Supplemental Material: Base Diagnostics

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Contents

Chapter 1

Introduction

This is the supplemental material for experiments with basic diagnostics.

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-Sch

# 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',
```

```r
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.
```

```r
# 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
```

Chapter 2

Exploitation rate results

Here we present the results for **best performances** found by each selection scheme on the exploitation rate diagnostic. 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)

sati_df <- read.csv(paste(DIR,'sol-fnd.csv', sep = "", collapse = NULL), header = TRUE, stringsAs
sati_df$acro <- factor(sati_df$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.

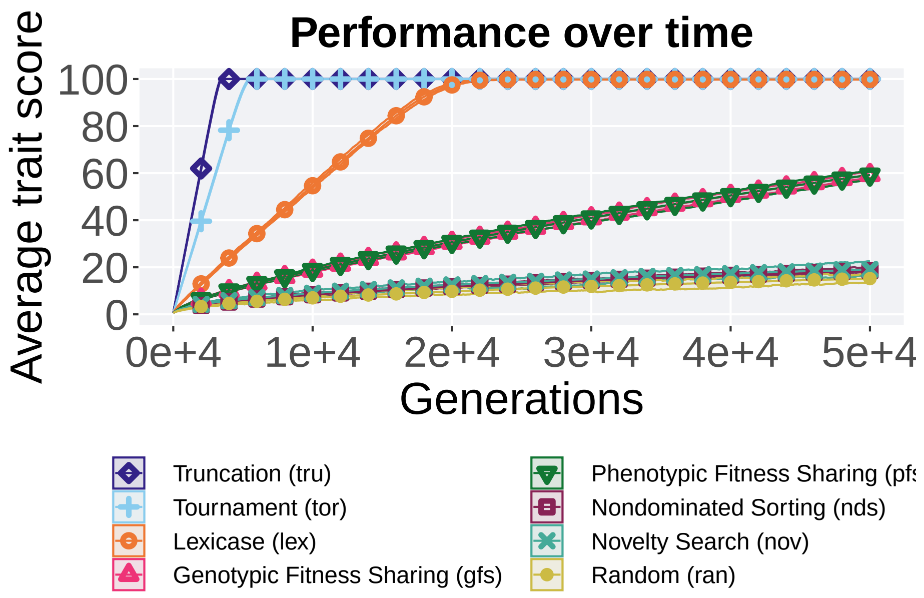
```
lines = over_time_df %>%
  group_by(scheme, gen) %>%
  dplyr::summarise(
    min = min(pop_fit_max) / DIMENSIONALITY,
    mean = mean(pop_fit_max) / DIMENSIONALITY,
    max = max(pop_fit_max) / DIMENSIONALITY
  )
```

```
## `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, 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('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

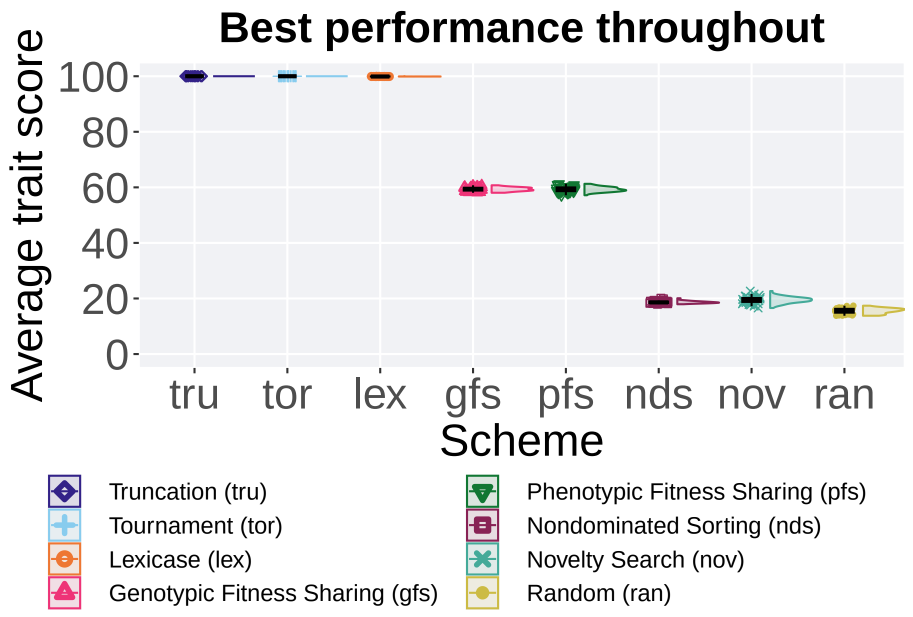
Best performance reached throughout 50,000 generations in a population.

```
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, 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 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.
```

```
## Warning: Removed 47 rows containing missing values (`geom_point()`).
```



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('tru','tor','lex','gfs','pfs','
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 tru      50      0 100    100   100   100   0
## 2 tor      50      0 100    100   100   100   0
## 3 lex      50      0  99.9   99.9  99.9  99.9 0.0137
## 4 gfs      50      0  58.1   59.3  59.3  60.7 1.01
## 5 pfs      50      0  57.2   59.2  59.3  61.3 1.33
## 6 nov      50      0  16.6   19.5  19.5  22.7 1.38
## 7 nds      50      0  17.9   18.6  18.7  20.1 0.513
## 8 ran      50      0  13.8   15.7  15.5  17.4 1.37
```

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 = 385.9, 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')
```

