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.

```r
# 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
```

```r
library(PupillometryR)
```

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

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

# data diractory for local testing
# DATA_DIR = '~/Desktop/Repositories/ECJ-2023-Suite-Of-Diagnostic-Metrics-For-Characterizing-Selection-

# graph variables
SHAPE = c(5,3,1,2,6,0,4,20,1)
cb_palette <- c('#332288','#88CCEE','#EE7733','#EE3377','#117733','#882255','#44AA99','#CCBB44', '#0000
TSIZE = 26
p_theme <- theme(
  plot.title = element_text( face = "bold", size = 20, hjust=0.5),
  panel.border = element_blank(),
  panel.grid.minor = element_blank(),
  legend.title=element_text(size=18, hjust = 0.5),
  legend.text=element_text(size=10),
  axis.title = element_text(size=18),
  axis.text = element_text(size=16),
  legend.position="bottom",
  panel.background = element_rect(fill = "#f1f2f5",
                                  colour = "white",
                                  linewidth = 0.5, linetype = "solid")
)

# default variables
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)','Ph
```

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 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, stringsA
over_time_df$scheme <- factor(over_time_df$scheme, levels = NAMES)

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

2.2 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.
```

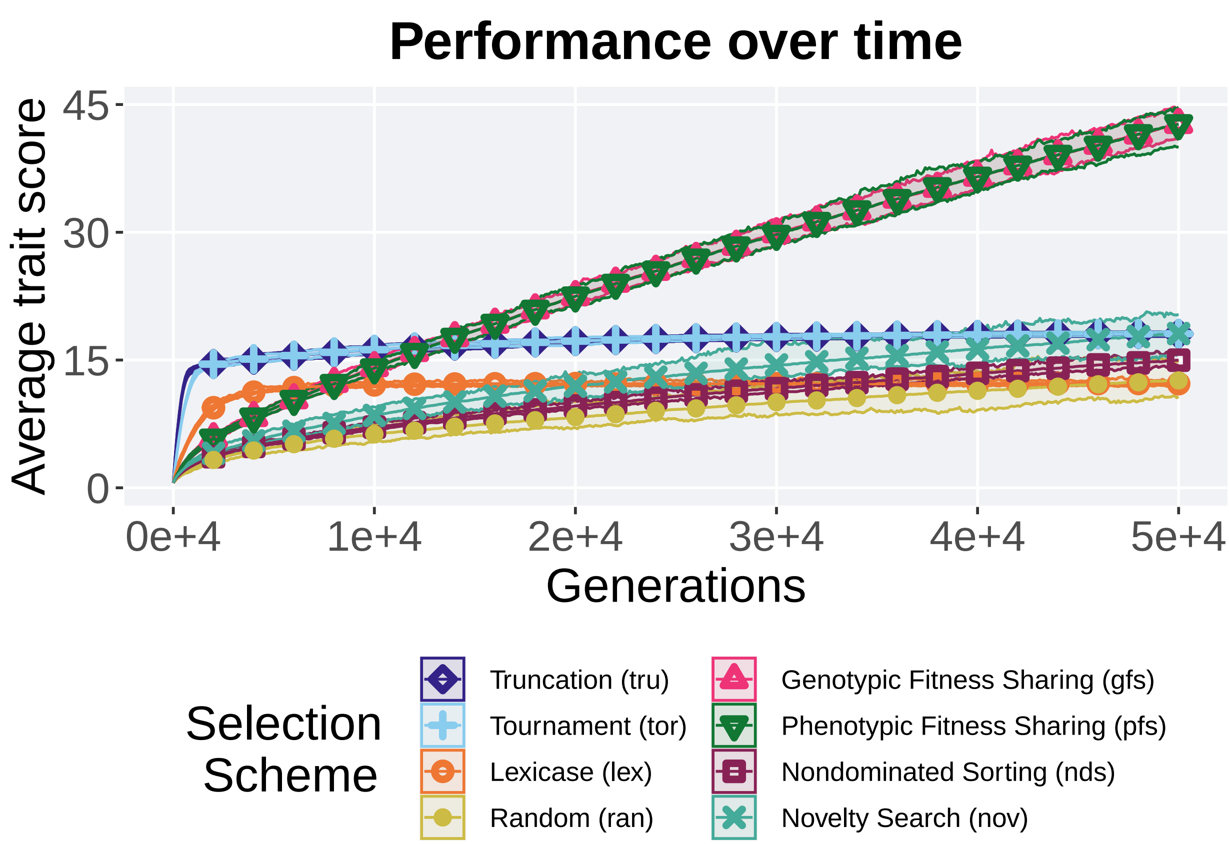
```
lines$scheme <- factor(lines$scheme, levels = c('Truncation (tru)','Tournament (tor)','Lexicase (lex)',

over_time_plot = ggplot(lines, aes(x=gen, y=mean, group = scheme, fill = scheme, color = scheme, shape =
  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 = 1.0) +
  scale_y_continuous(
    name="Average trait score",
    limits=c(0, 45),
```

```
    breaks=seq(0,45, 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=c(5,3,1,20,2,6,0,4))+
  scale_colour_manual(values = c('#332288','#88CCEE','#EE7733','#CCBB44','#EE3377','#117733','#882255',
  scale_fill_manual(values = c('#332288','#88CCEE','#EE7733','#CCBB44','#EE3377','#117733','#882255','#4
  ggtitle('Performance over time')+
  p_theme +
  guides(
    shape=guide_legend(ncol=2, title.position = "left", title = 'Selection \nScheme'),
    color=guide_legend(ncol=2, title.position = "left", title = 'Selection \nScheme'),
    fill=guide_legend(ncol=2, title.position = "left", title = 'Selection \nScheme')
  )

over_time_plot
```



2.3 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 = .1, y = 0), scale = 'width', alpha = 0.2, width = 1.5)
  geom_boxplot(color = 'black', width = .07, outlier.shape = NA, alpha = 0.0, size = 1.0, position = pos
  geom_point(position = position_jitter(width = 0.03, height = 0.02), size = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Average trait score",
    limits=c(0, 45),
    breaks=seq(0,45, 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')+
  p_theme

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

2.3.1 Stats

Summary statistics for the best performance.

```
performance = filter(best_df, var == 'pop_fit_max')
performance$acro = factor(performance$acro, levels = c('gfs','pfs','nov','tru','tor','nds','ran','lex'))
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  41.2   42.9  42.9  44.9 1.05
## 2 pfs      50      0  40.2   43.1  42.9  44.8 1.28
## 3 nov      50      0  16.0   18.6  18.6  20.9 1.07
## 4 tru      50      0  17.8   18.1  18.1  18.3 0.123
## 5 tor      50      0  17.9   18.1  18.1  18.3 0.0974
## 6 nds      50      0  14.7   15.3  15.4  16.1 0.378
## 7 ran      50      0  11.1   13.0  13.1  15.7 1.39
## 8 lex      50      0  12.5   12.7  12.7  13.1 0.128
```

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 = 366.61, 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     nov     tru     tor     nds     ran
## pfs 1.0000  -       -       -       -       -       -
## nov < 2e-16 < 2e-16 -       -       -       -       -
## tru < 2e-16 < 2e-16 0.0014  -       -       -       -
## tor < 2e-16 < 2e-16 0.0026  1.0000  -       -       -
## nds < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 -       -
## ran < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 1.2e-14 -
## lex < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 1.0000
```

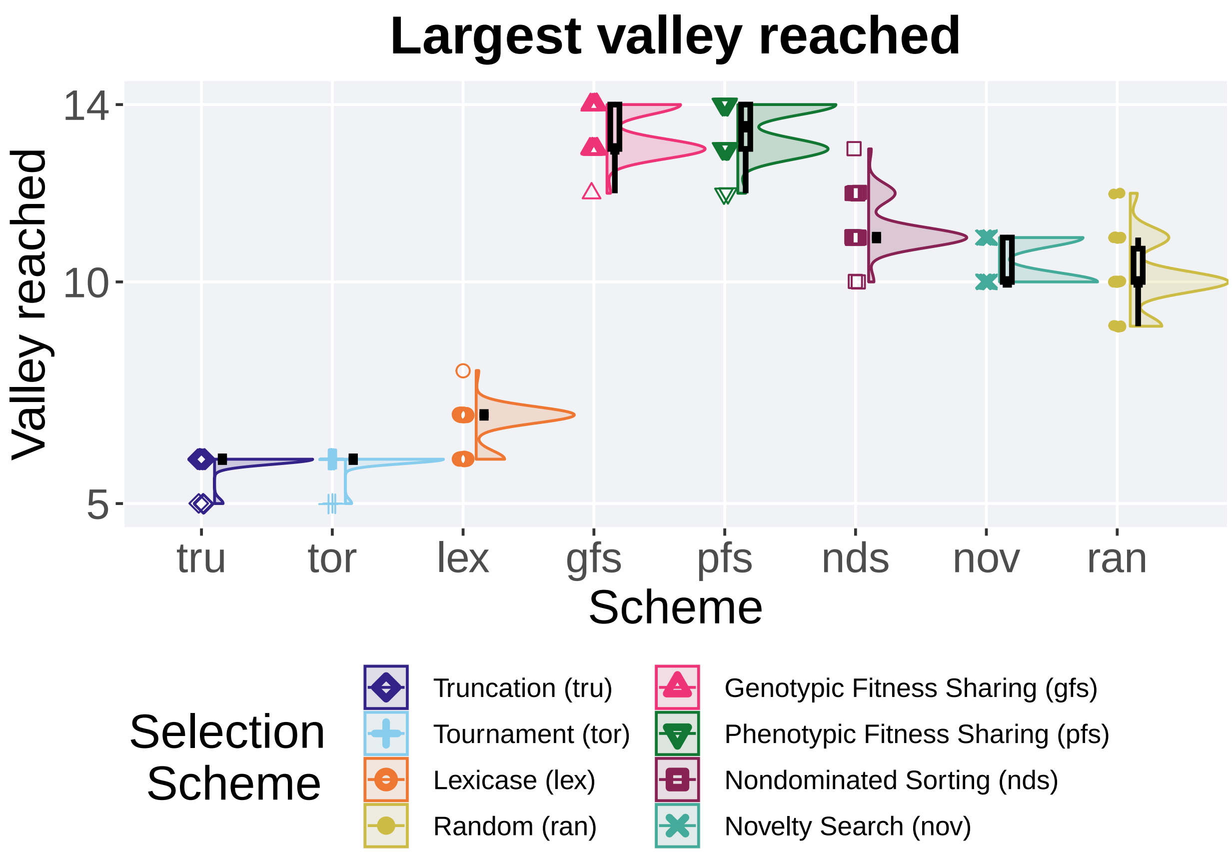
```
##
## P value adjustment method: bonferroni
```

2.4 Largest valley reached throughout

The largest valley reached in a single trait throughout an entire evolutionary run. To collect this value, we look through all the best-performing solutions each generation and find the largest valley reached.

