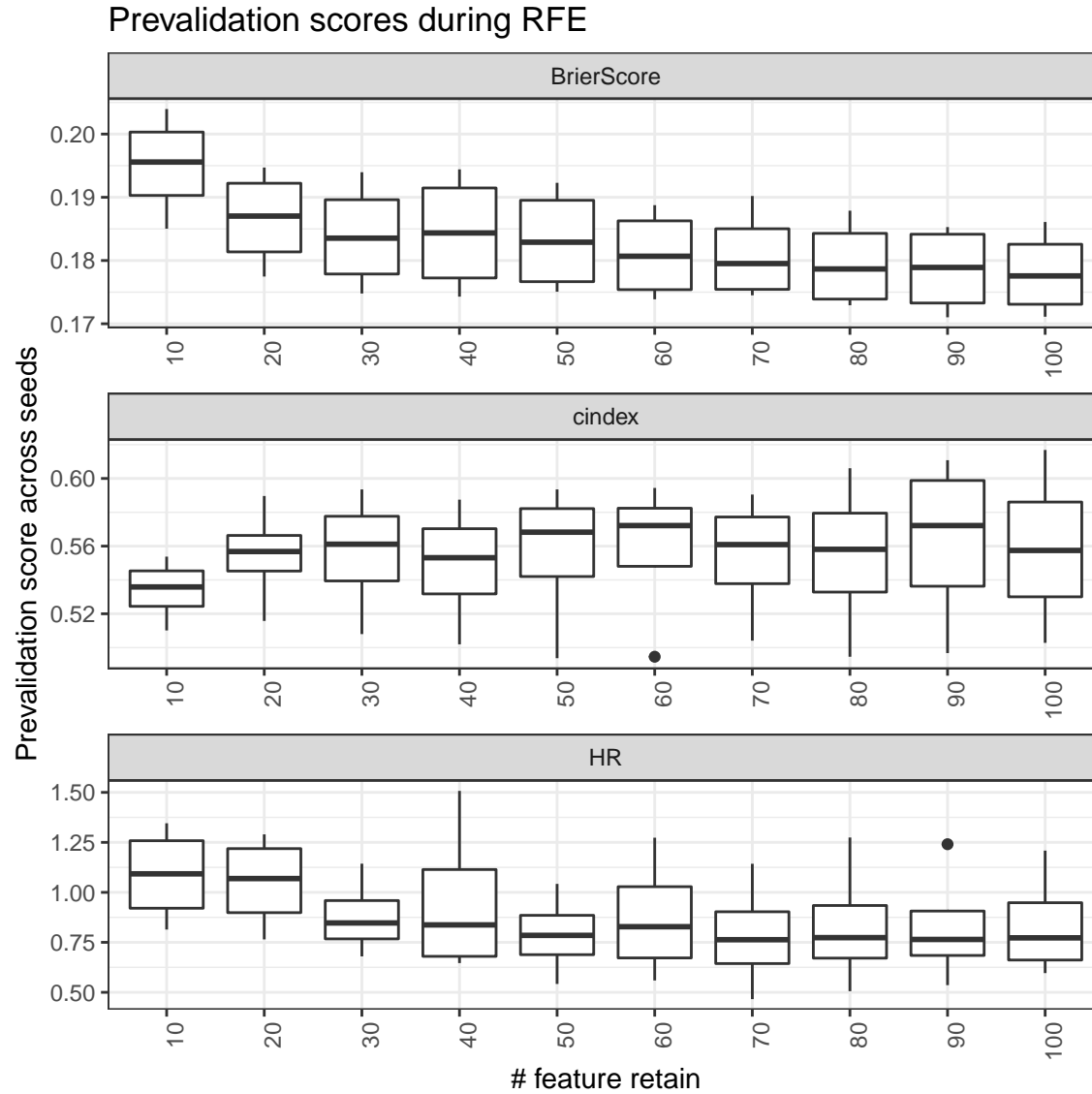
276 of samples were used

100 of full features

4 runs, each run contains 3 CVs.

run with rfeSRCC.r.