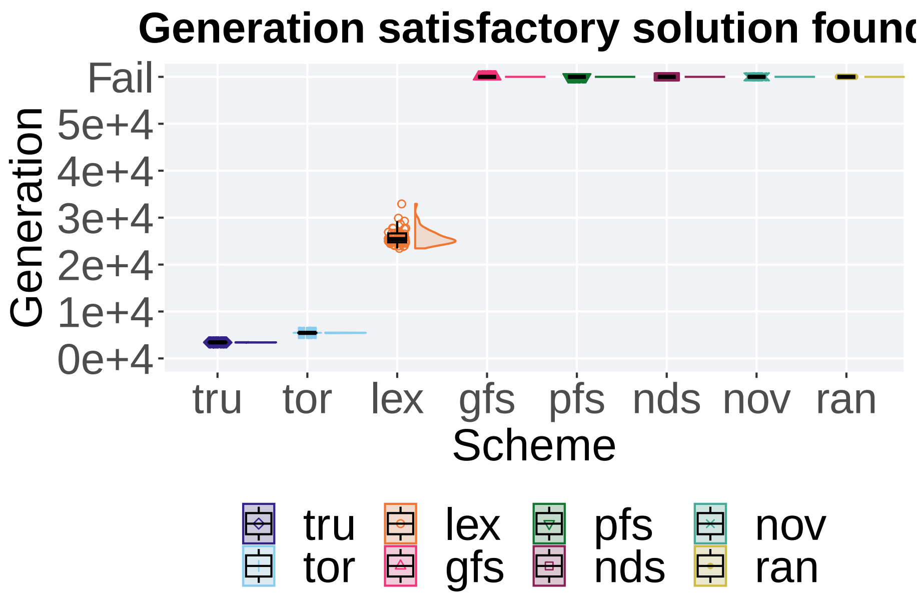
```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  performance$val and performance$acro
##
##     tru     tor     lex     gfs     pfs     nov     nds
## tor 1.00000 -       -       -       -       -       -
## lex < 2e-16 < 2e-16 -       -       -       -       -
## gfs < 2e-16 < 2e-16 < 2e-16 -       -       -       -
## pfs < 2e-16 < 2e-16 < 2e-16 1.00000 -       -       -
## nov < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 -       -
## nds < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 0.00014 -
## ran < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16
```

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

2.5 Generation satisfactory solution found

First generation a satisfactory solution is found throughout the 50,000 generations.

```
sati_df %>%
  ggplot(., aes(x = acro, y = gen , color = acro, fill = acro, shape = acro)) +
  geom_flat_violin(position = position_nudge(x = .2, y = 0), scale = 'width', alpha = 
  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="Generation",
    limits=c(0, 60001),
    breaks=c(0, 10000, 20000, 30000, 40000, 50000, 60000),
    labels=c("0e+4", "1e+4", "2e+4", "3e+4", "4e+4", "5e+4", "Fail")
  ) +
  scale_x_discrete(
    name="Scheme"
  )+
  scale_shape_manual(values=SHAPE)+
  scale_colour_manual(values = cb_palette, ) +
  scale_fill_manual(values = cb_palette) +
  ggtitle('Generation satisfactory solution found')+
  p_theme + theme(legend.title=element_blank()) +
  guides(
    shape=guide_legend(nrow=2, title.position = "bottom"),
    color=guide_legend(nrow=2, title.position = "bottom"),
    fill=guide_legend(nrow=2, title.position = "bottom")
  )
```



2.5.1 Stats

Summary statistics for the generation a satisfactory solution is found.

```
ssf = filter(sati_df, gen <= GENERATIONS)
ssf$acro = factor(ssf$acro, levels = c('tru','tor','lex'))
ssf %>%
  group_by(acro) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(gen)),
    min = min(gen, na.rm = TRUE),
    median = median(gen, na.rm = TRUE),
    mean = mean(gen, na.rm = TRUE),
    max = max(gen, na.rm = TRUE),
    IQR = IQR(gen, na.rm = TRUE)
  )
```

```
## # A tibble: 3 x 8
##   acro  count na_cnt   min median   mean   max   IQR
##   <fct> <int>  <int> <int>  <dbl>  <dbl> <int> <dbl>
## 1 tru      50      0  3384  3416.  3417.  3448   17
## 2 tor      50      0  5388  5453   5449.  5497   40
## 3 lex      50      0 23451 25436. 25865. 32924 1901.
```

Kruskal–Wallis test illustrates evidence of statistical differences.

```
kruskal.test(gen ~ acro, data = ssf)
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  gen by acro
## Kruskal-Wallis chi-squared = 132.46, df = 2, p-value < 2.2e-16
```

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

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

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  ssf$gen and ssf$acro
##
##     tru    tor
## tor <2e-16 -
## lex <2e-16 <2e-16
##
## 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. 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)

sati_df <- read.csv(paste(DIR,'sol-fnd.csv', sep = "", collapse = NULL), header = TRUE, stringsAs
sati_df$acro <- factor(sati_df$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.

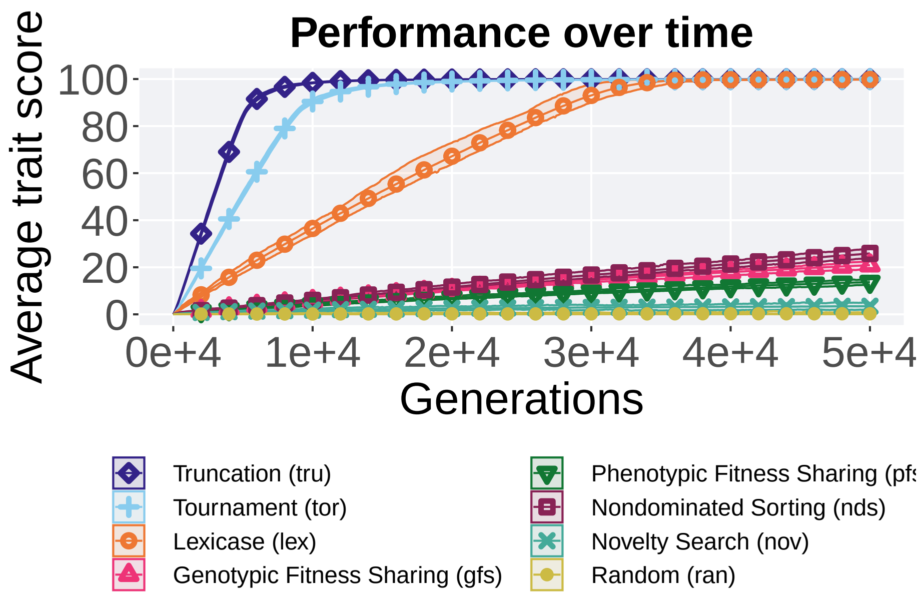
```
lines = over_time_df %>%
  group_by(scheme, gen) %>%
  dplyr::summarise(
    min = min(pop_fit_max) / DIMENSIONALITY,
    mean = mean(pop_fit_max) / DIMENSIONALITY,
    max = max(pop_fit_max) / DIMENSIONALITY
  )
```

```
## `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, 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('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
```

