

# Diagnostics Supplemental Material

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2022-10-28



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# Chapter 1

## Introduction

This is the supplemental material associated with our 2022 ECJ contribution entitled, *A suite of diagnostic metrics for characterizing selection schemes*. Preprint here.

### 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)

Additionally, our supplemental material includes the results from parameter tuning selection schemes:

- Truncation selection (Section 6)
- Tournament selection sharing (Section 7)
- Genotypic fitness sharing (Section 8)
- Phenotypic fitness sharing (Section 9)
- Nondominated sorting (Section 10)
- Novelty search (Section 11)

## 1.2 Contributing authors

- Jose Guadalupe Hernandez
- Alexander Lalejini
- Charles Ofria

## 1.3 Research overview

### **Abstract:**

Evolutionary algorithms typically consist of multiple interacting components, where each component influences an algorithm’s problem-solving abilities. Understanding how each component of an evolutionary algorithm influences problem-solving success can improve our ability to target particular problem domains. Benchmark suites provide insights into an evolutionary algorithm’s problem-solving capabilities, but benchmarking problems often have complex search space topologies, making it difficult to isolate and test an algorithm’s strengths and weaknesses. Our work focuses on diagnosing selection schemes, which identify individuals to contribute genetic material to the next generation, thus driving an evolutionary algorithm’s search strategy. We introduce four diagnostics for empirically testing the strengths and weaknesses of selection schemes: the exploitation rate diagnostic, ordered exploitation rate diagnostic, contradictory objectives diagnostic, and the multi-path exploration diagnostic. Each diagnostic is a handcrafted search space designed to isolate and measure the relative exploitation and exploration characteristics of selection schemes. Here, we use our diagnostics to evaluate six population selection methods: truncation selection, tournament selection, fitness sharing, lexicase selection, nondominated sorting, and novelty search. Expectedly, tournament and truncation selection excelled at gradient exploitation but poorly explored search spaces, while novelty search excelled at exploration but failed to exploit gradients. Fitness sharing performed poorly across all diagnostics, suggesting poor overall exploitation and exploration abilities. Nondominated sorting was best for maintaining diverse populations comprised of individuals inhabiting multiple optima, but struggled to effectively exploit gradients. Lexicase selection balanced search space exploration without sacrificing exploitation, generally performing well across diagnostics. Our work demonstrates the value of diagnostics for building a deeper understanding of selection schemes, which can then be used to improve or develop new selection methods.

## 1.4 Experimental setup

Setting up required variables variables.

```
library(ggplot2)
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

# variables used throughout
TRAITS = 100
TSIZE = 26
ORDER = c('Truncation (tru)', 'Tournament (tor)', 'Genotypic Fitness Sharing (gfs)', 'Phenotypic Fi
ACRON = tolower(c('TRU', 'TOR', 'GFS', 'PFS', 'LEX', 'NDS', 'NOV', 'RAN'))
SHAPE = c(5,3,2,6,1,0,4,20,1)
PARAM = c('8', '8', '0.3', '0.3', '0.0', '0.3', '15', '1')
cb_palette <- c('#332288', '#88CCEE', '#EE3377', '#117733', '#EE7733', '#882255', '#44AA99', '#CCBB44', '#FF9933', '#FF6633', '#FF3333', '#FF9966', '#FFCC99', '#FFCC66', '#FFCC33', '#FF99CC', '#FF6699', '#FF3399', '#CC99CC', '#CC6699', '#CC3399', '#99CC99', '#66CC66', '#33CC33', '#339999', '#336699', '#333399', '#3333CC', '#3366CC', '#3399CC', '#339999', '#666699', '#6666CC', '#999999', '#9999CC', '#CC9999', '#CC6666', '#CC3333', '#993333', '#663333', '#333333')

# selection scheme parameters
TR_LIST = c(1, 2, 4, 8, 16, 32, 64, 128, 256)
TS_LIST = c(2, 4, 8, 16, 32, 64, 128, 256)
FS_LIST = c(0.0, 0.1, 0.3, 0.6, 1.2, 2.5, 5.0)
ND_LIST = c(0.0, 0.1, 0.3, 0.6, 1.2, 2.5, 5.0)
NS_LIST = c(1, 2, 4, 8, 15, 30)

# theme that graphs will follow
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=18),
  legend.text=element_text(size=14),
  axis.title = element_text(size=18),
  axis.text = element_text(size=16),
  legend.position="bottom",
  panel.background = element_rect(fill = "#f1f2f5",
                                    colour = "white",
                                    size = 0.5, linetype = "solid")
)

# cross comparison data frames
cc_over_time <- read.csv('/opt/ECJ-2022-suite-of-diagnostics-for-selection-schemes/DATA-FINAL/POD'
colnames(cc_over_time)[19] <- 'Selection\nScheme'
cc_over_time$`Selection\nScheme` <- factor(cc_over_time$`Selection\nScheme`, levels = ORDER)

```

```

cc_best = read.csv('/opt/ECJ-2022-suite-of-diagnostics-for-selection-schemes/DATA-FINAL')
cc_best$acron <- factor(cc_best$acron, levels = ACRON)
cc_ssf = read.csv('/opt/ECJ-2022-suite-of-diagnostics-for-selection-schemes/DATA-FINAL')
cc_ssf$acron <- factor(cc_ssf$acron, levels = ACRON)
cc_ssf[is.na(cc_ssf)] <- 59999
cc_end <- filter(cc_over_time, gen == 50000)
cc_end$acron <- factor(cc_end$acron, levels = ACRON)

# selection scheme data frames
ss_over_time <- read.csv('/opt/ECJ-2022-suite-of-diagnostics-for-selection-schemes/DATA-FINAL')
ss_best <- read.csv('/opt/ECJ-2022-suite-of-diagnostics-for-selection-schemes/DATA-FINAL')
ss_ssf <- read.csv('/opt/ECJ-2022-suite-of-diagnostics-for-selection-schemes/DATA-FINAL')

## genotypic fitness sharing data frames
gfs_ot <- filter(ss_over_time, acron == 'gfs')
gfs_ot$Sigma <- factor(gfs_ot$trt, levels = FS_LIST)
gfs_best <- filter(ss_best, acron == 'gfs')
gfs_best$Sigma <- factor(gfs_best$trt, levels = FS_LIST)
gfs_end <- filter(gfs_ot, gen == 50000)

## phenotypic fitness sharing data frames
pfs_ot <- filter(ss_over_time, acron == 'pfs')
pfs_ot$Sigma <- factor(pfs_ot$trt, levels = FS_LIST)
pfs_best <- filter(ss_best, acron == 'pfs')
pfs_best$Sigma <- factor(pfs_best$trt, levels = FS_LIST)
pfs_end <- filter(pfs_ot, gen == 50000)

## nondominated sorting data frames
nds_ot <- filter(ss_over_time, acron == 'nds')
nds_ot$Sigma <- factor(nds_ot$trt, levels = ND_LIST)
nds_best <- filter(ss_best, acron == 'nds')
nds_best$Sigma <- factor(nds_best$trt, levels = ND_LIST)
nds_end <- filter(nds_ot, gen == 50000)

## novelty search data frames
nov_ot <- filter(ss_over_time, acron == 'nov' & trt != 0)
nov_ot$K <- factor(nov_ot$trt, levels = NS_LIST)
nov_best <- filter(ss_best, acron == 'nov' & trt != 0)
nov_best$K <- factor(nov_best$trt, levels = NS_LIST)
nov_end <- filter(nov_ot, gen == 50000)

## tournament data frames
tor_ot <- filter(ss_over_time, acron == 'tor' & trt != 1)
tor_ot$T <- factor(tor_ot$trt, levels = TS_LIST)
tor_best <- filter(ss_best, acron == 'tor' & trt != 1)

```

```

tor_best$T <- factor(tor_best$trt, levels = TS_LIST)
tor_end <- filter(tor_ot, gen == 50000)
tor_ssf <- filter(ss_ssf, acron == 'tor' & trt != 1)
tor_ssf$T <- factor(tor_ssf$trt, levels = TS_LIST)
tor_ssf[is.na(tor_ssf)] <- 59999

## truncation data frames
tru_ot <- filter(ss_over_time, acron == 'tru')
tru_ot$T <- factor(tru_ot$trt, levels = TR_LIST)
tru_best <- filter(ss_best, acron == 'tru')
tru_best$T <- factor(tru_best$trt, levels = TR_LIST)
tru_end <- filter(tru_ot, gen == 50000)
tru_ssf <- filter(ss_ssf, acron == 'tru')
tru_ssf$T <- factor(tru_ssf$trt, levels = TR_LIST)
tru_ssf[is.na(tru_ssf)] <- 59999

```

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         2.1
## year          2022
## month         06
## day           23
## svn rev       82513
## language      R
## version.string R version 4.2.1 (2022-06-23)
## nickname      Funny-Looking Kid

```



# Chapter 2

## Exploitation rate results

Here we present the results for **best performances** found by each selection scheme replicate on the exploitation rate diagnostic. Best performance found refers to the largest average trait score found in a given population. Note that performance values fall between 0 and 100.

### 2.1 Analysis dependencies

```
library(ggplot2)
library(cowplot)
library(dplyr)
library(PupilometryR)
```

### 2.2 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         2.1
## year          2022
## month         06
```

```
## day          23
## svn rev     82513
## language    R
## version.string R version 4.2.1 (2022-06-23)
## nickname    Funny-Looking Kid
```

## 2.3 Performance over time

Best performance in a population over time.

```
exploitation_rate = filter(cc_over_time, diagnostic == 'exploitation_rate')
lines = exploitation_rate %>%
  group_by(`Selection\nScheme`, gen) %>%
  dplyr::summarise(
    min = min(pop_fit_max),
    mean = mean(pop_fit_max),
    max = max(pop_fit_max)
  )

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

points = filter(lines, gen %% 2000 == 0 & gen != 0)

ot = ggplot(lines, aes(x=gen, y=mean / TRAITS, group = `Selection\nScheme`, fill = Selection))
  geom_ribbon(aes(ymin = min / TRAITS, ymax = max / TRAITS), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = points, size = 1.5, stroke = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Average trait score",
    limits=c(-1, 101),
    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+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6")
  ) +
  scale_shape_manual(values=SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  ggtitle("Best performance over time") +
  p_theme+
```

```

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")
) +
theme(
  legend.position = "bottom",
  legend.box="vertical",
  legend.justification="center",
  legend.title=element_blank()
)

```

ot



## 2.4 Best performance throughout

Best performance throughout 50,000 generations.

```

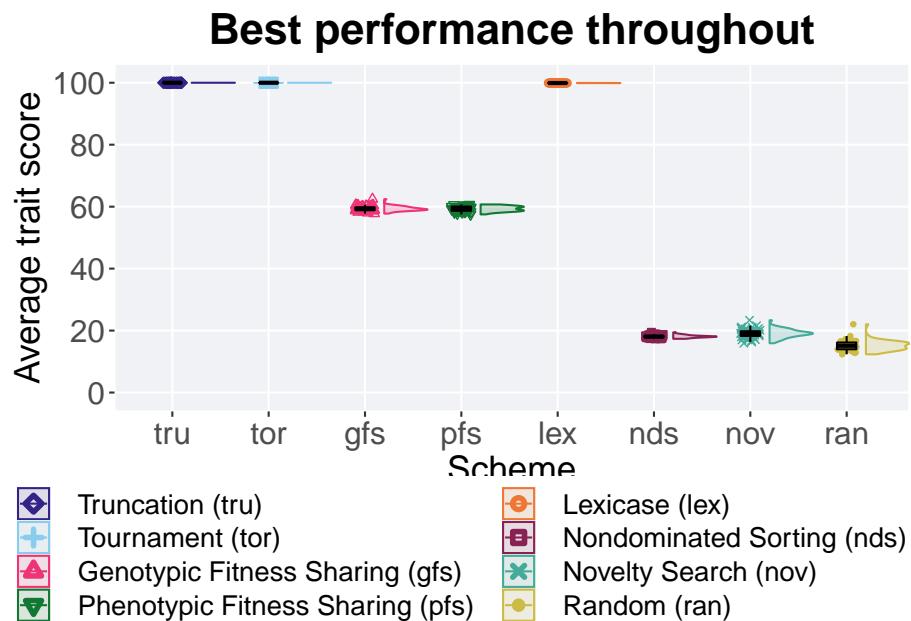
best = filter(cc_best, col == 'pop_fit_max' & diagnostic == 'exploitation_rate')
plot = ggplot(best, aes(x = acron, y = val / TRAITS, color = acron, fill = acron, shape = acron))
  geom_flat_violin(position = position_nudge(x = .2, y = 0), scale = 'width', alpha = 0.2) +
  geom_point(position = position_jitter(width = .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(-1, 101),
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) +
p_theme

plot_grid(
  plot +
  ggtitle("Best performance throughout") +
  theme(legend.position="none"),
  legend,
  nrow=2,
  rel_heights = c(2,.55),
  label_size = TSIZE
)

```



### 2.4.1 Stats

Summary statistics for the performance of the best performance throughout 50,000 generations.

```
best$acron <- factor(best$acron, levels = c('tru', 'tor', 'lex', 'gfs', 'pfs', 'nov', 'nds', 'ran')
group_by(best, acron) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(val)),
    min = min(val / TRAITS, na.rm = TRUE),
    median = median(val / TRAITS, na.rm = TRUE),
    mean = mean(val / TRAITS, na.rm = TRUE),
    max = max(val / TRAITS, na.rm = TRUE),
    IQR = IQR(val / TRAITS, na.rm = TRUE)
  )

## # A tibble: 8 x 8
##   acron 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   0.0183
## 4 gfs      50     0 57.8    59.2   59.4   62.4   0.921
## 5 pfs      50     0 57.5    59.4   59.3   60.7   1.37
## 6 nov      50     0 15.9    19.1   19.1   23.3   1.50
## 7 nds      50     0 17.3    18.0   18.1   19.4   0.482
## 8 ran      50     0 12.3    15.1   15.2   22.0   2.18
```

Kruskal–Wallis test provides evidence of statistical differences among best performance found throughout 50,000 generations.

```
kruskal.test(val ~ acron, data = best)

##
## Kruskal-Wallis rank sum test
##
## data: val by acron
## Kruskal-Wallis chi-squared = 384.12, df = 7, p-value < 2.2e-16
```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction on the best performance found throughout 50,000 generations.

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

##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
```

```

## data: best$val and best$acron
##
##    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 0.00012 -
##    ran < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 1.6e-14 1.3e-14
##
## P value adjustment method: bonferroni

```

## 2.5 Generation satisfactory solution found

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

```

ssf = filter(cc_ssf, diagnostic == 'exploitation_rate')
schemes = data.frame()

for (i in 1:8) {
  if(i == 5)
  {
    schemes = rbind(schemes, filter(ssf, acron == ACRON[i]))
    next
  }
  schemes = rbind(schemes, filter(ssf, acron == ACRON[i] & trt == PARAM[i]))
}

plot <- ggplot(schemes, aes(x = acron, y = generation, color = acron, fill = acron, shape = acron))
  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_shape_manual(values=SHAPE) +
  scale_y_continuous(
    name="Generation",
    limits=c(0, 60000),
    breaks=c(0, 10000, 20000, 30000, 40000, 50000, 60000),
    labels=c("0e+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6", "Fail"))
  ) +
  scale_x_discrete(
    name="Scheme"
  ) +
  scale_colour_manual(values = cb_palette) +

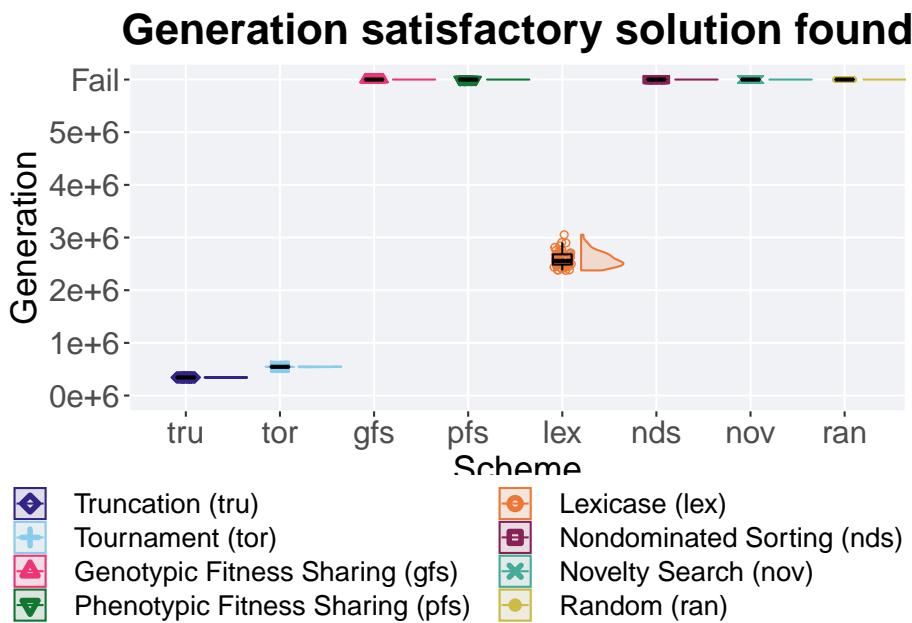
```

```

  scale_fill_manual(values = cb_palette) +
  p_theme

  plot_grid(
    plot +
      ggtitle("Generation satisfactory solution found") +
      theme(legend.position="none"),
    legend,
    nrow=2,
    rel_heights = c(2,.55),
    label_size = TSIZE
  )
)

```



### 2.5.1 Stats

Summary statistics for the first generation a satisfactory solution is found throughout the 50,000 generations.

```

schemes <- filter(schemes, acron == 'tru' | acron == 'tor' | acron == 'lex')
group_by(schemes, acron) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(generation)),
    min = min(generation, na.rm = TRUE),
    median = median(generation, na.rm = TRUE),
    max = max(generation, na.rm = TRUE),
    mean = mean(generation, na.rm = TRUE),
    sd = sd(generation, na.rm = TRUE)
  )

```

```

mean = mean(generation, na.rm = TRUE),
max = max(generation, na.rm = TRUE),
IQR = IQR(generation, na.rm = TRUE)
)

## # A tibble: 3 x 8
##   acron count na_cnt   min median   mean   max   IQR
##   <fct> <int> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 tru     50     0  3399  3430.  3432.  3478    18
## 2 tor     50     0  5379  5457   5453.  5529    56
## 3 lex     50     0 23761 25580. 25863. 30542   1935

```

Kruskal-Wallis test provides evidence of difference amoung selection schemes the first generation a satisfactory solution is found throughout the 50,000 generations.

```
kruskal.test(generation ~ acron, data = schemes)
```

```

##
## Kruskal-Wallis rank sum test
##
## data: generation by acron
## 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 on the first generation a satisfactory solution is found throughout the 50,000 generations.

```

pairwise.wilcox.test(x = schemes$generation, g = schemes$acron, p.adjust.method = "bonferroni",
                      paired = FALSE, conf.int = FALSE, alternative = 'g')

##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: schemes$generation and schemes$acron
##
##      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 replicate on the exploitation rate diagnostic. Best performance found refers to the largest average trait score found in a given population. Note that performance values fall between 0 and 100.

### 3.1 Analysis dependencies

```
library(ggplot2)
library(cowplot)
library(dplyr)
library(PupilometryR)
```

### 3.2 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         2.1
## year          2022
## month         06
```

```
## day          23
## svn rev     82513
## language    R
## version.string R version 4.2.1 (2022-06-23)
## nickname    Funny-Looking Kid
```

### 3.3 Performance over time

Best performance in a population over time.

```
ordered_exploitation = filter(cc_over_time, diagnostic == 'ordered_exploitation')
lines = ordered_exploitation %>%
  group_by(`Selection\nScheme`, gen) %>%
  dplyr::summarise(
    min = min(pop_fit_max),
    mean = mean(pop_fit_max),
    max = max(pop_fit_max)
  )

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

points = filter(lines, gen %% 2000 == 0 & gen != 0)

ot = ggplot(lines, aes(x=gen, y=mean / TRAITS, group = `Selection\nScheme`, fill = Selection))
  geom_ribbon(aes(ymin = min / TRAITS, ymax = max / TRAITS), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = points, size = 1.5, stroke = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Average trait score",
    limits=c(-1, 101),
    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+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6")
  ) +
  scale_shape_manual(values=SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  ggtitle("Best performance over time") +
  p_theme+
```

```

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")
) +
theme(
  legend.position = "bottom",
  legend.box="vertical",
  legend.justification="center",
  legend.title=element_blank()
)

```

ot



### 3.4 Best performance throughout

Best performance throughout 50,000 generations.

```

best = filter(cc_best, col == 'pop_fit_max' & diagnostic == 'ordered_exploitation')
plot = ggplot(best, aes(x = acron, y = val / TRAITS, color = acron, fill = acron, shape = acron))
  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(
    trans = log_trans(),
    labels = scales::label_percent()
  )

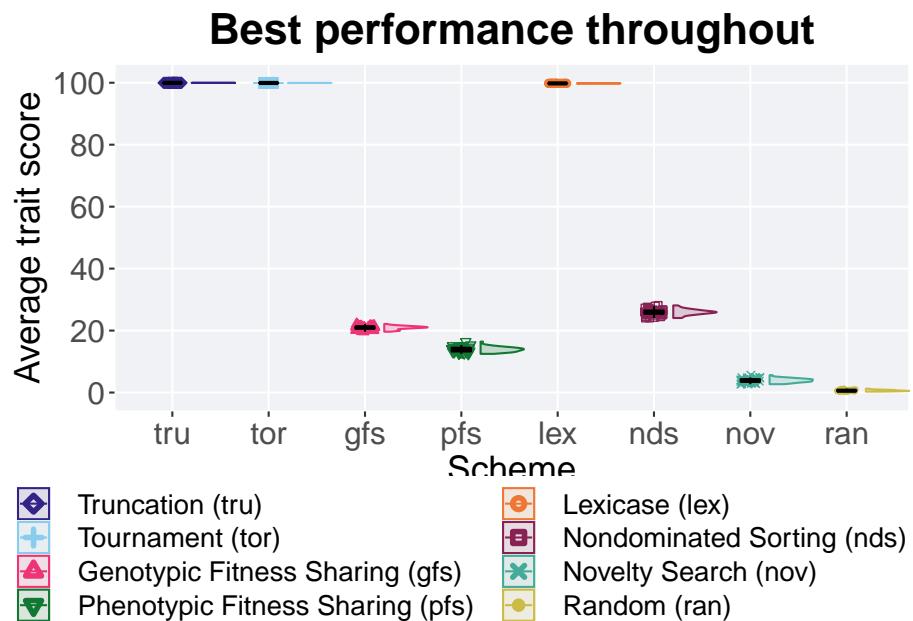
```

```

name="Average trait score",
limits=c(-1, 101),
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) +
p_theme

plot_grid(
  plot +
  ggtitle("Best performance throughout") +
  theme(legend.position="none"),
  legend,
  nrow=2,
  rel_heights = c(2,.55),
  label_size = TSIZE
)

```



### 3.4.1 Stats

Summary statistics for the performance of the best performance throughout 50,000 generations.

```
best$acron <- factor(best$acron, levels = c('tru', 'tor', 'lex', 'nds', 'gfs', 'pfs', 'nov', 'ran')
group_by(best, acron) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(val)),
    min = min(val / TRAITS, na.rm = TRUE),
    median = median(val / TRAITS, na.rm = TRUE),
    mean = mean(val / TRAITS, na.rm = TRUE),
    max = max(val / TRAITS, na.rm = TRUE),
    IQR = IQR(val / TRAITS, na.rm = TRUE)
  )

## # A tibble: 8 x 8
##   acron count na_cnt     min   median     mean     max     IQR
##   <fct> <int> <int>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>
## 1 tru      50     0 100.    100.    100.    100.    0.00225
## 2 tor      50     0 99.9    99.9    99.9    99.9    0.00540
## 3 lex      50     0 99.7    99.8    99.8    99.8    0.0239
## 4 nds      50     0 24.1    26.0    26.0    28.1    1.04
## 5 gfs      50     0 19.6    21.0    20.9    22.1    0.686
## 6 pfs      50     0 12.5    13.9    13.9    16.4    1.21
## 7 nov      50     0 2.70    3.88    3.89    5.62    0.846
## 8 ran      50     0 0.310   0.594   0.640   1.23    0.317
```

Kruskal–Wallis test provides evidence of statistical differences among best performance found throughout 50,000 generations.

```
kruskal.test(val ~ acron, data = best)

##
## Kruskal-Wallis rank sum test
##
## data: val by acron
## 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 on the best performance found throughout 50,000 generations.

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

##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
```

```

## data: best$val and best$acron
##
##   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.

```

ssf = filter(cc_ssf, diagnostic == 'ordered_exploitation')
schemes = data.frame()

for (i in 1:8) {
  if(i == 5)
  {
    schemes = rbind(schemes, filter(ssf, acron == ACRON[i]))
    next
  }
  schemes = rbind(schemes, filter(ssf, acron == ACRON[i] & trt == PARAM[i]))
}

plot <- ggplot(schemes, aes(x = acron, y = generation, color = acron, fill = acron, shape = acron))
  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_shape_manual(values=SHAPE) +
  scale_y_continuous(
    name="Generation",
    limits=c(0, 60000),
    breaks=c(0, 10000, 20000, 30000, 40000, 50000, 60000),
    labels=c("0e+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6", "Fail"))
  ) +
  scale_x_discrete(
    name="Scheme"
  ) +
  scale_colour_manual(values = cb_palette) +

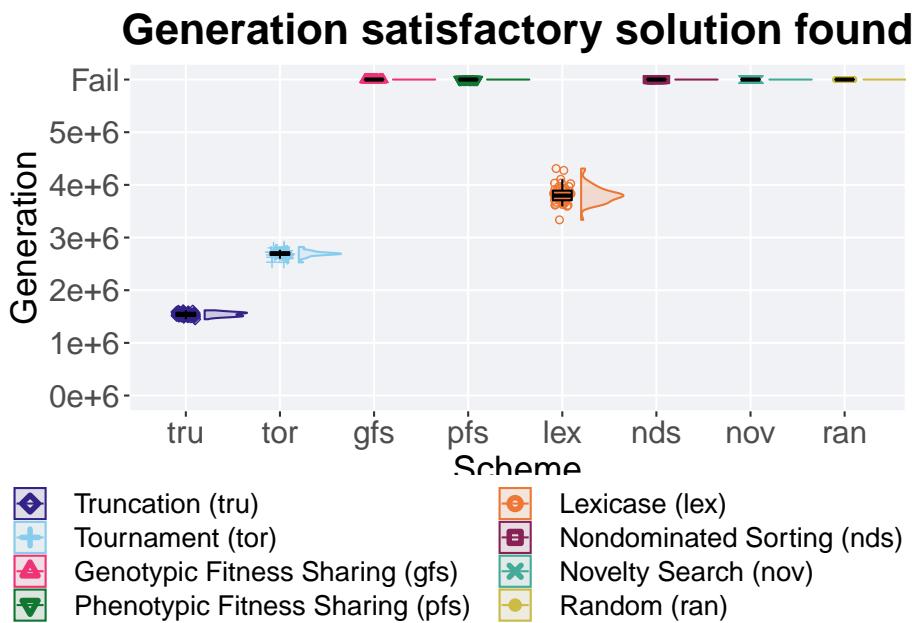
```

```

  scale_fill_manual(values = cb_palette) +
  p_theme

  plot_grid(
    plot +
      ggtitle("Generation satisfactory solution found") +
      theme(legend.position="none"),
    legend,
    nrow=2,
    rel_heights = c(2,.55),
    label_size = TSIZE
  )
)

```



### 3.5.1 Stats

Summary statistics for the first generation a satisfactory solution is found throughout the 50,000 generations.

```

schemes <- filter(schemes, acron == 'tru' | acron == 'tor' | acron == 'lex')
group_by(schemes, acron) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(generation)),
    min = min(generation, na.rm = TRUE),
    median = median(generation, na.rm = TRUE),
    max = max(generation, na.rm = TRUE),
    mean = mean(generation, na.rm = TRUE),
    sd = sd(generation, na.rm = TRUE)
  )

```

```

mean = mean(generation, na.rm = TRUE),
max = max(generation, na.rm = TRUE),
IQR = IQR(generation, na.rm = TRUE)
)

## # A tibble: 3 x 8
##   acron count na_cnt  min median   mean   max   IQR
##   <fct> <int> <int> <dbl> <dbl> <dbl> <dbl>
## 1 tru     50      0 14487 15446. 15428. 16184  609.
## 2 tor     50      0 25283 26926. 26922. 28222  496.
## 3 lex     50      0 33359 37966. 38119. 43099 1820.

```

Kruskal–Wallis test provides evidence of difference amoung selection schemes the first generation a satisfactory solution is found throughout the 50,000 generations..

```
kruskal.test(generation ~ acron, data = schemes)
```

```

##
##  Kruskal-Wallis rank sum test
##
## data:  generation by acron
## 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 on the first generation a satisfactory solution is found throughout the 50,000 generations.

```

pairwise.wilcox.test(x = schemes$generation, g = schemes$acron, p.adjust.method = "bonferroni",
                      paired = FALSE, conf.int = FALSE, alternative = 'g')

##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  schemes$generation and schemes$acron
##
##    tru    tor
## tor <2e-16 -
## lex <2e-16 <2e-16
##
## P value adjustment method: bonferroni

```

## 3.6 Streaks

### 3.6.1 Over time

Best streak in a population over time.

```

streaks_df = filter(ordered_exploitation, acron == 'pfs' | acron == 'nds' | acron == 'gfs' | acron == 'nondominated')
streaks_df$`Selection\`nScheme` <- factor(streaks_df$`Selection\`nScheme`, levels = c('Nondominated', 'pfs', 'nds', 'gfs'))

lines = streaks_df %>%
  group_by(`Selection\`nScheme`, gen) %>%
  dplyr::summarise(
    min = min(pop_str_max),
    mean = mean(pop_str_max),
    max = max(pop_str_max)
  )

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

points = filter(lines, gen %% 2000 == 0 & gen != 0)

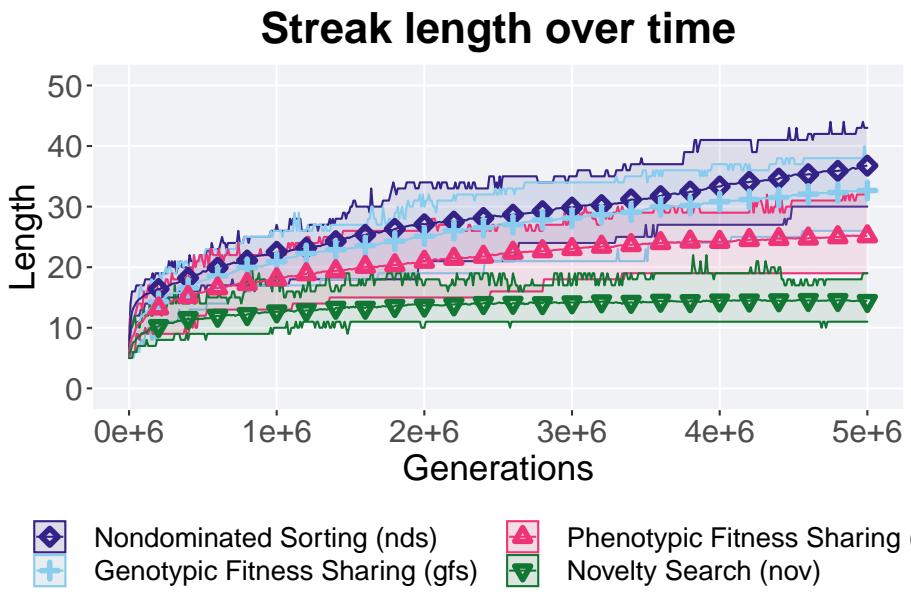
ot = ggplot(lines, aes(x=gen, y=mean, group = `Selection\`nScheme`, fill = `Selection\`nScheme`), color = `Selection\`nScheme`)
  geom_ribbon(aes(ymin = min, ymax = max), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = points, size = 1.5, stroke = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Length",
    limits=c(-1, 51),
    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+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6")
  ) +
  scale_shape_manual(values=SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  ggtitle("Streak length over time") +
  p_theme +
  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")
  ) +
  theme(
    legend.position = "bottom",
    legend.box="vertical",
    legend.title.position = "top"
  )

```

```

        legend.justification="center",
        legend.title=element_blank()
    )
}
ot

```



### 3.6.2 End of 50,000 generations

Best streak in the population at the end of 50,000 generations.

```

end <- filter(streaks_df, gen == 50000)
end = filter(end, acron == 'pfs' | acron == 'nds' | acron == 'gfs' | acron == 'nov')
end$acron <- factor(end$acron, levels = c('nds', 'gfs', 'pfs', 'nov'))

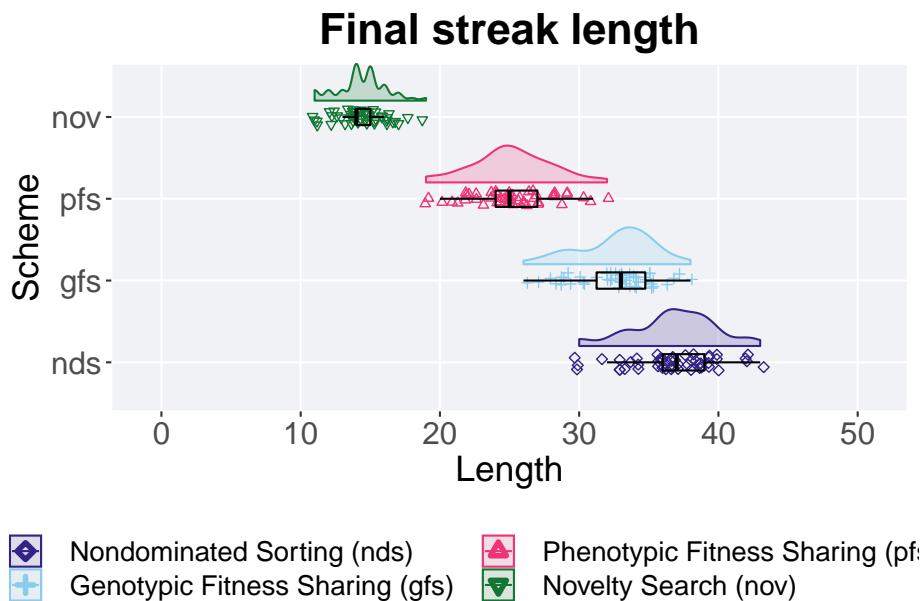
plot = ggplot(end, aes(x = acron, y = pop_str_max, color = acron, fill = acron, shape =
  geom_flat_violin(position = position_nudge(x = .2, y = 0), scale = 'width', alpha = 0.2) +
  geom_point(position = position_jitter(width = .1), size = 1.5, alpha = 1.0) +
  geom_boxplot(color = 'black', width = .2, outlier.shape = NA, alpha = 0.0) +
  scale_y_continuous(
    name="Length",
    limits=c(-1, 51),
    breaks=seq(0, 50, 10),
    labels=c("0", "10", "20", "30", "40", "50")
  ) +
  scale_x_discrete(
    name="Algorithm"
  )
}
```

```

    name="Scheme"
) +
  scale_shape_manual(values=SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  coord_flip() +
  p_theme

plot_grid(
  plot +
  ggtitle("Final streak length") +
  theme(legend.position="none"),
  legend,
  nrow=2,
  rel_heights = c(2,.55),
  label_size = TSIZE
)

```



### 3.6.2.1 Stats

Summary statistics for best streak in the population at the end of 50,000 generations.

```

group_by(end, acron) %>%
  dplyr::summarise(

```

```

count = n(),
na_cnt = sum(is.na(pop_str_max)),
min = min(pop_str_max, na.rm = TRUE),
median = median(pop_str_max, na.rm = TRUE),
mean = mean(pop_str_max, na.rm = TRUE),
max = max(pop_str_max, na.rm = TRUE),
IQR = IQR(pop_str_max, na.rm = TRUE)
)

## # A tibble: 4 x 8
##   acron count na_cnt   min median   mean   max   IQR
##   <fct> <int> <int> <int> <dbl> <dbl> <int> <dbl>
## 1 nds     50     0    30     37  36.8    43     3
## 2 gfs     50     0    26     33  32.7    38     3.5
## 3 pfs     50     0    19     25  25.1    32     3
## 4 nov     50     0    11     14  14.4    19     1

```

Kruskal–Wallis test provides evidence of difference among best performance in the population at the end of 50,000 generations.

```
kruskal.test(pop_str_max ~ acron, data = end)
```

```

##
## Kruskal-Wallis rank sum test
##
## data: pop_str_max by acron
## Kruskal-Wallis chi-squared = 174.19, df = 3, p-value < 2.2e-16

```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction on best performance in the population at the end of 50,000 generations.

```

pairwise.wilcox.test(x = end$pop_str_max, g = end$acron, p.adjust.method = "bonferroni"
                      paired = FALSE, conf.int = FALSE, alternative = 'l')

##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: end$pop_str_max and end$acron
##
##      nds      gfs      pfs
## gfs 4.9e-09 -       -
## pfs < 2e-16 1.9e-15 -
## nov < 2e-16 < 2e-16 < 2e-16
##
## P value adjustment method: bonferroni

```

# Chapter 4

## Contradictory objectives results

Here we present the results for the **satisfactory trait coverage** and **activation gene coverage** generated by each selection scheme replicate on the contradictory objectives diagnostic. Note both of these values are gathered at the population-level. Activation gene coverage refers to the count of unique activation genes in a given population; this gives us a range of integers between 0 and 100. Satisfactory trait coverage refers to the count of unique satisfied traits in a given population; this gives us a range of integers between 0 and 100.

### 4.1 Analysis dependencies

```
library(ggplot2)
library(cowplot)
library(dplyr)
library(Pupillometry)
```

### 4.2 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     2.1
## year     2022
## month     06
## day       23
## svn rev   82513
## language   R
## version.string R version 4.2.1 (2022-06-23)
## nickname   Funny-Looking Kid

```

## 4.3 Satisfactory trait coverage

Satisfactory trait coverage analysis.

### 4.3.1 Coverage over time

Satisfactory trait coverage over time.

```

contradictory_objectives = filter(cc_over_time, diagnostic == 'contradictory_objectives')
lines = contradictory_objectives %>%
  group_by(`Selection\nScheme`, gen) %>%
  dplyr::summarise(
    min = min(pop_uni_obj),
    mean = mean(pop_uni_obj),
    max = max(pop_uni_obj)
  )

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

points = filter(lines, gen %% 2000 == 0 & gen != 0)

ot = ggplot(lines, aes(x=gen, y=mean, group = `Selection\nScheme`, fill = `Selection\nScheme`),
            geom_ribbon(aes(ymin = min, ymax = max), alpha = 0.1) +
            geom_line(size = 0.5) +
            geom_point(data = points, size = 1.5, stroke = 2.0, alpha = 1.0) +
            scale_y_continuous(
              name="Coverage",
              limits=c(-1, 101),
              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+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6")

) +
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 +
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")
) +
theme(
  legend.position = "bottom",
  legend.box="vertical",
  legend.justification="center",
  legend.title=element_blank()
)

ot

```

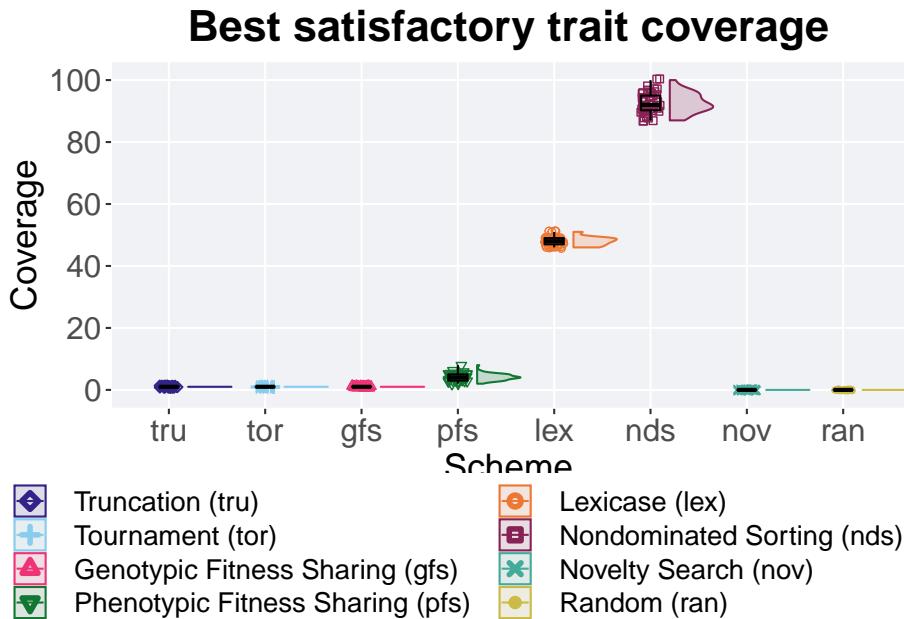


### 4.3.2 Best coverage throughout

Best satisfactory trait coverage throughout 50,000 generations.

```
best = filter(cc_best, col == 'pop_uni_obj' & diagnostic == 'contradictory_objectives')
plot = ggplot(best, aes(x = acron, y = val, color = acron, fill = acron, shape = acron))
  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(-1, 101),
    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) +
  p_theme

plot_grid(
  plot +
    ggtitle("Best satisfactory trait coverage") +
    theme(legend.position="none"),
  legend,
  nrow=2,
  rel_heights = c(2,.55),
  label_size = TSIZE
)
```



#### 4.3.2.1 Stats

Summary statistics for the best satisfactory trait coverage throughout 50,000 generations.

```
best$acron = factor(best$acron, levels = c('nds', 'lex', 'pfs', 'gfs', 'tor', 'tru', 'nov', 'ran')
group_by(best, acron) %>%
  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
##   acron count na_cnt  min median  mean  max   IQR
##   <fct> <int> <int> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 nds     50     0     87    92.6  92.6   100   4.75
## 2 lex     50     0     46    48.0   48.0    51    2
## 3 pfs     50     0      2     4     4.12    8    2
## 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 provides evidence of difference among satisfactory trait coverage throughout 50,000 generations.

```
kruskal.test(val ~ acron, data = best)
```

```
##
## Kruskal-Wallis rank sum test
##
## data: val by acron
## Kruskal-Wallis chi-squared = 396.62, df = 7, p-value < 2.2e-16
```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction on satisfactory trait coverage throughout 50,000 generations.

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

```
##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: best$val and best$acron
##
##    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
```

### 4.3.3 End of 50,000 generations

Satisfactory trait coverage in the population at the end of 50,000 generations.

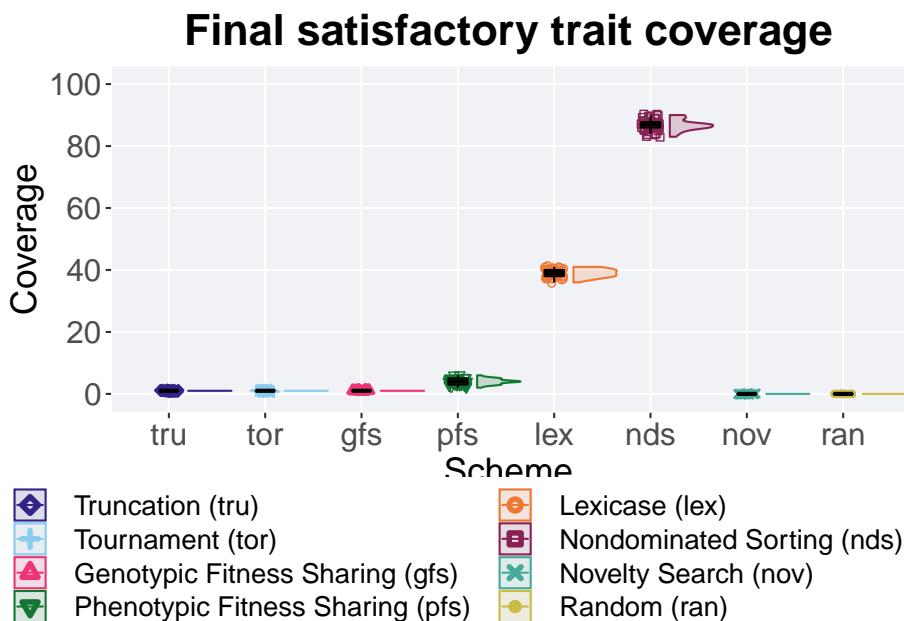
```
end = filter(cc_end, diagnostic == 'contradictory_objectives')
plot = ggplot(end, aes(x = acron, y = pop_uni_obj, color = acron, fill = acron, shape =
  geom_flat_violin(position = position_nudge(x = .2, y = 0), scale = 'width', alpha = 0.5) +
  geom_point(position = position_jitter(width = .1), 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(-1, 101),
    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) +
p_theme

plot_grid(
  plot +
  ggtitle("Final satisfactory trait coverage") +
  theme(legend.position="none"),
  legend,
  nrow=2,
  rel_heights = c(2,.55),
  label_size = TSIZE
)

```



#### 4.3.3.1 Stats

Summary statistics for satisfactory trait coverage in the population at the end of 50,000 generations.

```

end$acron = factor(end$acron, levels = c('nds', 'lex', 'pfs', 'gfs', 'tor', 'tru', 'nov')
group_by(end, acron) %>%
  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
##   acron count na_cnt   min median   mean   max   IQR
##   <fct> <int> <int> <dbl> <dbl> <dbl> <dbl>
## 1 nds     50     0     83     87   86.8    90   1.75
## 2 lex     50     0     36     39   39.0    41    2
## 3 pfs     50     0      2      4     4      6    2
## 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 provides evidence of difference among satisfactory trait coverage in the population at the end of 50,000 generations.

