

Supplemental Material for ‘Optimizing Model
Performance and Fairness Through Evolved
Sample Weights’

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2024-08-01

Contents

1	Introduction	5
1.1	Contributing authors	5
1.2	About our supplemental material	5
1.3	Supplemental material setup	6
2	Bias defintions	9
3	Heart Disease	11
3.1	Hypervolume	11
4	Student Math	15
4.1	Hypervolume	15
5	Student Por	19
5.1	Hypervolume	19
6	CreditG	23
6.1	Hypervolume	23
7	Titanic	27
7.1	Hypervolume	27
8	US Crime	31
8.1	Hypervolume	31

9 Compas Violent	35
9.1 Hypervolume	35
10 NLSY	39
10.1 Hypervolume	39
11 Compas	43
11.1 Hypervolume	43
12 Speeddating	47
12.1 Hypervolume	47
13 PMAD EPDS	51
13.1 Hypervolume	51
14 PMAD PHQ	55
14.1 Hypervolume	55

Chapter 1

Introduction

This is not intended as a stand-alone document, but as a companion to our manuscript.

1.1 Contributing authors

- Anil Kumar Saini
- Jose Guadalupe Hernandez
- Emily F. Wong
- Jason H. Moore

1.2 About our supplemental material

As you may have noticed (unless you're reading a pdf version of this), our supplemental material is hosted using GitHub pages. We compiled our data analyses and supplemental documentation into this nifty web-accessible book using bookdown.

The code used for this supplemental material can be found in this GitHub repository.

Our supplemental material includes the following:

- Metric definitions (Section ??)
- Heart disease results (Section 3)
- Student math results (Section 4)
- Student por results (Section 5)

- CreditG results (Section 6)
- Titanic results (Section 7)
- US Crime results (Section 8)
- Compas Violent results (Section 9)
- NLSY results (Section 10)
- Compas results (Section 11)
- Speed dating results (Section 12)
- PMAD EPDS results (Section 13)
- PMAD PHQ results (Section 14)

1.3 Supplemental material setup

1.3.1 Required packages and variables

Variable set up.

```
library(ggplot2)
library(cowplot)
library(dplyr)
library(PupillometryR)

NAMES <- c('Evolved','Calculated','None')
TASKS <- c('heart_disease', 'student_math', 'student_por', 'creditg', 'titanic', 'us_crime')
SHAPE <- c(21,24,22)
cb_palette <- c('#D81B60','#1E88E5','#FFC107')
TSIZE <- 19

p_theme <- theme(
  plot.title = element_text( face = "bold", size = 22, hjust=0.5),
  panel.border = element_blank(),
  panel.grid.minor = element_blank(),
  legend.title=element_text(size=18),
  legend.text=element_text(size=18),
  axis.title = element_text(size=18),
  axis.text = element_text(size=14),
  legend.position="bottom",
  panel.background = element_rect(fill = "#f1f2f5",
                                   colour = "white",
                                   linewidth = 0.5, linetype = "solid")
)

testing <- read.csv(paste('./', 'hv_test.csv', sep = "", collapse = NULL), header = TRUE)
testing$exp <- gsub('Evolved Weights', 'Evolved', testing$ex)
testing$exp <- gsub('Calculated Weights', 'Calculated', testing$ex)
```

```
testing$exp <- gsub('No Weights', 'None', testing$ex)
testing$exp <- factor(testing$exp, levels = NAMES)
```

1.3.2 Helper functions

Function to plot hypervolume results

```
# function to plot hyper-volume data
volume_plotter <- function(data, id)
{
  ggplot(data, aes(x = exp, y = hv, color = exp, fill = exp, shape = exp)) +
    geom_flat_violin(position = position_nudge(x = .1, y = 0), scale = 'width', alpha = 0.2, width = .05) +
    geom_boxplot(color = 'black', width = .07, outlier.shape = NA, alpha = 0.0, size = 1.0, position = position_nudge(x = .1, y = 0)) +
    geom_point(position = position_jitter(width = 0.02, height = 0.0001), size = 1.5, alpha = 1.0) +
    scale_y_continuous(
      name="Volume",
    ) +
    scale_x_discrete(
      name="Strategy"
    ) +
    scale_shape_manual(values=SHAPE, name="Weight\nStrategy") +
    scale_colour_manual(values = cb_palette, name="Weight\nStrategy") +
    scale_fill_manual(values = cb_palette, name="Weight\nStrategy") +
    ggtitle(TASKS[id]) +
    p_theme + coord_flip()
}
```

Function to summarize hypervolume results

```
# function to plot hyper-volume data
volume_summarize <- function(data)
{
  data %>%
    group_by(exp) %>%
    dplyr::summarise(
      count = n(),
      na_cnt = sum(is.na(hv)),
      min = min(hv, na.rm = TRUE),
      median = median(hv, na.rm = TRUE),
      mean = mean(hv, na.rm = TRUE),
      max = max(hv, na.rm = TRUE),
      IQR = IQR(hv, na.rm = TRUE)
    )
}
```


Chapter 2

Bias definitions

Multiple metrics exist to measure the fairness of predictions made by a machine learning model. Each metric is defined in relation to a specific application context and attempts to quantify different properties (false negative rate, accuracy, etc.) of the predictions for people belonging to different groups. Different metrics try to quantify different properties (false negative rate, accuracy, etc.) of the predictions for people belonging to different groups. For example, ‘Demographic parity’ measures whether the acceptance rates (proportion of individuals belonging to the group receiving positive prediction) are the same for all groups. ‘Error rate parity’ measures whether the false positive and false negative rates in all groups are equal, and ‘Predictive parity’ ensures an equal positive prediction rate across all groups. Here, we discuss in detail two commonly used metrics to measure the fairness in the predictions of a given model : ‘Subgroup False Positive Fairness’, and ‘Subgroup False Negative Fairness’. Before delving into the definitions of the above-mentioned metrics, we describe some terminologies here. Let $\mathcal{D} = \{(X, X', Y)_i\}_{i=1}^N$ be the dataset under consideration. For each data point (X, X', Y) , $X \in \mathcal{X}^d$ contains values corresponding to d *non-sensitive* features, $X' \in \mathcal{X}'^p$ contains values corresponding to p *sensitive* features, and Y contains the target variables. Features deemed ‘sensitive’, or ‘protected’, such as race, sex, and gender, are classified as sensitive features (X'). Here, we would assume X' and X do not overlap, and therefore, $X + X'$ would give us the full feature set for a particular data point. Based on the values of sensitive attributes, each data point can fall into one of the groups defined by those sensitive attributes. For example, ‘Black women younger than 25’ would be one of the groups when the sensitive attributes are race, gender, and age. Let $G \in \mathcal{G}$ be one such group. We show the membership to this group by $X' \in G$. Finally, let $\hat{Y} \in \{0, 1\}$ be the predicted target value output by the classifier. Finally, let $R(X, X') \in [0.0, 1.0]$ be the risk score output by a given ML model, $\hat{Y} \in \{0, 1\}$ is the predicted target value, and for simplicity, also the classifier, formed by applying a threshold on $R(X, X')$. False Positive Subgroup Fairness and False Negative Subgroup Fairness capture the maximum deviation of a model’s perfor-