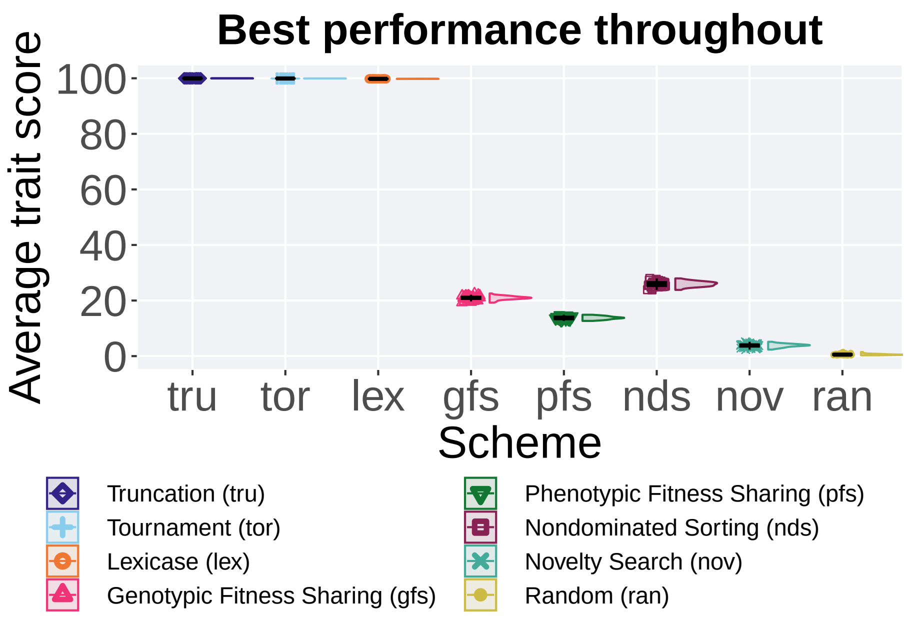


3.4 Best performance throughout

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 = .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, 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 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('tru','tor','lex','nds','gfs','
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 tru      50      0 100.    100.    100.    100.   0.00195
## 2 tor      50      0  99.9    99.9    99.9    99.9  0.00467
## 3 lex      50      0  99.7    99.8    99.8    99.8  0.0233
## 4 nds      50      0  23.8    26.0    25.9    28.0  1.38
## 5 gfs      50      0  19.2    21.0    20.9    22.6  0.760
## 6 pfs      50      0  12.7    13.7    13.8    14.9  0.937
## 7 nov      50      0   2.34    3.85    3.82    5.16 0.753
## 8 ran      50      0   0.289   0.538   0.593   1.47 0.269
```

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 = 392.77, df = 7, p-value < 2.2e-16
```

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

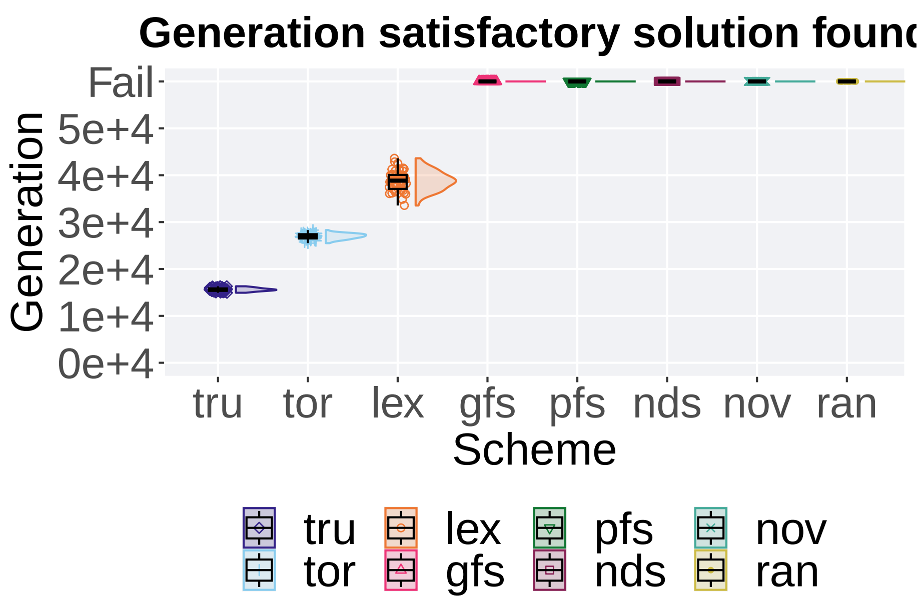
```r
pairwise.wilcox.test(x = performance$val, g = performance$acro, p.adjust.method = "bonferroni",
                     paired = FALSE, conf.int = FALSE, alternative = 'l')
```

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  performance$val and performance$acro
##
##     tru    tor    lex    nds    gfs    pfs    nov
## tor <2e-16 -      -      -      -      -      -
## lex <2e-16 <2e-16 -      -      -      -      -
## nds <2e-16 <2e-16 <2e-16 -      -      -      -
## gfs <2e-16 <2e-16 <2e-16 <2e-16 -      -      -
## pfs <2e-16 <2e-16 <2e-16 <2e-16 <2e-16 -      -
## nov <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 Generation satisfactory solution found

First generation a satisfactory solution is found throughout the 50,000 generations.

```
sati_df %>%
  ggplot(., aes(x = acro, y = gen , color = acro, fill = acro, shape = acro)) +
  geom_flat_violin(position = position_nudge(x = .2, y = 0), scale = 'width', alpha = 
  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="Generation",
    limits=c(0, 60001),
    breaks=c(0, 10000, 20000, 30000, 40000, 50000, 60000),
    labels=c("0e+4", "1e+4", "2e+4", "3e+4", "4e+4", "5e+4", "Fail")
  ) +
  scale_x_discrete(
    name="Scheme"
  )+
  scale_shape_manual(values=SHAPE)+
  scale_colour_manual(values = cb_palette, ) +
  scale_fill_manual(values = cb_palette) +
  ggtitle('Generation satisfactory solution found')+
  p_theme + theme(legend.title=element_blank()) +
  guides(
    shape=guide_legend(nrow=2, title.position = "bottom"),
    color=guide_legend(nrow=2, title.position = "bottom"),
    fill=guide_legend(nrow=2, title.position = "bottom")
  )
```