```
kruskal.test(pop_uni_obj ~ acron, data = end)
```

```
##
## Kruskal-Wallis rank sum test
##
## data: pop_uni_obj by acron
## Kruskal-Wallis chi-squared = 396.66, df = 7, p-value < 2.2e-16
```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction on satisfactory trait coverage in the population at the end of 50,000 generations.

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

##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: end$pop_uni_obj and end$acron
##
##   nds   lex   pfs   gfs   tor   tru   nov
##   lex <2e-16 -    -    -    -    -    -
```

```

## pfs <2e-16 <2e-16 - - - - -
## gfs <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 - -
## ran <2e-16 <2e-16 <2e-16 <2e-16 <2e-16 1
##
## P value adjustment method: bonferroni

```

## 4.4 Activation gene coverage

Activation gene coverage analysis.

### 4.4.1 Over time coverage

Activation gene coverage over time.

```

contradictory_objectives = filter(cc_over_time, diagnostic == 'contradictory_objectives')
contradictory_objectives$uni_str_pos = contradictory_objectives$uni_str_pos + contradictory_objectives
lines = contradictory_objectives %>%
  group_by(`Selection\nScheme`, gen) %>%
  dplyr::summarise(
    min = min(uni_str_pos),
    mean = mean(uni_str_pos),
    max = max(uni_str_pos)
  )

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

points = filter(lines, gen %% 2000 == 0 & gen != 0)

ot = ggplot(lines, aes(x=gen, y=mean, group = `Selection\nScheme`, fill = `Selection\nScheme`, color = `Selection\nScheme`)) +
  geom_ribbon(aes(ymin = min, ymax = max), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = points, size = 1.5, stroke = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Coverage",
    limits=c(-1, 101),
    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+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6")

) +
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+  

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")
) +
theme(  

legend.position = "bottom",  

legend.box="vertical",  

legend.justification="center",  

legend.title=element_blank()
)

ot

```

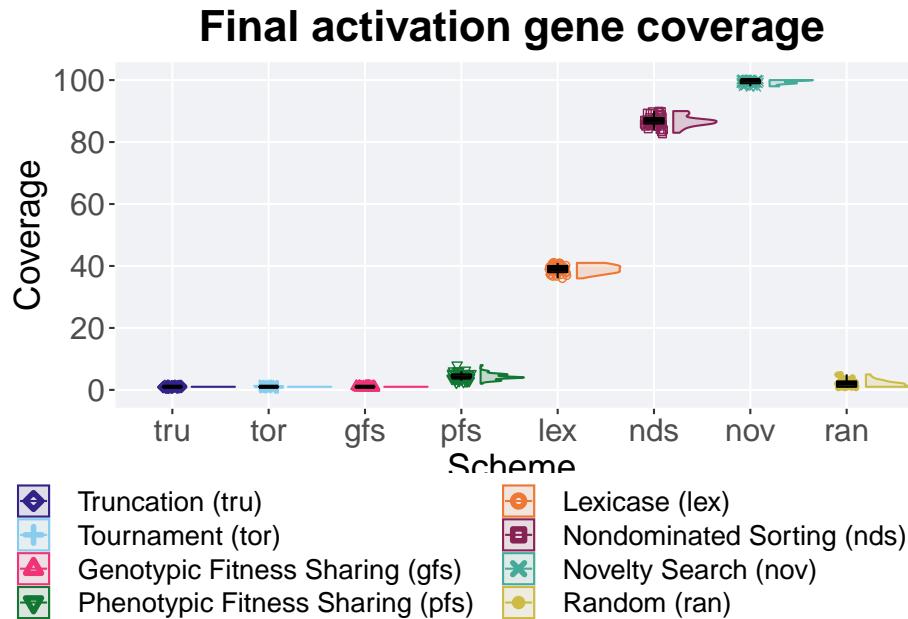


#### 4.4.2 End of 50,000 generations

Activation gene coverage in the population at the end of 50,000 generations.

```
end = filter(cc_end, diagnostic == 'contradictory_objectives')
end$uni_str_pos = end$uni_str_pos + end$arc_acti_gene - end$overlap
best = ggplot(end, aes(x = acron, y = uni_str_pos, color = acron, fill = acron, shape = acron)) +
  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(-1, 101),
    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) +
  p_theme

plot_grid(
  best +
  ggtitle("Final activation gene coverage") +
  theme(legend.position="none"),
  legend,
  nrow=2,
  rel_heights = c(2,.55),
  label_size = TSIZE
)
```



#### 4.4.2.1 Stats

Summary statistics for activation gene coverage in the population at the end of 50,000 generations.

```
end$acron = factor(end$acron, levels = c('nov', 'nds', 'lex', 'pfs', 'gfs', 'ran', 'tor'))
group_by(end, acron) %>%
  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
##   acron count na_cnt   min median   mean   max   IQR
##   <fct> <int> <int> <dbl> <dbl> <dbl> <int> <dbl>
## 1 nov     50     0     98  100  99.4    100    1
## 2 nds     50     0     83    87  86.8     90  1.75
## 3 lex     50     0     36    39  39.0     41    2
## 4 pfs     50     0      2     4  4.26      8    1
## 5 gfs     50     0      1     1     1      1    0
## 6 ran     50     0      1     2     2      5  1.75
```

```
## 7 tor      50      0      1      1  1      1  0
## 8 tru      50      0      1      1  1      1  0
```

Kruskal–Wallis test provides evidence of difference among activation gene coverage in the population at the end of 50,000 generations.

```
kruskal.test(uni_str_pos ~ acron, data = end)
```

```
##
## Kruskal-Wallis rank sum test
##
## data: uni_str_pos by acron
## Kruskal-Wallis chi-squared = 383.7, df = 7, p-value < 2.2e-16
```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction on activation gene coverage in the population at the end of 50,000 generations.

```
pairwise.wilcox.test(x = end$uni_str_pos, g = end$acron, p.adjust.method = "bonferroni",
                      paired = FALSE, conf.int = FALSE, alternative = '1')

##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: end$uni_str_pos and end$acron
##
##      nov     nds     lex     pfs     gfs ran    tor
## nds < 2e-16 -      -      -      -      -
## lex < 2e-16 < 2e-16 -      -      -      -
## pfs < 2e-16 < 2e-16 < 2e-16 -      -      -
## gfs < 2e-16 < 2e-16 < 2e-16 < 2e-16 -      -
## ran < 2e-16 < 2e-16 < 2e-16 2.1e-12 1      -
## tor < 2e-16 < 2e-16 < 2e-16 < 2e-16 1      2.2e-09 -
## tru < 2e-16 < 2e-16 < 2e-16 < 2e-16 1      2.2e-09 1
##
## P value adjustment method: bonferroni
```

## 4.5 Nondominated sorting split

Here analyze the satisfactory trait coverage and activation gene coverage results for nondominated sorting, nondominated front ranking (no fitness sharing between fronts), and phenotypic fitness sharing.

### 4.5.1 Coverage over time

Satisfactory trait coverage over time.

```
nds <- filter(cc_over_time, acron == 'nds' & diagnostic == 'contradictory_objectives')
nds$'Selection\nScheme' = 'Nondominated sorting (nds)'
```

```

nfr <- read.csv('./DATA-FINAL/NONDOMINATEDSORTING/over-time-contradictory_objectives-no'
nfr$acron = 'nfr'
nfr$'Selection\nScheme' = 'Nondominated front ranking (nfr)'
nfr$diagnostic = 'contradictory_objectives'
nfr <- filter(nfr, trt == 0.0)

pfs <- filter(cc_over_time, acron == 'pfs' & diagnostic == 'contradictory_objectives')
pfs$'Selection\nScheme' = 'Phenotypic fitness sharing (pfs)'

contradictory_objectives <- rbind(nds,nfr,pfs)
contradictory_objectives$`Selection\nScheme` <- factor(contradictory_objectives$`Selection\nScheme`)

lines = contradictory_objectives %>%
  group_by(`Selection\nScheme`, gen) %>%
  dplyr::summarise(
    min = min(pop_uni_obj),
    mean = mean(pop_uni_obj),
    max = max(pop_uni_obj)
  )

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

points = filter(lines, gen %% 2000 == 0 & gen != 0)

ot = ggplot(lines, aes(x=gen, y=mean, group = `Selection\nScheme`, fill = `Selection\nScheme`),
  geom_ribbon(aes(ymin = min, ymax = max), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = points, size = 1.5, stroke = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Coverage",
    limits=c(-1, 101),
    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+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6")
  ) +
  scale_shape_manual(values=SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +

```

```

ggtile("Satisfactory trait coverage over time") +
p_theme+
  guides(
    shape=guide_legend(ncol=1, title.position = "bottom"),
    color=guide_legend(ncol=1, title.position = "bottom"),
    fill=guide_legend(ncol=1, title.position = "bottom")
  ) +
  theme(
    legend.position = "bottom",
    legend.box="vertical",
    legend.justification="center",
    legend.title=element_blank()
  )

```

ot



#### 4.5.2 Best coverage throughout

Best satisfactory trait coverage throughout 50,000 generations.

```

nds <- filter(cc_best, diagnostic == 'contradictory_objectives' & acron == 'nds' & col == 'pop_un'
nds$'Selection\nScheme' = 'Nondominated sorting (nds)'
nds = subset(nds, select = -c(Selection.Scheme) )

nfr <- read.csv('./DATA-FINAL/NONDominatedSORTING/best-contradictory_objectives-nondominatedsorti

```

```

nfr$acron = 'nfr'
nfr$'Selection\nScheme' = 'Nondominated front ranking (nfr)'
nfr$diagnostic = 'contradictory_objectives'
nfr <- filter(nfr, trt == 0.0 & col == 'pop_uni_obj')

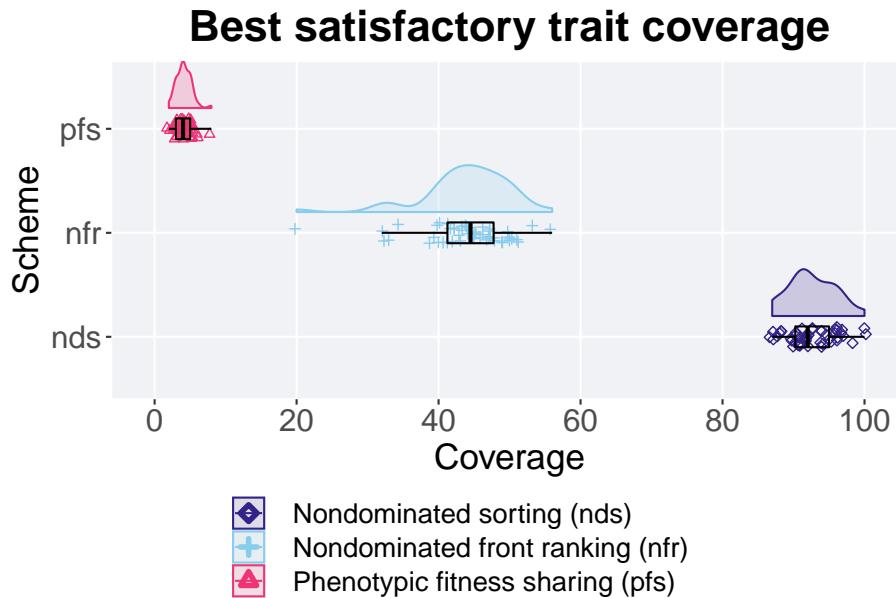
pfs <- filter(cc_best, diagnostic == 'contradictory_objectives' & acron == 'pfs' & col
pfs$'Selection\nScheme' = 'Phenotypic fitness sharing (pfs)'
pfs = subset(pfs, select = -c(Selection.Scheme) )

best <- rbind(nds, nfr, pfs)
best$`Selection\nScheme` <- factor(best$`Selection\nScheme`, levels = c('Nondominated s
best$acron <- factor(best$acron, levels = c('nds','nfr','pfs'))

plot = ggplot(best, aes(x = acron, y = val, color = acron, fill = acron, shape = acron))
  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(-1, 101),
    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) +
  coord_flip()+
  p_theme

plot_grid(
  plot +
  ggtitle("Best satisfactory trait coverage") +
  theme(legend.position="none"),
  legend,
  nrow=2,
  rel_heights = c(2,.6),
  label_size = TSIZE
)

```



#### 4.5.2.1 Stats

Summary statistics for the best satisfactory trait coverage throughout 50,000 generations.

```
group_by(best, acron) %>%
  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: 3 x 8
##   acron count na_cnt   min median   mean   max   IQR
##   <fct> <int> <int> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 nds     50     0     87     92     92.6    100    4.75
## 2 nfr     50     0    20    44.5    43.9     56     6.5
## 3 pfs     50     0      2      4     4.12      8      2
```

Kruskal–Wallis test provides evidence of difference among best satisfactory trait coverage throughout 50,000 generations

```

kruskal.test(val ~ acron,data = best)

##
## Kruskal-Wallis rank sum test
##
## data: val by acron
## Kruskal-Wallis chi-squared = 132.98, df = 2, p-value < 2.2e-16

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction on
best satisfactory trait coverage throughout 50,000 generations.

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

##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: best$val and best$acron
##
##      nds     nfr
## nfr <2e-16 -
## pfs <2e-16 <2e-16
##
## P value adjustment method: bonferroni

```

#### 4.5.3 End of 50,000 generations

Satisfactory trait coverage in the population at the end of 50,000 generations.

```

nds <- filter(cc_end, diagnostic == 'contradictory_objectives' & acron == 'nds')
nds$'Selection\nScheme' = 'Nondominated sorting (nds)'

nfr <- read.csv('./DATA-FINAL/NONDOMINATEDSORTING/over-time-contradictory_objectives-n')
nfr$acron = 'nfr'
nfr$Selection.Scheme = 'Nondominated front ranking (nfr)'
nfr$'Selection\nScheme' = 'Nondominated front ranking (nfr)'
nfr$diagnostic = 'contradictory_objectives'
nfr <- filter(nfr, trt == 0.0 & gen == 50000)
nfr = subset(nfr, select = -c(Selection.Scheme) )

pfs <- filter(cc_end, diagnostic == 'contradictory_objectives' & acron == 'pfs')
pfs$'Selection\nScheme' = 'Phenotypic fitness sharing (pfs)'

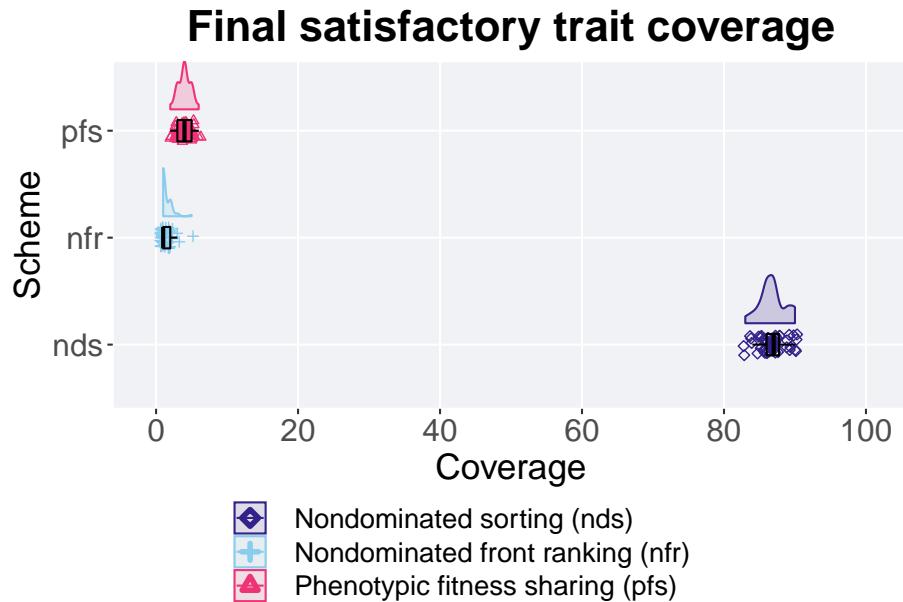
end <- rbind(nds, nfr, pfs)
end$acron <- factor(end$acron, levels = c('nds','nfr','pfs'))

best = ggplot(end, aes(x = acron, y = pop_uni_obj, color = acron, fill = acron, shape =

```

```
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(-1, 101),
    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) +
  coord_flip() +
  p_theme

plot_grid(
  best +
  ggtitle("Final satisfactory trait coverage") +
  theme(legend.position="none"),
  legend,
  nrow=2,
  rel_heights = c(2,.55),
  label_size = TSIZE
)
```



#### 4.5.3.1 Stats

Summary statistics for satisfactory trait coverage in the population at the end of 50,000 generations.

```
group_by(end, acron) %>%
  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: 3 x 8
##   acron count na_cnt   min median   mean   max   IQR
##   <fct>  <int>   <int>   <dbl>   <dbl>   <dbl>   <dbl>
## 1 nds      50       0     83     87   86.8     90   1.75
## 2 nfr      50       0      1      1    1.4      5     1
## 3 pfs      50       0      2      4     4      6     2
```

Kruskal–Wallis test provides evidence of difference among satisfactory trait coverage in the population at the end of 50,000 generations.

```
kruskal.test(pop_uni_obj ~ acron, data = end)

##
## Kruskal-Wallis rank sum test
##
## data: pop_uni_obj by acron
## Kruskal-Wallis chi-squared = 131.43, df = 2, p-value < 2.2e-16

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction on
satisfactory trait coverage in the population at the end of 50,000 generations.

pairwise.wilcox.test(x = end$pop_uni_obj, g = end$acron, p.adjust.method = "bonferroni",
                      paired = FALSE, conf.int = FALSE, alternative = 'l')

##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: end$pop_uni_obj and end$acron
##
##      nds     nfr
## nfr <2e-16 -
## pfs <2e-16 1
##
## P value adjustment method: bonferroni
```



# Chapter 5

## Multi-path exploration results

Here we present the results for the **best performances** and **activation gene coverage** generated by each selection scheme replicate on the contradictory objectives diagnostic. Best performance found refers to the largest average trait score found in a given population. Note that activation gene coverage values are gathered at the population-level. Activation gene coverage refers to the count of unique activation genes in a given population; this gives us a range of integers between 0 and 100.

### 5.1 Analysis dependencies

```
library(ggplot2)
library(cowplot)
library(dplyr)
library(Pupilometry)
```

### 5.2 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     2.1
## year     2022
## month     06
## day       23
## svn rev   82513
## language   R
## version.string R version 4.2.1 (2022-06-23)
## nickname   Funny-Looking Kid

```

## 5.3 Performance

Performance analysis.

### 5.3.1 Over time

Best performance in a population over time.

```

multipath_exploration = filter(cc_over_time, diagnostic == 'multipath_exploration')
lines = multipath_exploration %>%
  group_by(`Selection\nScheme`, gen) %>%
  dplyr::summarise(
    min = min(pop_fit_max),
    mean = mean(pop_fit_max),
    max = max(pop_fit_max)
  )

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

points = filter(lines, gen %% 2000 == 0 & gen != 0)

ot = ggplot(lines, aes(x=gen, y=mean / TRAITS, group = `Selection\nScheme`, fill = `Sel
  geom_ribbon(aes(ymin = min / TRAITS, ymax = max / TRAITS), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = points, size = 1.5, stroke = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Average trait score",
    limits=c(-1, 101),
    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+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6")

) +
scale_shape_manual(values=SHAPE) +
scale_colour_manual(values = cb_palette) +
scale_fill_manual(values = cb_palette) +
ggtitle("Best performance over time") +
p_theme+
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")
) +
theme(
legend.position = "bottom",
legend.box="vertical",
legend.justification="center",
legend.title=element_blank()
)
)

ot

```

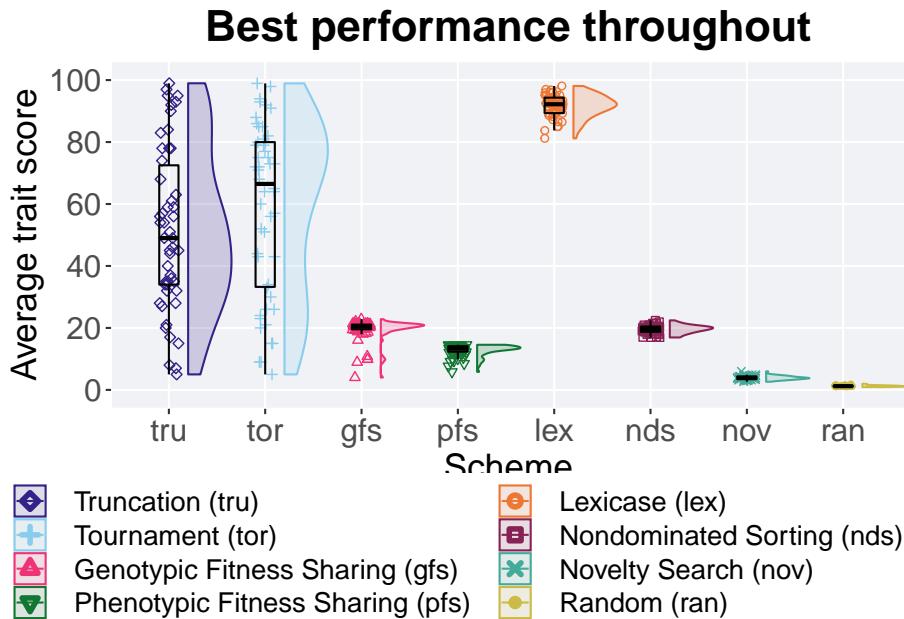


### 5.3.2 Best performance throughout

Best performance throughout 50,000 generations.

```
best = filter(cc_best, col == 'pop_fit_max' & diagnostic == 'multipath_exploration')
plot = ggplot(best, aes(x = acron, y = val / TRAITS, color = acron, fill = acron, shape = acron))
  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 = "Average trait score",
    limits = c(-1, 101),
    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) +
  p_theme

plot_grid(
  plot +
    ggtitle("Best performance throughout") +
    theme(legend.position = "none"),
  legend,
  nrow = 2,
  rel_heights = c(2, .55),
  label_size = TSIZE
)
```



#### 5.3.2.1 Stats

Summary statistics for the best performance throughout 50,000 generations.

```
best$acron <- factor(best$acron, levels = c('lex', 'tor', 'tru', 'nds', 'gfs', 'pfs', 'nov', 'ran'))
group_by(best, acron) %>%
  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
##   acron count na_cnt   min median   mean   max    IQR
##   <fct> <int>   <int>   <dbl>   <dbl>   <dbl>   <dbl>
## 1 lex      50       0  8119.  9221.  9165.  9810.   499.
## 2 tor      50       0   500    6649.  5873.  9894.  4673.
## 3 tru      50       0   500    4900.  5156.  9897.  3849.
## 4 nds      50       0  1692.  1971.  1957.  2244.   171.
## 5 gfs      50       0   400    2045.  1921.  2283.   152.
## 6 pfs      50       0  583.   1336.  1274.  1456.   177.
## 7 nov      50       0  263.   384.   389.   599.   86.5
```

```
## # 8 ran      50      0   90.1   121.   124.   199.   29.9
```

Kruskal–Wallis test provides evidence of difference among best performances throughout 50,000 generations.

```
kruskal.test(val ~ acron,data = best)
```

```
##  
## Kruskal-Wallis rank sum test  
##  
## data: val by acron  
## Kruskal-Wallis chi-squared = 353.07, df = 7, p-value < 2.2e-16
```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction on best performance throughout 50,000 generations.

```
pairwise.wilcox.test(x = best$val, g = best$acron, p.adjust.method = "bonferroni",  
                     paired = FALSE, conf.int = FALSE, alternative = '1')
```

```
##  
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction  
##  
## data: best$val and best$acron  
##  
##    lex     tor     tru     nds     gfs     pfs     nov  
## tor 2.0e-11 -      -      -      -      -      -  
## tru 7.8e-11 1      -      -      -      -      -  
## nds < 2e-16 2.7e-10 2.2e-10 -      -      -      -  
## gfs < 2e-16 3.6e-10 3.8e-10 1      -      -      -  
## pfs < 2e-16 3.5e-13 4.1e-13 < 2e-16 2.5e-11 -      -  
## nov < 2e-16 < 2e-16 < 2e-16 < 2e-16 2.7e-16 < 2e-16 -  
## ran < 2e-16  
##  
## P value adjustment method: bonferroni
```

### 5.3.3 End of 50,000 generations

Best performance in the population at the end of 50,000 generations.

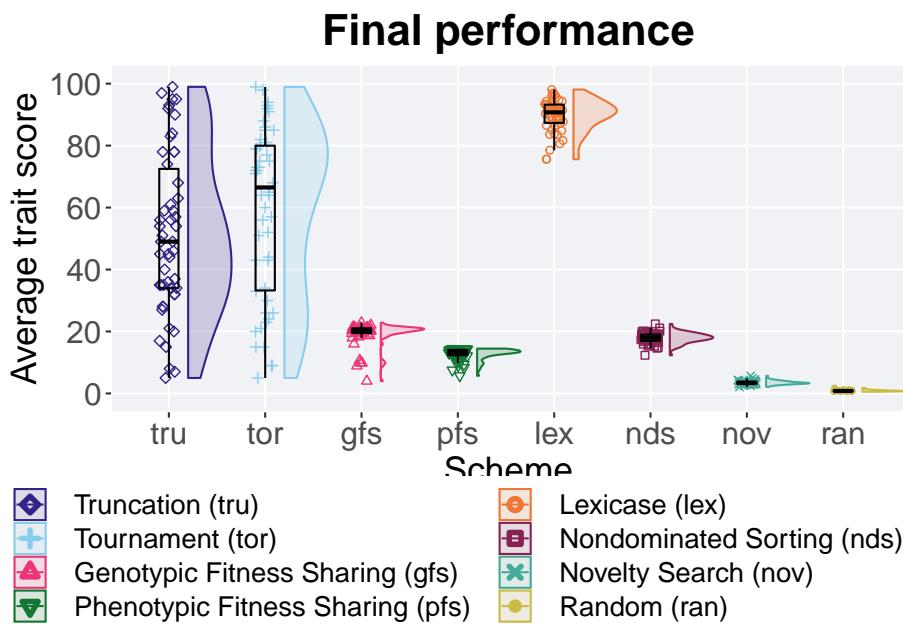
```
end = filter(cc_end, diagnostic == 'multipath_exploration')  
plot = ggplot(end, aes(x = acron, y = pop_fit_max / TRAITS, color = acron, fill = acron)  
  + geom_flat_violin(position = position_nudge(x = .2, y = 0), scale = 'width', alpha = 0.5)  
  + geom_point(position = position_jitter(width = .1), size = 1.5, alpha = 1.0) +  
  + geom_boxplot(color = 'black', width = .2, outlier.shape = NA, alpha = 0.0) +  
  + scale_y_continuous(  
    name = "Average trait score",  
    limits = c(-1, 101),  
    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) +
  p_theme

plot_grid(
  plot +
    ggtitle("Final performance") +
    theme(legend.position="none"),
  legend,
  nrow=2,
  rel_heights = c(2,.55),
  label_size = TSIZE
)

```



### 5.3.3.1 Stats

Summary statistics for best performance in the population at the end of 50,000 generations.

```

end$acron <- factor(end$acron, levels = c('lex','tor','tru','nds','gfs','pfs','nov','ran'))
group_by(end, acron) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(pop_fit_max)),
    min = min(pop_fit_max, na.rm = TRUE),
    median = median(pop_fit_max, na.rm = TRUE),
    mean = mean(pop_fit_max, na.rm = TRUE),
    max = max(pop_fit_max, na.rm = TRUE),
    IQR = IQR(pop_fit_max, na.rm = TRUE)
  )

## # A tibble: 8 x 8
##   acron count na_cnt     min median    mean    max    IQR
##   <fct> <int> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 lex      50     0 7559.  9074.  8969.  9810.  589.
## 2 tor      50     0  500   6649.  5873.  9894.  4673.
## 3 tru      50     0  500   4900.  5156.  9897.  3849.
## 4 nds      50     0 1232.  1800.  1791.  2244.  206.
## 5 gfs      50     0  399.  2041.  1916.  2283.  153.
## 6 pfs      50     0  570.  1333.  1268.  1448.  174.
## 7 nov      50     0 210.   336.   349.   568.   73.0
## 8 ran      50     0  55.0  79.9   87.0  183.   30.4

```

Kruskal–Wallis test provides evidence of difference among best performance in the population at the end of 50,000 generations.

```

kruskal.test(pop_fit_max ~ acron, data = end)

##
##  Kruskal-Wallis rank sum test
##
## data: pop_fit_max by acron
## Kruskal-Wallis chi-squared = 353.68, df = 7, p-value < 2.2e-16

```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction on best performance in the population at the end of 50,000 generations.

```

pairwise.wilcox.test(x = end$pop_fit_max, g = end$acron, p.adjust.method = "bonferroni",
                      paired = FALSE, conf.int = FALSE, alternative = 'l')

##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: end$pop_fit_max and end$acron
##
##    lex    tor    tru    nds    gfs    pfs    nov
##    tor 6.6e-10 -      -      -      -      -      -

```

```

## tru 6.0e-10 1      -      -      -      -      -
## nds < 2e-16 8.2e-11 4.8e-11 -      -      -      -
## gfs < 2e-16 3.4e-10 3.6e-10 1      -      -      -
## pfs < 2e-16 3.2e-13 4.1e-13 8.9e-16 2.5e-11 -      -
## nov < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 -
## ran < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16
##
## P value adjustment method: bonferroni

```

## 5.4 Activation gene coverage

Activation gene coverage analysis.

### 5.4.1 Over time coverage

Activation gene coverage over time.

```

multipath_exploration = filter(cc_over_time, diagnostic == 'multipath_exploration')
multipath_exploration$uni_str_pos = multipath_exploration$uni_str_pos + multipath_exploration$arc

lines = multipath_exploration %>%
  group_by(`Selection\nScheme`, gen) %>%
  dplyr::summarise(
    min = min(uni_str_pos),
    mean = mean(uni_str_pos),
    max = max(uni_str_pos)
  )

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

points = filter(lines, gen %% 2000 == 0 & gen != 0)

ot = ggplot(lines, aes(x=gen, y=mean, group = `Selection\nScheme`, fill = `Selection\nScheme`, col =
  geom_ribbon(aes(ymin = min, ymax = max), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = points, size = 1.5, stroke = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Coverage",
    limits=c(-1, 101),
    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+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6")

) +
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+
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")
) +
theme(
legend.position = "bottom",
legend.box="vertical",
legend.justification="center",
legend.title=element_blank()
)

)
ot

```

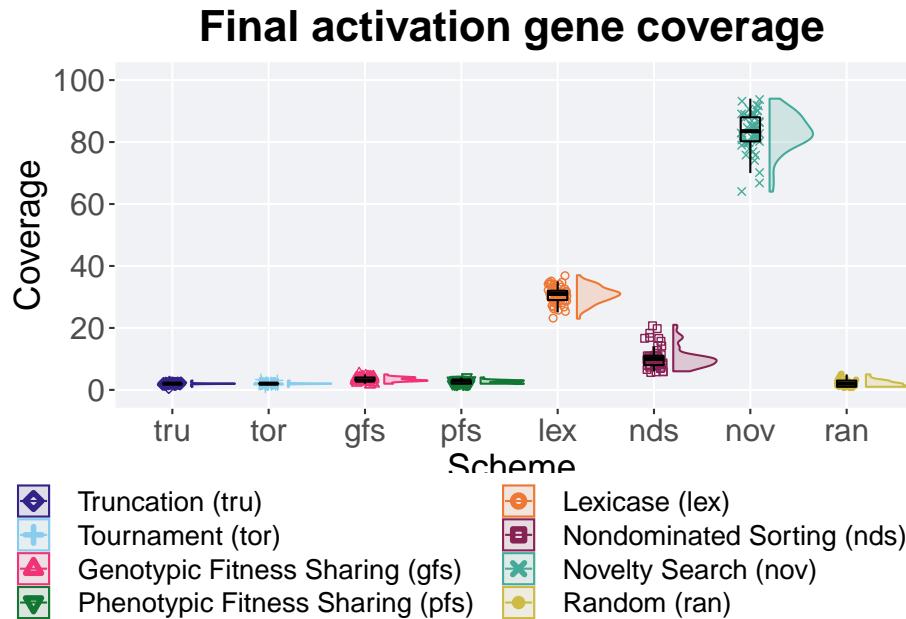


### 5.4.2 End of 50,000 generations

Activation gene coverage in the population at the end of 50,000 generations.

```
end = filter(cc_end, diagnostic == 'multipath_exploration')
end$uni_str_pos = end$uni_str_pos + end$arc_acti_gene - end$overlap
best = ggplot(end, aes(x = acron, y = uni_str_pos, color = acron, fill = acron, shape = acron)) +
  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(-1, 101),
    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) +
  p_theme

plot_grid(
  best +
    ggtitle("Final activation gene coverage") +
    theme(legend.position="none"),
  legend,
  nrow=2,
  rel_heights = c(2,.55),
  label_size = TSIZE
)
```



#### 5.4.2.1 Stats

Summary statistics for activation gene coverage in the population at the end of 50,000 generations.

```
end$acron <- factor(end$acron, levels = c('nov', 'lex', 'nds', 'gfs', 'pfs', 'tor', 'tru', 'ran'))
group_by(end, acron) %>%
  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
##   acron count na_cnt   min median   mean   max   IQR
##   <fct> <int> <int> <dbl> <dbl> <dbl> <int> <dbl>
## 1 nov     50     0     64  83.5  83.2    94  7.75
## 2 lex     50     0     23   31    30.7    37   3
## 3 nds     50     0      6   10    10.4    21   3
## 4 gfs     50     0      2    3    3.34     5   1
## 5 pfs     50     0      2    3    2.56     4   1
## 6 tor     50     0      1    2    2.02     3   0
```

```
## 7 tru      50      0      1      2      2      3      0
## 8 ran      50      0      1      2      2      5      2
```

Kruskal–Wallis test provides evidence of difference among activation gene coverage in the population at the end of 50,000 generations.

```
kruskal.test(uni_str_pos ~ acron, data = end)
```

```
##
## Kruskal-Wallis rank sum test
##
## data: uni_str_pos by acron
## Kruskal-Wallis chi-squared = 350.16, df = 7, p-value < 2.2e-16
```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction on activation gene coverage in the population at the end of 50,000 generations.

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

```
##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: end$uni_str_pos and end$acron
##
##    nov    lex    nds    gfs    pfs    tor    tru
## lex < 2e-16 -      -      -      -      -      -
## nds < 2e-16 < 2e-16 -      -      -      -      -
## gfs < 2e-16 < 2e-16 < 2e-16 -      -      -      -
## pfs < 2e-16 < 2e-16 < 2e-16 3.3e-06 -      -      -
## tor < 2e-16 < 2e-16 < 2e-16 1.7e-15 1.2e-06 -      -
## tru < 2e-16 < 2e-16 < 2e-16 5.0e-16 2.6e-07 1.0000 -
## ran < 2e-16 < 2e-16 < 2e-16 1.2e-08 0.0036 1.0000 1.0000
##
## P value adjustment method: bonferroni
```



# Chapter 6

## Truncation selection

We present the results from our parameter sweep on truncation selection. 50 replicates are conducted for each truncation size T parameter value explored.

```
library(ggplot2)
library(cowplot)
library(dplyr)
library(PupilometryR)
```

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         2.1
## year          2022
## month         06
## day           23
## svn rev       82513
## language      R
## version.string R version 4.2.1 (2022-06-23)
## nickname      Funny-Looking Kid
```

## 6.1 Exploitation rate results

Here we present the results for **best performances** found by each genotypic fitness sharing sigma value replicate on the exploitation rate diagnostic. Best performance found refers to the largest average trait score found in a given population. Note that performance values fall between 0 and 100.

### 6.1.1 Performance over time

Performance over time.

```
problem <- filter(tru_ot, diagnostic == 'exploitation_rate')
lines = problem %>%
  group_by(T, gen) %>%
  dplyr::summarise(
    min = min(pop_fit_max),
    mean = mean(pop_fit_max),
    max = max(pop_fit_max)
  )

## `summarise()` has grouped output by 'T'. You can override using the `.groups` argument.

points = filter(lines, gen %% 2000 == 0 & gen != 0)

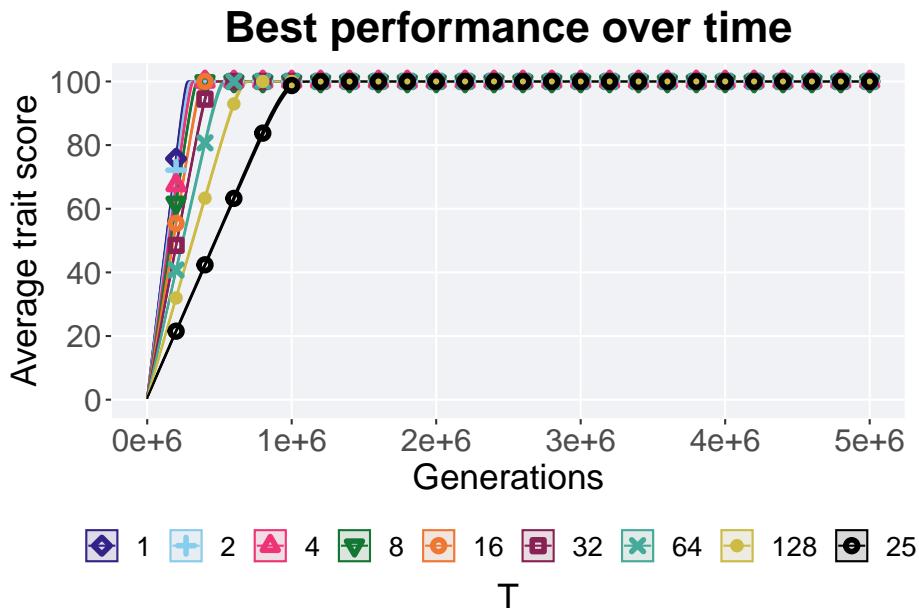
ot = ggplot(lines, aes(x=gen, y=mean / TRAITS, group = T, fill = T, color = T, shape =
  geom_ribbon(aes(ymin = min / TRAITS, ymax = max / TRAITS), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = points, size = 1.5, stroke = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Average trait score",
    limits=c(-1, 101),
    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+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6")
  ) +
  scale_shape_manual(values=SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  ggtitle("Best performance over time") +
  p_theme+
```

```

guides(
  shape=guide_legend(nrow=1, title.position = "bottom"),
  color=guide_legend(nrow=1, title.position = "bottom"),
  fill=guide_legend(nrow=1, title.position = "bottom")
) +
theme(
  legend.position = "bottom",
  legend.box="vertical",
  legend.justification="center",
  legend.title.align=0.5
)

```

ot



### 6.1.2 Generation satisfactory solution found

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

```

ssf = filter(tru_ssf, diagnostic == 'exploitation_rate')

plot <- ggplot(ssf, aes(x = T, y = generation, color = T, fill = T, shape = T)) +
  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) +

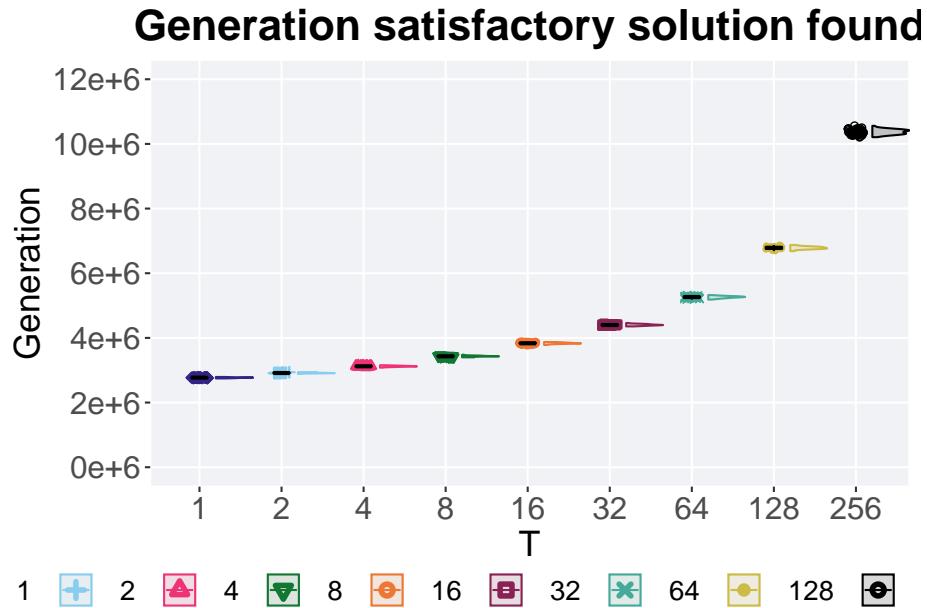
```

```

scale_shape_manual(values=SHAPE) +
scale_y_continuous(
  name="Generation",
  limits=c(0, 12000),
  breaks=c(0, 2000, 4000, 6000, 8000, 10000, 12000),
  labels=c("0e+6", "2e+6", "4e+6", "6e+6", "8e+6", "10e+6", "12e+6")
) +
scale_x_discrete(
  name="T"
) +
scale_colour_manual(values = cb_palette) +
scale_fill_manual(values = cb_palette) +
p_theme

plot_grid(
  plot +
  ggtitle("Generation satisfactory solution found") +
  theme(legend.position="none"),
  legend,
  nrow=2,
  rel_heights = c(2,.2),
  label_size = TSIZE
)

```



### 6.1.2.1 Stats

Summary statistics for the first generation a satisfactory solution is found throughout the 50,000 generations.

```
group_by(ssf, T) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(generation)),
    min = min(generation, na.rm = TRUE),
    median = median(generation, na.rm = TRUE),
    mean = mean(generation, na.rm = TRUE),
    max = max(generation, na.rm = TRUE),
    IQR = IQR(generation, na.rm = TRUE)
  )

## # A tibble: 9 x 8
##   T      count na_cnt   min median   mean   max   IQR
##   <fct> <int> <int> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 1       50     0  2746  2771  2769.  2792  15.5
## 2 2       50     0  2886  2914. 2917.  2941  19.8
## 3 4       50     0  3080  3122. 3121.  3154  19.8
## 4 8       50     0  3399  3430. 3432.  3478  18
## 5 16      50     0  3779  3833  3835.  3872  26.8
## 6 32      50     0  4355  4398. 4401.  4460  33.2
## 7 64      50     0  5185  5264  5261.  5324  44.5
## 8 128     50     0  6684  6784  6785.  6874  60.2
## 9 256     50     0 10209 10369 10371. 10559 109.
```

Kruskal–Wallis test provides evidence of significant differences among the generation a satisfactory solution is first found.

```
kruskal.test(generation ~ T,data = ssf)

##
## Kruskal-Wallis rank sum test
##
## data: generation by T
## Kruskal-Wallis chi-squared = 443.46, df = 8, p-value < 2.2e-16
```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction on the generation a satisfactory solution is first found. .

```
pairwise.wilcox.test(x = ssf$generation, g = ssf$T , p.adjust.method = "bonferroni",
                      paired = FALSE, conf.int = FALSE, alternative = 'g')

##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
```

```
## data: ssf$generation and ssf$T
##
##      1     2     4     8    16    32    64   128
## 2 <2e-16 - - - - - - -
## 4 <2e-16 <2e-16 - - - - - -
## 8 <2e-16 <2e-16 <2e-16 - - - - - -
## 16 <2e-16 <2e-16 <2e-16 <2e-16 - - - -
## 32 <2e-16 <2e-16 <2e-16 <2e-16 <2e-16 - - -
## 64 <2e-16 <2e-16 <2e-16 <2e-16 <2e-16 <2e-16 - -
## 128 <2e-16 <2e-16 <2e-16 <2e-16 <2e-16 <2e-16 <2e-16 - -
## 256 <2e-16 <2e-16 <2e-16 <2e-16 <2e-16 <2e-16 <2e-16 <2e-16
##
## P value adjustment method: bonferroni
```

## 6.2 Ordered exploitation results

Here we present the results for best performances found by each genotypic fitness sharing sigma value replicate on the ordered exploitation diagnostic. Best performance found refers to the largest average trait score found in a given population. Note that performance values fall between 0 and 100.