mance among any one group in \mathcal{G} , normalized by the probability of observing an individual from that group in the negative or positive labels, respectively. Since in most scenarios, we would want the model to perform similarly in all groups, lower values on these metrics denote more fair models. For a dataset \mathcal{D} , and risk model $R(X, X')$, the following are the definitions. False Positive (FP) Rate : False positive (FP) rate can be defined as

$$FP(R) = Pr[\hat{Y} = 1|Y = 0].$$

And the False Positive Rate for a group G can be defined as

$$FP(R, G) = Pr[\hat{Y} = 1|Y = 0, X' \in G].$$

False Negative (FN) Rate : False positive (FP) rate can be defined as

$$FN(R) = Pr[\hat{Y} = 0|Y = 1].$$

And the False Negative Rate for a group G can be defined as

$$FN(R, G) = Pr[\hat{Y} = 0|Y = 1, X' \in G].$$

False Positive Subgroup Fairness : Let the probability of getting negative labels in group G be

$$\alpha_{FP}(G) = Pr[X' \in G, Y = 0].$$

We also define the absolute difference in false positive rate between the whole population and for a specific group G as

$$\beta(R, G) = |FP(R) - FP(R, G)|.$$

Then the False Positive Subgroup Fairness (FPSF) is given by

$$FPSF(D, R) = \max_{G \in \mathcal{G}} \alpha_{FP}(G) \beta(R, G).$$

False Negative Subgroup Fairness : Let the probability of getting positive labels in group G be

$$\alpha_{FN}(G) = Pr[X' \in G, Y = 1].$$

We also define the absolute difference in false negative rate between the whole population and for a specific group G as

$$\beta(R, G) = |FN(R) - FN(R, G)|.$$

Then the False Positive Subgroup Fairness (FPSF) is given by

$$FNSF(D, R) = \max_{G \in \mathcal{G}} \alpha_{FN}(G) \beta(R, G).$$

Chapter 3

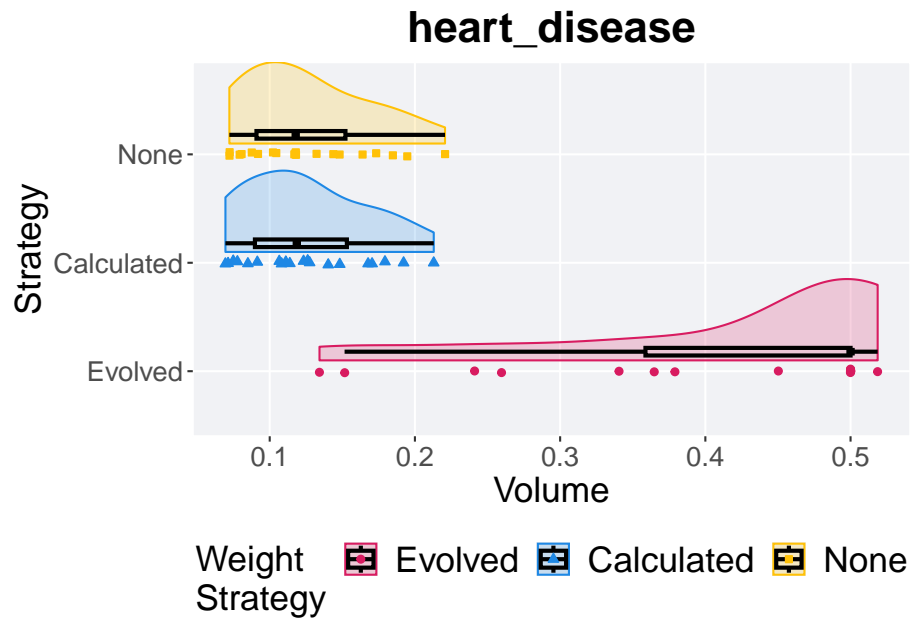
Heart Disease

Here we report the **hypervolume** achieved by evaluating the performance of each solution within the Pareto front on the test set of the `heart_disease` dataset.

```
# heart-disease data
data <- filter(testing, dataset == "heart_disease")
```

3.1 Hypervolume

```
volume_plotter(data, 1)
```



3.1.1 Summary stats

```
volume_summarize(data)
```

```
## # A tibble: 3 x 8
##   exp      count na_cnt   min median  mean  max  IQR
##   <fct>    <int> <int> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 Evolved      20     0 0.134   0.5  0.417 0.519 0.141
## 2 Calculated   20     0 0.0695 0.119 0.125 0.213 0.0633
## 3 None         20     0 0.0722 0.118 0.126 0.221 0.0613
```

3.1.2 Kruskal-Wallis test

Detected differences between weight strategies.

```
kruskal.test(hv ~ exp, data = data)
```

```
##
## Kruskal-Wallis rank sum test
##
## data: hv by exp
## Kruskal-Wallis chi-squared = 34.987, df = 2, p-value = 2.528e-08
```

3.1.3 Pairwise wilcoxon test

```
pairwise.wilcox.test(x = data$hv, g = data$exp, p.adjust.method = "bonferroni",
                    paired = FALSE, conf.int = FALSE, alternative = 'l')

##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: data$hv and data$exp
##
##           Evolved Calculated
## Calculated 4.5e-07 -
## None       4.5e-07 1
##
## P value adjustment method: bonferroni
```