3.5.1 Stats

Summary statistics for the generation a satisfactory solution is found.

```
ssf = filter(sati_df, gen <= GENERATIONS)
ssf$acro = factor(ssf$acro, levels = c('tru','tor','lex'))
ssf %>%
  group_by(acro) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(gen)),
    min = min(gen, na.rm = TRUE),
    median = median(gen, na.rm = TRUE),
    mean = mean(gen, na.rm = TRUE),
    max = max(gen, na.rm = TRUE),
    IQR = IQR(gen, na.rm = TRUE)
  )
```

```
## # A tibble: 3 x 8
##   acro  count na_cnt   min median   mean   max   IQR
##   <fct> <int>  <int> <int>  <dbl>  <dbl> <int> <dbl>
## 1 tru      50      0 14934 15599  15613. 16315  508.
## 2 tor      50      0 25512 27026  26961. 28298  904.
## 3 lex      50      0 33548 38842. 38804. 43613 2970.
```

Kruskal–Wallis test illustrates evidence of statistical differences.

```
kruskal.test(gen ~ acro, data = ssf)
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  gen by acro
## Kruskal-Wallis chi-squared = 132.45, df = 2, p-value < 2.2e-16
```

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

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

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  ssf$gen and ssf$acro
##
##     tru    tor
## tor <2e-16 -
## lex <2e-16 <2e-16
##
```

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

3.6 Streaks over time

Longest streak solution found in a population over time. A maximum streak value of 100 and a minimum streak value of 1 is possible. 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.

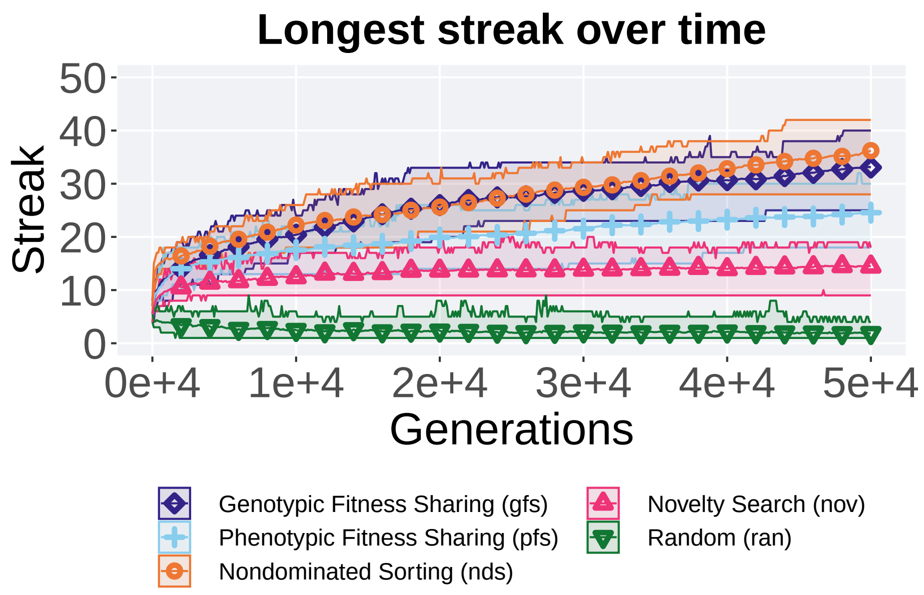
```
lines = filter(over_time_df, acro != 'tor' & acro != 'tru' & acro != 'lex') %>%
  group_by(scheme, gen) %>%
  dplyr::summarise(
    min = min(pop_str_max),
    mean = mean(pop_str_max),
    max = max(pop_str_max)
  )
```

```
## `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
  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="Streak",
    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('Longest streak 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
```

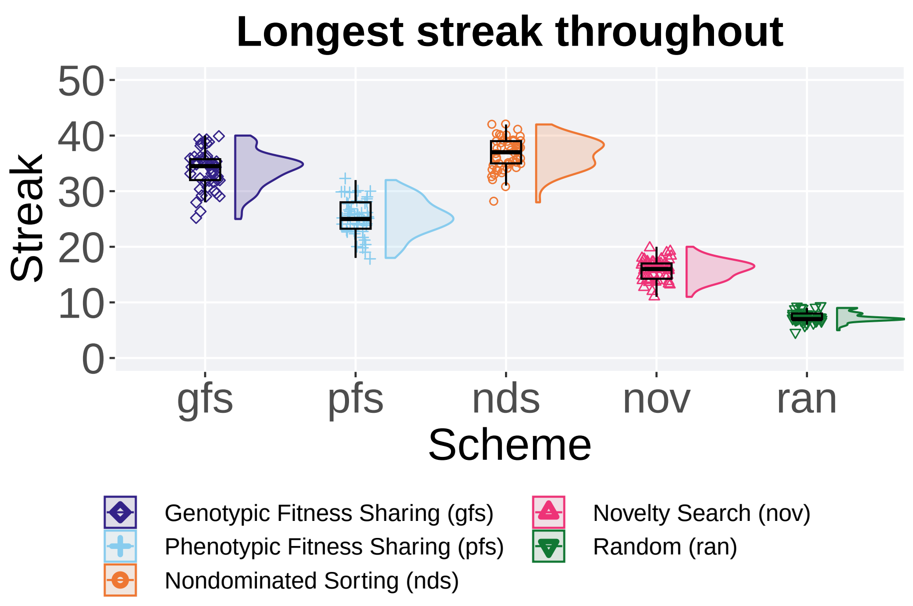


3.7 Longest streak throughout

Longest streak reached throughout 50,000 generations in a population.