### 6.2.1 Performance over time

Performance over time.

```
problem <- filter(tru_ot, diagnostic == 'ordered_exploitation')
lines = problem %>%
  group_by(T, gen) %>%
  dplyr::summarise(
    min = min(pop_fit_max),
    mean = mean(pop_fit_max),
    max = max(pop_fit_max)
  )

## `summarise()` has grouped output by 'T'. You can override using the `groups` argument.

points = filter(lines, gen %% 2000 == 0 & gen != 0)

ot = ggplot(lines, aes(x=gen, y=mean / TRAITS, group = T, fill = T, color = T, shape =
  geom_ribbon(aes(ymin = min / TRAITS, ymax = max / TRAITS), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = points, size = 1.5, stroke = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Average trait score",
    limits=c(-1, 101),
```

```
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+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6")

) +
scale_shape_manual(values=SHAPE) +
scale_colour_manual(values = cb_palette) +
scale_fill_manual(values = cb_palette) +
ggtitle("Best performance over time") +
p_theme+
guides(
  shape=guide_legend(nrow=1, title.position = "bottom"),
  color=guide_legend(nrow=1, title.position = "bottom"),
  fill=guide_legend(nrow=1, title.position = "bottom")
) +
theme(
  legend.position = "bottom",
  legend.box="vertical",
  legend.justification="center",
  legend.title.align=0.5
)

ot
```



### 6.2.2 Generation satisfactory solution found

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

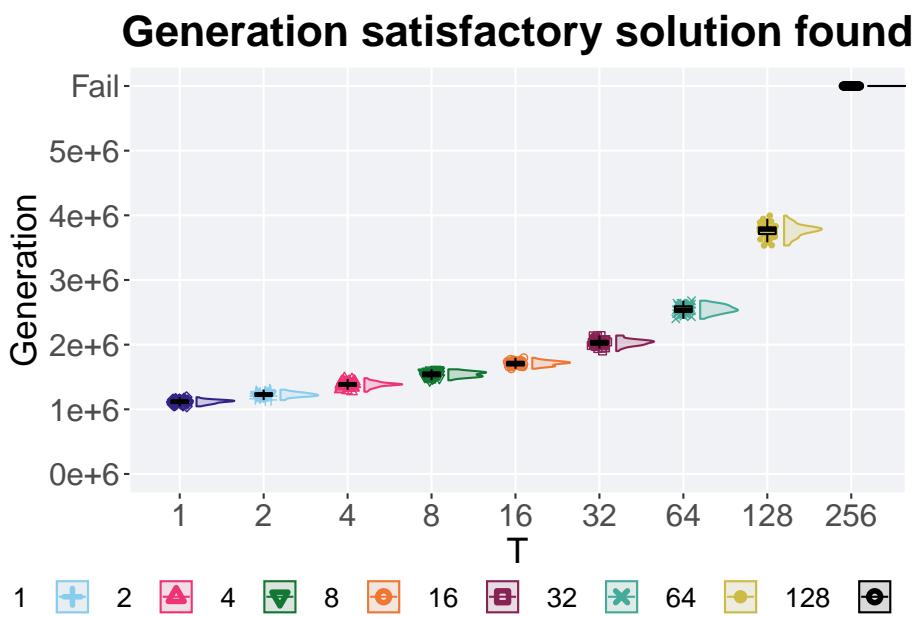
```
ssf = filter(tru_ssf, diagnostic == 'ordered_exploitation')

plot <- ggplot(ssf, aes(x = T, y = generation, color = T, fill = T, shape = T)) +
  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_shape_manual(values=SHAPE) +
  scale_y_continuous(
    name="Generation",
    limits=c(0, 60000),
    breaks=c(0, 10000, 20000, 30000, 40000, 50000, 60000),
    labels=c("0e+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6", "Fail"))
  ) +
  scale_x_discrete(
    name="T"
  ) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  p_theme
```

```

plot_grid(
  plot +
    ggtitle("Generation satisfactory solution found") +
    theme(legend.position="none"),
  legend,
  nrow=2,
  rel_heights = c(2,.2),
  label_size = TSIZE
)

```



### 6.2.2.1 Stats

Summary statistics for the first generation a satisfactory solution is found throughout the 50,000 generations.

```

ssf = filter(ssf, T != 2)

group_by(ssf, T) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(generation)),
    min = min(generation, na.rm = TRUE),
    median = median(generation, na.rm = TRUE),
    mean = mean(generation, na.rm = TRUE),
    max = max(generation, na.rm = TRUE),
    )

```

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

## # A tibble: 8 x 8
##   T     count na_cnt   min median   mean   max   IQR
##   <fct> <int> <int> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 1      50    0 10460 11241 11172. 11869 409.
## 2 4      50    0 12720 13842 13830. 14809 448.
## 3 8      50    0 14487 15446. 15428. 16184 609.
## 4 16     50    0 16269 17168. 17103. 17969 566.
## 5 32     50    0 19009 20381 20332. 21414 606.
## 6 64     50    0 23993 25418. 25485. 26795 885.
## 7 128    50    0 35340 37772 37632. 39953 1039.
## 8 256    50    0 59999 59999 59999 59999    0
```

Kruskal–Wallis test provides evidence of significant differences among the first generation a satisfactory solution is found throughout the 50,000 generations.

```
kruskal.test(generation ~ T, data = ssf)
```

```
##
## Kruskal-Wallis rank sum test
##
## data: generation by T
## Kruskal-Wallis chi-squared = 393.51, df = 7, p-value < 2.2e-16
```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction on the first generation a satisfactory solution is found throughout the 50,000 generations.

```
pairwise.wilcox.test(x = ssf$generation, g = ssf$T , p.adjust.method = "bonferroni",
                      paired = FALSE, conf.int = FALSE, alternative = 'g')

##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: ssf$generation and ssf$T
##
##   1     4     8     16    32    64    128
## 4 <2e-16 -     -     -     -     -     -
## 8 <2e-16 <2e-16 -     -     -     -     -
## 16 <2e-16 <2e-16 <2e-16 -     -     -     -
## 32 <2e-16 <2e-16 <2e-16 <2e-16 -     -     -
## 64 <2e-16 <2e-16 <2e-16 <2e-16 <2e-16 -     -
## 128 <2e-16 <2e-16 <2e-16 <2e-16 <2e-16 <2e-16 -
## 256 <2e-16 <2e-16 <2e-16 <2e-16 <2e-16 <2e-16 <2e-16
##
## P value adjustment method: bonferroni
```

## 6.3 Contraditruy objectives diagnostic

Here we present the results for **satisfactory trait coverage** and **activation gene coverage** found by each genotypic fitness sharing sigma value replicate on the ordered exploitation diagnostic. Satisfactruy trait coverage refers to the count of unique satisfied traits in the population, while activation gene coverage refers to the count of unique activation genes in the population. Note that both coverage values fall between 0 and 100.

### 6.3.1 Satisfactruy trait coverage

Satisfactruy trait coverage analysis.

#### 6.3.1.1 Coverage over time

Satisfactruy trait coverage over time.

```
problem <- filter(tru_ot, diagnostic == 'contradictory_objectives')
lines = problem %>%
  group_by(T, gen) %>%
  dplyr::summarise(
    min = min(pop_uni_obj),
    mean = mean(pop_uni_obj),
    max = max(pop_uni_obj)
  )
## `summarise()` has grouped output by 'T'. You can override using the `.groups` argument.
points = filter(lines, gen %% 2000 == 0 & gen != 0)

ot = ggplot(lines, aes(x=gen, y=mean, group = T, fill = T, color = T, shape = T)) +
  geom_ribbon(aes(ymin = min, ymax = max), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = points, size = 1.5, stroke = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Coverage",
    limits=c(0, 5)
  ) +
  scale_x_continuous(
    name="Generations",
    limits=c(0, 50000),
    breaks=c(0, 10000, 20000, 30000, 40000, 50000),
    labels=c("0e+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6")
  ) +
  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 +
guides(
  shape=guide_legend(nrow=1, title.position = "bottom"),
  color=guide_legend(nrow=1, title.position = "bottom"),
  fill=guide_legend(nrow=1, title.position = "bottom")
) +
theme(
  legend.position = "bottom",
  legend.box="vertical",
  legend.justification="center",
  legend.title.align=0.5
)
)

ot

```



### 6.3.1.2 Best coverage throughout

Best satisfactory trait coverage throughout 50,000 generations.

```

best = filter(tru_best, col == 'pop_uni_obj' & diagnostic == 'contradictory_objectives')

plot = ggplot(best, aes(x = T, y = val, color = T, fill = T, shape = T)) +

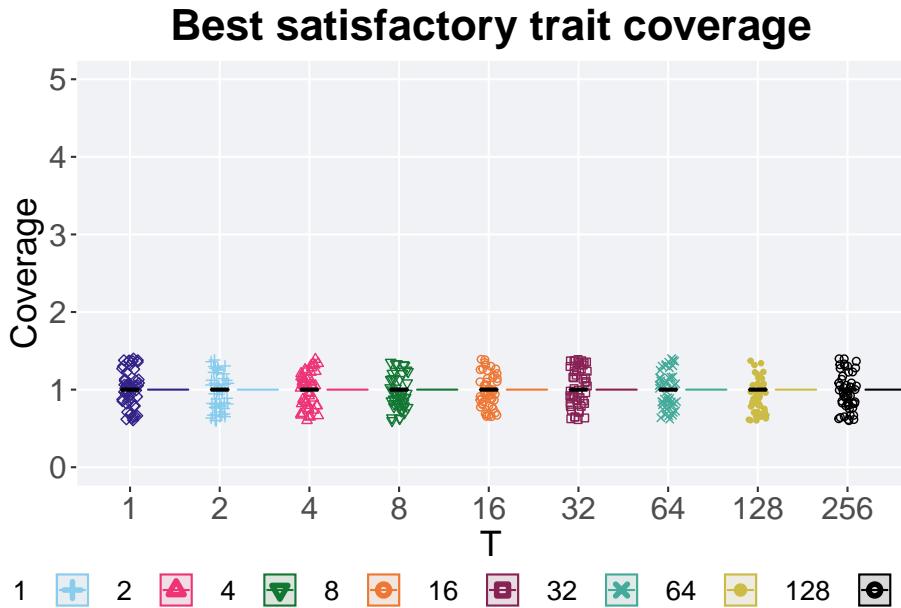
```

```

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, 5)
  ) +
  scale_x_discrete(
    name = "T"
  ) +
  scale_shape_manual(values = SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  p_theme

plot_grid(
  plot +
    ggtitle("Best satisfactory trait coverage") +
    theme(legend.position = "none"),
  legend,
  nrow = 2,
  rel_heights = c(2, .2),
  label_size = TSIZE
)

```



### 6.3.1.2.1 Stats

Summary statistics for the best satisfactory trait coverage throughout 50,000 generations.

```
group_by(best, T) %>%
  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: 9 x 8
##   T     count na_cnt  min median  mean  max  IQR
##   <fct> <int>   <int> <dbl> <dbl> <dbl> <dbl>
## 1 1       50      0     1     1     1     1     0
## 2 2       50      0     1     1     1     1     0
## 3 4       50      0     1     1     1     1     0
## 4 8       50      0     1     1     1     1     0
## 5 16      50      0     1     1     1     1     0
## 6 32      50      0     1     1     1     1     0
## 7 64      50      0     1     1     1     1     0
## 8 128     50      0     1     1     1     1     0
## 9 256     50      0     1     1     1     1     0
```

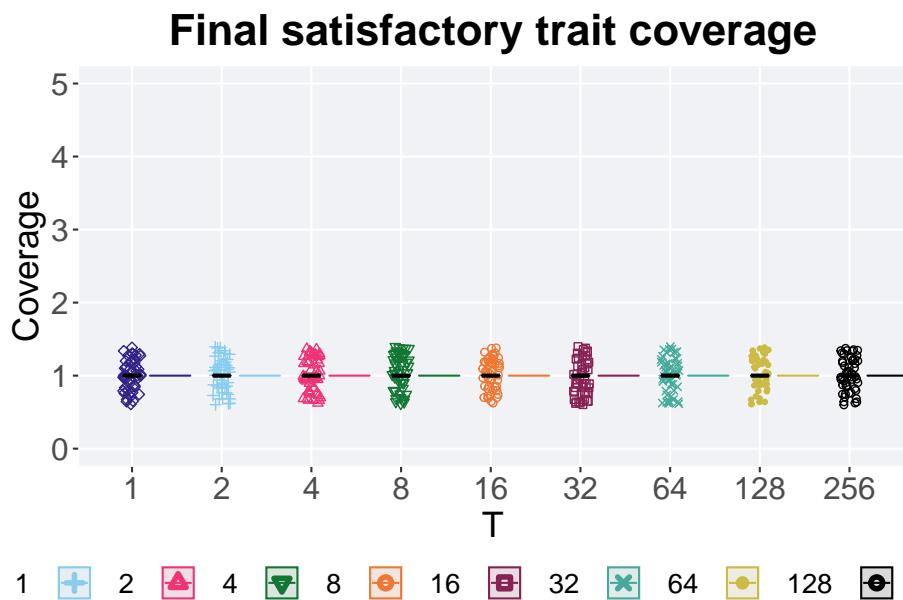
### 6.3.1.3 End of 50,000 generations

Satisfactory trait coverage in the population at the end of 50,000 generations.

```
end = filter(tru_end, diagnostic == 'contradictory_objectives')
plot = ggplot(end, aes(x = T, y = pop_uni_obj, color = T, fill = T, shape = T)) +
  geom_flat_violin(position = position_nudge(x = .2, y = 0), scale = 'width', alpha = 0.0) +
  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, 5)
  ) +
  scale_x_discrete(
    name="T"
  ) +
  scale_shape_manual(values=SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
```

```
p_theme
```

```
plot_grid(
  plot +
    ggtitle("Final satisfactory trait coverage") +
    theme(legend.position="none"),
  legend,
  nrow=2,
  rel_heights = c(2,.3),
  label_size = TSIZE
)
```



#### 6.3.1.3.1 Stats

Summary statistics for satisfactory trait coverage in the population at the end of 50,000 generations.

```
group_by(end, T) %>%
  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: 9 x 8
##   T      count na_cnt  min median  mean  max  IQR
##   <fct> <int> <int> <dbl> <dbl> <dbl> <int> <dbl>
## 1 1       50     0     1     1     1     1     0
## 2 2       50     0     1     1     1     1     0
## 3 4       50     0     1     1     1     1     0
## 4 8       50     0     1     1     1     1     0
## 5 16      50     0     1     1     1     1     0
## 6 32      50     0     1     1     1     1     0
## 7 64      50     0     1     1     1     1     0
## 8 128     50     0     1     1     1     1     0
## 9 256     50     0     1     1     1     1     0

```

### 6.3.2 Activation gene coverage

Here we analyze the activation gene coverage for each parameter replicate on the contradictory objectives diagnostic.

#### 6.3.2.1 Coverage over time

Activation gene coverage over time.

```

problem <- filter(tru_ot, diagnostic == 'contradictory_objectives')
lines = problem %>%
  group_by(T, gen) %>%
  dplyr::summarise(
    min = min(uni_str_pos),
    mean = mean(uni_str_pos),
    max = max(uni_str_pos)
  )

## `summarise()` has grouped output by 'T'. You can override using the `.groups`#
## argument.

points = filter(lines, gen %% 2000 == 0 & gen != 0)

ot = ggplot(lines, aes(x=gen, y=mean, group = T, fill = T, color = T, shape = T)) +
  geom_ribbon(aes(ymin = min, ymax = max), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = points, size = 1.5, stroke = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Coverage",
    limits=c(-1, 101),
    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+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6")

) +
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 +
guides(
  shape=guide_legend(nrow=1, title.position = "bottom"),
  color=guide_legend(nrow=1, title.position = "bottom"),
  fill=guide_legend(nrow=1, title.position = "bottom")
) +
theme(
  legend.position = "bottom",
  legend.box="vertical",
  legend.justification="center",
  legend.title.align=0.5
)

)
ot
```



#### 6.3.2.2 End of 50,000 generations

Activation gene coverage in the population at the end of 50,000 generations.

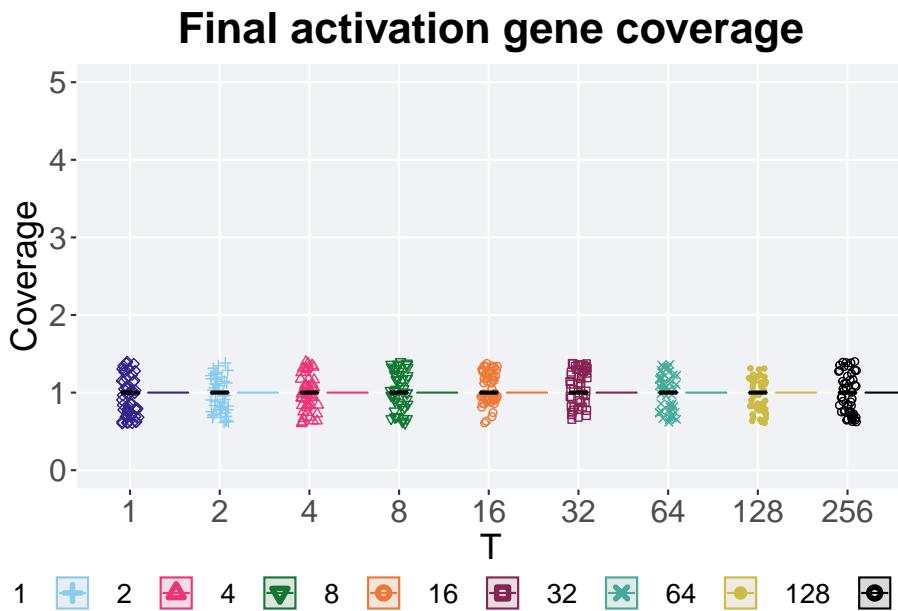
```
end = filter(tru_end, diagnostic == 'contradictory_objectives')
plot = ggplot(end, aes(x = T, y = uni_str_pos, color = T, fill = T, shape = T)) +
  geom_flat_violin(position = position_nudge(x = .2, y = 0), scale = 'width', alpha = 0.5) +
  geom_point(position = position_jitter(width = .1), size = 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, 5)
  ) +
  scale_x_discrete(
    name = "T"
  ) +
  scale_shape_manual(values = SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  p_theme

plot_grid(
  plot +
    ggtitle("Final activation gene coverage") +
    theme(legend.position = "none"),
  nrow = 1,
  ncol = 1
)
```

```

legend,
nrow=2,
rel_heights = c(2,.2),
label_size = TSIZE
)

```



#### 6.3.2.2.1 Stats

Summary statistics for activation gene coverage in the population at the end of 50,000 generations.

```

group_by(end, T) %>%
  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: 9 x 8
##   T      count  na_cnt  min  median  mean   max   IQR
##   <fct> <int>   <int> <dbl> <dbl> <dbl> <int> <dbl>
## 1 1        50       0     1      1      1     1      0

```

```
## 2 2      50    0    1    1    1    1    0
## 3 4      50    0    1    1    1    1    0
## 4 8      50    0    1    1    1    1    0
## 5 16     50    0    1    1    1    1    0
## 6 32     50    0    1    1    1    1    0
## 7 64     50    0    1    1    1    1    0
## 8 128    50    0    1    1    1    1    0
## 9 256    50    0    1    1    1    1    0
```

## 6.4 Multi-path exploration results

Here we present the results for **best performances** and **activation gene coverage** found by each genotypic fitness sharing sigma value replicate on the multi-path exploration diagnostic. Best performance found refers to the largest average trait score found in a given population, while activation gene coverage refers to the count of unique activation genes in the population. Note that both values fall between 0 and 100.

### 6.4.1 Performance

Here we analyze the performances for each parameter replicate on the multi-path exploration diagnostic.

#### 6.4.1.1 Performance over time

Performance over time.

```
problem <- filter(tru_ot, diagnostic == 'multipath_exploration')
lines = problem %>%
  group_by(T, gen) %>%
  dplyr::summarise(
    min = min(pop_fit_max),
    mean = mean(pop_fit_max),
    max = max(pop_fit_max)
  )

## `summarise()` has grouped output by 'T'. You can override using the `.groups` argument.

points = filter(lines, gen %% 2000 == 0 & gen != 0)

ot = ggplot(lines, aes(x=gen, y=mean / TRAITS, group = T, fill = T, color = T, shape =
  geom_ribbon(aes(ymin = min / TRAITS, ymax = max / TRAITS), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = points, size = 1.5, stroke = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Average trait score",
```

```
limits=c(-1, 101),
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+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6")

) +
scale_shape_manual(values=SHAPE) +
scale_colour_manual(values = cb_palette) +
scale_fill_manual(values = cb_palette) +
ggtitle("Best performance over time") +
p_theme +
guides(
  shape=guide_legend(nrow=1, title.position = "bottom"),
  color=guide_legend(nrow=1, title.position = "bottom"),
  fill=guide_legend(nrow=1, title.position = "bottom")
) +
theme(
  legend.position = "bottom",
  legend.box="vertical",
  legend.justification="center",
  legend.title.align=0.5
)

ot
```



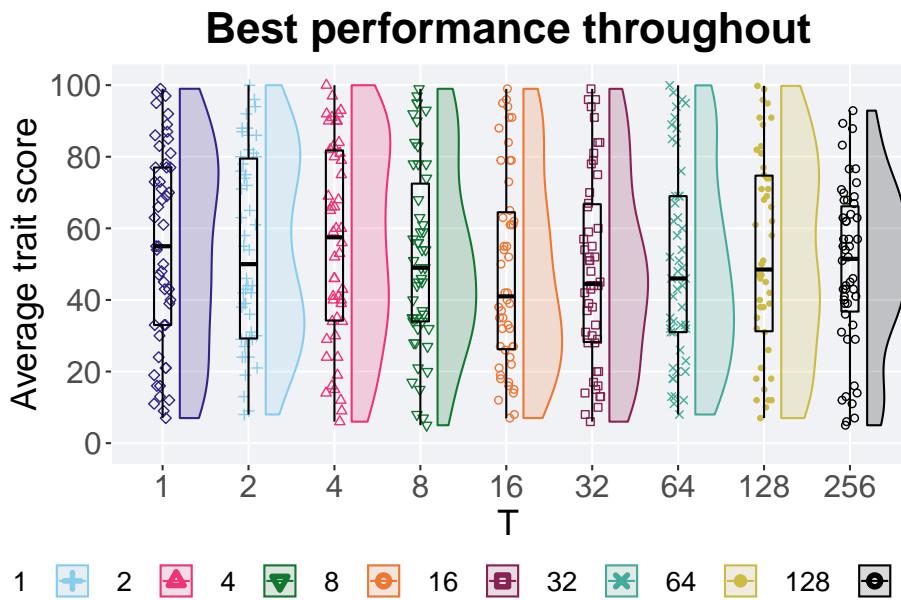
#### 6.4.1.2 Best performance throughout

Here we plot the performance of the best performing solution found throughout 50,000 generations.

```
best = filter(tru_best, col == 'pop_fit_max' & diagnostic == 'multipath_exploration')

plot = ggplot(best, aes(x = T, y = val / TRAITS, color = T, fill = T, shape = T)) +
  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="Average trait score",
    limits=c(-1, 101),
    breaks=seq(0,100, 20),
    labels=c("0", "20", "40", "60", "80", "100"))
  ) +
  scale_x_discrete(
    name="T"
  ) +
  scale_shape_manual(values=SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  p_theme
```

```
plot_grid(
  plot +
    ggtitle("Best performance throughout") +
    theme(legend.position="none"),
  legend,
  nrow=2,
  rel_heights = c(2,.3),
  label_size = TSIZE
)
```



#### 6.4.1.2.1 Stats

Summary statistics for the performance of the best performing solution found throughout 50,000 generations.

```
group_by(best, T) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(val)),
    min = min(val / TRAITS, na.rm = TRUE),
    median = median(val / TRAITS, na.rm = TRUE),
    mean = mean(val / TRAITS, na.rm = TRUE),
    max = max(val / TRAITS, na.rm = TRUE),
    IQR = IQR(val / TRAITS, na.rm = TRUE)
)
```

```
## # A tibble: 9 x 8
##   T      count na_cnt   min median   mean   max   IQR
##   <fct> <int> <int> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 1       50     0    7     55.0  54.6  99.0  44.0
## 2 2       50     0    8     50.0  54.0  100.   50.2
## 3 4       50     0    6     57.5  56.0  100.   47.5
## 4 8       50     0    5     49.0  51.6  99.0  38.5
## 5 16      50     0    7     41.0  47.8  99.0  38.2
## 6 32      50     0    6     44.5  48.1  99.0  38.5
## 7 64      50     0    8     46.0  49.8  99.9  38.0
## 8 128     50     0  7.00   48.5  52.2  99.8  43.5
## 9 256     50     0    5     51.5  49.0  92.9  29.4
```

Kruskal–Wallis test provides evidence of no statistical differences among the best performing solution found throughout 50,000 generations.

```
kruskal.test(val ~ T, data = best)

##
##  Kruskal-Wallis rank sum test
##
## data: val by T
## Kruskal-Wallis chi-squared = 5.0721, df = 8, p-value = 0.7498
```

#### 6.4.1.3 End of 50,000 generations

Best performance in the population at the end of 50,000 generations.

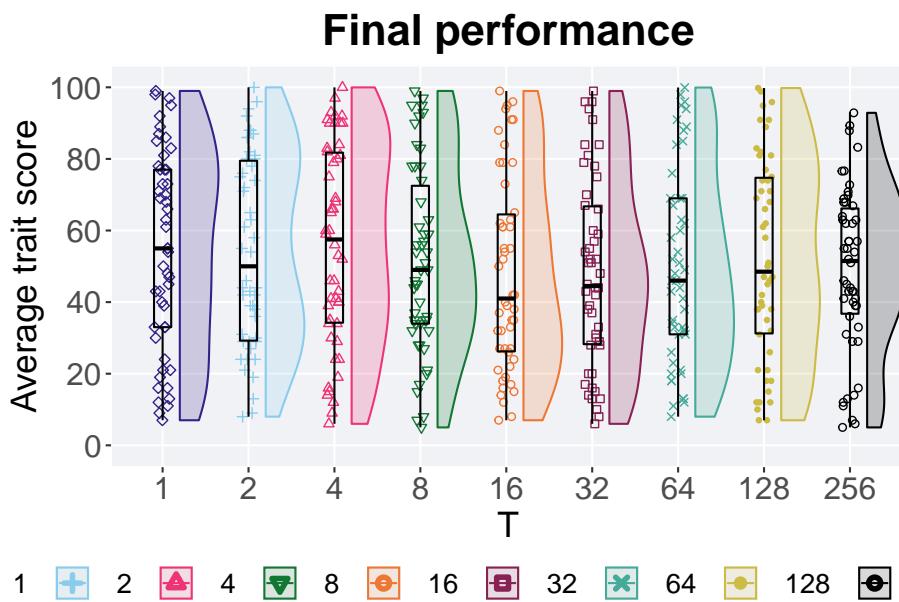
```
end = filter(tru_end, diagnostic == 'multipath_exploration')
plot = ggplot(end, aes(x = T, y = pop_fit_max / TRAITS, color = T, fill = T, shape = T))
  geom_flat_violin(position = position_nudge(x = .2, y = 0), scale = 'width', alpha = 0.5) +
  geom_point(position = position_jitter(width = .1), size = 1.5, alpha = 1.0) +
  geom_boxplot(color = 'black', width = .2, outlier.shape = NA, alpha = 0.0) +
  scale_y_continuous(
    name = "Average trait score",
    limits = c(-1, 101),
    breaks = seq(0, 100, 20),
    labels = c("0", "20", "40", "60", "80", "100"))
  ) +
  scale_x_discrete(
    name = "T")
  ) +
  scale_shape_manual(values = SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  p_theme

plot_grid(
```

```

plot +
  ggtitle("Final performance") +
  theme(legend.position="none"),
  legend,
  nrow=2,
  rel_heights = c(2,.3),
  label_size = TSIZE
)

```



#### 6.4.1.3.1 Stats

Summary statistics for the best performance in the population at the end of 50,000 generations.

```

group_by(end, T) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(pop_fit_max / TRAITS)),
    min = min(pop_fit_max / TRAITS, na.rm = TRUE),
    median = median(pop_fit_max / TRAITS, na.rm = TRUE),
    mean = mean(pop_fit_max / TRAITS, na.rm = TRUE),
    max = max(pop_fit_max / TRAITS, na.rm = TRUE),
    IQR = IQR(pop_fit_max / TRAITS, na.rm = TRUE)
  )

```

## # A tibble: 9 x 8

```
##   T      count na_cnt    min median   mean   max   IQR
##   <fct> <int> <int> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 1      50     0  7    55.0  54.6  99.0  44.0
## 2 2      50     0  8    50.0  54.0 100.   50.2
## 3 4      50     0  6    57.5  56.0 100.   47.5
## 4 8      50     0  5    49.0  51.6  99.0  38.5
## 5 16     50     0  7    41.0  47.8  99.0  38.2
## 6 32     50     0  6    44.5  48.1  99.0  38.5
## 7 64     50     0  8    46.0  49.8  99.9  38.0
## 8 128    50     0 7.00  48.5  52.2  99.8  43.5
## 9 256    50     0  5    51.5  49.0  92.9  29.4
```

Kruskal–Wallis test provides evidence of statistical differences among best performance in the population at the end of 50,000 generations.

```
kruskal.test(pop_fit_max ~ T, data = end)
```

```
##
## Kruskal-Wallis rank sum test
##
## data: pop_fit_max by T
## Kruskal-Wallis chi-squared = 5.0721, df = 8, p-value = 0.7498
```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction on the best performance in the population at the end of 50,000 generations.

```
pairwise.wilcox.test(x = end$pop_fit_max, g = end$T, p.adjust.method = "bonferroni",
                      paired = FALSE, conf.int = FALSE, alternative = 'l')
```

```
##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: end$pop_fit_max and end$T
##
##   1 2 4 8 16 32 64 128
## 2  1 - - - - - - -
## 4  1 1 - - - - - -
## 8  1 1 1 - - - - -
## 16 1 1 1 1 - - - -
## 32 1 1 1 1 1 - - -
## 64 1 1 1 1 1 1 - -
## 128 1 1 1 1 1 1 1 -
## 256 1 1 1 1 1 1 1 1
##
## P value adjustment method: bonferroni
```

### 6.4.2 Activation gene coverage

Here we analyze the activation gene coverage for each parameter replicate on the multi-path exploration diagnostic.

#### 6.4.2.1 Coverage over time

Activation gene coverage over time.

```
problem <- filter(tru_ot, diagnostic == 'multipath_exploration')
lines = problem %>%
  group_by(T, gen) %>%
  dplyr::summarise(
    min = min(uni_str_pos),
    mean = mean(uni_str_pos),
    max = max(uni_str_pos)
  )

## `summarise()` has grouped output by 'T'. You can override using the ` `.groups` ` argument.

points = filter(lines, gen %% 2000 == 0 & gen != 0)

ot = ggplot(lines, aes(x=gen, y=mean, group = T, fill = T, color = T, shape = T)) +
  geom_ribbon(aes(ymin = min, ymax = max), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = points, size = 1.5, stroke = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Coverage",
    limits=c(-1, 101),
    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+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6")
  ) +
  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 +
  guides(
    shape=guide_legend(nrow=1, title.position = "bottom"),
    color=guide_legend(nrow=1, title.position = "bottom"),
    fill=guide_legend(nrow=1, title.position = "bottom")
  )
```

```

    fill=guide_legend(nrow=1, title.position = "bottom")
) +
theme(
  legend.position = "bottom",
  legend.box="vertical",
  legend.justification="center",
  legend.title.align=0.5
)
ot

```



#### 6.4.2.2 End of 50,000 generations

Activation gene coverage in the population at the end of 50,000 generations.

```

end = filter(tru_end, diagnostic == 'multipath_exploration')
plot = ggplot(end, aes(x = T, y = uni_str_pos, color = T, fill = T, shape = T)) +
  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(-1, 10),
    breaks=seq(0,10, 2),
    labels=c("0", "2", "4", "6", "8", "10"))

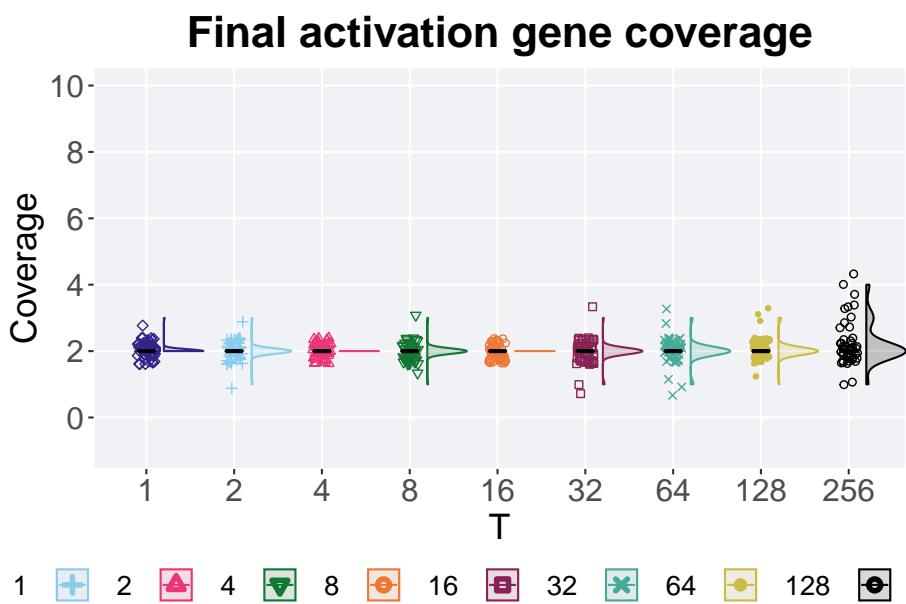
```

```

) +
  scale_x_discrete(
    name="T"
) +
  scale_shape_manual(values=SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  p_theme

plot_grid(
  plot +
    ggtitle("Final activation gene coverage") +
    theme(legend.position="none"),
  legend,
  nrow=2,
  rel_heights = c(2,.3),
  label_size = TSIZE
)

```



#### 6.4.2.2.1 Stats

Summary statistics for the activation gene coverage in the population at the end of 50,000 generations.

```

group_by(end, T) %>%
  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: 9 x 8
##   T      count na_cnt  min median  mean  max  IQR
##   <fct> <int> <int> <dbl> <dbl> <int> <dbl>
## 1 1       50     0     2     2  2.02     3     0
## 2 2       50     0     1     2     2     3     0
## 3 4       50     0     2     2     2     2     0
## 4 8       50     0     1     2     2     3     0
## 5 16      50     0     2     2     2     2     0
## 6 32      50     0     1     2  1.98     3     0
## 7 64      50     0     1     2  1.98     3     0
## 8 128     50     0     1     2  2.04     3     0
## 9 256     50     0     1     2  2.22     4     0

```

Kruskal–Wallis test provides evidence of statistical differences among activation gene coverage in the population at the end of 50,000 generations.

```
kruskal.test(uni_str_pos ~ T, data = end)
```

```

##
##  Kruskal-Wallis rank sum test
##
## data:  uni_str_pos by T
## Kruskal-Wallis chi-squared = 19.931, df = 8, p-value = 0.0106

```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction on the activation gene coverage in the population at the end of 50,000 generations.

```

pairwise.wilcox.test(x = end$uni_str_pos, g = end$T , p.adjust.method = "bonferroni",
                      paired = FALSE, conf.int = FALSE, alternative = 't')

##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  end$uni_str_pos and end$T
##
##   1   2   4   8   16   32   64   128
## 2  1.00 - - - - - - - - - - - - - - -

```

```
## 4  1.00 1.00 -  -  -  -  -  -
## 8  1.00 1.00 1.00 -  -  -  -  -  -
## 16 1.00 1.00 -  1.00 -  -  -  -  -
## 32 1.00 1.00 1.00 1.00 1.00 -  -  -  -
## 64 1.00 1.00 1.00 1.00 1.00 1.00 -  -
## 128 1.00 1.00 1.00 1.00 1.00 1.00 1.00 -  -
## 256 1.00 0.85 0.52 0.85 0.52 0.56 0.83 1.00
##
## P value adjustment method: bonferroni
```



# Chapter 7

## Tournament selection

We present the results from our parameter sweep on tournament selection. 50 replicates are conducted for each tournament size T parameter value explored.

```
library(ggplot2)
library(cowplot)
library(dplyr)
library(PupilometryR)
```

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         2.1
## year          2022
## month         06
## day           23
## svn rev       82513
## language      R
## version.string R version 4.2.1 (2022-06-23)
## nickname      Funny-Looking Kid
```

## 7.1 Exploitation rate results

Here we present the results for **best performances** found by each tournament selection value replicate on the exploitation rate diagnostic.

### 7.1.1 Performance over time

Performance over time.

```
problem <- filter(tor_ot, diagnostic == 'exploitation_rate')
lines = problem %>%
  group_by(T, gen) %>%
  dplyr::summarise(
    min = min(pop_fit_max),
    mean = mean(pop_fit_max),
    max = max(pop_fit_max)
  )

## `summarise()` has grouped output by 'T'. You can override using the `groups` argument.

points = filter(lines, gen %% 2000 == 0 & gen != 0)

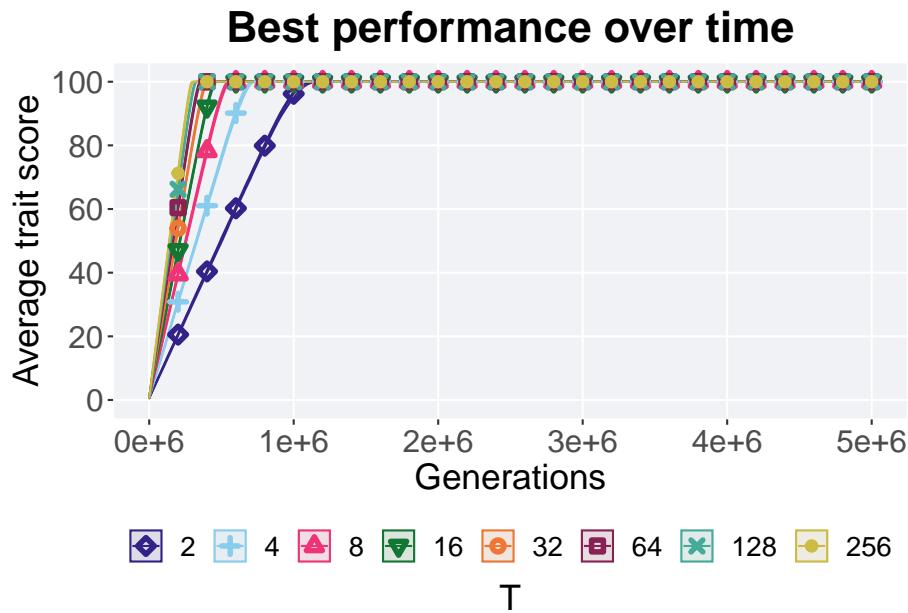
ot = ggplot(lines, aes(x=gen, y=mean / TRAITS, group = T, fill = T, color = T, shape =
  geom_ribbon(aes(ymin = min / TRAITS, ymax = max / TRAITS), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = points, size = 1.5, stroke = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Average trait score",
    limits=c(-1, 101),
    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+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6")
  ) +
  scale_shape_manual(values=SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  ggtitle("Best performance over time") +
  p_theme +
  guides(
    shape=guide_legend(nrow=1, title.position = "bottom"),
    color=guide_legend(nrow=1, title.position = "bottom"),
    fill=guide_legend(nrow=1, title.position = "bottom")
  )
print(ot)
```

```

color=guide_legend(nrow=1, title.position = "bottom"),
fill=guide_legend(nrow=1, title.position = "bottom")
) +
theme(
  legend.position = "bottom",
  legend.box="vertical",
  legend.justification="center",
  legend.title.align=0.5
)

```

ot



#### 7.1.2 Generation satisfactory solution found

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

```

ssf = filter(tor_ssf, diagnostic == 'exploitation_rate')

plot <- ggplot(ssf, aes(x = T, y = generation, color = T, fill = T, shape = T)) +
  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_shape_manual(values=SHAPE) +
  scale_y_continuous()

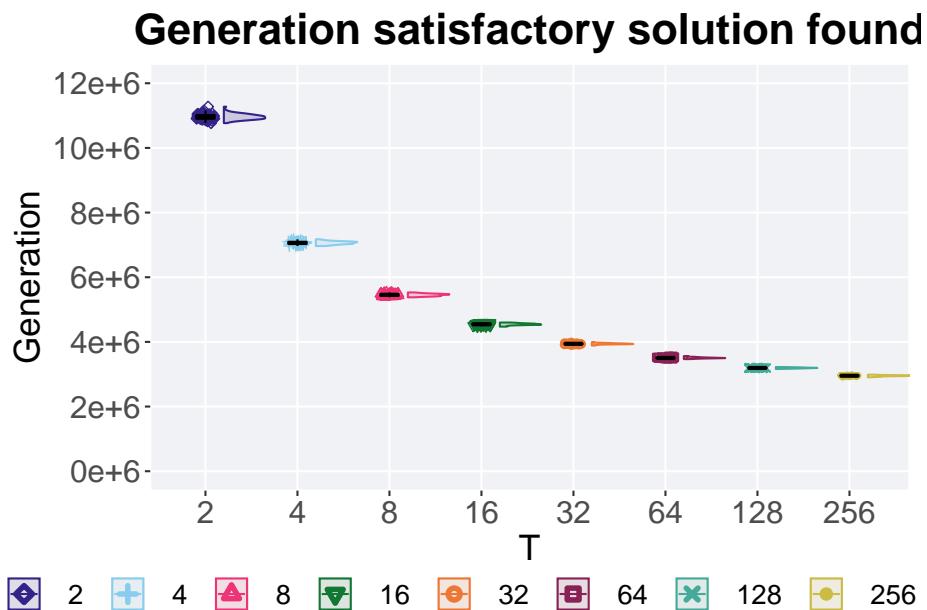
```

```

name="Generation",
limits=c(0, 12000),
breaks=c(0, 2000, 4000, 6000, 8000, 10000, 12000),
labels=c("0e+6", "2e+6", "4e+6", "6e+6", "8e+6", "10e+6", "12e+6")
) +
scale_x_discrete(
  name="T"
) +
scale_colour_manual(values = cb_palette) +
scale_fill_manual(values = cb_palette) +
p_theme

plot_grid(
  plot +
  ggtitle("Generation satisfactory solution found") +
  theme(legend.position="none"),
legend,
nrow=2,
rel_heights = c(2,.2),
label_size = TSIZE
)

```



### 7.1.2.1 Stats

Summary statistics for the best performance found throughout 50,000 generations.

```
group_by(ssf, T) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(generation)),
    min = min(generation, na.rm = TRUE),
    median = median(generation, na.rm = TRUE),
    mean = mean(generation, na.rm = TRUE),
    max = max(generation, na.rm = TRUE),
    IQR = IQR(generation, na.rm = TRUE)
  )

## # A tibble: 8 x 8
##   T      count na_cnt   min median   mean   max   IQR
##   <fct> <int> <int> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 2        50     0 10767 10964. 10963. 11275 112.
## 2 4        50     0  6965  7059   7062.  7173   62.5
## 3 8        50     0  5379  5457   5453.  5529   56
## 4 16       50     0  4472  4544   4545.  4599   34
## 5 32       50     0  3889  3941   3941.  3992   21.5
## 6 64       50     0  3468  3502.  3506.  3562   20.8
## 7 128      50     0  3162  3194   3194.  3222   19.5
## 8 256      50     0  2905  2954.  2952.  2986   21.5
```

Kruskal–Wallis test provides evidence of significant differences among the generation a satisfactory solution is first found.

```
kruskal.test(generation ~ T,data = ssf)

##
## Kruskal-Wallis rank sum test
##
## data: generation by T
## 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 on the generation a satisfactory solution is first found. .

```
pairwise.wilcox.test(x = ssf$generation, g = ssf$T , p.adjust.method = "bonferroni",
                      paired = FALSE, conf.int = FALSE, alternative = 'l')

##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: ssf$generation and ssf$T
```

```

##          2      4      8     16     32     64    128
## 4 <2e-16 -      -      -      -      -      -
## 8 <2e-16 <2e-16 -      -      -      -      -
## 16 <2e-16 <2e-16 <2e-16 -      -      -      -
## 32 <2e-16 <2e-16 <2e-16 <2e-16 -      -      -
## 64 <2e-16 <2e-16 <2e-16 <2e-16 <2e-16 -      -
## 128 <2e-16 <2e-16 <2e-16 <2e-16 <2e-16 <2e-16 -
## 256 <2e-16 <2e-16 <2e-16 <2e-16 <2e-16 <2e-16 <2e-16
##
## P value adjustment method: bonferroni

```

## 7.2 Ordered exploitation results

Here we present the results for **best performances** found by each genotypic fitness sharing sigma value replicate on the ordered exploitation diagnostic. Best performance found refers to the largest average trait score found in a given population. Note that performance values fall between 0 and 100.

### 7.2.1 Performance over time

Performance over time.

