

Supplemental Material: Base Diagnostics

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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.

```
# 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',
```

```

TSIZE = 26
p_theme <- theme(
  text = element_text(size = 28),
  plot.title = element_text(face = "bold", size = 22, hjust=0.5),
  panel.border = element_blank(),
  panel.grid.minor = element_blank(),
  legend.title=element_text(size=22),
  legend.text=element_text(size=23),
  axis.title = element_text(size=23),
  axis.text = element_text(size=22),
  legend.position="bottom",
  panel.background = element_rect(fill = "#f1f2f5",
                                   colour = "white",
                                   size = 0.5, linetype = "solid")
)

```

```

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

```

```

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

```

```

# selection scheme related stuff

```

```

ACRO = c('tru', 'tor', 'lex', 'gfs', 'pfs', 'nds', 'nov', 'ran')

```

```

NAMES = c('Truncation (tru)', 'Tournament (tor)', 'Lexicase (lex)', 'Genotypic Fitness Sharing (gfs)'

```


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, stringsAsFactors = FALSE)
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 = FALSE)
best_df$acro <- factor(best_df$acro, levels = ACRO)

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

2.3 Performance over time

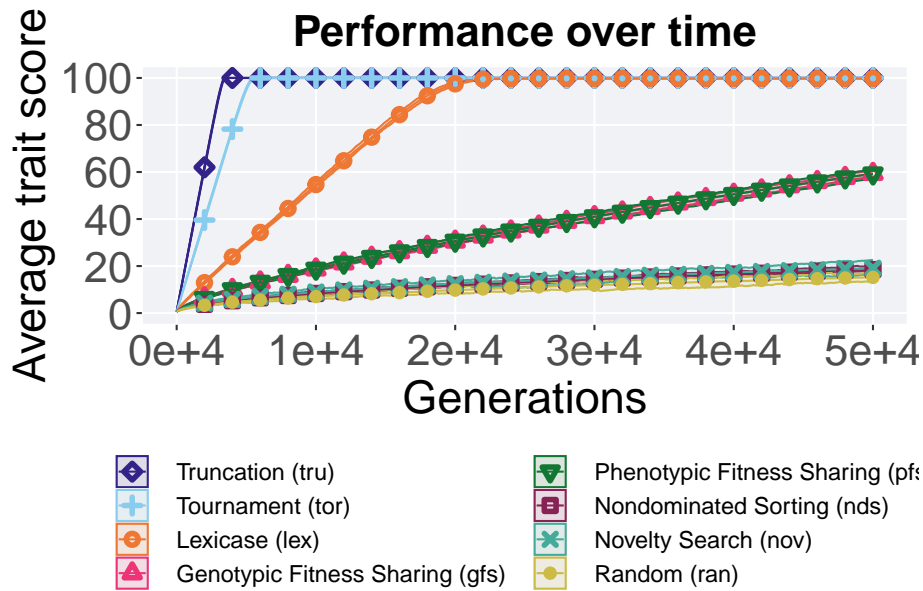
Best performance in a population over time. Data points on the graph is the average performance across 50 replicates every 2000 generations. Shading comes from the best and worse performance across 50 replicates.

```
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

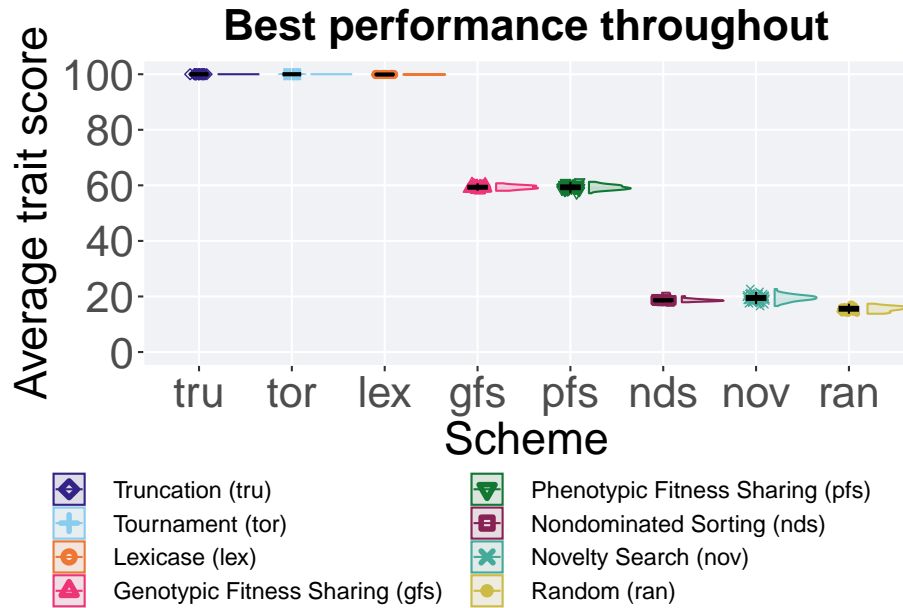
Best performance reached throughout 50,000 generations in a population.

