Supplemental Material: Valley Crossing Diagnostics

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Contents

Chapter 1

Introduction

This is the supplemental material for experiments with diagnostics and integrated valleys.

1.1 About our supplemental material

This supplemental material is hosted on GitHub using GitHub pages. The source code and configuration files used to generate this supplemental material can be found in this GitHub repository. We compiled our data analyses and supplemental documentation into this nifty web-accessible book using bookdown.

Our supplemental material includes the following paper figures and statistics:

- Exploitation rate results (Section 2)
- Ordered exploitation results (Section 3)
- Contradictory objectives results (Section 4)
- Multi-path exploration results (Section 5)

1.2 Contributing authors

- Jose Guadalupe Hernandez
- Alexander Lalejini
- Charles Ofria

1.3 Computer Setup

These analyses were conducted in the following computing environment:

```
print(version)
```

```
##                _
## platform       x86_64-pc-linux-gnu
## arch           x86_64
## os             linux-gnu
## system         x86_64, linux-gnu
## status
## major          4
## minor          3.1
## year           2023
## month          06
## day            16
## svn rev        84548
## language       R
## version.string R version 4.3.1 (2023-06-16)
## nickname       Beagle Scouts
```

1.4 Experimental setup

Setting up required variables variables.

```
# libraries we are using
library(ggplot2)
library(cowplot)
library(dplyr)
```

```
##
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':
##
##     filter, lag
```

```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
library(PupillometryR)
```

```
## Loading required package: rlang
```

```
# data diractory for gh-pages
DATA_DIR = '/opt/ECJ-2023-Suite-Of-Diagnostic-Metrics-For-Characterizing-Selection-Sche

# data diractory for local testing
# DATA_DIR = 'C:/Users/jgh9094/Desktop/Research/Projects/SelectionDiagnostics/ECJ-2023

# graph variables
SHAPE = c(5,3,1,2,6,0,4,20,1)
```

```
cb_palette <- c('#332288','#88CCEE','#EE7733','#EE3377','#117733','#882255','#44AA99','#CCBB44',
TSIZE = 26
p_theme <- theme(
  text = element_text(size = 28),
  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=22),
  legend.text=element_text(size=23),
  axis.title = element_text(size=23),
  axis.text = element_text(size=22),
  legend.position="bottom",
  panel.background = element_rect(fill = "#f1f2f5",
                                  colour = "white",
                                  size = 0.5, linetype = "solid")
)
```

```
## Warning: The `size` argument of `element_rect()` is deprecated as of ggplot2 3.4.0.
## i Please use the `linewidth` argument instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```

```
# default variables
REPLICATES = 50
DIMENSIONALITY = 100
GENERATIONS = 50000

# selection scheme related stuff
ACRO = c('tru','tor','lex','gfs','pfs','nds','nov','ran')
NAMES = c('Truncation (tru)','Tournament (tor)','Lexicase (lex)', 'Genotypic Fitness Sharing (gfs

# valley crossing comparisons
mvc_col = c('#1A85FF','#D41159')
```

Chapter 2

Exploitation rate results

Here we present the results for **best performances** found by each selection scheme on the exploitation rate diagnostic with valley crossing integrated. 50 replicates are conducted for each scheme explored.

2.1 Analysis dependencies

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

2.2 Data setup

```
DIR = paste(DATA_DIR,'EXPLOITATION_RATE/', sep = "", collapse = NULL)
over_time_df <- read.csv(paste(DIR,'over-time.csv', sep = "", collapse = NULL), header = TRUE, st
over_time_df$scheme <- factor(over_time_df$scheme, levels = NAMES)

best_df <- read.csv(paste(DIR,'best.csv', sep = "", collapse = NULL), header = TRUE, stringsAsFac
best_df$acro <- factor(best_df$acro, levels = ACRO)
```

2.3 Performance over time

Best performance in a population over time. Data points on the graph is the average performance across 50 replicates every 2000 generations. Shading comes from the best and worse performance across 50 replicates.

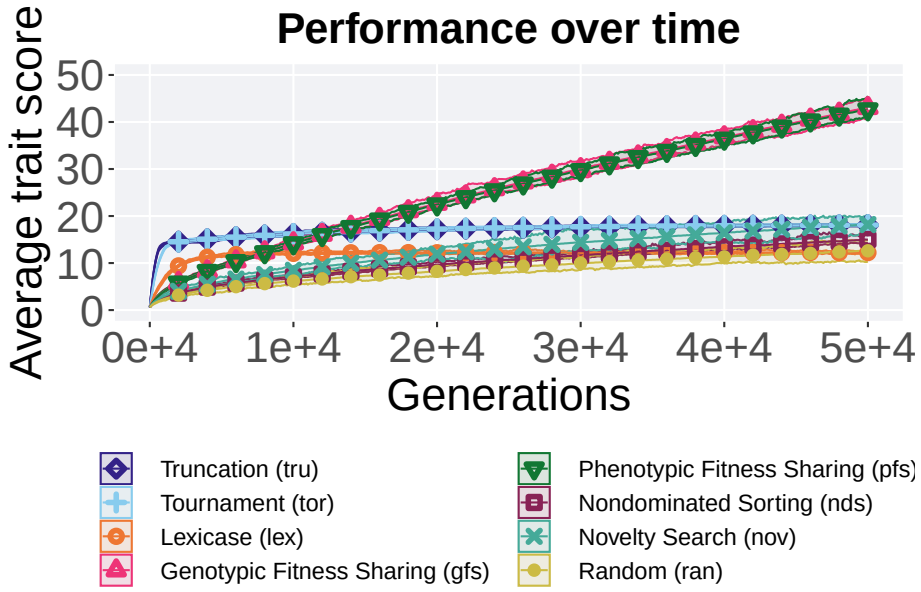
```
lines = over_time_df %>%
  group_by(scheme, gen) %>%
  dplyr::summarise(
    min = min(pop_fit_max) / DIMENSIONALITY,
    mean = mean(pop_fit_max) / DIMENSIONALITY,
    max = max(pop_fit_max) / DIMENSIONALITY
  )
```

```
## `summarise()` has grouped output by 'scheme'. You can override using the
## `.groups` argument.
```

```
over_time_plot = ggplot(lines, aes(x=gen, y=mean, group = scheme, fill = scheme, color
  geom_ribbon(aes(ymin = min, ymax = max), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = filter(lines, gen %% 2000 == 0 & gen != 0), size = 1.5, stroke = 2
  scale_y_continuous(
    name="Average trait score",
    limits=c(0, 50),
    breaks=seq(0,50, 10),
    labels=c("0", "10", "20", "30", "40", "50")
  ) +
  scale_x_continuous(
    name="Generations",
    limits=c(0, 50000),
    breaks=c(0, 10000, 20000, 30000, 40000, 50000),
    labels=c("0e+4", "1e+4", "2e+4", "3e+4", "4e+4", "5e+4")

  ) +
  scale_shape_manual(values=SHAPE)+
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  ggtitle('Performance over time')+
  p_theme + theme(legend.title=element_blank(),legend.text=element_text(size=12)) +
  guides(
    shape=guide_legend(ncol=2, title.position = "bottom"),
    color=guide_legend(ncol=2, title.position = "bottom"),
    fill=guide_legend(ncol=2, title.position = "bottom")
  )

over_time_plot
```



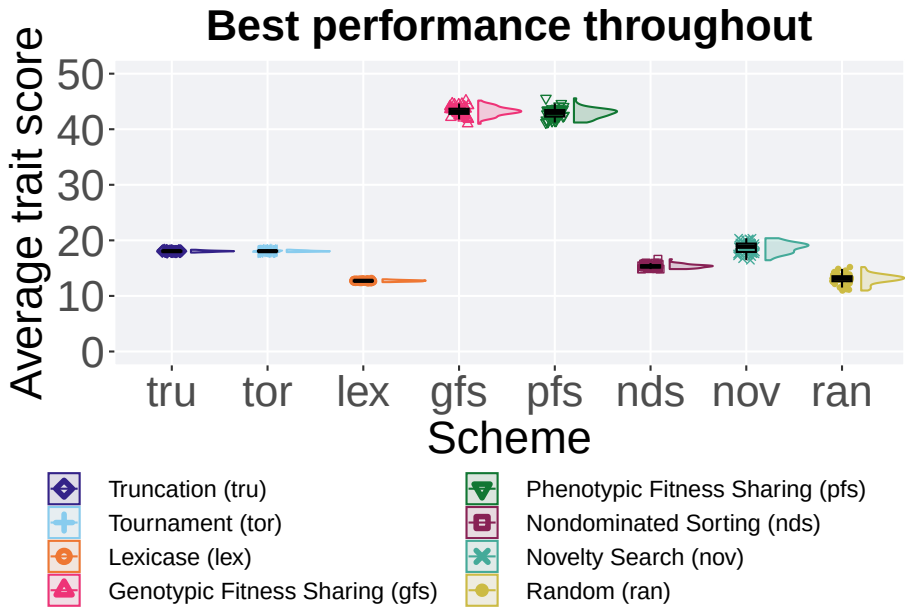
2.4 Best performance throughout

Best performance reached throughout 50,000 generations in a population.

```
plot = filter(best_df, var == 'pop_fit_max') %>%
  ggplot(., aes(x = acro, y = val / DIMENSIONALITY, color = acro, fill = acro, shape = acro)) +
  geom_flat_violin(position = position_nudge(x = .2, y = 0), scale = 'width', alpha = 0.2) +
  geom_point(position = position_jitter(width = .1), size = 1.5, alpha = 1.0) +
  geom_boxplot(color = 'black', width = .2, outlier.shape = NA, alpha = 0.0) +
  scale_y_continuous(
    name="Average trait score",
    limits=c(0, 50),
    breaks=seq(0,50, 10),
    labels=c("0", "10", "20", "30", "40", "50")
  ) +
  scale_x_discrete(
    name="Scheme"
  )+
  scale_shape_manual(values=SHAPE)+
  scale_colour_manual(values = cb_palette, ) +
  scale_fill_manual(values = cb_palette) +
  ggtitle('Best performance throughout')+
  p_theme + theme(legend.title=element_blank())
```

```
plot_grid(
  plot +
    theme(legend.position="none"),
  legend,
  nrow=2,
  rel_heights = c(3,1)
)
```

```
## Warning: Using the `size` aesthetic with geom_polygon was deprecated in ggplot2 3.4
## i Please use the `linewidth` aesthetic instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```



2.4.1 Stats

Summary statistics for the best performance.

```
performance = filter(best_df, var == 'pop_fit_max')
performance$acro = factor(performance$acro, levels = c('gfs','pfs','tru','tor','nov','r
performance %>%
  group_by(acro) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(val)),
```

```
    min = min(val / DIMENSIONALITY, na.rm = TRUE),
    median = median(val / DIMENSIONALITY, na.rm = TRUE),
    mean = mean(val / DIMENSIONALITY, na.rm = TRUE),
    max = max(val / DIMENSIONALITY, na.rm = TRUE),
    IQR = IQR(val / DIMENSIONALITY, na.rm = TRUE)
  )
```

```
## # A tibble: 8 x 8
##   acro  count na_cnt   min median  mean   max   IQR
##   <fct> <int>  <int> <dbl>  <dbl> <dbl> <dbl> <dbl>
## 1 gfs      50      0  41.0   43.2  43.2  45.2 0.923
## 2 pfs      50      0  41.2   43.0  42.9  45.6 1.17
## 3 tru      50      0  17.8   18.1  18.0  18.3 0.140
## 4 tor      50      0  17.9   18.1  18.1  18.3 0.150
## 5 nov      50      0  16.4   18.8  18.7  20.4 1.51
## 6 nds      50      0  14.8   15.3  15.4  16.6 0.418
## 7 ran      50      0  11.0   13.2  13.1  15.2 0.900
## 8 lex      50      0  12.5   12.7  12.7  13.0 0.154
```

Kruskal–Wallis test illustrates evidence of statistical differences.

```
kruskal.test(val ~ acro, data = performance)
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  val by acro
## Kruskal-Wallis chi-squared = 367.97, df = 7, p-value < 2.2e-16
```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction.

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

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  performance$val and performance$acro
##
##     gfs     pfs     tru     tor     nov     nds     ran
## pfs 0.4845  -       -       -       -       -       -
## tru < 2e-16 < 2e-16 -       -       -       -       -
## tor < 2e-16 < 2e-16 1.0000  -       -       -       -
## nov < 2e-16 < 2e-16 1.0000  1.0000  -       -       -
## nds < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 -       -
## ran < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 2.9e-16 -
## lex < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 0.0035
##
```

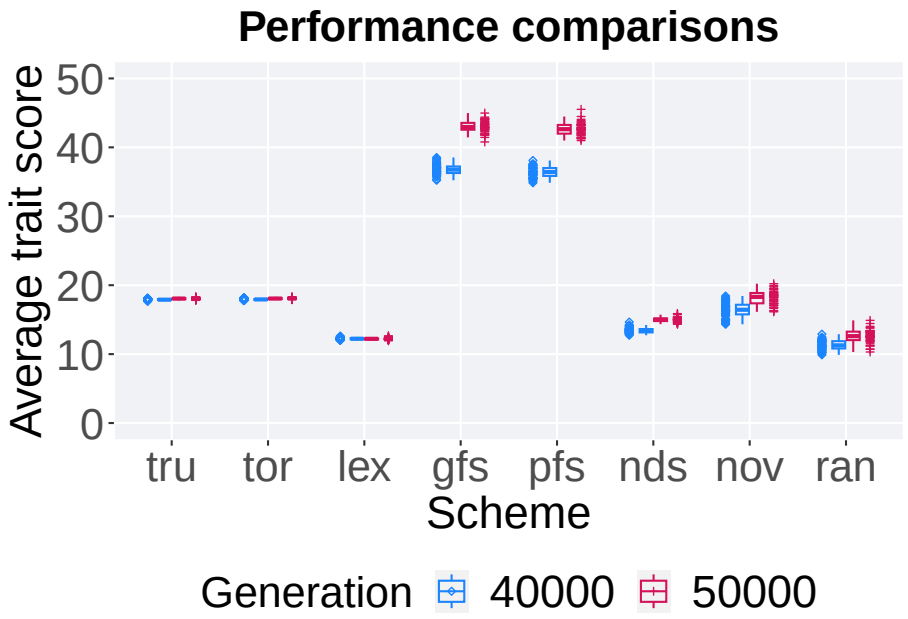
```
## P value adjustment method: bonferroni
```

2.5 Performance interval comparison

Here we compare the best performance found in the population at generation 40,000 & 50,000 for all selection schemes.

```
interval_df = filter(filter(over_time_df, (gen == 50000 | gen == 40000)))
interval_df$Generation <- factor(interval_df$gen, levels = c(40000,50000))
interval_df$acro <- factor(interval_df$acro, levels = ACRO)

ggplot(interval_df, aes(x=acro, y=pop_fit_max/DIMENSIONALITY,fill=Generation,color=Gene
  geom_boxplot(width = .3, outlier.shape = NA, alpha = 0.0) +
    geom_point(size = 1.0, alpha = 1.0, position=position_dodge(width=1.0)) +
    scale_y_continuous(
      name="Average trait score",
      limits=c(0, 50),
      breaks=seq(0,50, 10),
      labels=c("0","10", "20", "30", "40", "50")
    ) +
    scale_x_discrete(
      name="Scheme"
    ) +
  scale_shape_manual(values=SHAPE)+
  scale_colour_manual(values = mvc_col, ) +
  scale_fill_manual(values = mvc_col) +
  ggtitle('Performance comparisons')+
  p_theme
```



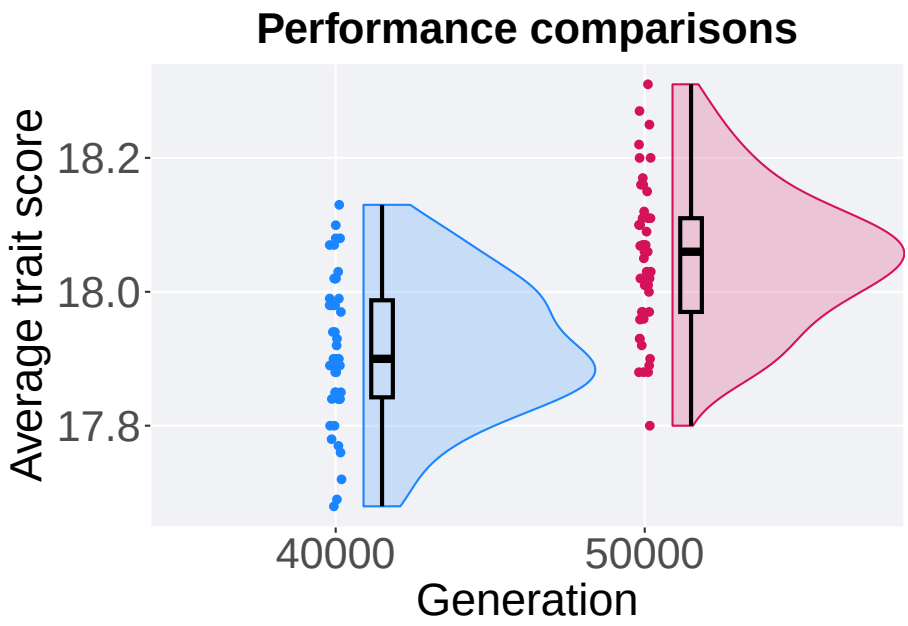
2.5.1 Stats by interval comparisons

Here we present statistical analysis between the performances found at different generation intervals.

2.5.1.1 Truncation

Plot for comparing performances at interval 40,000 & 50,000.