```
plot = filter(best_df, var == 'ele_big_peak') %>%
  ggplot(., aes(x = acro, y = val, color = acro, fill = acro, shape = acro)) +
  geom_flat_violin(position = position_nudge(x = .1, y = 0), scale = 'width', alpha = 0.2, width = 1.5)
  geom_boxplot(color = 'black', width = .07, outlier.shape = NA, alpha = 0.0, size = 1.0, position = po
  geom_point(position = position_jitter(width = 0.03, height = 0.02), size = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Valley reached",
    limits=c(4.9,14.1),
    breaks=c(5,10,14)
  ) +
  scale_x_discrete(
    name="Scheme"
  )+
  scale_shape_manual(values=SHAPE)+
  scale_colour_manual(values = cb_palette, ) +
  scale_fill_manual(values = cb_palette) +
  ggtitle('Largest valley reached')+
  p_theme

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



2.4.1 Stats

Summary statistics for the largest valley crossed.

```
valleys = filter(best_df, var == 'ele_big_peak')
valleys$acro = factor(valleys$acro, levels = c('gfs','pfs','nds','nov','ran','lex','tru','tor'))
valleys %>%
  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 gfs      50      0    12   13    13.4    14  1
## 2 pfs      50      0    12   13.5  13.5    14  1
## 3 nds      50      0    10   11    11.2    13  0
## 4 nov      50      0    10   10    10.5    11  1
## 5 ran      50      0     9   10    10.1    12  0.75
## 6 lex      50      0     6    7     6.8     8  0
```

```
## 7 tru      50      0     5    6    5.92     6  0
## 8 tor      50      0     5    6    5.94     6  0
```

Kruskal–Wallis test illustrates evidence of statistical differences.

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

```
##
##  Kruskal-Wallis rank sum test
##
## data:  val by acro
## Kruskal-Wallis chi-squared = 377.23, df = 7, p-value < 2.2e-16
```

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

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

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  valleys$val and valleys$acro
##
##     gfs     pfs     nds     nov     ran     lex     tru
## pfs 1.000   -       -       -       -       -       -
## nds < 2e-16 < 2e-16 -       -       -       -       -
## nov < 2e-16 < 2e-16 3.9e-08 -       -       -       -
## ran < 2e-16 < 2e-16 2.1e-10 0.099   -       -       -
## lex < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 -       -
## tru < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 4.6e-14 -
## tor < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 4.3e-14 1.000
##
## P value adjustment method: bonferroni
```

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 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, stringsAs
over_time_df$scheme <- factor(over_time_df$scheme, levels = NAMES)

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

3.2 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.
```

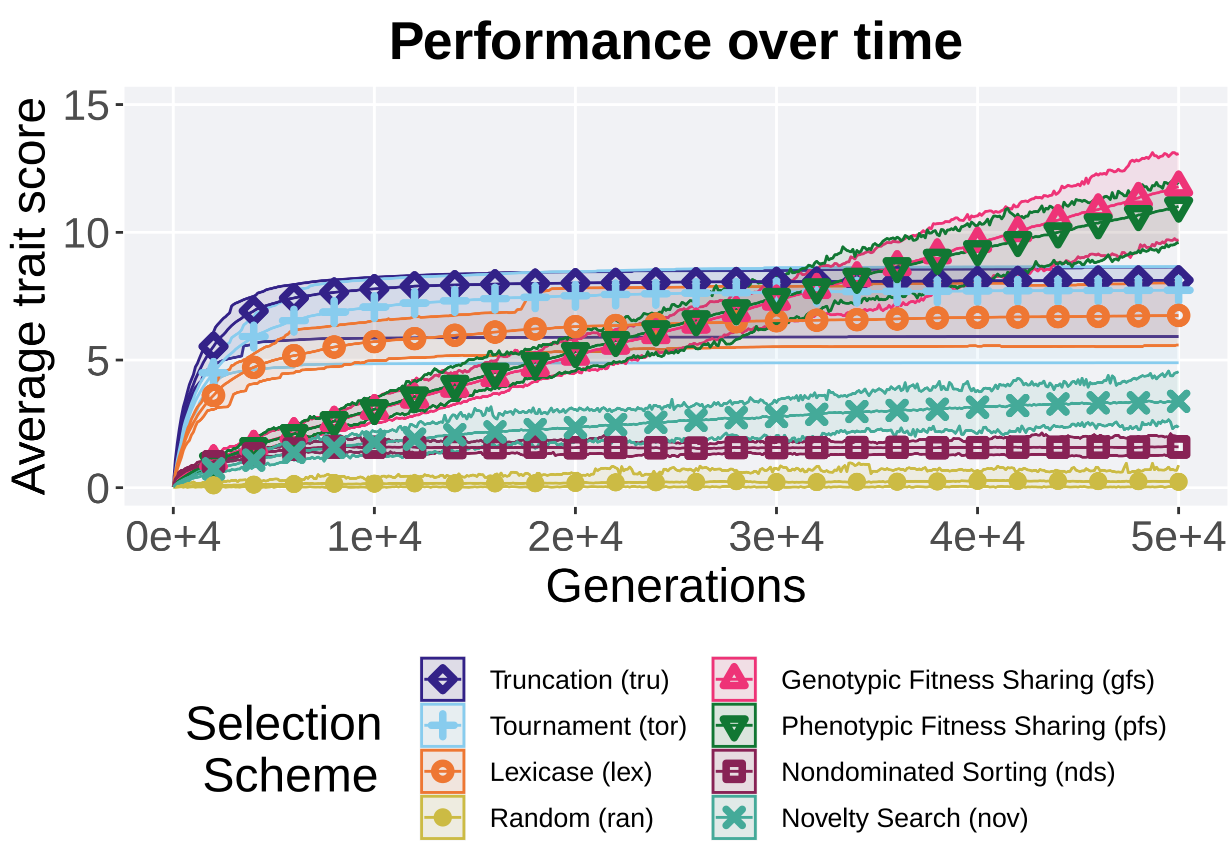
```
lines$scheme <- factor(lines$scheme, levels = c('Truncation (tru)','Tournament (tor)','Lexicase (lex)',

over_time_plot = ggplot(lines, aes(x=gen, y=mean, group = scheme, fill = scheme, color = scheme, shape =
  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 = 1.0) +
  scale_y_continuous(
    name="Average trait score",
    limits=c(0, 15),
```

```
    breaks=c(0,5,10,15)
  ) +
  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=c(5,3,1,20,2,6,0,4))+
  scale_colour_manual(values = c('#332288','#88CCEE','#EE7733','#CCBB44','#EE3377','#117733','#882255',
  scale_fill_manual(values = c('#332288','#88CCEE','#EE7733','#CCBB44','#EE3377','#117733','#882255','#4
  ggtitle('Performance over time')+
  p_theme +
  guides(
    shape=guide_legend(ncol=2, title.position = "left", title = 'Selection \nScheme'),
    color=guide_legend(ncol=2, title.position = "left", title = 'Selection \nScheme'),
    fill=guide_legend(ncol=2, title.position = "left", title = 'Selection \nScheme')
  )

over_time_plot
```

