

# Evaluate testing data (survival) - rfsrc

*EVE W.*

*2019-11-16*

## 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

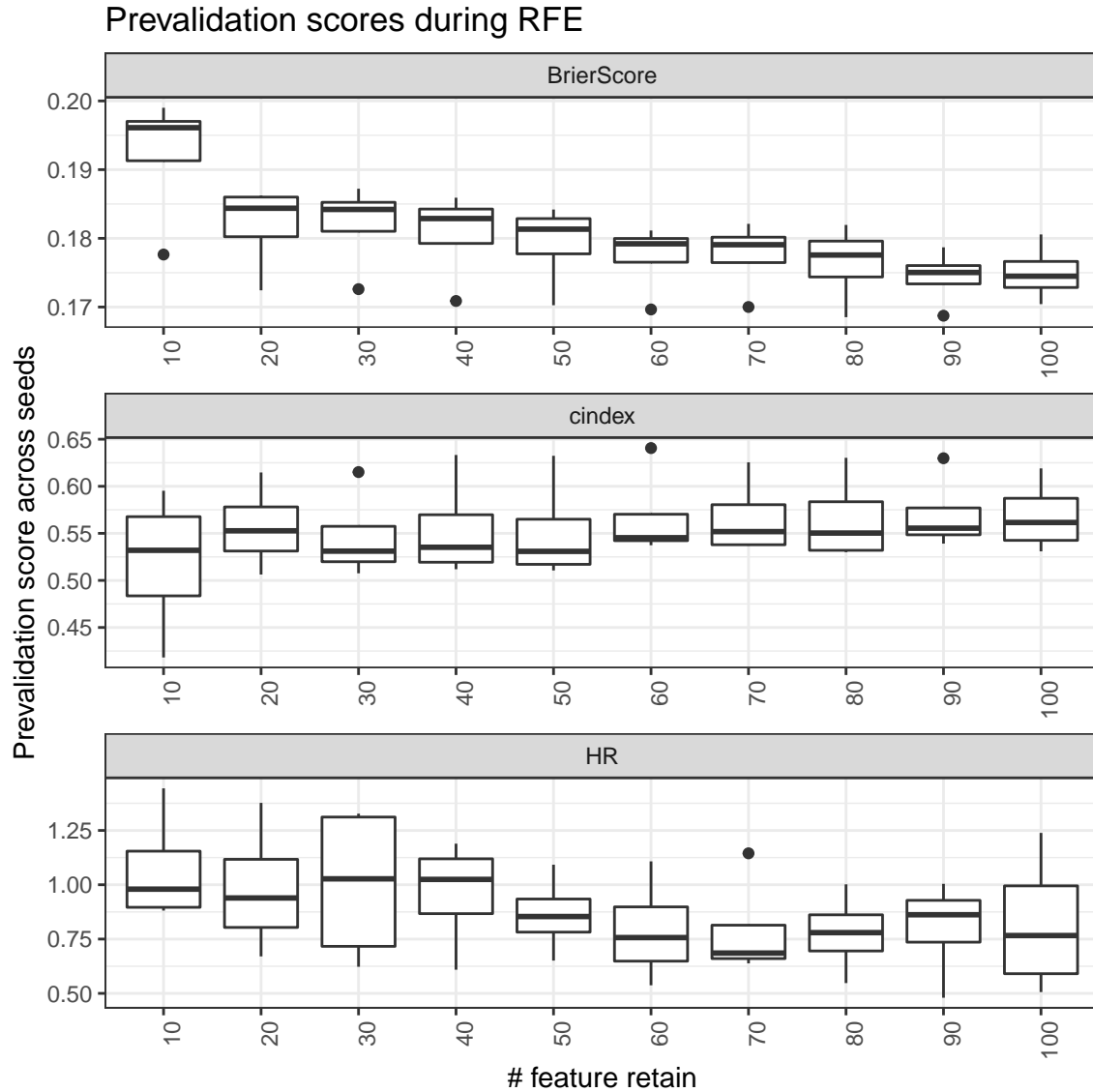
276 of samples were used

100 of full features

4 runs, each run contains 3 CVs.