```
filter(interval_df, acro == 'tru') %>%
ggplot(., aes(x=Generation, y=pop_fit_max/DIMENSIONALITY,fill=Generation,color=Generation,shape=G
  geom_flat_violin(position = position_nudge(x = .09, y = 0), scale = 'width', alpha = 0.2, width
  geom_boxplot(color = 'black', width = .07, outlier.shape = NA, alpha = 0.0, size = 1.0, positio
  geom_point(position = position_jitter(width = .02), size = 2.0, alpha = 1.0) +
    scale_y_continuous(
      name="Average trait score",
    ) +
    scale_x_discrete(
      name="Generation"
    ) +
  scale_shape_manual(values=c(16,16))+
  scale_colour_manual(values = mvc_col, ) +
  scale_fill_manual(values = mvc_col) +
  ggtitle('Performance comparisons')+
  p_theme + theme(legend.position="none")
```



Summary statistics for the best performance.

```
filter(interval_df, acro == 'tru') %>%
  group_by(Generation) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(pop_fit_max)),
    min = min(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    median = median(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    mean = mean(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    max = max(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    IQR = IQR(pop_fit_max / DIMENSIONALITY, na.rm = TRUE)
  )
```

```
## # A tibble: 2 x 8
##   Generation count na_cnt   min median  mean   max   IQR
##   <fct>      <int>  <int> <dbl>  <dbl> <dbl> <dbl> <dbl>
## 1 40000         50      0  17.7   17.9  17.9  18.1 0.145
## 2 50000         50      0  17.8   18.1  18.0  18.3 0.140
```

Results for post-hoc Wilcoxon rank-sum test.

```
wilcox.test(x = filter(interval_df, acro == 'tru' & Generation == 50000)$pop_fit_max,
            y = filter(interval_df, acro == 'tru' & Generation == 40000)$pop_fit_max,
            alternative = 'g')
```

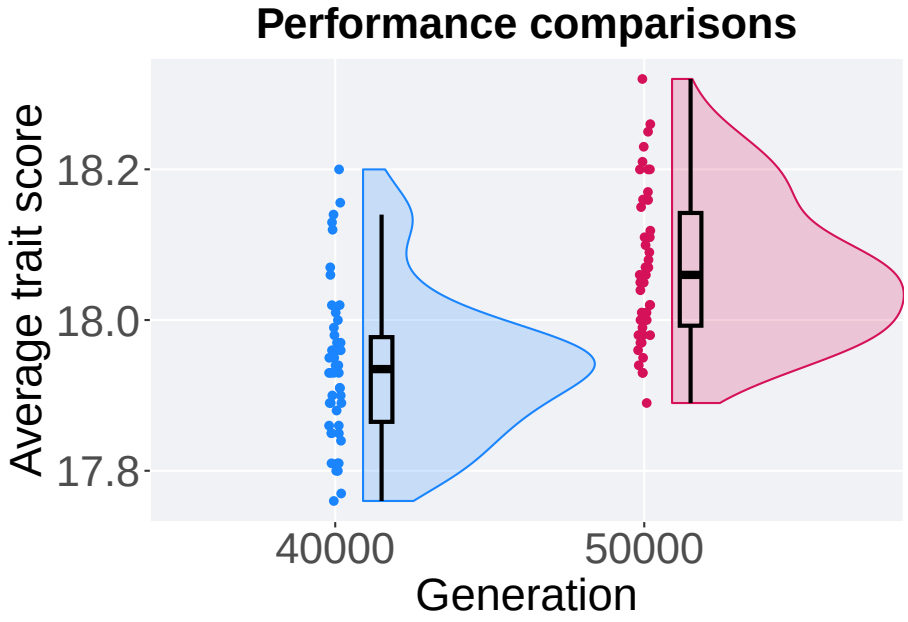
```
##
```

```
##  Wilcoxon rank sum test with continuity correction
##
## data:  filter(interval_df, acro == "tru" & Generation == 50000)$pop_fit_max and filter(interva
## W = 2013.5, p-value = 7.103e-08
## alternative hypothesis: true location shift is greater than 0
```

2.5.1.2 Tournament

Plot for comparing performances at interval 40,000 & 50,000.

```
filter(interval_df, acro == 'tor') %>%
ggplot(., aes(x=Generation, y=pop_fit_max/DIMENSIONALITY,fill=Generation,color=Generation,shape=C
  geom_flat_violin(position = position_nudge(x = .09, y = 0), scale = 'width', alpha = 0.2, width
  geom_boxplot(color = 'black', width = .07, outlier.shape = NA, alpha = 0.0, size = 1.0, positio
  geom_point(position = position_jitter(width = .02), size = 2.0, alpha = 1.0) +
    scale_y_continuous(
      name="Average trait score",
    ) +
    scale_x_discrete(
      name="Generation"
    ) +
  scale_shape_manual(values=c(16,16))+
  scale_colour_manual(values = mvc_col, ) +
  scale_fill_manual(values = mvc_col) +
  ggtitle('Performance comparisons')+
  p_theme + theme(legend.position="none")
```



Summary statistics for the best performance.

```
filter(interval_df, acro == 'tor') %>%
  group_by(Generation) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(pop_fit_max)),
    min = min(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    median = median(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    mean = mean(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    max = max(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    IQR = IQR(pop_fit_max / DIMENSIONALITY, na.rm = TRUE)
  )
```

```
## # A tibble: 2 x 8
##   Generation count na_cnt   min median  mean   max   IQR
##   <fct>      <int>  <int> <dbl>  <dbl> <dbl> <dbl> <dbl>
## 1 40000         50      0  17.8   17.9  17.9  18.2 0.112
## 2 50000         50      0  17.9   18.1  18.1  18.3 0.150
```

Results for post-hoc Wilcoxon rank-sum test.

```
wilcox.test(x = filter(interval_df, acro == 'tor' & Generation == 50000)$pop_fit_max,
            y = filter(interval_df, acro == 'tor' & Generation == 40000)$pop_fit_max,
            alternative = 'g')
```

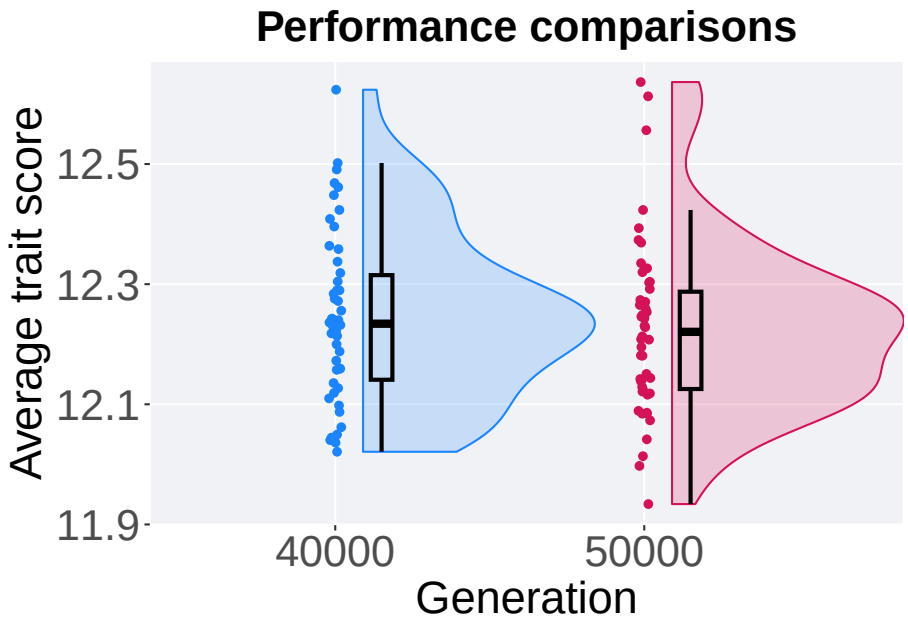
```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  filter(interval_df, acro == "tor" & Generation == 50000)$pop_fit_max and filt
## W = 2095.5, p-value = 2.818e-09
## alternative hypothesis: true location shift is greater than 0
```

2.5.1.3 Lexicase

Plot for comparing performances at interval 40,000 & 50,000.

```
filter(interval_df, acro == 'lex') %>%
ggplot(., aes(x=Generation, y=pop_fit_max/DIMENSIONALITY,fill=Generation,color=Generati
  geom_flat_violin(position = position_nudge(x = .09, y = 0), scale = 'width', alpha =
  geom_boxplot(color = 'black', width = .07, outlier.shape = NA, alpha = 0.0, size = 1
  geom_point(position = position_jitter(width = .02), size = 2.0, alpha = 1.0) +
    scale_y_continuous(
      name="Average trait score",
    ) +
    scale_x_discrete(
      name="Generation"
    ) +
```

```
  scale_shape_manual(values=c(16,16))+
  scale_colour_manual(values = mvc_col, ) +
  scale_fill_manual(values = mvc_col) +
  ggtitle('Performance comparisons')+
  p_theme + theme(legend.position="none")
```



Summary statistics for the best performance.

```
filter(interval_df, acro == 'lex') %>%
  group_by(Generation) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(pop_fit_max)),
    min = min(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    median = median(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    mean = mean(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    max = max(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    IQR = IQR(pop_fit_max / DIMENSIONALITY, na.rm = TRUE)
  )
```

```
## # A tibble: 2 x 8
##   Generation count na_cnt   min median  mean   max   IQR
##   <fct>      <int>  <int> <dbl>  <dbl> <dbl> <dbl> <dbl>
## 1 40000         50      0  12.0   12.2  12.2  12.6 0.174
## 2 50000         50      0  11.9   12.2  12.2  12.6 0.162
```

Results for post-hoc Wilcoxon rank-sum test.

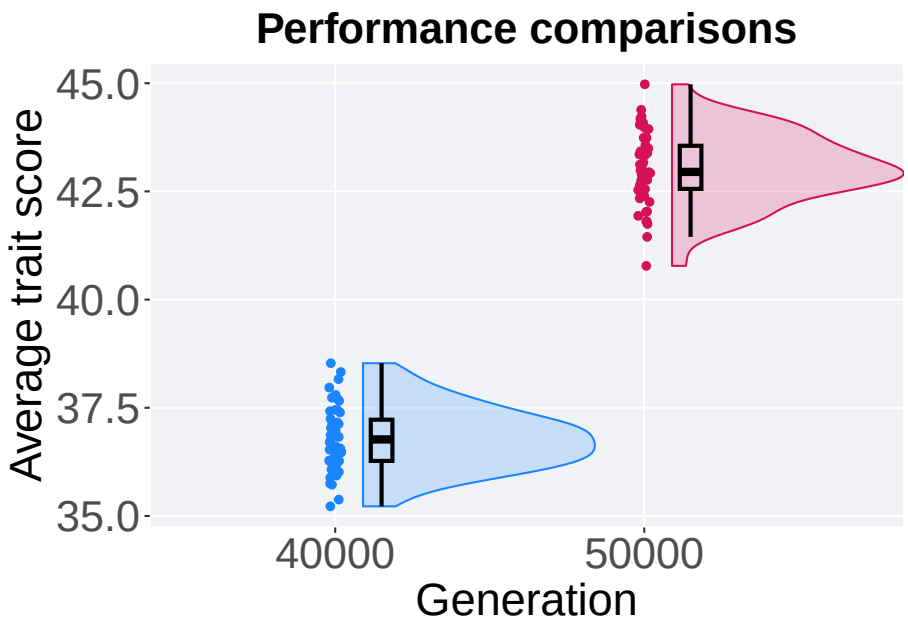
```
wilcox.test(x = filter(interval_df, acro == 'lex' & Generation == 50000)$pop_fit_max,
            y = filter(interval_df, acro == 'lex' & Generation == 40000)$pop_fit_max,
            alternative = 't')
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  filter(interval_df, acro == "lex" & Generation == 50000)$pop_fit_max and filt
## W = 1155, p-value = 0.5147
## alternative hypothesis: true location shift is not equal to 0
```

2.5.1.4 Genotypic fitness sharing

Plot for comparing performances at interval 40,000 & 50,000.

```
filter(interval_df, acro == 'gfs') %>%
ggplot(., aes(x=Generation, y=pop_fit_max/DIMENSIONALITY,fill=Generation,color=Generati
  geom_flat_violin(position = position_nudge(x = .09, y = 0), scale = 'width', alpha =
  geom_boxplot(color = 'black', width = .07, outlier.shape = NA, alpha = 0.0, size = 1
  geom_point(position = position_jitter(width = .02), size = 2.0, alpha = 1.0) +
    scale_y_continuous(
      name="Average trait score",
    ) +
    scale_x_discrete(
      name="Generation"
    ) +
  scale_shape_manual(values=c(16,16))+
  scale_colour_manual(values = mvc_col, ) +
  scale_fill_manual(values = mvc_col) +
  ggtitle('Performance comparisons')+
  p_theme + theme(legend.position="none")
```



Summary statistics for the best performance.

```
filter(interval_df, acro == 'gfs') %>%
  group_by(Generation) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(pop_fit_max)),
    min = min(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    median = median(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    mean = mean(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    max = max(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    IQR = IQR(pop_fit_max / DIMENSIONALITY, na.rm = TRUE)
  )
```

```
## # A tibble: 2 x 8
##   Generation count na_cnt   min median  mean   max   IQR
##   <fct>      <int>  <int> <dbl>  <dbl> <dbl> <dbl> <dbl>
## 1 40000         50      0  35.2   36.8  36.8  38.5 0.952
## 2 50000         50      0  40.8   43.0  43.0  45.0 0.996
```

Results for post-hoc Wilcoxon rank-sum test.

```
wilcox.test(x = filter(interval_df, acro == 'gfs' & Generation == 50000)$pop_fit_max,
            y = filter(interval_df, acro == 'gfs' & Generation == 40000)$pop_fit_max,
            alternative = 'g')
```

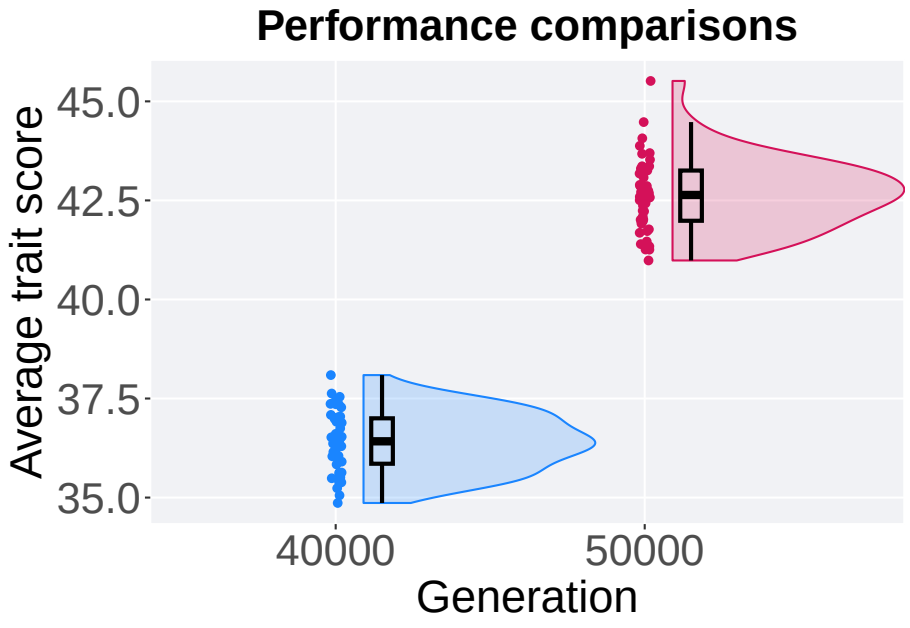
```
##
```

```
##  Wilcoxon rank sum test with continuity correction
##
## data:  filter(interval_df, acro == "gfs" & Generation == 50000)$pop_fit_max and filt
## W = 2500, p-value < 2.2e-16
## alternative hypothesis: true location shift is greater than 0
```

2.5.1.5 Phenotypic fitness sharing

Plot for comparing performances at interval 40,000 & 50,000.

```
filter(interval_df, acro == 'pfs') %>%
ggplot(., aes(x=Generation, y=pop_fit_max/DIMENSIONALITY,fill=Generation,color=Generati
  geom_flat_violin(position = position_nudge(x = .09, y = 0), scale = 'width', alpha =
  geom_boxplot(color = 'black', width = .07, outlier.shape = NA, alpha = 0.0, size = 1
  geom_point(position = position_jitter(width = .02), size = 2.0, alpha = 1.0) +
    scale_y_continuous(
      name="Average trait score",
    ) +
    scale_x_discrete(
      name="Generation"
    ) +
  scale_shape_manual(values=c(16,16))+
  scale_colour_manual(values = mvc_col, ) +
  scale_fill_manual(values = mvc_col) +
  ggtitle('Performance comparisons')+
  p_theme + theme(legend.position="none")
```



Summary statistics for the best performance.

```
filter(interval_df, acro == 'pfs') %>%
  group_by(Generation) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(pop_fit_max)),
    min = min(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    median = median(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    mean = mean(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    max = max(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    IQR = IQR(pop_fit_max / DIMENSIONALITY, na.rm = TRUE)
  )
```

```
## # A tibble: 2 x 8
##   Generation count na_cnt   min median  mean   max   IQR
##   <fct>      <int>  <int> <dbl>  <dbl> <dbl> <dbl> <dbl>
## 1 40000         50      0  34.9   36.4  36.4  38.1  1.15
## 2 50000         50      0  41.0   42.6  42.6  45.5  1.27
```

Results for post-hoc Wilcoxon rank-sum test.