```
plot = filter(best_df, var == 'pop_str_max' &  acro != 'tor' & acro != 'tru' & acro != 'lex') %>
  ggplot(., aes(x = acro, y = val, 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="Streak",
    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('Longest streak throughout')+
  p_theme + theme(legend.title=element_blank())

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



3.7.1 Stats

Summary statistics for the longest streak

```
streak = filter(best_df, var == 'pop_str_max' &  acro != 'tor' & acro != 'tru' & acro
streak$acro = factor(streak$acro, levels = c('nds','gfs','pfs','nov','ran'))
streak %>%
  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: 5 x 8
##   acro  count na_cnt   min median  mean   max   IQR
##   <fct> <int>  <int> <dbl>  <dbl> <dbl> <dbl> <dbl>
## 1 nds      50      0    28   37    36.7    42  4
## 2 gfs      50      0    25   34.5  33.8    40  3.75
## 3 pfs      50      0    18   25    25.4    32  4.75
## 4 nov      50      0    11   16    15.8    20  2.75
## 5 ran      50      0     5    7     7.4     9  1
```

Kruskal–Wallis test illustrates evidence of statistical differences.

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

```
##
##  Kruskal-Wallis rank sum test
##
## data:  val by acro
## Kruskal-Wallis chi-squared = 227.37, df = 4, p-value < 2.2e-16
```

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

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

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  streak$val and streak$acro
##
##     nds     gfs     pfs     nov
## gfs 0.00026 -       -       -
## pfs < 2e-16 9.2e-15 -       -
## nov < 2e-16 < 2e-16 < 2e-16 -
## ran < 2e-16 < 2e-16 < 2e-16 < 2e-16
##
## 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. 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.

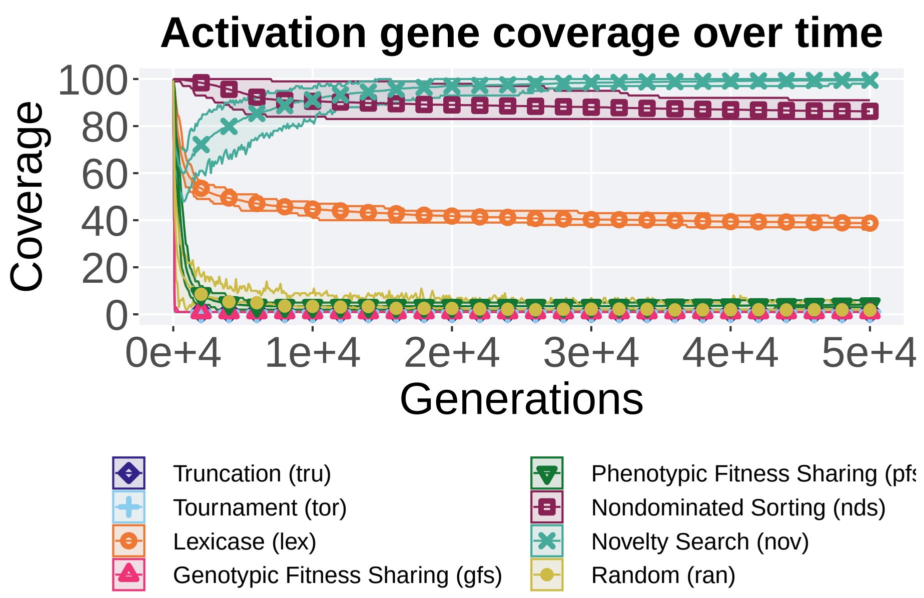
```
lines = over_time_df %>%
  group_by(scheme, gen) %>%
  dplyr::summarise(
    min = min(uni_str_pos),
    mean = mean(uni_str_pos),
    max = max(uni_str_pos)
  )
```

```
## `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
```



