

CODECHECK certificate 2020-001



Item	Value
Title	ShinyLearner: A containerized benchmarking tool for machine-learning classification of tabular data.
Authors	Terry J Lee; Erica Suh; Kimball Hill; Stephen R Piccolo
Reference	Paper to appear in Gigascience.
Codechecker	Stephen J. Eglen https://orcid.org/0000-0001-8607-8025
Date of check:	2019-02-14 10:00:00
Date of check:	2019-02-14 10:00:00
Repository:	https://github.com/codecheckers/Piccolo-2020

Table 1: CODECHECK summary

File	Comment	Size
Figures/Datasets_Basic_AUROC.pdf	Figure 2 of manuscript	8078
Figures/Predictions_Histograms.pdf	Figure 3 of manuscript	8727
Figures/Algorithms_ParamsImprovement_AUROC.pdf	Figure 4 of manuscript	7837
Figures/Algorithms_FSIImprovement_AUROC.pdf	Figure 5 of manuscript	8190
Figures/FS_vs_CL.pdf	Figure 6 of manuscript	6521
Figures/FS_NumFeatures.pdf	Figure 7 of manuscript	5810
Tables/Basic_DiffFromMedian.tsv	Example output table 1 (not in manuscript)	619
Tables/ParamOpt_Improvement.tsv	Example output table 2 (not in manuscript)	14216

Table 2: Summary of output files generated

Summary

The reproduction of the figures in the manuscript was straightforward given that the authors provided a Rmarkdown document that processed the results data files. The results data files were not independently reproduced at this stage because of the long compute time.

CODECHECKER notes

Data and Code

After creating an empty repository, the following data and results folders were copied from CODE OCEAN capsule (<https://codeocean.com/capsule/5449763/tree>) for the paper: Datasets, Results_Basic, Results_FeatureSelection and Results_ParamsOptimized. One of the data files Results_ParamsOptimized/diabetes/Nested_Predictions.tsv.gz needed to be compressed to reduce the file size from 160 Mb to 9 Mb (Github has limit on individual files of 100 Mb.)

The main Rmd and helper script were downloaded from <https://github.com/srp33/ShinyLearner/>. The Rmd file was edited to read the compressed version of the .tsv file.

As no MANIFEST was provided by the author, SJE made one.

Extra software installations

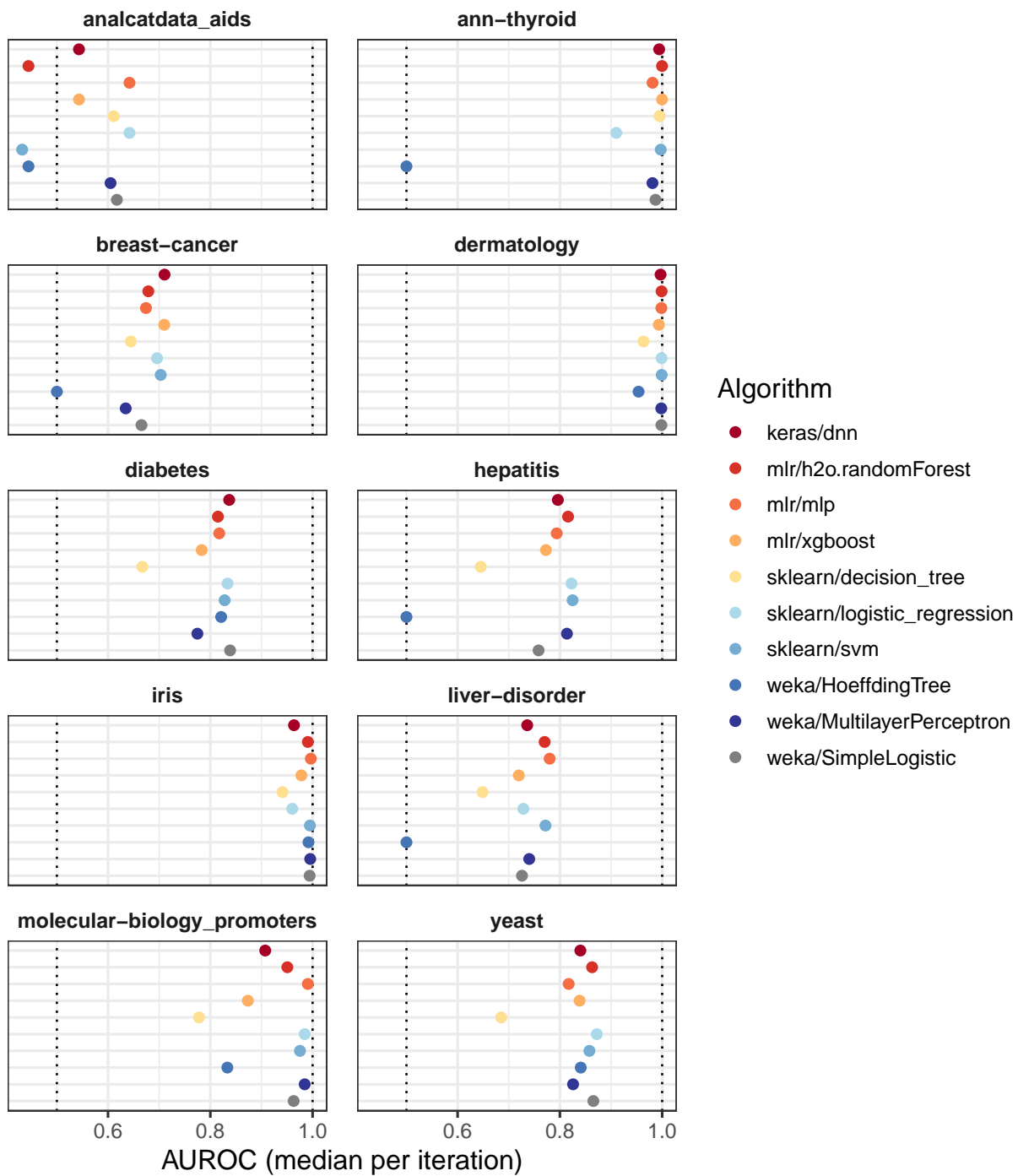
To run this script, I needed to install the following R packages

```
install.packages("tidyverse")
install.packages("cowplot")
```