Chapter 4

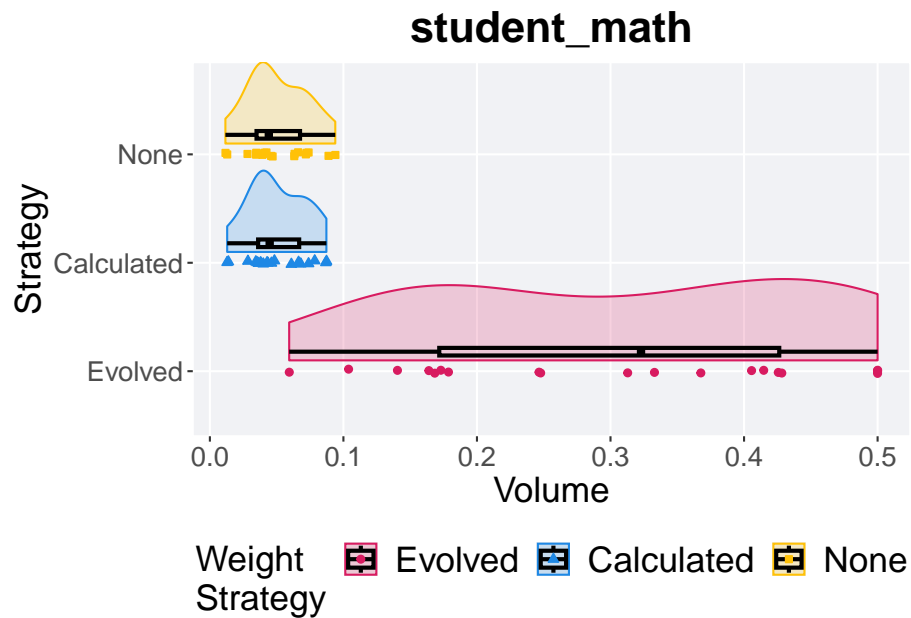
Student Math

Here we report the **hypervolume** achieved by evaluating the performance of each solution within the Pareto front on the test set of the `student_math` dataset.

```
# heart-disease data  
data <- filter(testing, dataset == "student_math")
```

4.1 Hypervolume

```
volume_plotter(data, 2)
```



4.1.1 Summary stats

```
volume_summarize(data)
```

```
## # A tibble: 3 x 8
##   exp      count na_cnt    min median  mean   max   IQR
##   <fct>    <int> <int>  <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 Evolved      20     0 0.0594 0.323 0.308 0.5   0.255
## 2 Calculated   20     0 0.0129 0.0448 0.0504 0.0873 0.0307
## 3 None         20     0 0.0116 0.0441 0.0503 0.0939 0.0326
```

4.1.2 Kruskal-Wallis test

Detected differences between weight strategies.

```
kruskal.test(hv ~ exp, data = data)
```

```
##
## Kruskal-Wallis rank sum test
##
## data: hv by exp
## Kruskal-Wallis chi-squared = 36.282, df = 2, p-value = 1.323e-08
```


4.1.3 Pairwise wilcoxon test

```
pairwise.wilcox.test(x = data$hv, g = data$exp, p.adjust.method = "bonferroni",
                    paired = FALSE, conf.int = FALSE, alternative = 'l')

##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: data$hv and data$exp
##
##           Evolved Calculated
## Calculated 3.3e-07 -
## None       3.3e-07 1
##
## P value adjustment method: bonferroni
```


Chapter 5

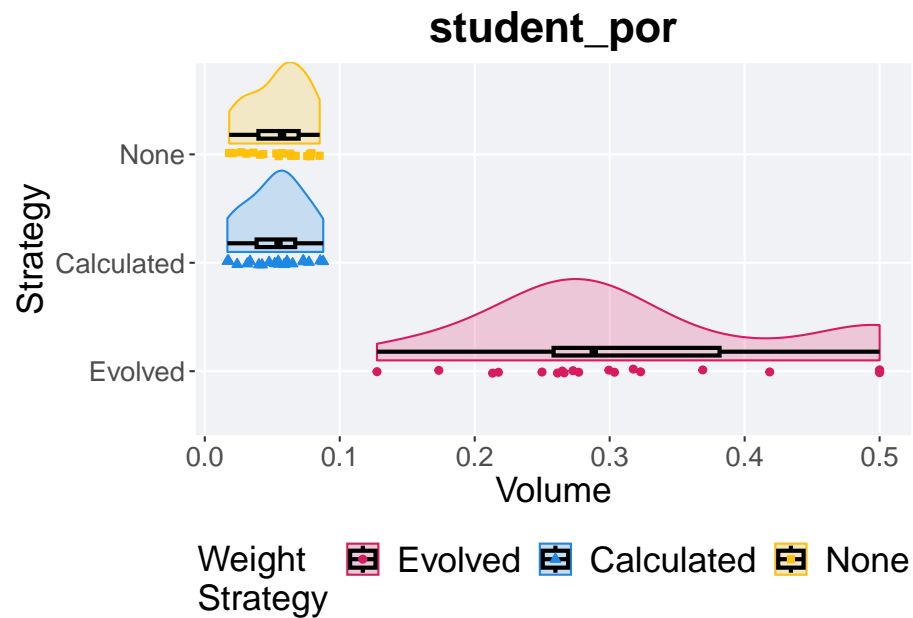
Student Por

Here we report the **hypervolume** achieved by evaluating the performance of each solution within the Pareto front on the test set of the `student_por` dataset.

```
# heart-disease data  
data <- filter(testing, dataset == "student_por")
```

5.1 Hypervolume

```
volume_plotter(data,3)
```



5.1.1 Summary stats

```
volume_summarize(data)
```

```
## # A tibble: 3 x 8
##   exp      count na_cnt   min median   mean   max   IQR
##   <fct>    <int> <int> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 Evolved      20     0 0.128 0.288 0.318 0.5   0.123
## 2 Calculated   20     0 0.0168 0.0546 0.0528 0.0878 0.0286
## 3 None         20     0 0.0181 0.0573 0.0547 0.0851 0.0298
```

5.1.2 Kruskal-Wallis test

Detected differences between weight strategies.

```
kruskal.test(hv ~ exp, data = data)
```

```
##
## Kruskal-Wallis rank sum test
##
## data: hv by exp
## Kruskal-Wallis chi-squared = 39.429, df = 2, p-value = 2.742e-09
```

