Random Forest with ranger using fold sampling

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04/01/2022

Random Forest Regression using sample summaries runs faster, retains accuracy

Summarising or Folding the samples is a way of reducing the total number of samples to a manageable number in order to run prediction algorithms on modern day machines. The folded samples are then unfolded to predict the full dataset.

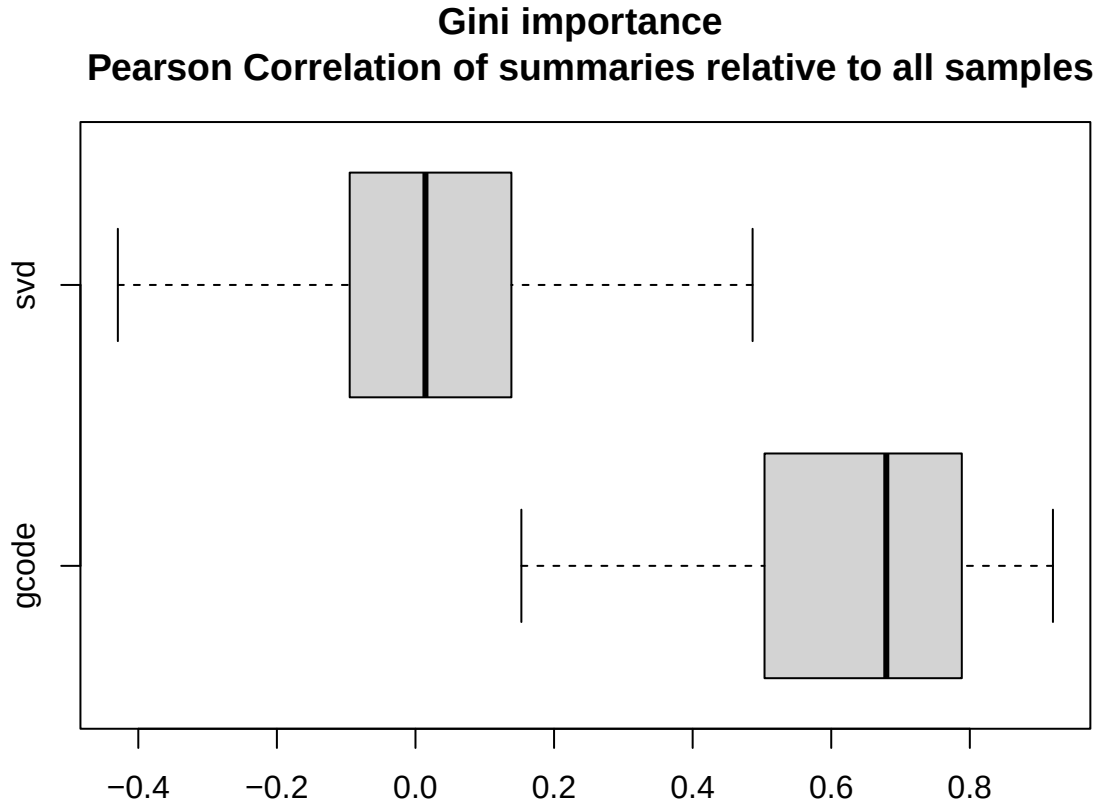
```
# Removes one feature at a time and uses it as the variable to be predicted (y variable)


# Total permutations :

permutation_test_number <- 100




# Run SVD decomposition of samples to a reduced sample space

source("./decompose_sample_space.R")


# Run gcode encoding of samples to a reduced sample space

source("./encode_sample_space.R")
```

A way to fold the total number of samples while retaining the original sample structure is done via Generative Encoding (gcode): https://github.com/AskExplain/gcode/tree/alpha_test_v2022.1

Boxplots of Gini importance Correlation for the features after summarisation compared to using all samples

```
boxplot(data.frame(gcode = total_cor.gcode,
                   svd = total_cor.svd),
        outline = F,
        horizontal = T,
        main = "Gini importance \n Pearson Correlation of summaries relative to all samples")
```

In essence, the Gini Importance is calculated for the features using all samples, and then correlated with the corresponding Importance values when using the summary samples from either SVD or gcode. The output is a correlation R^2 value for each run, giving a distribution for multiple runs on different permutations of the training set.