```
wilcox.test(x = filter(interval_df, acro == 'pfs' & Generation == 50000)$pop_fit_max,
            y = filter(interval_df, acro == 'pfs' & Generation == 40000)$pop_fit_max,
            alternative = 'g')
```

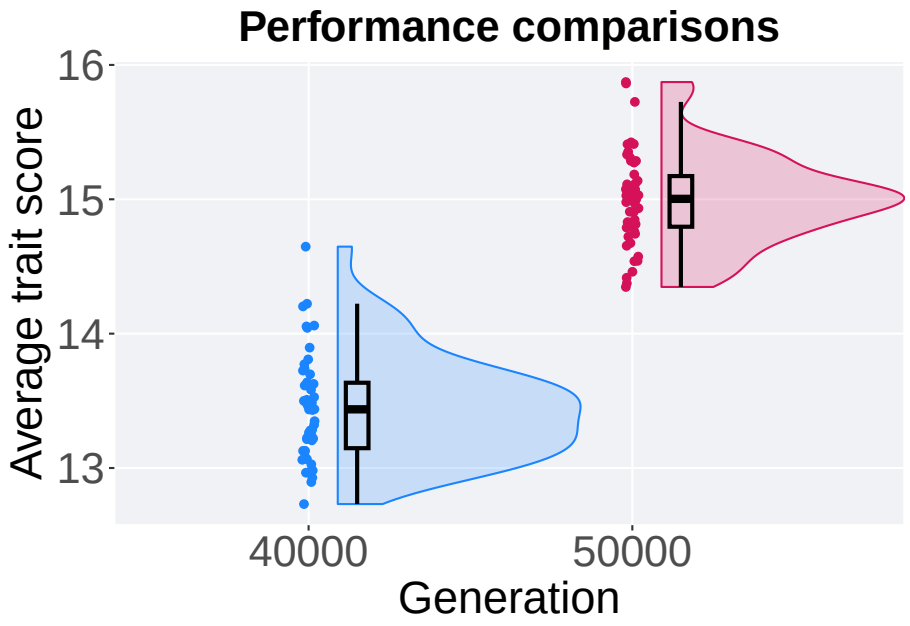
```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  filter(interval_df, acro == "pfs" & Generation == 50000)$pop_fit_max and filter(interva
## W = 2500, p-value < 2.2e-16
## alternative hypothesis: true location shift is greater than 0
```

2.5.1.6 Nondominated sorting

Plot for comparing performances at interval 40,000 & 50,000.

```
filter(interval_df, acro == 'nds') %>%
ggplot(., aes(x=Generation, y=pop_fit_max/DIMENSIONALITY,fill=Generation,color=Generation,shape=G
  geom_flat_violin(position = position_nudge(x = .09, y = 0), scale = 'width', alpha = 0.2, width
  geom_boxplot(color = 'black', width = .07, outlier.shape = NA, alpha = 0.0, size = 1.0, positio
  geom_point(position = position_jitter(width = .02), size = 2.0, alpha = 1.0) +
    scale_y_continuous(
      name="Average trait score",
    ) +
    scale_x_discrete(
      name="Generation"
    ) +
```

```
  scale_shape_manual(values=c(16,16))+
  scale_colour_manual(values = mvc_col, ) +
  scale_fill_manual(values = mvc_col) +
  ggtitle('Performance comparisons')+
  p_theme + theme(legend.position="none")
```



Summary statistics for the best performance.

```
filter(interval_df, acro == 'nds') %>%
  group_by(Generation) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(pop_fit_max)),
    min = min(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    median = median(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    mean = mean(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    max = max(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    IQR = IQR(pop_fit_max / DIMENSIONALITY, na.rm = TRUE)
  )
```

```
## # A tibble: 2 x 8
##   Generation count na_cnt   min median  mean   max   IQR
##   <fct>      <int>  <int> <dbl>  <dbl> <dbl> <dbl> <dbl>
## 1 40000         50      0  12.7   13.4  13.5  14.6 0.487
## 2 50000         50      0  14.3   15.0  15.0  15.9 0.377
```

Results for post-hoc Wilcoxon rank-sum test.

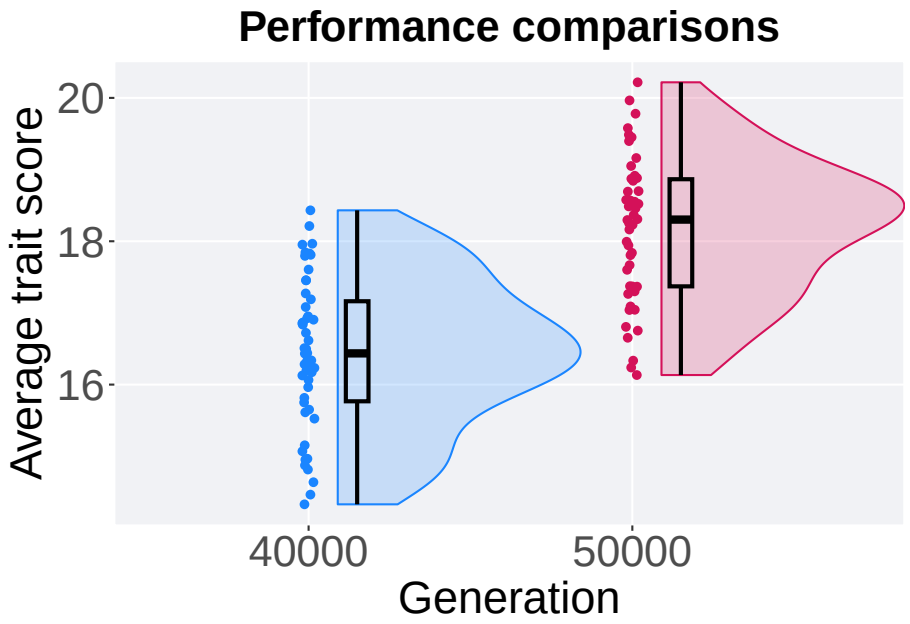
```
wilcox.test(x = filter(interval_df, acro == 'nds' & Generation == 50000)$pop_fit_max,
            y = filter(interval_df, acro == 'nds' & Generation == 40000)$pop_fit_max,
            alternative = 'g')
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  filter(interval_df, acro == "nds" & Generation == 50000)$pop_fit_max and filter(interva
## W = 2493, p-value < 2.2e-16
## alternative hypothesis: true location shift is greater than 0
```

2.5.1.7 Novelty search

Plot for comparing performances at interval 40,000 & 50,000.

```
filter(interval_df, acro == 'nov') %>%
ggplot(., aes(x=Generation, y=pop_fit_max/DIMENSIONALITY,fill=Generation,color=Generation,shape=G
  geom_flat_violin(position = position_nudge(x = .09, y = 0), scale = 'width', alpha = 0.2, width
  geom_boxplot(color = 'black', width = .07, outlier.shape = NA, alpha = 0.0, size = 1.0, positio
  geom_point(position = position_jitter(width = .02), size = 2.0, alpha = 1.0) +
    scale_y_continuous(
      name="Average trait score",
    ) +
    scale_x_discrete(
      name="Generation"
    ) +
  scale_shape_manual(values=c(16,16))+
  scale_colour_manual(values = mvc_col, ) +
  scale_fill_manual(values = mvc_col) +
  ggtitle('Performance comparisons')+
  p_theme + theme(legend.position="none")
```



Summary statistics for the best performance.

```
filter(interval_df, acro == 'nov') %>%
  group_by(Generation) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(pop_fit_max)),
    min = min(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    median = median(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    mean = mean(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    max = max(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    IQR = IQR(pop_fit_max / DIMENSIONALITY, na.rm = TRUE)
  )
```

```
## # A tibble: 2 x 8
##   Generation count na_cnt   min median  mean   max   IQR
##   <fct>      <int>  <int> <dbl>  <dbl> <dbl> <dbl> <dbl>
## 1 40000         50      0  14.3   16.4  16.4  18.4  1.40
## 2 50000         50      0  16.1   18.3  18.2  20.2  1.49
```

Results for post-hoc Wilcoxon rank-sum test.

```
wilcox.test(x = filter(interval_df, acro == 'nov' & Generation == 50000)$pop_fit_max,
            y = filter(interval_df, acro == 'nov' & Generation == 40000)$pop_fit_max,
            alternative = 'g')
```

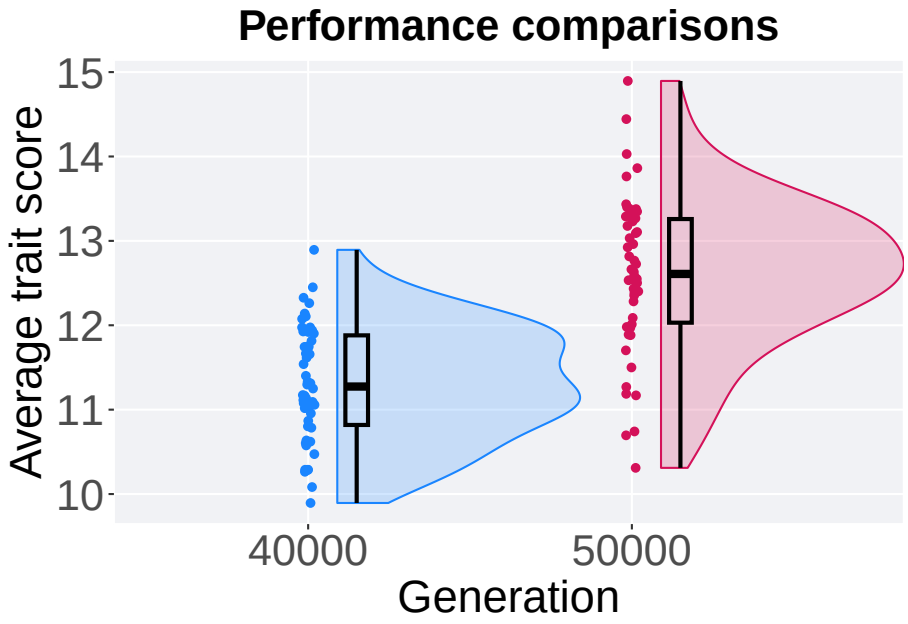
```
##
```

```
##  Wilcoxon rank sum test with continuity correction
##
## data:  filter(interval_df, acro == "nov" & Generation == 50000)$pop_fit_max and filter(interva
## W = 2209, p-value = 1.951e-11
## alternative hypothesis: true location shift is greater than 0
```

2.5.1.8 Random

Plot for comparing performances at interval 40,000 & 50,000.

```
filter(interval_df, acro == 'ran') %>%
ggplot(., aes(x=Generation, y=pop_fit_max/DIMENSIONALITY,fill=Generation,color=Generation,shape=C
  geom_flat_violin(position = position_nudge(x = .09, y = 0), scale = 'width', alpha = 0.2, width
  geom_boxplot(color = 'black', width = .07, outlier.shape = NA, alpha = 0.0, size = 1.0, positio
  geom_point(position = position_jitter(width = .02), size = 2.0, alpha = 1.0) +
    scale_y_continuous(
      name="Average trait score",
    ) +
    scale_x_discrete(
      name="Generation"
    ) +
  scale_shape_manual(values=c(16,16))+
  scale_colour_manual(values = mvc_col, ) +
  scale_fill_manual(values = mvc_col) +
  ggtitle('Performance comparisons')+
  p_theme + theme(legend.position="none")
```



Summary statistics for the best performance.

```
filter(interval_df, acro == 'ran') %>%
  group_by(Generation) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(pop_fit_max)),
    min = min(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    median = median(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    mean = mean(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    max = max(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    IQR = IQR(pop_fit_max / DIMENSIONALITY, na.rm = TRUE)
  )
```

```
## # A tibble: 2 x 8
##   Generation count na_cnt   min median  mean   max   IQR
##   <fct>      <int>  <int> <dbl>  <dbl> <dbl> <dbl> <dbl>
## 1 40000         50      0  9.89   11.3  11.3  12.9  1.06
## 2 50000         50      0 10.3    12.6  12.6  14.9  1.23
```

Results for post-hoc Wilcoxon rank-sum test.

```
wilcox.test(x = filter(interval_df, acro == 'ran' & Generation == 50000)$pop_fit_max,
            y = filter(interval_df, acro == 'ran' & Generation == 40000)$pop_fit_max,
            alternative = 'g')
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  filter(interval_df, acro == "ran" & Generation == 50000)$pop_fit_max and filt
## W = 2185, p-value = 5.885e-11
## alternative hypothesis: true location shift is greater than 0
```

Chapter 3

Ordered exploitation results

Here we present the results for **best performances** found by each selection scheme on the ordered exploitation diagnostic with valley crossing integrated. 50 replicates are conducted for each scheme explored.

3.1 Analysis dependencies

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

3.2 Data setup

```
DIR = paste(DATA_DIR,'ORDERED_EXPLOITATION/', sep = "", collapse = NULL)
over_time_df <- read.csv(paste(DIR,'over-time.csv', sep = "", collapse = NULL), header = TRUE, st
over_time_df$scheme <- factor(over_time_df$scheme, levels = NAMES)

best_df <- read.csv(paste(DIR,'best.csv', sep = "", collapse = NULL), header = TRUE, stringsAsFac
best_df$acro <- factor(best_df$acro, levels = ACRO)
```

3.3 Performance over time

Best performance in a population over time. Data points on the graph is the average performance across 50 replicates every 2000 generations. Shading comes from the best and worse performance across 50 replicates.

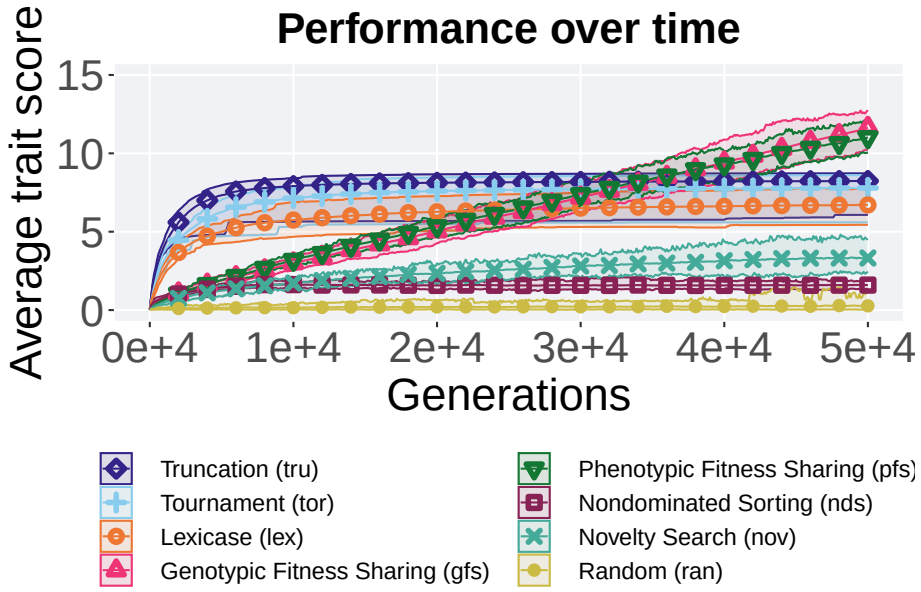
```
lines = over_time_df %>%
  group_by(scheme, gen) %>%
  dplyr::summarise(
    min = min(pop_fit_max) / DIMENSIONALITY,
    mean = mean(pop_fit_max) / DIMENSIONALITY,
    max = max(pop_fit_max) / DIMENSIONALITY
  )
```

```
## `summarise()` has grouped output by 'scheme'. You can override using the
## `.groups` argument.
```

```
over_time_plot = ggplot(lines, aes(x=gen, y=mean, group = scheme, fill = scheme, color
  geom_ribbon(aes(ymin = min, ymax = max), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = filter(lines, gen %% 2000 == 0 & gen != 0), size = 1.5, stroke = 2
  scale_y_continuous(
    name="Average trait score",
    limits=c(0, 15),
  ) +
  scale_x_continuous(
    name="Generations",
    limits=c(0, 50000),
    breaks=c(0, 10000, 20000, 30000, 40000, 50000),
    labels=c("0e+4", "1e+4", "2e+4", "3e+4", "4e+4", "5e+4")

  ) +
  scale_shape_manual(values=SHAPE)+
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  ggtitle('Performance over time')+
  p_theme + theme(legend.title=element_blank(),legend.text=element_text(size=12)) +
  guides(
    shape=guide_legend(ncol=2, title.position = "bottom"),
    color=guide_legend(ncol=2, title.position = "bottom"),
    fill=guide_legend(ncol=2, title.position = "bottom")
  )

over_time_plot
```



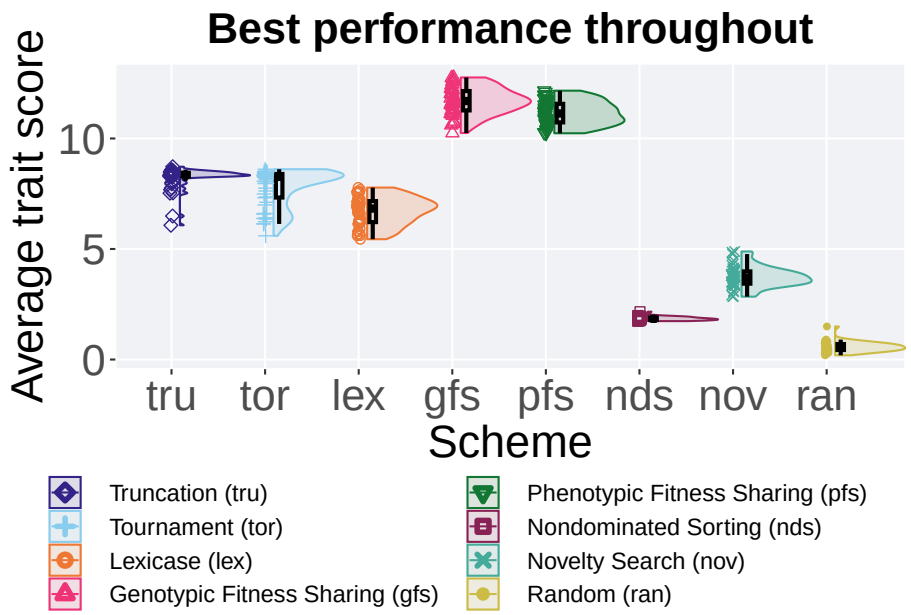
3.4 Best performance throughout

Best performance reached throughout 50,000 generations in a population.