5.1.3 Pairwise wilcoxon test

```
pairwise.wilcox.test(x = data$hv, g = data$exp, p.adjust.method = "bonferroni",
                    paired = FALSE, conf.int = FALSE, alternative = 'l')

##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: data$hv and data$exp
##
##           Evolved Calculated
## Calculated 1e-07      -
## None       1e-07      1
##
## P value adjustment method: bonferroni
```


Chapter 6

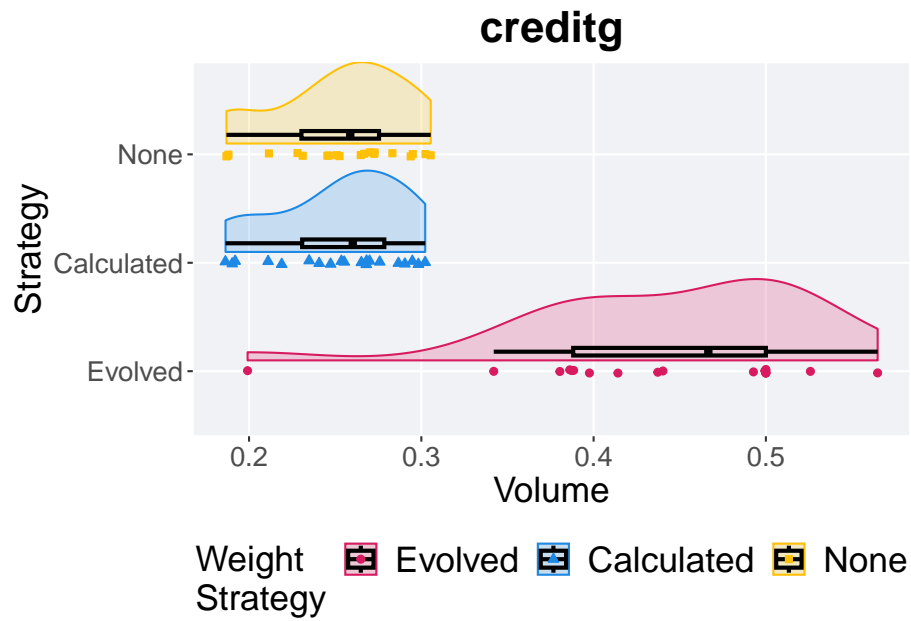
CreditG

Here we report the **hypervolume** achieved by evaluating the performance of each solution within the Pareto front on the test set of the `creditg` dataset.

```
# heart-disease data  
data <- filter(testing, dataset == "creditg")
```

6.1 Hypervolume

```
volume_plotter(data, 4)
```



6.1.1 Summary stats

```
volume_summarize(data)
```

```
## # A tibble: 3 x 8
##   exp      count na_cnt  min median  mean  max  IQR
##   <fct>    <int> <int> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 Evolved      20     0 0.199  0.467 0.443 0.565 0.112
## 2 Calculated   20     0 0.186  0.260 0.252 0.302 0.0477
## 3 None         20     0 0.187  0.259 0.253 0.305 0.0450
```

6.1.2 Kruskal-Wallis test

Detected differences between weight strategies.

```
kruskal.test(hv ~ exp, data = data)
```

```
##
## Kruskal-Wallis rank sum test
##
## data:  hv by exp
## Kruskal-Wallis chi-squared = 32.972, df = 2, p-value = 6.922e-08
```


6.1.3 Pairwise wilcoxon test

```
pairwise.wilcox.test(x = data$hv, g = data$exp, p.adjust.method = "bonferroni",
                    paired = FALSE, conf.int = FALSE, alternative = 'l')

##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: data$hv and data$exp
##
##           Evolved Calculated
## Calculated 1.1e-06 -
## None       1.1e-06 1
##
## P value adjustment method: bonferroni
```


Chapter 7

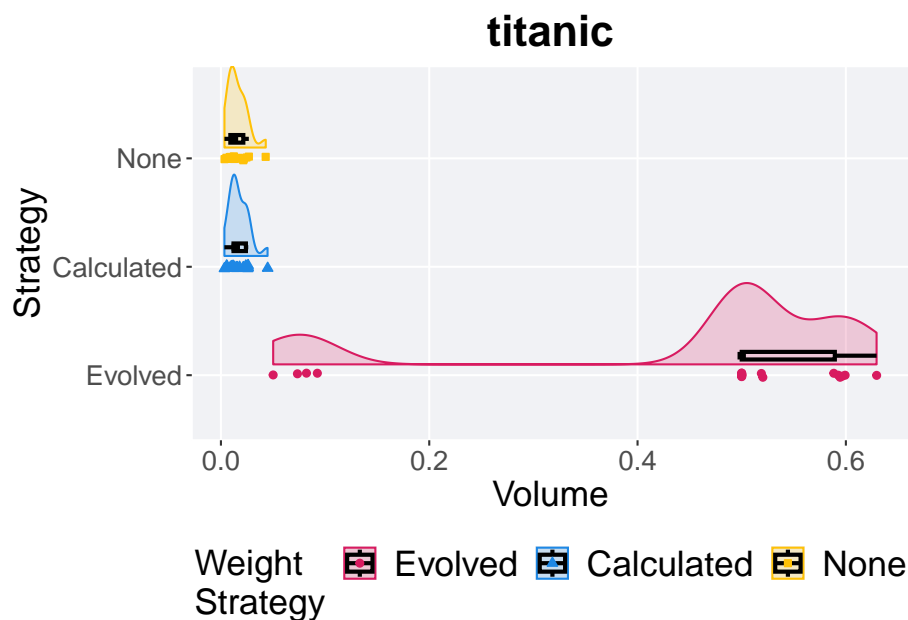
Titanic

Here we report the **hypervolume** achieved by evaluating the performance of each solution within the Pareto front on the test set of the `titanic` dataset.

```
# heart-disease data  
data <- filter(testing, dataset == "titanic")
```

7.1 Hypervolume

```
volume_plotter(data,5)
```



7.1.1 Summary stats

```
volume_summarize(data)
```

```
## # A tibble: 3 x 8
##   exp      count na_cnt    min median  mean   max   IQR
##   <fct>    <int> <int>  <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 Evolved      20     0 0.0502  0.5   0.447  0.629 0.0894
## 2 Calculated   20     0 0.00334 0.0143 0.0171 0.0448 0.0119
## 3 None         20     0 0.00340 0.0126 0.0157 0.0430 0.0125
```