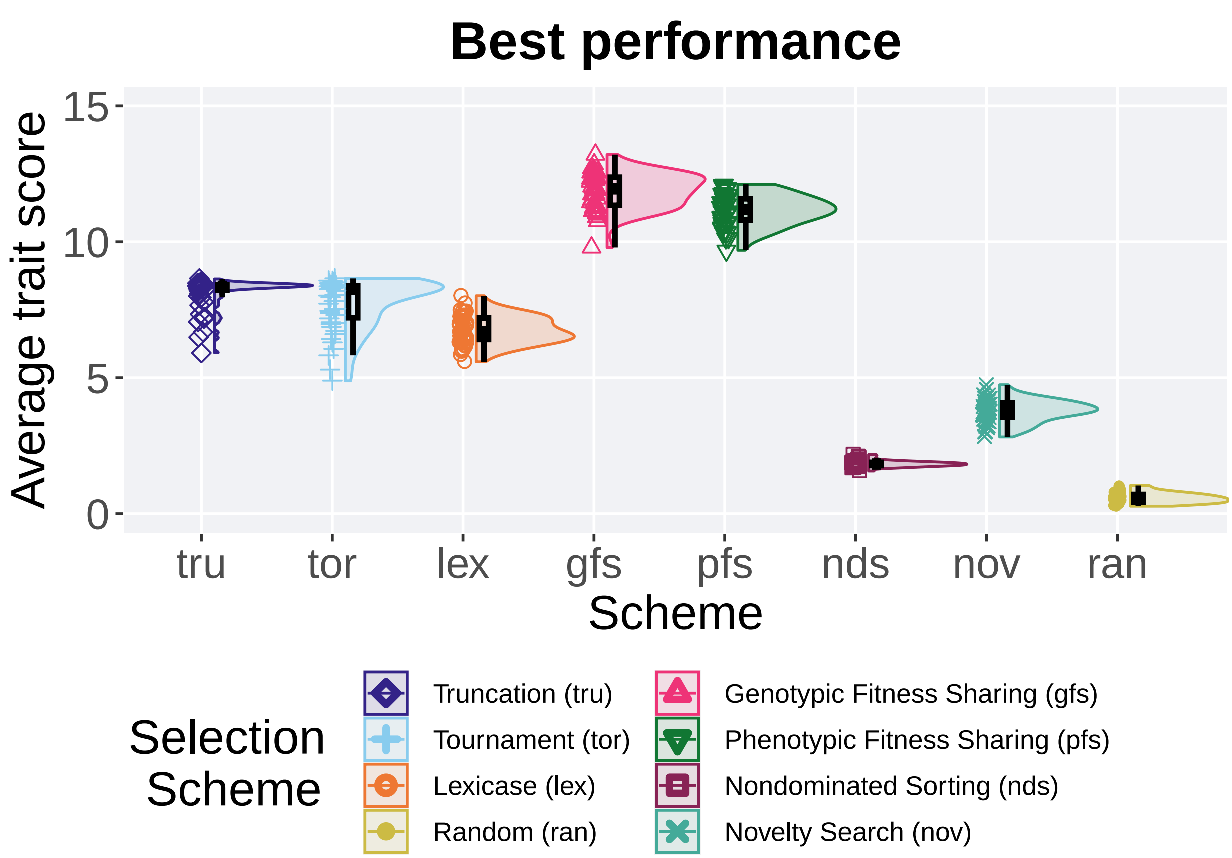


3.3 Best performance throughout

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 = .1, y = 0), scale = 'width', alpha = 0.2, width = 1.5)
  geom_boxplot(color = 'black', width = .07, outlier.shape = NA, alpha = 0.0, size = 1.0, position = pos
  geom_point(position = position_jitter(width = 0.03, height = 0.02), size = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Average trait score",
    limits=c(0, 15),
    breaks=c(0,5,10,15)
  ) +
  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')+
  p_theme

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



3.3.1 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','nov','nds','ran'))
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 9.79  11.9   11.9   13.2  1.03 
## 2 pfs      50      0 9.69  11.2   11.2   12.1  0.779
## 3 tru      50      0 5.92   8.36   8.13   8.63 0.203
## 4 tor      50      0 4.89   8.26   7.73   8.65 1.17 
## 5 lex      50      0 5.59   6.70   6.76   8.02 0.792
## 6 nov      50      0 2.82   3.82   3.79   4.74 0.515
## 7 nds      50      0 1.57   1.83   1.84   2.18 0.116
## 8 ran      50      0 0.279  0.568  0.587  1.04 0.280
```

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 = 379.83, 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 5.0e-06 -       -       -       -       -       -      
## tru < 2e-16 < 2e-16 -       -       -       -       -      
## tor < 2e-16 < 2e-16 0.33    -       -       -       -      
## lex < 2e-16 < 2e-16 7.8e-13 2.8e-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
```

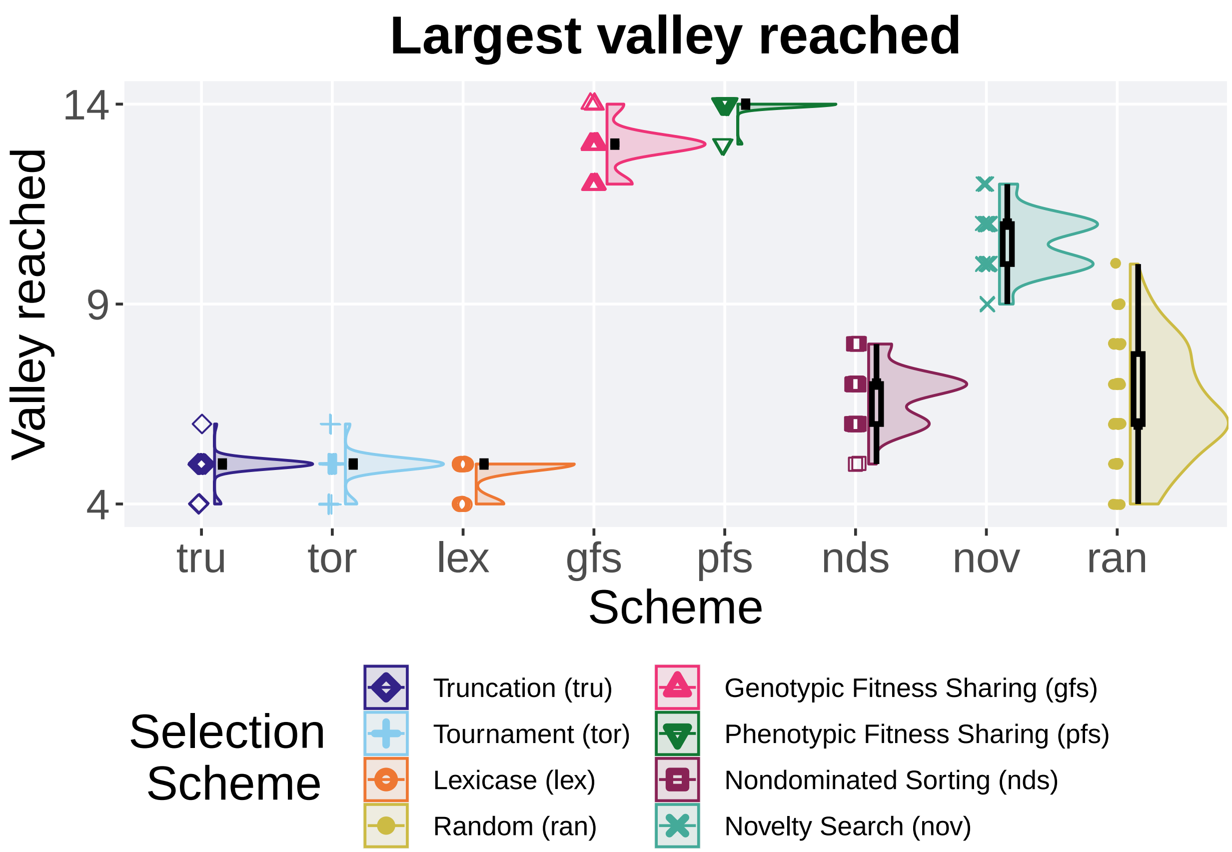
```
##
## P value adjustment method: bonferroni
```

3.4 Largest valley reached throughout

The largest valley reached in a single trait throughout an entire evolutionary run. To collect this value, we look through all the best-performing solutions each generation and find the largest valley reached.

```
plot = filter(best_df, var == 'ele_big_peak') %>%
  ggplot(., aes(x = acro, y = val, color = acro, fill = acro, shape = acro)) +
  geom_flat_violin(position = position_nudge(x = .1, y = 0), scale = 'width', alpha = 0.2, width = 1.5)
  geom_boxplot(color = 'black', width = .07, outlier.shape = NA, alpha = 0.0, size = 1.0, position = po
  geom_point(position = position_jitter(width = 0.03, height = 0.02), size = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Valley reached",
    limits=c(3.9,14.1),
    breaks=c(4,9,14)
  ) +
  scale_x_discrete(
    name="Scheme"
  )+
  scale_shape_manual(values=SHAPE)+
  scale_colour_manual(values = cb_palette, ) +
  scale_fill_manual(values = cb_palette) +
  ggtitle('Largest valley reached')+
  p_theme

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



3.4.1 Stats

Summary statistics for the largest valley crossed.

```
valleys = filter(best_df, var == 'ele_big_peak')
valleys$acro = factor(valleys$acro, levels = c('pfs','gfs','nov','nds','ran','tru','tor','lex'))
valleys %>%
  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    13     14 14.0     14  0
## 2 gfs      50      0    12     13 12.9     14  0
## 3 nov      50      0     9     11 10.5     12  1
## 4 nds      50      0     5      7  6.72     8  1
## 5 ran      50      0     4      6  6.48    10  1.75
## 6 tru      50      0     4      5  4.96     6  0
```

```
## 7 tor      50      0     4      5  4.94     6  0
## 8 lex      50      0     4      5  4.78     5  0
```

Kruskal–Wallis test illustrates evidence of statistical differences.

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

```
##
##  Kruskal-Wallis rank sum test
##
## data:  val by acro
## Kruskal-Wallis chi-squared = 364.41, df = 7, p-value < 2.2e-16
```

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

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

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  valleys$val and valleys$acro
##
##     pfs     gfs     nov     nds     ran     tru  tor
## gfs 3.3e-15 -       -       -       -       -    -
## nov < 2e-16 < 2e-16 -       -       -       -    -
## nds < 2e-16 < 2e-16 < 2e-16 -       -       -    -
## ran < 2e-16 < 2e-16 < 2e-16 1.00    -       -    -
## tru < 2e-16 < 2e-16 < 2e-16 < 2e-16 1.6e-09 -    -
## tor < 2e-16 < 2e-16 < 2e-16 < 2e-16 2.8e-09 1.00 -
## lex < 2e-16 < 2e-16 < 2e-16 < 2e-16 2.9e-10 0.21 0.72
##
## P value adjustment method: bonferroni
```

Chapter 4

Contradictory objectives results

Here we present the results for **activation gene coverage** and **satisfactory 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 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, stringsAs
over_time_df$uni_str_pos = over_time_df$uni_str_pos + over_time_df$arc_acti_gene - over_time_df$overlap
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, stringsAsFactors =
best_df$acro <- factor(best_df$acro, levels = ACRO)
```

4.2 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.
```