Running the software to regenerate outputs.

A few small edits were made to the Analyze_Results.Rmd, see the git history,

To regenerate the Figures/ folder, we simply ran `make run` in the Makefile, created by SJE.



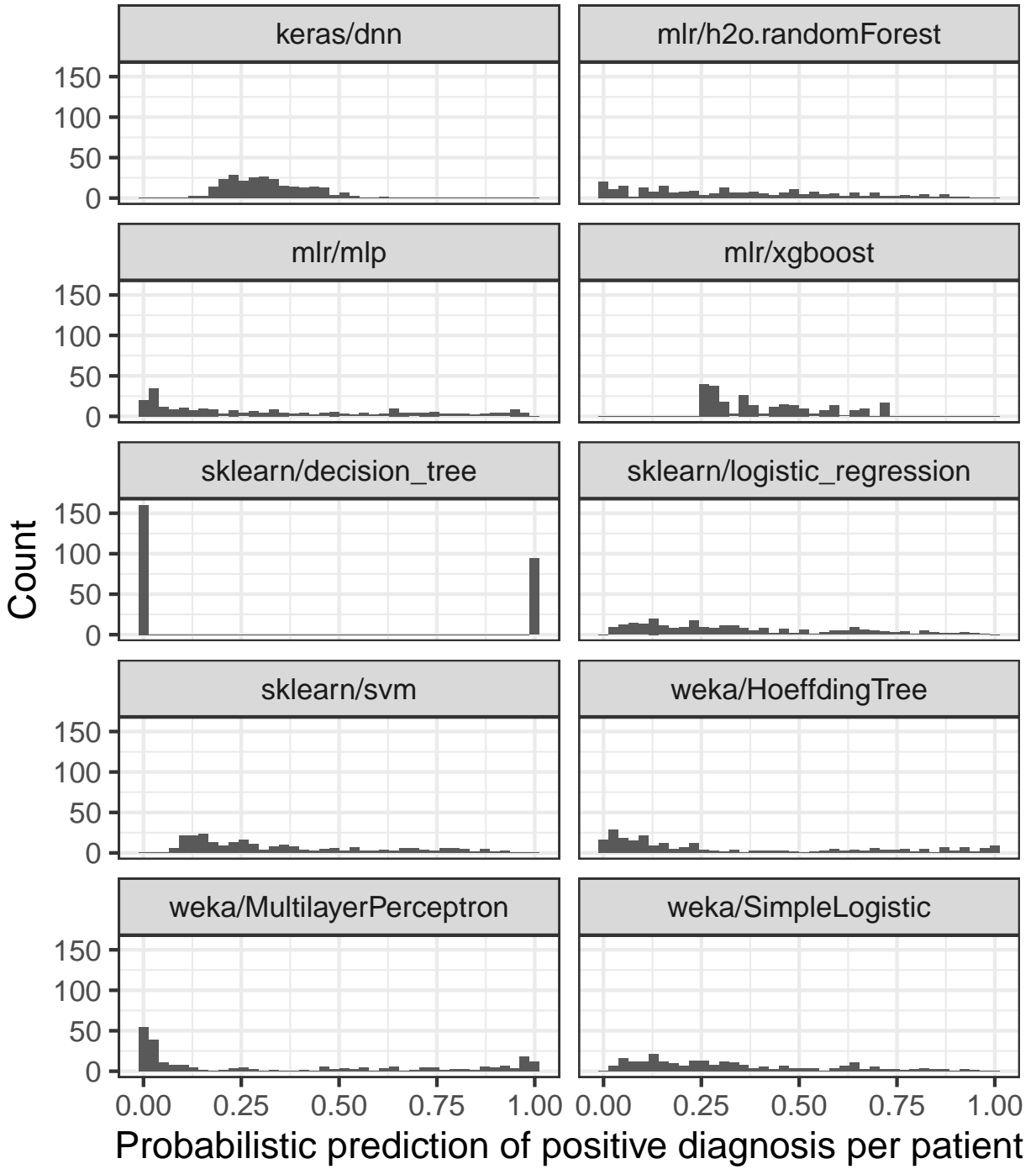


Figure 2: Figure 3 of manuscript

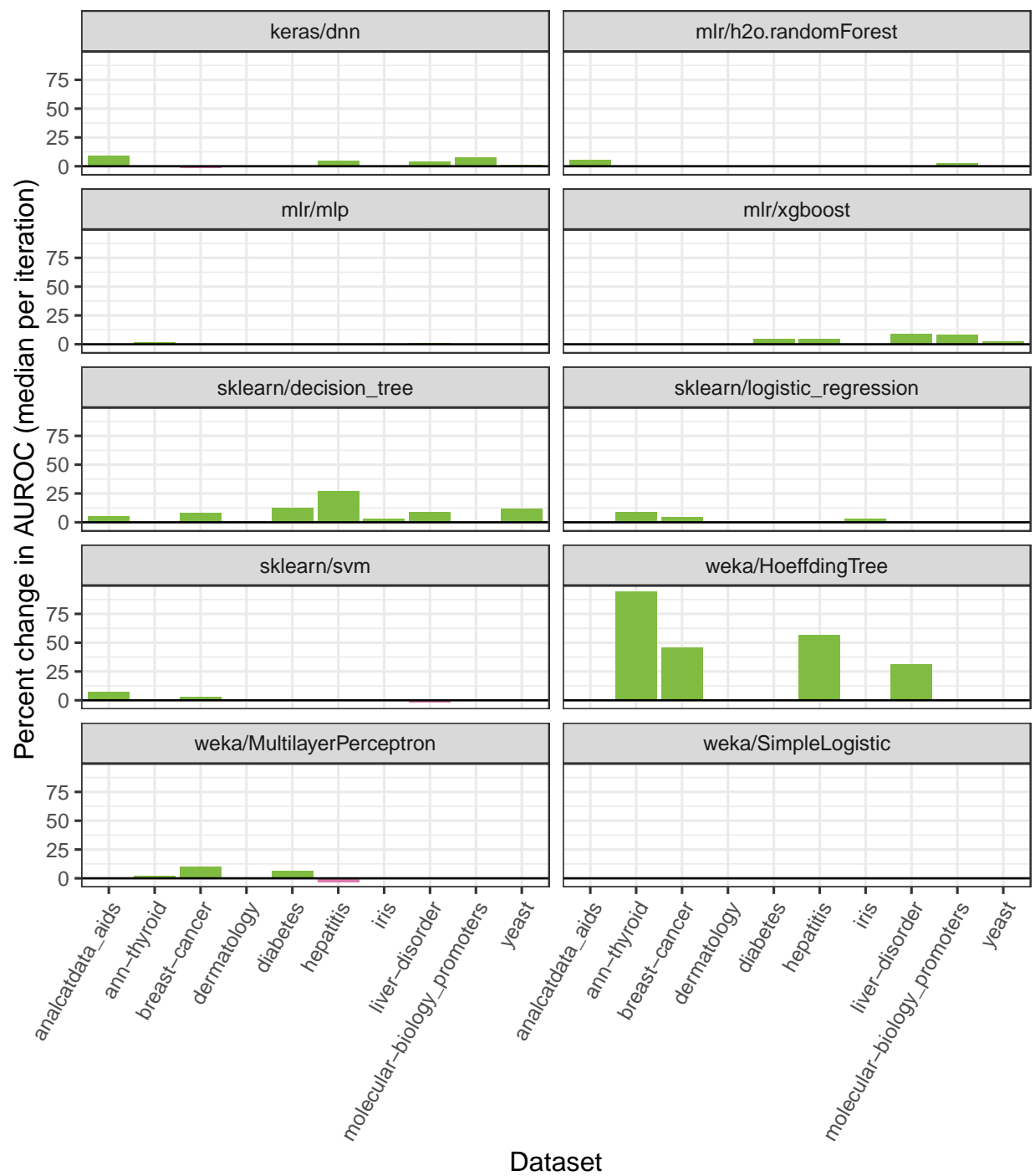


Figure 3: Figure 4 of manuscript

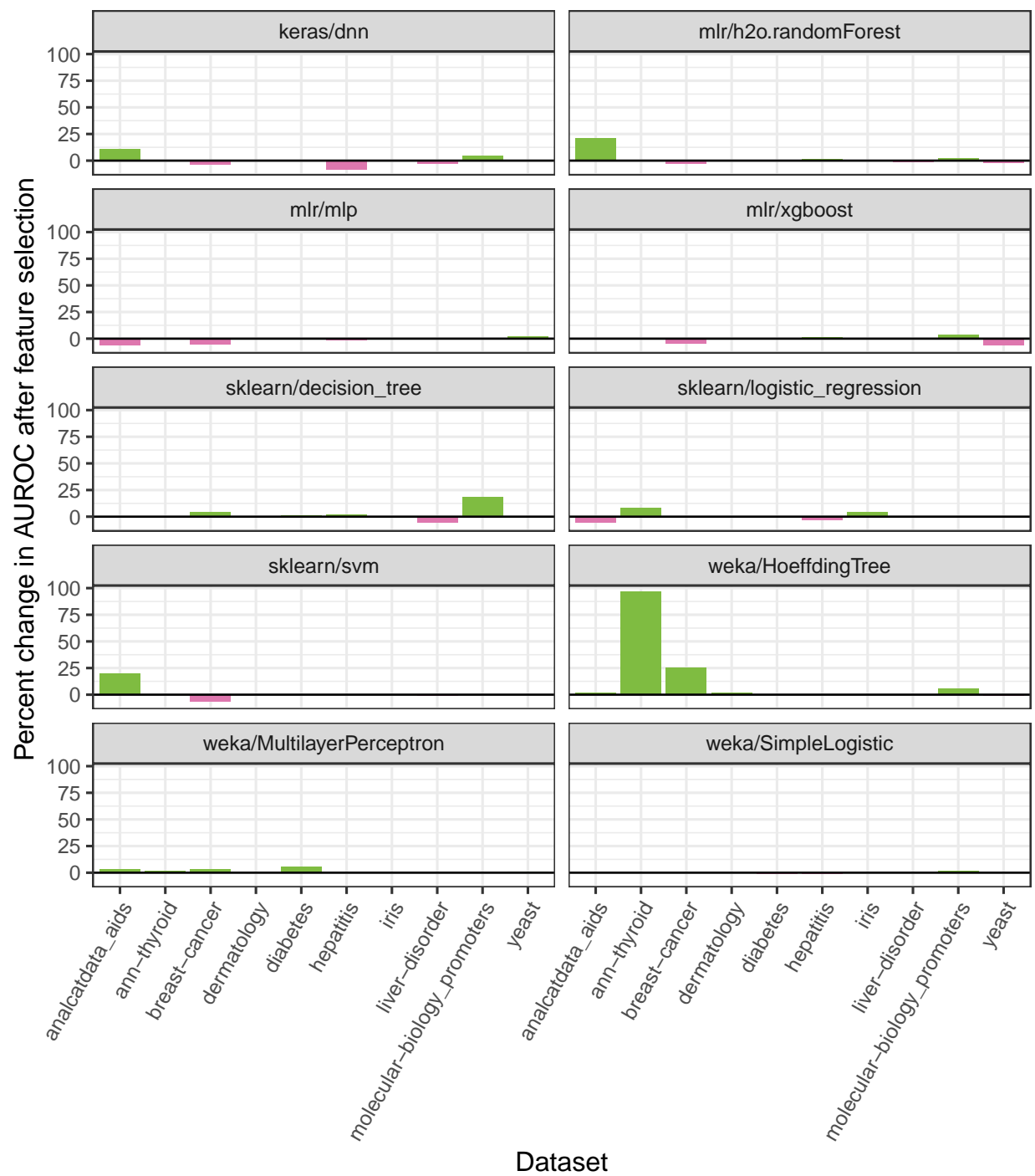


Figure 4: Figure 5 of manuscript

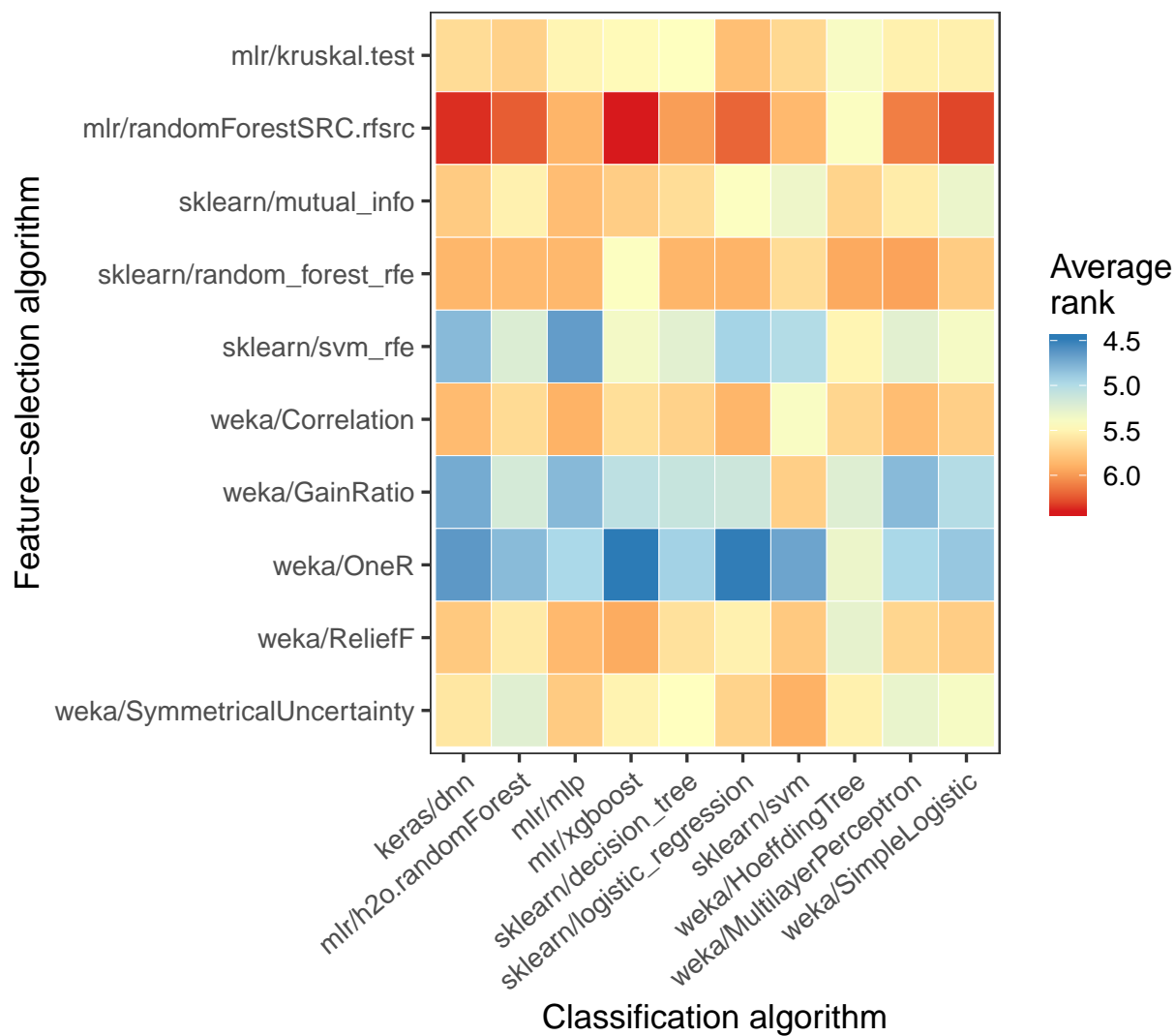


Figure 5: Figure 6 of manuscript

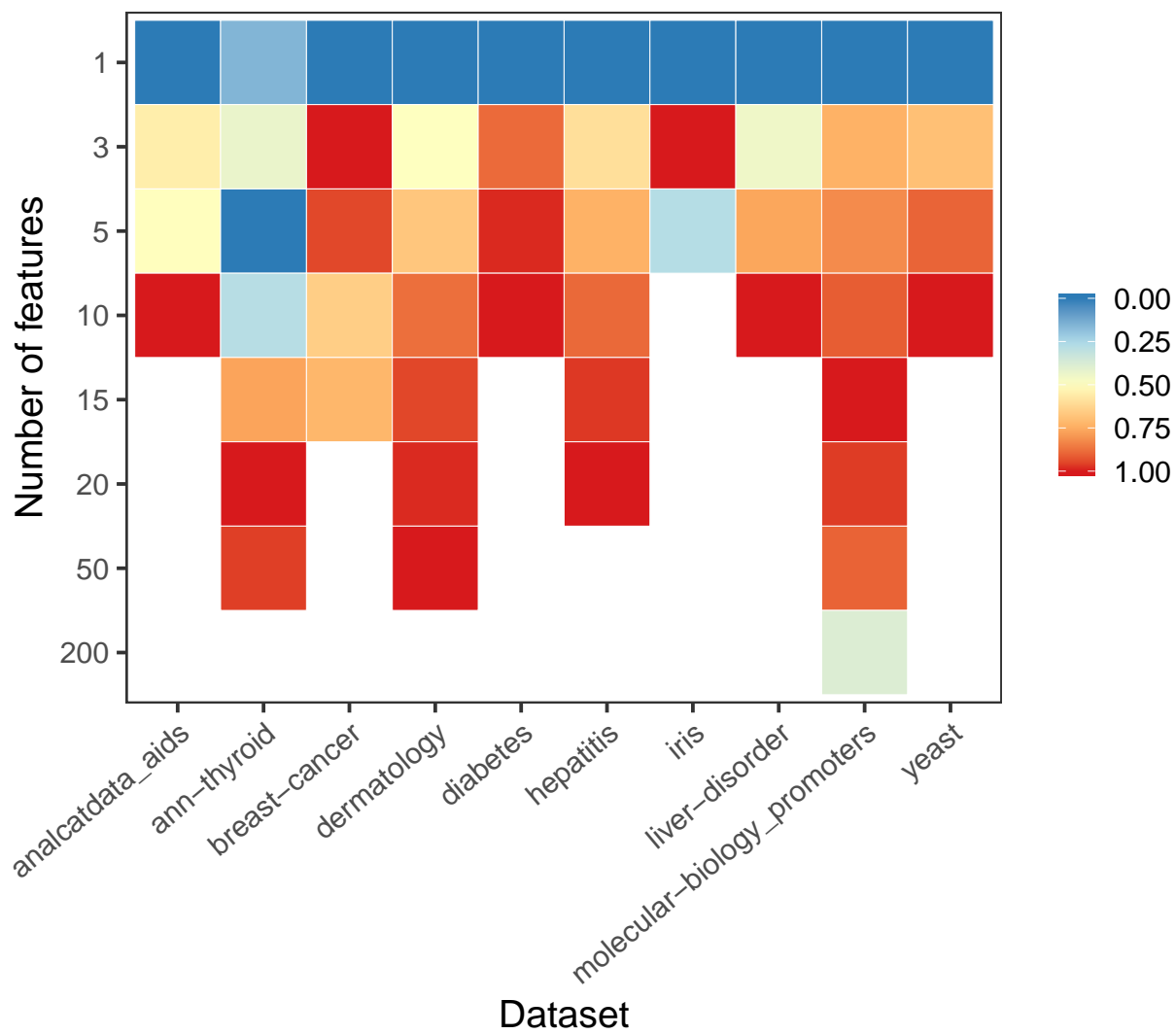


Figure 6: Figure 7 of manuscript

Table 1

```
read_tsv(dest_files[7])
```

```