```

problem <- filter(tor_ot, diagnostic == 'ordered_exploitation')
lines = problem %>%
  group_by(T, gen) %>%
  dplyr::summarise(
    min = min(pop_fit_max),
    mean = mean(pop_fit_max),
    max = max(pop_fit_max)
  )

## `summarise()` has grouped output by 'T'. You can override using the `.groups` argument.

points = filter(lines, gen %% 2000 == 0 & gen != 0)

ot = ggplot(lines, aes(x=gen, y=mean / TRAITS, group = T, fill = T, color = T, shape =
  geom_ribbon(aes(ymin = min / TRAITS, ymax = max / TRAITS), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = points, size = 1.5, stroke = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Average trait score",
    limits=c(-1, 101),
    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+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6"))

) +
  scale_shape_manual(values=SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  ggtitle("Best performance over time") +
  p_theme +
  guides(
    shape=guide_legend(nrow=1, title.position = "bottom"),
    color=guide_legend(nrow=1, title.position = "bottom"),
    fill=guide_legend(nrow=1, title.position = "bottom")
  ) +
  theme(
    legend.position = "bottom",
    legend.box="vertical",
    legend.justification="center",
    legend.title.align=0.5
  )
)
ot
```



### 7.2.2 Generation satisfactory solution found

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

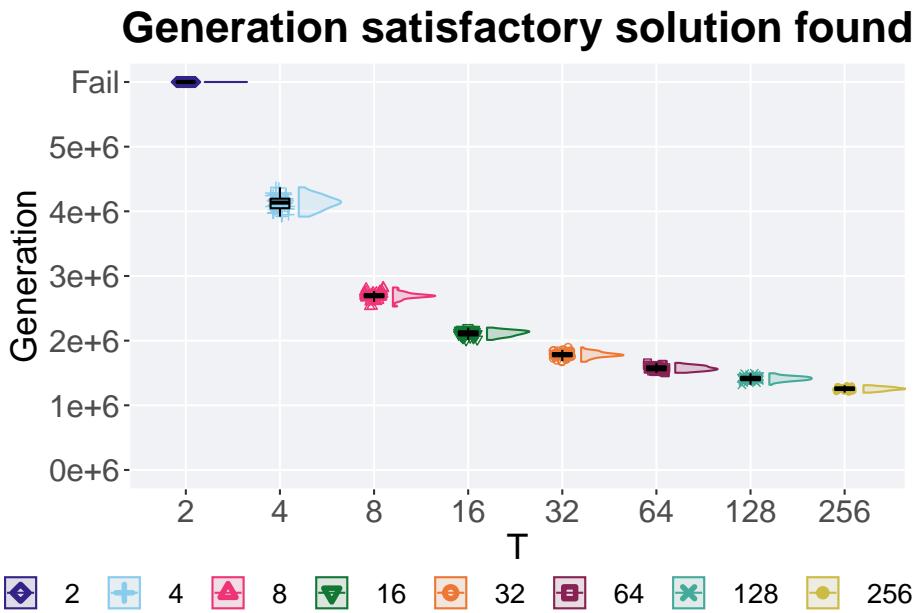
```
ssf = filter(tor_ssf, diagnostic == 'ordered_exploitation')

plot <- ggplot(ssf, aes(x = T, y = generation, color = T, fill = T, shape = T)) +
  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_shape_manual(values=SHAPE) +
  scale_y_continuous(
    name="Generation",
    limits=c(0, 60000),
    breaks=c(0, 10000, 20000, 30000, 40000, 50000, 60000),
    labels=c("0e+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6", "Fail"))
  ) +
  scale_x_discrete(
    name="T"
  ) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  p_theme
```

```

plot_grid(
  plot +
    ggtitle("Generation satisfactory solution found") +
    theme(legend.position="none"),
  legend,
  nrow=2,
  rel_heights = c(2,.2),
  label_size = TSIZE
)

```



### 7.2.2.1 Stats

Summary statistics for the first generation a satisfactory solution is found throughout the 50,000 generations.

```

ssf = filter(ssf, T != 2)

group_by(ssf, T) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(generation)),
    min = min(generation, na.rm = TRUE),
    median = median(generation, na.rm = TRUE),
    mean = mean(generation, na.rm = TRUE),
    max = max(generation, na.rm = TRUE),
    )

```

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

## # A tibble: 7 x 8
##   T      count na_cnt   min median   mean   max   IQR
##   <fct> <int> <int> <dbl> <dbl> <dbl> <dbl>
## 1 4       50     0 39186 41352. 41339. 43712 1474.
## 2 8       50     0 25283 26926. 26922. 28222 496.
## 3 16      50     0 20113 21130. 21135. 22015 642.
## 4 32      50     0 16732 17819 17821. 18957 499.
## 5 64      50     0 15028 15683 15722. 16562 608.
## 6 128     50     0 13171 14148. 14142. 14954 524
## 7 256     50     0 11964 12546. 12548. 13104 402.
```

Kruskal–Wallis test provides evidence of significant differences among the first generation a satisfactory solution is found throughout the 50,000 generations.

```
kruskal.test(generation ~ T, data = ssf)
```

```
##
## Kruskal-Wallis rank sum test
##
## data: generation by T
## Kruskal-Wallis chi-squared = 341.88, df = 6, p-value < 2.2e-16
```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction on the first generation a satisfactory solution is found throughout the 50,000 generations.

```
pairwise.wilcox.test(x = ssf$generation, g = ssf$T, p.adjust.method = "bonferroni",
                      paired = FALSE, conf.int = FALSE, alternative = 'l')

##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: ssf$generation and ssf$T
##
##    4      8      16      32      64      128
## 8 <2e-16 -      -      -      -      -
## 16 <2e-16 <2e-16 -      -      -      -
## 32 <2e-16 <2e-16 <2e-16 -      -      -
## 64 <2e-16 <2e-16 <2e-16 <2e-16 -      -
## 128 <2e-16 <2e-16 <2e-16 <2e-16 <2e-16 -
## 256 <2e-16 <2e-16 <2e-16 <2e-16 <2e-16 <2e-16
##
## P value adjustment method: bonferroni
```

## 7.3 Contradictory objectives diagnostic

Here we present the results for **satisfactory trait coverage** and **activation gene coverage** found by each genotypic fitness sharing sigma value replicate on the ordered exploitation diagnostic. Satisfactory trait coverage refers to the count of unique satisfied traits in the population, while activation gene coverage refers to the count of unique activation genes in the population. Note that both coverage values fall between 0 and 100.

### 7.3.1 Satisfactory trait coverage

Satisfactory trait coverage analysis.

#### 7.3.1.1 Coverage over time

Satisfactory trait coverage over time.

```
problem <- filter(tor_ot, diagnostic == 'contradictory_objectives')
lines = problem %>%
  group_by(T, gen) %>%
  dplyr::summarise(
    min = min(pop_uni_obj),
    mean = mean(pop_uni_obj),
    max = max(pop_uni_obj)
  )
## `summarise()` has grouped output by 'T'. You can override using the ` .groups` argument.
points = filter(lines, gen %% 2000 == 0 & gen != 0)

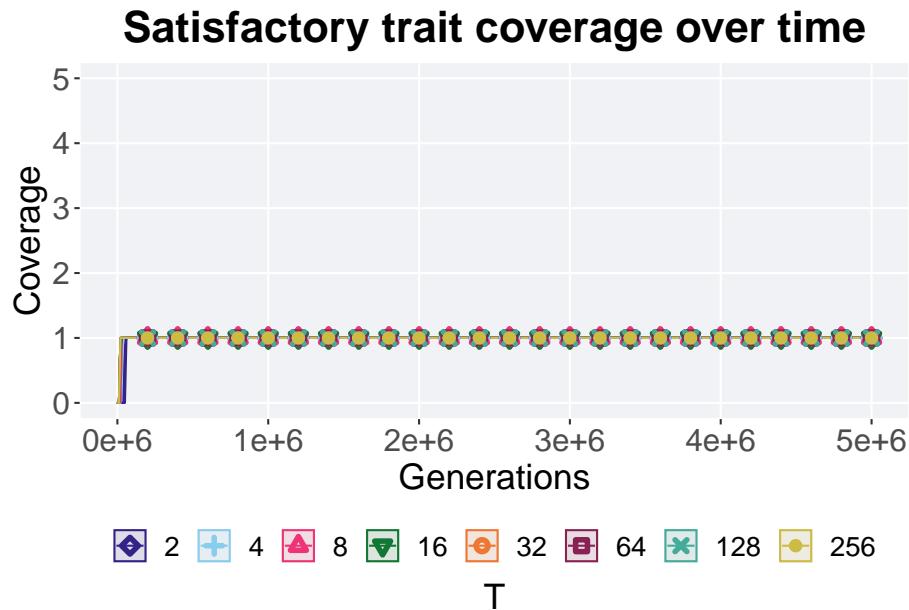
ot = ggplot(lines, aes(x=gen, y=mean, group = T, fill = T, color = T, shape = T)) +
  geom_ribbon(aes(ymin = min, ymax = max), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = points, size = 1.5, stroke = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Coverage",
    limits=c(0, 5)
  ) +
  scale_x_continuous(
    name="Generations",
    limits=c(0, 50000),
    breaks=c(0, 10000, 20000, 30000, 40000, 50000),
    labels=c("0e+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6")
  ) +
  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 +
guides(
  shape=guide_legend(nrow=1, title.position = "bottom"),
  color=guide_legend(nrow=1, title.position = "bottom"),
  fill=guide_legend(nrow=1, title.position = "bottom")
) +
theme(
  legend.position = "bottom",
  legend.box="vertical",
  legend.justification="center",
  legend.title.align=0.5
)

ot

```



### 7.3.1.2 Best coverage throughout

Best satisfactory trait coverage throughout 50,000 generations.

```

best = filter(tor_best, col == 'pop_uni_obj' & diagnostic == 'contradictory_objectives')

plot = ggplot(best, aes(x = T, y = val, color = T, fill = T, shape = T)) +

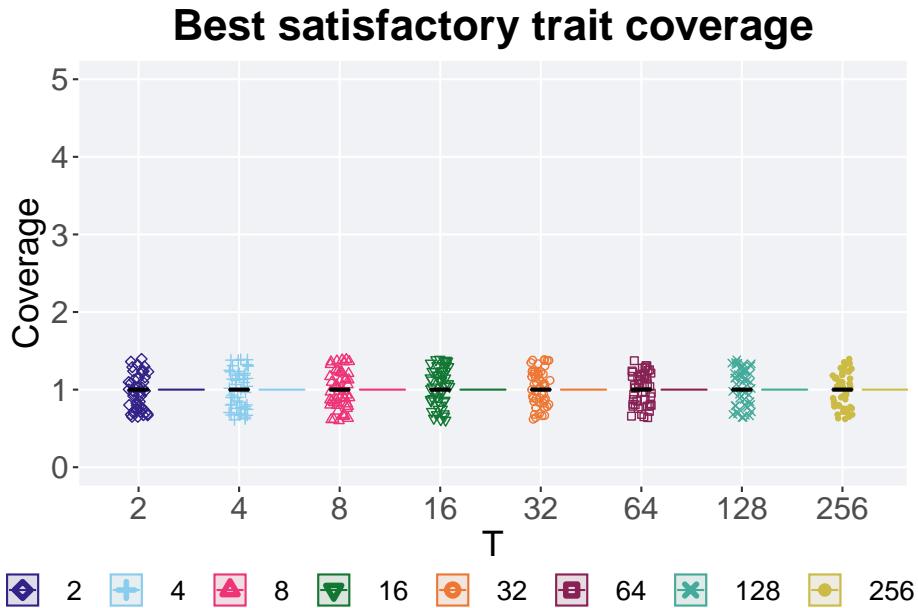
```

```

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, 5)
  ) +
  scale_x_discrete(
    name = "T"
  ) +
  scale_shape_manual(values = SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  p_theme

plot_grid(
  plot +
    ggtitle("Best satisfactory trait coverage") +
    theme(legend.position = "none"),
  legend,
  nrow = 2,
  rel_heights = c(2, .2),
  label_size = TSIZE
)

```



### 7.3.1.2.1 Stats

Summary statistics for the best satisfactory trait coverage throughout 50,000 generations.

```
group_by(best, T) %>%
  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)
  )

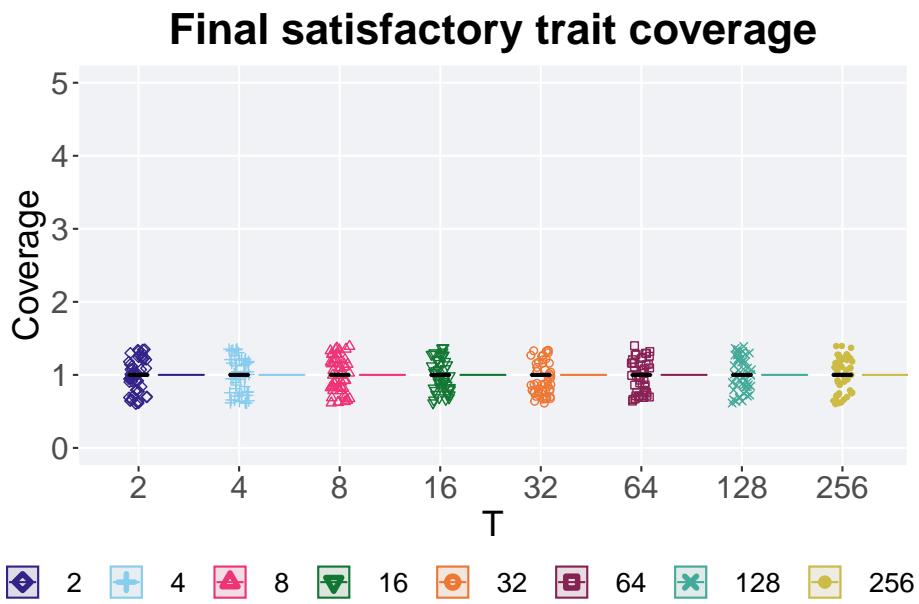
## # A tibble: 8 x 8
##   T     count na_cnt  min median  mean  max  IQR
##   <fct> <int>   <int> <dbl> <dbl> <dbl> <dbl>
## 1 2      50      0     1     1     1     1     0
## 2 4      50      0     1     1     1     1     0
## 3 8      50      0     1     1     1     1     0
## 4 16     50      0     1     1     1     1     0
## 5 32     50      0     1     1     1     1     0
## 6 64     50      0     1     1     1     1     0
## 7 128    50      0     1     1     1     1     0
## 8 256    50      0     1     1     1     1     0
```

### 7.3.1.3 End of 50,000 generations

Satisfactory trait coverage in the population at the end of 50,000 generations.

```
end = filter(tor_end, diagnostic == 'contradictory_objectives')
plot = ggplot(end, aes(x = T, y = pop_uni_obj, color = T, fill = T), shape = T)) +
  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, 5)
  ) +
  scale_x_discrete(
    name = "T"
  ) +
  scale_shape_manual(values = SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  p_theme
```

```
plot_grid(
  plot +
    ggtitle("Final satisfactory trait coverage") +
    theme(legend.position="none"),
  legend,
  nrow=2,
  rel_heights = c(2,.3),
  label_size = TSIZE
)
```



#### 7.3.1.3.1 Stats

Summary statistics for satisfactory trait coverage in the population at the end of 50,000 generations.

```
group_by(end, T) %>%
  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
##   T     count na_cnt  min median  mean  max  IQR
##   <fct> <int> <int> <dbl> <dbl> <dbl> <dbl>
## 1 2      50     0     1     1     1     1     0
## 2 4      50     0     1     1     1     1     0
## 3 8      50     0     1     1     1     1     0
## 4 16     50     0     1     1     1     1     0
## 5 32     50     0     1     1     1     1     0
## 6 64     50     0     1     1     1     1     0
## 7 128    50     0     1     1     1     1     0
## 8 256    50     0     1     1     1     1     0
```

### 7.3.2 Activation gene coverage

Here we analyze the activation gene coverage for each parameter replicate on the contradictory objectives diagnostic.

#### 7.3.2.1 Coverage over time

Activation gene coverage over time.

```
problem <- filter(tor_ot, diagnostic == 'contradictory_objectives')
lines = problem %>%
  group_by(T, gen) %>%
  dplyr::summarise(
    min = min(uni_str_pos),
    mean = mean(uni_str_pos),
    max = max(uni_str_pos)
  )

## `summarise()` has grouped output by 'T'. You can override using the `.groups` argument.

points = filter(lines, gen %% 2000 == 0 & gen != 0)

ot = ggplot(lines, aes(x=gen, y=mean, group = T, fill = T, color = T, shape = T)) +
  geom_ribbon(aes(ymin = min, ymax = max), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = points, size = 1.5, stroke = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Coverage",
    limits=c(-1, 101),
    breaks=seq(0,100, 20),
    labels=c("0", "20", "40", "60", "80", "100")
  ) +
  scale_x_continuous(
    name="Generations",
```

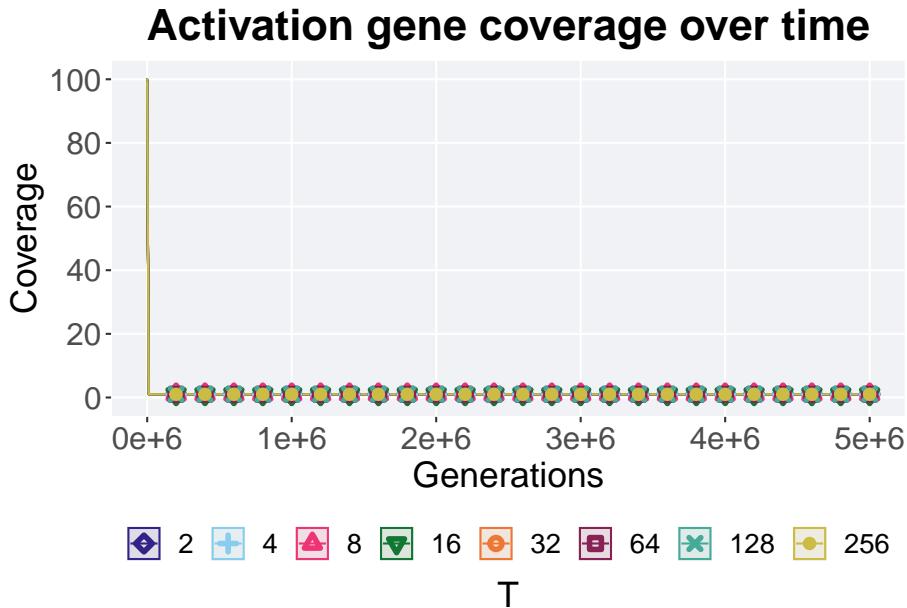
```

limits=c(0, 50000),
breaks=c(0, 10000, 20000, 30000, 40000, 50000),
labels=c("0e+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6")

) +
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+
guides(
shape=guide_legend(nrow=1, title.position = "bottom"),
color=guide_legend(nrow=1, title.position = "bottom"),
fill=guide_legend(nrow=1, title.position = "bottom")
) +
theme(
legend.position = "bottom",
legend.box="vertical",
legend.justification="center",
legend.title.align=0.5
)
)

ot

```

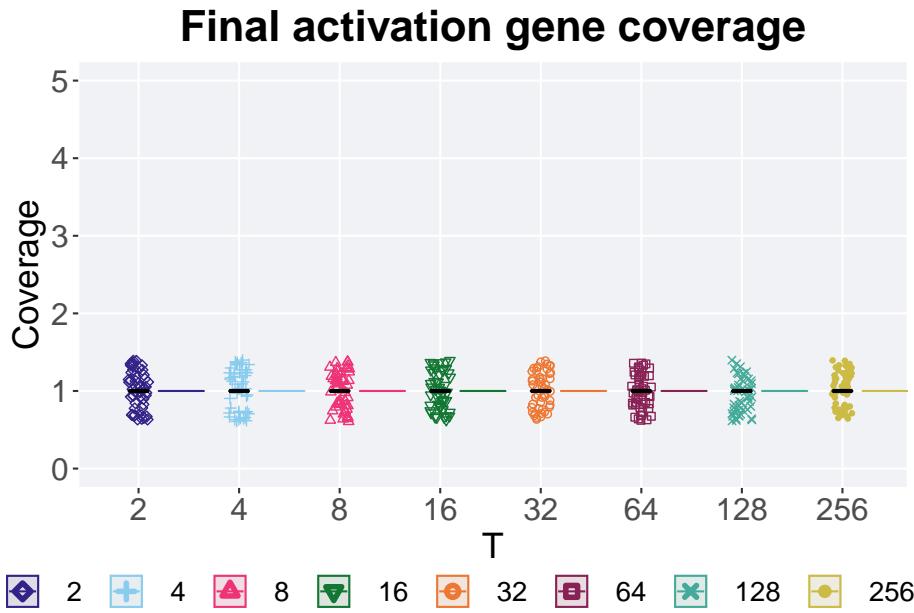


### 7.3.2.2 End of 50,000 generations

Activation gene coverage in the population at the end of 50,000 generations.

```
end = filter(tor_end, diagnostic == 'contradictory_objectives')
plot = ggplot(end, aes(x = T, y = uni_str_pos, color = T, fill = T, shape = T)) +
  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, 5)
  ) +
  scale_x_discrete(
    name = "T"
  ) +
  scale_shape_manual(values = SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  p_theme

plot_grid(
  plot +
    ggtitle("Final activation gene coverage") +
    theme(legend.position = "none"),
  legend,
  nrow = 2,
  rel_heights = c(2, .2),
  label_size = TSIZE
)
```



#### 7.3.2.2.1 Stats

Summary statistics for activation gene coverage in the population at the end of 50,000 generations.

```
group_by(end, T) %>%
  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
##   T      count na_cnt  min median  mean   max  IQR
##   <fct> <int>   <int> <dbl> <dbl> <dbl> <dbl>
## 1 2        50      0     1     1     1     1     0
## 2 4        50      0     1     1     1     1     0
## 3 8        50      0     1     1     1     1     0
## 4 16       50      0     1     1     1     1     0
## 5 32       50      0     1     1     1     1     0
## 6 64       50      0     1     1     1     1     0
## 7 128      50      0     1     1     1     1     0
```

```
## 8 256      50      0      1      1      1      1      0
```

## 7.4 Multi-path exploration results

Here we present the results for **best performances** and **activation gene coverage** found by each genotypic fitness sharing sigma value replicate on the multi-path exploration diagnostic. Best performance found refers to the largest average trait score found in a given population, while activation gene coverage refers to the count of unique activation genes in the population. Note that both values fall between 0 and 100.

### 7.4.1 Performance

Here we analyze the performances for each parameter replicate on the multi-path exploration diagnostic.

#### 7.4.1.1 Performance over time

Performance over time.

```
problem <- filter(tor_ot, diagnostic == 'multipath_exploration')
lines = problem %>%
  group_by(T, gen) %>%
  dplyr::summarise(
    min = min(pop_fit_max),
    mean = mean(pop_fit_max),
    max = max(pop_fit_max)
  )

## `summarise()` has grouped output by 'T'. You can override using the `.groups` argument.

points = filter(lines, gen %% 2000 == 0 & gen != 0)

ot = ggplot(lines, aes(x=gen, y=mean / TRAITS, group = T, fill = T, color = T, shape =
  geom_ribbon(aes(ymin = min / TRAITS, ymax = max / TRAITS), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = points, size = 1.5, stroke = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Average trait score",
    limits=c(-1, 101),
    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+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6")

) +
scale_shape_manual(values=SHAPE) +
scale_colour_manual(values = cb_palette) +
scale_fill_manual(values = cb_palette) +
ggtitle("Best performance over time") +
p_theme+
guides(
shape=guide_legend(nrow=1, title.position = "bottom"),
color=guide_legend(nrow=1, title.position = "bottom"),
fill=guide_legend(nrow=1, title.position = "bottom")
) +
theme(
legend.position = "bottom",
legend.box="vertical",
legend.justification="center",
legend.title.align=0.5
)
)

ot

```



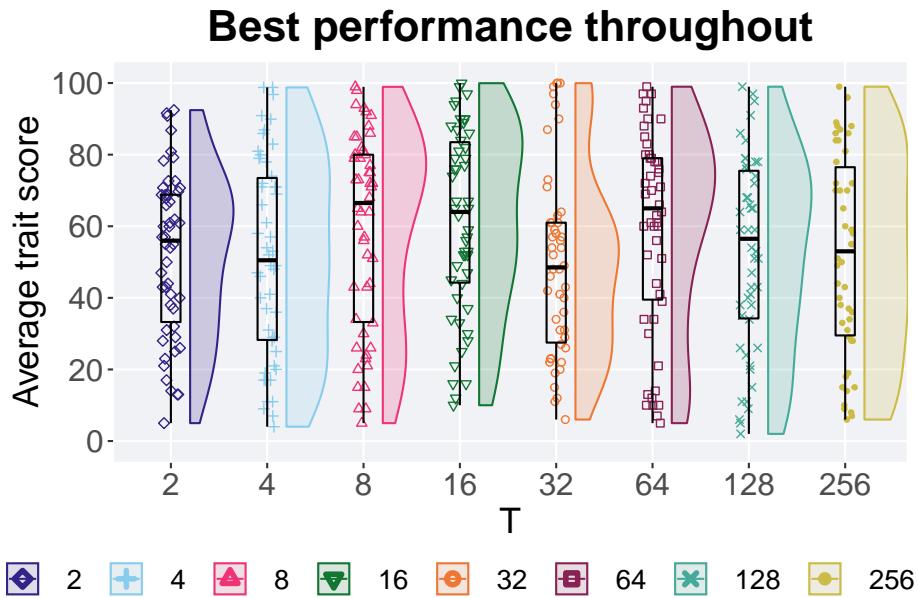
### 7.4.1.2 Best performance throughout

Here we plot the performance of the best performing solution found throughout 50,000 generations.

```
best = filter(tor_best, col == 'pop_fit_max' & diagnostic == 'multipath_exploration')

plot = ggplot(best, aes(x = T, y = val / TRAITS, color = T, fill = T, shape = T)) +
  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 = "Average trait score",
    limits = c(-1, 101),
    breaks = seq(0, 100, 20),
    labels = c("0", "20", "40", "60", "80", "100")
  ) +
  scale_x_discrete(
    name = "T"
  ) +
  scale_shape_manual(values = SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  p_theme

plot_grid(
  plot +
    ggtitle("Best performance throughout") +
    theme(legend.position = "none"),
  legend,
  nrow = 2,
  rel_heights = c(2, .3),
  label_size = TSIZE
)
```



#### 7.4.1.2.1 Stats

Summary statistics for the performance of the best performing solution found throughout 50,000 generations.

```
group_by(best, T) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(val)),
    min = min(val / TRAITS, na.rm = TRUE),
    median = median(val / TRAITS, na.rm = TRUE),
    mean = mean(val / TRAITS, na.rm = TRUE),
    max = max(val / TRAITS, na.rm = TRUE),
    IQR = IQR(val / TRAITS, na.rm = TRUE)
  )

## # A tibble: 8 x 8
##   T      count na_cnt   min median   mean   max   IQR
##   <fct> <int>   <int> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 2        50       0  5     56.0  52.1  92.4  35.5
## 2 4        50       0  4     50.5  51.3  98.8  45.2
## 3 8        50       0  5     66.5  58.7  98.9  46.7
## 4 16       50       0 10.0   64.0  61.2 100.   39.2
## 5 32       50       0  6.00   48.5  49.9 100.   33.5
## 6 64       50       0  5     65.0  59.1  99.0  39.5
## 7 128      50       0  2     56.5  52.5  99.0  41.2
```

```
## 8 256      50      0  6      53.0  52.0  99.0  47.0
```

Kruskal–Wallis test provides evidence of no statistical differences among the best performing solution found throughout 50,000 generations.

```
kruskal.test(val ~ T, data = best)

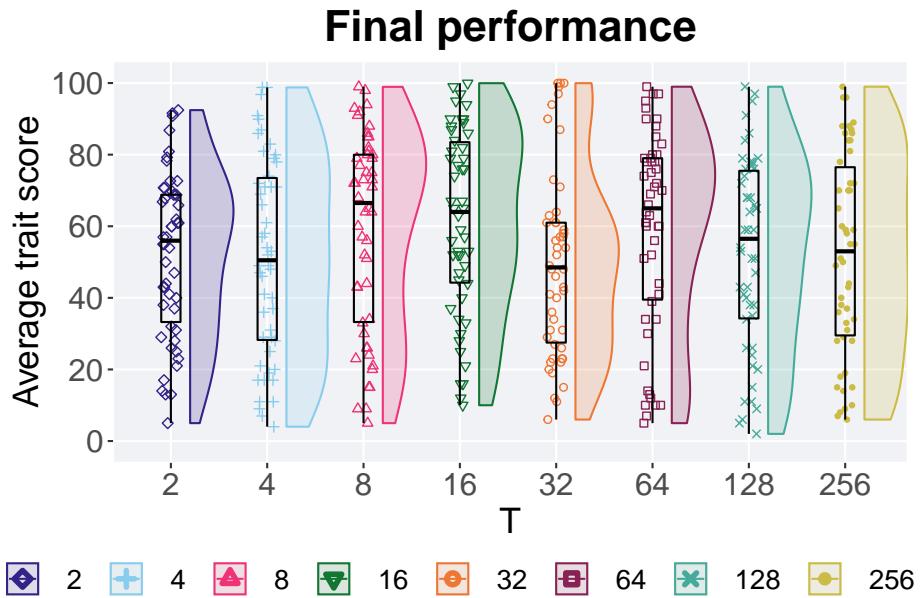
##
## Kruskal-Wallis rank sum test
##
## data: val by T
## Kruskal-Wallis chi-squared = 9.9954, df = 7, p-value = 0.1888
```

#### 7.4.1.3 End of 50,000 generations

Best performance in the population at the end of 50,000 generations.

```
end = filter(tor_end, diagnostic == 'multipath_exploration')
plot = ggplot(end, aes(x = T, y = pop_fit_max / TRAITS, color = T, fill = T, shape = T))
  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 = "Average trait score",
    limits = c(-1, 101),
    breaks = seq(0, 100, 20),
    labels = c("0", "20", "40", "60", "80", "100"))
  ) +
  scale_x_discrete(
    name = "T"
  ) +
  scale_shape_manual(values = SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  p_theme

plot_grid(
  plot +
    ggtitle("Final performance") +
    theme(legend.position = "none"),
  legend,
  nrow = 2,
  rel_heights = c(2, .3),
  label_size = TSIZE
)
```



#### 7.4.1.3.1 Stats

Summary statistics for the best performance in the population at the end of 50,000 generations.

```
group_by(end, T) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(pop_fit_max / TRAITS)),
    min = min(pop_fit_max / TRAITS, na.rm = TRUE),
    median = median(pop_fit_max / TRAITS, na.rm = TRUE),
    mean = mean(pop_fit_max / TRAITS, na.rm = TRUE),
    max = max(pop_fit_max / TRAITS, na.rm = TRUE),
    IQR = IQR(pop_fit_max / TRAITS, na.rm = TRUE)
  )

## # A tibble: 8 x 8
##   T      count na_cnt  min median  mean   max   IQR
##   <fct> <int>   <int> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 2        50       0  5     56.0  52.1  92.4  35.5
## 2 4        50       0  4     50.5  51.3  98.8  45.2
## 3 8        50       0  5     66.5  58.7  98.9  46.7
## 4 16       50      10.0 64.0  61.2 100.   39.2
## 5 32       50      6.00 48.5  49.9 100.   33.5
## 6 64       50       0  5     65.0  59.1  99.0  39.5
## 7 128      50       0  2     56.5  52.5  99.0  41.2
```

```
## 8 256      50      0 6      53.0 52.0 99.0 47.0
```

Kruskal–Wallis test provides evidence of statistical differences among best performance in the population at the end of 50,000 generations.

```
kruskal.test(pop_fit_max ~ T, data = end)
```

```
##  
## Kruskal-Wallis rank sum test  
##  
## data: pop_fit_max by T  
## Kruskal-Wallis chi-squared = 9.9954, df = 7, p-value = 0.1888
```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction on the best performance in the population at the end of 50,000 generations.

```
pairwise.wilcox.test(x = end$pop_fit_max, g = end$T, p.adjust.method = "bonferroni",  
                     paired = FALSE, conf.int = FALSE, alternative = 'l')
```

```
##  
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction  
##  
## data: end$pop_fit_max and end$T  
##  
##      2     4     8    16    32    64   128  
## 4  1.00 - - - - - -  
## 8  1.00 1.00 - - - - - -  
## 16 1.00 1.00 1.00 - - - -  
## 32 1.00 1.00 1.00 0.59 - - - -  
## 64 1.00 1.00 1.00 1.00 1.00 - -  
## 128 1.00 1.00 1.00 1.00 1.00 1.00 -  
## 256 1.00 1.00 1.00 1.00 1.00 1.00 1.00  
##  
## P value adjustment method: bonferroni
```

## 7.4.2 Activation gene coverage

Here we analyze the activation gene coverage for each parameter replicate on the multi-path exploration diagnostic.

### 7.4.2.1 Coverage over time

Activation gene coverage over time.

```
problem <- filter(tor_ot, diagnostic == 'multipath_exploration')  
lines = problem %>%  
  group_by(T, gen) %>%  
  dplyr::summarise(  
    min = min(uni_str_pos),
```

```
    mean = mean(uni_str_pos),
    max = max(uni_str_pos)
  )

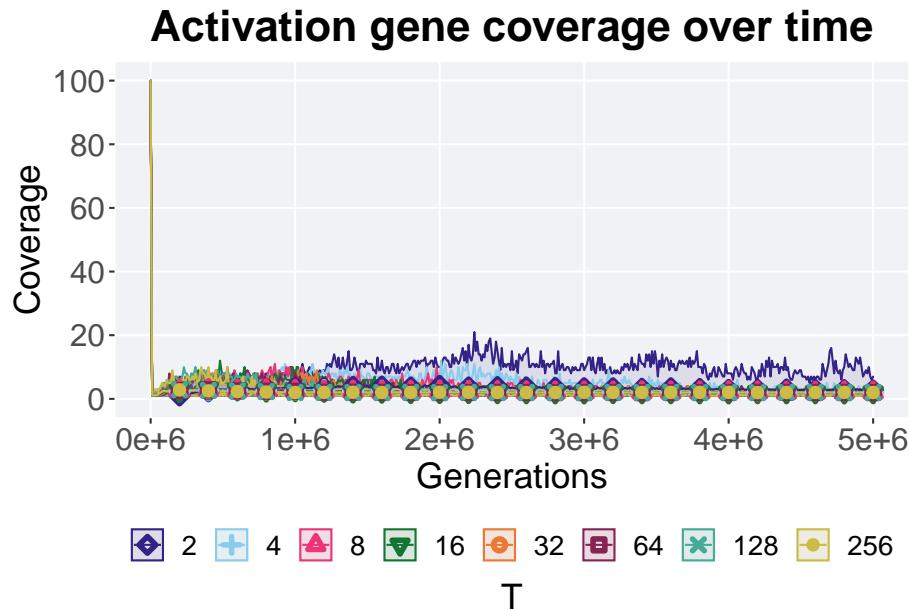
## `summarise()` has grouped output by 'T'. You can override using the `groups`#
## argument.

points = filter(lines, gen %% 2000 == 0 & gen != 0)

ot = ggplot(lines, aes(x=gen, y=mean, group = T, fill = T, color = T, shape = T)) +
  geom_ribbon(aes(ymin = min, ymax = max), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = points, size = 1.5, stroke = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Coverage",
    limits=c(-1, 101),
    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+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6")

  ) +
  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 +
  guides(
    shape=guide_legend(nrow=1, title.position = "bottom"),
    color=guide_legend(nrow=1, title.position = "bottom"),
    fill=guide_legend(nrow=1, title.position = "bottom")
  ) +
  theme(
    legend.position = "bottom",
    legend.box="vertical",
    legend.justification="center",
    legend.title.align=0.5
  )

ot
```



#### 7.4.2.2 End of 50,000 generations

Activation gene coverage in the population at the end of 50,000 generations.

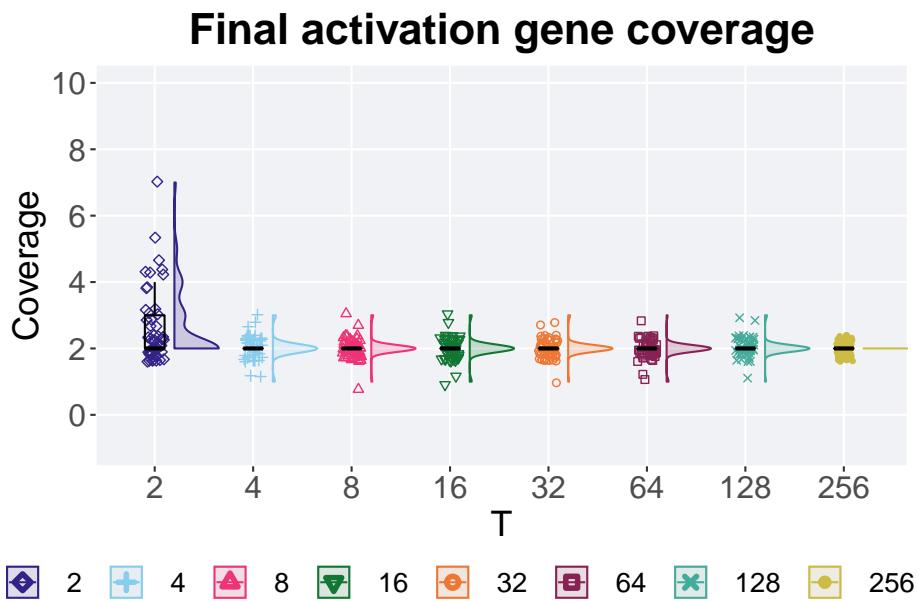
```
end = filter(tor_end, diagnostic == 'multipath_exploration')
plot = ggplot(end, aes(x = T, y = uni_str_pos, color = T, fill = T, shape = T)) +
  geom_flat_violin(position = position_nudge(x = .2, y = 0), scale = 'width', alpha = 0.5) +
  geom_point(position = position_jitter(width = .1), size = 1.5, alpha = 1.0) +
  geom_boxplot(color = 'black', width = .2, outlier.shape = NA, alpha = 0.0) +
  scale_y_continuous(
    name="Coverage",
    limits=c(-1, 10),
    breaks=seq(0,10, 2),
    labels=c("0", "2", "4", "6", "8", "10"))
  ) +
  scale_x_discrete(
    name="T"
  ) +
  scale_shape_manual(values=SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  p_theme

plot_grid(
  plot +
```

```

ggtile("Final activation gene coverage") +
  theme(legend.position="none"),
  legend,
  nrow=2,
  rel_heights = c(2,.3),
  label_size = TSIZE
)

```



#### 7.4.2.2.1 Stats

Summary statistics for the activation gene coverage in the population at the end of 50,000 generations.

```

group_by(end, T) %>%
  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
##   T      count  na_cnt  min  median  mean   max    IQR
##   <dbl>    <int>   <dbl> <dbl>    <dbl> <dbl> <dbl>   <dbl>
## 1 2       100000 100000 0.00  1.00  1.00  1.00  1.00
## 2 4       100000 100000 0.00  2.00  2.00  2.00  2.00
## 3 8       100000 100000 0.00  2.00  2.00  2.00  2.00
## 4 16      100000 100000 0.00  2.00  2.00  2.00  2.00
## 5 32      100000 100000 0.00  2.00  2.00  2.00  2.00
## 6 64      100000 100000 0.00  2.00  2.00  2.00  2.00
## 7 128     100000 100000 0.00  2.00  2.00  2.00  2.00
## 8 256     100000 100000 0.00  2.00  2.00  2.00  2.00

```

```
##   <fct> <int> <int> <int> <dbl> <dbl> <int> <dbl>
## 1 2      50     0     2     2  2.62    7     1
## 2 4      50     0     1     2  2.02    3     0
## 3 8      50     0     1     2  2.02    3     0
## 4 16     50     0     1     2  2       3     0
## 5 32     50     0     1     2  2.02    3     0
## 6 64     50     0     1     2  1.98    3     0
## 7 128    50     0     1     2  2.02    3     0
## 8 256    50     0     2     2  2       2     0
```

Kruskal–Wallis test provides evidence of statistical differences among activation gene coverage in the population at the end of 50,000 generations.

```
kruskal.test(uni_str_pos ~ T, data = end)
```

```
##
## Kruskal-Wallis rank sum test
##
## data: uni_str_pos by T
## Kruskal-Wallis chi-squared = 55.517, df = 7, p-value = 1.178e-09
```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction on the activation gene coverage in the population at the end of 50,000 generations.

```
pairwise.wilcox.test(x = end$uni_str_pos, g = end$T, p.adjust.method = "bonferroni",
                      paired = FALSE, conf.int = FALSE, alternative = 't')
```

```
##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: end$uni_str_pos and end$T
##
##   2      4      8      16     32     64     128
## 4 0.00454 -      -      -      -      -      -
## 8 0.00217 1.00000 -      -      -      -      -
## 16 0.00151 1.00000 1.00000 -      -      -      -
## 32 0.00217 1.00000 1.00000 1.00000 -      -      -
## 64 0.00044 1.00000 1.00000 1.00000 1.00000 -      -
## 128 0.00217 1.00000 1.00000 1.00000 1.00000 1.00000 -
## 256 0.00021 1.00000 1.00000 1.00000 1.00000 1.00000 1.00000
##
## P value adjustment method: bonferroni
```

## Chapter 8

# Genotypic fitness sharing

We present the results from our parameter sweep on genotypic fitness sharing. 50 replicates are conducted for each sigma parameter value explored. Note that when `sigma = 0.0`, performance with no similarity penalty and stochastic remainder selection is used to identify parent solutions.

```
library(ggplot2)
library(cowplot)
library(dplyr)
library(Pupillometry)
```

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          2.1
## year          2022
## month         06
## day           23
## svn rev       82513
## language      R
## version.string R version 4.2.1 (2022-06-23)
## nickname      Funny-Looking Kid
```

## 8.1 Exploitation rate results

Here we present the results for **best performances** found by each genotypic fitness sharing sigma value replicate on the exploitation rate diagnostic. 50 replicates are conducted for each sigma parameter value explored. Note that when `sigma = 0.0`, performance with no similarity penalty and stochastic remainder selection is used to identify parent solutions.

### 8.1.1 Performance over time

Performance over time.

```
problem <- filter(gfs_ot, diagnostic == 'exploitation_rate')
lines = problem %>%
  group_by(Sigma, gen) %>%
  dplyr::summarise(
    min = min(pop_fit_max),
    mean = mean(pop_fit_max),
    max = max(pop_fit_max)
  )

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

points = filter(lines, gen %% 2000 == 0 & gen != 0)

ot = ggplot(lines, aes(x=gen, y=mean / TRAITS, group = Sigma, fill = Sigma, color = Sigma))
  geom_ribbon(aes(ymin = min / TRAITS, ymax = max / TRAITS), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = points, size = 1.5, stroke = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Average trait score",
    limits=c(-1, 101),
    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+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6")
  ) +
  scale_shape_manual(values=SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  ggtitle("Best performance over time") +
```

```

p_theme +
  guides(
    shape=guide_legend(nrow=1, title.position = "bottom"),
    color=guide_legend(nrow=1, title.position = "bottom"),
    fill=guide_legend(nrow=1, title.position = "bottom")
  ) +
  theme(
    legend.position = "bottom",
    legend.box="vertical",
    legend.justification="center",
    legend.title.align=0.5
  )
)

ot

```



### 8.1.2 Best performance throughout

The best performance found throughout 50,000 generations.

```

best = filter(gfs_best, col == 'pop_fit_max' & diagnostic == 'exploitation_rate')

plot = ggplot(best, aes(x = Sigma, y = val / TRAITS, color = Sigma, fill = Sigma, shape = Sigma))
  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(-1, 101),
  breaks=seq(0,100, 20),
  labels=c("0", "20", "40", "60", "80", "100")
) +
scale_x_discrete(
  name="Sigma"
) +
scale_shape_manual(values=SHAPE) +
scale_colour_manual(values = cb_palette) +
scale_fill_manual(values = cb_palette) +
p_theme

plot_grid(
  plot +
  ggtitle("Best performance throughout") +
  theme(legend.position="none"),
  legend,
  nrow=2,
  rel_heights = c(2,.3),
  label_size = TSIZE
)

```



### 8.1.2.1 Stats

Summary statistics for the best performance found throughout 50,000 generations.

```
group_by(best, Sigma) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(val)),
    min = min(val / TRAITS, na.rm = TRUE),
    median = median(val / TRAITS, na.rm = TRUE),
    mean = mean(val / TRAITS, na.rm = TRUE),
    max = max(val / TRAITS, na.rm = TRUE),
    IQR = IQR(val / TRAITS, na.rm = TRUE)
  )

## # A tibble: 7 x 8
##   Sigma count na_cnt   min median   mean   max   IQR
##   <fct> <int> <int> <dbl> <dbl> <dbl> <dbl>
## 1 0         50     0  63.7   65.1   65.2   66.7 1.02
## 2 0.1       50     0  58.8   60.4   60.4   61.7 1.02
## 3 0.3       50     0  57.8   59.2   59.4   62.4 0.921
## 4 0.6       50     0  55.8   57.4   57.4   59.2 0.698
## 5 1.2       50     0  50.2   52.1   52.5   64.1 1.03
## 6 2.5       50     0  38.7   40.5   40.6   43.1 1.38
## 7 5         50     0  41.4   43.5   43.4   45.2 1.33
```

Kruskal–Wallis test provides evidence of significant differences among sigma values on the best performance found throughout 50,000 generations

```
kruskal.test(val ~ Sigma, data = best)

##
## Kruskal-Wallis rank sum test
##
## data: val by Sigma
## Kruskal-Wallis chi-squared = 333.76, df = 6, p-value < 2.2e-16
```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction on the best performance found throughout 50,000 generations.

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

##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: best$val and best$Sigma
##
```

```

##      0     0.1     0.3     0.6     1.2     2.5
## 0.1 < 2e-16 -     -     -     -     -
## 0.3 < 2e-16 6.6e-08 -     -     -     -
## 0.6 < 2e-16 < 2e-16 7.4e-15 -     -     -
## 1.2 < 2e-16 1.4e-15 1.4e-15 1.4e-15 -     -
## 2.5 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 -
## 5    < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 1
##
## P value adjustment method: bonferroni

```

## 8.2 Ordered exploitation results

Here we present the results for **best performances** found by each genotypic fitness sharing sigma value replicate on the ordered exploitation diagnostic. Best performance found refers to the largest average trait score found in a given population. Note that performance values fall between 0 and 100.