```
plot = filter(best_df, var == 'pop_fit_max') %>%
  ggplot(., aes(x = acro, y = val / DIMENSIONALITY, color = acro, fill = acro, shape = acro)) +
  geom_flat_violin(position = position_nudge(x = .09, y = 0), scale = 'width', alpha = 0.2, width
  geom_boxplot(color = 'black', width = .07, outlier.shape = NA, alpha = 0.0, size = 1.0, positio
  geom_point(position = position_jitter(width = .02), size = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Average trait score"
  ) +
  scale_x_discrete(
    name="Scheme"
  )+
  scale_shape_manual(values=SHAPE)+
  scale_colour_manual(values = cb_palette, ) +
  scale_fill_manual(values = cb_palette) +
  ggtitle('Best performance throughout')+
  p_theme + theme(legend.title=element_blank())

plot_grid(
  plot +
    theme(legend.position="none"),
```

```
  legend,
  nrow=2,
  rel_heights = c(3,1)
)
```



3.4.1 Stats

Summary statistics for the best performance.

```
performance = filter(best_df, var == 'pop_fit_max')
performance$acro = factor(performance$acro, levels = c('gfs','pfs','tru','tor','lex','r
performance %>%
  group_by(acro) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(val)),
    min = min(val / DIMENSIONALITY, na.rm = TRUE),
    median = median(val / DIMENSIONALITY, na.rm = TRUE),
    mean = mean(val / DIMENSIONALITY, na.rm = TRUE),
    max = max(val / DIMENSIONALITY, na.rm = TRUE),
    IQR = IQR(val / DIMENSIONALITY, na.rm = TRUE)
  )
```

```
## # A tibble: 8 x 8
##   acro  count na_cnt    min median   mean    max   IQR
```

```
##   <fct> <int>  <int>  <dbl>  <dbl>  <dbl> <dbl> <dbl>
## 1 gfs      50      0 10.2   11.7   11.7   12.8  0.876
## 2 pfs      50      0 10.2   11.1   11.2   12.2  0.840
## 3 tru      50      0  6.07   8.35   8.23   8.72 0.166
## 4 tor      50      0  5.60   8.26   7.79   8.61 1.07
## 5 lex      50      0  5.44   6.83   6.72   7.78 0.949
## 6 nov      50      0  2.84   3.70   3.74   4.89 0.555
## 7 nds      50      0  1.74   1.84   1.85   2.16 0.114
## 8 ran      50      0  0.192  0.552  0.570  1.50 0.269
```

Kruskal–Wallis test illustrates evidence of statistical differences.

```
kruskal.test(val ~ acro, data = performance)
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  val by acro
## Kruskal-Wallis chi-squared = 380.24, df = 7, p-value < 2.2e-16
```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction.

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

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  performance$val and performance$acro
##
##     gfs     pfs     tru     tor     lex     nov     nds
## pfs 0.00041 -       -       -       -       -       -
## tru < 2e-16 < 2e-16 -       -       -       -       -
## tor < 2e-16 < 2e-16 0.09539 -       -       -       -
## lex < 2e-16 < 2e-16 2.1e-14 2.0e-07 -       -       -
## nov < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 -       -
## nds < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 -
## ran < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16
##
## P value adjustment method: bonferroni
```

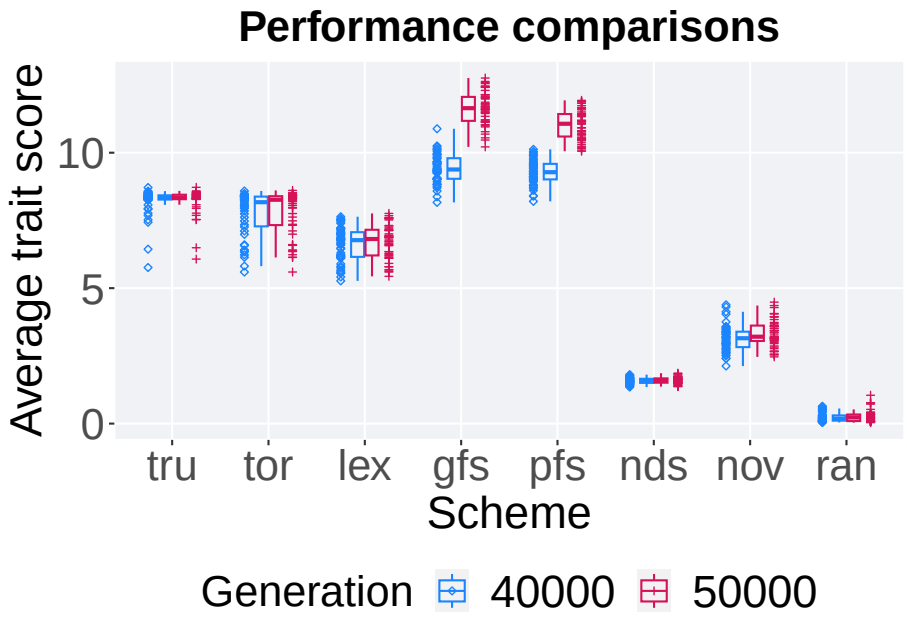
3.5 Performance interval comparison

Here we compare the best performance found in the population at generation 40,000 & 50,000 for all selection schemes.

```
interval_df = filter(filter(over_time_df, (gen == 50000 | gen == 40000)))
interval_df$Generation <- factor(interval_df$gen, levels = c(40000,50000))
```

```
interval_df$acro <- factor(interval_df$acro, levels = ACRO)

ggplot(interval_df, aes(x=acro, y=pop_fit_max/DIMENSIONALITY,fill=Generation,color=Gene
  geom_boxplot(width = .3, outlier.shape = NA, alpha = 0.0) +
  geom_point(size = 1.0, alpha = 1.0, position=position_dodge(width=1.0)) +
    scale_y_continuous(
      name="Average trait score"
    ) +
    scale_x_discrete(
      name="Scheme"
    ) +
  scale_shape_manual(values=SHAPE)+
  scale_colour_manual(values = mvc_col, ) +
  scale_fill_manual(values = mvc_col) +
  ggtitle('Performance comparisons')+
  p_theme
```



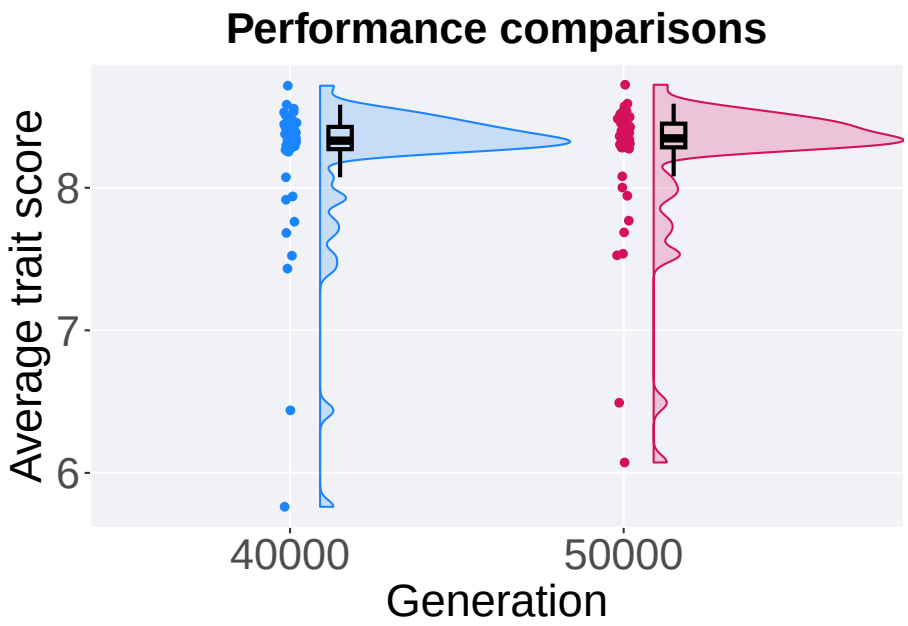
3.5.1 Stats by interval comparisons

Here we present statistical analysis between the performances found at different generation intervals.

3.5.1.1 Truncation

Plot for comparing performances at interval 40,000 & 50,000.

```
filter(interval_df, acro == 'tru') %>%
ggplot(., aes(x=Generation, y=pop_fit_max/DIMENSIONALITY,fill=Generation,color=Generation,shape=C
  geom_flat_violin(position = position_nudge(x = .09, y = 0), scale = 'width', alpha = 0.2, width
  geom_boxplot(color = 'black', width = .07, outlier.shape = NA, alpha = 0.0, size = 1.0, positio
  geom_point(position = position_jitter(width = .02), size = 2.0, alpha = 1.0) +
    scale_y_continuous(
      name="Average trait score",
    ) +
    scale_x_discrete(
      name="Generation"
    ) +
  scale_shape_manual(values=c(16,16))+
  scale_colour_manual(values = mvc_col, ) +
  scale_fill_manual(values = mvc_col) +
  ggtitle('Performance comparisons')+
  p_theme + theme(legend.position="none")
```



Summary statistics for the best performance.

```
filter(interval_df, acro == 'tru') %>%
  group_by(Generation) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(pop_fit_max)),
    min = min(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
```

```
    median = median(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    mean = mean(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    max = max(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    IQR = IQR(pop_fit_max / DIMENSIONALITY, na.rm = TRUE)
  )
```

```
## # A tibble: 2 x 8
##   Generation count na_cnt   min median  mean   max   IQR
##   <fct>      <int>  <int> <dbl>  <dbl> <dbl> <dbl> <dbl>
## 1 40000         50      0  5.76   8.33  8.21  8.72 0.156
## 2 50000         50      0  6.07   8.35  8.23  8.72 0.166
```

Results for post-hoc Wilcoxon rank-sum test.

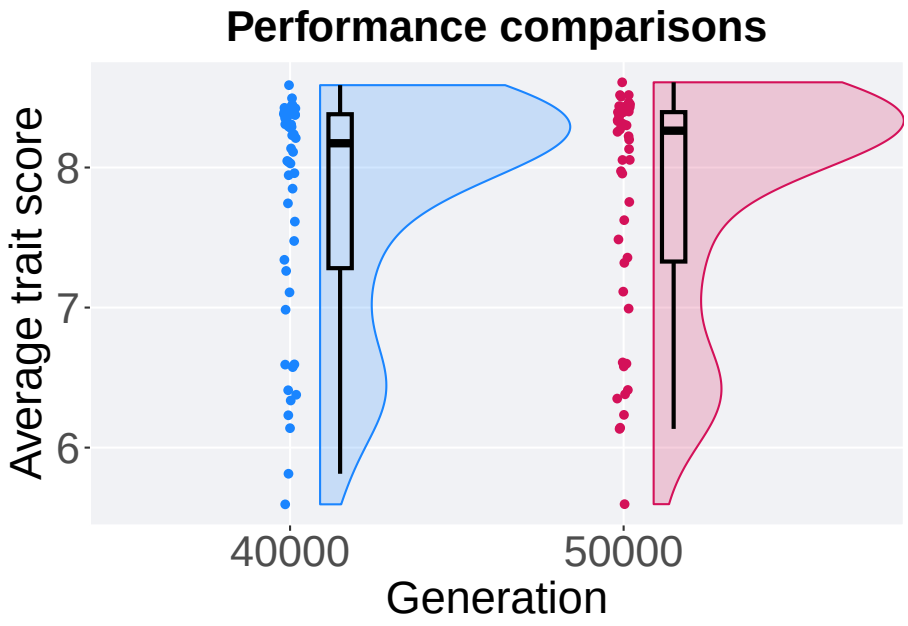
```
wilcox.test(x = filter(interval_df, acro == 'tru' & Generation == 50000)$pop_fit_max,
            y = filter(interval_df, acro == 'tru' & Generation == 40000)$pop_fit_max,
            alternative = 't')
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  filter(interval_df, acro == "tru" & Generation == 50000)$pop_fit_max and filt
## W = 1351, p-value = 0.4884
## alternative hypothesis: true location shift is not equal to 0
```

3.5.1.2 Tournament

Plot for comparing performances at interval 40,000 & 50,000.

```
filter(interval_df, acro == 'tor') %>%
ggplot(., aes(x=Generation, y=pop_fit_max/DIMENSIONALITY,fill=Generation,color=Generati
  geom_flat_violin(position = position_nudge(x = .09, y = 0), scale = 'width', alpha =
  geom_boxplot(color = 'black', width = .07, outlier.shape = NA, alpha = 0.0, size = 1
  geom_point(position = position_jitter(width = .02), size = 2.0, alpha = 1.0) +
    scale_y_continuous(
      name="Average trait score",
    ) +
    scale_x_discrete(
      name="Generation"
    ) +
  scale_shape_manual(values=c(16,16))+
  scale_colour_manual(values = mvc_col, ) +
  scale_fill_manual(values = mvc_col) +
  ggtitle('Performance comparisons')+
  p_theme + theme(legend.position="none")
```



Summary statistics for the best performance.

```
filter(interval_df, acro == 'tor') %>%
  group_by(Generation) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(pop_fit_max)),
    min = min(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    median = median(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    mean = mean(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    max = max(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    IQR = IQR(pop_fit_max / DIMENSIONALITY, na.rm = TRUE)
  )
```

```
## # A tibble: 2 x 8
##   Generation count na_cnt   min median  mean   max   IQR
##   <fct>      <int>  <int> <dbl>  <dbl> <dbl> <dbl> <dbl>
## 1 40000         50      0  5.59   8.17  7.75  8.59  1.10
## 2 50000         50      0  5.60   8.26  7.79  8.61  1.07
```

Results for post-hoc Wilcoxon rank-sum test.

```
wilcox.test(x = filter(interval_df, acro == 'tor' & Generation == 50000)$pop_fit_max,
            y = filter(interval_df, acro == 'tor' & Generation == 40000)$pop_fit_max,
            alternative = 't')
```

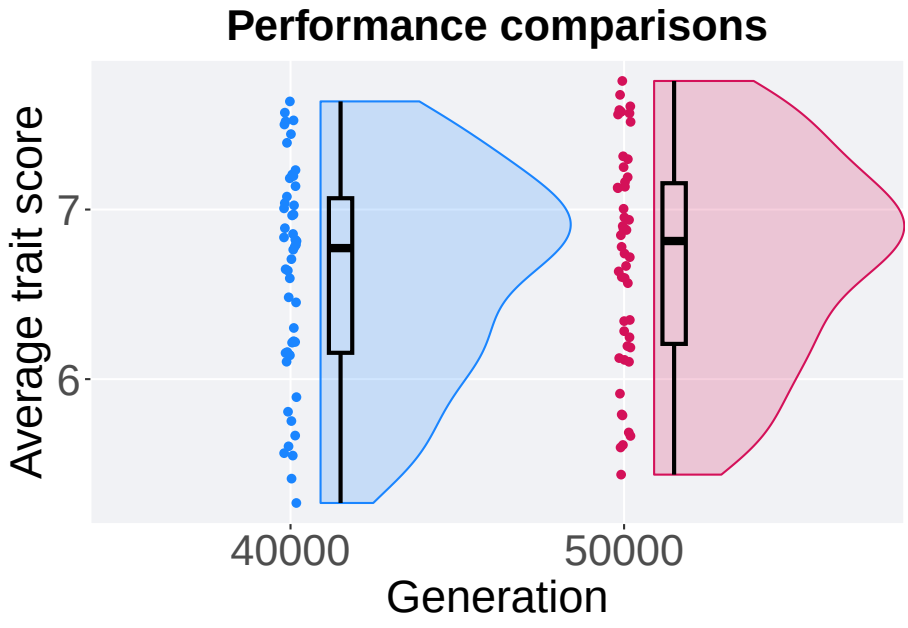
```
##
```

```
##  Wilcoxon rank sum test with continuity correction
##
## data:  filter(interval_df, acro == "tor" & Generation == 50000)$pop_fit_max and filt
## W = 1343, p-value = 0.5237
## alternative hypothesis: true location shift is not equal to 0
```

3.5.1.3 Lexicase

Plot for comparing performances at interval 40,000 & 50,000.

```
filter(interval_df, acro == 'lex') %>%
ggplot(., aes(x=Generation, y=pop_fit_max/DIMENSIONALITY,fill=Generation,color=Generati
  geom_flat_violin(position = position_nudge(x = .09, y = 0), scale = 'width', alpha =
  geom_boxplot(color = 'black', width = .07, outlier.shape = NA, alpha = 0.0, size = 1
  geom_point(position = position_jitter(width = .02), size = 2.0, alpha = 1.0) +
    scale_y_continuous(
      name="Average trait score",
    ) +
    scale_x_discrete(
      name="Generation"
    ) +
  scale_shape_manual(values=c(16,16))+
  scale_colour_manual(values = mvc_col, ) +
  scale_fill_manual(values = mvc_col) +
  ggtitle('Performance comparisons')+
  p_theme + theme(legend.position="none")
```



Summary statistics for the best performance.

```
filter(interval_df, acro == 'lex') %>%
  group_by(Generation) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(pop_fit_max)),
    min = min(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    median = median(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    mean = mean(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    max = max(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    IQR = IQR(pop_fit_max / DIMENSIONALITY, na.rm = TRUE)
  )
```

```
## # A tibble: 2 x 8
##   Generation count na_cnt   min median  mean   max   IQR
##   <fct>      <int>  <int> <dbl>  <dbl> <dbl> <dbl> <dbl>
## 1 40000         50      0  5.27   6.77  6.62  7.64 0.912
## 2 50000         50      0  5.44   6.81  6.71  7.76 0.948
```

Results for post-hoc Wilcoxon rank-sum test.

```
wilcox.test(x = filter(interval_df, acro == 'lex' & Generation == 50000)$pop_fit_max,
            y = filter(interval_df, acro == 'lex' & Generation == 40000)$pop_fit_max,
            alternative = 't')
```