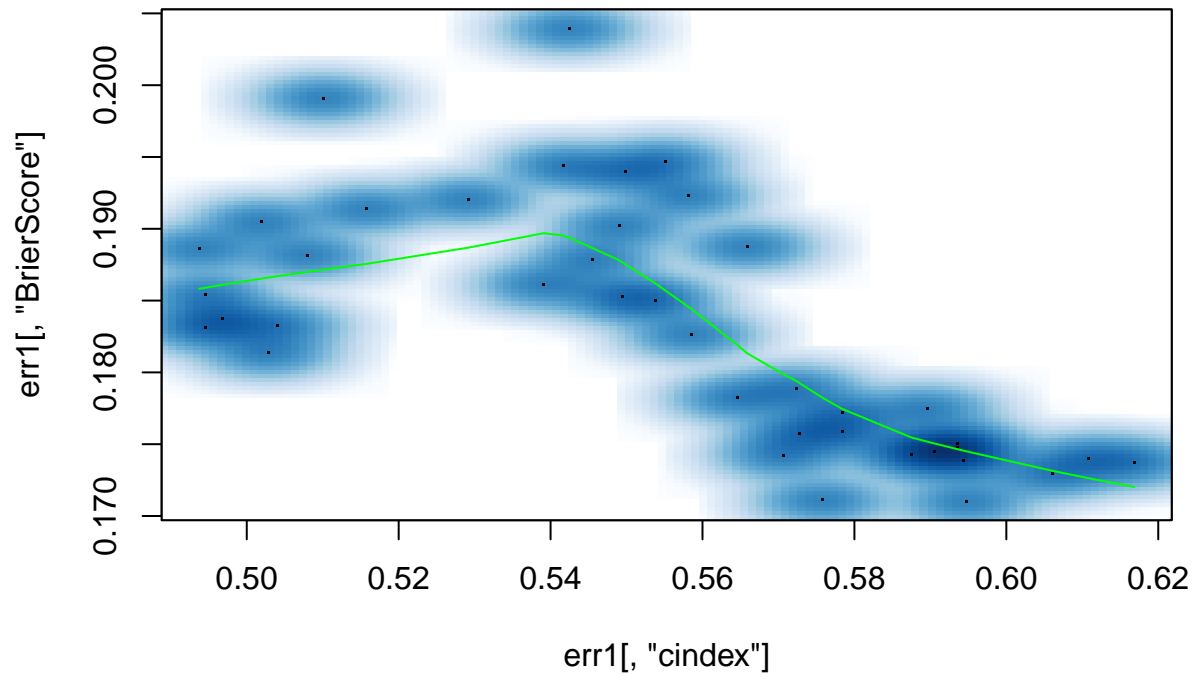
## 1. Scores



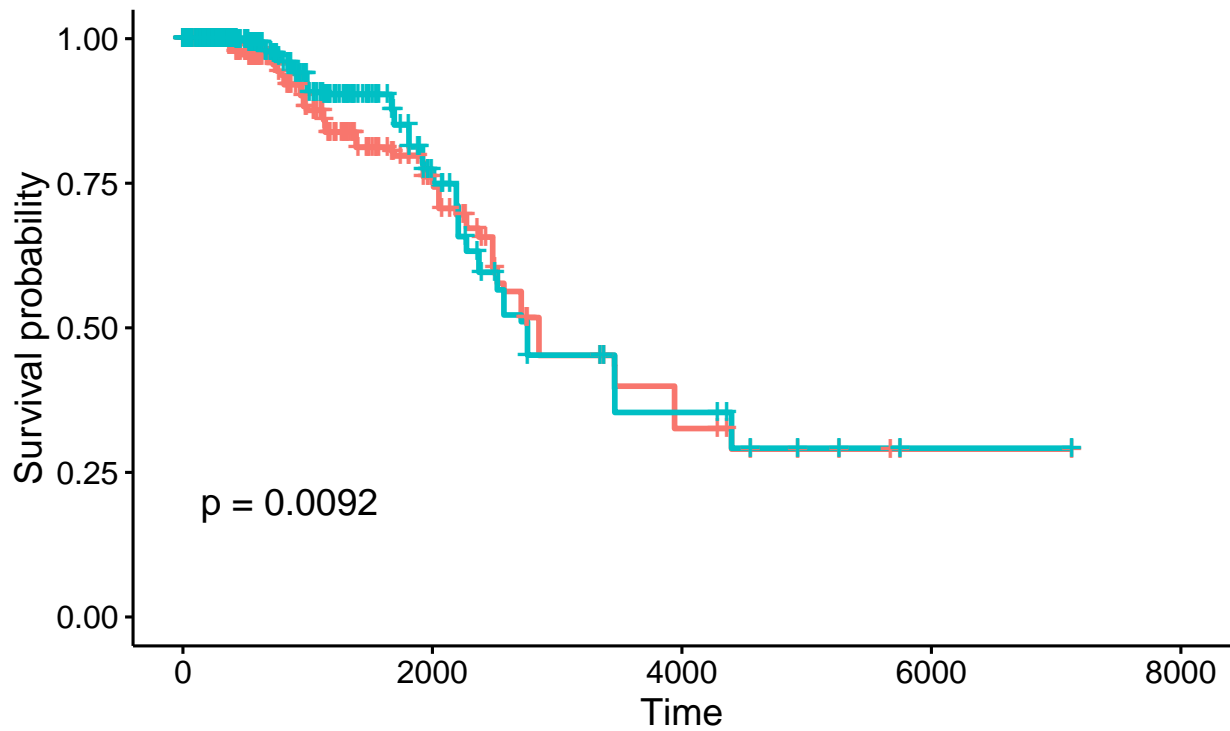
Note for the **HR plot**: A HR value (per seed) is calculated by comparing the survival time between 'long' and 'short' survivors. These two groups are defined by splitting samples based on *median* predicted risk score; group\_0 is predicted risk scores > median, which can be viewed as 'short survivors'. On the other hand, group\_1 can be viewed as 'long survivors'. If the prediction is reasonable, the hazard ratio of group\_1/group\_0 should be < 1. The actual function used in calculating HR is `coxph(Surv(time, status) ~ group.binary, df)`.

metrics	size.max	median.max	size.min	median.min
BrierScore	10	0.196	100	0.178
cindex	90	0.572	10	0.536
HR	10	1.093	70	0.763

pearson corr:  $-0.64$



The following plot is to quickly see how well the prediction can separate long and short survivor.  
Strata + pred.binary=0 + pred.binary=1



## 2. Important Features

From 100 feature step based on vimp