### 8.2.1 Performance over time

Performance over time.

```

problem <- filter(gfs_ot, diagnostic == 'ordered_exploitation')
lines = problem %>%
  group_by(Sigma, gen) %>%
  dplyr::summarise(
    min = min(pop_fit_max),
    mean = mean(pop_fit_max),
    max = max(pop_fit_max)
  )

## `summarise()` has grouped output by 'Sigma'. You can override using the
## `.groups` argument.
points = filter(lines, gen %% 2000 == 0 & gen != 0)

ot = ggplot(lines, aes(x=gen, y=mean / TRAITS, group = Sigma, fill = Sigma, color = Sigma))
  geom_ribbon(aes(ymin = min / TRAITS, ymax = max / TRAITS), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = points, size = 1.5, stroke = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Average trait score",
    limits=c(-1, 30),
    breaks=seq(0, 30, 10),
    labels=c("0", "10", "20", "30")
  ) +
  scale_x_continuous(

```

```

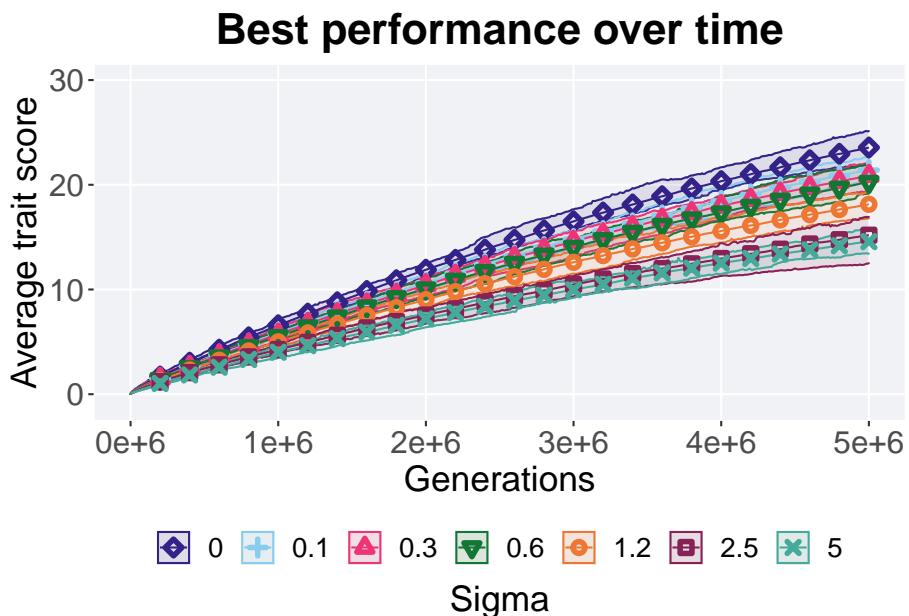
name="Generations",
limits=c(0, 50000),
breaks=c(0, 10000, 20000, 30000, 40000, 50000),
labels=c("0e+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6")

) +
scale_shape_manual(values=SHAPE) +
scale_colour_manual(values = cb_palette) +
scale_fill_manual(values = cb_palette) +
ggtitle("Best performance over time") +
p_theme +
guides(
shape=guide_legend(nrow=1, title.position = "bottom"),
color=guide_legend(nrow=1, title.position = "bottom"),
fill=guide_legend(nrow=1, title.position = "bottom")
) +
theme(
legend.position = "bottom",
legend.box="vertical",
legend.justification="center",
legend.title.align=0.5
)

)

```

ot



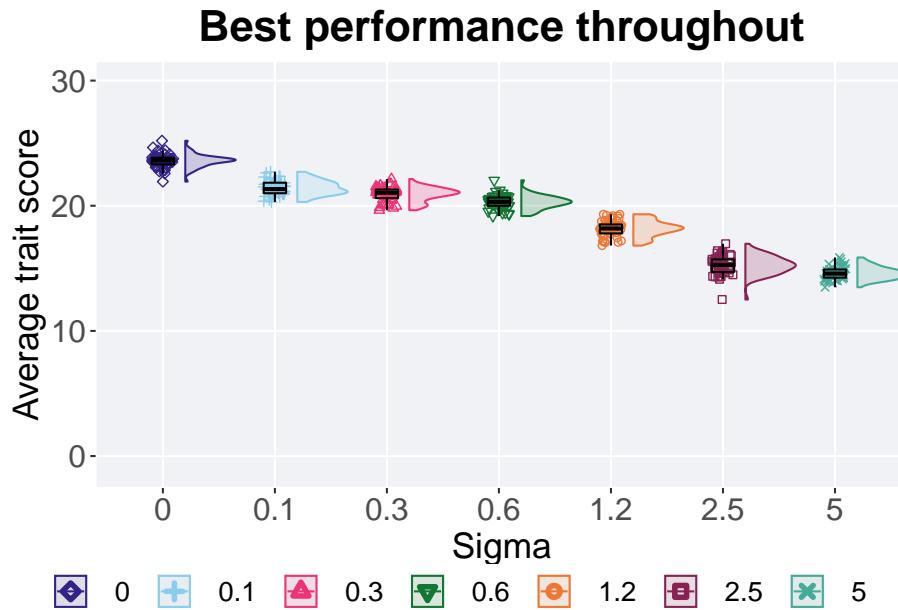
### 8.2.2 Best performance throughout

The best performance found throughout 50,000 generations.

```
best = filter(gfs_best, col == 'pop_fit_max' & diagnostic == 'ordered_exploitation')

plot = ggplot(best, aes(x = Sigma, y = val / TRAITS, color = Sigma, fill = Sigma, shape = Sigma))
  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 = "Average trait score",
    limits = c(-1, 30),
    breaks = seq(0, 30, 10),
    labels = c("0", "10", "20", "30"))
) +
  scale_x_discrete(
    name = "Sigma"
) +
  scale_shape_manual(values = SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  p_theme

plot_grid(
  plot +
    ggtitle("Best performance throughout") +
    theme(legend.position = "none"),
  legend,
  nrow = 2,
  rel_heights = c(2, .2),
  label_size = TSIZE
)
```



#### 8.2.2.1 Stats

Summary statistics about the best performance found.

```
group_by(best, Sigma) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(val)),
    min = min(val / TRAITS, na.rm = TRUE),
    median = median(val / TRAITS, na.rm = TRUE),
    mean = mean(val / TRAITS, na.rm = TRUE),
    max = max(val / TRAITS, na.rm = TRUE),
    IQR = IQR(val / TRAITS, na.rm = TRUE)
  )

## # A tibble: 7 x 8
##   Sigma count na_cnt   min median   mean   max   IQR
##   <fct> <int>   <int>   <dbl>   <dbl>   <dbl>   <dbl>
## 1 0        50      0  21.9   23.6   23.6   25.2  0.531
## 2 0.1     50      0  20.3   21.3   21.4   22.7  0.841
## 3 0.3     50      0  19.6   21.0   20.9   22.1  0.686
## 4 0.6     50      0  19.2   20.3   20.3   22.0  0.660
## 5 1.2     50      0  16.8   18.2   18.2   19.3  0.717
## 6 2.5     50      0  12.5   15.3   15.2   17.0  1.01 
## 7 5       50      0  13.5   14.6   14.6   15.9  0.654
```

Kruskal–Wallis test provides evidence of statistical differences for the best performance found in the population throughout 50,000 generations.

```
kruskal.test(val ~ Sigma, data = best)

##
##  Kruskal-Wallis rank sum test
##
## data: val by Sigma
## Kruskal-Wallis chi-squared = 325.01, df = 6, p-value < 2.2e-16
```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction on the best performance found in the population throughout 50,000 generations.

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

##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: best$val and best$Sigma
##
##    0      0.1     0.3     0.6     1.2     2.5
## 0.1 < 2e-16 -      -      -      -      -
## 0.3 < 2e-16 0.00086 -      -      -      -
## 0.6 < 2e-16 6.2e-13 2.5e-06 -      -      -
## 1.2 < 2e-16 < 2e-16 < 2e-16 < 2e-16 -      -
## 2.5 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 -
## 5 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 2.6e-05
##
## P value adjustment method: bonferroni
```

## 8.3 Contraditory objectives diagnostic

Here we present the results for **satisfactory trait coverage** and **activation gene coverage** found by each genotypic fitness sharing sigma value replicate on the ordered exploitation diagnostic. Satisfactory trait coverage refers to the count of unique satisfied traits in the population, while activation gene coverage refers to the count of unique activation genes in the population. Note that both coverage values fall between 0 and 100.

### 8.3.1 Satisfactory trait coverage

Satisfactory trait coverage analysis.

#### 8.3.1.1 Coverage over time

Satisfactory trait coverage over time.

```

problem <- filter(gfs_ot, diagnostic == 'contradictory_objectives')
lines = problem %>%
  group_by(Sigma, gen) %>%
  dplyr::summarise(
    min = min(pop_uni_obj),
    mean = mean(pop_uni_obj),
    max = max(pop_uni_obj)
  )

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

points = filter(lines, gen %% 2000 == 0 & gen != 0)

ot = ggplot(lines, aes(x=gen, y=mean, group = Sigma, fill = Sigma, color = Sigma, shape = Sigma))
  geom_ribbon(aes(ymin = min, ymax = max), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = points, size = 1.5, stroke = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Coverage",
    limits=c(0, 5)
  ) +
  scale_x_continuous(
    name="Generations",
    limits=c(0, 50000),
    breaks=c(0, 10000, 20000, 30000, 40000, 50000),
    labels=c("0e+0", "1e+0", "2e+0", "3e+0", "4e+0", "5e+0")
  ) +
  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 +
  guides(
    shape=guide_legend(nrow=1, title.position = "bottom"),
    color=guide_legend(nrow=1, title.position = "bottom"),
    fill=guide_legend(nrow=1, title.position = "bottom")
  ) +
  theme(
    legend.position = "bottom",
    legend.box="vertical",
    legend.justification="center",
    legend.title.align=0.5
  )

```

```
ot
```



#### 8.3.1.2 Best coverage throughout

Best satisfactory trait coverage throughout 50,000 generations.

```
best = filter(gfs_best, col == 'pop_uni_obj' & diagnostic == 'contradictory_objectives')

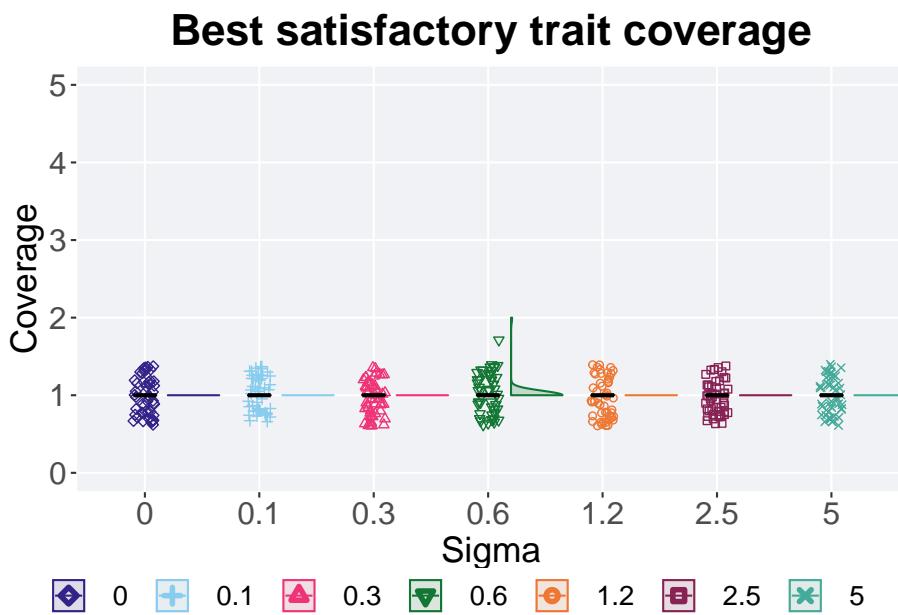
plot = ggplot(best, aes(x = Sigma, y = val, color = Sigma, fill = Sigma, shape = Sigma))
  geom_flat_violin(position = position_nudge(x = .2, y = 0), scale = 'width', alpha = 0.5) +
  geom_point(position = position_jitter(width = .1), size = 1.5, alpha = 1.0) +
  geom_boxplot(color = 'black', width = .2, outlier.shape = NA, alpha = 0.0) +
  scale_y_continuous(
    name="Coverage",
    limits=c(0, 5)
  ) +
  scale_x_discrete(
    name="Sigma"
  ) +
  scale_shape_manual(values=SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  p_theme

plot_grid(
```

```

plot +
  ggtitle("Best satisfactory trait coverage") +
  theme(legend.position="none"),
legend,
nrow=2,
rel_heights = c(2,.2),
label_size = TSIZE
)

```



### 8.3.1.2.1 Stats

Summary statistics for the best satisfactory trait coverage throughout 50,000 generations.

```

group_by(best, Sigma) %>%
  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: 7 x 8

```

```
##   Sigma count na_cnt   min median   mean   max   IQR
##   <fct> <int> <int> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 0      50     0     1     1     1     1     0
## 2 0.1    50     0     1     1     1     1     0
## 3 0.3    50     0     1     1     1     1     0
## 4 0.6    50     0     1     1     1.02   2     0
## 5 1.2    50     0     1     1     1     1     0
## 6 2.5    50     0     1     1     1     1     0
## 7 5      50     0     1     1     1     1     0
```

Kruskal–Wallis test provides evidence of no statistical difference among satisfactory trait coverage throughout 50,000 generations.

```
kruskal.test(val ~ Sigma, data = best)

##
## Kruskal-Wallis rank sum test
##
## data: val by Sigma
## Kruskal-Wallis chi-squared = 6, df = 6, p-value = 0.4232
```

### 8.3.1.3 End of 50,000 generations

Satisfactory trait coverage in the population at the end of 50,000 generations.

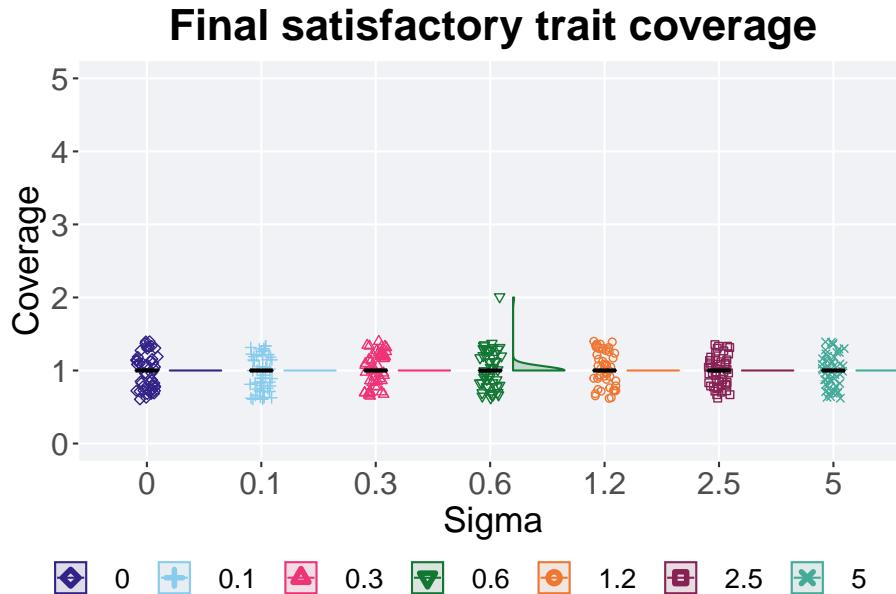
```
end = filter(gfs_end, diagnostic == 'contradictory_objectives')
plot = ggplot(end, aes(x = Sigma, y = pop_uni_obj, color = Sigma, fill = Sigma, shape =
  geom_flat_violin(position = position_nudge(x = .2, y = 0), scale = 'width', alpha = 0.5) +
  geom_point(position = position_jitter(width = .1), 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, 5)
  ) +
  scale_x_discrete(
    name="Sigma"
  ) +
  scale_shape_manual(values=SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  p_theme

plot_grid(
  plot +
  ggtitle("Final satisfactory trait coverage") +
  theme(legend.position="none"),
  legend,
  nrow=2,
```

```

rel_heights = c(2,.3),
label_size = TSIZE
)

```



### 8.3.1.3.1 Stats

Summary statistics for satisfactory trait coverage in the population at the end of 50,000 generations.

```

group_by(end, Sigma) %>%
  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: 7 x 8
##   Sigma count na_cnt  min median  mean  max   IQR
##   <fct> <int>   <int> <dbl> <dbl> <dbl> <dbl>
## 1 0        50      0     1     1     1       1     0
## 2 0.1      50      0     1     1     1       1     0
## 3 0.3      50      0     1     1     1       1     0

```

```
## 4 0.6      50     0     1     1  1.02     2     0
## 5 1.2      50     0     1     1  1       1     0
## 6 2.5      50     0     1     1  1       1     0
## 7 5        50     0     1     1  1       1     0
```

Kruskal–Wallis test provides evidence of no statistical difference among satisfactory trait coverage throughout 50,000 generations.

```
kruskal.test(pop_uni_obj ~ Sigma, data = end)
```

```
##
## Kruskal-Wallis rank sum test
##
## data: pop_uni_obj by Sigma
## Kruskal-Wallis chi-squared = 6, df = 6, p-value = 0.4232
```

### 8.3.2 Activation gene coverage

Here we analyze the activation gene coverage for each parameter replicate on the contradictory objectives diagnostic.

#### 8.3.2.1 Coverage over time

Activation gene coverage over time.

```
problem <- filter(gfs_ot, diagnostic == 'contradictory_objectives')
lines = problem %>%
  group_by(Sigma, gen) %>%
  dplyr::summarise(
    min = min(uni_str_pos),
    mean = mean(uni_str_pos),
    max = max(uni_str_pos)
  )

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

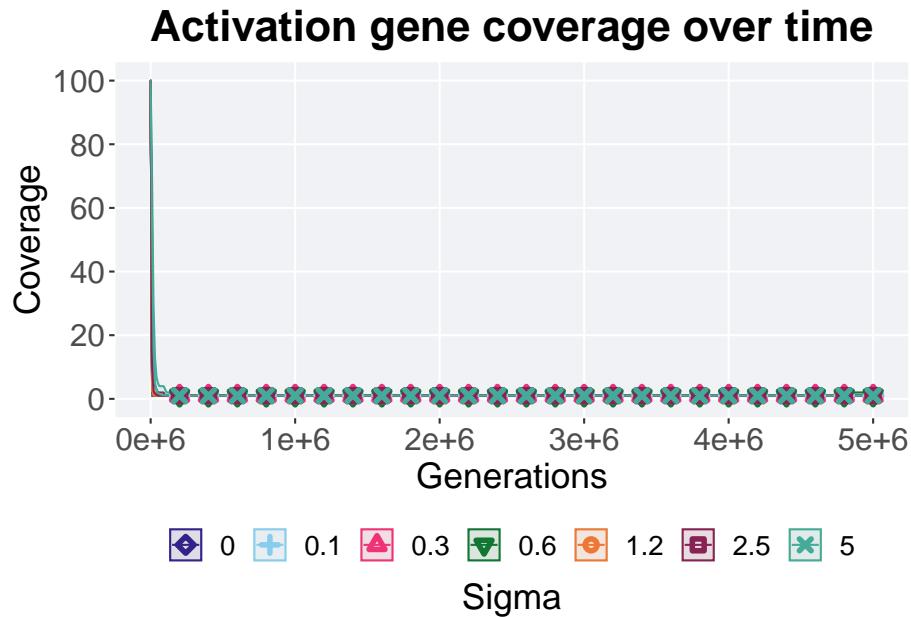
points = filter(lines, gen %% 2000 == 0 & gen != 0)

ot = ggplot(lines, aes(x=gen, y=mean, group = Sigma, fill = Sigma, color = Sigma, shape = Sigma,
  geom_ribbon(aes(ymin = min, ymax = max), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = points, size = 1.5, stroke = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Coverage",
    limits=c(-1, 101),
    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+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6")

) +
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 +
guides(
  shape=guide_legend(nrow=1, title.position = "bottom"),
  color=guide_legend(nrow=1, title.position = "bottom"),
  fill=guide_legend(nrow=1, title.position = "bottom")
) +
theme(
  legend.position = "bottom",
  legend.box="vertical",
  legend.justification="center",
  legend.title.align=0.5
)

)
ot
```



#### 8.3.2.2 End of 50,000 generations

Activation gene coverage in the population at the end of 50,000 generations.

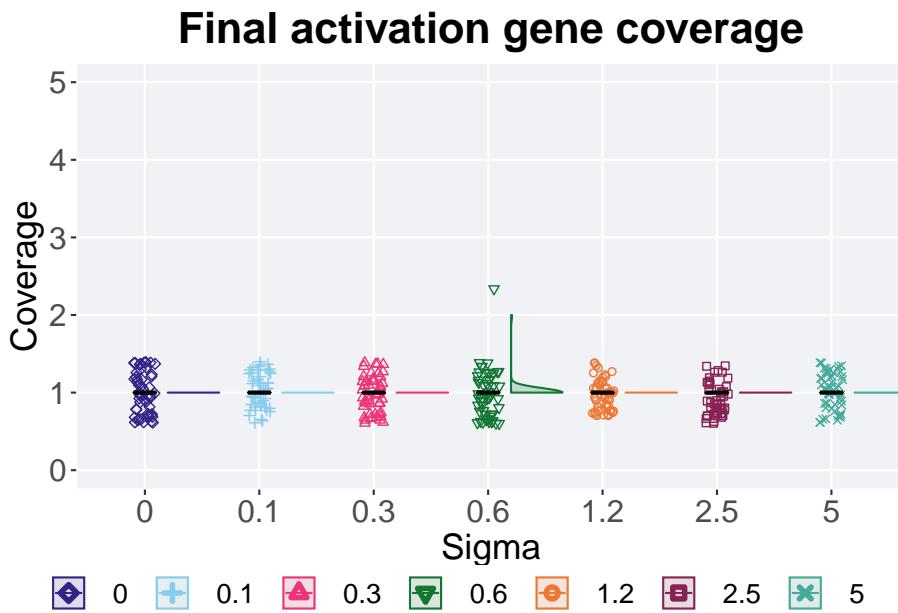
```
end = filter(gfs_end, diagnostic == 'contradictory_objectives')
plot = ggplot(end, aes(x = Sigma, y = uni_str_pos, color = Sigma, fill = Sigma, shape =
  geom_flat_violin(position = position_nudge(x = .2, y = 0), scale = 'width', alpha = 0.2) +
  geom_point(position = position_jitter(width = .1), 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, 5)
  ) +
  scale_x_discrete(
    name="Sigma"
  ) +
  scale_shape_manual(values=SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  p_theme

plot_grid(
  plot +
  ggtitle("Final activation gene coverage") +
  theme(legend.position="none"),
```

```

legend,
nrow=2,
rel_heights = c(2,.2),
label_size = TSIZE
)

```



#### 8.3.2.2.1 Stats

Summary statistics for activation gene coverage in the population at the end of 50,000 generations.

```

group_by(end, Sigma) %>%
  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: 7 x 8
##   Sigma count na_cnt  min median  mean   max   IQR
##   <fct> <int>   <int> <dbl> <dbl> <dbl> <int> <dbl>
## 1 0         50       0     0     1     1     1     0
## 2 0.1        50       0     0     1     1     1     0
## 3 0.3        50       0     0     1     1     1     0
## 4 0.6        50       0     0     1     1     1     0
## 5 1.2        50       0     0     1     1     1     0
## 6 2.5        50       0     0     1     1     1     0
## 7 5          50       0     0     1     1     1     0

```

```
## 2 0.1      50     0     1     1   1     1     0
## 3 0.3      50     0     1     1   1     1     0
## 4 0.6      50     0     1     1   1.02   2     0
## 5 1.2      50     0     1     1   1     1     0
## 6 2.5      50     0     1     1   1     1     0
## 7 5        50     0     1     1   1     1     0
```

Kruskal–Wallis test provides evidence of no statistical difference for activation gene coverage in the population at the end of 50,000 generations.

```
kruskal.test(uni_str_pos ~ Sigma, data = end)

##
## Kruskal-Wallis rank sum test
##
## data: uni_str_pos by Sigma
## Kruskal-Wallis chi-squared = 6, df = 6, p-value = 0.4232
```

## 8.4 Multi-path exploration results

Here we present the results for **best performances** and **activation gene coverage** found by each genotypic fitness sharing sigma value replicate on the multi-path exploration diagnostic. Best performance found refers to the largest average trait score found in a given population, while activation gene coverage refers to the count of unique activation genes in the population. Note that both values fall between 0 and 100.

### 8.4.1 Performance

Here we analyze the performances for each parameter replicate on the multi-path exploration diagnostic.

#### 8.4.1.1 Performance over time

Performance over time.

```
problem <- filter(gfs_ot, diagnostic == 'multipath_exploration')
lines = problem %>%
  group_by(Sigma, gen) %>%
  dplyr::summarise(
    min = min(pop_fit_max),
    mean = mean(pop_fit_max),
    max = max(pop_fit_max)
  )

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

```
points = filter(lines, gen %% 2000 == 0 & gen != 0)

ot = ggplot(lines, aes(x=gen, y=mean / TRAITS, group = Sigma, fill = Sigma, color = Sigma, shape = Sigma) +
  geom_ribbon(aes(ymin = min / TRAITS, ymax = max / TRAITS), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = points, size = 1.5, stroke = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Average trait score",
    limits=c(-1, 30)
  ) +
  scale_x_continuous(
    name="Generations",
    limits=c(0, 50000),
    breaks=c(0, 10000, 20000, 30000, 40000, 50000),
    labels=c("0e+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6")
  ) +
  scale_shape_manual(values=SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  ggtitle("Best performance over time") +
  p_theme +
  guides(
    shape=guide_legend(nrow=1, title.position = "bottom"),
    color=guide_legend(nrow=1, title.position = "bottom"),
    fill=guide_legend(nrow=1, title.position = "bottom")
  ) +
  theme(
    legend.position = "bottom",
    legend.box="vertical",
    legend.justification="center",
    legend.title.align=0.5
  )
)

ot
```



#### 8.4.1.2 Best performance throughout

Here we plot the performance of the best performing solution found throughout 50,000 generations.

```
best = filter(gfs_best, col == 'pop_fit_max' & diagnostic == 'multipath_exploration')

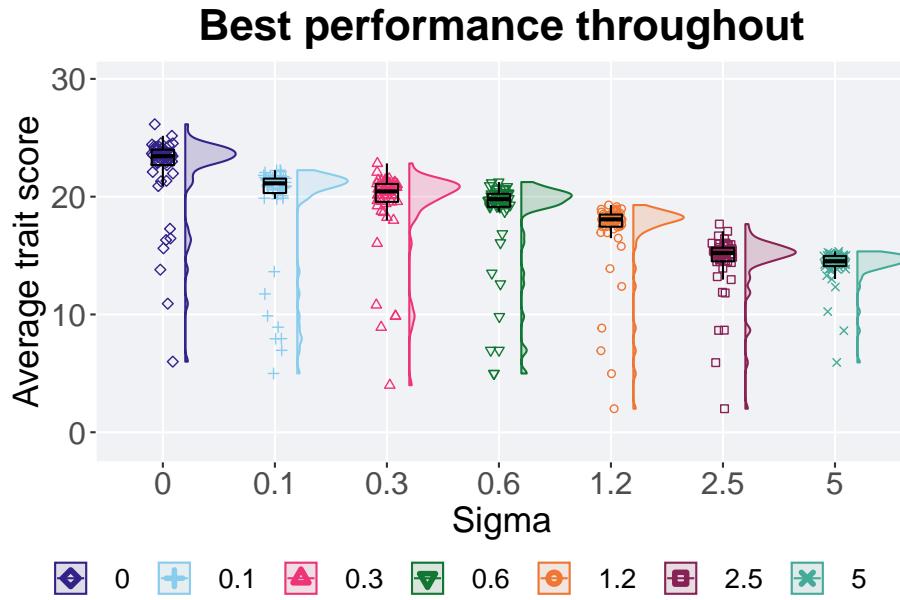
plot = ggplot(best, aes(x = Sigma, y = val / TRAITS, color = Sigma, fill = Sigma, shape = Sigma))
  + geom_flat_violin(position = position_nudge(x = .2, y = 0), scale = 'width', alpha = 0.5)
  + geom_point(position = position_jitter(width = .1), size = 1.5, alpha = 1.0) +
  + geom_boxplot(color = 'black', width = .2, outlier.shape = NA, alpha = 0.0) +
  + scale_y_continuous(
    name="Average trait score",
    limits=c(-1, 30)
  ) +
  + scale_x_discrete(
    name="Sigma"
  ) +
  + scale_shape_manual(values=SHAPE) +
  + scale_colour_manual(values = cb_palette) +
  + scale_fill_manual(values = cb_palette) +
  p_theme

plot_grid(
  plot +
```

```

ggtile("Best performance throughout") +
  theme(legend.position="none"),
  legend,
  nrow=2,
  rel_heights = c(2,.3),
  label_size = TSIZE
)

```



#### 8.4.1.2.1 Stats

Summary statistics for the performance of the best performing solution found throughout 50,000 generations.

```

group_by(best, Sigma) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(val)),
    min = min(val / TRAITS, na.rm = TRUE),
    median = median(val / TRAITS, na.rm = TRUE),
    mean = mean(val / TRAITS, na.rm = TRUE),
    max = max(val / TRAITS, na.rm = TRUE),
    IQR = IQR(val / TRAITS, na.rm = TRUE)
  )

## # A tibble: 7 x 8
##   Sigma count na_cnt   min median   mean   max    IQR

```

```
##   <fct> <int> <int> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 0      50     0  5.99  23.4  22.1  26.1 1.30
## 2 0.1    50     0  4.99  21.1  19.2  22.2 1.22
## 3 0.3    50     0  4.00  20.4  19.2  22.8 1.52
## 4 0.6    50     0  4.99  19.8  18.2  21.2 1.11
## 5 1.2    50     0  2.00  18.1  16.9  19.3 1.03
## 6 2.5    50     0  2.00  15.2  14.4  17.7 1.15
## 7 5      50     0  5.93  14.5  14.1  15.4 0.860
```

Kruskal–Wallis test provides evidence of statistical differences among the best performing solution found throughout 50,000 generations.

```
kruskal.test(val ~ Sigma, data = best)
```

```
##
## Kruskal-Wallis rank sum test
##
## data: val by Sigma
## Kruskal-Wallis chi-squared = 190.72, df = 6, p-value < 2.2e-16
```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction on the best performing solution found throughout 50,000 generations.

```
pairwise.wilcox.test(x = best$val, g = best$Sigma, p.adjust.method = "bonferroni",
                      paired = FALSE, conf.int = FALSE, alternative = '1')

##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: best$val and best$Sigma
##
##   0     0.1    0.3    0.6    1.2    2.5
## 0.1 1.9e-08 -     -     -     -     -
## 0.3 6.7e-09 0.07457 -     -     -     -
## 0.6 8.6e-10 6.0e-06 0.03482 -     -     -
## 1.2 9.0e-10 1.5e-08 4.1e-09 1.6e-07 -     -
## 2.5 5.3e-13 1.6e-08 3.4e-11 2.7e-09 7.5e-10 -
## 5    2.1e-13 2.5e-08 3.8e-11 3.2e-09 2.7e-10 0.00083
##
## P value adjustment method: bonferroni
```

#### 8.4.1.3 End of 50,000 generations

Best performance in the population at the end of 50,000 generations.

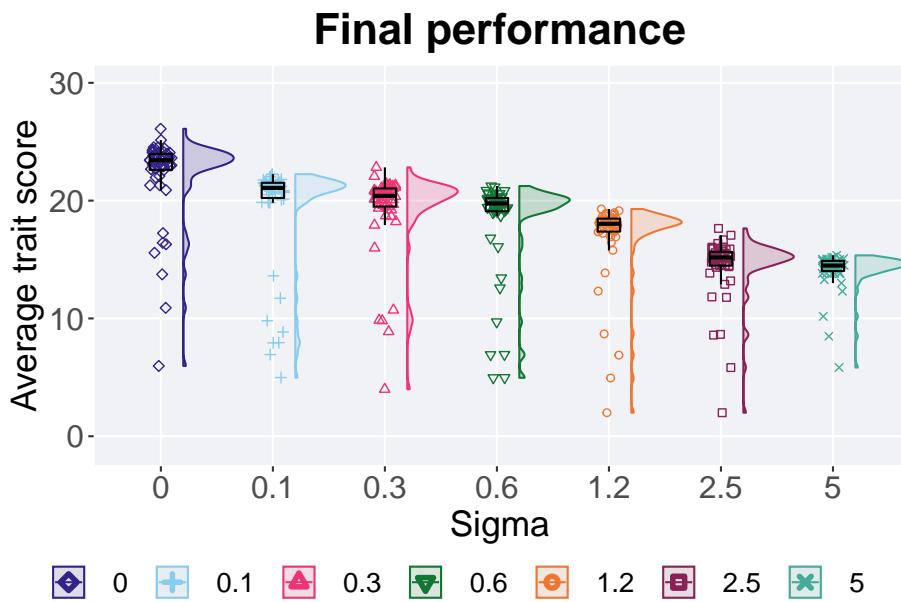
```
end = filter(gfs_end, diagnostic == 'multipath_exploration')
plot = ggplot(end, aes(x = Sigma, y = pop_fit_max / TRAITS, color = Sigma, fill = Sigma))
  geom_flat_violin(position = position_nudge(x = .2, y = 0), scale = 'width', alpha = .5)
  geom_point(position = position_jitter(width = .1), size = 1.5, alpha = 1.0) +
```

```

geom_boxplot(color = 'black', width = .2, outlier.shape = NA, alpha = 0.0) +
  scale_y_continuous(
    name="Average trait score",
    limits=c(-1, 30)
  ) +
  scale_x_discrete(
    name="Sigma"
  ) +
  scale_shape_manual(values=SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  p_theme

plot_grid(
  plot +
  ggtitle("Final performance") +
  theme(legend.position="none"),
  legend,
  nrow=2,
  rel_heights = c(2,.3),
  label_size = TSIZE
)

```



#### 8.4.1.3.1 Stats

Summary statistics for the best performance in the population at the end of 50,000 generations.

```
group_by(end, Sigma) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(pop_fit_max / TRAITS)),
    min = min(pop_fit_max / TRAITS, na.rm = TRUE),
    median = median(pop_fit_max / TRAITS, na.rm = TRUE),
    mean = mean(pop_fit_max / TRAITS, na.rm = TRUE),
    max = max(pop_fit_max / TRAITS, na.rm = TRUE),
    IQR = IQR(pop_fit_max / TRAITS, na.rm = TRUE)
  )

## # A tibble: 7 x 8
##   Sigma count na_cnt   min median   mean   max   IQR
##   <fct> <int>   <int> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 0         50      0  5.97  23.4  22.1  26.1 1.35
## 2 0.1       50      0  4.98  21.1  19.2  22.2 1.29
## 3 0.3       50      0  3.99  20.4  19.2  22.8 1.53
## 4 0.6       50      0  4.96  19.8  18.2  21.2 1.12
## 5 1.2       50      0  2.00  18.0  16.9  19.3 1.10
## 6 2.5       50      0  2.00  15.2  14.4  17.6 1.16
## 7 5         50      0  5.83  14.5  14.1  15.4 0.855
```

Kruskal–Wallis test provides evidence of statistical differences among best performance in the population at the end of 50,000 generations.

```
kruskal.test(pop_fit_max ~ Sigma, data = end)

##
##  Kruskal-Wallis rank sum test
##
## data: pop_fit_max by Sigma
## Kruskal-Wallis chi-squared = 190.85, df = 6, p-value < 2.2e-16
```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction on the best performance in the population at the end of 50,000 generations.

```
pairwise.wilcox.test(x = end$pop_fit_max, g = end$Sigma , p.adjust.method = "bonferroni",
                      paired = FALSE, conf.int = FALSE, alternative = '1')

##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: end$pop_fit_max and end$Sigma
##
##   0     0.1    0.3    0.6    1.2    2.5
## 0.1 1.7e-08 -      -      -      -      -
```

```

## 0.3 5.6e-09 0.06245 - - - -
## 0.6 8.2e-10 5.6e-06 0.03847 - - - -
## 1.2 9.0e-10 1.5e-08 4.0e-09 1.7e-07 - - -
## 2.5 5.6e-13 1.6e-08 3.4e-11 2.7e-09 7.1e-10 - -
## 5 2.1e-13 2.5e-08 3.8e-11 3.2e-09 2.6e-10 0.00076
##
## P value adjustment method: bonferroni

```

### 8.4.2 Activation gene coverage

Here we analyze the activation gene coverage for each parameter replicate on the multi-path exploration diagnostic.

#### 8.4.2.1 Coverage over time

Activation gene coverage over time.

```

problem <- filter(gfs_ot, diagnostic == 'multipath_exploration')
lines = problem %>%
  group_by(Sigma, gen) %>%
  dplyr::summarise(
    min = min(uni_str_pos),
    mean = mean(uni_str_pos),
    max = max(uni_str_pos)
  )

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

points = filter(lines, gen %% 2000 == 0 & gen != 0)

ot = ggplot(lines, aes(x=gen, y=mean, group = Sigma, fill = Sigma, color = Sigma, shape = Sigma))
  geom_ribbon(aes(ymin = min, ymax = max), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = points, size = 1.5, stroke = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Coverage",
    limits=c(-1, 101),
    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+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6")

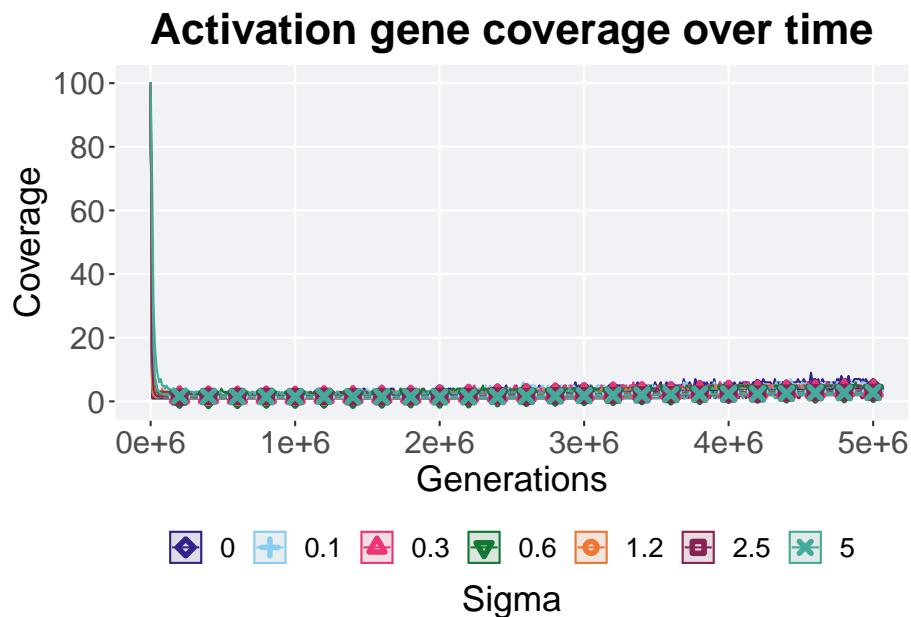
```

```

) +
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+
guides(
shape=guide_legend(nrow=1, title.position = "bottom"),
color=guide_legend(nrow=1, title.position = "bottom"),
fill=guide_legend(nrow=1, title.position = "bottom")
) +
theme(
legend.position = "bottom",
legend.box="vertical",
legend.justification="center",
legend.title.align=0.5
)
)

```

ot

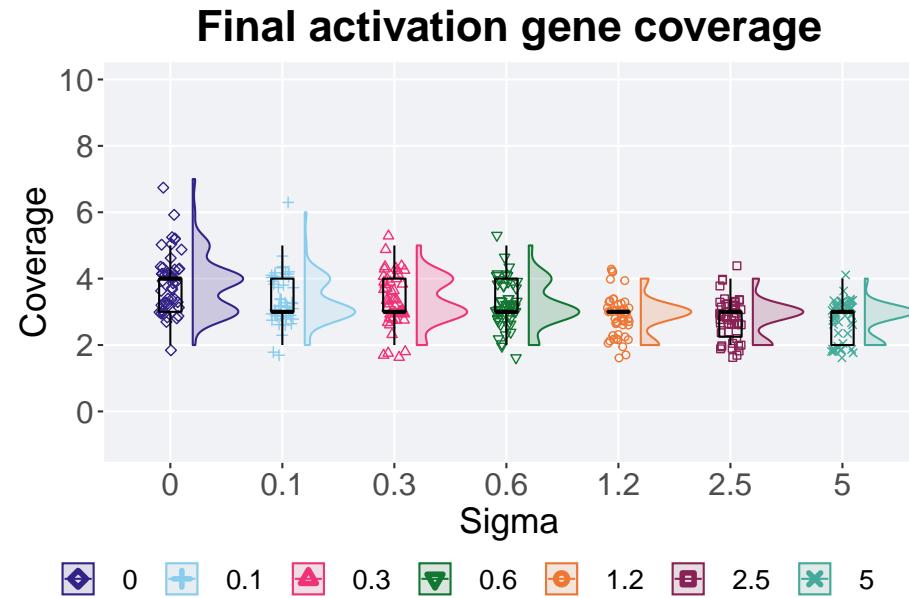


#### 8.4.2.2 End of 50,000 generations

Activation gene coverage in the population at the end of 50,000 generations.

```
end = filter(gfs_end, diagnostic == 'multipath_exploration')
plot = ggplot(end, aes(x = Sigma, y = uni_str_pos, color = Sigma, fill = Sigma, shape = Sigma)) +
  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(-1, 10),
    breaks=seq(0,10, 2),
    labels=c("0", "2", "4", "6", "8", "10")
  ) +
  scale_x_discrete(
    name="Sigma"
  ) +
  scale_shape_manual(values=SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  p_theme

plot_grid(
  plot +
  ggtitle("Final activation gene coverage") +
  theme(legend.position="none"),
  legend,
  nrow=2,
  rel_heights = c(2,.3),
  label_size = TSIZE
)
```



#### 8.4.2.2.1 Stats

Summary statistics for the activation gene coverage in the population at the end of 50,000 generations.

```
group_by(end, Sigma) %>%
  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: 7 x 8
##   Sigma count na_cnt   min median   mean   max   IQR
##   <dbl> <int>   <int> <dbl> <dbl> <dbl> <dbl>
## 1 0      50      0     2     4  3.82    7   1
## 2 0.1    50      0     2     3  3.34    6   1
## 3 0.3    50      0     2     3  3.34    5   1
## 4 0.6    50      0     2     3  3.22    5   1
## 5 1.2    50      0     2     3  2.86    4   0
## 6 2.5    50      0     2     3  2.82    4  0.75
## 7 5      50      0     2     3  2.76    4   1
```

Kruskal–Wallis test provides evidence of statistical differences among activation gene coverage in the population at the end of 50,000 generations.

```
kruskal.test(uni_str_pos ~ Sigma, data = end)

##
## Kruskal-Wallis rank sum test
##
## data: uni_str_pos by Sigma
## Kruskal-Wallis chi-squared = 72.787, df = 6, p-value = 1.095e-13
```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction on the activation gene coverage in the population at the end of 50,000 generations.

```
pairwise.wilcox.test(x = end$uni_str_pos, g = end$Sigma, p.adjust.method = "bonferroni",
                      paired = FALSE, conf.int = FALSE, alternative = 't')

##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: end$uni_str_pos and end$Sigma
##
##      0      0.1      0.3      0.6      1.2      2.5
## 0.1 0.08211  -      -      -      -      -
## 0.3 0.20516 1.00000  -      -      -      -
## 0.6 0.01338 1.00000 1.00000  -      -      -
## 1.2 4.4e-07 0.01017 0.01086 0.18315  -      -
## 2.5 1.2e-07 0.00303 0.00366 0.07131 1.00000  -
## 5   1.1e-08 0.00032 0.00050 0.01272 1.00000 1.00000
##
## P value adjustment method: bonferroni
```



## Chapter 9

# Phenotypic fitness sharing

We present the results from our parameter sweep on phenotypic fitness sharing. 50 replicates are conducted for each sigma parameter value explored. Note that when `sigma = 0.0`, performance with no similarity penalty and stochastic remainder selection is used to identify parent solutions.

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

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          2.1
## year          2022
## month         06
## day           23
## svn rev       82513
## language      R
## version.string R version 4.2.1 (2022-06-23)
## nickname      Funny-Looking Kid
```

## 9.1 Exploitation rate results

Here we present the results for **best performances** found by each phenotypic fitness sharing sigma value replicate on the exploitation rate diagnostic. 50 replicates are conducted for each sigma parameter value explored. Note that when `sigma = 0.0`, performance with no similarity penalty and stochastic remainder selection is used to identify parent solutions.

### 9.1.1 Performance over time

Performance over time.

```
problem <- filter(pfs_ot, diagnostic == 'exploitation_rate')
lines = problem %>%
  group_by(Sigma, gen) %>%
  dplyr::summarise(
    min = min(pop_fit_max),
    mean = mean(pop_fit_max),
    max = max(pop_fit_max)
  )

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

points = filter(lines, gen %% 2000 == 0 & gen != 0)

ot = ggplot(lines, aes(x=gen, y=mean / TRAITS, group = Sigma, fill = Sigma, color = Sigma))
  geom_ribbon(aes(ymin = min / TRAITS, ymax = max / TRAITS), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = points, size = 1.5, stroke = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Average trait score",
    limits=c(-1, 101),
    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+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6")
  ) +
  scale_shape_manual(values=SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  ggtitle("Best performance over time") +
```

```

p_theme +
  guides(
    shape=guide_legend(nrow=1, title.position = "bottom"),
    color=guide_legend(nrow=1, title.position = "bottom"),
    fill=guide_legend(nrow=1, title.position = "bottom")
  ) +
  theme(
    legend.position = "bottom",
    legend.box="vertical",
    legend.justification="center",
    legend.title.align=0.5
  )
)

```

ot



### 9.1.2 Best performance throughout

The best performance found throughout 50,000 generations.