```
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 50 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', 'nds', 'nov', '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 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

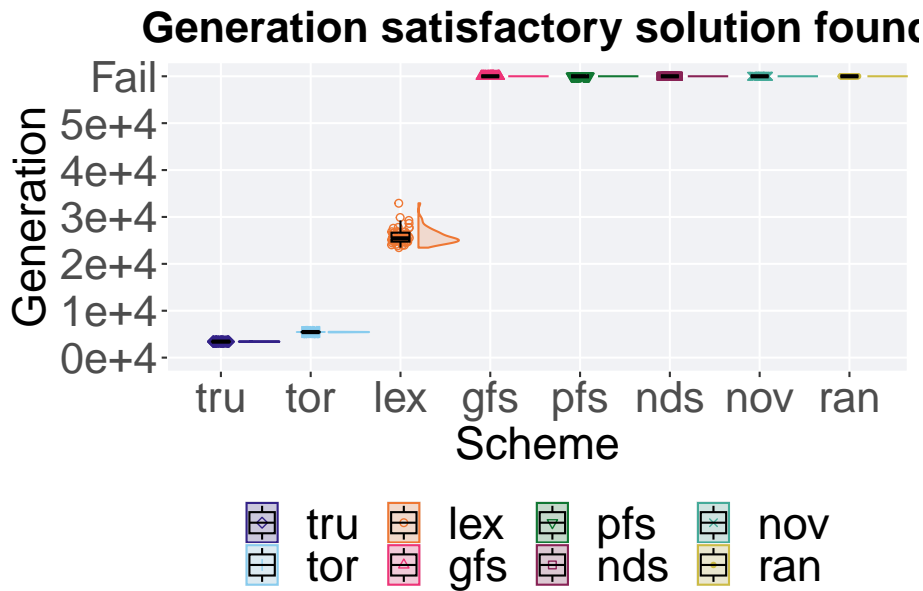
```

```
##
## 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 = 0.5) +
  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, stringsAsFactors = FALSE)
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 = FALSE)
best_df$acro <- factor(best_df$acro, levels = ACRO)

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

3.3 Performance over time

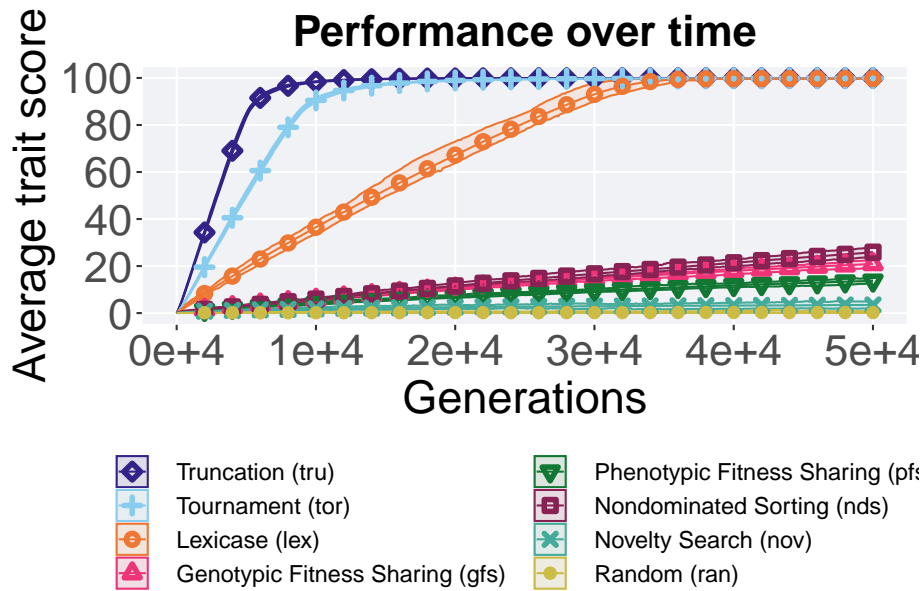
Best performance in a population over time. Data points on the graph is the average performance across 50 replicates every 2000 generations. Shading comes from the best and worse performance across 50 replicates.

```
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
```