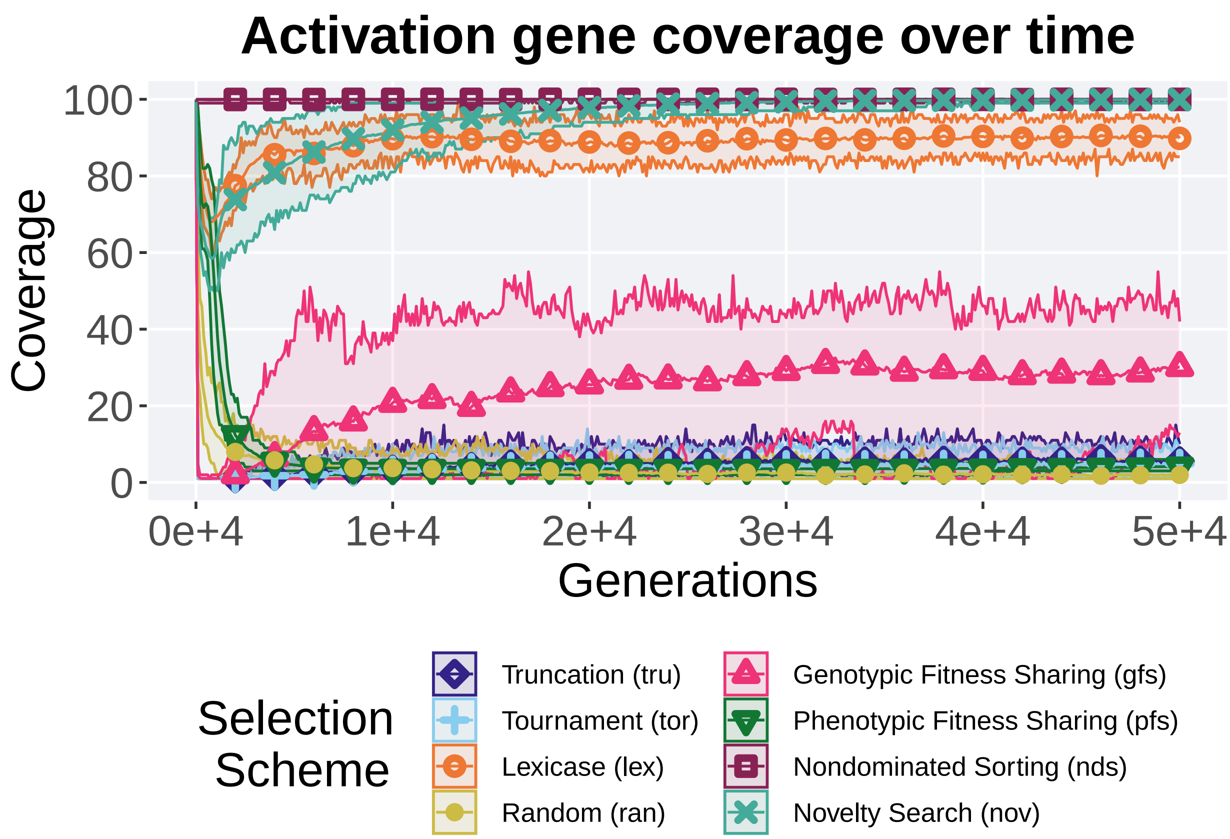
```
lines$scheme <- factor(lines$scheme, levels = c('Truncation (tru)','Tournament (tor)','Lexicase (lex)',

over_time_plot = ggplot(lines, aes(x=gen, y=mean, group = scheme, fill = scheme, color = scheme, shape =
  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 = 1.0) +
  scale_y_continuous(
    name="Coverage",
    limits=c(0, 100.1),
    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=c(5,3,1,20,2,6,0,4))+
  scale_colour_manual(values = c('#332288','#88CCEE','#EE7733','#CCBB44','#EE3377','#117733','#882255',
  scale_fill_manual(values = c('#332288','#88CCEE','#EE7733','#CCBB44','#EE3377','#117733','#882255','#
  ggtitle('Activation gene coverage over time')+
  p_theme +
  guides(
    shape=guide_legend(ncol=2, title.position = "left", title = 'Selection \nScheme'),
    color=guide_legend(ncol=2, title.position = "left", title = 'Selection \nScheme'),
    fill=guide_legend(ncol=2, title.position = "left", title = 'Selection \nScheme')
  )

over_time_plot
```



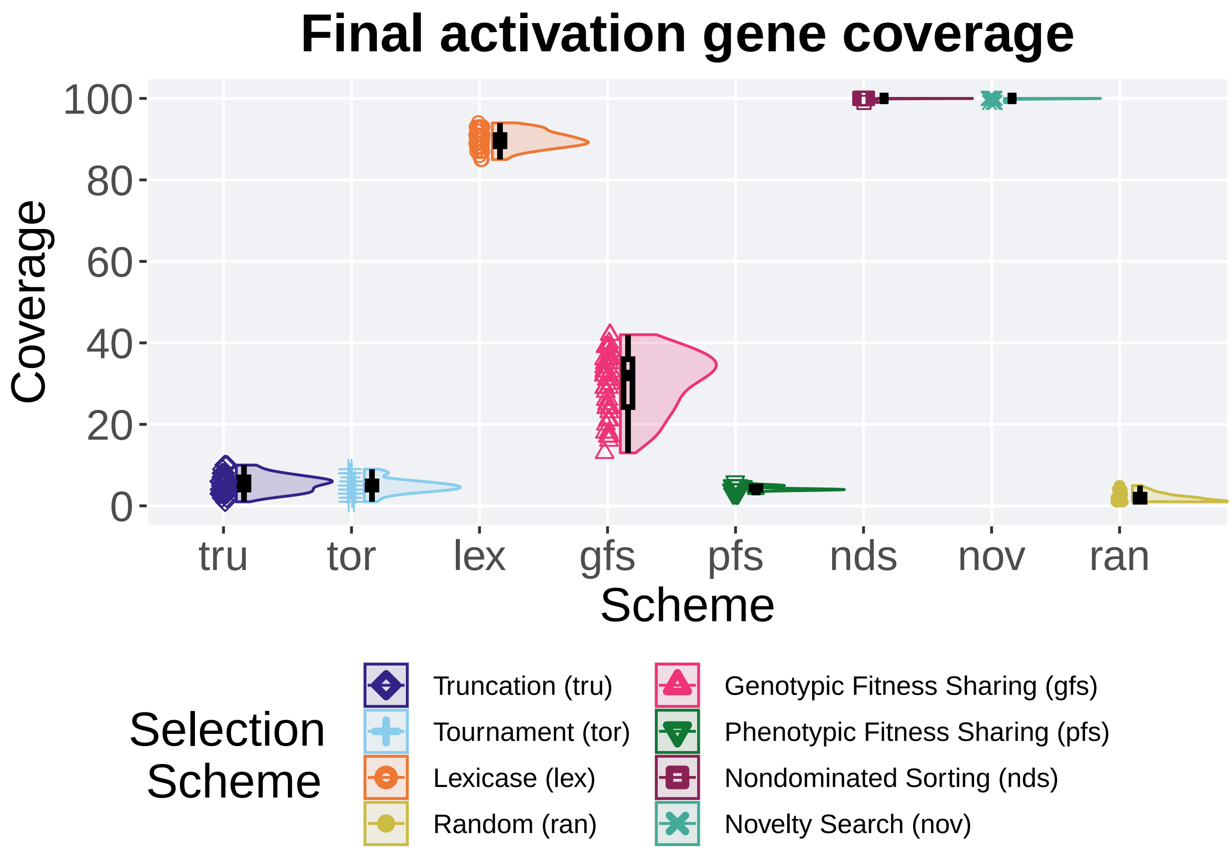
4.3 Final activation gene coverage

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 = .1, y = 0), scale = 'width', alpha = 0.2, width = 1.5)
  geom_boxplot(color = 'black', width = .07, outlier.shape = NA, alpha = 0.0, size = 1.0, position = pos
  geom_point(position = position_jitter(width = 0.03, height = 0.02), size = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Coverage",
    limits=c(0, 100.1),
    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

plot_grid(
```

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



4.3.1 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('nds','nov','lex','gfs','tru','tor','pfs','ran
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 nds      50      0    99    100 100.     100  0
## 2 nov      50      0    99    100  99.9    100  0
## 3 lex      50      0    85     90  89.8     94  2.75
## 4 gfs      50      0    13     32  30.1     42 11.8
## 5 tru      50      0     1      6   5.5     10  3
## 6 tor      50      0     1      5   4.86     9  2
## 7 pfs      50      0     3      4   4.18     6  0.75
## 8 ran      50      0     1      2   1.96     5  1.75
```

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 = 369.27, 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 = "bonferroni
                     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
##
##     nds     nov     lex     gfs     tru     tor     pfs
## nov 1.0000  -       -       -       -       -       -
## lex < 2e-16 < 2e-16 -       -       -       -       -
## gfs < 2e-16 < 2e-16 < 2e-16 -       -       -       -
## tru < 2e-16 < 2e-16 < 2e-16 < 2e-16 -       -       -
## tor < 2e-16 < 2e-16 < 2e-16 < 2e-16 1.0000  -       -
## pfs < 2e-16 < 2e-16 < 2e-16 < 2e-16 0.0095  0.1827  -
## ran < 2e-16 < 2e-16 < 2e-16 < 2e-16 1.7e-12 1.3e-11 5.0e-13
##
## P value adjustment method: bonferroni
```

4.4 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)
  )
```