```

best = filter(pfs_best, col == 'pop_fit_max' & diagnostic == 'exploitation_rate')

plot = ggplot(best, aes(x = Sigma, y = val / TRAITS, color = Sigma, fill = Sigma, shape = Sigma))
  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) +

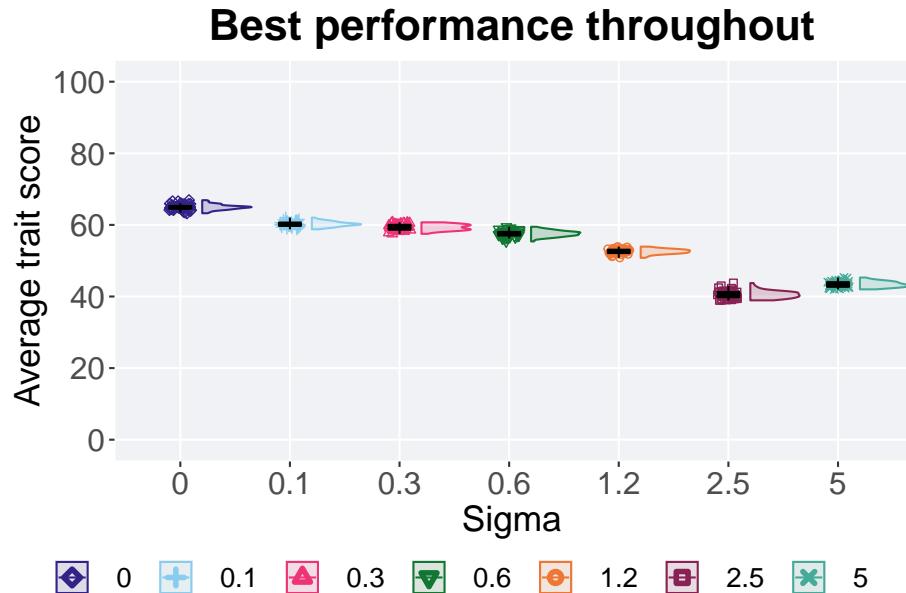
```

```

scale_y_continuous(
  name="Average trait score",
  limits=c(-1, 101),
  breaks=seq(0,100, 20),
  labels=c("0", "20", "40", "60", "80", "100")
) +
scale_x_discrete(
  name="Sigma"
) +
scale_shape_manual(values=SHAPE) +
scale_colour_manual(values = cb_palette) +
scale_fill_manual(values = cb_palette) +
p_theme

plot_grid(
  plot +
  ggtitle("Best performance throughout") +
  theme(legend.position="none"),
  legend,
  nrow=2,
  rel_heights = c(2,.3),
  label_size = TSIZE
)

```



### 9.1.2.1 Stats

Summary statistics for the best performance found throughout 50,000 generations.

```
group_by(best, Sigma) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(val)),
    min = min(val / TRAITS, na.rm = TRUE),
    median = median(val / TRAITS, na.rm = TRUE),
    mean = mean(val / TRAITS, na.rm = TRUE),
    max = max(val / TRAITS, na.rm = TRUE),
    IQR = IQR(val / TRAITS, na.rm = TRUE)
  )

## # A tibble: 7 x 8
##   Sigma count na_cnt   min median   mean   max   IQR
##   <fct> <int> <int> <dbl> <dbl> <dbl> <dbl>
## 1 0      50     0  63.3  65.0  65.0  66.9  0.772
## 2 0.1    50     0  58.8  60.2  60.2  62.0  0.928
## 3 0.3    50     0  57.5  59.4  59.3  60.7  1.37
## 4 0.6    50     0  55.4  57.6  57.6  59.5  0.985
## 5 1.2    50     0  50.8  52.6  52.6  53.9  0.942
## 6 2.5    50     0  38.9  40.5  40.5  43.8  1.43
## 7 5      50     0  42.0  43.3  43.4  45.3  1.29
```

Kruskal–Wallis test provides evidence of significant differences among sigma values on the best performance found throughout 50,000 generations

```
kruskal.test(val ~ Sigma, data = best)

##
## Kruskal-Wallis rank sum test
##
## data: val by Sigma
## Kruskal-Wallis chi-squared = 335, df = 6, p-value < 2.2e-16
```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction on the best performance found throughout 50,000 generations.

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

##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: best$val and best$Sigma
##
```

```

##      0     0.1     0.3     0.6     1.2     2.5
## 0.1 < 2e-16 -     -     -     -     -
## 0.3 < 2e-16 1.8e-05 -     -     -     -
## 0.6 < 2e-16 < 2e-16 9.9e-13 -     -     -
## 1.2 < 2e-16 < 2e-16 < 2e-16 < 2e-16 -     -
## 2.5 < 2e-16 < 2e-16 < 2e-16 < 2e-16 -     -
## 5    < 2e-16 < 2e-16 < 2e-16 < 2e-16 1
##
## P value adjustment method: bonferroni

```

## 9.2 Ordered exploitation results

Here we present the results for **best performances** found by each phenotypic fitness sharing sigma value replicate on the ordered exploitation diagnostic. Best performance found refers to the largest average trait score found in a given population. Note that performance values fall between 0 and 100.

### 9.2.1 Performance over time

Performance over time.

```

problem <- filter(pfs_ot, diagnostic == 'ordered_exploitation')
lines = problem %>%
  group_by(Sigma, gen) %>%
  dplyr::summarise(
    min = min(pop_fit_max),
    mean = mean(pop_fit_max),
    max = max(pop_fit_max)
  )

## `summarise()` has grouped output by 'Sigma'. You can override using the
## `.groups` argument.
points = filter(lines, gen %% 2000 == 0 & gen != 0)

ot = ggplot(lines, aes(x=gen, y=mean / TRAITS, group = Sigma, fill = Sigma, color = Sigma))
  geom_ribbon(aes(ymin = min / TRAITS, ymax = max / TRAITS), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = points, size = 1.5, stroke = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name = "Average trait score",
    limits = c(-1, 30),
    breaks = seq(0, 30, 10),
    labels = c("0", "10", "20", "30")
  ) +
  scale_x_continuous(

```

```

name="Generations",
limits=c(0, 50000),
breaks=c(0, 10000, 20000, 30000, 40000, 50000),
labels=c("0e+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6")

) +
scale_shape_manual(values=SHAPE) +
scale_colour_manual(values = cb_palette) +
scale_fill_manual(values = cb_palette) +
ggtitle("Best performance over time") +
p_theme +
guides(
shape=guide_legend(nrow=1, title.position = "bottom"),
color=guide_legend(nrow=1, title.position = "bottom"),
fill=guide_legend(nrow=1, title.position = "bottom")
) +
theme(
legend.position = "bottom",
legend.box="vertical",
legend.justification="center",
legend.title.align=0.5
)

)

```

ot



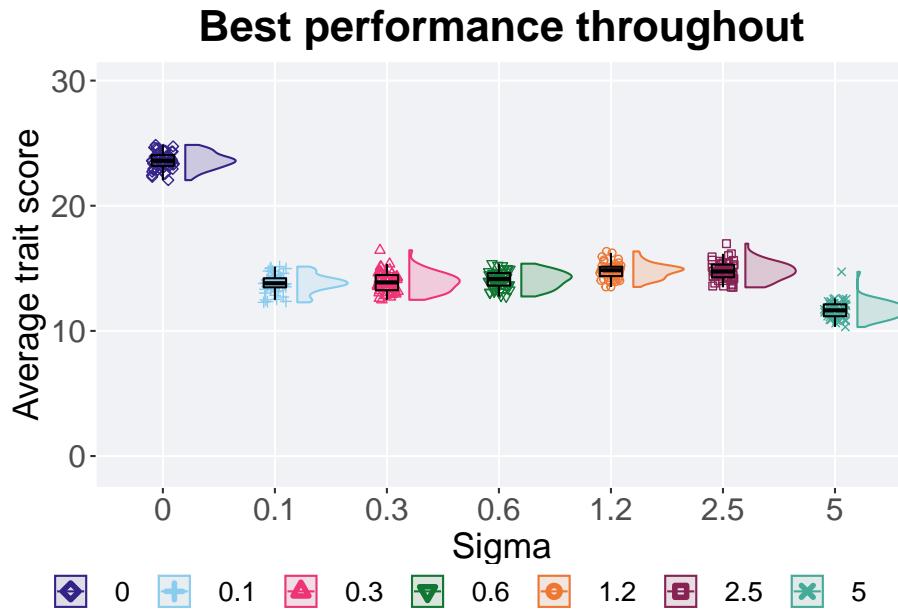
### 9.2.2 Best performance throughout

The best performance found throughout 50,000 generations.

```
best = filter(pfs_best, col == 'pop_fit_max' & diagnostic == 'ordered_exploitation')

plot = ggplot(best, aes(x = Sigma, y = val / TRAITS, color = Sigma, fill = Sigma, shape = Sigma))
  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 = "Average trait score",
    limits = c(-1, 30),
    breaks = seq(0, 30, 10),
    labels = c("0", "10", "20", "30"))
) +
  scale_x_discrete(
    name = "Sigma"
) +
  scale_shape_manual(values = SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  p_theme

plot_grid(
  plot +
    ggtitle("Best performance throughout") +
    theme(legend.position = "none"),
  legend,
  nrow = 2,
  rel_heights = c(2, .2),
  label_size = TSIZE
)
```



#### 9.2.2.1 Stats

Summary statistics about the best performance found.

```
group_by(best, Sigma) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(val)),
    min = min(val / TRAITS, na.rm = TRUE),
    median = median(val / TRAITS, na.rm = TRUE),
    mean = mean(val / TRAITS, na.rm = TRUE),
    max = max(val / TRAITS, na.rm = TRUE),
    IQR = IQR(val / TRAITS, na.rm = TRUE)
  )

## # A tibble: 7 x 8
##   Sigma count na_cnt   min median   mean   max   IQR
##   <fct> <int>   <int> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 0        50      0  22.0  23.6  23.6  24.9  0.874
## 2 0.1     50      0  12.3  13.8  13.8  15.1  0.725
## 3 0.3     50      0  12.5  13.9  13.9  16.4  1.21
## 4 0.6     50      0  12.8  14.1  14.1  15.4  1.01
## 5 1.2     50      0  13.5  14.8  14.8  16.4  0.745
## 6 2.5     50      0  13.5  14.8  14.8  17.0  1.01
## 7 5       50      0  10.3  11.6  11.7  14.7  0.949
```

Kruskal–Wallis test provides evidence of statistical differences for the best performance found in the population throughout 50,000 generations.

```
kruskal.test(val ~ Sigma, data = best)

##
## Kruskal-Wallis rank sum test
##
## data: val by Sigma
## Kruskal-Wallis chi-squared = 248.09, df = 6, p-value < 2.2e-16
```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction on the best performance found in the population throughout 50,000 generations.

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

##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: best$val and best$Sigma
##
##    0      0.1     0.3     0.6     1.2     2.5
## 0.1 < 2e-16 -      -      -      -      -
## 0.3 < 2e-16 1      -      -      -      -
## 0.6 < 2e-16 1      1      -      -      -
## 1.2 < 2e-16 1      1      1      -      -
## 2.5 < 2e-16 1      1      1      1      -
## 5    < 2e-16 4.5e-15 1.2e-15 7.9e-16 2.8e-16 3.1e-16
##
## P value adjustment method: bonferroni
```

## 9.3 Contraditory objectives diagnostic

Here we present the results for **satisfactory trait coverage** and **activation gene coverage** found by each phenotypic fitness sharing sigma value replicate on the ordered exploitation diagnostic. Satisfactory trait coverage refers to the count of unique satisfied traits in the population, while activation gene coverage refers to the count of unique activation genes in the population. Note that both coverage values fall between 0 and 100.

### 9.3.1 Satisfactory trait coverage

Satisfactory trait coverage analysis.

#### 9.3.1.1 Coverage over time

Satisfactory trait coverage over time.

```

problem <- filter(pfs_ot, diagnostic == 'contradictory_objectives')
lines = problem %>%
  group_by(Sigma, gen) %>%
  dplyr::summarise(
    min = min(pop_uni_obj),
    mean = mean(pop_uni_obj),
    max = max(pop_uni_obj)
  )

## `summarise()` has grouped output by 'Sigma'. You can override using the
## `.groups` argument.
points = filter(lines, gen %% 2000 == 0 & gen != 0)

ot = ggplot(lines, aes(x=gen, y=mean, group = Sigma, fill = Sigma, color = Sigma, shape = Sigma))
  geom_ribbon(aes(ymin = min, ymax = max), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = points, size = 1.5, stroke = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Coverage",
    limits=c(0, 30)
  ) +
  scale_x_continuous(
    name="Generations",
    limits=c(0, 50000),
    breaks=c(0, 10000, 20000, 30000, 40000, 50000),
    labels=c("0e+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6")
  ) +
  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 +
  guides(
    shape=guide_legend(nrow=1, title.position = "bottom"),
    color=guide_legend(nrow=1, title.position = "bottom"),
    fill=guide_legend(nrow=1, title.position = "bottom")
  ) +
  theme(
    legend.position = "bottom",
    legend.box="vertical",
    legend.justification="center",
    legend.title.align=0.5
  )

```

```
ot
```



#### 9.3.1.2 Best coverage throughout

Best satisfactory trait coverage throughout 50,000 generations.

```
best = filter(pfs_best, col == 'pop_uni_obj' & diagnostic == 'contradictory_objectives')

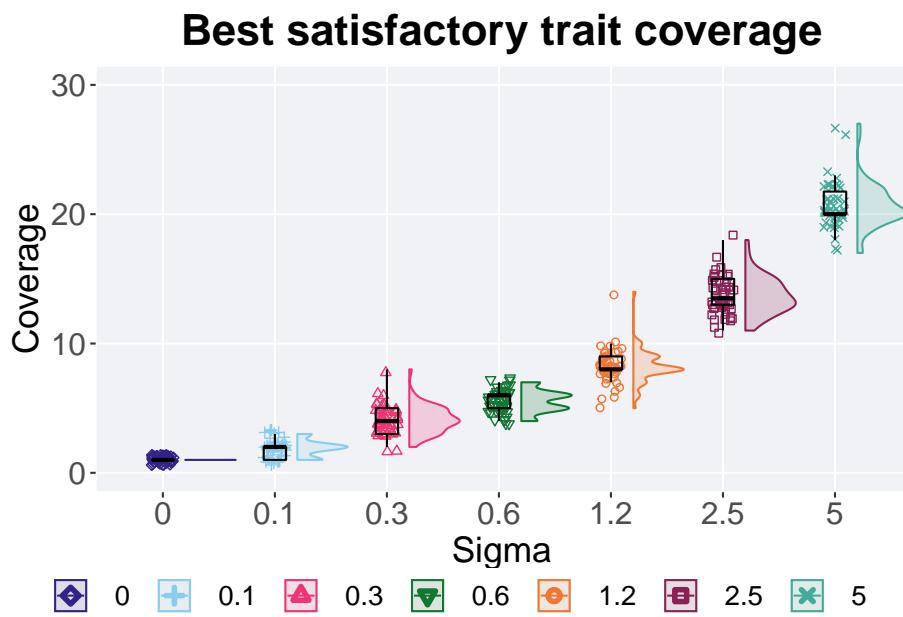
plot = ggplot(best, aes(x = Sigma, y = val, color = Sigma, fill = Sigma, shape = Sigma))
  geom_flat_violin(position = position_nudge(x = .2, y = 0), scale = 'width', alpha = 0.2) +
  geom_point(position = position_jitter(width = .1), size = 1.5, alpha = 1.0) +
  geom_boxplot(color = 'black', width = .2, outlier.shape = NA, alpha = 0.0) +
  scale_y_continuous(
    name="Coverage",
    limits=c(0, 30)
  ) +
  scale_x_discrete(
    name="Sigma"
  ) +
  scale_shape_manual(values=SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  p_theme

plot_grid(
```

```

plot +
  ggtitle("Best satisfactory trait coverage") +
  theme(legend.position="none"),
  legend,
  nrow=2,
  rel_heights = c(2,.2),
  label_size = TSIZE
)

```



#### 9.3.1.2.1 Stats

Summary statistics for the best satisfactory trait coverage throughout 50,000 generations.

```

group_by(best, Sigma) %>%
  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: 7 x 8
```

```
##   Sigma count na_cnt   min median   mean   max   IQR
##   <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 0      50     0     1     1     1       1     0
## 2 0.1    50     0     1     2     1.88    3     1
## 3 0.3    50     0     2     4     4.12    8     2
## 4 0.6    50     0     4     6     5.54    7     1
## 5 1.2    50     0     5     8     8.22   14     1
## 6 2.5    50     0    11    13.5  13.7   18     2
## 7 5      50     0    17    20    20.7   27   1.75
```

Kruskal–Wallis test provides evidence of statistical difference among the best satisfactory trait coverage throughout 50,000 generations.

```
kruskal.test(val ~ Sigma, data = best)
```

```
##
## Kruskal-Wallis rank sum test
##
## data: val by Sigma
## Kruskal-Wallis chi-squared = 335.64, df = 6, p-value < 2.2e-16
```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction on the best satisfactory trait coverage throughout 50,000 generations.

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

```
##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: best$val and best$Sigma
##
##          0      0.1     0.3     0.6     1.2     2.5
## 0.1 2.4e-12 -      -      -      -      -
## 0.3 < 2e-16 3.1e-15 -      -      -      -
## 0.6 < 2e-16 < 2e-16 8.0e-09 -      -      -
## 1.2 < 2e-16 < 2e-16 < 2e-16 1.1e-14 -      -
## 2.5 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 -
## 5   < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16
##
## P value adjustment method: bonferroni
```

### 9.3.1.3 End of 50,000 generations

Satisfactory trait coverage in the population at the end of 50,000 generations.

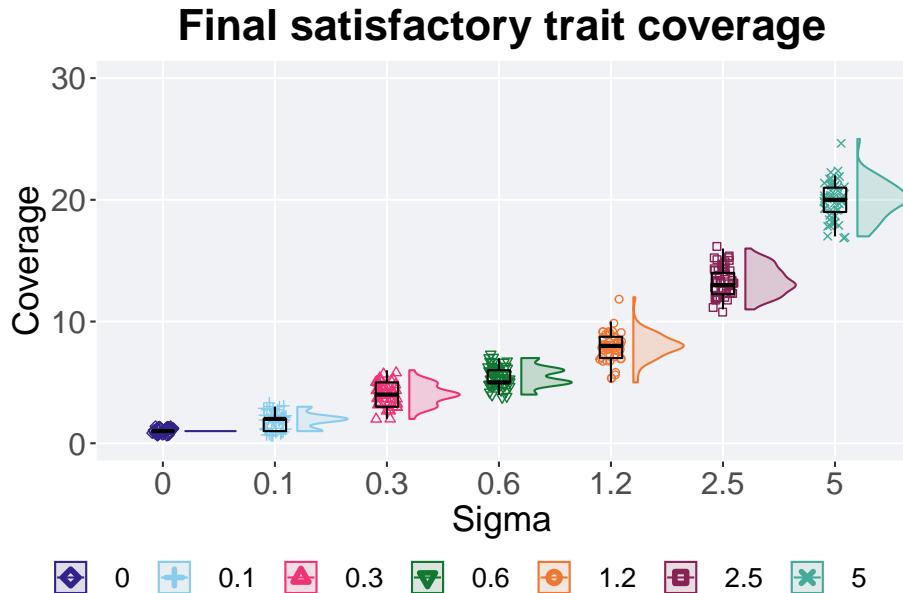
```
end = filter(pfs_end, diagnostic == 'contradictory_objectives')
plot = ggplot(end, aes(x = Sigma, y = pop_uni_obj, color = Sigma, fill = Sigma, shape =
geom_flat_violin(position = position_nudge(x = .2, y = 0), scale = 'width', alpha = 0.5)
```

```

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, 30)
  ) +
  scale_x_discrete(
    name="Sigma"
  ) +
  scale_shape_manual(values=SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  p_theme

plot_grid(
  plot +
    ggtitle("Final satisfactory trait coverage") +
    theme(legend.position="none"),
  legend,
  nrow=2,
  rel_heights = c(2,.3),
  label_size = TSIZE
)

```



### 9.3.1.3.1 Stats

Summary statistics for satisfactory trait coverage in the population at the end of 50,000 generations.

```
group_by(end, Sigma) %>%
  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: 7 x 8
##   Sigma count na_cnt   min median   mean   max   IQR
##   <fct> <int> <int> <dbl> <dbl> <int> <dbl>
## 1 0      50     0     1     1     1     1     0
## 2 0.1    50     0     1     2     1.88   3     1
## 3 0.3    50     0     2     4     4     6     2
## 4 0.6    50     0     4     5     5.5    7     1
## 5 1.2    50     0     5     8     7.94   12    1.75
## 6 2.5    50     0    11    13    13.3   16    1.75
## 7 5      50     0    17    20    20.0   25    2
```

Kruskal–Wallis test provides evidence of statistical difference among satisfactory trait coverage in the population at the end of 50,000 generations.

```
kruskal.test(pop_uni_obj ~ Sigma, data = end)

##
## Kruskal-Wallis rank sum test
##
## data: pop_uni_obj by Sigma
## Kruskal-Wallis chi-squared = 336.38, df = 6, p-value < 2.2e-16
```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction on the best satisfactory trait coverage in the population at the end of 50,000 generations.

```
pairwise.wilcox.test(x = end$pop_uni_obj, g = end$Sigma, p.adjust.method = "bonferroni",
                      paired = FALSE, conf.int = FALSE, alternative = 'g')

##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: end$pop_uni_obj and end$Sigma
##
```

```

##      0      0.1      0.3      0.6      1.2      2.5
## 0.1 2.4e-12 -      -      -      -      -
## 0.3 < 2e-16 2.8e-15 -      -      -      -
## 0.6 < 2e-16 < 2e-16 5.2e-10 -      -      -
## 1.2 < 2e-16 < 2e-16 < 2e-16 5.0e-14 -      -
## 2.5 < 2e-16 < 2e-16 < 2e-16 < 2e-16 -      -
## 5   < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16
##
## P value adjustment method: bonferroni

```

### 9.3.2 Activation gene coverage

Here we analyze the activation gene coverage for each parameter replicate on the contradictory objectives diagnostic.

#### 9.3.2.1 Coverage over time

Activation gene coverage over time.

```

problem <- filter(pfs_ot, diagnostic == 'contradictory_objectives')
lines = problem %>%
    group_by(Sigma, gen) %>%
    dplyr::summarise(
        min = min(uni_str_pos),
        mean = mean(uni_str_pos),
        max = max(uni_str_pos)
    )

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

points = filter(lines, gen %% 2000 == 0 & gen != 0)

ot = ggplot(lines, aes(x=gen, y=mean, group = Sigma, fill = Sigma, color = Sigma, shape = Sigma))
    geom_ribbon(aes(ymin = min, ymax = max), alpha = 0.1) +
    geom_line(size = 0.5) +
    geom_point(data = points, size = 1.5, stroke = 2.0, alpha = 1.0) +
    scale_y_continuous(
        name="Coverage",
        limits=c(-1, 101),
        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),

```

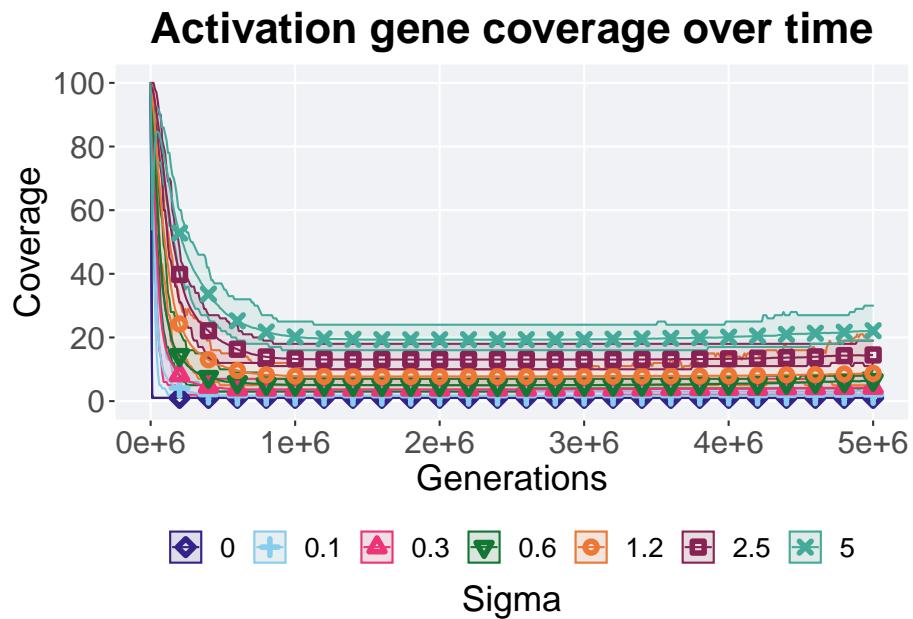
```

    labels=c("0e+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6")

) +
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+
guides(
shape=guide_legend(nrow=1, title.position = "bottom"),
color=guide_legend(nrow=1, title.position = "bottom"),
fill=guide_legend(nrow=1, title.position = "bottom")
) +
theme(
legend.position = "bottom",
legend.box="vertical",
legend.justification="center",
legend.title.align=0.5
)
)

ot

```



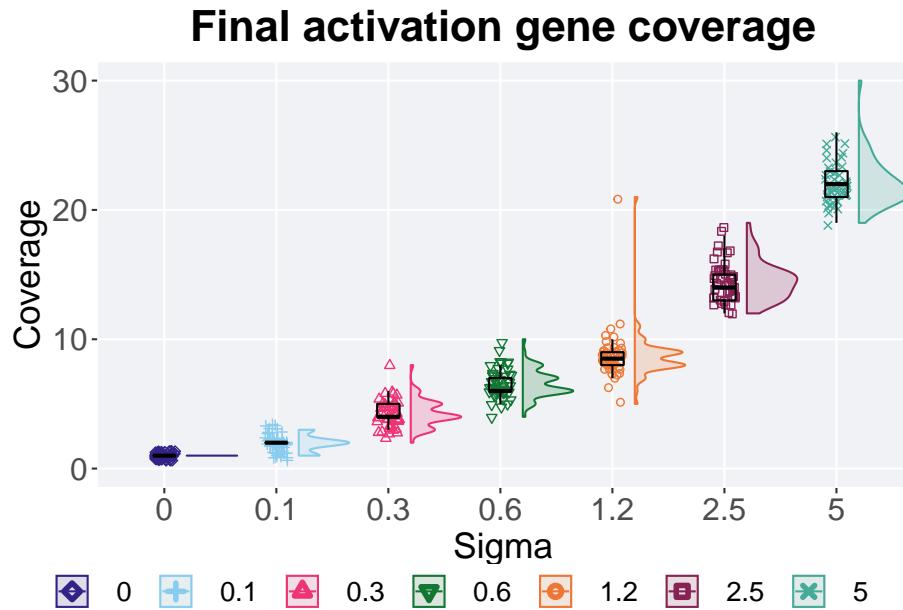
### 9.3.2.2 End of 50,000 generations

Activation gene coverage in the population at the end of 50,000 generations.

```
end = filter(pfs_end, diagnostic == 'contradictory_objectives')
plot = ggplot(end, aes(x = Sigma, y = uni_str_pos, color = Sigma, fill = Sigma, shape = Sigma)) +
  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, 30)
  ) +
  scale_x_discrete(
    name="Sigma"
  ) +
  scale_shape_manual(values=SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  p_theme

plot_grid(
  plot +
    ggtitle("Final activation gene coverage") +
    theme(legend.position="none"),
  legend,
  nrow=2,
  rel_heights = c(2,.2),
  label_size = TSIZE
)
```

## Warning: Removed 1 rows containing missing values (geom\_point).



#### 9.3.2.2.1 Stats

Summary statistics for the best activation gene coverage in the population at the end of 50,000 generations.

```
group_by(end, Sigma) %>%
  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: 7 x 8
##   Sigma count na_cnt   min median   mean   max   IQR
##   <dbl> <int>   <int> <dbl> <dbl> <dbl> <int> <dbl>
## 1 0      50       0     1     1     1     1     0
## 2 0.1    50       0     1     2     1.94   3     0
## 3 0.3    50       0     2     4     4.26   8     1
## 4 0.6    50       0     4     6     6.6    10    1
## 5 1.2    50       0     5     8.5   8.72   21    1
## 6 2.5    50       0    12    14    14.5   19    2
## 7 5      50       0    19    22    22.1   30    2
```

Kruskal–Wallis test provides evidence of no statistical difference among activation gene coverage in the population at the end of 50,000 generations.

```
kruskal.test(uni_str_pos ~ Sigma, data = end)

##
## Kruskal-Wallis rank sum test
##
## data: uni_str_pos by Sigma
## Kruskal-Wallis chi-squared = 335.75, df = 6, p-value < 2.2e-16
```

## 9.4 Multi-path exploration results

Here we present the results for **best performances** and **activation gene coverage** found by each phenotypic fitness sharing sigma value replicate on the multi-path exploration diagnostic. Best performance found refers to the largest average trait score found in a given population, while activation gene coverage refers to the count of unique activation genes in the population. Note that both values fall between 0 and 100.

### 9.4.1 Performance

Here we analyze the performances for each parameter replicate on the multi-path exploration diagnostic.

#### 9.4.1.1 Performance over time

Performance over time.

```
problem <- filter(pfs_ot, diagnostic == 'multipath_exploration')
lines = problem %>%
  group_by(Sigma, gen) %>%
  dplyr::summarise(
    min = min(pop_fit_max),
    mean = mean(pop_fit_max),
    max = max(pop_fit_max)
  )

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

points = filter(lines, gen %% 2000 == 0 & gen != 0)

ot = ggplot(lines, aes(x=gen, y=mean / TRAITS, group = Sigma, fill = Sigma, color = Sigma, shape = Sigma))
  geom_ribbon(aes(ymin = min / TRAITS, ymax = max / TRAITS), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = points, size = 1.5, stroke = 2.0, alpha = 1.0) +
```

```
scale_y_continuous(
  name="Average trait score",
  limits=c(-1, 30)
) +
scale_x_continuous(
  name="Generations",
  limits=c(0, 50000),
  breaks=c(0, 10000, 20000, 30000, 40000, 50000),
  labels=c("0e+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6")

) +
scale_shape_manual(values=SHAPE) +
scale_colour_manual(values = cb_palette) +
scale_fill_manual(values = cb_palette) +
ggtitle("Best performance over time") +
p_theme +
guides(
  shape=guide_legend(nrow=1, title.position = "bottom"),
  color=guide_legend(nrow=1, title.position = "bottom"),
  fill=guide_legend(nrow=1, title.position = "bottom")
) +
theme(
  legend.position = "bottom",
  legend.box="vertical",
  legend.justification="center",
  legend.title.align=0.5
)

ot
```



#### 9.4.1.2 Best performance throughout

Here we plot the performance of the best performing solution found throughout 50,000 generations.

```
best = filter(pfs_best, col == 'pop_fit_max' & diagnostic == 'multipath_exploration')

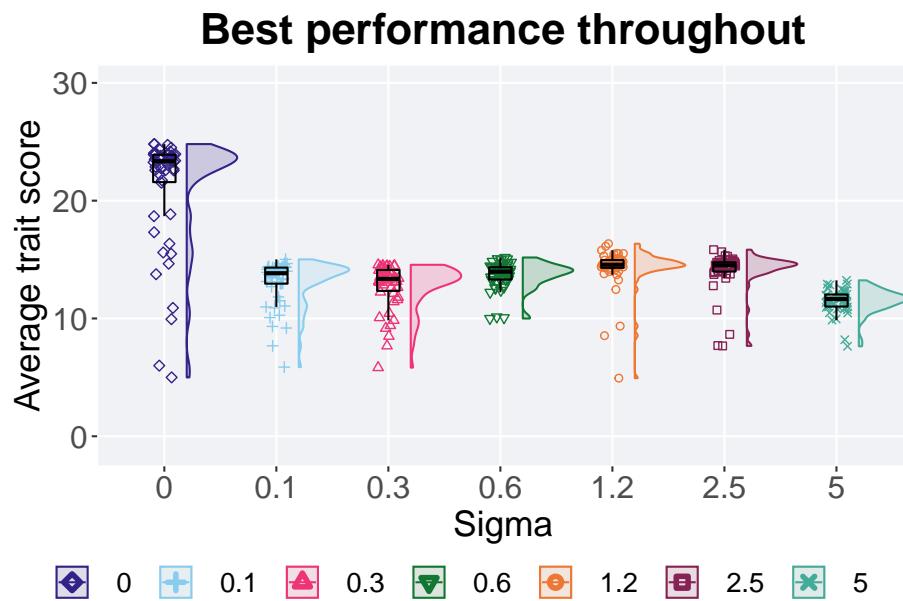
plot = ggplot(best, aes(x = Sigma, y = val / TRAITS, color = Sigma, fill = Sigma, shape = Sigma))
  geom_flat_violin(position = position_nudge(x = .2, y = 0), scale = 'width', alpha = 0.2) +
  geom_point(position = position_jitter(width = .1), size = 1.5, alpha = 1.0) +
  geom_boxplot(color = 'black', width = .2, outlier.shape = NA, alpha = 0.0) +
  scale_y_continuous(
    name="Average trait score",
    limits=c(-1, 30)
  ) +
  scale_x_discrete(
    name="Sigma"
  ) +
  scale_shape_manual(values=SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  p_theme

plot_grid(
  plot +
```

```

ggtile("Best performance throughout") +
  theme(legend.position="none"),
  legend,
  nrow=2,
  rel_heights = c(2,.3),
  label_size = TSIZE
)

```



#### 9.4.1.2.1 Stats

Summary statistics for the performance of the best performing solution found throughout 50,000 generations.

```

group_by(best, Sigma) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(val)),
    min = min(val / TRAITS, na.rm = TRUE),
    median = median(val / TRAITS, na.rm = TRUE),
    mean = mean(val / TRAITS, na.rm = TRUE),
    max = max(val / TRAITS, na.rm = TRUE),
    IQR = IQR(val / TRAITS, na.rm = TRUE)
  )

## # A tibble: 7 x 8
##   Sigma count na_cnt   min median   mean   max   IQR
##   <dbl> <int>   <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1     0     7     0.0  22.5  23.0  23.0  23.0  23.0
## 2     0.1    7     0.0  13.5  14.0  14.0  14.0  14.0
## 3     0.3    7     0.0  13.0  13.5  13.5  13.5  13.5
## 4     0.6    7     0.0  14.0  14.5  14.5  14.5  14.5
## 5     1.2    7     0.0  14.5  15.0  15.0  15.0  15.0
## 6     2.5    7     0.0  14.0  14.5  14.5  14.5  14.5
## 7     5      7     0.0  11.0  11.5  11.5  11.5  11.5

```

```
##   <fct> <int> <int> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 0      50     0  5.00  23.3  21.1  24.8  2.32
## 2 0.1    50     0  5.87  13.8  13.0  15.0  1.36
## 3 0.3    50     0  5.83  13.4  12.7  14.6  1.77
## 4 0.6    50     0 10.0   14.0  13.7  15.2  1.04
## 5 1.2    50     0  4.93  14.6  14.2  16.3  0.659
## 6 2.5    50     0  7.67  14.5  14.0  15.8  0.785
## 7 5      50     0  7.64  11.7  11.5  13.2  1.02
```

Kruskal–Wallis test provides evidence of statistical differences among the best performing solution found throughout 50,000 generations.

```
kruskal.test(val ~ Sigma, data = best)
```

```
##
## Kruskal-Wallis rank sum test
##
## data: val by Sigma
## Kruskal-Wallis chi-squared = 178.85, df = 6, p-value < 2.2e-16
```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction on the best performing solution found throughout 50,000 generations.

```
pairwise.wilcox.test(x = best$val, g = best$Sigma, p.adjust.method = "bonferroni",
                      paired = FALSE, conf.int = FALSE, alternative = 't')
```

```
##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: best$val and best$Sigma
##
##   0     0.1    0.3    0.6    1.2    2.5
## 0.1 2.4e-11 -     -     -     -     -
## 0.3 1.0e-11 1.00000 -     -     -     -
## 0.6 5.1e-11 1.00000 0.13442 -     -     -
## 1.2 2.6e-10 1.4e-06 2.6e-08 0.00019 -     -
## 2.5 1.8e-10 0.00011 6.1e-07 0.01206 1.00000 -
## 5   5.0e-12 1.1e-06 4.8e-06 2.7e-12 8.5e-13 7.2e-12
##
## P value adjustment method: bonferroni
```

#### 9.4.1.3 End of 50,000 generations

Best performance in the population at the end of 50,000 generations.

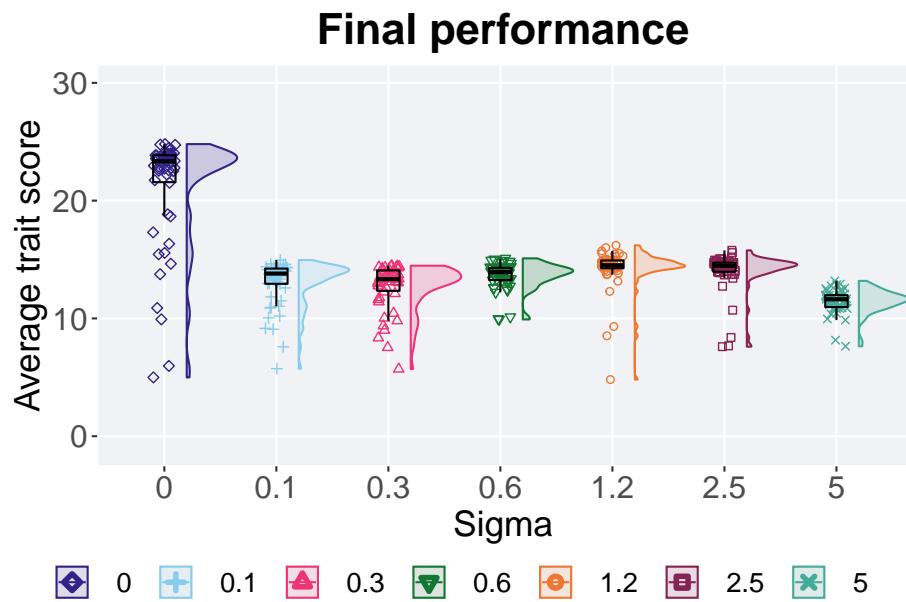
```
end = filter(pfs_end, diagnostic == 'multipath_exploration')
plot = ggplot(end, aes(x = Sigma, y = pop_fit_max / TRAITS, color = Sigma, fill = Sigma, shape =
  geom_flat_violin(position = position_nudge(x = .2, y = 0), scale = 'width', alpha = 0.2) +
  geom_point(position = position_jitter(width = .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(-1, 30)
  ) +
  scale_x_discrete(
    name="Sigma"
  ) +
  scale_shape_manual(values=SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  p_theme

plot_grid(
  plot +
  ggtitle("Final performance") +
  theme(legend.position="none"),
  legend,
  nrow=2,
  rel_heights = c(2,.3),
  label_size = TSIZE
)

```



#### 9.4.1.3.1 Stats

Summary statistics for the best performance in the population at the end of 50,000 generations.

```
group_by(end, Sigma) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(pop_fit_max / TRAITS)),
    min = min(pop_fit_max / TRAITS, na.rm = TRUE),
    median = median(pop_fit_max / TRAITS, na.rm = TRUE),
    mean = mean(pop_fit_max / TRAITS, na.rm = TRUE),
    max = max(pop_fit_max / TRAITS, na.rm = TRUE),
    IQR = IQR(pop_fit_max / TRAITS, na.rm = TRUE)
  )

## # A tibble: 7 x 8
##   Sigma count na_cnt   min median   mean   max   IQR
##   <fct> <int>   <int> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 0         50      0  4.99  23.3  21.1  24.8  2.28
## 2 0.1       50      0  5.73  13.8  13.0  15.0  1.29
## 3 0.3       50      0  5.70  13.3  12.7  14.5  1.74
## 4 0.6       50      0  9.91  13.9  13.6  15.1  1.04
## 5 1.2       50      0  4.81  14.5  14.2  16.2  0.660
## 6 2.5       50      0  7.60  14.5  14.0  15.8  0.773
## 7 5         50      0  7.64  11.6  11.5  13.2  1.01
```

Kruskal–Wallis test provides evidence of statistical differences among best performance in the population at the end of 50,000 generations.

```
kruskal.test(pop_fit_max ~ Sigma, data = end)

##
##  Kruskal-Wallis rank sum test
##
## data: pop_fit_max by Sigma
## Kruskal-Wallis chi-squared = 179.82, df = 6, p-value < 2.2e-16
```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction on the best performance in the population at the end of 50,000 generations.

```
pairwise.wilcox.test(x = end$pop_fit_max, g = end$Sigma , p.adjust.method = "bonferroni",
                      paired = FALSE, conf.int = FALSE, alternative = 't')

##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: end$pop_fit_max and end$Sigma
##
##   0      0.1     0.3     0.6     1.2     2.5
## 0.1 2.0e-11 -      -      -      -      -
```

```

## 0.3 1.0e-11 1.00000 -      -      -      -
## 0.6 4.8e-11 1.00000 0.13725 -      -      -
## 1.2 2.5e-10 1.3e-06 1.5e-08 0.00016 -      -
## 2.5 1.3e-10 8.5e-05 3.8e-07 0.00718 1.00000 -
## 5   5.0e-12 9.8e-07 4.8e-06 2.7e-12 1.0e-12 7.6e-12
##
## P value adjustment method: bonferroni

```

## 9.4.2 Activation gene coverage

Here we analyze the activation gene coverage for each parameter replicate on the multi-path exploration diagnostic.

### 9.4.2.1 Coverage over time

Activation gene coverage over time.

```

problem <- filter(pfs_ot, diagnostic == 'multipath_exploration')
lines = problem %>%
  group_by(Sigma, gen) %>%
  dplyr::summarise(
    min = min(uni_str_pos),
    mean = mean(uni_str_pos),
    max = max(uni_str_pos)
  )

## `summarise()` has grouped output by 'Sigma'. You can override using the
## `.groups` argument.
points = filter(lines, gen %% 2000 == 0 & gen != 0)

ot = ggplot(lines, aes(x=gen, y=mean, group = Sigma, fill = Sigma, color = Sigma, shape = Sigma,
  geom_ribbon(aes(ymin = min, ymax = max), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = points, size = 1.5, stroke = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Coverage",
    limits=c(-1, 101),
    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+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6")

```

```

) +
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+
guides(
shape=guide_legend(nrow=1, title.position = "bottom"),
color=guide_legend(nrow=1, title.position = "bottom"),
fill=guide_legend(nrow=1, title.position = "bottom")
) +
theme(
legend.position = "bottom",
legend.box="vertical",
legend.justification="center",
legend.title.align=0.5
)
)

ot

```

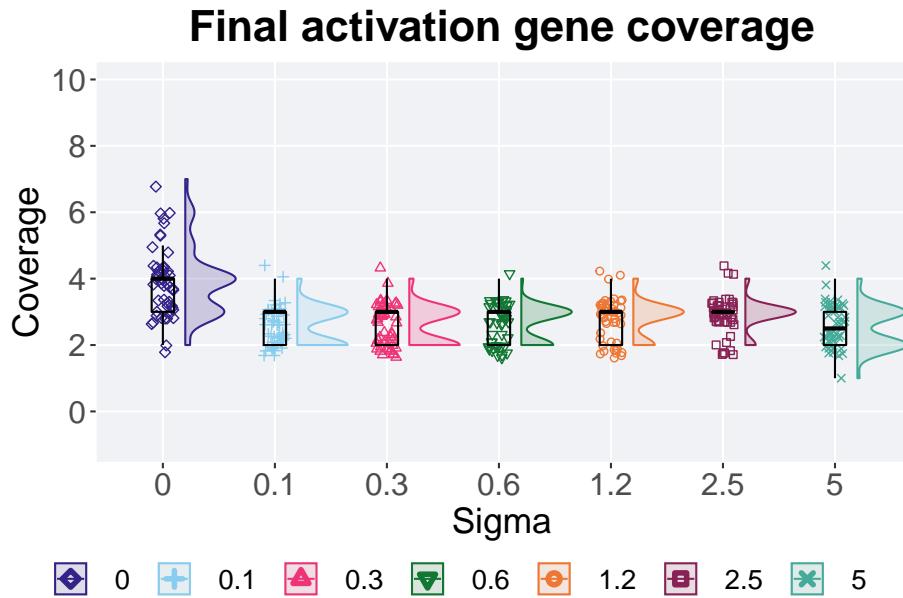


#### 9.4.2.2 End of 50,000 generations

Activation gene coverage in the population at the end of 50,000 generations.