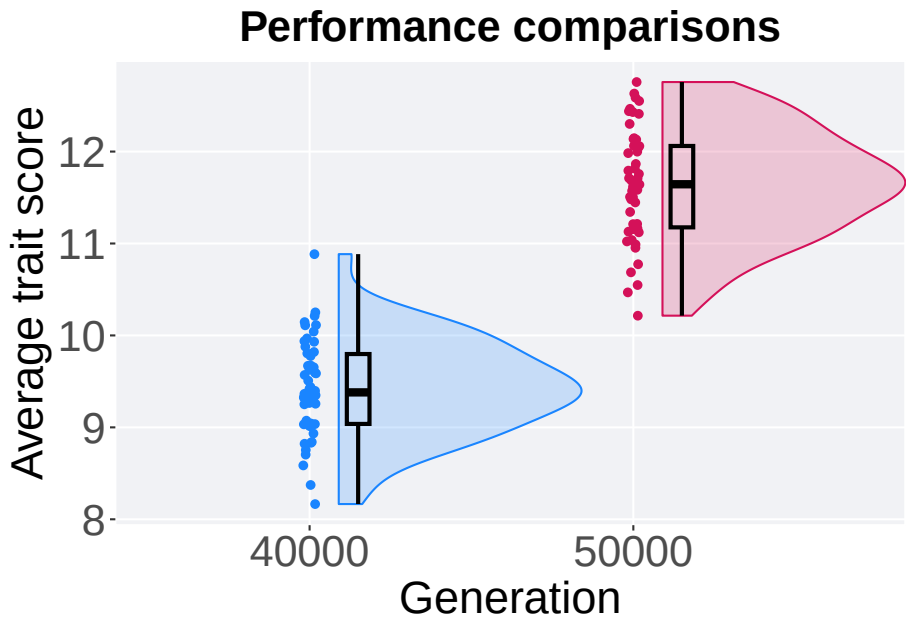
```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  filter(interval_df, acro == "lex" & Generation == 50000)$pop_fit_max and filter(interva
## W = 1346, p-value = 0.5103
## alternative hypothesis: true location shift is not equal to 0
```

3.5.1.4 Genotypic fitness sharing

Plot for comparing performances at interval 40,000 & 50,000.

```
filter(interval_df, acro == 'gfs') %>%
ggplot(., aes(x=Generation, y=pop_fit_max/DIMENSIONALITY,fill=Generation,color=Generation,shape=G
  geom_flat_violin(position = position_nudge(x = .09, y = 0), scale = 'width', alpha = 0.2, width
  geom_boxplot(color = 'black', width = .07, outlier.shape = NA, alpha = 0.0, size = 1.0, positio
  geom_point(position = position_jitter(width = .02), size = 2.0, alpha = 1.0) +
    scale_y_continuous(
      name="Average trait score",
    ) +
    scale_x_discrete(
      name="Generation"
    ) +
```

```
  scale_shape_manual(values=c(16,16))+
  scale_colour_manual(values = mvc_col, ) +
  scale_fill_manual(values = mvc_col) +
  ggtitle('Performance comparisons')+
  p_theme + theme(legend.position="none")
```



Summary statistics for the best performance.

```
filter(interval_df, acro == 'gfs') %>%
  group_by(Generation) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(pop_fit_max)),
    min = min(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    median = median(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    mean = mean(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    max = max(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    IQR = IQR(pop_fit_max / DIMENSIONALITY, na.rm = TRUE)
  )
```

```
## # A tibble: 2 x 8
##   Generation count na_cnt   min median  mean   max   IQR
##   <fct>      <int>  <int> <dbl>  <dbl> <dbl> <dbl> <dbl>
## 1 40000         50      0  8.17   9.38  9.43  10.9 0.760
## 2 50000         50      0 10.2   11.6  11.6   12.8 0.885
```

Results for post-hoc Wilcoxon rank-sum test.

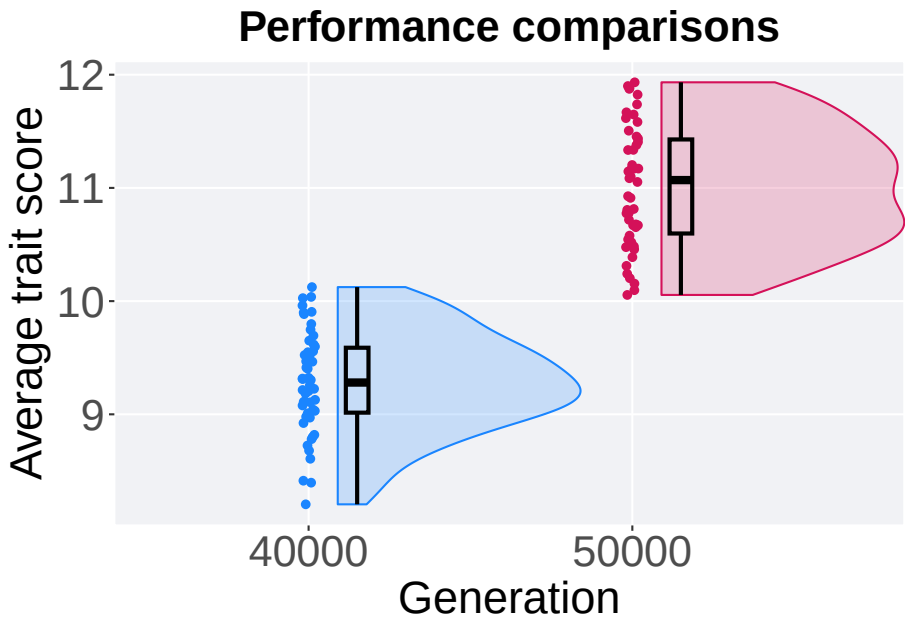
```
wilcox.test(x = filter(interval_df, acro == 'gfs' & Generation == 50000)$pop_fit_max,
            y = filter(interval_df, acro == 'gfs' & Generation == 40000)$pop_fit_max,
            alternative = 'g')
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  filter(interval_df, acro == "gfs" & Generation == 50000)$pop_fit_max and filter(interva
## W = 2494, p-value < 2.2e-16
## alternative hypothesis: true location shift is greater than 0
```

3.5.1.5 Phenotypic fitness sharing

Plot for comparing performances at interval 40,000 & 50,000.

```
filter(interval_df, acro == 'pfs') %>%
ggplot(., aes(x=Generation, y=pop_fit_max/DIMENSIONALITY,fill=Generation,color=Generation,shape=G
  geom_flat_violin(position = position_nudge(x = .09, y = 0), scale = 'width', alpha = 0.2, width
  geom_boxplot(color = 'black', width = .07, outlier.shape = NA, alpha = 0.0, size = 1.0, positio
  geom_point(position = position_jitter(width = .02), size = 2.0, alpha = 1.0) +
    scale_y_continuous(
      name="Average trait score",
    ) +
    scale_x_discrete(
      name="Generation"
    ) +
  scale_shape_manual(values=c(16,16))+
  scale_colour_manual(values = mvc_col, ) +
  scale_fill_manual(values = mvc_col) +
  ggtitle('Performance comparisons')+
  p_theme + theme(legend.position="none")
```



Summary statistics for the best performance.

```
filter(interval_df, acro == 'pfs') %>%
  group_by(Generation) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(pop_fit_max)),
    min = min(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    median = median(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    mean = mean(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    max = max(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    IQR = IQR(pop_fit_max / DIMENSIONALITY, na.rm = TRUE)
  )
```

```
## # A tibble: 2 x 8
##   Generation count na_cnt   min median  mean   max   IQR
##   <fct>      <int>  <int> <dbl>  <dbl> <dbl> <dbl> <dbl>
## 1 40000         50      0  8.20   9.28  9.28  10.1 0.574
## 2 50000         50      0 10.1   11.1  11.0   11.9 0.831
```

Results for post-hoc Wilcoxon rank-sum test.

```
wilcox.test(x = filter(interval_df, acro == 'pfs' & Generation == 50000)$pop_fit_max,
            y = filter(interval_df, acro == 'pfs' & Generation == 40000)$pop_fit_max,
            alternative = 'g')
```

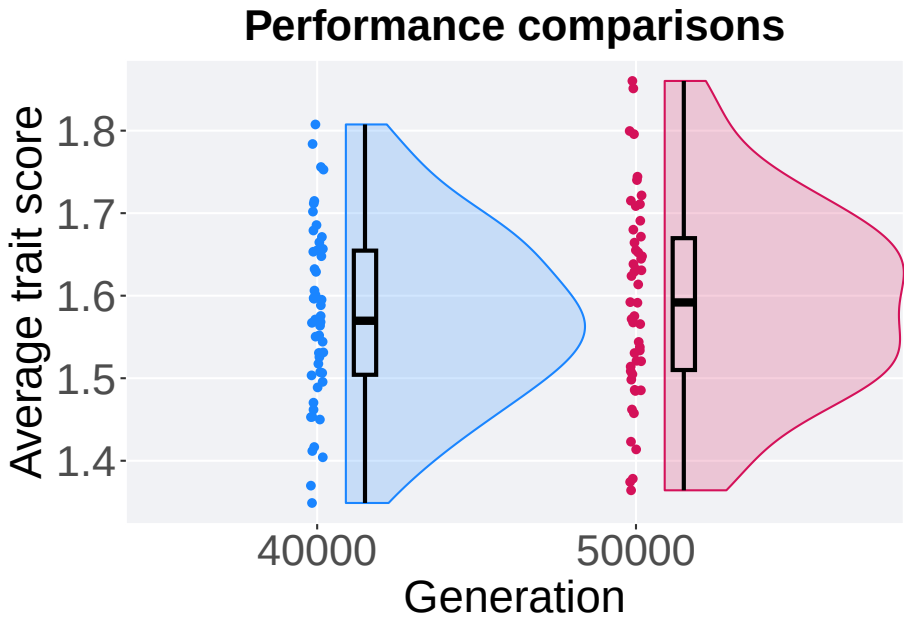
```
##
```

```
##  Wilcoxon rank sum test with continuity correction
##
## data:  filter(interval_df, acro == "pfs" & Generation == 50000)$pop_fit_max and filter(interva
## W = 2498, p-value < 2.2e-16
## alternative hypothesis: true location shift is greater than 0
```

3.5.1.6 Nondominated sorting

Plot for comparing performances at interval 40,000 & 50,000.

```
filter(interval_df, acro == 'nds') %>%
ggplot(., aes(x=Generation, y=pop_fit_max/DIMENSIONALITY,fill=Generation,color=Generation,shape=C
  geom_flat_violin(position = position_nudge(x = .09, y = 0), scale = 'width', alpha = 0.2, width
  geom_boxplot(color = 'black', width = .07, outlier.shape = NA, alpha = 0.0, size = 1.0, positio
  geom_point(position = position_jitter(width = .02), size = 2.0, alpha = 1.0) +
    scale_y_continuous(
      name="Average trait score",
    ) +
    scale_x_discrete(
      name="Generation"
    ) +
  scale_shape_manual(values=c(16,16))+
  scale_colour_manual(values = mvc_col, ) +
  scale_fill_manual(values = mvc_col) +
  ggtitle('Performance comparisons')+
  p_theme + theme(legend.position="none")
```



Summary statistics for the best performance.

```
filter(interval_df, acro == 'nds') %>%
  group_by(Generation) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(pop_fit_max)),
    min = min(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    median = median(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    mean = mean(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    max = max(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    IQR = IQR(pop_fit_max / DIMENSIONALITY, na.rm = TRUE)
  )
```

```
## # A tibble: 2 x 8
##   Generation count na_cnt   min median  mean   max   IQR
##   <fct>      <int>  <int> <dbl>  <dbl> <dbl> <dbl> <dbl>
## 1 40000         50      0  1.35   1.57  1.57  1.81 0.150
## 2 50000         50      0  1.36   1.59  1.59  1.86 0.160
```

Results for post-hoc Wilcoxon rank-sum test.

```
wilcox.test(x = filter(interval_df, acro == 'nds' & Generation == 50000)$pop_fit_max,
            y = filter(interval_df, acro == 'nds' & Generation == 40000)$pop_fit_max,
            alternative = 't')
```

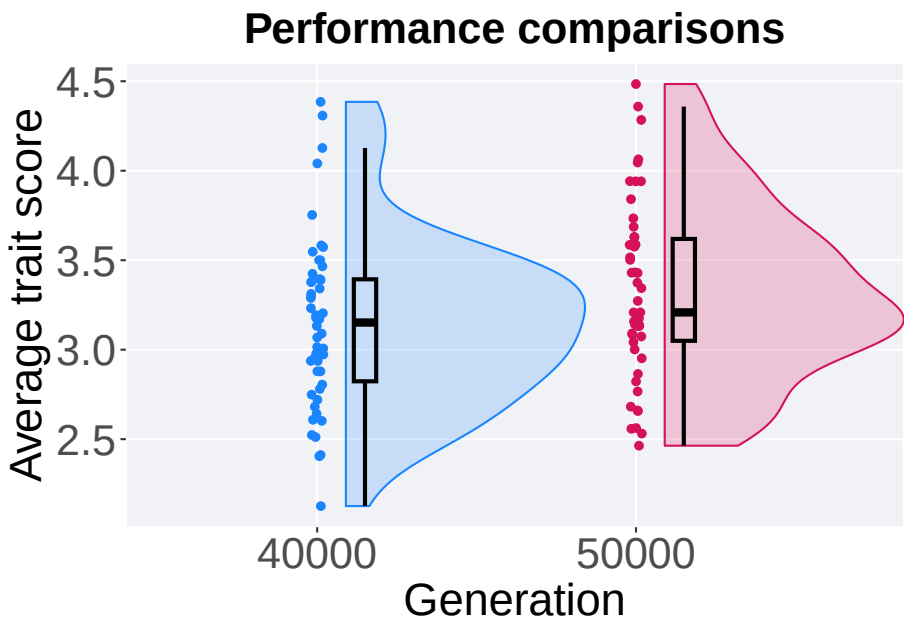
```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  filter(interval_df, acro == "nds" & Generation == 50000)$pop_fit_max and filt
## W = 1359, p-value = 0.4545
## alternative hypothesis: true location shift is not equal to 0
```

3.5.1.7 Novelty search

Plot for comparing performances at interval 40,000 & 50,000.

```
filter(interval_df, acro == 'nov') %>%
ggplot(., aes(x=Generation, y=pop_fit_max/DIMENSIONALITY,fill=Generation,color=Generati
  geom_flat_violin(position = position_nudge(x = .09, y = 0), scale = 'width', alpha =
  geom_boxplot(color = 'black', width = .07, outlier.shape = NA, alpha = 0.0, size = 1
  geom_point(position = position_jitter(width = .02), size = 2.0, alpha = 1.0) +
    scale_y_continuous(
      name="Average trait score",
    ) +
    scale_x_discrete(
      name="Generation"
    ) +
```

```
  scale_shape_manual(values=c(16,16))+
  scale_colour_manual(values = mvc_col, ) +
  scale_fill_manual(values = mvc_col) +
  ggtitle('Performance comparisons')+
  p_theme + theme(legend.position="none")
```



Summary statistics for the best performance.

```
filter(interval_df, acro == 'nov') %>%
  group_by(Generation) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(pop_fit_max)),
    min = min(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    median = median(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    mean = mean(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    max = max(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    IQR = IQR(pop_fit_max / DIMENSIONALITY, na.rm = TRUE)
  )
```

```
## # A tibble: 2 x 8
##   Generation count na_cnt   min median  mean   max   IQR
##   <fct>      <int>  <int> <dbl>  <dbl> <dbl> <dbl> <dbl>
## 1 40000         50      0  2.13   3.15  3.15  4.38 0.570
## 2 50000         50      0  2.46   3.21  3.32  4.48 0.569
```

Results for post-hoc Wilcoxon rank-sum test.