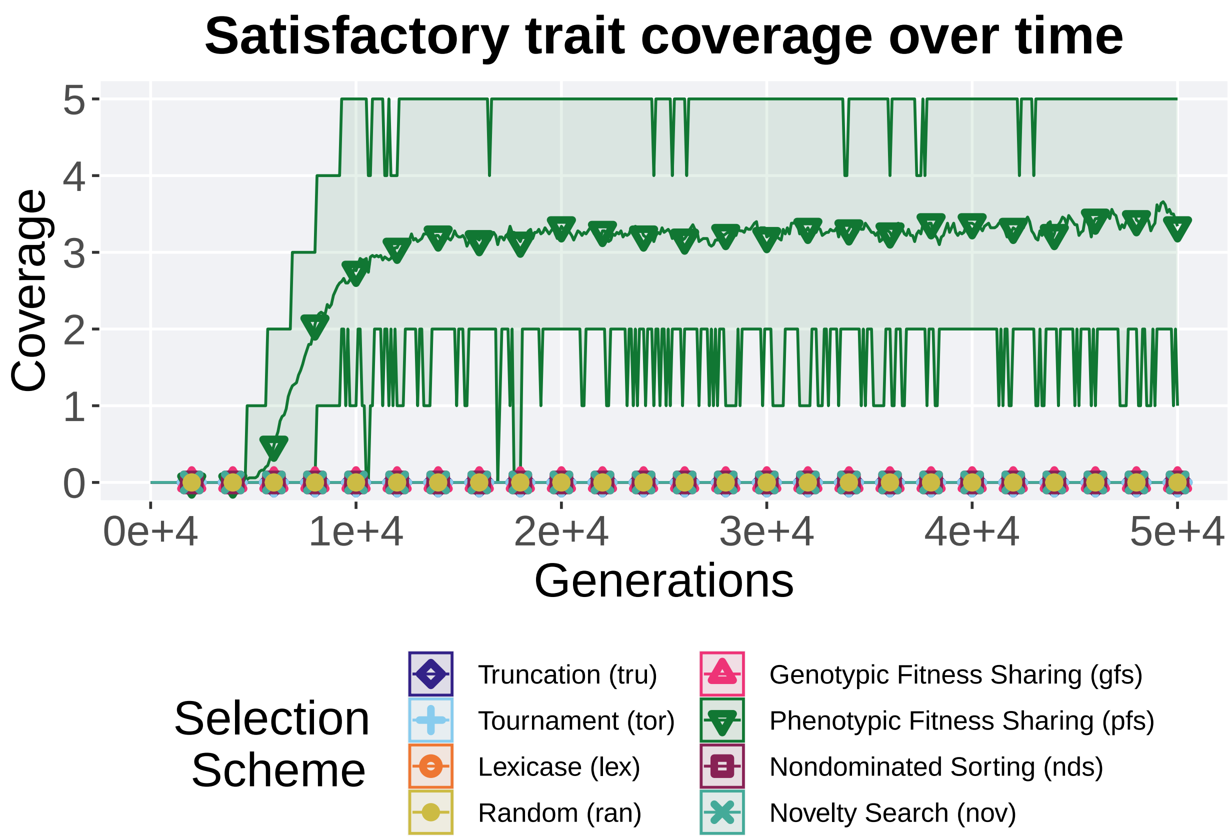
```
## `summarise()` has grouped output by 'scheme'. You can override using the
## `.groups` argument.
```

```
lines$scheme <- factor(lines$scheme, levels = c('Truncation (tru)','Tournament (tor)','Lexicase (lex)',

over_time_plot = ggplot(lines, aes(x=gen, y=mean, group = scheme, fill = scheme, color = scheme, shape =
  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 = 1.0)
  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=c(5,3,1,20,2,6,0,4))+
  scale_colour_manual(values = c('#332288','#88CCEE','#EE7733','#CCBB44','#EE3377','#117733','#882255',
  scale_fill_manual(values = c('#332288','#88CCEE','#EE7733','#CCBB44','#EE3377','#117733','#882255','#
  ggtitle('Satisfactory trait coverage over time')+
  p_theme +
  guides(
    shape=guide_legend(ncol=2, title.position = "left", title = 'Selection \nScheme'),
    color=guide_legend(ncol=2, title.position = "left", title = 'Selection \nScheme'),
    fill=guide_legend(ncol=2, title.position = "left", title = 'Selection \nScheme')
  )

over_time_plot
```



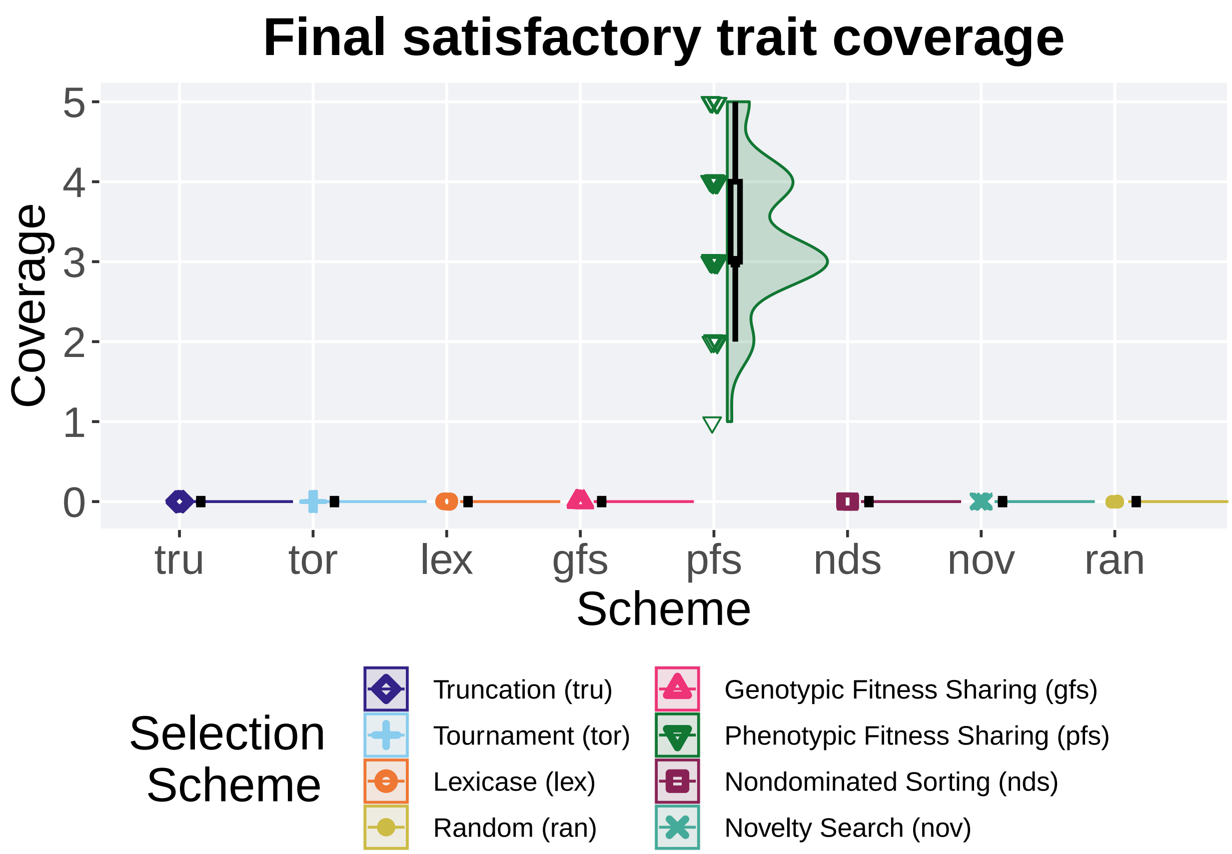
4.5 Final satisfactory trait coverage

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 = .1, y = 0), scale = 'width', alpha = 0.2, width = 1.5)
  geom_boxplot(color = 'black', width = .07, outlier.shape = NA, alpha = 0.0, size = 1.0, position = pos
  geom_point(position = position_jitter(width = 0.03, height = 0.02), size = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Coverage",
    limits=c(-0.1, 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

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

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



4.5.1 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','ran
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     1      3  3.34     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.

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

```
##
##  Kruskal-Wallis rank sum test
##
## data:  pop_uni_obj by acro
## Kruskal-Wallis chi-squared = 396.94, df = 7, p-value < 2.2e-16
```

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

```r
pairwise.wilcox.test(x = act_coverage$pop_uni_obj, g = act_coverage$acro, p.adjust.method = "bonferroni
                     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
```