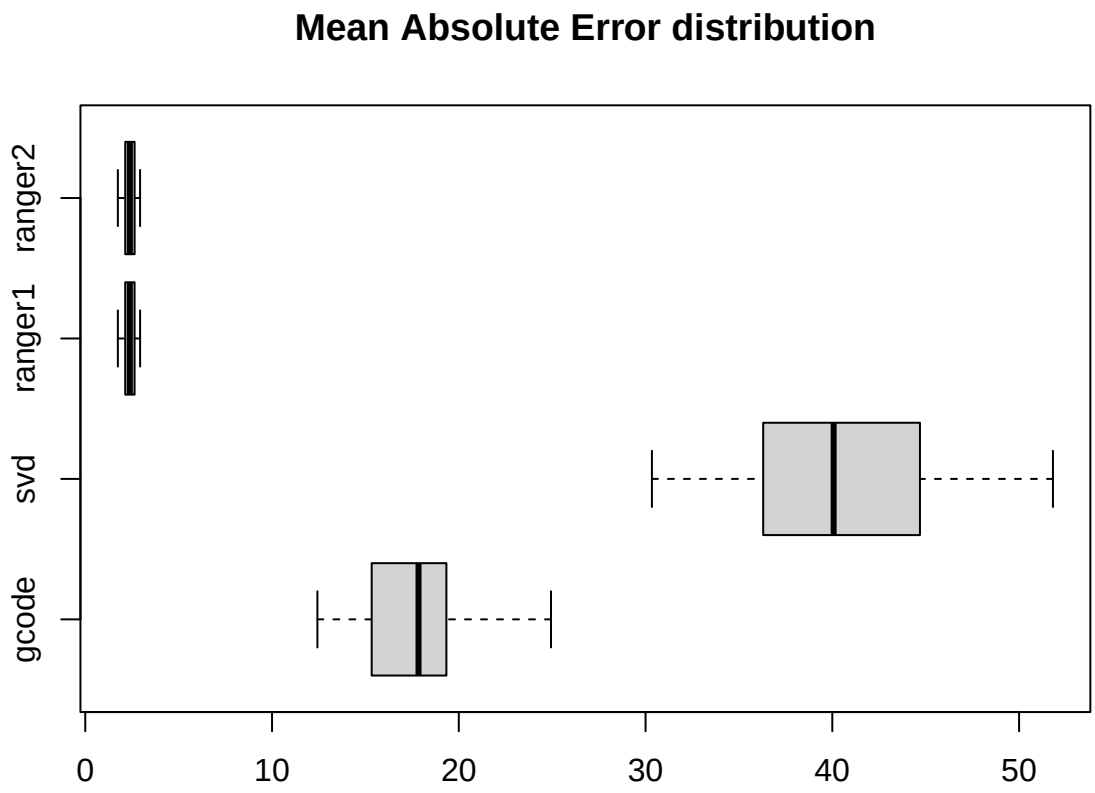


Boxplots of mean absolute error and runtime are plotted for every unique run of random forest regression via ranger package.

```
# Mean Absolute Error

boxplot(data.frame(gcode = total_mae.gcode,
```

```
                    svd = total_mae.svd,
                    ranger1 = total_mae.lreg.1,
                    ranger2 = total_mae.lreg.2),
        outline = F,
        horizontal = T,
        main = "Mean Absolute Error distribution")
```

Of great importance, the runtime does not include the running of the SVD or gcode algorithms.




```
# Runtime




boxplot(data.frame(gcode = total_time.gcode,
                   svd = total_time.svd,
                   ranger1 = total_time.lreg.1,
                   ranger2 = total_time.lreg.2),
        outline = F,
```

```
        horizontal = T,
        main = "Runtime distribution")
```