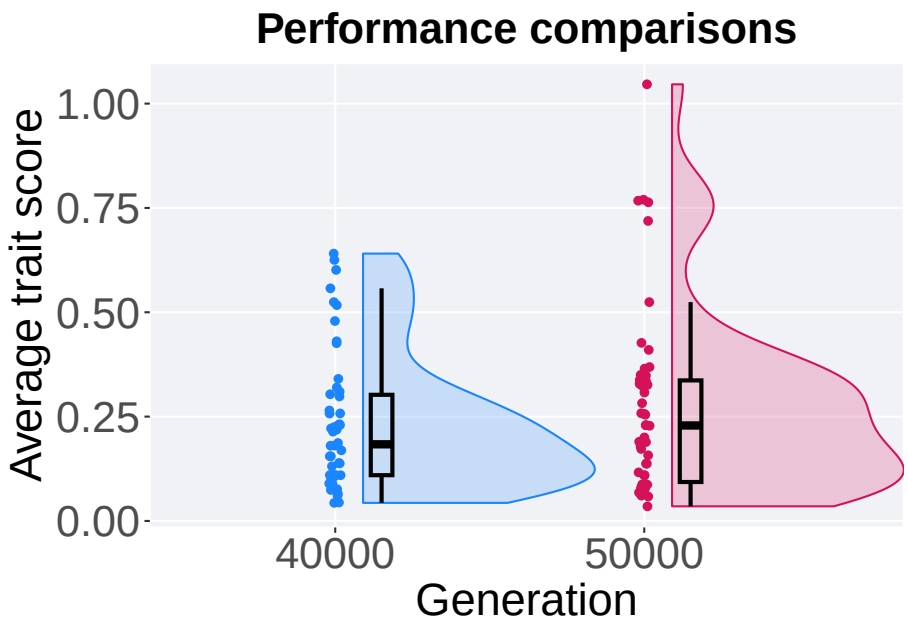
```
wilcox.test(x = filter(interval_df, acro == 'nov' & Generation == 50000)$pop_fit_max,
            y = filter(interval_df, acro == 'nov' & Generation == 40000)$pop_fit_max,
            alternative = 't')
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  filter(interval_df, acro == "nov" & Generation == 50000)$pop_fit_max and filt
## W = 1506, p-value = 0.07818
## alternative hypothesis: true location shift is not equal to 0
```

3.5.1.8 Random

Plot for comparing performances at interval 40,000 & 50,000.

```
filter(interval_df, acro == 'ran') %>%
ggplot(., aes(x=Generation, y=pop_fit_max/DIMENSIONALITY,fill=Generation,color=Generati
  geom_flat_violin(position = position_nudge(x = .09, y = 0), scale = 'width', alpha =
  geom_boxplot(color = 'black', width = .07, outlier.shape = NA, alpha = 0.0, size = 1
  geom_point(position = position_jitter(width = .02), size = 2.0, alpha = 1.0) +
    scale_y_continuous(
      name="Average trait score",
    ) +
    scale_x_discrete(
      name="Generation"
    ) +
  scale_shape_manual(values=c(16,16))+
  scale_colour_manual(values = mvc_col, ) +
  scale_fill_manual(values = mvc_col) +
  ggtitle('Performance comparisons')+
  p_theme + theme(legend.position="none")
```



Summary statistics for the best performance.

```
filter(interval_df, acro == 'ran') %>%
  group_by(Generation) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(pop_fit_max)),
    min = min(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    median = median(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    mean = mean(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    max = max(pop_fit_max / DIMENSIONALITY, na.rm = TRUE),
    IQR = IQR(pop_fit_max / DIMENSIONALITY, na.rm = TRUE)
  )
```

```
## # A tibble: 2 x 8
##   Generation count na_cnt    min median  mean   max   IQR
##   <fct>      <int>  <int>  <dbl>  <dbl> <dbl> <dbl> <dbl>
## 1 40000         50      0 0.0433  0.184 0.233 0.641 0.193
## 2 50000         50      0 0.0350  0.229 0.270 1.05  0.243
```

Results for post-hoc Wilcoxon rank-sum test.

```
wilcox.test(x = filter(interval_df, acro == 'ran' & Generation == 50000)$pop_fit_max,
            y = filter(interval_df, acro == 'ran' & Generation == 40000)$pop_fit_max,
            alternative = 't')
```

```
##
```

```
##  Wilcoxon rank sum test with continuity correction
##
## data:  filter(interval_df, acro == "ran" & Generation == 50000)$pop_fit_max and filt
## W = 1335, p-value = 0.5602
## alternative hypothesis: true location shift is not equal to 0
```

Chapter 4

Contradictory objectives results

Here we present the results for **activation gene coverage** and **satisfacotory trait coverage** found by each selection scheme on the contradictory objectives diagnostic with valley crossing integrated. 50 replicates are conducted for each scheme explored.

4.1 Analysis dependencies

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

4.2 Data setup

```
DIR = paste(DATA_DIR,'CONTRADICTORY_OBJECTIVES/', sep = "", collapse = NULL)
over_time_df <- read.csv(paste(DIR,'over-time.csv', sep = "", collapse = NULL), header = TRUE, st
over_time_df$uni_str_pos = over_time_df$uni_str_pos + over_time_df$arc_acti_gene - over_time_df$c
over_time_df$scheme <- factor(over_time_df$scheme, levels = NAMES)
over_time_df$acro <- factor(over_time_df$acro, levels = ACRO)

best_df <- read.csv(paste(DIR,'best.csv', sep = "", collapse = NULL), header = TRUE, stringsAsFac
best_df$acro <- factor(best_df$acro, levels = ACRO)
```

4.3 Activation gene coverage over time

Activation gene coverage in a population over time. Data points on the graph is the average activation gene coverage across 50 replicates every 2000 generations. Shading comes from the best and worse coverage across 50 replicates.

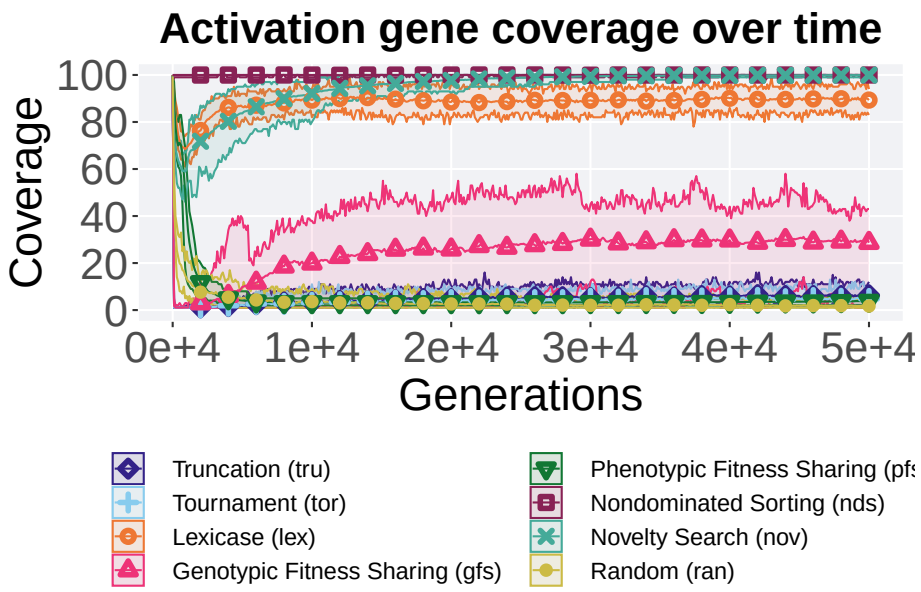
```
lines = over_time_df %>%
  group_by(scheme, gen) %>%
  dplyr::summarise(
    min = min(uni_str_pos),
    mean = mean(uni_str_pos),
    max = max(uni_str_pos)
  )
```

```
## `summarise()` has grouped output by 'scheme'. You can override using the
## `.groups` argument.
```

```
over_time_plot = ggplot(lines, aes(x=gen, y=mean, group = scheme, fill = scheme, color
  geom_ribbon(aes(ymin = min, ymax = max), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = filter(lines, gen %% 2000 == 0 & gen != 0), size = 1.5, stroke = 2
  scale_y_continuous(
    name="Coverage",
    limits=c(0, 100),
    breaks=seq(0,100, 20),
    labels=c("0", "20", "40", "60", "80", "100")
  ) +
  scale_x_continuous(
    name="Generations",
    limits=c(0, 50000),
    breaks=c(0, 10000, 20000, 30000, 40000, 50000),
    labels=c("0e+4", "1e+4", "2e+4", "3e+4", "4e+4", "5e+4")

  ) +
  scale_shape_manual(values=SHAPE)+
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  ggtitle('Activation gene coverage over time')+
  p_theme + theme(legend.title=element_blank(),legend.text=element_text(size=12)) +
  guides(
    shape=guide_legend(ncol=2, title.position = "bottom"),
    color=guide_legend(ncol=2, title.position = "bottom"),
    fill=guide_legend(ncol=2, title.position = "bottom")
  )

over_time_plot
```



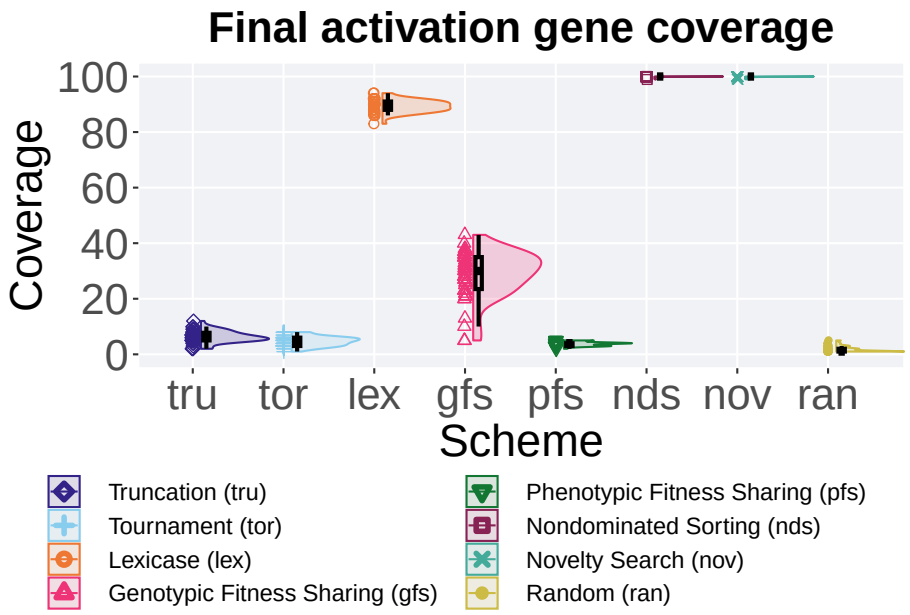
4.4 Final activation gene coverage

Activation gene coverage found in the final population at 50,000 generations.

```
plot = filter(over_time_df, gen == 50000) %>%
  ggplot(., aes(x = acro, y = uni_str_pos, color = acro, fill = acro, shape = acro)) +
  geom_flat_violin(position = position_nudge(x = .09, y = 0), scale = 'width', alpha = 0.2, width
  geom_boxplot(color = 'black', width = .07, outlier.shape = NA, alpha = 0.0, size = 1.0, positio
  geom_point(position = position_jitter(width = 0.01, height = 0.1), size = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Coverage",
    limits=c(0, 100),
    breaks=seq(0,100, 20),
    labels=c("0", "20", "40", "60", "80", "100")
  ) +
  scale_x_discrete(
    name="Scheme"
  )+
  scale_shape_manual(values=SHAPE)+
  scale_colour_manual(values = cb_palette, ) +
  scale_fill_manual(values = cb_palette) +
  ggtitle('Final activation gene coverage')+
  p_theme + theme(legend.title=element_blank())
```

```
plot_grid(
  plot +
    theme(legend.position="none"),
  legend,
  nrow=2,
  rel_heights = c(3,1)
)
```

```
## Warning: Removed 55 rows containing missing values (`geom_point()`).
```



4.4.1 Stats

Summary statistics for the coverage found in the final population.

```
act_coverage = filter(over_time_df, gen == 50000)
act_coverage$acro = factor(act_coverage$acro, levels = c('nov','nds','lex','gfs','tor'
act_coverage %>%
  group_by(acro) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(uni_str_pos)),
    min = min(uni_str_pos, na.rm = TRUE),
    median = median(uni_str_pos, na.rm = TRUE),
    mean = mean(uni_str_pos, na.rm = TRUE),
    max = max(uni_str_pos, na.rm = TRUE),
```

```
    IQR = IQR(uni_str_pos, na.rm = TRUE)
  )
```

```
## # A tibble: 8 x 8
##   acro  count na_cnt   min median   mean   max   IQR
##   <fct> <int>  <int> <int>  <dbl>  <dbl> <int> <dbl>
## 1 nov      50      0    99    100  99.9    100  0
## 2 nds      50      0    99    100 100.     100  0
## 3 lex      50      0    83     89  89.3     94  3
## 4 gfs      50      0     5     30  28.7     43 11.5
## 5 tor      50      0     1      5   4.72     8  3
## 6 tru      50      0     2      6   6.28    12  2.75
## 7 pfs      50      0     2      4   3.84     5  1
## 8 ran      50      0     1      1   1.72     5  1
```

Kruskal–Wallis test illustrates evidence of statistical differences.

```
kruskal.test(uni_str_pos ~ acro, data = act_coverage)
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  uni_str_pos by acro
## Kruskal-Wallis chi-squared = 373.95, df = 7, p-value < 2.2e-16
```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction.

```
pairwise.wilcox.test(x = act_coverage$uni_str_pos, g = act_coverage$acro, p.adjust.method = "bonf
                     paired = FALSE, conf.int = FALSE, alternative = 'l')
```

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  act_coverage$uni_str_pos and act_coverage$acro
##
##     nov     nds     lex     gfs     tor     tru     pfs
## nds 1.00    -       -       -       -       -       -
## lex < 2e-16 < 2e-16 -       -       -       -       -
## gfs < 2e-16 < 2e-16 < 2e-16 -       -       -       -
## tor < 2e-16 < 2e-16 < 2e-16 1.3e-15 -       -       -
## tru < 2e-16 < 2e-16 < 2e-16 7.3e-15 1.00    -       -
## pfs < 2e-16 < 2e-16 < 2e-16 < 2e-16 0.05    3.4e-10 -
## ran < 2e-16 < 2e-16 < 2e-16 < 2e-16 1.4e-12 1.9e-15 1.8e-12
##
## P value adjustment method: bonferroni
```

4.5 Satisfactory trait coverage over time

Satisfactory trait coverage in a population over time. Data points on the graph is the average activation gene coverage across 50 replicates every 2000 generations. Shading comes from the best and worse coverage across 50 replicates.

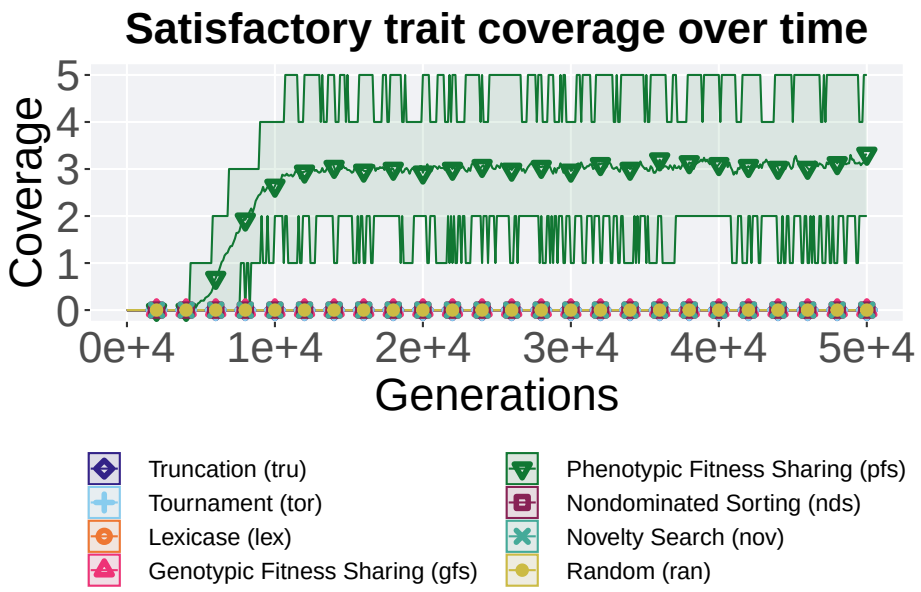
```
lines = over_time_df %>%
  group_by(scheme, gen) %>%
  dplyr::summarise(
    min = min(pop_uni_obj),
    mean = mean(pop_uni_obj),
    max = max(pop_uni_obj)
  )
```

```
## `summarise()` has grouped output by 'scheme'. You can override using the
## `.groups` argument.
```

```
over_time_plot = ggplot(lines, aes(x=gen, y=mean, group = scheme, fill = scheme, color
  geom_ribbon(aes(ymin = min, ymax = max), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = filter(lines, gen %% 2000 == 0 & gen != 0), size = 1.5, stroke = 2
  scale_y_continuous(
    name="Coverage"
  ) +
  scale_x_continuous(
    name="Generations",
    limits=c(0, 50000),
    breaks=c(0, 10000, 20000, 30000, 40000, 50000),
    labels=c("0e+4", "1e+4", "2e+4", "3e+4", "4e+4", "5e+4")

  ) +
  scale_shape_manual(values=SHAPE)+
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  ggtitle('Satisfactory trait coverage over time')+
  p_theme + theme(legend.title=element_blank(),legend.text=element_text(size=12)) +
  guides(
    shape=guide_legend(ncol=2, title.position = "bottom"),
    color=guide_legend(ncol=2, title.position = "bottom"),
    fill=guide_legend(ncol=2, title.position = "bottom")
  )

over_time_plot
```



4.6 Best satisfactory trait coverage throughout

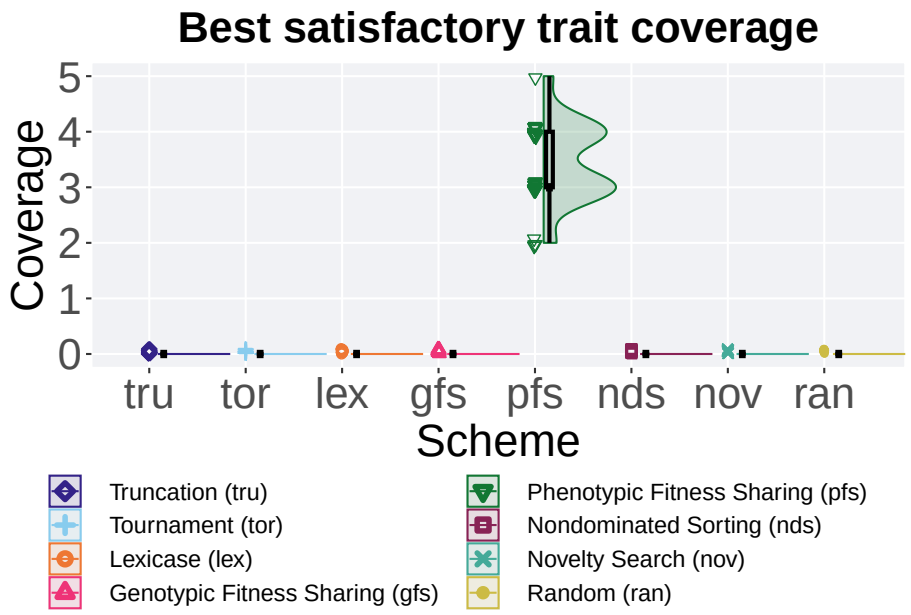
Best satisfactory trait coverage reached throughout 50,000 generations in a population.