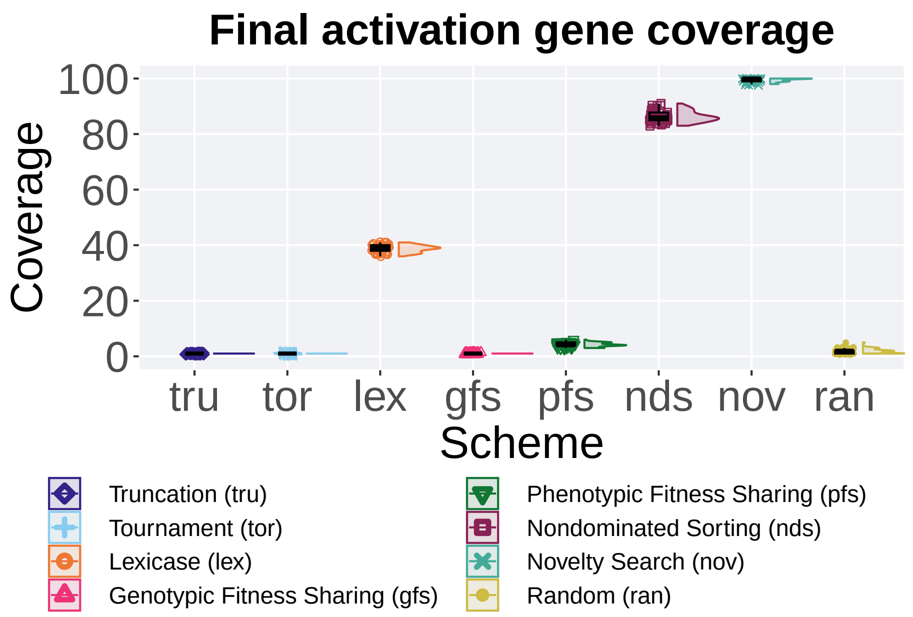
4.4 Final activation gene coverage

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 = .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="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 13 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','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 nov      50      0    98    100 99.5    100  1
## 2 nds      50      0    83     86 86.3     91  2.75
## 3 lex      50      0    36     39 38.8     41  2
## 4 pfs      50      0     3      4  4.12     6  1
## 5 ran      50      0     1      2  1.78     5  1
## 6 gfs      50      0     1      1  1        1  0
## 7 tor      50      0     1      1  1        1  0
## 8 tru      50      0     1      1  1        1  0
```

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 = 384.61, 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     pfs     ran     gfs tor
## nds < 2e-16 -       -       -       -       -   -
## lex < 2e-16 < 2e-16 -       -       -       -   -
## pfs < 2e-16 < 2e-16 < 2e-16 -       -       -   -
## ran < 2e-16 < 2e-16 < 2e-16 4.8e-15 -       -   -
## gfs < 2e-16 < 2e-16 < 2e-16 < 2e-16 3.2e-08 -   -
## tor < 2e-16 < 2e-16 < 2e-16 < 2e-16 3.2e-08 1   -
## tru < 2e-16 < 2e-16 < 2e-16 < 2e-16 3.2e-08 1   1
##
## 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.

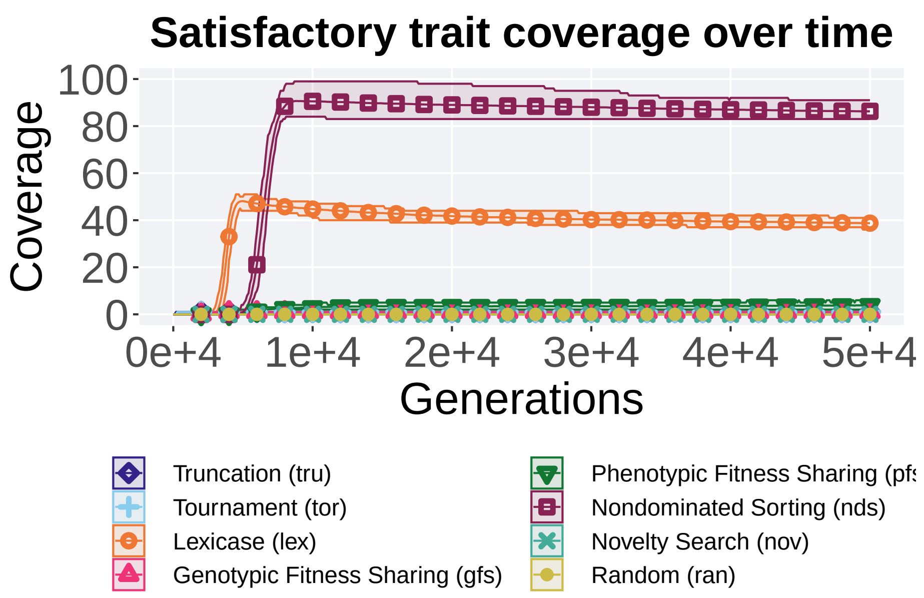
```
lines = over_time_df %>%
  group_by(scheme, gen) %>%
  dplyr::summarise(
    min = min(pop_uni_obj),
    mean = mean(pop_uni_obj),
    max = max(pop_uni_obj)
  )
```

```
## `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",
    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('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
```



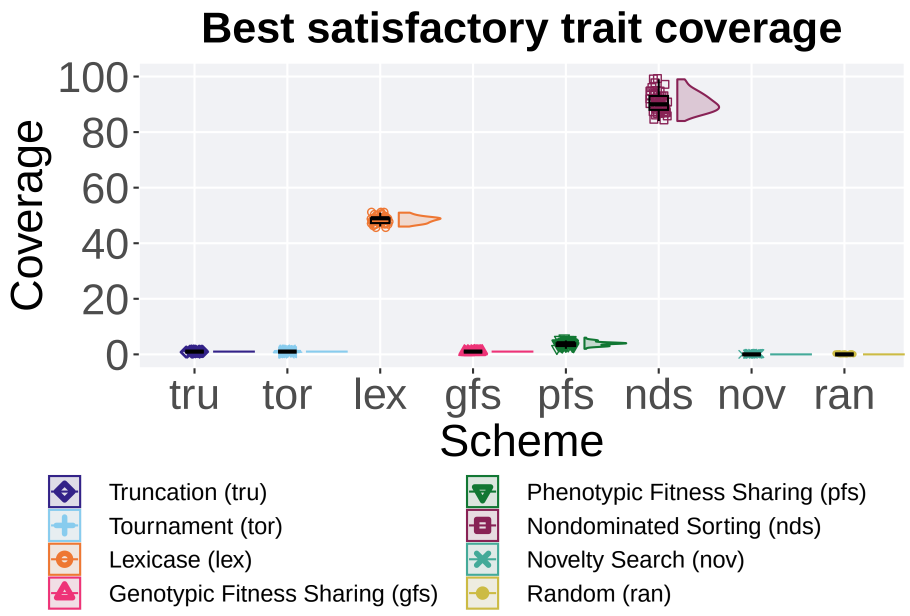
4.6 Best satisfactory trait coverage throughout

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 = .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="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('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 44 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('nds','lex','pfs','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 nds      50      0    84     90 90.8     99  5
## 2 lex      50      0    46     49 48.5     51  1.75
## 3 pfs      50      0     2      4  3.86     6  1
## 4 gfs      50      0     1      1  1        1  0
## 5 tor      50      0     1      1  1        1  0
## 6 tru      50      0     1      1  1        1  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 = 396.67, 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
##
##     nds    lex    pfs    gfs    tor    tru    nov
## lex <2e-16 -      -      -      -      -      -
## pfs <2e-16 <2e-16 -      -      -      -      -
## gfs <2e-16 <2e-16 <2e-16 -      -      -      -
## tor <2e-16 <2e-16 <2e-16 1      -      -      -
## tru <2e-16 <2e-16 <2e-16 1      1      -      -
## nov <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 1
##
## P value adjustment method: bonferroni
```