```
end = filter(pfs_end, diagnostic == 'multipath_exploration')
plot = ggplot(end, aes(x = Sigma, y = uni_str_pos, color = Sigma, fill = Sigma, shape =
  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(-1, 10),
    breaks=seq(0,10, 2),
    labels=c("0", "2", "4", "6", "8", "10")
  ) +
  scale_x_discrete(
    name="Sigma"
  ) +
  scale_shape_manual(values=SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  p_theme

plot_grid(
  plot +
  ggtitle("Final activation gene coverage") +
  theme(legend.position="none"),
  legend,
  nrow=2,
  rel_heights = c(2,.3),
  label_size = TSIZE
)
```



#### 9.4.2.2.1 Stats

Summary statistics for the activation gene coverage in the population at the end of 50,000 generations.

```
group_by(end, Sigma) %>%
  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: 7 x 8
##   Sigma count na_cnt   min median   mean   max   IQR
##   <fct> <int>   <int> <dbl> <dbl> <dbl> <int> <dbl>
## 1 0      50      0     2     4    3.88     7     1
## 2 0.1    50      0     2     3    2.56     4     1
## 3 0.3    50      0     2     3    2.56     4     1
## 4 0.6    50      0     2     3    2.64     4     1
## 5 1.2    50      0     2     3    2.78     4     1
## 6 2.5    50      0     2     3    2.9      4     0
## 7 5      50      0     1     2.5   2.52     4     1
```

Kruskal–Wallis test provides evidence of statistical differences among activation gene coverage in the population at the end of 50,000 generations.

```
kruskal.test(uni_str_pos ~ Sigma, data = end)
```

```
##  
## Kruskal-Wallis rank sum test  
##  
## data: uni_str_pos by Sigma  
## Kruskal-Wallis chi-squared = 90.932, df = 6, p-value < 2.2e-16
```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction on the activation gene coverage in the population at the end of 50,000 generations.

```
pairwise.wilcox.test(x = end$uni_str_pos, g = end$Sigma , p.adjust.method = "bonferroni"  
                      paired = FALSE, conf.int = FALSE, alternative = 't')  
  
##  
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction  
##  
## data: end$uni_str_pos and end$Sigma  
##  
##      0       0.1     0.3     0.6     1.2     2.5  
## 0.1 6.6e-10 -      -      -      -  
## 0.3 6.6e-10 1.000 -      -      -  
## 0.6 1.4e-09 1.000 1.000 -      -  
## 1.2 5.4e-08 0.963 0.963 1.000 -  
## 2.5 2.6e-07 0.026 0.026 0.219 1.000 -  
## 5   4.5e-10 1.000 1.000 1.000 0.549 0.013  
##  
## P value adjustment method: bonferroni
```

# Chapter 10

## Nondominated sorting

We present the results from our parameter sweep on genotypic fitness sharing. 50 replicates are conducted for each sigma parameter value explored. Note that when `sigma = 0.0`, performance with no similarity penalty and stochastic remainder selection is used to identify parent solutions.

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

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        2.1
## year         2022
## month        06
## day          23
## svn rev      82513
## language     R
## version.string R version 4.2.1 (2022-06-23)
## nickname     Funny-Looking Kid
```

## 10.1 Exploitation rate results

Here we present the results for **best performances** found by each genotypic fitness sharing sigma value replicate on the exploitation rate diagnostic. Best performance found refers to the largest average trait score found in a given population. Note that performance values fall between 0 and 100.

### 10.1.1 Performance over time

Performance over time.

```
problem <- filter(nds_ot, diagnostic == 'exploitation_rate')
lines = problem %>%
  group_by(Sigma, gen) %>%
  dplyr::summarise(
    min = min(pop_fit_max),
    mean = mean(pop_fit_max),
    max = max(pop_fit_max)
  )

## `summarise()` has grouped output by 'Sigma'. You can override using the
## ` `.groups` argument.
points = filter(lines, gen %% 2000 == 0 & gen != 0)

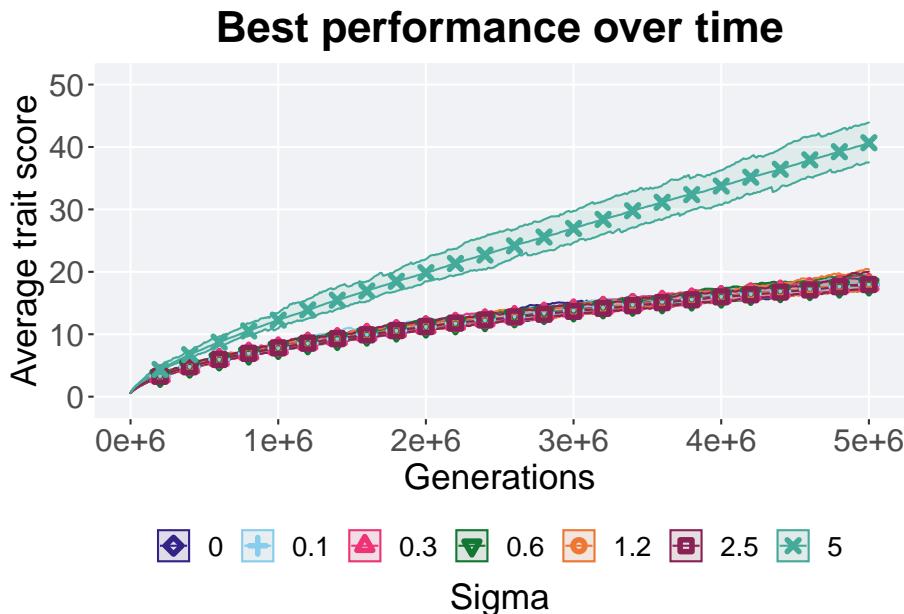
ot = ggplot(lines, aes(x=gen, y=mean / TRAITS, group = Sigma, fill = Sigma, color = Sigma))
  geom_ribbon(aes(ymin = min / TRAITS, ymax = max / TRAITS), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = points, size = 1.5, stroke = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Average trait score",
    limits=c(-1, 51),
    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+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6")
  ) +
  scale_shape_manual(values=SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  ggtitle("Best performance over time") +
  p_theme+
```

```

guides(
  shape=guide_legend(nrow=1, title.position = "bottom"),
  color=guide_legend(nrow=1, title.position = "bottom"),
  fill=guide_legend(nrow=1, title.position = "bottom")
) +
theme(
  legend.position = "bottom",
  legend.box="vertical",
  legend.justification="center",
  legend.title.align=0.5
)

```

ot



#### 10.1.2 Best performance throughout

The best performance found throughout 50,000 generations.

```

best = filter(nds_best, col == 'pop_fit_max' & diagnostic == 'exploitation_rate')

plot = ggplot(best, aes(x = Sigma, y = val / TRAITS, color = Sigma, fill = Sigma, shape = Sigma))
  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()

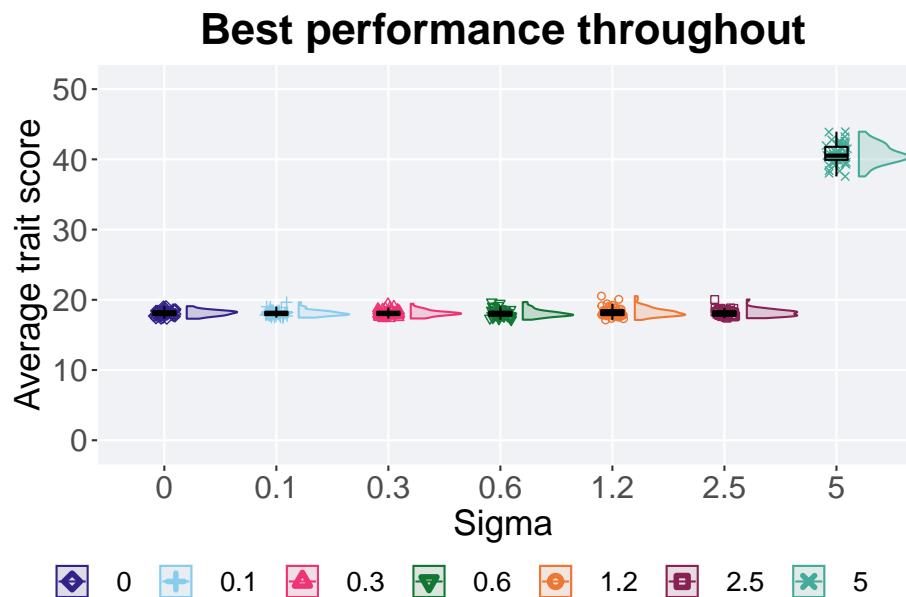
```

```

name="Average trait score",
limits=c(-1, 51),
breaks=seq(0,50, 10),
labels=c("0", "10", "20", "30", "40", "50")
) +
scale_x_discrete(
  name="Sigma"
) +
scale_shape_manual(values=SHAPE) +
scale_colour_manual(values = cb_palette) +
scale_fill_manual(values = cb_palette) +
p_theme

plot_grid(
  plot +
  ggtitle("Best performance throughout") +
  theme(legend.position="none"),
  legend,
  nrow=2,
  rel_heights = c(2,.3),
  label_size = TSIZE
)

```



### 10.1.2.1 Stats

Summary statistics for the best performance found throughout 50,000 generations.

```
group_by(best, Sigma) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(val)),
    min = min(val / TRAITS, na.rm = TRUE),
    median = median(val / TRAITS, na.rm = TRUE),
    mean = mean(val / TRAITS, na.rm = TRUE),
    max = max(val / TRAITS, na.rm = TRUE),
    IQR = IQR(val / TRAITS, na.rm = TRUE)
  )

## # A tibble: 7 x 8
##   Sigma count na_cnt   min median   mean   max   IQR
##   <fct> <int> <int> <dbl> <dbl> <dbl> <dbl>
## 1 0         50     0  17.3  18.1  18.1  19.1  0.567
## 2 0.1       50     0  17.5  18.0  18.1  19.6  0.483
## 3 0.3       50     0  17.3  18.0  18.1  19.4  0.482
## 4 0.6       50     0  17.2  18.0  18.1  19.7  0.567
## 5 1.2       50     0  17.1  18.1  18.3  20.5  0.704
## 6 2.5       50     0  17.4  18.1  18.1  20.0  0.649
## 7 5         50     0  37.6  40.5  40.8  43.9  1.87
```

Kruskal–Wallis test provides evidence of significant differences among sigma values on the best performance found throughout 50,000 generations

```
kruskal.test(val ~ Sigma, data = best)

##
## Kruskal-Wallis rank sum test
##
## data: val by Sigma
## Kruskal-Wallis chi-squared = 129.86, df = 6, p-value < 2.2e-16
```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction on the best performance found throughout 50,000 generations.

```
pairwise.wilcox.test(x = best$val, g = best$Sigma, p.adjust.method = "bonferroni",
                      paired = FALSE, conf.int = FALSE, alternative = 't')

##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: best$val and best$Sigma
##
```

```

##      0     0.1    0.3    0.6    1.2    2.5
## 0.1 1     -     -     -     -     -
## 0.3 1     1     -     -     -     -
## 0.6 1     1     1     -     -     -
## 1.2 1     1     1     1     -     -
## 2.5 1     1     1     1     1     -
## 5 <2e-16 <2e-16 <2e-16 <2e-16 <2e-16 <2e-16
##
## P value adjustment method: bonferroni

```

## 10.2 Ordered exploitation results

Here we present the results for **best performances** found by each genotypic fitness sharing sigma value replicate on the ordered exploitation diagnostic. Best performance found refers to the largest average trait score found in a given population. Note that performance values fall between 0 and 100.

### 10.2.1 Performance over time

Performance over time.

```

problem <- filter(nds_ot, diagnostic == 'ordered_exploitation')
lines = problem %>%
  group_by(Sigma, gen) %>%
  dplyr::summarise(
    min = min(pop_fit_max),
    mean = mean(pop_fit_max),
    max = max(pop_fit_max)
  )

## `summarise()` has grouped output by 'Sigma'. You can override using the
## `.groups` argument.
points = filter(lines, gen %% 2000 == 0 & gen != 0)

ot = ggplot(lines, aes(x=gen, y=mean / TRAITS, group = Sigma, fill = Sigma, color = Sigma))
  geom_ribbon(aes(ymin = min / TRAITS, ymax = max / TRAITS), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = points, size = 1.5, stroke = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name = "Average trait score",
    limits = c(-1, 51),
    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+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6")

) +
scale_shape_manual(values=SHAPE) +
scale_colour_manual(values = cb_palette) +
scale_fill_manual(values = cb_palette) +
ggtitle("Best performance over time") +
p_theme +
guides(
shape=guide_legend(nrow=1, title.position = "bottom"),
color=guide_legend(nrow=1, title.position = "bottom"),
fill=guide_legend(nrow=1, title.position = "bottom")
) +
theme(
legend.position = "bottom",
legend.box="vertical",
legend.justification="center",
legend.title.align=0.5
)

)

```

ot



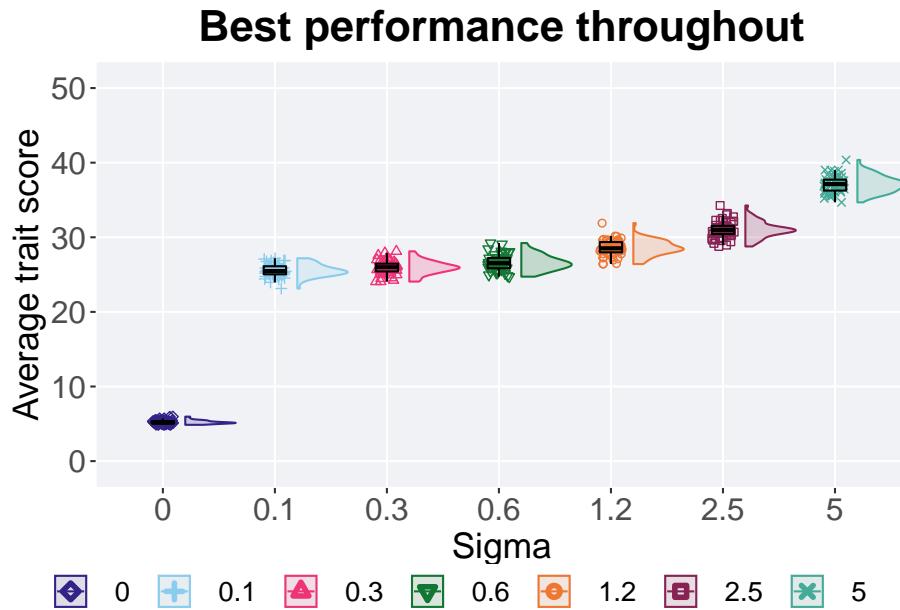
### 10.2.2 Best performance throughout

The best performance found throughout 50,000 generations.

```
best = filter(nds_best, col == 'pop_fit_max' & diagnostic == 'ordered_exploitation')

plot = ggplot(best, aes(x = Sigma, y = val / TRAITS, color = Sigma, fill = Sigma, shape = Sigma))
  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 = "Average trait score",
    limits = c(-1, 51),
    breaks = seq(0, 50, 10),
    labels = c("0", "10", "20", "30", "40", "50")
  ) +
  scale_x_discrete(
    name = "Sigma"
  ) +
  scale_shape_manual(values = SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  p_theme

plot_grid(
  plot +
    ggtitle("Best performance throughout") +
    theme(legend.position = "none"),
  legend,
  nrow = 2,
  rel_heights = c(2, .2),
  label_size = TSIZE
)
```



#### 10.2.2.1 Stats

Summary statistics about the best performance found.

```
group_by(best, Sigma) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(val)),
    min = min(val / TRAITS, na.rm = TRUE),
    median = median(val / TRAITS, na.rm = TRUE),
    mean = mean(val / TRAITS, na.rm = TRUE),
    max = max(val / TRAITS, na.rm = TRUE),
    IQR = IQR(val / TRAITS, na.rm = TRUE)
  )

## # A tibble: 7 x 8
##   Sigma count na_cnt   min median   mean   max   IQR
##   <fct> <int>   <int> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 0        50      0  4.86   5.15   5.22   5.96  0.289
## 2 0.1     50      0 23.1    25.5   25.5   27.2   1.08
## 3 0.3     50      0 24.1    26.0   26.0   28.1   1.04
## 4 0.6     50      0 24.7    26.5   26.6   29.2   1.38
## 5 1.2     50      0 26.4    28.5   28.6   31.9   1.37
## 6 2.5     50      0 28.8    31.0   31.0   34.3   1.10
## 7 5       50      0 34.7    37.1   37.1   40.4   1.46
```

Kruskal–Wallis test provides evidence of statistical differences for the best performance found in the population throughout 50,000 generations.

```
kruskal.test(val ~ Sigma, data = best)

##
## Kruskal-Wallis rank sum test
##
## data: val by Sigma
## Kruskal-Wallis chi-squared = 315.25, df = 6, p-value < 2.2e-16
```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction on the best performance found in the population throughout 50,000 generations.

```
pairwise.wilcox.test(x = best$val, g = best$Sigma, p.adjust.method = "bonferroni",
                      paired = FALSE, conf.int = FALSE, alternative = 't')

##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: best$val and best$Sigma
##
##    0     0.1    0.3    0.6    1.2    2.5
## 0.1 < 2e-16 -      -      -      -      -
## 0.3 < 2e-16 0.34   -      -      -      -
## 0.6 < 2e-16 2.8e-05 0.11   -      -      -
## 1.2 < 2e-16 7.4e-16 9.4e-15 6.8e-11 -      -
## 2.5 < 2e-16 < 2e-16 < 2e-16 < 2e-16 1.8e-13 -
## 5    < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16
##
## P value adjustment method: bonferroni
```

## 10.3 Contradictory objectives diagnostic

Here we present the results for **satisfactory trait coverage** and **activation gene coverage** found by each genotypic fitness sharing sigma value replicate on the contradictory objectives diagnostic. Satisfactory trait coverage refers to the count of unique satisfied traits in the population, while activation gene coverage refers to the count of unique activation genes in the population. Note that both coverage values fall between 0 and 100.

### 10.3.1 Satisfactory trait coverage

Here we analyze the satisfactory trait coverage for each parameter replicate on the contradictory objectives diagnostic.

### 10.3.1.1 Coverage over time

Satisfactory trait coverage over time.

```
problem <- filter(nds_ot, diagnostic == 'contradictory_objectives')
lines = problem %>%
  group_by(Sigma, gen) %>%
  dplyr::summarise(
    min = min(pop_uni_obj),
    mean = mean(pop_uni_obj),
    max = max(pop_uni_obj)
  )

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

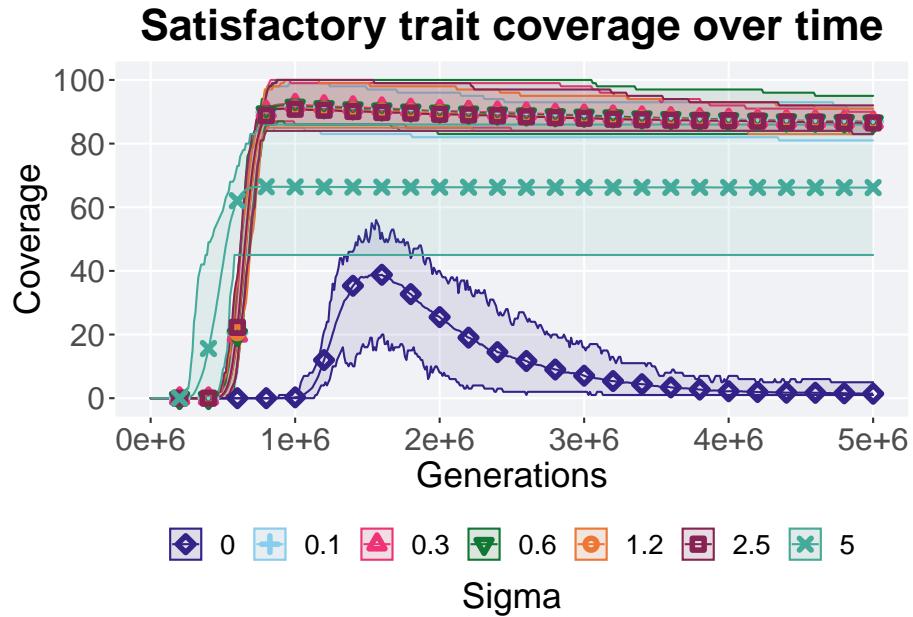
points = filter(lines, gen %% 2000 == 0 & gen != 0)

ot = ggplot(lines, aes(x=gen, y=mean, group = Sigma, fill = Sigma, color = Sigma, shape = Sigma))
  geom_ribbon(aes(ymin = min, ymax = max), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = points, size = 1.5, stroke = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Coverage",
    limits=c(-1, 101),
    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+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6")
  ) +
  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 +
  guides(
    shape=guide_legend(nrow=1, title.position = "bottom"),
    color=guide_legend(nrow=1, title.position = "bottom"),
    fill=guide_legend(nrow=1, title.position = "bottom")
  ) +
  theme(
    legend.position = "bottom",
```

```

        legend.box="vertical",
        legend.justification="center",
        legend.title.align=0.5
    )
}

ot
```



### 10.3.1.2 Best coverage throughout

Best satisfactory trait coverage throughout 50,000 generations.

```

best = filter(nds_best, col == 'pop_uni_obj' & diagnostic == 'contradictory_objectives')

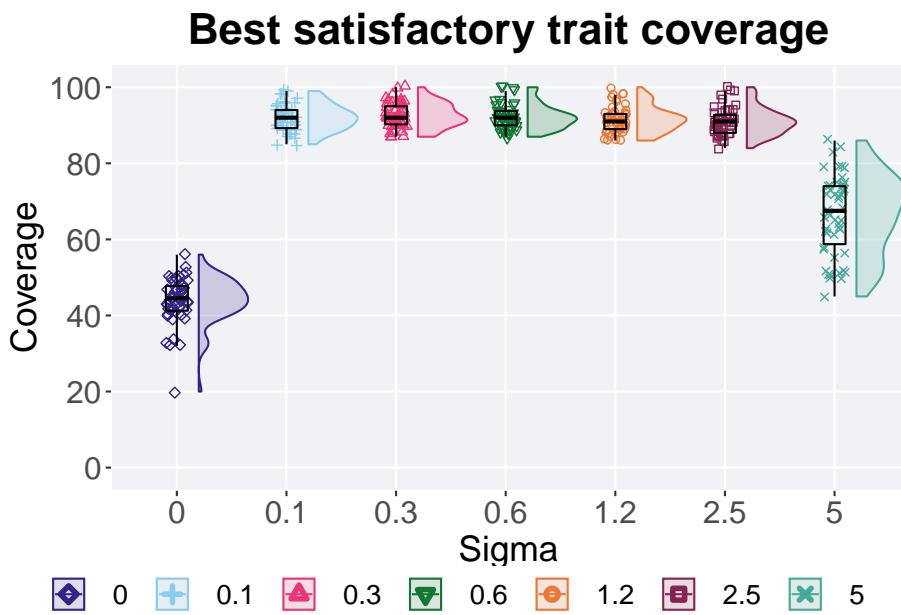
plot = ggplot(best, aes(x = Sigma, y = val, color = Sigma, fill = Sigma, shape = Sigma,
                        geom_flat_violin(position = position_nudge(x = .2, y = 0), scale = 'width', alpha = 0.5),
                        geom_point(position = position_jitter(width = .1), size = 1.5, alpha = 1.0) +
                        geom_boxplot(color = 'black', width = .2, outlier.shape = NA, alpha = 0.0) +
                        scale_y_continuous(
                            name = "Coverage",
                            limits = c(-1, 101),
                            breaks = seq(0, 100, 20),
                            labels = c("0", "20", "40", "60", "80", "100")
                        ) +
                        scale_x_discrete(
                            name = "Sigma"
                        )
)
}
```

```

) +
  scale_shape_manual(values=SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  p_theme

plot_grid(
  plot +
    ggtitle("Best satisfactory trait coverage") +
    theme(legend.position="none"),
  legend,
  nrow=2,
  rel_heights = c(2,.2),
  label_size = TSIZE
)

```



#### 10.3.1.2.1 Stats

Summary statistics for the best satisfactory trait coverage throughout 50,000 generations.

```

group_by(best, Sigma) %>%
  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: 7 x 8
##   Sigma count na_cnt   min median  mean   max   IQR
##   <fct> <int> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 0      50     0     20   44.5  43.9   56   6.5
## 2 0.1    50     0     85   92    92.0   99   4.75
## 3 0.3    50     0     87   92    92.6   100  4.75
## 4 0.6    50     0     87   92    92.2   100  3.75
## 5 1.2    50     0     86   91    91.6   100   4
## 6 2.5    50     0     84   91    91.0   100  4.75
## 7 5      50     0     45   67.5  66.5   86  15.2

```

Kruskal–Wallis test provides evidence of statistical difference for the best satisfactory trait coverage throughout 50,000 generations.

```
kruskal.test(val ~ Sigma, data = best)
```

```

##
## Kruskal-Wallis rank sum test
##
## data: val by Sigma
## Kruskal-Wallis chi-squared = 223.58, df = 6, p-value < 2.2e-16

```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction for the best satisfactory trait coverage throughout 50,000 generations..

```

pairwise.wilcox.test(x = best$val, g = best$Sigma , p.adjust.method = "bonferroni",
                      paired = FALSE, conf.int = FALSE, alternative = 't')

##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: best$val and best$Sigma
##
##      0      0.1     0.3     0.6     1.2     2.5
## 0.1 < 2e-16 -      -      -      -      -
## 0.3 < 2e-16 1.00 -      -      -      -      -
## 0.6 < 2e-16 1.00 1.00 -      -      -      -
## 1.2 < 2e-16 1.00 1.00 1.00 -      -      -
## 2.5 < 2e-16 1.00 0.28 1.00 1.00 -      -
## 5    3.3e-15 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16
##
```

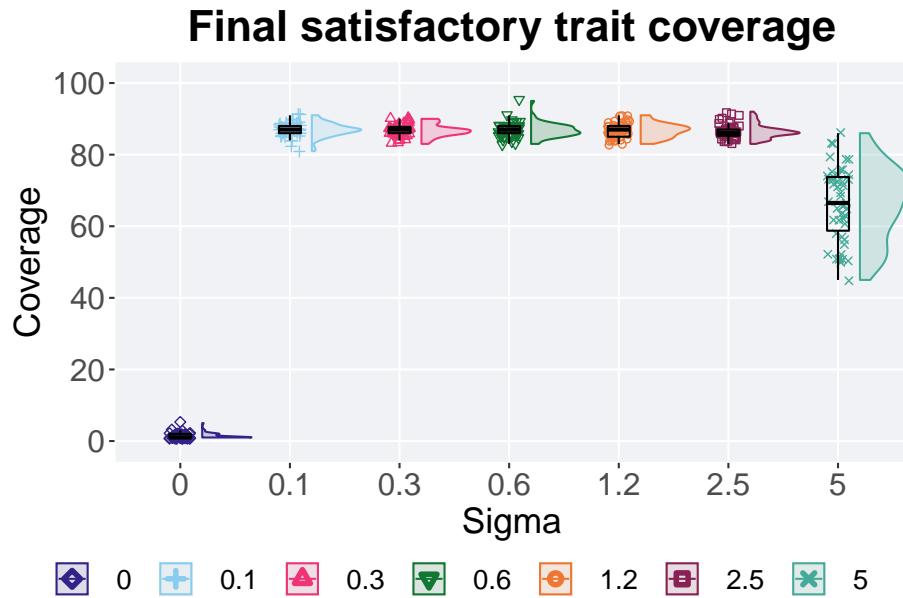
```
## P value adjustment method: bonferroni
```

### 10.3.1.3 End of 50,000 generations

Satisfactory trait coverage in the population at the end of 50,000 generations.

```
end = filter(nds_end, diagnostic == 'contradictory_objectives')
plot = ggplot(end, aes(x = Sigma, y = pop_uni_obj, color = Sigma, fill = Sigma, shape = Sigma)) +
  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(-1, 101),
    breaks=seq(0, 100, 20),
    labels=c("0", "20", "40", "60", "80", "100"))
  ) +
  scale_x_discrete(
    name="Sigma")
  )+
  scale_shape_manual(values=SHAPE)+
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  p_theme

plot_grid(
  plot +
    ggtitle("Final satisfactory trait coverage") +
    theme(legend.position="none"),
  legend,
  nrow=2,
  rel_heights = c(2,.3),
  label_size = TSIZE
)
```



#### 10.3.1.3.1 Stats

Summary statistics for satisfactory trait coverage in the population at the end of 50,000 generations.

```
group_by(end, Sigma) %>%
  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: 7 x 8
##   Sigma count na_cnt   min median   mean   max   IQR
##   <dbl> <int>   <int> <dbl> <dbl> <dbl> <dbl>
## 1 0      50      0     1     1     1.4     5     1
## 2 0.1    50      0    81     87    86.9    91     2
## 3 0.3    50      0    83     87    86.8    90    1.75
## 4 0.6    50      0    83     87    86.8    95     2
## 5 1.2    50      0    83     87    86.7    91     3
## 6 2.5    50      0    83     86    86.5    92    1.75
## 7 5      50      0    45    66.5   66.2    86    15
```

Kruskal–Wallis test provides evidence of statistical difference for satisfactory trait coverage in the population at the end of 50,000 generations.

```
kruskal.test(pop_uni_obj ~ Sigma, data = end)

##
## Kruskal-Wallis rank sum test
##
## data: pop_uni_obj by Sigma
## Kruskal-Wallis chi-squared = 221.3, df = 6, p-value < 2.2e-16
```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction for satisfactory trait coverage in the population at the end of 50,000 generations.

```
pairwise.wilcox.test(x = end$pop_uni_obj, g = end$Sigma, p.adjust.method = "bonferroni",
                      paired = FALSE, conf.int = FALSE, alternative = 't')

##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: end$pop_uni_obj and end$Sigma
##
##      0      0.1     0.3     0.6     1.2     2.5
## 0.1 < 2e-16 -      -      -      -      -
## 0.3 < 2e-16 1      -      -      -      -
## 0.6 < 2e-16 1      1      -      -      -
## 1.2 < 2e-16 1      1      1      -      -
## 2.5 < 2e-16 1      1      1      1      -
## 5    < 2e-16 3.5e-16 3.6e-16 4.1e-16 4.3e-16 4.3e-16
##
## P value adjustment method: bonferroni
```

### 10.3.2 Activation gene coverage

Here we analyze the activation gene coverage for each parameter replicate on the contradictory objectives diagnostic.

#### 10.3.2.1 Coverage over time

Activation gene coverage over time.

```
problem <- filter(nds_ot, diagnostic == 'contradictory_objectives')
lines = problem %>%
  group_by(Sigma, gen) %>%
  dplyr::summarise(
    min = min(uni_str_pos),
    mean = mean(uni_str_pos),
    max = max(uni_str_pos)
```

```
)
```

```
## `summarise()` has grouped output by 'Sigma'. You can override using the
## `.`groups` argument.
points = filter(lines, gen %% 2000 == 0 & gen != 0)

ot = ggplot(lines, aes(x=gen, y=mean, group = Sigma, fill = Sigma, color = Sigma, shape = Sigma))
  geom_ribbon(aes(ymin = min, ymax = max), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = points, size = 1.5, stroke = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Coverage",
    limits=c(-1, 101),
    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+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6")
  ) +
  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 +
  guides(
    shape=guide_legend(nrow=1, title.position = "bottom"),
    color=guide_legend(nrow=1, title.position = "bottom"),
    fill=guide_legend(nrow=1, title.position = "bottom")
  ) +
  theme(
    legend.position = "bottom",
    legend.box="vertical",
    legend.justification="center",
    legend.title.align=0.5
  )

ot
```



#### 10.3.2.2 End of 50,000 generations

Activation gene coverage in the population at the end of 50,000 generations.

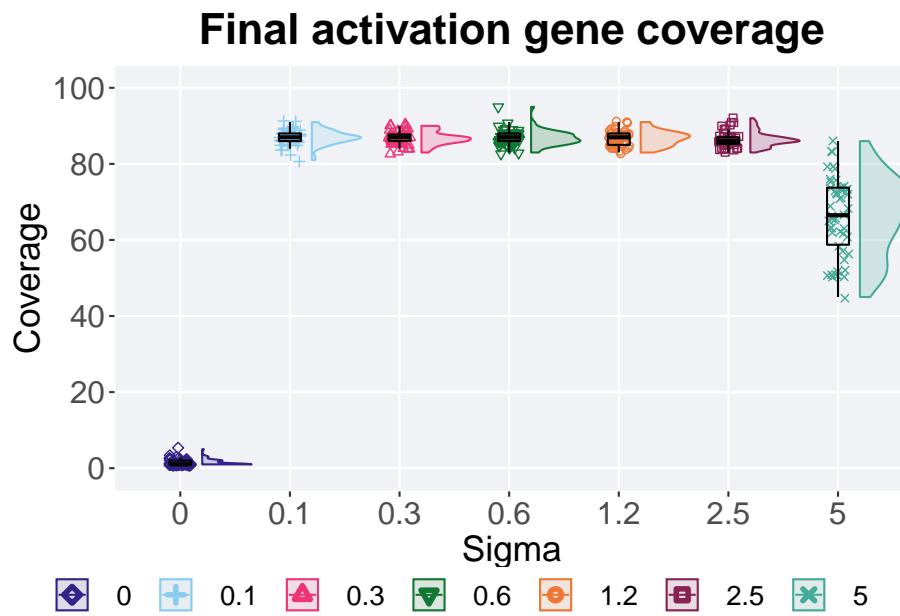
```
end = filter(nds_end, diagnostic == 'contradictory_objectives')
plot = ggplot(end, aes(x = Sigma, y = uni_str_pos, color = Sigma, fill = Sigma, shape = Sigma)) +
  geom_flat_violin(position = position_nudge(x = .2, y = 0), scale = 'width', alpha = 0.2) +
  geom_point(position = position_jitter(width = .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(-1, 101),
    breaks=seq(0, 100, 20),
    labels=c("0", "20", "40", "60", "80", "100"))
  ) +
  scale_x_discrete(
    name="Sigma")
) +
  scale_shape_manual(values=SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  p_theme

plot_grid(
  plot +
```

```

ggtile("Final activation gene coverage") +
  theme(legend.position="none"),
  legend,
  nrow=2,
  rel_heights = c(2,.2),
  label_size = TSIZE
)

```



### 10.3.2.2.1 Stats

Summary statistics for activation gene coverage in the population at the end of 50,000 generations.

```

group_by(end, Sigma) %>%
  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: 7 x 8
##   Sigma count na_cnt   min median   mean   max   IQR
##   <dbl> <int>   <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1     0     1       0     0     0     0     0     0
## 2     0.1    1       0     0     0     0     0     0
## 3     0.3    1       0     0     0     0     0     0
## 4     0.6    1       0     0     0     0     0     0
## 5     1.2    1       0     0     0     0     0     0
## 6     2.5    1       0     0     0     0     0     0
## 7     5      1       0     0     0     0     0     0

```

```
##   <fct> <int> <int> <dbl> <dbl> <int> <dbl>
## 1 0      50     0     1     1    1.5     5   1
## 2 0.1    50     0    81    87   86.9    91   2
## 3 0.3    50     0    83    87   86.8    90  1.75
## 4 0.6    50     0    83    87   86.8    95   2
## 5 1.2    50     0    83    87   86.7    91   3
## 6 2.5    50     0    83    86   86.5    92  1.75
## 7 5      50     0    45   66.5   66.2    86  15
```

Kruskal–Wallis test provides evidence of statistical difference for activation gene coverage in the population at the end of 50,000 generations.

```
kruskal.test(uni_str_pos ~ Sigma, data = end)
```

```
##
## Kruskal-Wallis rank sum test
##
## data: uni_str_pos by Sigma
## Kruskal-Wallis chi-squared = 221.25, df = 6, p-value < 2.2e-16
```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction for activation gene coverage in the population at the end of 50,000 generations.

```
pairwise.wilcox.test(x = end$uni_str_pos, g = end$Sigma, p.adjust.method = "bonferroni",
                      paired = FALSE, conf.int = FALSE, alternative = 't')

##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: end$uni_str_pos and end$Sigma
##
##   0      0.1     0.3     0.6     1.2     2.5
## 0.1 < 2e-16 -      -      -      -      -
## 0.3 < 2e-16 1      -      -      -      -
## 0.6 < 2e-16 1      1      -      -      -
## 1.2 < 2e-16 1      1      1      -      -
## 2.5 < 2e-16 1      1      1      1      -
## 5   < 2e-16 3.5e-16 3.6e-16 4.1e-16 4.3e-16 4.3e-16
##
## P value adjustment method: bonferroni
```

## 10.4 Multi-path exploration results

Here we present the results for **best performances** and **activation gene coverage** found by each nondominated sorting sigma value replicate on the multi-path exploration diagnostic. Best performance found refers to the largest average trait score found in a given population, while activation gene coverage

refers to the count of unique activation genes in the population. Note that both values fall between 0 and 100.

### 10.4.1 Performance

Here we analyze the performances for each parameter replicate on the multi-path exploration diagnostic.

#### 10.4.1.1 Performance over time

Performance over time.

```
problem <- filter(nds_ot, diagnostic == 'multipath_exploration')
lines = problem %>%
  group_by(Sigma, gen) %>%
  dplyr::summarise(
    min = min(pop_fit_max),
    mean = mean(pop_fit_max),
    max = max(pop_fit_max)
  )

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

points = filter(lines, gen %% 2000 == 0 & gen != 0)

ot = ggplot(lines, aes(x=gen, y=mean / TRAITS, group = Sigma, fill = Sigma, color = Sigma))
  geom_ribbon(aes(ymin = min / TRAITS, ymax = max / TRAITS), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = points, size = 1.5, stroke = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Average trait score",
    limits=c(-1, 30)
  ) +
  scale_x_continuous(
    name="Generations",
    limits=c(0, 50000),
    breaks=c(0, 10000, 20000, 30000, 40000, 50000),
    labels=c("0e+0", "1e+0", "2e+0", "3e+0", "4e+0", "5e+0")
  ) +
  scale_shape_manual(values=SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  ggtitle("Best performance over time") +
  p_theme +
  guides(
```

```

shape=guide_legend(nrow=1, title.position = "bottom"),
color=guide_legend(nrow=1, title.position = "bottom"),
fill=guide_legend(nrow=1, title.position = "bottom")
) +
theme(
  legend.position = "bottom",
  legend.box="vertical",
  legend.justification="center",
  legend.title.align=0.5
)

```

ot



#### 10.4.1.2 Best performance throughout

Here we plot the performance of the best performing solution found throughout 50,000 generations.

```

best = filter(nds_best, col == 'pop_fit_max' & diagnostic == 'multipath_exploration')

plot = ggplot(best, aes(x = Sigma, y = val / TRAITS, color = Sigma, fill = Sigma, shape = Sigma))
  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()

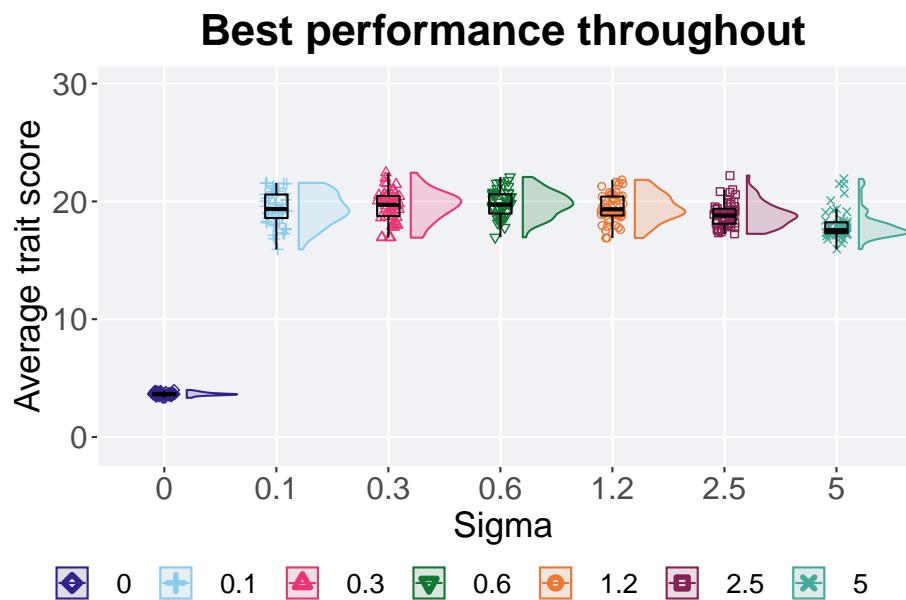
```

```

    name="Average trait score",
    limits=c(-1, 30)
) +
scale_x_discrete(
  name="Sigma"
) +
scale_shape_manual(values=SHAPE) +
scale_colour_manual(values = cb_palette) +
scale_fill_manual(values = cb_palette) +
p_theme

plot_grid(
  plot +
  ggtitle("Best performance throughout") +
  theme(legend.position="none"),
legend,
nrow=2,
rel_heights = c(2,.3),
label_size = TSIZE
)

```



#### 10.4.1.2.1 Stats

Summary statistics for the performance of the best performing solution found throughout 50,000 generations.

```

group_by(best, Sigma) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(val)),
    min = min(val / TRAITS, na.rm = TRUE),
    median = median(val / TRAITS, na.rm = TRUE),
    mean = mean(val / TRAITS, na.rm = TRUE),
    max = max(val / TRAITS, na.rm = TRUE),
    IQR = IQR(val / TRAITS, na.rm = TRUE)
  )

## # A tibble: 7 x 8
##   Sigma count na_cnt   min median   mean   max   IQR
##   <fct> <int>   <int> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 0         50      0  3.33   3.63   3.65   3.99  0.165
## 2 0.1       50      0 15.9    19.4   19.4   21.6   2.00
## 3 0.3       50      0 16.9    19.7   19.6   22.4   1.71
## 4 0.6       50      0 17.0    19.7   19.8   22.1   1.64
## 5 1.2       50      0 16.9    19.3   19.5   21.8   1.61
## 6 2.5       50      0 17.2    18.8   18.9   22.2   1.27
## 7 5         50      0 16.0    17.6   18.0   21.9   0.924

```

Kruskal–Wallis test provides evidence of statistical differences among the best performing solution found throughout 50,000 generations.

```

kruskal.test(val ~ Sigma, data = best)

##
## Kruskal-Wallis rank sum test
##
## data: val by Sigma
## Kruskal-Wallis chi-squared = 173.69, df = 6, p-value < 2.2e-16

```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction on the best performing solution found throughout 50,000 generations.

```

pairwise.wilcox.test(x = best$val, g = best$Sigma, p.adjust.method = "bonferroni",
                      paired = FALSE, conf.int = FALSE, alternative = 't')

##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: best$val and best$Sigma
##
##    0     0.1    0.3    0.6    1.2    2.5
## 0.1 < 2e-16 -     -     -     -     -
## 0.3 < 2e-16 1.00000 -     -     -     -
## 0.6 < 2e-16 1.00000 1.00000 -     -     -

```

```

## 1.2 < 2e-16 1.00000 1.00000 1.00000 -
## 2.5 < 2e-16 0.36861 0.04081 0.00117 0.14914 -
## 5   < 2e-16 2.0e-05 2.0e-06 4.4e-09 1.0e-06 0.00012
##
## P value adjustment method: bonferroni

```

#### 10.4.1.3 End of 50,000 generations

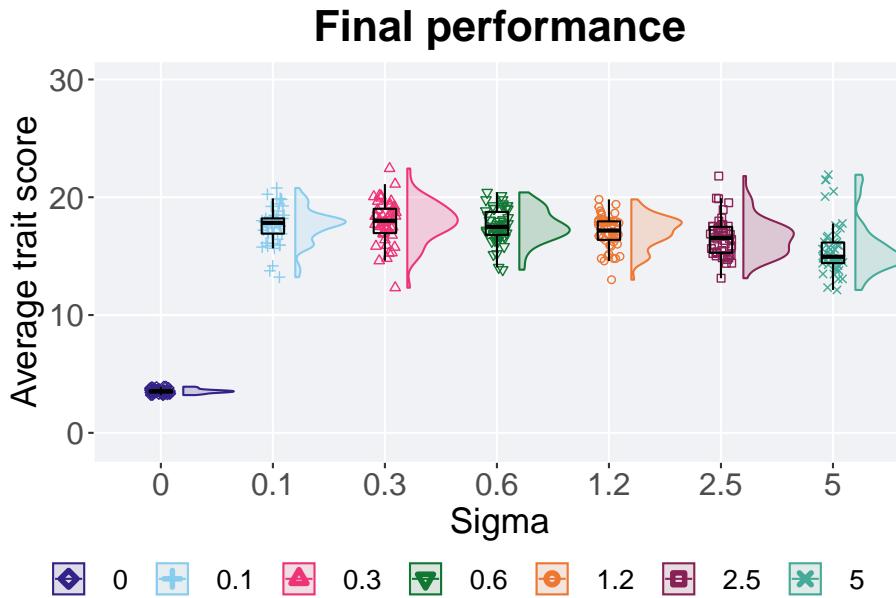
Best performance in the population at the end of 50,000 generations.

```

end = filter(nds_end, diagnostic == 'multipath_exploration')
plot = ggplot(end, aes(x = Sigma, y = pop_fit_max / TRAITS, color = Sigma, fill = Sigma))
  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 = "Average trait score",
    limits = c(-1, 30)
  ) +
  scale_x_discrete(
    name = "Sigma"
  ) +
  scale_shape_manual(values = SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  p_theme

plot_grid(
  plot +
    ggtitle("Final performance") +
    theme(legend.position = "none"),
  legend,
  nrow = 2,
  rel_heights = c(2, .3),
  label_size = TSIZE
)

```



#### 10.4.1.3.1 Stats

Summary statistics for the best performance in the population at the end of 50,000 generations.

```
group_by(end, Sigma) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(pop_fit_max / TRAITS)),
    min = min(pop_fit_max / TRAITS, na.rm = TRUE),
    median = median(pop_fit_max / TRAITS, na.rm = TRUE),
    mean = mean(pop_fit_max / TRAITS, na.rm = TRUE),
    max = max(pop_fit_max / TRAITS, na.rm = TRUE),
    IQR = IQR(pop_fit_max / TRAITS, na.rm = TRUE)
  )

## # A tibble: 7 x 8
##   Sigma count na_cnt   min median   mean   max   IQR
##   <fct> <int> <int> <dbl> <dbl> <dbl> <dbl>
## 1 0      50     0  3.21   3.53   3.53   3.92  0.189
## 2 0.1    50     0 13.2    17.8   17.6   20.8   1.30
## 3 0.3    50     0 12.3    18.0   17.9   22.4   2.06
## 4 0.6    50     0 13.8    17.5   17.6   20.4   1.95
## 5 1.2    50     0 13.0    17.2   17.1   19.8   1.57
## 6 2.5    50     0 13.1    16.5   16.6   21.8   2.21
## 7 5      50     0 12.1    15.0   15.6   21.9   1.74
```

Kruskal–Wallis test provides evidence of statistical differences among best performance in the population at the end of 50,000 generations.

```
kruskal.test(pop_fit_max ~ Sigma, data = end)

##
##  Kruskal-Wallis rank sum test
##
## data: pop_fit_max by Sigma
## Kruskal-Wallis chi-squared = 174.25, df = 6, p-value < 2.2e-16
```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction on the best performance in the population at the end of 50,000 generations.

```
pairwise.wilcox.test(x = end$pop_fit_max, g = end$Sigma , p.adjust.method = "bonferroni",
                      paired = FALSE, conf.int = FALSE, alternative = 't')

##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: end$pop_fit_max and end$Sigma
##
##      0      0.1     0.3     0.6     1.2     2.5
## 0.1 < 2e-16 -      -      -      -      -
## 0.3 < 2e-16 1.00000 -      -      -      -
## 0.6 < 2e-16 1.00000 1.00000 -      -      -
## 1.2 < 2e-16 1.00000 0.13442 1.00000 -      -
## 2.5 < 2e-16 0.00346 0.00069 0.01477 0.69032 -
## 5    < 2e-16 1.6e-06 5.7e-07 8.1e-07 2.4e-05 0.00612
##
## P value adjustment method: bonferroni
```

### 10.4.2 Activation gene coverage

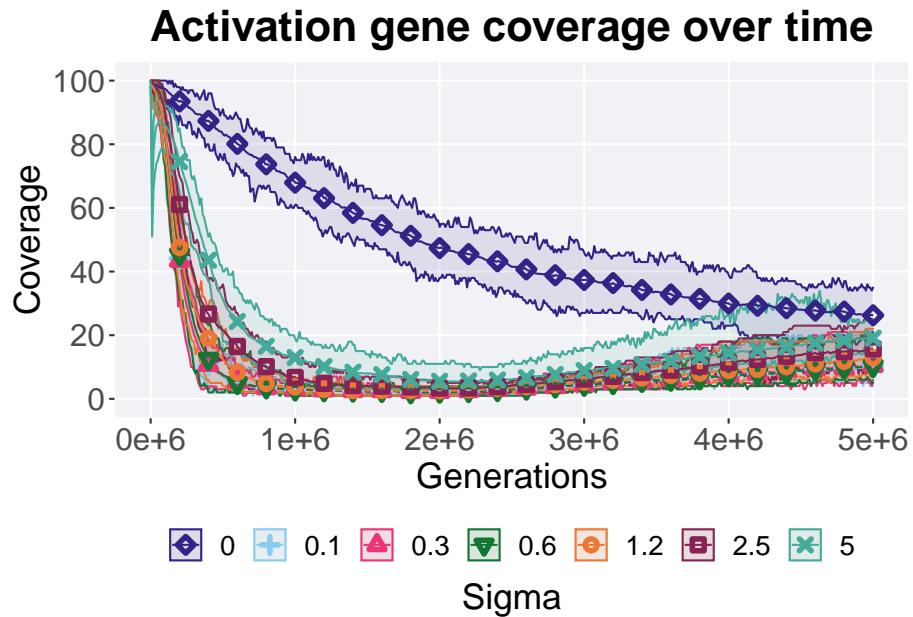
Here we analyze the activation gene coverage for each parameter replicate on the multi-path exploration diagnostic.