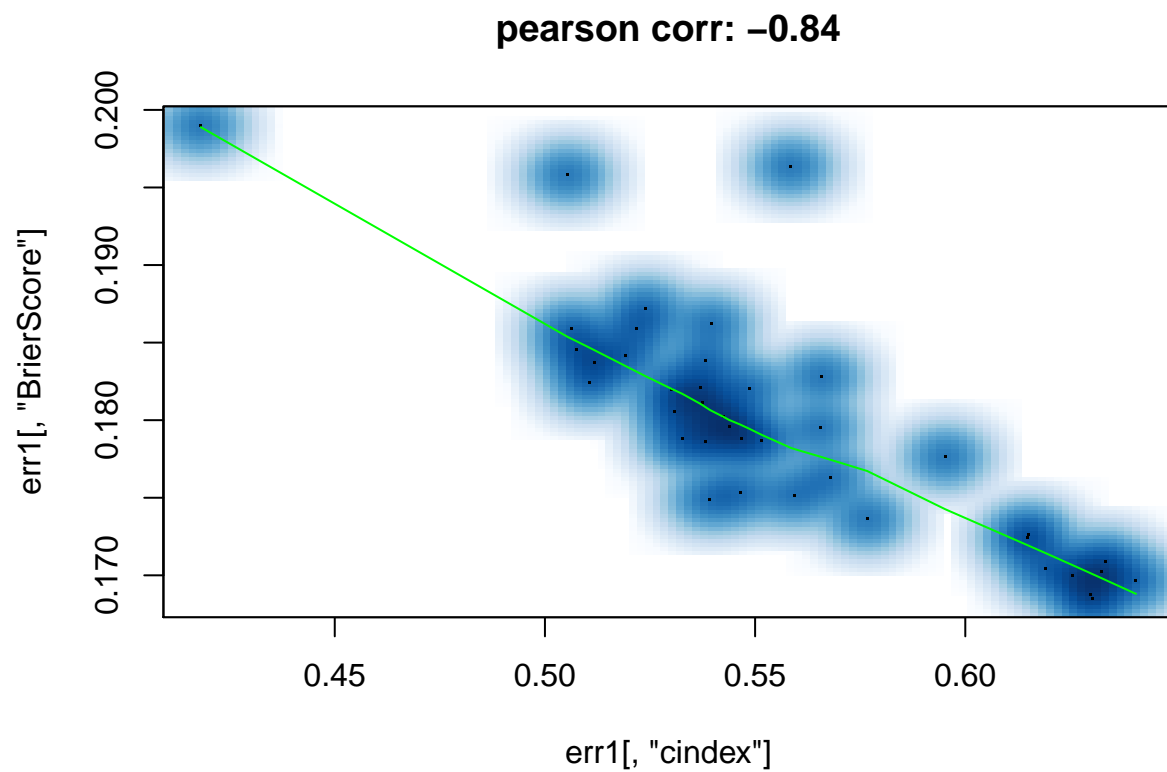
run with rfeSRCC.r.

## 1. Scores

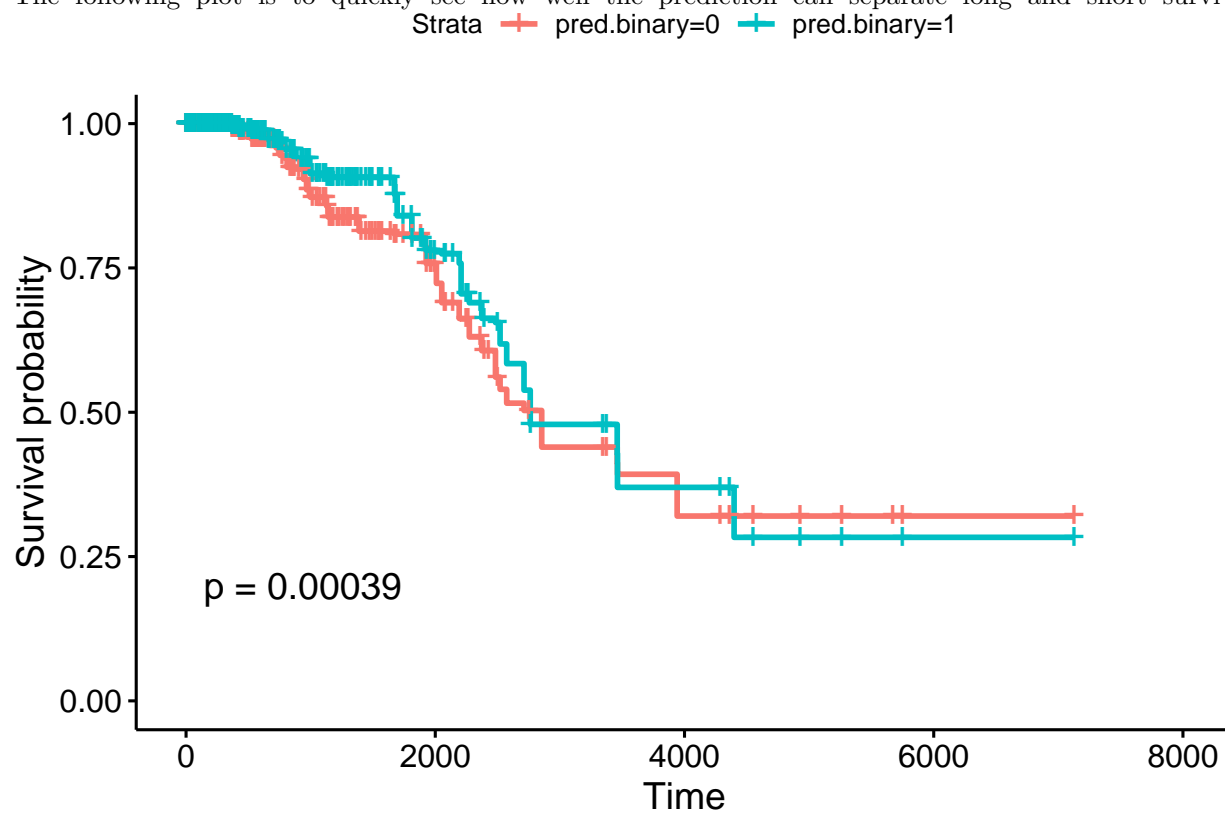


Note for the **HR plot**: A HR value (per seed) is calculated by comparing the survival time between 'long' and 'short' survivors. These two group is defined by splitting samples based on *median* predicted risk score; group\_0 is predicted risk scores > median, which can be viewed as 'short survivors'. 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	0.174
cindex	100	0.562	50	0.531
HR	30	1.027	70	0.686



The following plot is to quickly see how well the prediction can separate long and short survivor.



2. Important Features

From 100 feature step based on vimp

