Evaluate testing data (regression) - Lasso

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Contents

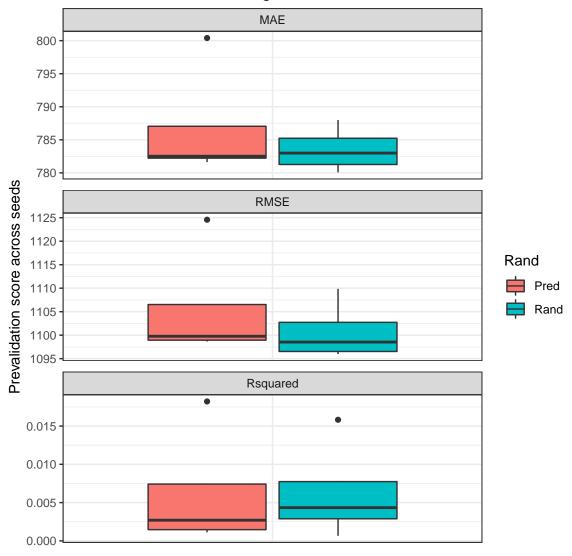
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# user input	
roject_home <- "~/EVE/examples"	
roject_name <- "lasso_regression_outCV_test"	

0. Load Data

```
## Error : $ operator is invalid for atomic vectors
## 300 of samples were used
## 100 of full features
## 4 runs, each run contains 3 CVs.
## os_time :
## Min. 1st Qu. Median Mean 3rd Qu. Max.
## 0.0 182.8 480.0 889.4 1221.2 7125.0
run with lasso.r.
```

1. Scores

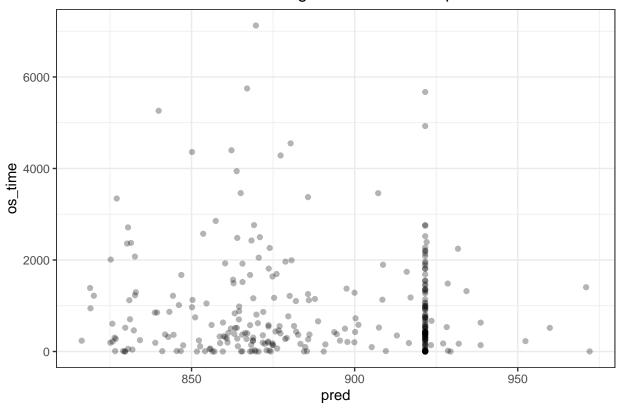
Prevalidation scores during RFE



'Pred' compares the actual CV prediction with observed value. 'Rand' compares permuted CV prediction with observed to mimic random prediction.

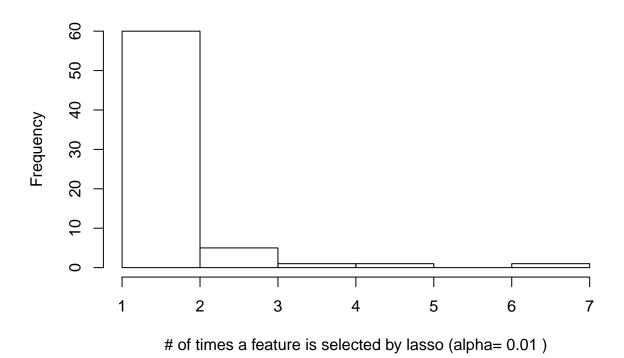
correlation

Correlation at seed = 1003 using 100 feature set input



2. Important Features

distribution across 4 seed x 3 CV



```
## [1] "there are 68 unique features used from the 100 feature set"
```

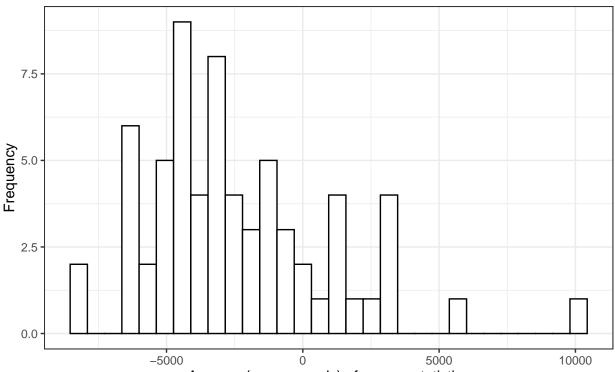
[1] "summary of number of features used in each run under 4 seeds and 3 CVs"

```
## Min. 1st Qu. Median Mean 3rd Qu. Max. NA's ## 1.00 4.00 9.00 15.14 14.50 59.00 5
```

`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.