7.1.2 Kruskal-Wallis test

Detected differences between weight strategies.

```
kruskal.test(hv ~ exp, data = data)
```

```
##
## Kruskal-Wallis rank sum test
##
## data: hv by exp
## Kruskal-Wallis chi-squared = 39.658, df = 2, p-value = 2.445e-09
```

7.1.3 Pairwise wilcoxon test

```
pairwise.wilcox.test(x = data$hv, g = data$exp, p.adjust.method = "bonferroni",
                    paired = FALSE, conf.int = FALSE, alternative = 'l')

##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: data$hv and data$exp
##
##           Evolved Calculated
## Calculated 9e-08      -
## None       9e-08    0.74
##
## P value adjustment method: bonferroni
```


Chapter 8

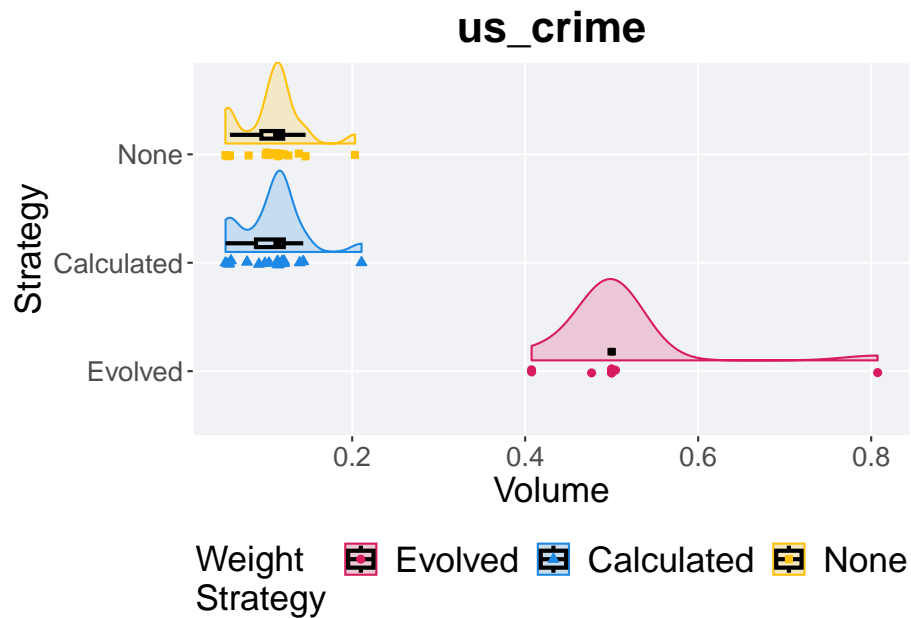
US Crime

Here we report the **hypervolume** achieved by evaluating the performance of each solution within the Pareto front on the test set of the `us_crime` dataset.

```
# heart-disease data  
data <- filter(testing, dataset == "us_crime")
```

8.1 Hypervolume

```
volume_plotter(data, 6)
```



8.1.1 Summary stats

```
volume_summarize(data)
```

```
## # A tibble: 3 x 8
##   exp      count na_cnt    min median  mean   max   IQR
##   <fct>    <int>  <int>  <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 Evolved      20      0 0.407   0.5  0.505 0.807  0
## 2 Calculated   20      0 0.0536 0.114 0.108 0.211 0.0322
## 3 None        20      0 0.0534 0.113 0.107 0.203 0.0252
```

8.1.2 Kruskal-Wallis test

Detected differences between weight strategies.

```
kruskal.test(hv ~ exp, data = data)
```

```
##
## Kruskal-Wallis rank sum test
##
## data: hv by exp
## Kruskal-Wallis chi-squared = 39.978, df = 2, p-value = 2.084e-09
```


8.1.3 Pairwise wilcoxon test

```
pairwise.wilcox.test(x = data$hv, g = data$exp, p.adjust.method = "bonferroni",
                    paired = FALSE, conf.int = FALSE, alternative = 'l')

##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: data$hv and data$exp
##
##           Evolved Calculated
## Calculated 4.4e-08 -
## None       4.4e-08 1
##
## P value adjustment method: bonferroni
```


Chapter 9

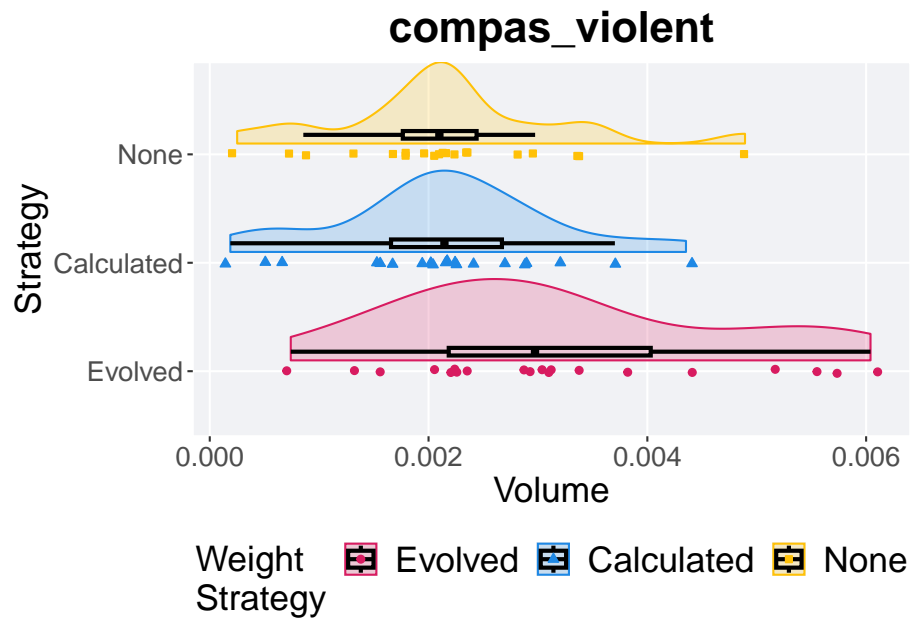
Compas Violent

Here we report the **hypervolume** achieved by evaluating the performance of each solution within the Pareto front on the test set of the `compas_violent` dataset.

```
# heart-disease data
data <- filter(testing, dataset == "compas_violent")
```