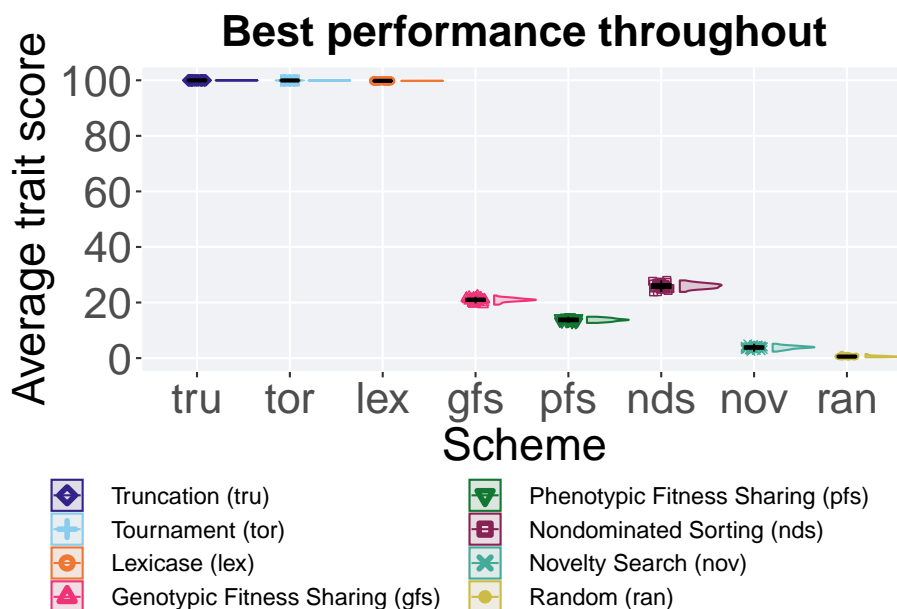


3.4 Best performance throughout

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','pfs','nov','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 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.

```
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.

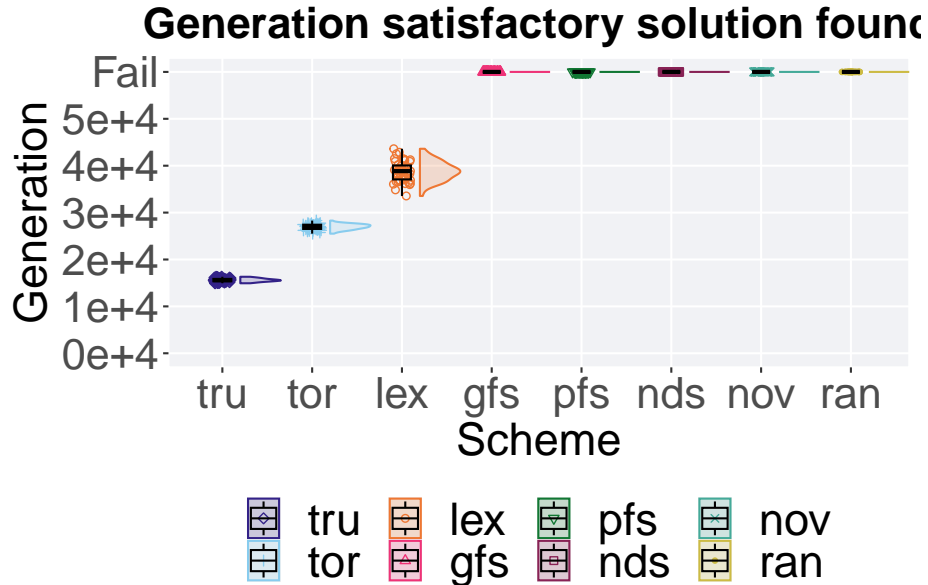
```
pairwise.wilcox.test(x = performance$val, g = performance$acro, p.adjust.method = "bonferroni",
                     paired = FALSE, conf.int = FALSE, alternative = 'l')
```

