Prediction using fold sampling

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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.

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

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



# Total permutations :

permutation_test_number <- 1000









# 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
```

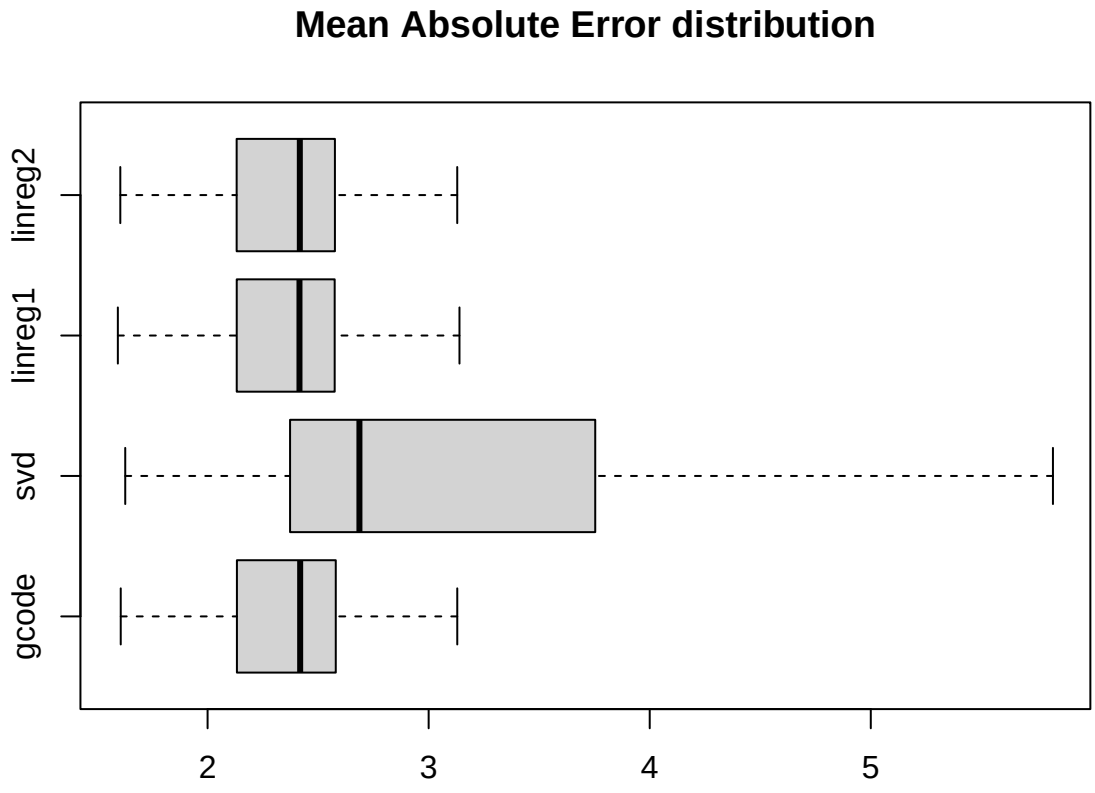
```
source("./encode_sample_space.R")
```

Boxplots of mean absolute error and runtime are plotted for every unique run of linear regression .

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

```
# Mean Absolute Error


boxplot(data.frame(gcode = total_mae.gcode,
                   svd = total_mae.svd,
                   linreg1 = total_mae.lreg.1,
                   linreg2 = total_mae.lreg.2),
        outline = F,
        horizontal = T,
        main = "Mean Absolute Error distribution")
```



```
# Runtime
```

```
boxplot(data.frame(gcode = total_time.gcode,
                   svd = total_time.svd,
                   linreg1 = total_time.lreg.1,
                   linreg2 = total_time.lreg.2),
        outline = F,
        horizontal = T,
        main = "Runtime distribution")
```