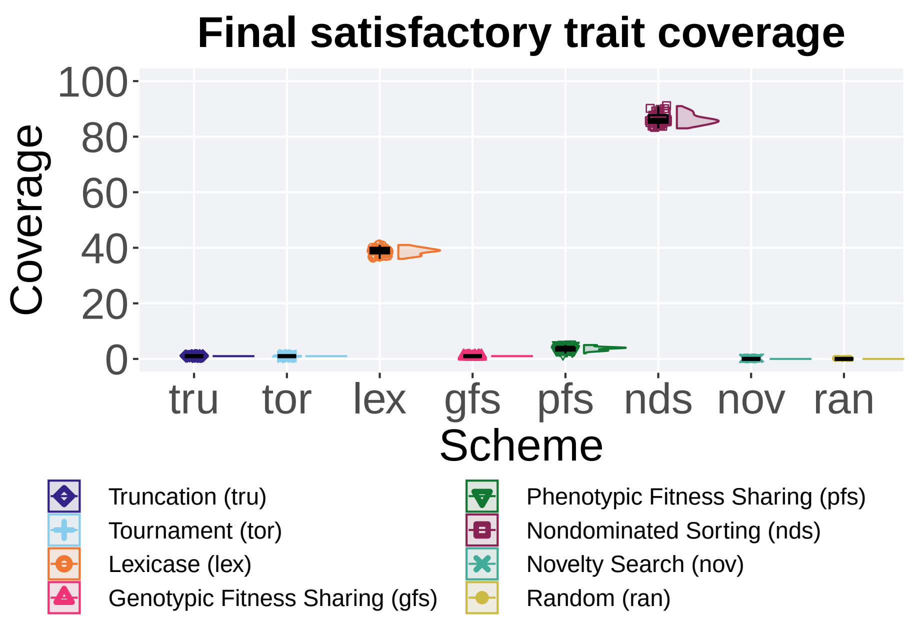
4.7 Final satisfactory trait coverage

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 = .2, y = 0), scale = 'width', alpha = (
  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="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 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 49 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('nds','lex','pfs','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 nds      50      0    83     86 86.3     91  2.75
## 2 lex      50      0    36     39 38.8     41  2
## 3 pfs      50      0     2      4  3.82     5  1
## 4 gfs      50      0     1      1  1        1  0
## 5 tor       50       0      1       1  1         1  0
## 6 tru       50       0      1       1  1         1  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 = 396.72, 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.meth
                     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
##
##     nds    lex    pfs    gfs    tor    tru    nov
## lex <2e-16 -      -      -      -      -      -
## pfs <2e-16 <2e-16 -      -      -      -      -
## gfs <2e-16 <2e-16 <2e-16 -      -      -      -
## tor <2e-16 <2e-16 <2e-16 1      -      -      -
## tru <2e-16 <2e-16 <2e-16 1      1      -      -
## nov <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 1
##
## P value adjustment method: bonferroni
```

Chapter 5

Multi-path exploration results

Here we present the results for **best performances** and **activation gene coverage** found by each selection scheme on the multi-path exploration diagnostic. 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.

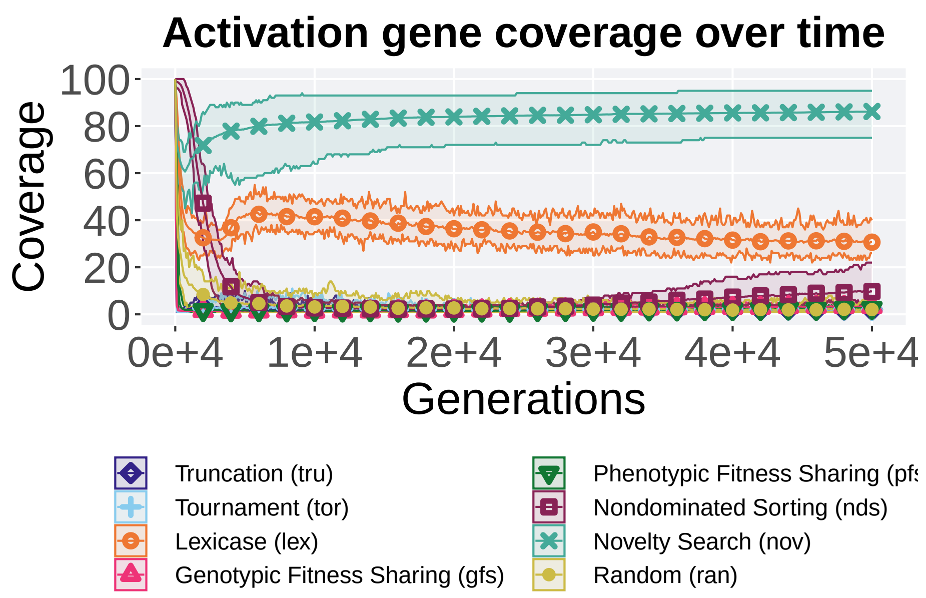
```
lines = over_time_df %>%
  group_by(scheme, gen) %>%
  dplyr::summarise(
    min = min(uni_str_pos),
    mean = mean(uni_str_pos),
    max = max(uni_str_pos)
  )
```

```
## `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
```

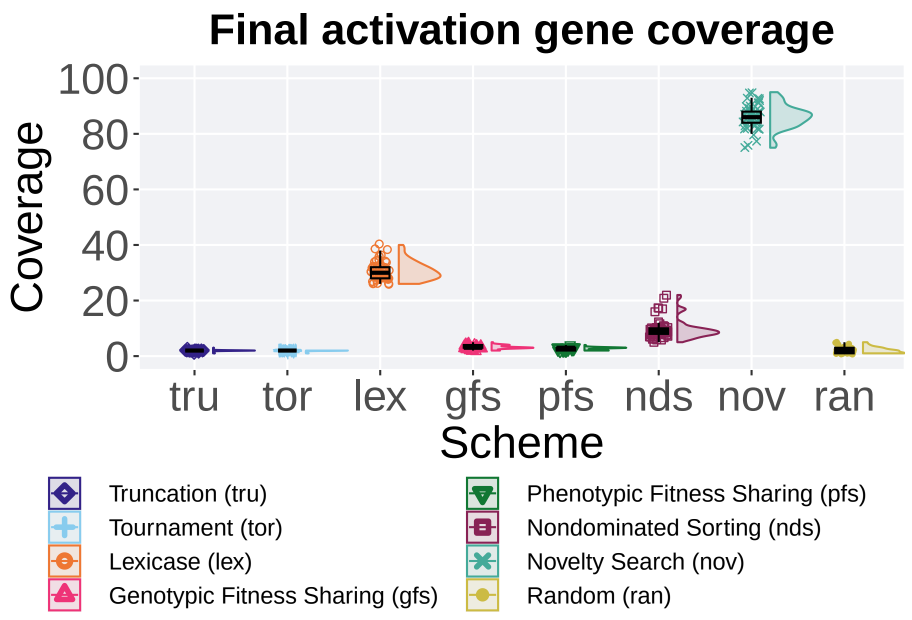


5.4 Final activation gene coverage

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