```
plot = filter(best_df, var == 'pop_uni_obj') %>%
  ggplot(., aes(x = acro, y = val, color = acro, fill = acro, shape = acro)) +
  geom_flat_violin(position = position_nudge(x = .09, y = 0), scale = 'width', alpha = 0.2, width
  geom_boxplot(color = 'black', width = .07, outlier.shape = NA, alpha = 0.0, size = 1.0, positio
  geom_point(position = position_jitter(width = 0.01, height = 0.1), size = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Coverage",
    limits=c(0, 5)
  ) +
  scale_x_discrete(
    name="Scheme"
  )+
  scale_shape_manual(values=SHAPE)+
  scale_colour_manual(values = cb_palette, ) +
  scale_fill_manual(values = cb_palette) +
  ggtitle('Best satisfactory trait coverage')+
  p_theme + theme(legend.title=element_blank())

plot_grid(
```

```
  plot +
    theme(legend.position="none"),
  legend,
  nrow=2,
  rel_heights = c(3,1)
)
```

```
## Warning: Removed 174 rows containing missing values (`geom_point()`).
```



4.6.1 Stats

Summary statistics for the best coverage.

```
sat_coverage = filter(best_df, var == 'pop_uni_obj')
sat_coverage$acro = factor(sat_coverage$acro, levels = c('pfs','nds','lex','gfs','tor'
sat_coverage %>%
  group_by(acro) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(val)),
    min = min(val, na.rm = TRUE),
    median = median(val, na.rm = TRUE),
    mean = mean(val, na.rm = TRUE),
    max = max(val, na.rm = TRUE),
    IQR = IQR(val, na.rm = TRUE)
```

```
  )
```

```
## # A tibble: 8 x 8
##   acro  count na_cnt   min median  mean   max   IQR
##   <fct> <int>  <int> <dbl>  <dbl> <dbl> <dbl> <dbl>
## 1 pfs      50      0     2      3  3.44     5     1
## 2 nds      50      0     0      0  0        0     0
## 3 lex      50      0     0      0  0        0     0
## 4 gfs      50      0     0      0  0        0     0
## 5 tor      50      0     0      0  0        0     0
## 6 tru      50      0     0      0  0        0     0
## 7 nov      50      0     0      0  0        0     0
## 8 ran      50      0     0      0  0        0     0
```

Kruskal–Wallis test illustrates evidence of statistical differences.

```
kruskal.test(val ~ acro, data = sat_coverage)
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  val by acro
## Kruskal-Wallis chi-squared = 397.02, df = 7, p-value < 2.2e-16
```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction.

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

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  sat_coverage$val and sat_coverage$acro
##
##     pfs    nds lex gfs tor tru nov
## nds <2e-16 -   -   -   -   -   -
## lex <2e-16 1   -   -   -   -   -
## gfs <2e-16 1   1   -   -   -   -
## tor <2e-16 1   1   1   -   -   -
## tru <2e-16 1   1   1   1   -   -
## nov <2e-16 1   1   1   1   1   -
## ran <2e-16 1   1   1   1   1   1
##
## P value adjustment method: bonferroni
```

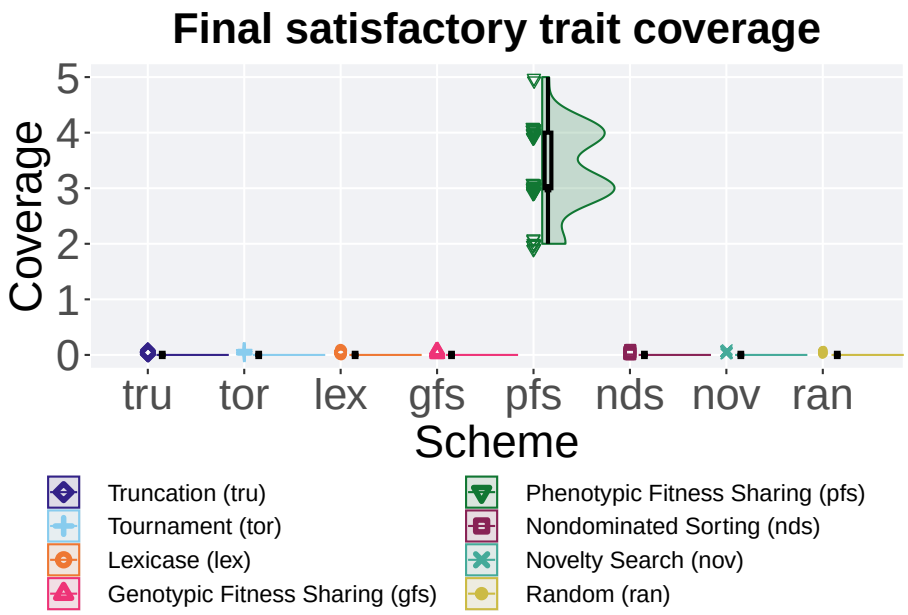
4.7 Final satisfactory trait coverage

Satisfactory trait coverage found in the final population at 50,000 generations.

```
plot = filter(over_time_df, gen == 50000) %>%
  ggplot(., aes(x = acro, y = pop_uni_obj, color = acro, fill = acro, shape = acro)) +
  geom_flat_violin(position = position_nudge(x = .09, y = 0), scale = 'width', alpha =
  geom_boxplot(color = 'black', width = .07, outlier.shape = NA, alpha = 0.0, size = 1
  geom_point(position = position_jitter(width = 0.01, height = 0.1), size = 2.0, alpha
  scale_y_continuous(
    name="Coverage",
    limits=c(0, 5)
  ) +
  scale_x_discrete(
    name="Scheme"
  )+
  scale_shape_manual(values=SHAPE)+
  scale_colour_manual(values = cb_palette, ) +
  scale_fill_manual(values = cb_palette) +
  ggtitle('Final satisfactory trait coverage')+
  p_theme + theme(legend.title=element_blank())

plot_grid(
  plot +
    theme(legend.position="none"),
  legend,
  nrow=2,
  rel_heights = c(3,1)
)
```

```
## Warning: Removed 166 rows containing missing values (`geom_point()`).
```



4.7.1 Stats

Summary statistics for the coverage found in the final population.

```
act_coverage = filter(over_time_df, gen == 50000)
act_coverage$acro = factor(act_coverage$acro, levels = c('pfs','nds','lex','gfs','tor','tru','nov
act_coverage %>%
  group_by(acro) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(pop_uni_obj)),
    min = min(pop_uni_obj, na.rm = TRUE),
    median = median(pop_uni_obj, na.rm = TRUE),
    mean = mean(pop_uni_obj, na.rm = TRUE),
    max = max(pop_uni_obj, na.rm = TRUE),
    IQR = IQR(pop_uni_obj, na.rm = TRUE)
  )
```

```
## # A tibble: 8 x 8
##   acro  count na_cnt   min median  mean   max   IQR
##   <fct> <int>  <int> <int>  <dbl> <dbl> <int> <dbl>
## 1 pfs      50      0     2      3  3.32     5     1
## 2 nds      50      0     0      0  0        0     0
## 3 lex      50      0     0      0  0        0     0
## 4 gfs      50      0     0      0  0        0     0
```

```
## 5 tor      50      0     0      0  0        0     0
## 6 tru      50      0     0      0  0        0     0
## 7 nov      50      0     0      0  0        0     0
## 8 ran      50      0     0      0  0        0     0
```

Kruskal–Wallis test illustrates evidence of statistical differences.

```
kruskal.test(pop_uni_obj ~ acro, data = act_coverage)
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  pop_uni_obj by acro
## Kruskal-Wallis chi-squared = 396.97, df = 7, p-value < 2.2e-16
```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction.

```
pairwise.wilcox.test(x = act_coverage$pop_uni_obj, g = act_coverage$acro, p.adjust.metl
                     paired = FALSE, conf.int = FALSE, alternative = 'l')
```

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  act_coverage$pop_uni_obj and act_coverage$acro
##
##     pfs    nds lex gfs tor tru nov
## nds <2e-16 -   -   -   -   -   -
## lex <2e-16 1   -   -   -   -   -
## gfs <2e-16 1   1   -   -   -   -
## tor <2e-16 1   1   1   -   -   -
## tru <2e-16 1   1   1   1   -   -
## nov <2e-16 1   1   1   1   1   -
## ran <2e-16 1   1   1   1   1   1
##
## P value adjustment method: bonferroni
```

4.8 Best trait value over time

Best trait value in a population over time. Data points on the graph is the average trait value across 50 replicates every 2000 generations. Shading comes from the best and worse trait value across 50 replicates.

```
lines = over_time_df %>%
  group_by(scheme, gen) %>%
  dplyr::summarise(
    min = min(pop_fit_max),
    mean = mean(pop_fit_max),
    max = max(pop_fit_max)
```

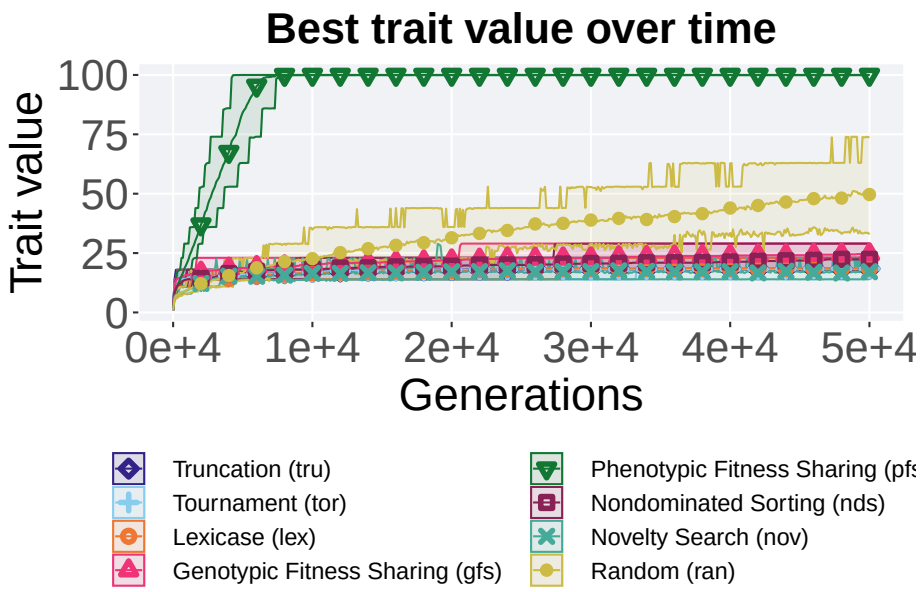
```
  )
```

```
## `summarise()` has grouped output by 'scheme'. You can override using the
## `.groups` argument.
```

```
over_time_plot = ggplot(lines, aes(x=gen, y=mean, group = scheme, fill = scheme, color = scheme,
  geom_ribbon(aes(ymin = min, ymax = max), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = filter(lines, gen %% 2000 == 0 & gen != 0), size = 1.5, stroke = 2.0, alpha =
  scale_y_continuous(
    name="Trait value"
  ) +
  scale_x_continuous(
    name="Generations",
    limits=c(0, 50000),
    breaks=c(0, 10000, 20000, 30000, 40000, 50000),
    labels=c("0e+4", "1e+4", "2e+4", "3e+4", "4e+4", "5e+4")

  ) +
  scale_shape_manual(values=SHAPE)+
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  ggtitle('Best trait value over time')+
  p_theme + theme(legend.title=element_blank(),legend.text=element_text(size=12)) +
  guides(
    shape=guide_legend(ncol=2, title.position = "bottom"),
    color=guide_legend(ncol=2, title.position = "bottom"),
    fill=guide_legend(ncol=2, title.position = "bottom")
  )

over_time_plot
```



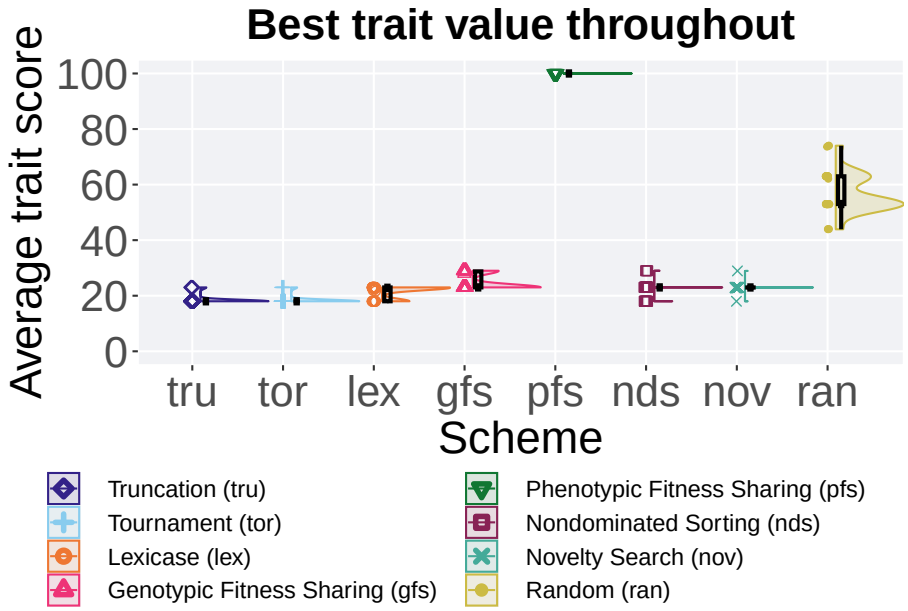
4.9 Best trait value throughout

Best trait value reached throughout 50,000 generations in a population.

```
plot = filter(best_df, var == 'pop_fit_max') %>%
  ggplot(., aes(x = acro, y = val, color = acro, fill = acro, shape = acro)) +
  geom_flat_violin(position = position_nudge(x = .09, y = 0), scale = 'width', alpha =
  geom_boxplot(color = 'black', width = .07, outlier.shape = NA, alpha = 0.0, size = 1
  geom_point(position = position_jitter(width = .02), size = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Average trait score",
    limits=c(0, 100),
    breaks=seq(0,100, 20),
    labels=c("0", "20", "40", "60", "80", "100")
  ) +
  scale_x_discrete(
    name="Scheme"
  )+
  scale_shape_manual(values=SHAPE)+
  scale_colour_manual(values = cb_palette, ) +
  scale_fill_manual(values = cb_palette) +
  ggtitle('Best trait value throughout')+
  p_theme + theme(legend.title=element_blank())
```

```
plot_grid(
  plot +
    theme(legend.position="none"),
  legend,
  nrow=2,
  rel_heights = c(3,1)
)
```

```
## Warning: Removed 15 rows containing missing values (`geom_point()`).
```



4.9.1 Stats

Summary statistics for the best trait value.

```
trait_val = filter(best_df, var == 'pop_fit_max')
trait_val$acro = factor(trait_val$acro, levels = c('pfs','ran','gfs','nov','nds','lex','tru','tor
trait_val %>%
  group_by(acro) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(val)),
    min = min(val, na.rm = TRUE),
    median = median(val, na.rm = TRUE),
    mean = mean(val, na.rm = TRUE),
    max = max(val, na.rm = TRUE),
```

```
    IQR = IQR(val, na.rm = TRUE)
  )
```

```
## # A tibble: 8 x 8
##   acro  count na_cnt   min median  mean   max      IQR
##   <fct> <int>  <int> <dbl>  <dbl> <dbl> <dbl>    <dbl>
## 1 pfs      50      0 100.   100   100.  100   0.000100
## 2 ran      50      0  43.9   53.0  56.7  74.0 9.99
## 3 gfs      50      0  23.0   23    24.7  29   5.76
## 4 nov      50      0  18.0   23.0  23.0  28.9 0.0528
## 5 nds      50      0  18     23    22.4  29   0.00328
## 6 lex      50      0  18     22.9  21.5  23   4.98
## 7 tru      50      0  18.0   18    18.4  23   0
## 8 tor      50      0  18.0   18    18.4  23   0
```

Kruskal–Wallis test illustrates evidence of statistical differences.

```
kruskal.test(val ~ acro, data = trait_val)
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  val by acro
## Kruskal-Wallis chi-squared = 337.68, df = 7, p-value < 2.2e-16
```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction.

```
pairwise.wilcox.test(x = trait_val$val, g = trait_val$acro, p.adjust.method = "bonferr
                     paired = FALSE, conf.int = FALSE, alternative = 'l')
```

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  trait_val$val and trait_val$acro
##
##     pfs     ran     gfs     nov     nds     lex     tru
## ran < 2e-16 -       -       -       -       -       -
## gfs < 2e-16 < 2e-16 -       -       -       -       -
## nov < 2e-16 < 2e-16 3.2e-16 -       -       -       -
## nds < 2e-16 < 2e-16 0.00015 1.00000 -       -       -
## lex < 2e-16 < 2e-16 3.7e-15 0.00722 1.4e-05 -       -
## tru < 2e-16 < 2e-16 < 2e-16 4.5e-12 3.0e-11 1.0e-07 -
## tor < 2e-16 < 2e-16 < 2e-16 6.3e-12 7.2e-11 9.4e-08 1.00000
##
## P value adjustment method: bonferroni
```

Chapter 5

Multi-path exploration results

Here we present the results for **best performances** found by each selection scheme on the multi-path exploration diagnostic with valley crossing integrated. 50 replicates are conducted for each scheme explored.

5.1 Analysis dependencies

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

5.2 Data setup

```
DIR = paste(DATA_DIR,'MULTIPATH_EXPLORATION/', sep = "", collapse = NULL)
over_time_df <- read.csv(paste(DIR,'over-time.csv', sep = "", collapse = NULL), header = TRUE, st
over_time_df$uni_str_pos = over_time_df$uni_str_pos + over_time_df$arc_acti_gene - over_time_df$c
over_time_df$scheme <- factor(over_time_df$scheme, levels = NAMES)
over_time_df$acro <- factor(over_time_df$acro, levels = ACRO)

best_df <- read.csv(paste(DIR,'best.csv', sep = "", collapse = NULL), header = TRUE, stringsAsFac
best_df$acro <- factor(best_df$acro, levels = ACRO)
```

5.3 Activation gene coverage over time

Activation gene coverage in a population over time. Data points on the graph is the average activation gene coverage across 50 replicates every 2000 generations. Shading comes from the best and worse coverage across 50 replicates.