```
##
##   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 = 0.5) +
  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
```

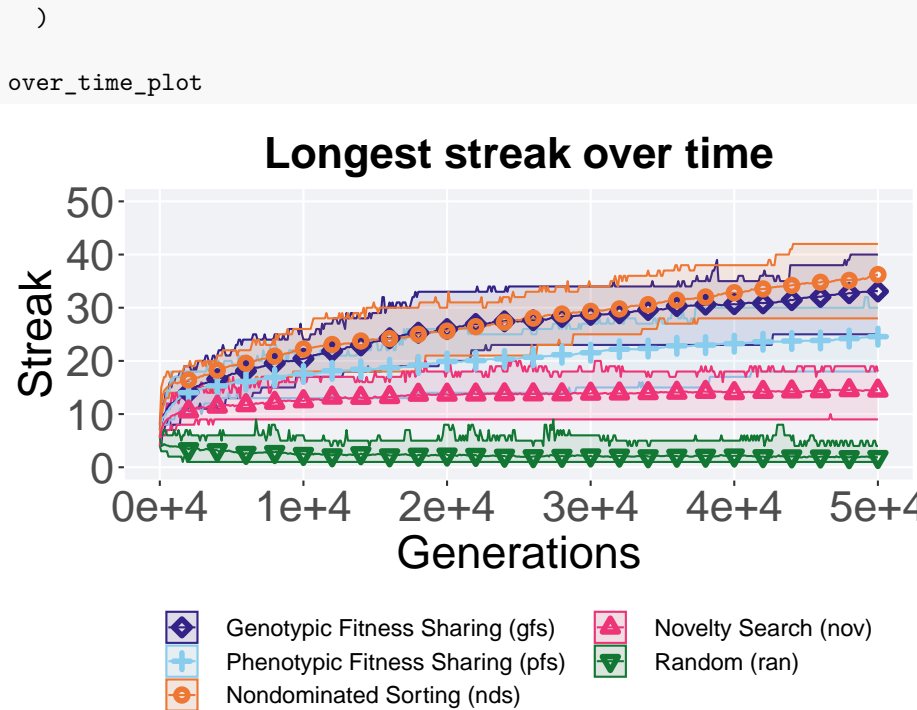
3.6 Streaks over time

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")
  )
```

3.7 Longest streak throughout

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

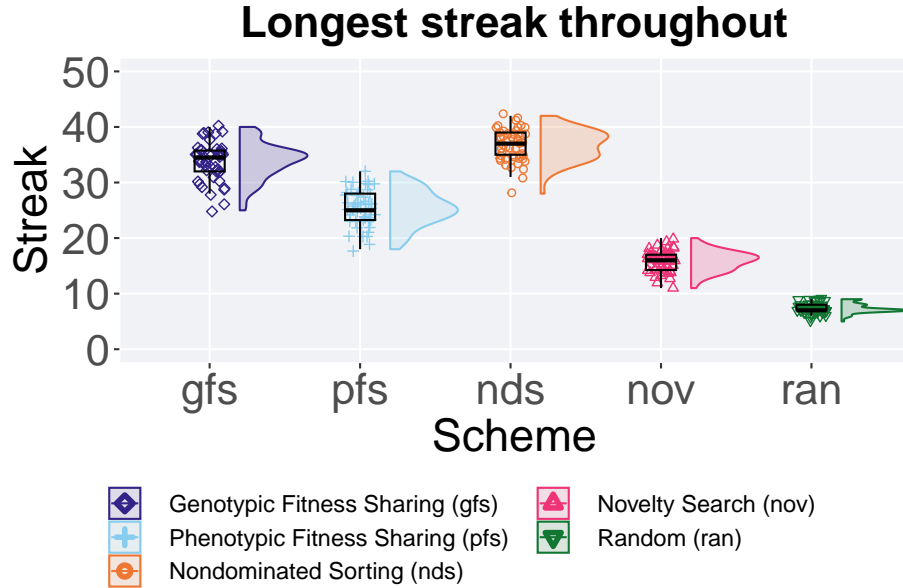
```
plot = filter(best_df, var == 'pop_str_max' & acro != 'tor' & acro != 'tru' & acro != 'lex') %>%
  ggplot(., aes(x = acro, y = val, color = acro, fill = acro, shape = acro)) +
  geom_flat_violin(position = position_nudge(x = .2, y = 0), scale = 'width', alpha = 0.2) +
  geom_point(position = position_jitter(width = .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, 'CONTRADICTIONARY_OBJECTIVES/', sep = "", collapse = NULL)
over_time_df <- read.csv(paste(DIR, 'over-time.csv', sep = "", collapse = NULL), header = TRUE, stringsAsFactors = FALSE)
over_time_df$uni_str_pos = over_time_df$uni_str_pos + over_time_df$arc_acti_gene - over_time_df$arc_acti_gene
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 = FALSE)
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
```