```r
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 = .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="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','gfs','pfs'
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    75     86 86.2     95     4
## 2 lex      50      0    26     30 30.7     40     4
## 3 nds      50      0     5      9  9.68    22     2
## 4 gfs      50      0     2      3  3.18     5     1
## 5 pfs      50      0     2      3  2.66     4     1
## 6 ran      50      0     1      2  2.02     5     2
## 7 tor      50      0     1      2  1.94     2     0
## 8 tru      50      0     1      2  1.98     3     0
```

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 = 350.22, 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     gfs     pfs     ran     tor
## lex < 2e-16 -       -       -       -       -       -
## nds < 2e-16 < 2e-16 -       -       -       -       -
## gfs < 2e-16 < 2e-16 < 2e-16 -       -       -       -
## pfs < 2e-16 < 2e-16 < 2e-16 0.00097 -       -       -
## ran < 2e-16 < 2e-16 < 2e-16 2.2e-07 0.00068 -       -
## tor < 2e-16 < 2e-16 < 2e-16 4.9e-16 1.2e-10 1.00000 -
## tru < 2e-16 < 2e-16 < 2e-16 1.7e-15 7.1e-10 1.00000 1.00000
##
## 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.

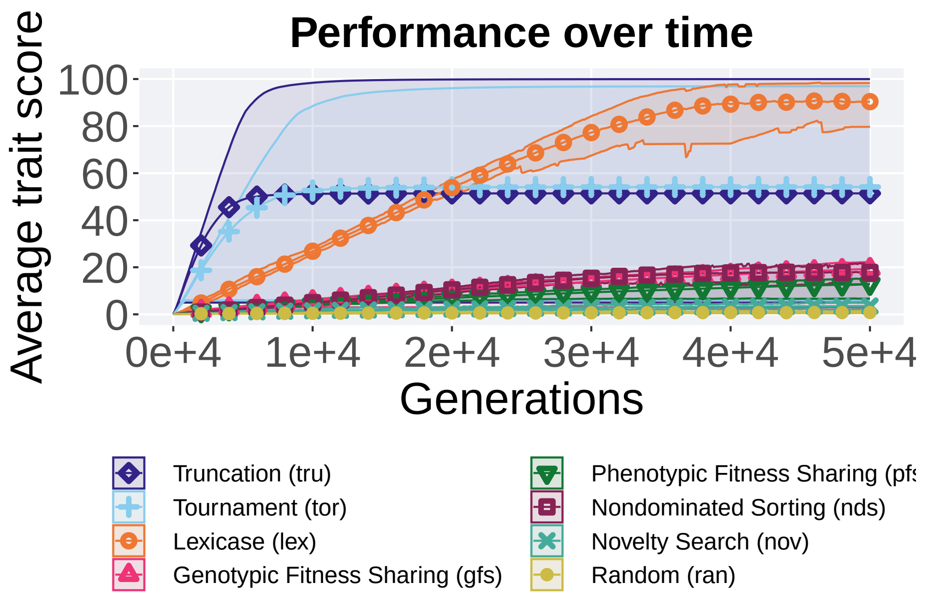
```r
lines = over_time_df %>%
  group_by(scheme, gen) %>%
  dplyr::summarise(
    min = min(pop_fit_max) / DIMENSIONALITY,
    mean = mean(pop_fit_max) / DIMENSIONALITY,
    max = max(pop_fit_max) / DIMENSIONALITY
  )
```

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

```r
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, 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('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
```

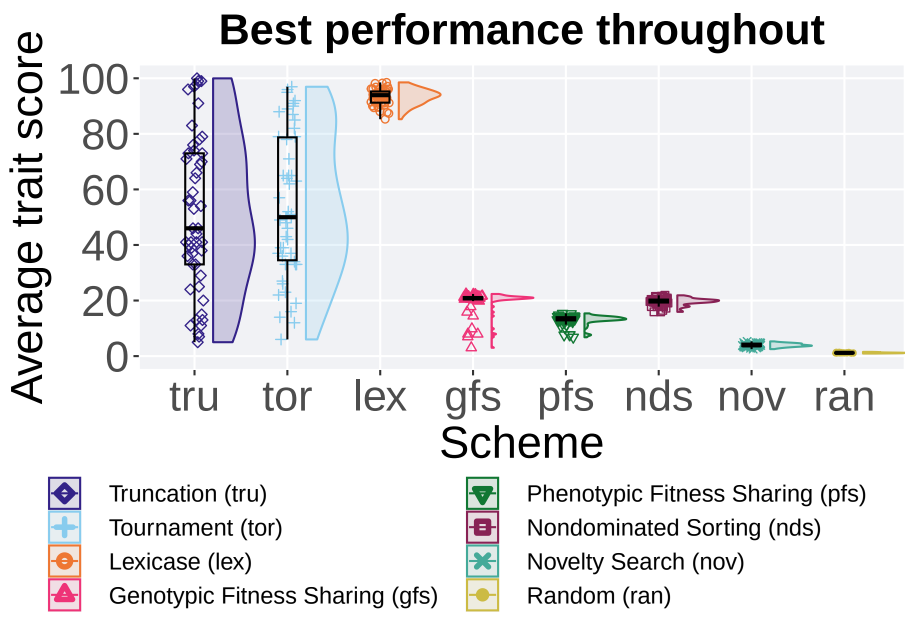


5.6 Best performance throughout

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 = .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, 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 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('lex','tru','tor','gfs','nds','
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 lex      50      0 85.3    93.9  93.3   98.5   4.02
## 2 tru      50      0  5      46.0  51.4  100.   40.0
## 3 tor      50      0  6      50.0  54.1   96.9  44.2
## 4 gfs      50      0  3.00   20.9  19.4   22.4   0.843
## 5 nds      50      0 15.9    19.8  19.6   21.9   1.05
## 6 pfs      50      0  6.78   13.4  12.9   15.4   1.15
## 7 nov      50      0  2.51    3.87  3.95   5.30  0.895
## 8 ran      50      0  0.919   1.17  1.18   1.52  0.209
```

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 = 348.24, 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
##
##     lex     tru     tor     gfs     nds     pfs     nov
## tru 5.7e-10 -       -       -       -       -       -
## tor 8.7e-13 1.00000 -       -       -       -       -
## gfs < 2e-16 8.8e-08 2.5e-11 -       -       -       -
## nds < 2e-16 1.7e-07 4.1e-11 0.00099 -       -       -
## pfs < 2e-16 1.0e-09 4.5e-14 5.0e-11 < 2e-16 -       -
## nov < 2e-16 < 2e-16 < 2e-16 1.5e-15 < 2e-16 < 2e-16 -
## ran < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16
##
## P value adjustment method: bonferroni
```