## Parsed with column specification:
## cols(
##   Algorithm = col_character(),
##   Min_Diff = col_double(),
##   Max_Diff = col_double()
## )
```

```
## # A tibble: 10 x 3
##   Algorithm      Min_Diff Max_Diff
##   <chr>          <dbl>   <dbl>
## 1 keras/dnn      -0.0494  0.0340
## 2 mlr/h2o.randomForest -0.130   0.0379
## 3 mlr/mlp        -0.0233  0.0679
## 4 mlr/xgboost    -0.0833  0.0335
## 5 sklearn/decision_tree -0.179   0.0370
## 6 sklearn/logistic_regression -0.0803  0.0679
## 7 sklearn/svm    -0.142   0.0395
## 8 weka/HoeffdingTree -0.491   0.00187
## 9 weka/MultilayerPerceptron -0.0446  0.0309
## 10 weka/SimpleLogistic -0.0366  0.0432
```

Table 2

```
print(read_tsv(dest_files[8]))
```

```
## Parsed with column specification:
## cols(
##   Params = col_character(),
##   analcatdata_aids = col_double(),
##   `ann-thyroid` = col_double(),
##   `breast-cancer` = col_double(),
##   dermatology = col_double(),
##   diabetes = col_double(),
##   hepatitis = col_double(),
##   iris = col_double(),
##   `liver-disorder` = col_double(),
##   `molecular-biology_promoters` = col_double(),
##   yeast = col_double()
## )

## # A tibble: 53 x 11
##   Params analcatdata_aids `ann-thyroid` `breast-cancer`
##   <chr>          <dbl>          <dbl>          <dbl>
## 1 dropo~      -0.0833      0.00266      -0.00819
## 2 dropo~       0.0833     -0.000223    -0.0251
## 3 dropo~      -0.0278     -0.00301     0.0158
## 4 dropo~      -0.0278     0.00221    -0.00234
## 5 dropo~      -0.139      -0.00152    -0.0327
## 6 dropo~      -0.0278     0.00259    -0.00994
## 7 dropo~      -0.0278     -0.00405    -0.0655
## 8 dropo~      -0.0278     -0.00734    -0.0965
## 9 dropo~       0        -0.00800    -0.0550
## 10 dropo~    -0.0833     -0.0112    -0.0690
## # ... with 43 more rows, and 7 more variables:
## #   dermatology <dbl>, diabetes <dbl>, hepatitis <dbl>,
## #   iris <dbl>, `liver-disorder` <dbl>,
## #   `molecular-biology_promoters` <dbl>, yeast <dbl>
```

About this document

This document was created using Rmarkdown. `make codecheck.pdf` will regenerate the file.

```
sessionInfo()
```

```
## R version 3.6.2 (2019-12-12)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: Ubuntu 16.04.5 LTS
##
## Matrix products: default
## BLAS: /usr/lib/openblas-base/libblas.so.3
## LAPACK: /usr/lib/libopenblas-r0.2.18.so
##
## locale:
##  [1] LC_CTYPE=en_GB.UTF-8      LC_NUMERIC=C
##  [3] LC_TIME=en_GB.UTF-8      LC_COLLATE=en_GB.UTF-8
##  [5] LC_MONETARY=en_GB.UTF-8  LC_MESSAGES=en_GB.UTF-8
##  [7] LC_PAPER=en_GB.UTF-8     LC_NAME=C
##  [9] LC_ADDRESS=C             LC_TELEPHONE=C
## [11] LC_MEASUREMENT=en_GB.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets
## [6] methods    base
##
## other attached packages:
## [1] rprojroot_1.3-2 readr_1.3.1      tibble_2.1.3
## [4] yaml_2.2.1      DT_0.8          xtable_1.8-3
## [7] knitr_1.20
##
## loaded via a namespace (and not attached):
##  [1] Rcpp_1.0.1      magrittr_1.5      hms_0.5.3
##  [4] R6_2.3.0        rlang_0.4.4       fansi_0.4.0
##  [7] stringr_1.4.0   highr_0.8         tools_3.6.2
## [10] utf8_1.1.4      cli_1.1.0         htmltools_0.3.6
## [13] assertthat_0.2.1 digest_0.6.19     crayon_1.3.4
## [16] htmlwidgets_1.3 vctrs_0.2.2       evaluate_0.13
## [19] rmarkdown_1.10  stringi_1.2.4     compiler_3.6.2
## [22] pillar_1.4.2    backports_1.1.2   pkgconfig_2.0.2
```