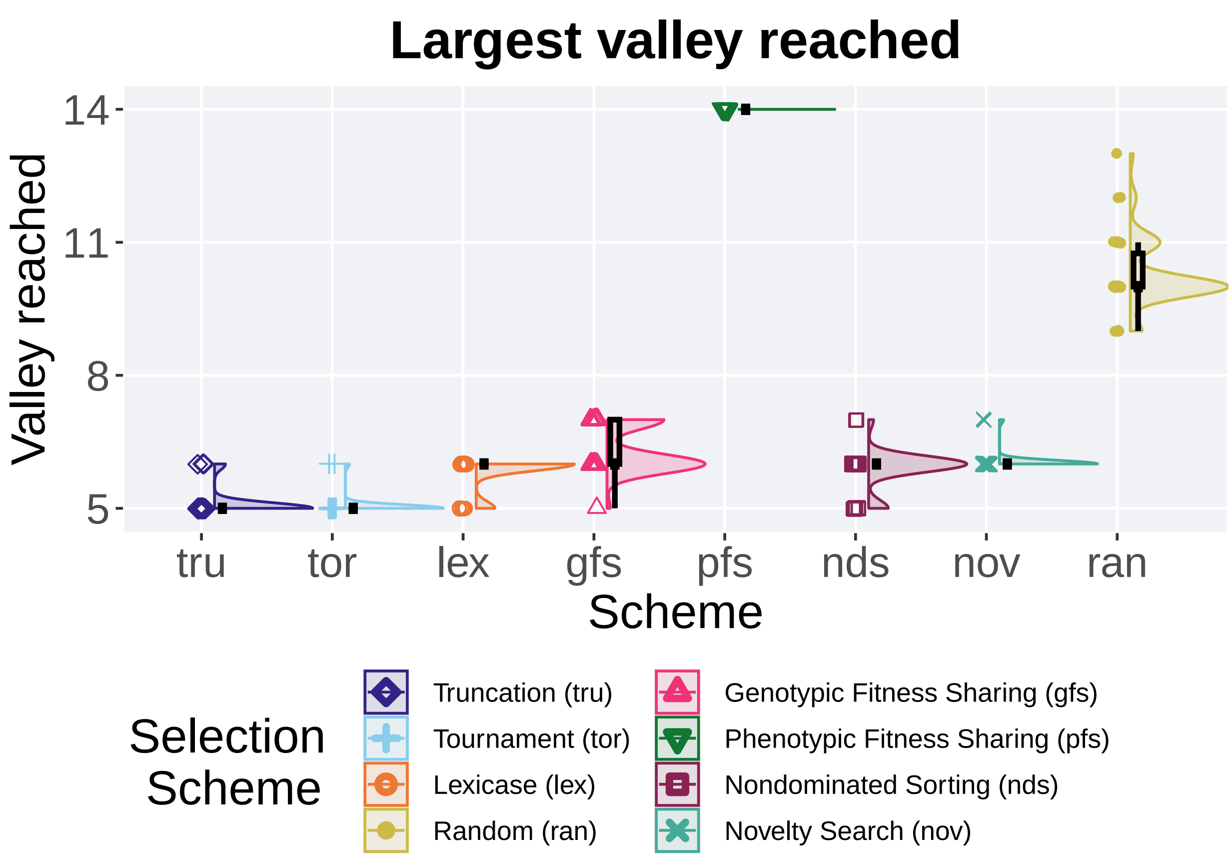
4.6 Largest valley reached throughout

The largest valley reached in a single trait throughout an entire evolutionary run. To collect this value, we look through all the best-performing solutions each generation and find the largest valley reached.

```r
plot = filter(best_df, var == 'ele_big_peak') %>%
  ggplot(., aes(x = acro, y = val, color = acro, fill = acro, shape = acro)) +
  geom_flat_violin(position = position_nudge(x = .1, y = 0), scale = 'width', alpha = 0.2, width = 1.5)
  geom_boxplot(color = 'black', width = .07, outlier.shape = NA, alpha = 0.0, size = 1.0, position = pos
  geom_point(position = position_jitter(width = 0.03, height = 0.02), size = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Valley reached",
    limits=c(4.9,14.1),
    breaks=c(5,8,11,14)
  ) +
  scale_x_discrete(
    name="Scheme"
```

```
  )+
  scale_shape_manual(values=SHAPE)+
  scale_colour_manual(values = cb_palette, ) +
  scale_fill_manual(values = cb_palette) +
  ggtitle('Largest valley reached')+
  p_theme

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



4.6.1 Stats

Summary statistics for the largest valley crossed.

```
valleys = filter(best_df, var == 'ele_big_peak')
valleys$acro = factor(valleys$acro, levels = c('pfs','ran','gfs','nov','nds','lex','tru','tor'))
valleys %>%
  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    14     14 14       14  0
## 2 ran      50      0     9     10 10.3     13  0.75
## 3 gfs      50      0     5      6  6.34     7  1
## 4 nov      50      0     6      6  6.04     7  0
## 5 nds      50      0     5      6  5.88     7  0
## 6 lex      50      0     5      6  5.84     6  0
## 7 tru      50      0     5      5  5.1      6  0
## 8 tor      50      0     5      5  5.04     6  0
```

Kruskal–Wallis test illustrates evidence of statistical differences.

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

```
##
##  Kruskal-Wallis rank sum test
##
## data:  val by acro
## Kruskal-Wallis chi-squared = 352.03, df = 7, p-value < 2.2e-16
```

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

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

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  valleys$val and valleys$acro
##
##     pfs     ran     gfs     nov     nds     lex     tru
## ran < 2e-16 -       -       -       -       -       -
## gfs < 2e-16 < 2e-16 -       -       -       -       -
## nov < 2e-16 < 2e-16 0.00347 -       -       -       -
## nds < 2e-16 < 2e-16 0.00018 0.26915 -       -       -
## lex < 2e-16 < 2e-16 1.3e-05 0.01917 1.00000 -       -
## tru < 2e-16 < 2e-16 < 2e-16 < 2e-16 2.8e-12 2.3e-12 -
## tor < 2e-16 < 2e-16 < 2e-16 < 2e-16 2.2e-14 1.6e-14 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 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, stringsAs
over_time_df$uni_str_pos = over_time_df$uni_str_pos + over_time_df$arc_acti_gene - over_time_df$overlap
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, stringsAsFactors =
best_df$acro <- factor(best_df$acro, levels = ACRO)
```

5.2 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.
```

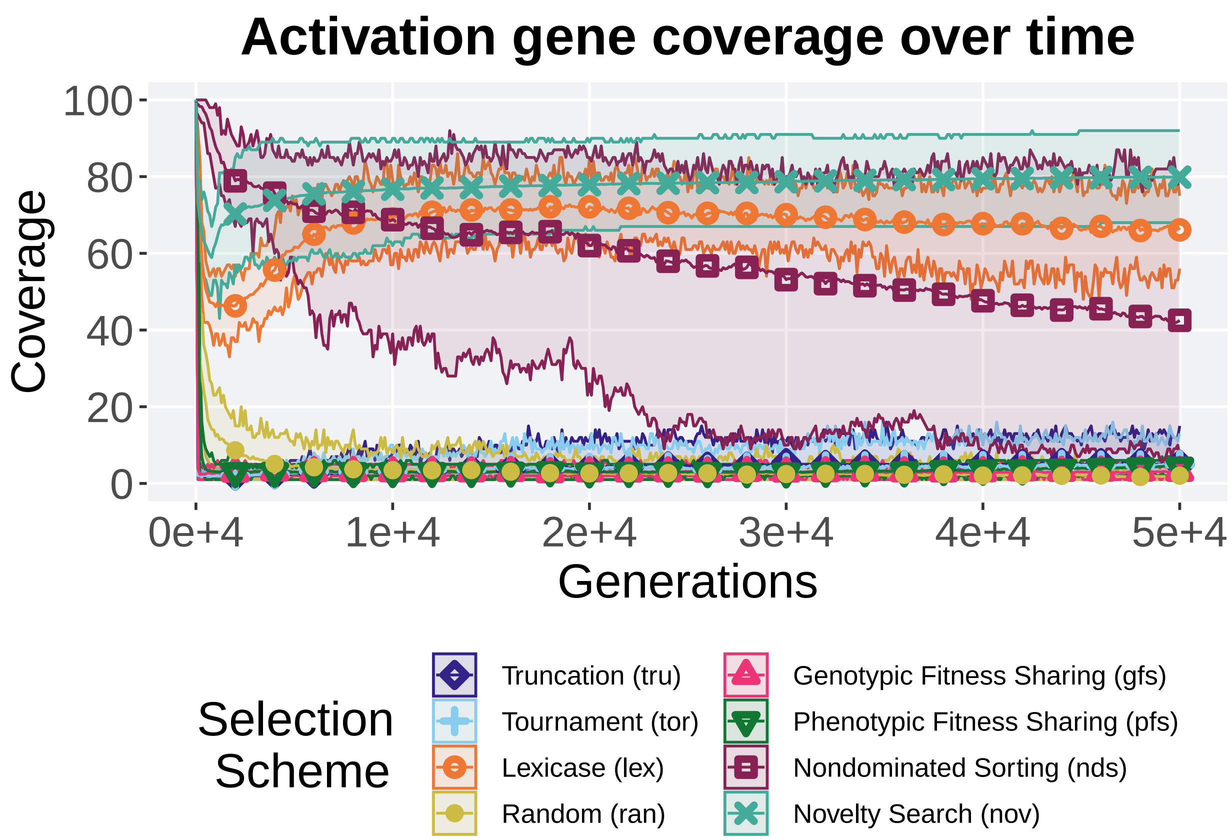
```
lines$scheme <- factor(lines$scheme, levels = c('Truncation (tru)','Tournament (tor)','Lexicase (lex)',

over_time_plot = ggplot(lines, aes(x=gen, y=mean, group = scheme, fill = scheme, color = scheme, shape =
  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 = 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_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=c(5,3,1,20,2,6,0,4))+
  scale_colour_manual(values = c('#332288','#88CCEE','#EE7733','#CCBB44','#EE3377','#117733','#882255',
  scale_fill_manual(values = c('#332288','#88CCEE','#EE7733','#CCBB44','#EE3377','#117733','#882255','#4
  ggtitle('Activation gene coverage over time')+
  p_theme +
  guides(
    shape=guide_legend(ncol=2, title.position = "left", title = 'Selection \nScheme'),
    color=guide_legend(ncol=2, title.position = "left", title = 'Selection \nScheme'),
    fill=guide_legend(ncol=2, title.position = "left", title = 'Selection \nScheme')
  )