9.1 Hypervolume

```
volume_plotter(data, 7)
```



9.1.1 Summary stats

```
volume_summarize(data)
```

```
## # A tibble: 3 x 8
##   exp      count na_cnt      min median    mean    max    IQR
##   <fct>    <int> <int>    <dbl> <dbl>  <dbl> <dbl> <dbl>
## 1 Evolved      20     0 0.000741 0.00297 0.00319 0.00604 0.00185
## 2 Calculated   20     0 0.000188 0.00215 0.00215 0.00435 0.00101
## 3 None         20     0 0.000251 0.00210 0.00217 0.00489 0.000675
```

9.1.2 Kruskal-Wallis test

Detected differences between weight strategies.

```
kruskal.test(hv ~ exp, data = data)
```

```
##
## Kruskal-Wallis rank sum test
##
## data: hv by exp
## Kruskal-Wallis chi-squared = 6.7764, df = 2, p-value = 0.03377
```

9.1.3 Pairwise wilcoxon test

```
pairwise.wilcox.test(x = data$hv, g = data$exp, p.adjust.method = "bonferroni",  
                    paired = FALSE, conf.int = FALSE, alternative = 'l')
```

```
##  
## Pairwise comparisons using Wilcoxon rank sum exact test  
##  
## data: data$hv and data$exp  
##  
##           Evolved Calculated  
## Calculated 0.034 -  
## None       0.039 1.000  
##  
## P value adjustment method: bonferroni
```


Chapter 10

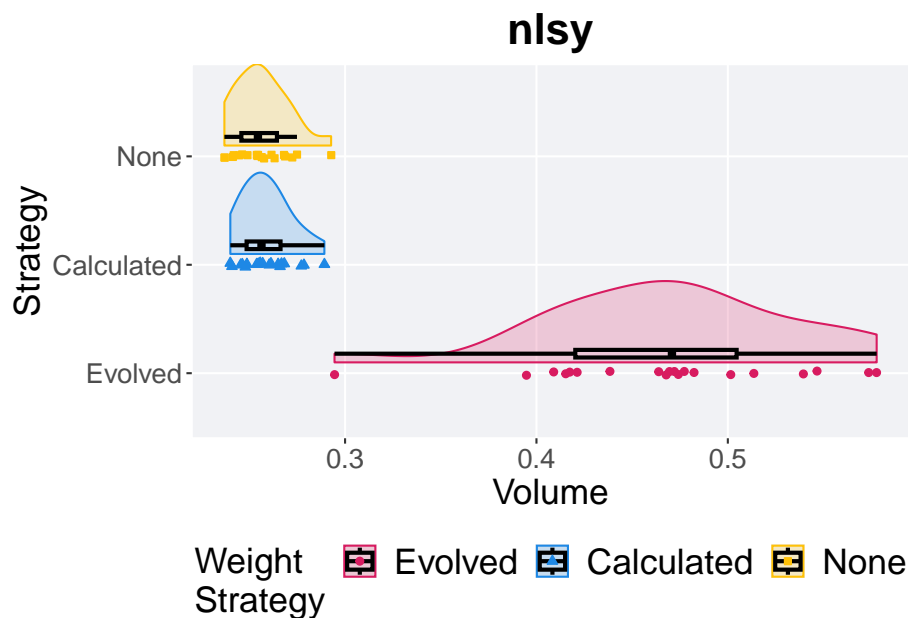
NLSY

Here we report the **hypervolume** achieved by evaluating the performance of each solution within the Pareto front on the test set of the `nlsy` dataset.

```
# heart-disease data  
data <- filter(testing, dataset == "nlsy")
```

10.1 Hypervolume

```
volume_plotter(data,8)
```



10.1.1 Summary stats

```
volume_summarize(data)
```

```
## # A tibble: 3 x 8
##   exp      count na_cnt   min median  mean   max   IQR
##   <fct>    <int>  <int> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 Evolved      20      0 0.294  0.471 0.468 0.578 0.0843
## 2 Calculated   20      0 0.240  0.256 0.259 0.289 0.0177
## 3 None         20      0 0.237  0.254 0.256 0.293 0.0186
```

10.1.2 Kruskal-Wallis test

Detected differences between weight strategies.

```
kruskal.test(hv ~ exp, data = data)
```

```
##
## Kruskal-Wallis rank sum test
##
## data:  hv by exp
## Kruskal-Wallis chi-squared = 39.518, df = 2, p-value = 2.623e-09
```


10.1.3 Pairwise wilcoxon test

```
pairwise.wilcox.test(x = data$hv, g = data$exp, p.adjust.method = "bonferroni",  
                    paired = FALSE, conf.int = FALSE, alternative = 'l')
```

```
##  
## Pairwise comparisons using Wilcoxon rank sum exact test  
##  
## data: data$hv and data$exp  
##  
##           Evolved Calculated  
## Calculated 2.2e-11 -  
## None       2.2e-11 0.82  
##  
## P value adjustment method: bonferroni
```


Chapter 11

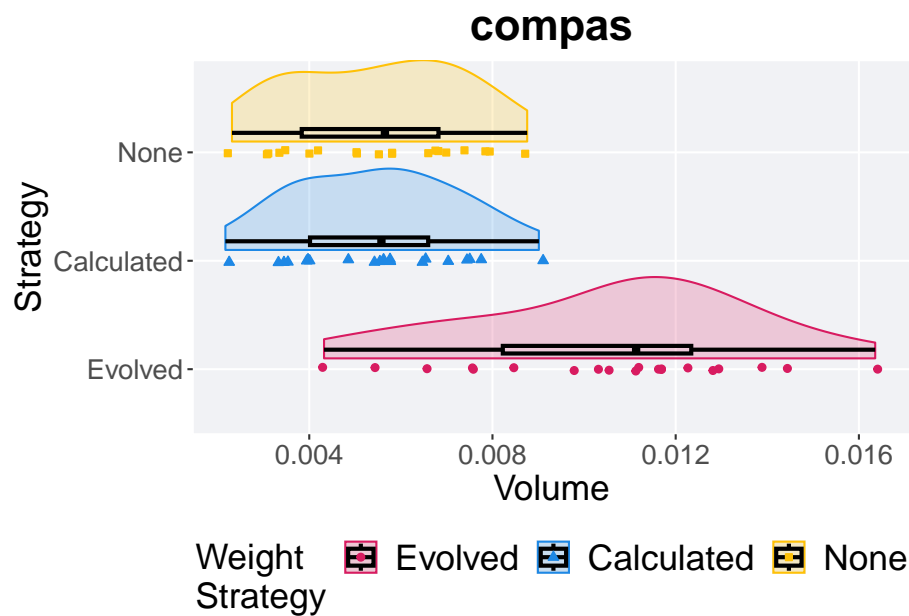
Compas

Here we report the **hypervolume** achieved by evaluating the performance of each solution within the Pareto front on the test set of the **compas** dataset.

```
# heart-disease data  
data <- filter(testing, dataset == "compas")
```