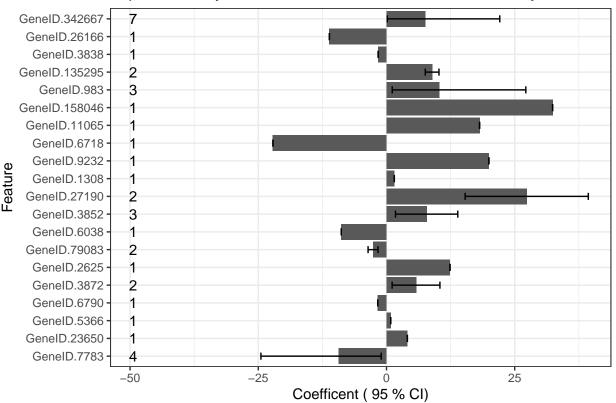
Warning: Removed 2 rows containing non-finite values (stat_bin).

Distribution across all 68 features



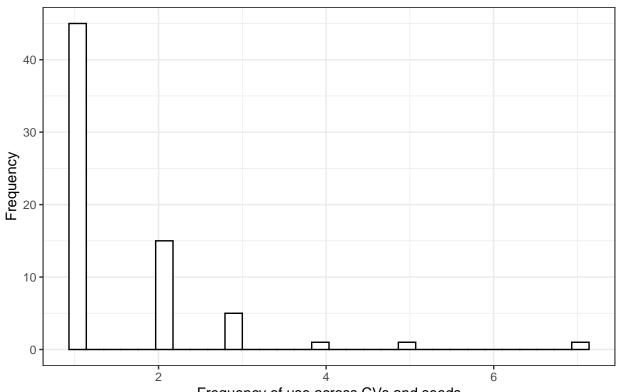
Average (across seeds) of worsen statistics from NextDoor analysis (summed across all CVs per seed)

Top feature, by the worsen statistic from NextDoor analysis

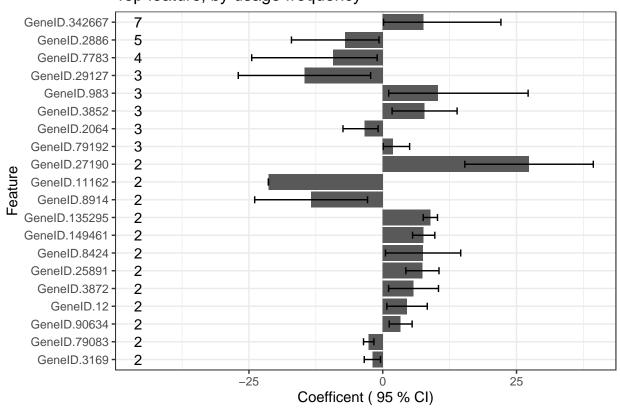


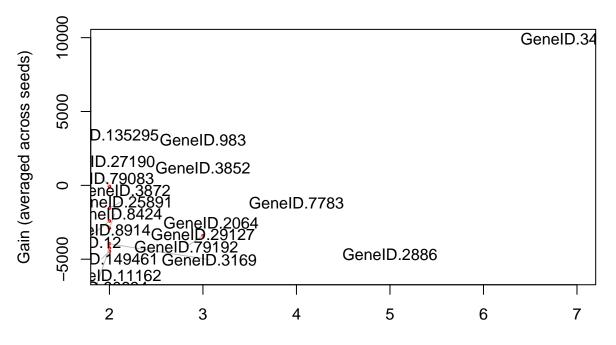
`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.

Distribution across all 68 features



Frequency of use across CVs and seeds Top feature, by usage frequency





Frequency (summed across CVs/seeds)

Heatmap of top 20 important features