over_time_plot
```

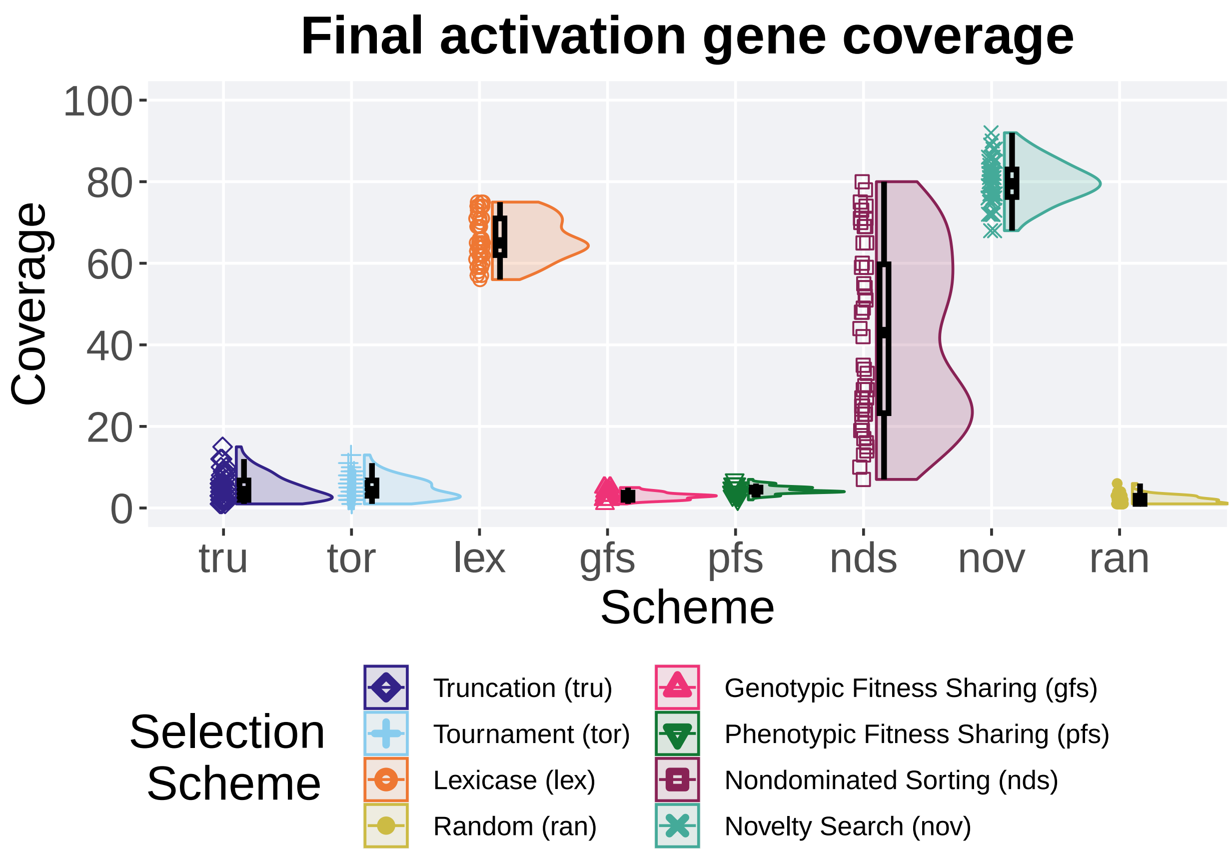


5.3 Final activation gene coverage

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 = .1, y = 0), scale = 'width', alpha = 0.2, width = 1.5)
  geom_boxplot(color = 'black', width = .07, outlier.shape = NA, alpha = 0.0, size = 1.0, position = pos
  geom_point(position = position_jitter(width = 0.03, height = 0.02), 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

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



5.3.1 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','pfs','gfs','ran
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    68   79.5 79.9     92  6.75
## 2 lex      50      0    56   65   66.1     75  9
## 3 nds      50      0     7   43   42.5     80 36.5
## 4 tor      50      0     1    4    4.84    13  3.75
## 5 tru      50      0     1    4    4.9     15  4.75
## 6 pfs      50      0     2    4    4.4      7  1
```

```
## 7 gfs      50      0     1    3    3         5  1.75
## 8 ran      50      0     1    2    2.02      6  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 = 324.89, 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 = "bonferroni
                     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     pfs     gfs
## lex 1.4e-14 -       -       -       -       -       -
## nds 8.1e-15 1.5e-06 -       -       -       -       -
## tor < 2e-16 < 2e-16 < 2e-16 -       -       -       -
## tru < 2e-16 < 2e-16 2.7e-16 1.000   -       -       -
## pfs < 2e-16 < 2e-16 < 2e-16 1.000   1.000   -       -
## gfs < 2e-16 < 2e-16 < 2e-16 0.011   0.157   3.8e-08 -
## ran < 2e-16 < 2e-16 < 2e-16 3.7e-08 2.7e-06 1.3e-13 4.0e-05
##
## P value adjustment method: bonferroni
```

5.4 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.
```

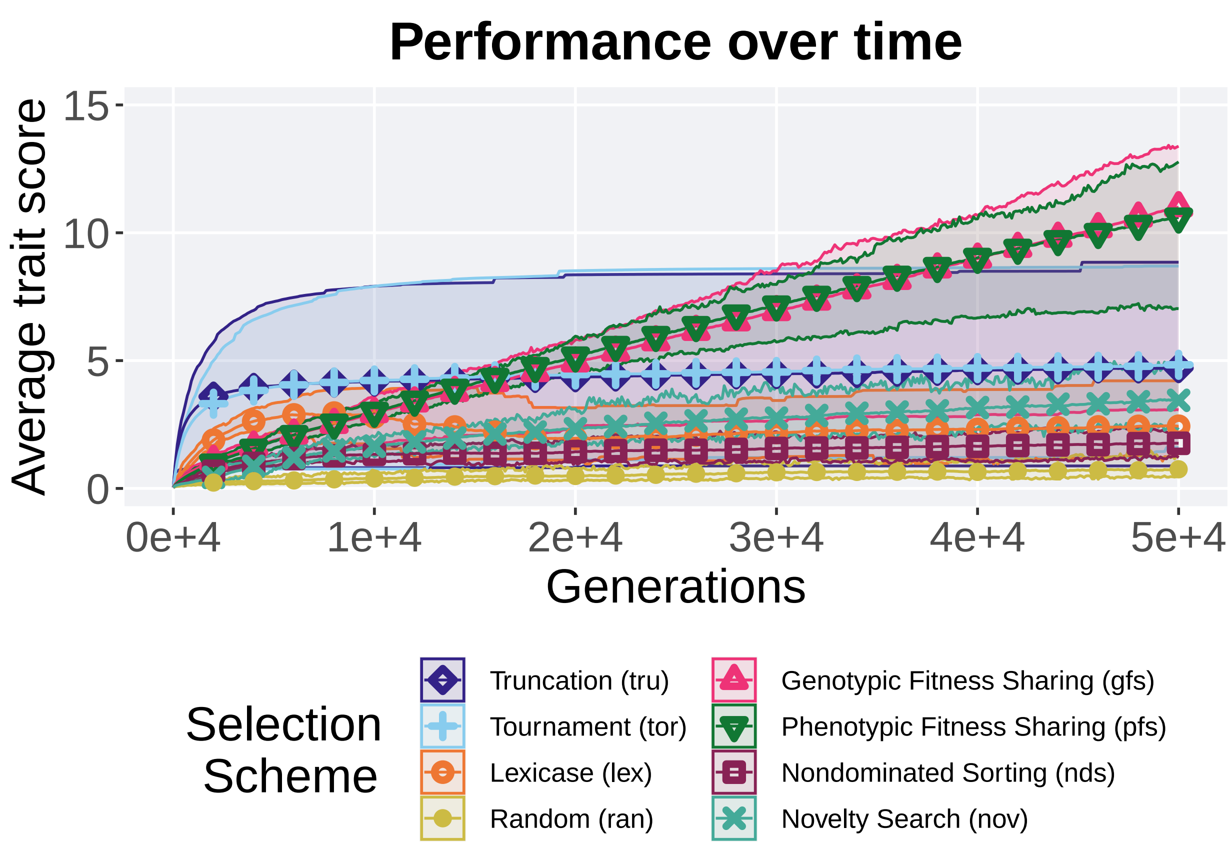
```
lines$scheme <- factor(lines$scheme, levels = c('Truncation (tru)','Tournament (tor)','Lexicase (lex)',

over_time_plot = ggplot(lines, aes(x=gen, y=mean, group = scheme, fill = scheme, color = scheme, shape =
  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 = 1.0) +
  scale_y_continuous(
```

```
    name="Average trait score",
    limits=c(0, 15),
    breaks=c(0,5,10,15)
  ) +
  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=c(5,3,1,20,2,6,0,4))+
  scale_colour_manual(values = c('#332288','#88CCEE','#EE7733','#CCBB44','#EE3377','#117733','#882255',
  scale_fill_manual(values = c('#332288','#88CCEE','#EE7733','#CCBB44','#EE3377','#117733','#882255','#
  ggtitle('Performance over time')+
  p_theme +
  guides(
    shape=guide_legend(ncol=2, title.position = "left", title = 'Selection \nScheme'),
    color=guide_legend(ncol=2, title.position = "left", title = 'Selection \nScheme'),
    fill=guide_legend(ncol=2, title.position = "left", title = 'Selection \nScheme')
  )