11.1 Hypervolume

```
volume_plotter(data, 9)
```



11.1.1 Summary stats

```
volume_summarize(data)
```

```
## # A tibble: 3 x 8
##   exp      count na_cnt    min median   mean   max   IQR
##   <fct>    <int> <int>  <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 Evolved      20     0 0.00432 0.0111 0.0105 0.0164 0.00411
## 2 Calculated   20     0 0.00217 0.00558 0.00546 0.00901 0.00258
## 3 None         20     0 0.00231 0.00565 0.00548 0.00876 0.00299
```

11.1.2 Kruskal-Wallis test

Detected differences between weight strategies.

```
kruskal.test(hv ~ exp, data = data)
```

```
##
## Kruskal-Wallis rank sum test
##
## data: hv by exp
## Kruskal-Wallis chi-squared = 26.298, df = 2, p-value = 1.947e-06
```

11.1.3 Pairwise wilcoxon test

```
pairwise.wilcox.test(x = data$hv, g = data$exp, p.adjust.method = "bonferroni",  
                    paired = FALSE, conf.int = FALSE, alternative = 'l')
```

```
##  
## Pairwise comparisons using Wilcoxon rank sum exact test  
##  
## data: data$hv and data$exp  
##  
##           Evolved Calculated  
## Calculated 1.4e-06 -  
## None       3.6e-06 1  
##  
## P value adjustment method: bonferroni
```


Chapter 12

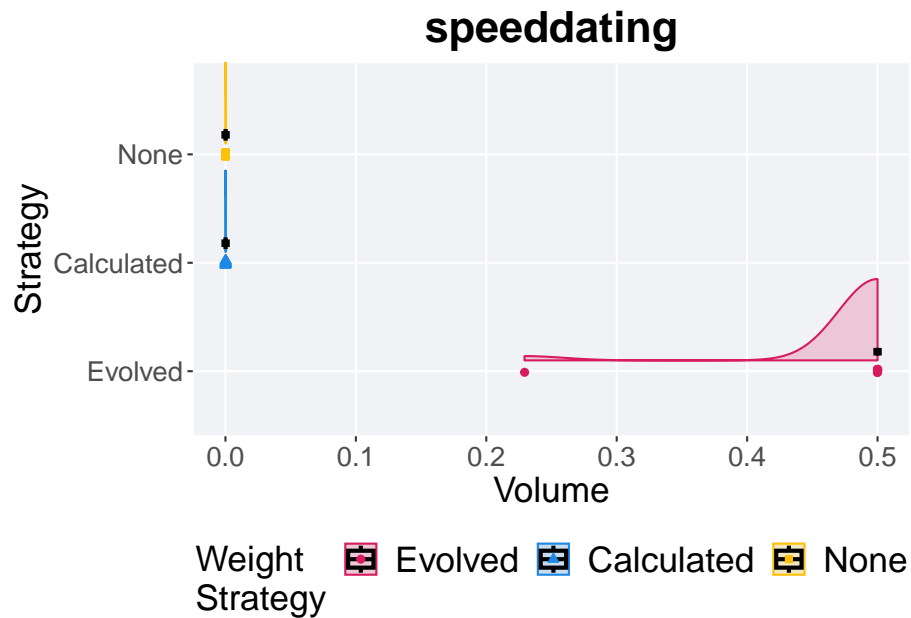
Speeddating

Here we report the **hypervolume** achieved by evaluating the performance of each solution within the Pareto front on the test set of the **speeddating** dataset.

```
# heart-disease data  
data <- filter(testing, dataset == "speeddating")
```

12.1 Hypervolume

```
volume_plotter(data, 10)
```



12.1.1 Summary stats

```
volume_summarize(data)
```

```
## # A tibble: 3 x 8
##   exp      count na_cnt      min  median    mean    max    IQR
##   <fct>    <int> <int>    <dbl>  <dbl>  <dbl>  <dbl>  <dbl>
## 1 Evolved      20     0 0.229    0.5    0.486    0.5    0
## 2 Calculated   20     0 0.0000388 0.000102 0.000114 0.000239 0.000121
## 3 None        20     0 0.0000297 0.000109 0.000124 0.000255 0.000122
```

12.1.2 Kruskal-Wallis test

Detected differences between weight strategies.

```
kruskal.test(hv ~ exp, data = data)
```

```
##
## Kruskal-Wallis rank sum test
##
## data: hv by exp
## Kruskal-Wallis chi-squared = 40.672, df = 2, p-value = 1.473e-09
```


12.1.3 Pairwise wilcoxon test

```
pairwise.wilcox.test(x = data$hv, g = data$exp, p.adjust.method = "bonferroni",
                    paired = FALSE, conf.int = FALSE, alternative = 'l')

##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: data$hv and data$exp
##
##           Evolved Calculated
## Calculated 1.7e-08 -
## None       1.7e-08 1
##
## P value adjustment method: bonferroni
```