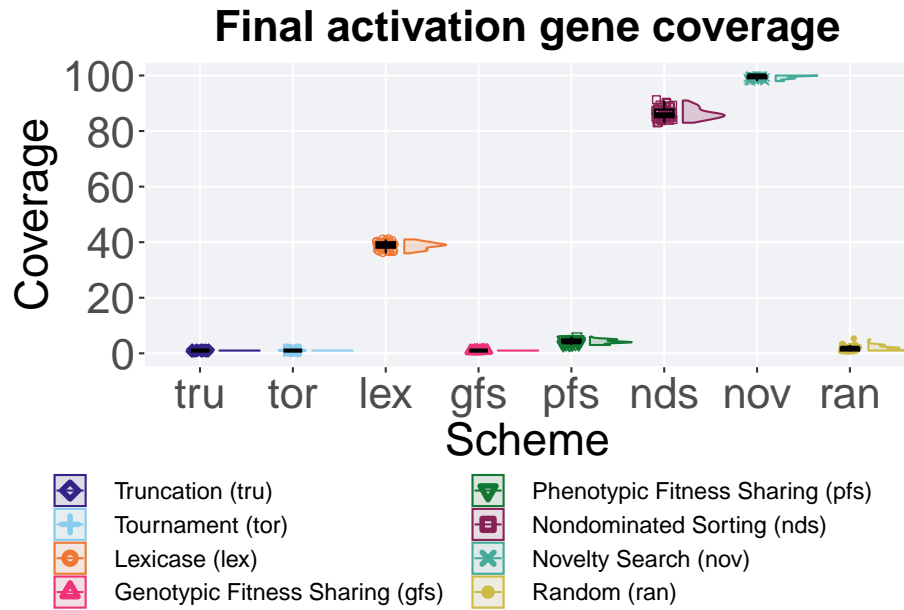
4.4 Final activation gene coverage

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 18 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

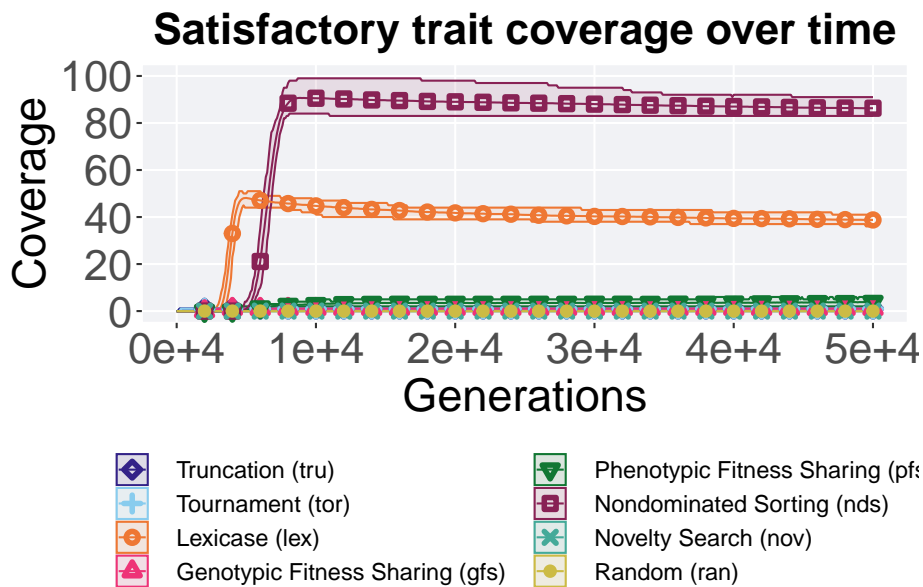
Satisfactory trait coverage in a population over time. Data points on the graph is the average activation gene coverage across 50 replicates every 2000 generations. Shading comes from the best and worse coverage across 50 replicates.

```
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
```