over_time_plot
```

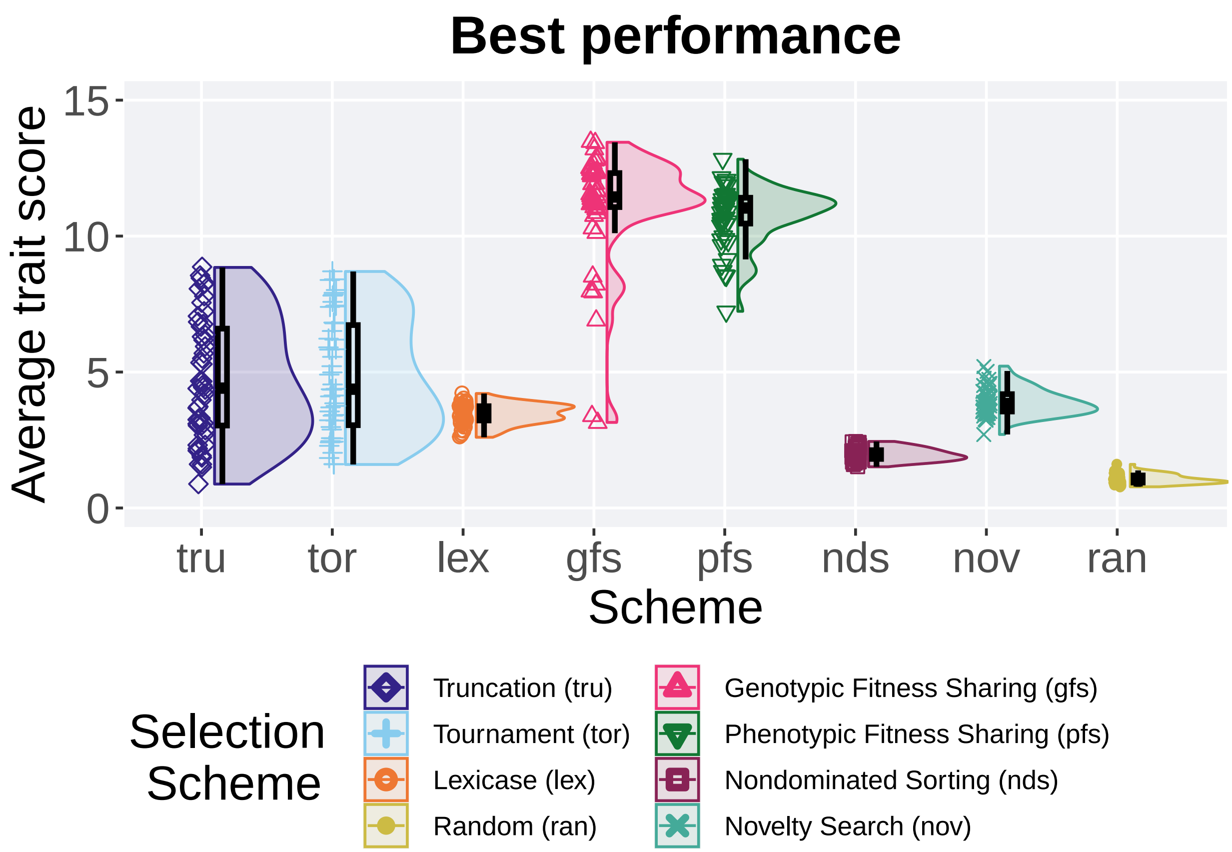


5.5 Best performance throughout

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 = .1, y = 0), scale = 'width', alpha = 0.2, width = 1.5)
  geom_boxplot(color = 'black', width = .07, outlier.shape = NA, alpha = 0.0, size = 1.0, position = pos
  geom_point(position = position_jitter(width = 0.03, height = 0.02), size = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Average trait score",
    limits=c(0, 15),
    breaks=c(0,5,10,15)
  ) +
  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')+
  p_theme

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



5.5.1 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','lex','nds','ran'))
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 3.15   11.4  11.1  13.4  1.25
## 2 pfs      50      0 7.23   11.0  10.8  12.8  0.949
## 3 tru      50      0 0.880   4.41  4.71  8.85 3.56
## 4 tor      50      0 1.60    4.37  4.84  8.70 3.68
## 5 nov      50      0 2.70    3.84  3.89  5.22 0.639
## 6 lex      50      0 2.60    3.44  3.45  4.21 0.523
```

```
## 7 nds      50      0 1.52   1.93   1.97  2.45 0.322
## 8 ran      50      0 0.780  0.998  1.06  1.60 0.261
```

Kruskal–Wallis test illustrates evidence of statistical differences.

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

```
##
##  Kruskal-Wallis rank sum test
##
## data:  val by acro
## Kruskal-Wallis chi-squared = 327.4, df = 7, p-value < 2.2e-16
```

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

```r
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 0.03925 -       -       -       -       -       -
## tru 2.2e-14 < 2e-16 -       -       -       -       -
## tor 2.4e-14 < 2e-16 1.00000 -       -       -       -
## nov 2.1e-14 < 2e-16 1.00000 1.00000 -       -       -
## lex 5.3e-15 < 2e-16 0.23671 0.04294 0.00042 -       -
## nds < 2e-16 < 2e-16 5.5e-10 8.2e-13 < 2e-16 < 2e-16 -
## ran < 2e-16 < 2e-16 1.4e-15 < 2e-16 < 2e-16 < 2e-16 < 2e-16
##
## P value adjustment method: bonferroni
```

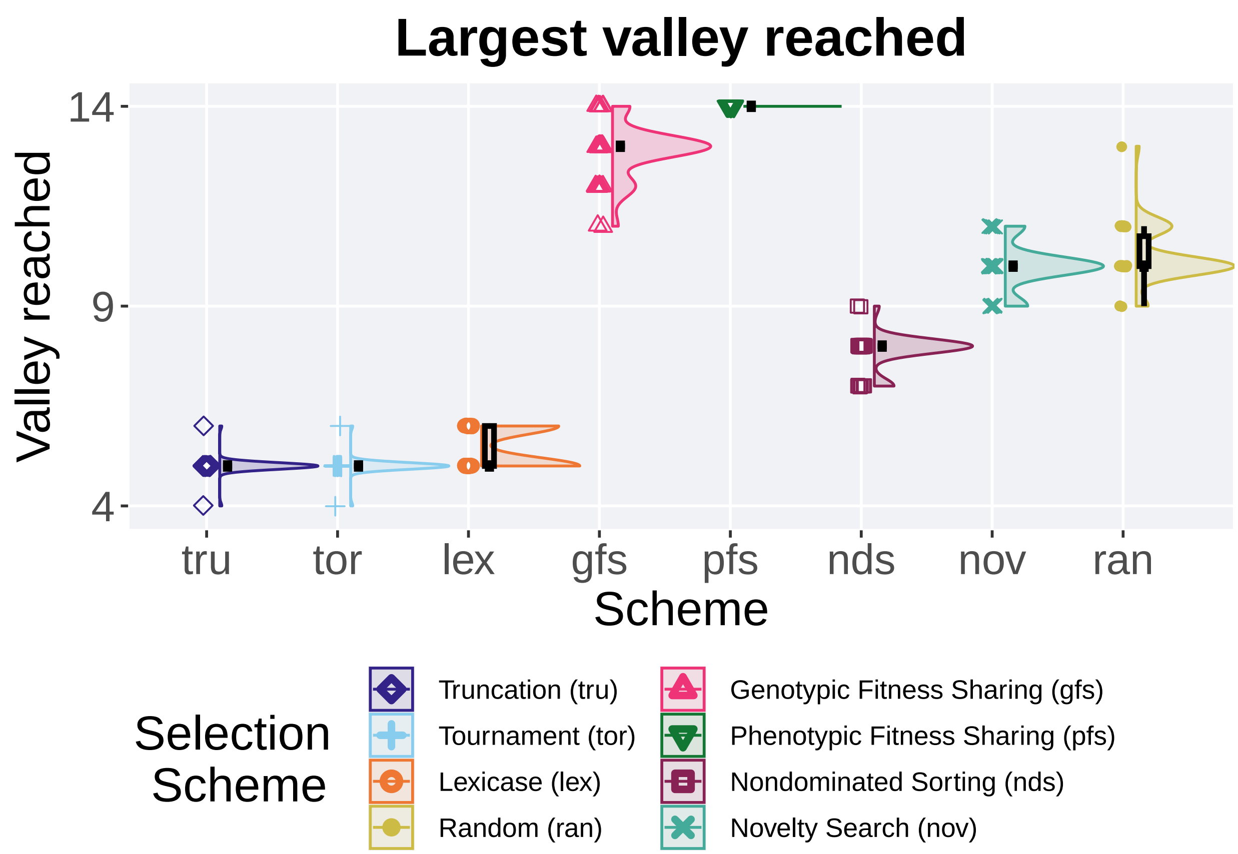
5.6 Largest valley reached throughout

The largest valley reached in a single trait throughout an entire evolutionary run. To collect this value, we look through all the best-performing solutions each generation and find the largest valley reached.

```r
plot = filter(best_df, var == 'ele_big_peak') %>%
  ggplot(., aes(x = acro, y = val, color = acro, fill = acro, shape = acro)) +
  geom_flat_violin(position = position_nudge(x = .1, y = 0), scale = 'width', alpha = 0.2, width = 1.5)
  geom_boxplot(color = 'black', width = .07, outlier.shape = NA, alpha = 0.0, size = 1.0, position = po
  geom_point(position = position_jitter(width = 0.03, height = 0.02), size = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Valley reached",
    limits=c(3.9,14.1),
    breaks=c(4,9,14)
  ) +
  scale_x_discrete(
    name="Scheme"
  )+
  scale_shape_manual(values=SHAPE)+
  scale_colour_manual(values = cb_palette, ) +
  scale_fill_manual(values = cb_palette) +
  ggtitle('Largest valley reached')+
```

```
  p_theme

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



5.6.1 Stats

Summary statistics for the largest valley crossed.

```
valleys = filter(best_df, var == 'ele_big_peak')
valleys$acro = factor(valleys$acro, levels = c('pfs','gfs','ran','nov','nds','lex','tru','tor'))
valleys %>%
  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    14     14 14       14  0
## 2 gfs      50      0    11     13 12.9     14  0
## 3 ran      50      0     9     10 10.2     13  0.75
## 4 nov      50      0     9     10  9.98    11  0
## 5 nds      50      0     7      8  7.88     9  0
## 6 lex      50      0     5      5  5.44     6  1
## 7 tru      50      0     4      5  5        6  0
## 8 tor      50      0     4      5  5        6  0
```

Kruskal–Wallis test illustrates evidence of statistical differences.

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

```
##
##  Kruskal-Wallis rank sum test
##
## data:  val by acro
## Kruskal-Wallis chi-squared = 385.68, df = 7, p-value < 2.2e-16
```

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

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

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  valleys$val and valleys$acro
##
##     pfs     gfs     ran     nov     nds     lex     tru
## gfs < 2e-16 -       -       -       -       -       -
## ran < 2e-16 < 2e-16 -       -       -       -       -
## nov < 2e-16 < 2e-16 1       -       -       -       -
## nds < 2e-16 < 2e-16 < 2e-16 < 2e-16 -       -       -
## lex < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 -       -
## tru < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 7.6e-06 -
## tor < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 7.6e-06 1
##
## P value adjustment method: bonferroni
```