Chapter 13

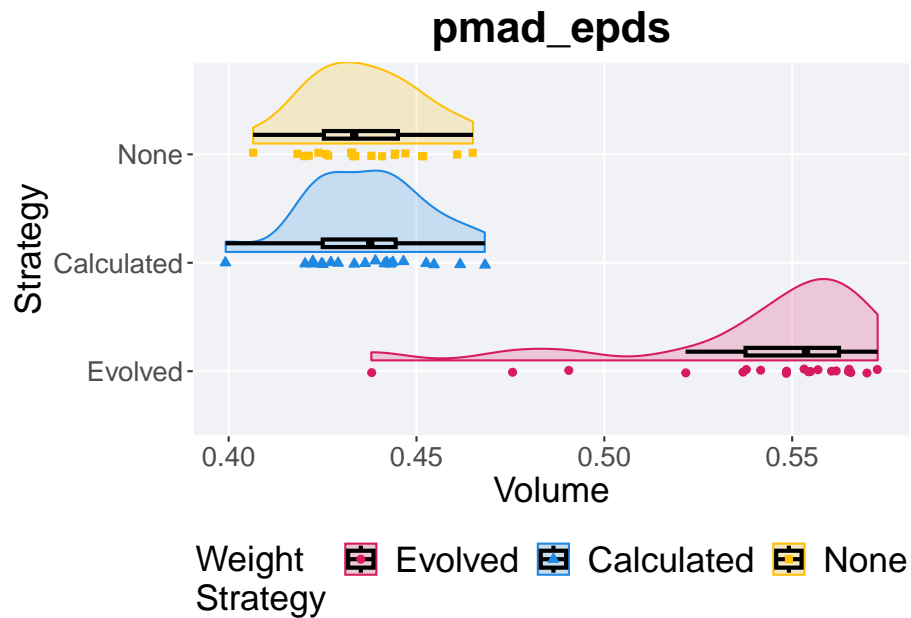
PMAD EPDS

Here we report the **hypervolume** achieved by evaluating the performance of each solution within the Pareto front on the test set of the `pmad_epds` dataset.

```
# heart-disease data  
data <- filter(testing, dataset == "pmad_epds")
```

13.1 Hypervolume

```
volume_plotter(data, 11)
```



13.1.1 Summary stats

```
volume_summarize(data)
```

```
## # A tibble: 3 x 8
##   exp      count na_cnt   min median  mean   max   IQR
##   <fct>    <int>  <int> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 Evolved      20      0 0.438  0.554 0.541 0.573 0.0249
## 2 Calculated   20      0 0.399  0.438 0.437 0.468 0.0194
## 3 None         20      0 0.407  0.433 0.436 0.465 0.0197
```

13.1.2 Kruskal-Wallis test

Detected differences between weight strategies.

```
kruskal.test(hv ~ exp, data = data)
```

```
##
## Kruskal-Wallis rank sum test
##
## data: hv by exp
## Kruskal-Wallis chi-squared = 35.731, df = 2, p-value = 1.742e-08
```

13.1.3 Pairwise wilcoxon test

```
pairwise.wilcox.test(x = data$hv, g = data$exp, p.adjust.method = "bonferroni",  
                    paired = FALSE, conf.int = FALSE, alternative = 'l')
```

```
##  
## Pairwise comparisons using Wilcoxon rank sum exact test  
##  
## data: data$hv and data$exp  
##  
##           Evolved Calculated  
## Calculated 3.0e-09 -  
## None       2.1e-09 1  
##  
## P value adjustment method: bonferroni
```


Chapter 14

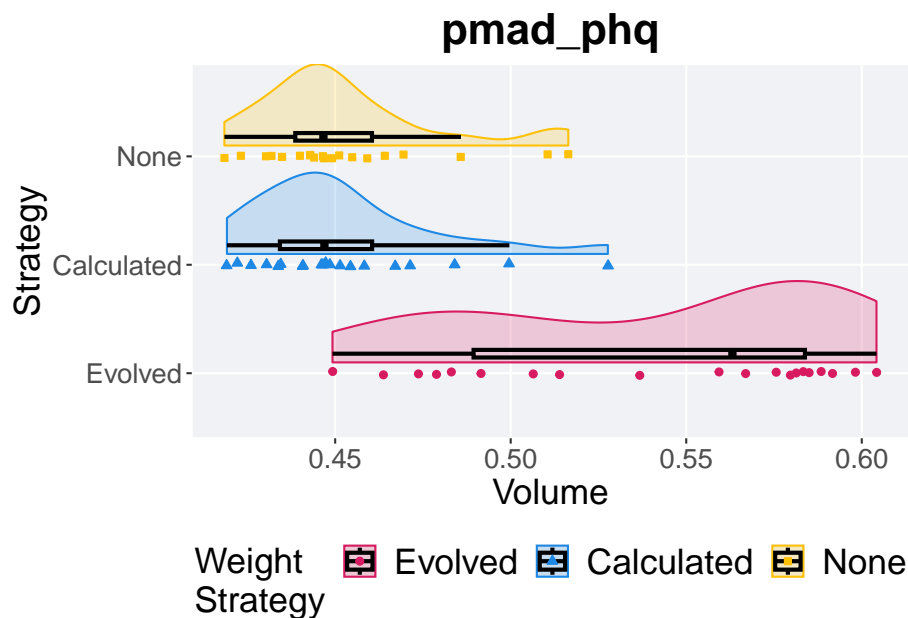
PMAD PHQ

Here we report the **hypervolume** achieved by evaluating the performance of each solution within the Pareto front on the test set of the `pmad_phq` dataset.

```
# heart-disease data  
data <- filter(testing, dataset == "pmad_phq")
```

14.1 Hypervolume

```
volume_plotter(data, 13)
```



14.1.1 Summary stats

```
volume_summarize(data)
```

```
## # A tibble: 3 x 8
##   exp      count na_cnt   min median  mean   max   IQR
##   <fct>    <int>  <int> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 Evolved      20      0 0.449  0.563 0.541 0.604 0.0944
## 2 Calculated   20      0 0.419  0.447 0.452 0.528 0.0263
## 3 None         20      0 0.418  0.447 0.453 0.516 0.0218
```

14.1.2 Kruskal-Wallis test

Detected differences between weight strategies.

```
kruskal.test(hv ~ exp, data = data)
```

```
##
## Kruskal-Wallis rank sum test
##
## data: hv by exp
## Kruskal-Wallis chi-squared = 29.615, df = 2, p-value = 3.708e-07
```


14.1.3 Pairwise wilcoxon test

```
pairwise.wilcox.test(x = data$hv, g = data$exp, p.adjust.method = "bonferroni",  
                    paired = FALSE, conf.int = FALSE, alternative = 'l')
```

```
##  
## Pairwise comparisons using Wilcoxon rank sum exact test  
##  
## data: data$hv and data$exp  
##  
##           Evolved Calculated  
## Calculated 2.5e-07 -  
## None       3.2e-07 1  
##  
## P value adjustment method: bonferroni
```