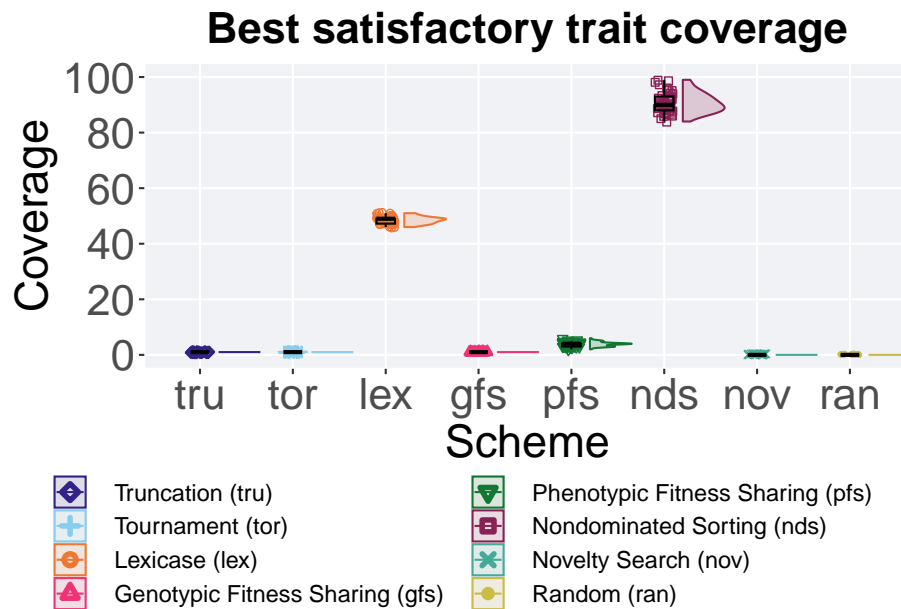
4.6 Best satisfactory trait coverage throughout

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 55 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
```

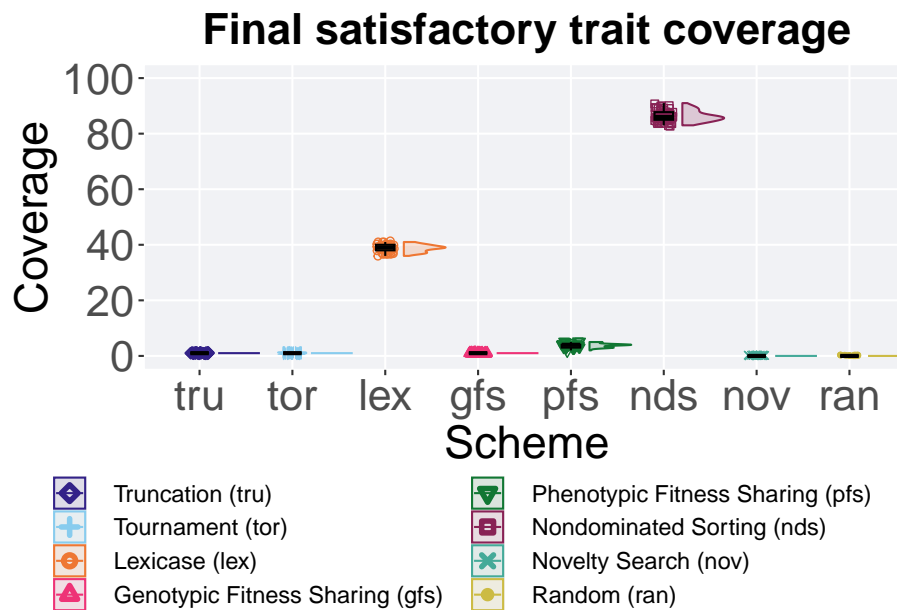
4.7 Final satisfactory trait coverage

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 = 0.5) +
  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 54 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', '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 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.

```
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.

```
pairwise.wilcox.test(x = act_coverage$pop_uni_obj, g = act_coverage$acro, p.adjust.method = 'p.adjust.method',
                    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, stringsAsFactors = FALSE)
over_time_df$uni_str_pos = over_time_df$uni_str_pos + over_time_df$arc_acti_gene - over_time_df$arc_acti_gene
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 = FALSE)
best_df$acro <- factor(best_df$acro, levels = ACRO)
```