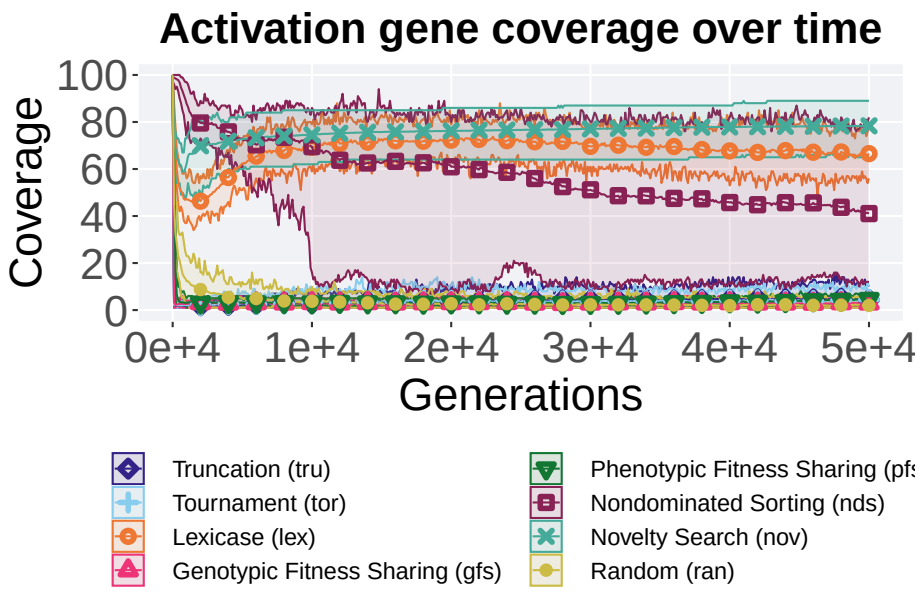
```
lines = over_time_df %>%
  group_by(scheme, gen) %>%
  dplyr::summarise(
    min = min(uni_str_pos),
    mean = mean(uni_str_pos),
    max = max(uni_str_pos)
  )
```

```
## `summarise()` has grouped output by 'scheme'. You can override using the
## `.groups` argument.
```

```
over_time_plot = ggplot(lines, aes(x=gen, y=mean, group = scheme, fill = scheme, color
  geom_ribbon(aes(ymin = min, ymax = max), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = filter(lines, gen %% 2000 == 0 & gen != 0), size = 1.5, stroke = 2
  scale_y_continuous(
    name="Coverage",
    limits=c(0, 100),
    breaks=seq(0,100, 20),
    labels=c("0", "20", "40", "60", "80", "100")
  ) +
  scale_x_continuous(
    name="Generations",
    limits=c(0, 50000),
    breaks=c(0, 10000, 20000, 30000, 40000, 50000),
    labels=c("0e+4", "1e+4", "2e+4", "3e+4", "4e+4", "5e+4")

  ) +
  scale_shape_manual(values=SHAPE)+
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  ggtitle('Activation gene coverage over time')+
  p_theme + theme(legend.title=element_blank(),legend.text=element_text(size=12)) +
  guides(
    shape=guide_legend(ncol=2, title.position = "bottom"),
    color=guide_legend(ncol=2, title.position = "bottom"),
    fill=guide_legend(ncol=2, title.position = "bottom")
  )

over_time_plot
```

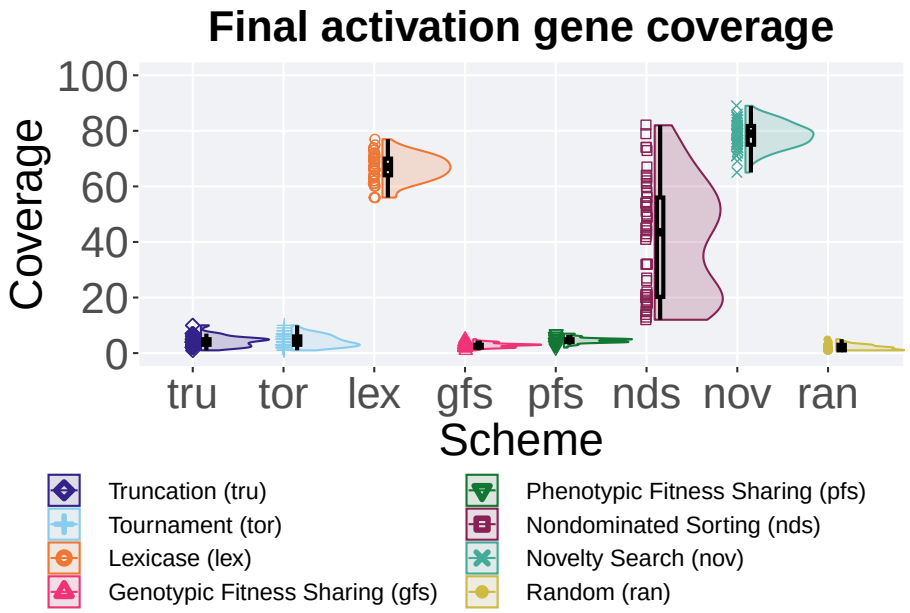


5.4 Final activation gene coverage

Activation gene coverage found in the final population at 50,000 generations.

```
plot = filter(over_time_df, gen == 50000) %>%
  ggplot(., aes(x = acro, y = uni_str_pos, color = acro, fill = acro, shape = acro)) +
  geom_flat_violin(position = position_nudge(x = .09, y = 0), scale = 'width', alpha = 0.2, width
  geom_boxplot(color = 'black', width = .07, outlier.shape = NA, alpha = 0.0, size = 1.0, positio
  geom_point(position = position_jitter(width = 0.01, height = 0.1), size = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Coverage",
    limits=c(0, 100),
    breaks=seq(0,100, 20),
    labels=c("0", "20", "40", "60", "80", "100")
  ) +
  scale_x_discrete(
    name="Scheme"
  )+
  scale_shape_manual(values=SHAPE)+
  scale_colour_manual(values = cb_palette, ) +
  scale_fill_manual(values = cb_palette) +
  ggtitle('Final activation gene coverage')+
  p_theme + theme(legend.title=element_blank())
```

```
plot_grid(
  plot +
    theme(legend.position="none"),
  legend,
  nrow=2,
  rel_heights = c(3,1)
)
```



5.4.1 Stats

Summary statistics for the coverage found in the final population.

```
act_coverage = filter(over_time_df, gen == 50000)
act_coverage$acro = factor(act_coverage$acro, levels = c('nov','lex','nds','tor','tru'
act_coverage %>%
  group_by(acro) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(uni_str_pos)),
    min = min(uni_str_pos, na.rm = TRUE),
    median = median(uni_str_pos, na.rm = TRUE),
    mean = mean(uni_str_pos, na.rm = TRUE),
    max = max(uni_str_pos, na.rm = TRUE),
    IQR = IQR(uni_str_pos, na.rm = TRUE)
  )
```

```
## # A tibble: 8 x 8
##   acro  count na_cnt   min median  mean   max   IQR
##   <fct> <int>  <int> <int>  <dbl> <dbl> <int> <dbl>
## 1 nov      50      0    65   79   78.4     89  6.75
## 2 lex      50      0    56   67   66.5     77  6
## 3 nds      50      0    12   43.5 41.0     82 35.8
## 4 tor      50      0     1    4    4.4     10  3
## 5 tru      50      0     1    4    4.28    10  2
## 6 gfs      50      0     1    3    2.88     5  1
## 7 pfs      50      0     2    5    4.64     7  1
## 8 ran      50      0     1    2    1.98     5  2
```

Kruskal–Wallis test illustrates evidence of statistical differences.

```
kruskal.test(uni_str_pos ~ acro, data = act_coverage)
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  uni_str_pos by acro
## Kruskal-Wallis chi-squared = 333.43, df = 7, p-value < 2.2e-16
```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction.

```
pairwise.wilcox.test(x = act_coverage$uni_str_pos, g = act_coverage$acro, p.adjust.method = "bonf
                     paired = FALSE, conf.int = FALSE, alternative = 'l')
```

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  act_coverage$uni_str_pos and act_coverage$acro
##
##     nov     lex     nds     tor     tru     gfs     pfs
## lex 3.0e-14 -       -       -       -       -       -
## nds 1.5e-14 2.0e-09 -       -       -       -       -
## tor < 2e-16 < 2e-16 < 2e-16 -       -       -       -
## tru < 2e-16 < 2e-16 < 2e-16 1.0000  -       -       -
## gfs < 2e-16 < 2e-16 < 2e-16 0.0032  0.0012  -       -
## pfs < 2e-16 < 2e-16 < 2e-16 1.0000  1.0000  1.0000  -
## ran < 2e-16 < 2e-16 < 2e-16 1.6e-08 1.1e-08 5.8e-05 2.2e-14
##
## P value adjustment method: bonferroni
```

5.5 Performance over time

Best performance in a population over time. Data points on the graph is the average performance across 50 replicates every 2000 generations. Shading comes

from the best and worse performance across 50 replicates.

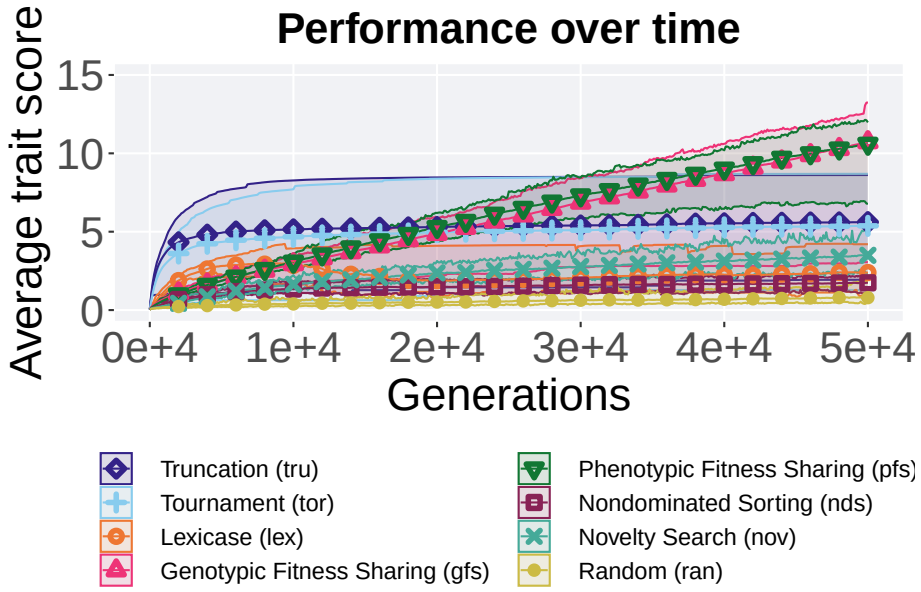
```
lines = over_time_df %>%
  group_by(scheme, gen) %>%
  dplyr::summarise(
    min = min(pop_fit_max) / DIMENSIONALITY,
    mean = mean(pop_fit_max) / DIMENSIONALITY,
    max = max(pop_fit_max) / DIMENSIONALITY
  )
```

```
## `summarise()` has grouped output by 'scheme'. You can override using the
## `.groups` argument.
```

```
over_time_plot = ggplot(lines, aes(x=gen, y=mean, group = scheme, fill = scheme, color
  geom_ribbon(aes(ymin = min, ymax = max), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = filter(lines, gen %% 2000 == 0 & gen != 0), size = 1.5, stroke = 2
  scale_y_continuous(
    name="Average trait score",
    limits=c(0, 15),
  ) +
  scale_x_continuous(
    name="Generations",
    limits=c(0, 50000),
    breaks=c(0, 10000, 20000, 30000, 40000, 50000),
    labels=c("0e+4", "1e+4", "2e+4", "3e+4", "4e+4", "5e+4")

  ) +
  scale_shape_manual(values=SHAPE)+
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  ggtitle('Performance over time')+
  p_theme + theme(legend.title=element_blank(),legend.text=element_text(size=12)) +
  guides(
    shape=guide_legend(ncol=2, title.position = "bottom"),
    color=guide_legend(ncol=2, title.position = "bottom"),
    fill=guide_legend(ncol=2, title.position = "bottom")
  )

over_time_plot
```



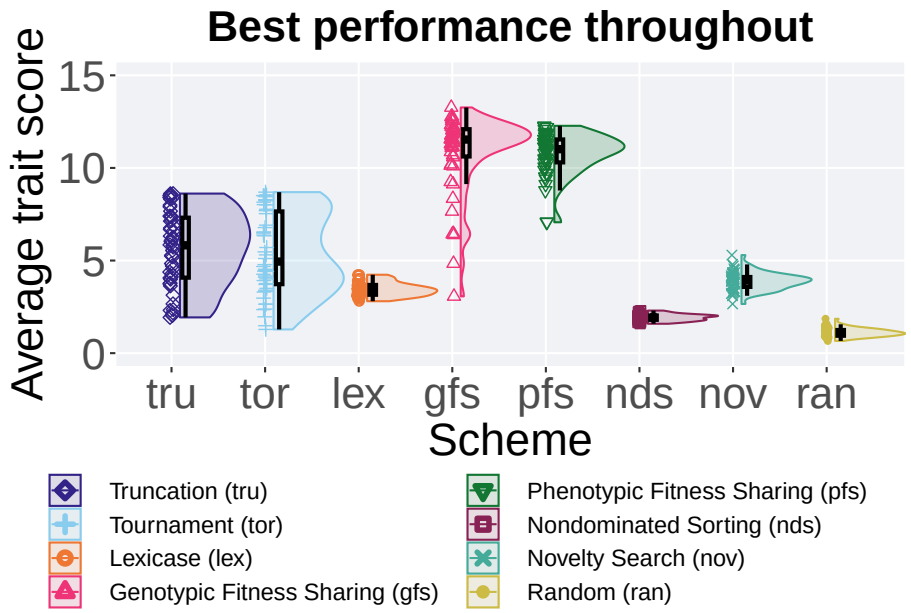
5.6 Best performance throughout

Best performance reached throughout 50,000 generations in a population.

```
plot = filter(best_df, var == 'pop_fit_max') %>%
  ggplot(., aes(x = acro, y = val / DIMENSIONALITY, color = acro, fill = acro, shape = acro)) +
  geom_flat_violin(position = position_nudge(x = .09, y = 0), scale = 'width', alpha = 0.2, width
  geom_boxplot(color = 'black', width = .07, outlier.shape = NA, alpha = 0.0, size = 1.0, positio
  geom_point(position = position_jitter(width = .02), size = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Average trait score",
    limits=c(0, 15),
  ) +
  scale_x_discrete(
    name="Scheme"
  )+
  scale_shape_manual(values=SHAPE)+
  scale_colour_manual(values = cb_palette, ) +
  scale_fill_manual(values = cb_palette) +
  ggtitle('Best performance throughout')+
  p_theme + theme(legend.title=element_blank())

plot_grid(
  plot +
```

```
    theme(legend.position="none"),
  legend,
  nrow=2,
  rel_heights = c(3,1)
)
```



5.6.1 Stats

Summary statistics for the best performance.

```
performance = filter(best_df, var == 'pop_fit_max')
performance$acro = factor(performance$acro, levels = c('gfs','pfs','tru','tor','nov','l
performance %>%
  group_by(acro) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(val)),
    min = min(val / DIMENSIONALITY, na.rm = TRUE),
    median = median(val / DIMENSIONALITY, na.rm = TRUE),
    mean = mean(val / DIMENSIONALITY, na.rm = TRUE),
    max = max(val / DIMENSIONALITY, na.rm = TRUE),
    IQR = IQR(val / DIMENSIONALITY, na.rm = TRUE)
  )
```

```
## # A tibble: 8 x 8
```

```
##   acro  count na_cnt   min median  mean   max   IQR
##   <fct> <int>  <int> <dbl>  <dbl> <dbl> <dbl> <dbl>
## 1 gfs      50      0 3.07   11.5  10.8  13.3  1.48
## 2 pfs      50      0 7.07   11.0  10.8  12.3  1.24
## 3 tru      50      0 1.93    5.82  5.61  8.62 3.24
## 4 tor      50      0 1.28    4.94  5.37  8.69 3.93
## 5 nov      50      0 2.66    3.92  3.88  5.29 0.536
## 6 lex      50      0 2.80    3.41  3.45  4.23 0.531
## 7 nds      50      0 1.59    1.95  1.92  2.30 0.235
## 8 ran      50      0 0.659   1.08  1.11  1.86 0.311
```

Kruskal–Wallis test illustrates evidence of statistical differences.

```
kruskal.test(val ~ acro, data = performance)
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  val by acro
## Kruskal-Wallis chi-squared = 341.54, df = 7, p-value < 2.2e-16
```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction.

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

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  performance$val and performance$acro
##
##     gfs     pfs     tru     tor     nov     lex     nds
## pfs 0.3635  -       -       -       -       -       -
## tru 4.1e-13 5.9e-16 -       -       -       -       -
## tor 3.2e-13 5.2e-16 1.0000  -       -       -       -
## nov 1.9e-15 < 2e-16 3.2e-05 0.0055  -       -       -
## lex 1.1e-15 < 2e-16 3.1e-07 1.6e-05 6.3e-05 -       -
## nds < 2e-16 < 2e-16 2.5e-15 1.2e-13 < 2e-16 < 2e-16 -
## ran < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 3.5e-16
##
## P value adjustment method: bonferroni
```