5.3 Activation gene coverage over time

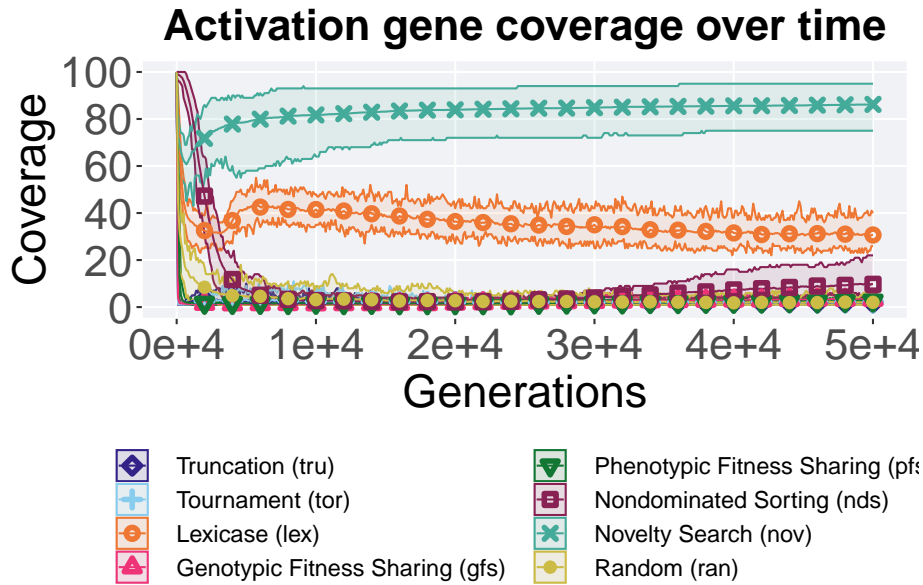
Activation gene coverage in a population over time. Data points on the graph is the average activation gene coverage across 50 replicates every 2000 generations. Shading comes from the best and worse coverage across 50 replicates.

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

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

over_time_plot = ggplot(lines, aes(x=gen, y=mean, group = scheme, fill = scheme, color
  geom_ribbon(aes(ymin = min, ymax = max), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = filter(lines, gen %% 2000 == 0 & gen != 0), size = 1.5, stroke = 2
  scale_y_continuous(
    name="Coverage",
    limits=c(0, 100),
    breaks=seq(0,100, 20),
    labels=c("0", "20", "40", "60", "80", "100")
  ) +
  scale_x_continuous(
    name="Generations",
    limits=c(0, 50000),
    breaks=c(0, 10000, 20000, 30000, 40000, 50000),
    labels=c("0e+4", "1e+4", "2e+4", "3e+4", "4e+4", "5e+4")
  ) +
  scale_shape_manual(values=SHAPE)+
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  ggtitle('Activation gene coverage over time')+
  p_theme + theme(legend.title=element_blank(),legend.text=element_text(size=12)) +
  guides(
    shape=guide_legend(ncol=2, title.position = "bottom"),
    color=guide_legend(ncol=2, title.position = "bottom"),
    fill=guide_legend(ncol=2, title.position = "bottom")
  )

over_time_plot
```

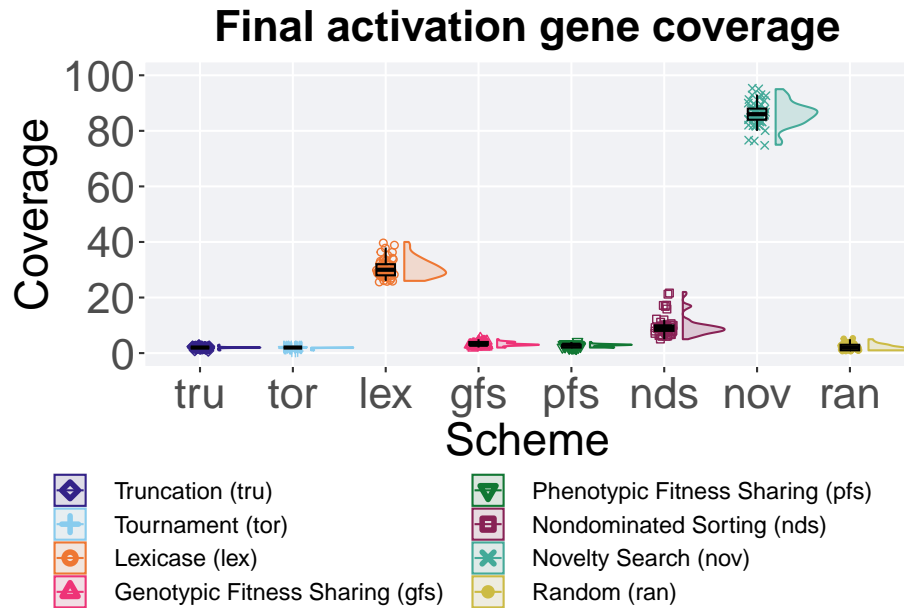


5.4 Final activation gene coverage

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

```
plot = filter(over_time_df, gen == 50000) %>%
  ggplot(., aes(x = acro, y = uni_str_pos, color = acro, fill = acro, shape = acro)) +
  geom_flat_violin(position = position_nudge(x = .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

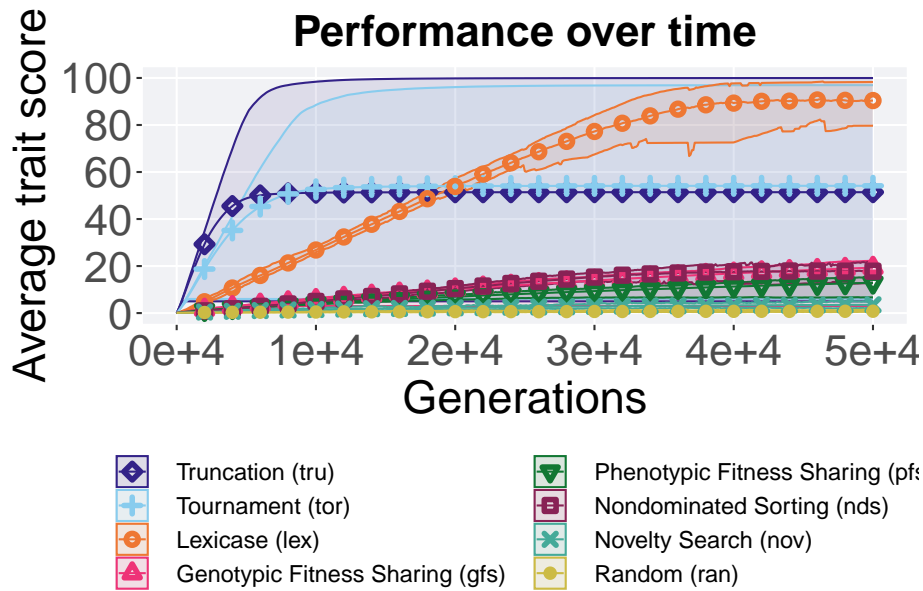
Best performance in a population over time. Data points on the graph is the average performance across 50 replicates every 2000 generations. Shading comes

from the best and worse performance across 50 replicates.

```
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
```

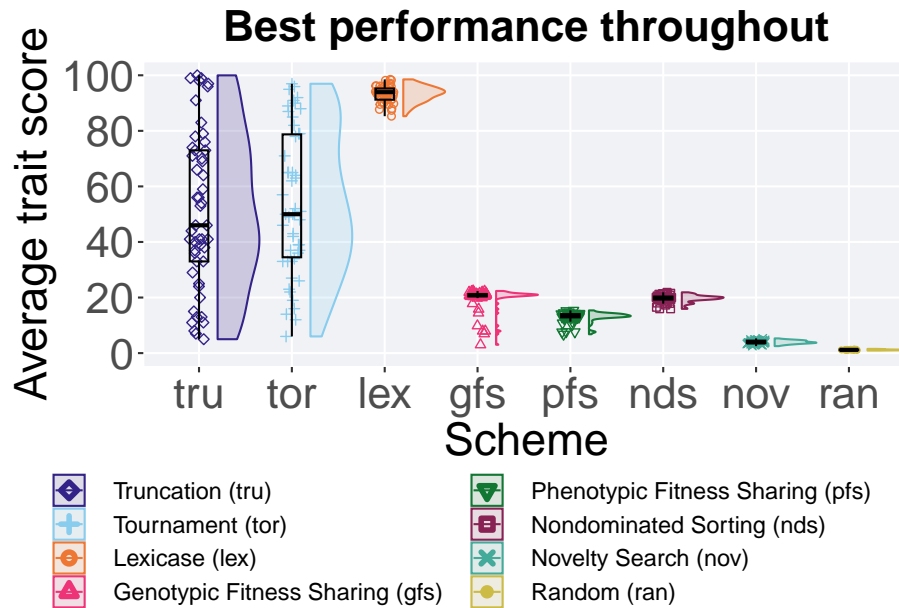


5.6 Best performance throughout

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', 'pfs', 'nov', '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 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
```