#### 10.4.2.1 Coverage over time

Activation gene coverage over time.

```
problem <- filter(nds_ot, diagnostic == 'multipath_exploration')
lines = problem %>%
  group_by(Sigma, gen) %>%
  dplyr::summarise(
    min = min(uni_str_pos),
    mean = mean(uni_str_pos),
    max = max(uni_str_pos)
```

```
)  
  
## `summarise()` has grouped output by 'Sigma'. You can override using the  
## `.`groups` argument.  
points = filter(lines, gen %% 2000 == 0 & gen != 0)  
  
ot = ggplot(lines, aes(x=gen, y=mean, group = Sigma, fill = Sigma, color = Sigma, shape = Sigma))  
  geom_ribbon(aes(ymin = min, ymax = max), alpha = 0.1) +  
  geom_line(size = 0.5) +  
  geom_point(data = points, size = 1.5, stroke = 2.0, alpha = 1.0) +  
  scale_y_continuous(  
    name="Coverage",  
    limits=c(-1, 101),  
    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+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6")  
) +  
  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+  
  guides(  
    shape=guide_legend(nrow=1, title.position = "bottom"),  
    color=guide_legend(nrow=1, title.position = "bottom"),  
    fill=guide_legend(nrow=1, title.position = "bottom")  
) +  
  theme(  
    legend.position = "bottom",  
    legend.box="vertical",  
    legend.justification="center",  
    legend.title.align=0.5  
)  
  
ot
```



#### 10.4.2.2 End of 50,000 generations

Activation gene coverage in the population at the end of 50,000 generations.

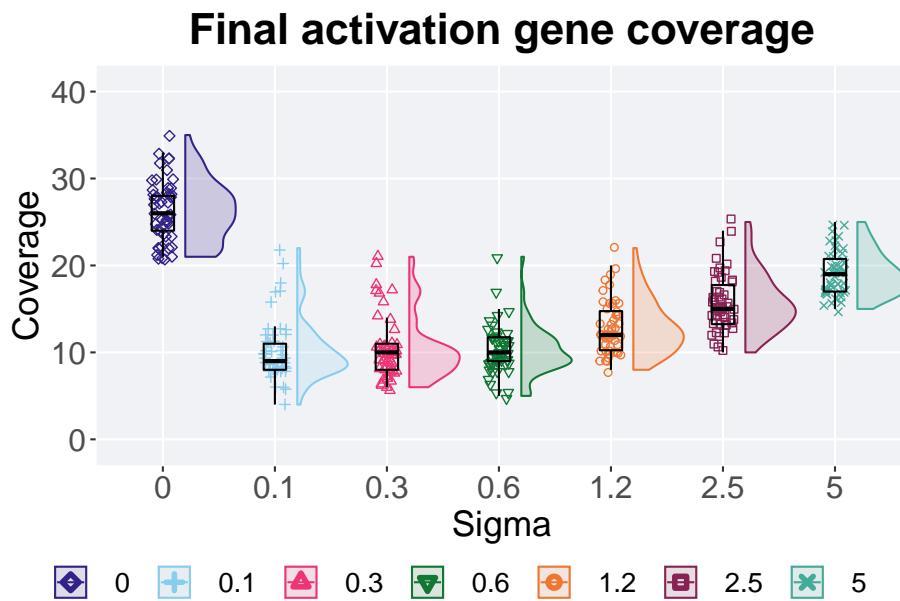
```
end = filter(nds_end, diagnostic == 'multipath_exploration')
plot = ggplot(end, aes(x = Sigma, y = uni_str_pos, color = Sigma, fill = Sigma, shape =
  geom_flat_violin(position = position_nudge(x = .2, y = 0), scale = 'width', alpha = 0.2) +
  geom_point(position = position_jitter(width = .1), size = 1.5, alpha = 1.0) +
  geom_boxplot(color = 'black', width = .2, outlier.shape = NA, alpha = 0.0) +
  scale_y_continuous(
    name="Coverage",
    limits=c(-1, 41),
    breaks=seq(0,40, 10),
    labels=c("0", "10", "20", "30", "40"))
  ) +
  scale_x_discrete(
    name="Sigma")
  )+
  scale_shape_manual(values=SHAPE)+
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  p_theme

plot_grid(
  plot +
```

```

ggtile("Final activation gene coverage") +
  theme(legend.position="none"),
  legend,
  nrow=2,
  rel_heights = c(2,.3),
  label_size = TSIZE
)

```



#### 10.4.2.2.1 Stats

Summary statistics for the activation gene coverage in the population at the end of 50,000 generations.

```

group_by(end, Sigma) %>%
  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: 7 x 8
##   Sigma count na_cnt  min median  mean   max    IQR
##   <dbl> <int>   <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1     0     7     0.0  0.0  2.0  2.0  35.0  2.0
## 2     0.1    7     0.0  0.0  10.0 10.0  20.0  1.0
## 3     0.3    7     0.0  0.0  10.0 10.0  20.0  1.0
## 4     0.6    7     0.0  0.0  10.0 10.0  20.0  1.0
## 5     1.2    7     0.0  0.0  10.0 10.0  20.0  1.0
## 6     2.5    7     0.0  0.0  10.0 10.0  20.0  1.0
## 7     5      7     0.0  0.0  10.0 10.0  20.0  1.0

```

```

##   <fct> <int> <int> <int> <dbl> <dbl> <int> <dbl>
## 1 0      50     0    21     26  26.3    35   4
## 2 0.1    50     0     4      9  10.3    22   3
## 3 0.3    50     0     6     10  10.4    21   3
## 4 0.6    50     0     5     10  10.2    21  2.75
## 5 1.2    50     0     8     12  12.9    22  4.5
## 6 2.5    50     0    10     15  15.7    25  4.5
## 7 5      50     0    15     19  19.1    25  3.75

```

Kruskal–Wallis test provides evidence of statistical differences among activation gene coverage in the population at the end of 50,000 generations.

```
kruskal.test(uni_str_pos ~ Sigma, data = end)
```

```

##
## Kruskal-Wallis rank sum test
##
## data: uni_str_pos by Sigma
## Kruskal-Wallis chi-squared = 240.04, df = 6, p-value < 2.2e-16

```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction on the activation gene coverage in the population at the end of 50,000 generations.

```

pairwise.wilcox.test(x = end$uni_str_pos, g = end$Sigma , p.adjust.method = "bonferroni"
                      paired = FALSE, conf.int = FALSE, alternative = 't')

##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: end$uni_str_pos and end$Sigma
##
##   0     0.1    0.3    0.6    1.2    2.5
## 0.1 < 2e-16 -     -     -     -     -
## 0.3 < 2e-16 1.00000 -     -     -     -
## 0.6 < 2e-16 1.00000 1.00000 -     -     -
## 1.2 < 2e-16 0.00015 0.00030 0.00015 -     -
## 2.5 2.1e-15 7.2e-10 3.7e-09 1.1e-11 0.00043 -
## 5   1.1e-13 1.5e-13 2.3e-13 2.4e-15 2.7e-12 2.8e-06
##
## P value adjustment method: bonferroni

```

# Chapter 11

## Novelty Search

We present the results from our parameter sweep on novelty search. 50 replicates are conducted for each K-nearest neighbors parameter value explored.

```
library(ggplot2)
library(cowplot)
library(dplyr)
library(PupilometryR)
```

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         2.1
## year          2022
## month         06
## day           23
## svn rev       82513
## language      R
## version.string R version 4.2.1 (2022-06-23)
## nickname      Funny-Looking Kid
```

## 11.1 Exploitation rate results

Here we present the results for **best performances** found by each novelty search K value replicate on the exploitation rate diagnostic. Best performance found refers to the largest average trait score found in a given population. Note that performance values fall between 0 and 100.

### 11.1.1 Performance over time

Performance over time.

```
problem <- filter(nov_ot, diagnostic == 'exploitation_rate')
lines = problem %>%
  group_by(K, gen) %>%
  dplyr::summarise(
    min = min(pop_fit_max),
    mean = mean(pop_fit_max),
    max = max(pop_fit_max)
  )

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

points = filter(lines, gen %% 2000 == 0 & gen != 0)

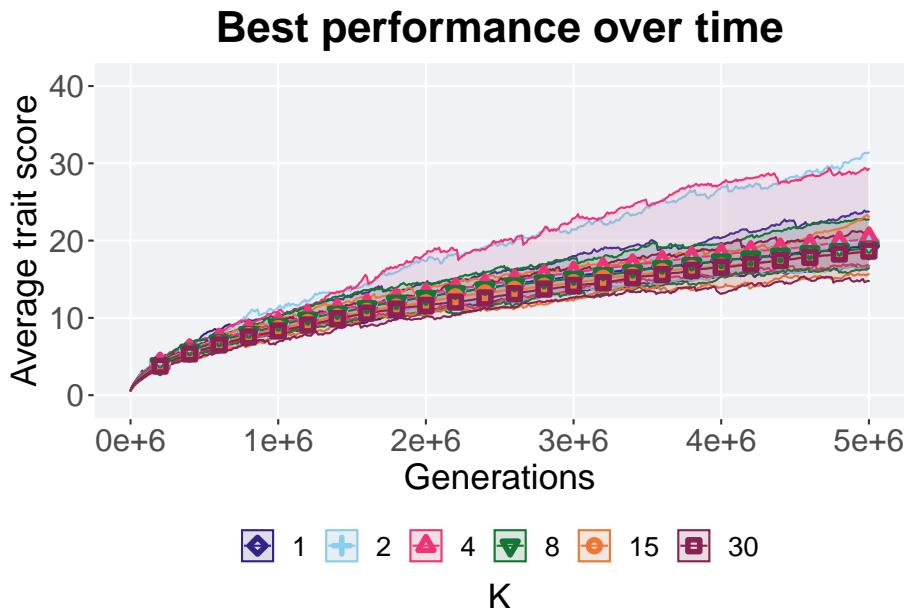
ot = ggplot(lines, aes(x=gen, y=mean / TRAITS, group = K, fill = K, color = K, shape =
  geom_ribbon(aes(ymin = min / TRAITS, ymax = max / TRAITS), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = points, size = 1.5, stroke = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Average trait score",
    limits=c(-1, 41),
    breaks=seq(0, 40, 10),
    labels=c("0", "10", "20", "30", "40")
  ) +
  scale_x_continuous(
    name="Generations",
    limits=c(0, 50000),
    breaks=c(0, 10000, 20000, 30000, 40000, 50000),
    labels=c("0e+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6")
  ) +
  scale_shape_manual(values=SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  ggtitle("Best performance over time") +
  p_theme+
```

```

guides(
  shape=guide_legend(nrow=1, title.position = "bottom"),
  color=guide_legend(nrow=1, title.position = "bottom"),
  fill=guide_legend(nrow=1, title.position = "bottom")
) +
theme(
  legend.position = "bottom",
  legend.box="vertical",
  legend.justification="center",
  legend.title.align=0.5
)

```

ot



#### 11.1.2 Best performance throughout

The best performance found throughout 50,000 generations.

```

best = filter(nov_best, col == 'pop_fit_max' & diagnostic == 'exploitation_rate')

plot = ggplot(best, aes(x = K, y = val / TRAITS, color = K, fill = K, shape = K)) +
  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()

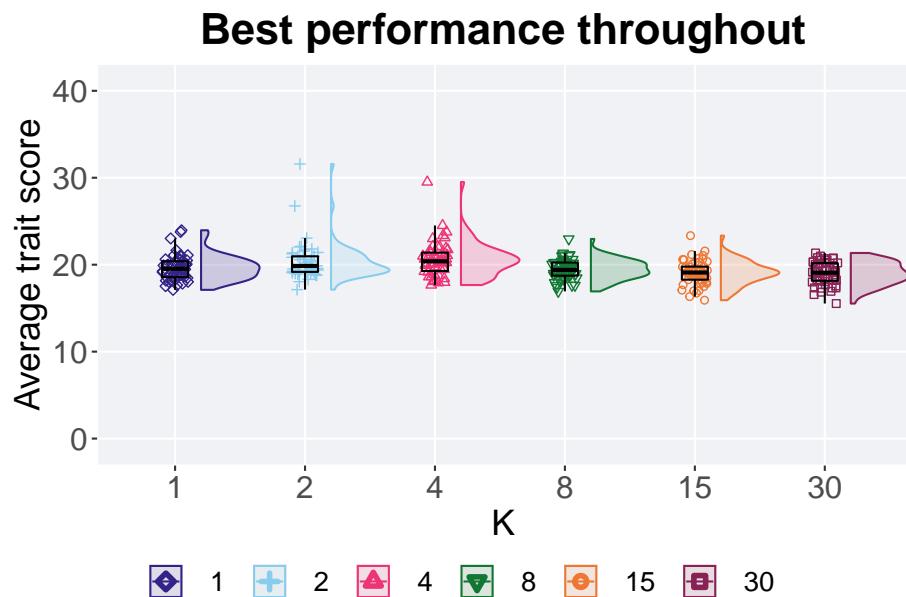
```

```

name = "Average trait score",
limits = c(-1, 41),
breaks = seq(0, 40, 10),
labels = c("0", "10", "20", "30", "40")
) +
scale_x_discrete(
  name = "K"
) +
scale_shape_manual(values = SHAPE) +
scale_colour_manual(values = cb_palette) +
scale_fill_manual(values = cb_palette) +
p_theme

plot_grid(
  plot +
  ggtitle("Best performance throughout") +
  theme(legend.position = "none"),
  legend,
  nrow = 2,
  rel_heights = c(2, .3),
  label_size = TSIZE
)

```



### 11.1.2.1 Stats

Summary statistics for the best performance found throughout 50,000 generations.

```
group_by(best, K) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(val)),
    min = min(val / TRAITS, na.rm = TRUE),
    median = median(val / TRAITS, na.rm = TRUE),
    mean = mean(val / TRAITS, na.rm = TRUE),
    max = max(val / TRAITS, na.rm = TRUE),
    IQR = IQR(val / TRAITS, na.rm = TRUE)
  )

## # A tibble: 6 x 8
##   K     count na_cnt   min median   mean   max   IQR
##   <fct> <int> <int> <dbl> <dbl> <dbl> <dbl>
## 1 1      50     0  17.1  19.5  19.7  24.0  1.83
## 2 2      50     0  17.1  19.9  20.4  31.6  1.79
## 3 4      50     0  17.7  20.4  20.6  29.5  2.11
## 4 8      50     0  16.9  19.4  19.5  23.0  1.51
## 5 15     50     0  15.9  19.1  19.1  23.3  1.50
## 6 30     50     0  15.5  19.1  19.0  21.3  2.03
```

Kruskal-Wallis test provides evidence of significant differences among K values on the best performance found throughout 50,000 generations

```
kruskal.test(val ~ K, data = best)

##
## Kruskal-Wallis rank sum test
##
## data: val by K
## Kruskal-Wallis chi-squared = 34.37, df = 5, p-value = 2.009e-06
```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction on the best performance found throughout 50,000 generations.

```
pairwise.wilcox.test(x = best$val, g = best$K, p.adjust.method = "bonferroni",
                      paired = FALSE, conf.int = FALSE, alternative = 't')

##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: best$val and best$K
##
##   1     2     4     8     15
```

```

## 2 0.96256 - - - -
## 4 0.11806 1.00000 - - - -
## 8 1.00000 0.27841 0.02146 - - -
## 15 1.00000 0.00404 0.00064 1.00000 - -
## 30 0.68378 0.00241 0.00024 1.00000 1.00000
##
## P value adjustment method: bonferroni

```

## 11.2 Ordered exploitation results

Here we present the results for **best performances** found by each novelty search K value replicate on the ordered exploitation diagnostic. Best performance found refers to the largest average trait score found in a given population. Note that performance values fall between 0 and 100.

### 11.2.1 Performance over time

Performance over time.

```

problem <- filter(nov_ot, diagnostic == 'ordered_exploitation')
lines = problem %>%
  group_by(K, gen) %>%
  dplyr::summarise(
    min = min(pop_fit_max),
    mean = mean(pop_fit_max),
    max = max(pop_fit_max)
  )

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

points = filter(lines, gen %% 2000 == 0 & gen != 0)

ot = ggplot(lines, aes(x=gen, y=mean / TRAITS, group = K, fill = K, color = K, shape =
  geom_ribbon(aes(ymin = min / TRAITS, ymax = max / TRAITS), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = points, size = 1.5, stroke = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Average trait score",
    limits=c(-1, 11),
    breaks=seq(0,10, 2),
    labels=c("0", "2", "4", "6", "8", "10")
  ) +
  scale_x_continuous(
    name="Generations",
    limits=c(0, 50000),

```

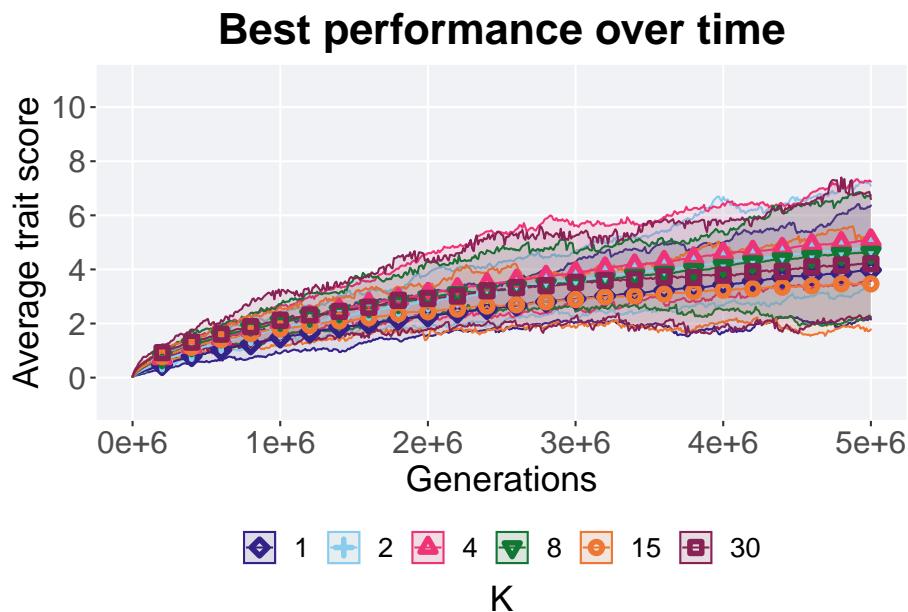
```

breaks=c(0, 10000, 20000, 30000, 40000, 50000),
labels=c("0e+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6")

) +
scale_shape_manual(values=SHAPE) +
scale_colour_manual(values = cb_palette) +
scale_fill_manual(values = cb_palette) +
ggtitle("Best performance over time") +
p_theme+
guides(
shape=guide_legend(nrow=1, title.position = "bottom"),
color=guide_legend(nrow=1, title.position = "bottom"),
fill=guide_legend(nrow=1, title.position = "bottom")
) +
theme(
legend.position = "bottom",
legend.box="vertical",
legend.justification="center",
legend.title.align=0.5
)
)

ot

```



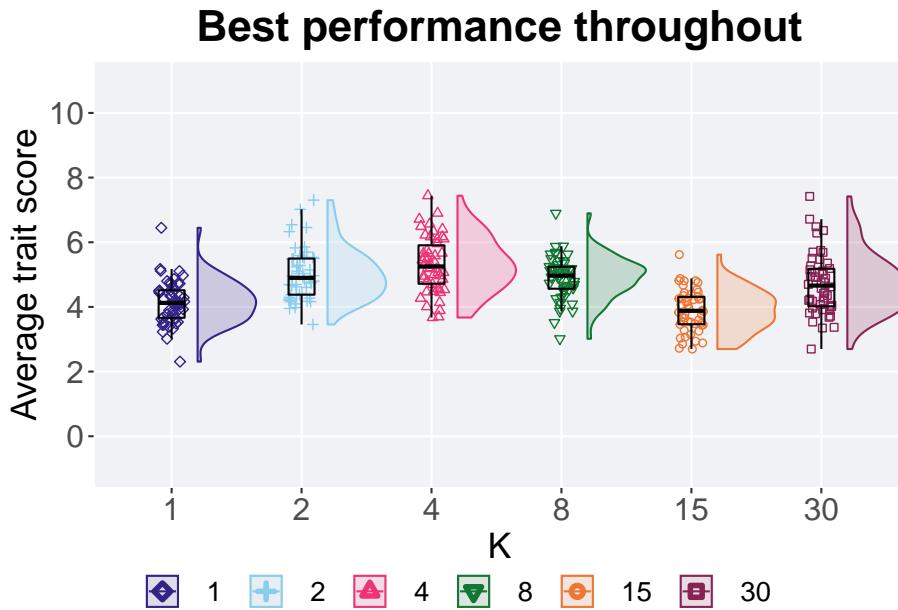
### 11.2.2 Best performance throughout

The best performance found throughout 50,000 generations.

```
best = filter(nov_best, col == 'pop_fit_max' & diagnostic == 'ordered_exploitation')

plot = ggplot(best, aes(x = K, y = val / TRAITS, color = K, fill = K, shape = K)) +
  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 = "Average trait score",
    limits = c(-1, 11),
    breaks = seq(0, 10, 2),
    labels = c("0", "2", "4", "6", "8", "10")
  ) +
  scale_x_discrete(
    name = "K"
  ) +
  scale_shape_manual(values = SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  p_theme

plot_grid(
  plot +
    ggtitle("Best performance throughout") +
    theme(legend.position = "none"),
  legend,
  nrow = 2,
  rel_heights = c(2, .2),
  label_size = TSIZE
)
```



#### 11.2.2.1 Stats

Summary statistics about the best performance found.

```
group_by(best, K) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(val)),
    min = min(val / TRAITS, na.rm = TRUE),
    median = median(val / TRAITS, na.rm = TRUE),
    mean = mean(val / TRAITS, na.rm = TRUE),
    max = max(val / TRAITS, na.rm = TRUE),
    IQR = IQR(val / TRAITS, na.rm = TRUE)
  )

## # A tibble: 6 x 8
##   K     count na_cnt   min median   mean   max   IQR
##   <fct> <int>   <int> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 1       50      0  2.31  4.12  4.14  6.45  0.852
## 2 2       50      0  3.46  4.90  5.01  7.30  1.12
## 3 4       50      0  3.67  5.25  5.30  7.44  1.19
## 4 8       50      0  3.01  4.97  4.90  6.89  0.677
## 5 15      50      0  2.70  3.88  3.89  5.62  0.846
## 6 30      50      0  2.70  4.66  4.72  7.42  1.16
```

Kruskal–Wallis test provides evidence of statistical differences for the best

performance found in the population throughout 50,000 generations.

```
kruskal.test(val ~ K, data = best)

##
## Kruskal-Wallis rank sum test
##
## data: val by K
## Kruskal-Wallis chi-squared = 94.864, df = 5, p-value < 2.2e-16

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction on
the best performance found in the population throughout 50,000 generations.

pairwise.wilcox.test(x = best$val, g = best$K, p.adjust.method = "bonferroni",
                      paired = FALSE, conf.int = FALSE, alternative = 't')

##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: best$val and best$K
##
##    1      2      4      8      15
## 2 1.8e-06 -
## 4 6.2e-09 0.905 -
## 8 1.6e-06 1.000 0.353 -
## 15 1.000 4.3e-09 2.3e-11 3.6e-09 -
## 30 0.020 1.000 0.021 1.000 9.3e-05
##
## P value adjustment method: bonferroni
```

## 11.3 Contradictory objectives diagnostic

Here we present the results for **satisfactory trait coverage** and **activation gene coverage** found by each novelty search K value replicate on the contradictory objectives diagnostic. Satisfactory trait coverage refers to the count of unique satisfied traits in the population, while activation gene coverage refers to the count of unique activation genes in the population. Note that both coverage values fall between 0 and 100.

### 11.3.1 Satisfactory trait coverage

Here we analyze the satisfactory trait coverage for each parameter replicate on the contradictory objectives diagnostic.

#### 11.3.1.1 Coverage over time

Satisfactory trait coverage over time.

```

problem <- filter(nov_ot, diagnostic == 'contradictory_objectives')
lines = problem %>%
  group_by(K, gen) %>%
  dplyr::summarise(
    min = min(pop_uni_obj),
    mean = mean(pop_uni_obj),
    max = max(pop_uni_obj)
  )

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

points = filter(lines, gen %% 2000 == 0 & gen != 0)

ot = ggplot(lines, aes(x=gen, y=mean, group = K, fill = K, color = K, shape = K)) +
  geom_ribbon(aes(ymin = min, ymax = max), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = points, size = 1.5, stroke = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Coverage",
    limits=c(-1, 5)
  ) +
  scale_x_continuous(
    name="Generations",
    limits=c(0, 50000),
    breaks=c(0, 10000, 20000, 30000, 40000, 50000),
    labels=c("0e+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6")
  ) +
  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 +
  guides(
    shape=guide_legend(nrow=1, title.position = "bottom"),
    color=guide_legend(nrow=1, title.position = "bottom"),
    fill=guide_legend(nrow=1, title.position = "bottom")
  ) +
  theme(
    legend.position = "bottom",
    legend.box="vertical",
    legend.justification="center",
    legend.title.align=0.5
  )

```

```
ot
```



#### 11.3.1.2 Best coverage throughout

Best satisfactory trait coverage throughout 50,000 generations.

```
best = filter(nov_best, col == 'pop_uni_obj' & diagnostic == 'contradictory_objectives')

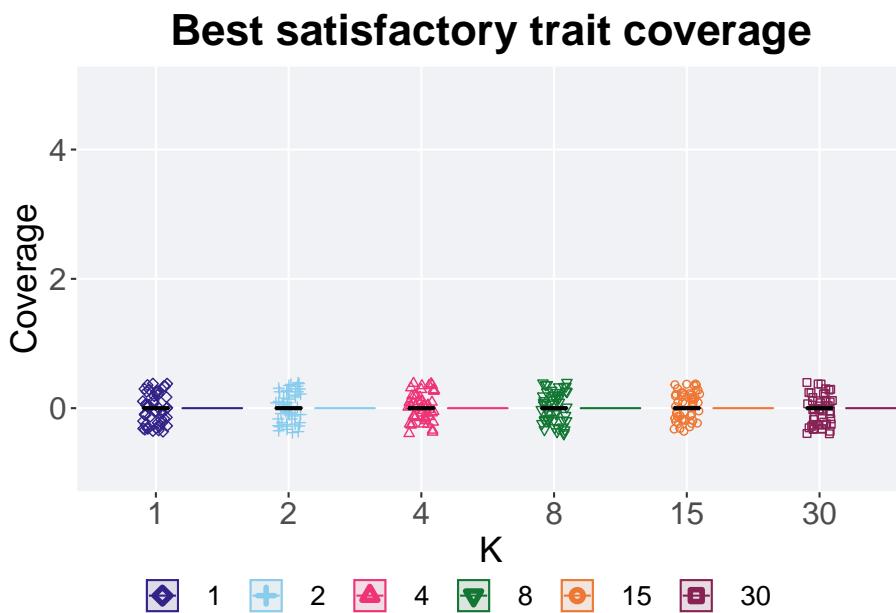
plot = ggplot(best, aes(x = K, y = val, color = K, fill = K, shape = K)) +
  geom_flat_violin(position = position_nudge(x = .2, y = 0), scale = 'width', alpha = 0.5) +
  geom_point(position = position_jitter(width = .1), size = 1.5, alpha = 1.0) +
  geom_boxplot(color = 'black', width = .2, outlier.shape = NA, alpha = 0.0) +
  scale_y_continuous(
    name = "Coverage",
    limits = c(-1, 5)
  ) +
  scale_x_discrete(
    name = "K"
  ) +
  scale_shape_manual(values = SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  p_theme

plot_grid(
```

```

plot +
  ggtitle("Best satisfactory trait coverage") +
  theme(legend.position="none"),
legend,
nrow=2,
rel_heights = c(2,.2),
label_size = TSIZE
)

```



#### 11.3.1.2.1 Stats

Summary statistics for the best satisfactory trait coverage throughout 50,000 generations.

```

group_by(best, K) %>%
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: 6 x 8
```

```
##   K      count na_cnt    min median   mean    max    IQR
##   <fct> <int> <int> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 1      50     0     0     0     0     0     0     0
## 2 2      50     0     0     0     0     0     0     0
## 3 4      50     0     0     0     0     0     0     0
## 4 8      50     0     0     0     0     0     0     0
## 5 15     50     0     0     0     0     0     0     0
## 6 30     50     0     0     0     0     0     0     0
```

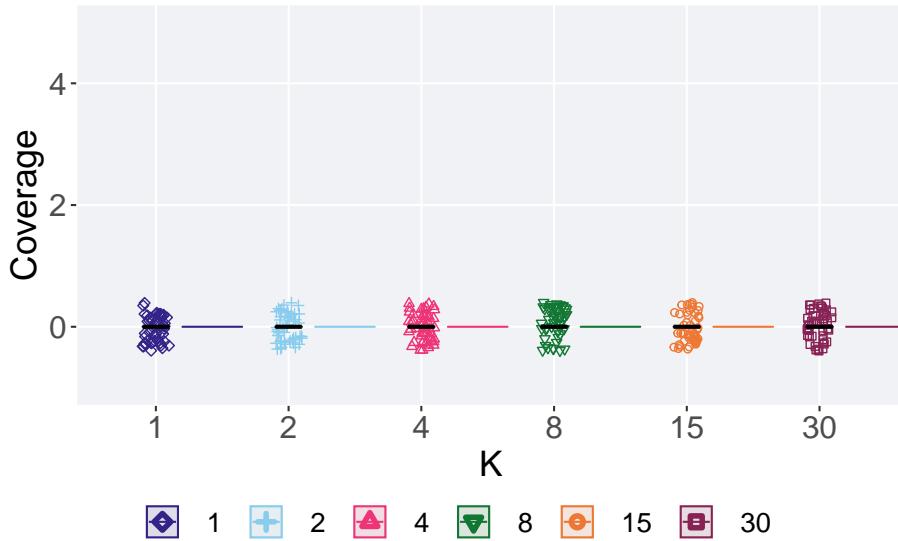
### 11.3.1.3 End of 50,000 generations

Satisfactory trait coverage in the population at the end of 50,000 generations.

```
end = filter(nov_end, diagnostic == 'contradictory_objectives')
plot = ggplot(end, aes(x = K, y = pop_uni_obj, color = K, fill = K, shape = K)) +
  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(-1, 5)
  ) +
  scale_x_discrete(
    name = "K"
  ) +
  scale_shape_manual(values = SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  p_theme

plot_grid(
  plot +
    ggtitle("Final satisfactory trait coverage") +
    theme(legend.position = "none"),
  legend,
  nrow = 2,
  rel_heights = c(2, .3),
  label_size = TSIZE
)
```

## Final satisfactory trait coverage



### 11.3.1.3.1 Stats

Summary statistics for satisfactory trait coverage in the population at the end of 50,000 generations.

```
group_by(end, K) %>%
  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: 6 x 8
##   K      count na_cnt  min median  mean  max  IQR
##   <fct> <int>   <int> <dbl> <dbl> <dbl> <dbl>
## 1 1       50      0     0     0     0     0     0
## 2 2       50      0     0     0     0     0     0
## 3 4       50      0     0     0     0     0     0
## 4 8       50      0     0     0     0     0     0
## 5 15      50      0     0     0     0     0     0
## 6 30      50      0     0     0     0     0     0
```

### 11.3.2 Activation gene coverage

Here we analyze the activation gene coverage for each parameter replicate on the contradictory objectives diagnostic.

#### 11.3.2.1 Coverage over time

Activation gene coverage over time.

```
problem <- filter(nov_ot, diagnostic == 'contradictory_objectives')
lines = problem %>%
  group_by(K, gen) %>%
  dplyr::summarise(
    min = min(uni_str_pos),
    mean = mean(uni_str_pos),
    max = max(uni_str_pos)
  )

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

points = filter(lines, gen %% 2000 == 0 & gen != 0)

ot = ggplot(lines, aes(x=gen, y=mean, group = K, fill = K, color = K, shape = K)) +
  geom_ribbon(aes(ymin = min, ymax = max), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = points, size = 1.5, stroke = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Coverage",
    limits=c(-1, 101),
    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+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6")
  ) +
  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 +
  guides(
    shape=guide_legend(nrow=1, title.position = "bottom"),
    color=guide_legend(nrow=1, title.position = "bottom"),
    fill=guide_legend(nrow=1, title.position = "bottom")
  )
```

```

    fill=guide_legend(nrow=1, title.position = "bottom")
) +
theme(
  legend.position = "bottom",
  legend.box="vertical",
  legend.justification="center",
  legend.title.align=0.5
)
)

ot

```



### 11.3.2.2 End of 50,000 generations

Activation gene coverage in the population at the end of 50,000 generations.

```

end = filter(nov_end, diagnostic == 'contradictory_objectives')
plot = ggplot(end, aes(x = K, y = uni_str_pos, color = K, fill = K, shape = K)) +
  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(-1, 41),
    breaks=seq(0, 40, 10),
    labels=c("0", "10", "20", "30", "40")

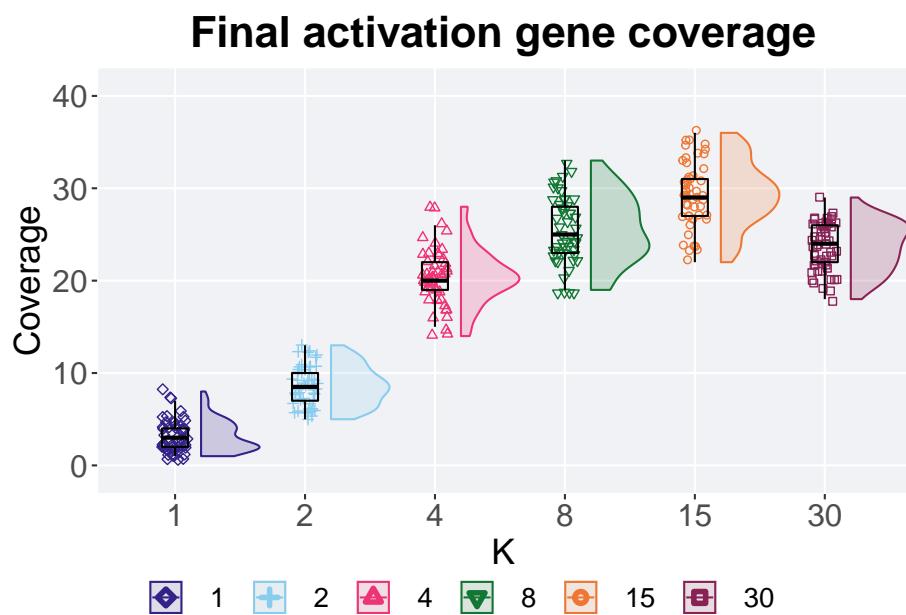
```

```

) +
  scale_x_discrete(
    name="K"
  ) +
  scale_shape_manual(values=SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  p_theme

plot_grid(
  plot +
  ggtitle("Final activation gene coverage") +
  theme(legend.position="none"),
  legend,
  nrow=2,
  rel_heights = c(2,.2),
  label_size = TSIZE
)

```



#### 11.3.2.2.1 Stats

Summary statistics for the activation gene coverage in the population at the end of 50,000 generations.

```

group_by(end, K) %>%
  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: 6 x 8
##   K     count  na_cnt  min  median  mean  max  IQR
##   <fct> <int> <int> <int> <dbl> <dbl> <int> <dbl>
## 1 1      50     0     1     3     3.16     8     2
## 2 2      50     0     5     8.5    8.6     13     3
## 3 4      50     0    14    20     20.4    28     3
## 4 8      50     0    19    25     25.5    33     5
## 5 15     50     0    22    29     29.4    36     4
## 6 30     50     0    18    24     23.6    29     4

```

Kruskal–Wallis test provides evidence of statistical differences among activation gene coverage in the population at the end of 50,000 generations.

```

kruskal.test(uni_str_pos ~ K, data = end)

##
##  Kruskal-Wallis rank sum test
##
## data: uni_str_pos by K
## Kruskal-Wallis chi-squared = 251.87, df = 5, p-value < 2.2e-16

```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction on the activation gene coverage in the population at the end of 50,000 generations.

```

pairwise.wilcox.test(x = end$uni_str_pos, g = end$K, p.adjust.method = "bonferroni",
                      paired = FALSE, conf.int = FALSE, alternative = 't')

##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: end$uni_str_pos and end$K
##
##    1     2     4     8     15
## 2 2.7e-15 -     -     -
## 4 < 2e-16 < 2e-16 -     -
## 8 < 2e-16 < 2e-16 1.5e-08 -     -
## 15 < 2e-16 < 2e-16 5.9e-15 4.0e-05 -

```

```
## 30 < 2e-16 < 2e-16 1.2e-05 0.15    2.9e-11
##
## P value adjustment method: bonferroni
```

## 11.4 Multi-path exploration results

Here we present the results for **best performances** and **activation gene coverage** found by each novelty search K value replicate on the multi-path exploration diagnostic. Best performance found refers to the largest average trait score found in a given population, while activation gene coverage refers to the count of unique activation genes in the population. Note that both values fall between 0 and 100.

### 11.4.1 Performance

Here we analyze the performances for each parameter replicate on the multi-path exploration diagnostic.

#### 11.4.1.1 Performance over time

Performance over time.

```
problem <- filter(nov_ot, diagnostic == 'multipath_exploration')
lines = problem %>%
  group_by(K, gen) %>%
  dplyr::summarise(
    min = min(pop_fit_max),
    mean = mean(pop_fit_max),
    max = max(pop_fit_max)
  )

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

points = filter(lines, gen %% 2000 == 0 & gen != 0)

ot = ggplot(lines, aes(x=gen, y=mean / TRAITS, group = K, fill = K, color = K, shape = K))
ot + geom_ribbon(aes(ymin = min / TRAITS, ymax = max / TRAITS), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = points, size = 1.5, stroke = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name = "Average trait score",
    limits = c(-1, 11),
    breaks = seq(0, 10, 2),
    labels = c("0", "2", "4", "6", "8", "10")
  ) +
  scale_x_continuous()
```

```

name="Generations",
limits=c(0, 50000),
breaks=c(0, 10000, 20000, 30000, 40000, 50000),
labels=c("0e+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6")

) +
scale_shape_manual(values=SHAPE) +
scale_colour_manual(values = cb_palette) +
scale_fill_manual(values = cb_palette) +
ggtitle("Best performance over time") +
p_theme +
guides(
shape=guide_legend(nrow=1, title.position = "bottom"),
color=guide_legend(nrow=1, title.position = "bottom"),
fill=guide_legend(nrow=1, title.position = "bottom")
) +
theme(
legend.position = "bottom",
legend.box="vertical",
legend.justification="center",
legend.title.align=0.5
)

)

```

ot



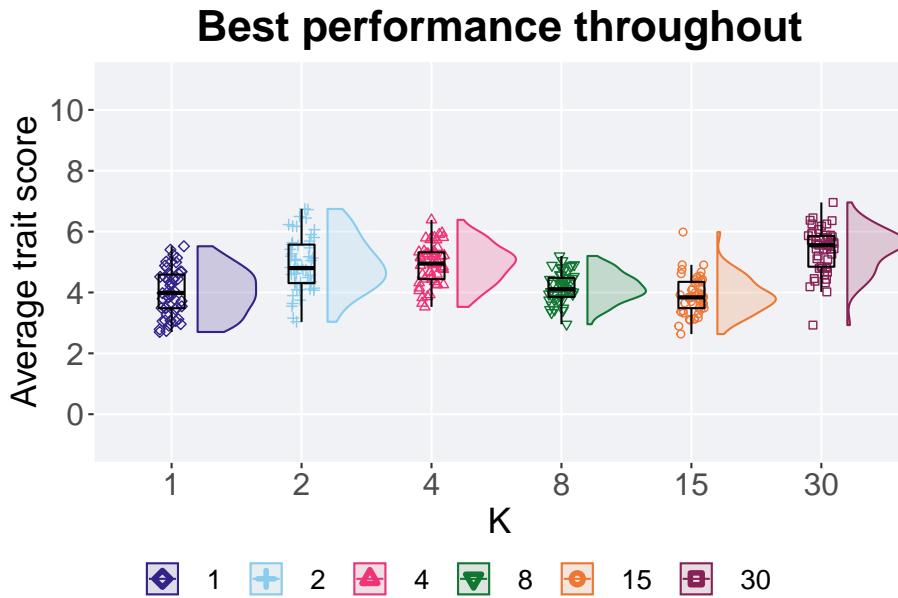
#### 11.4.1.2 Best performance throughout

Here we plot the performance of the best performing solution found throughout 50,000 generations.

```
best = filter(nov_best, col == 'pop_fit_max' & diagnostic == 'multipath_exploration')

plot = ggplot(best, aes(x = K, y = val / TRAITS, color = K, fill = K, shape = K)) +
  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 = "Average trait score",
    limits = c(-1, 11),
    breaks = seq(0, 10, 2),
    labels = c("0", "2", "4", "6", "8", "10")
  ) +
  scale_x_discrete(
    name = "K"
  ) +
  scale_shape_manual(values = SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  p_theme

plot_grid(
  plot +
    ggtitle("Best performance throughout") +
    theme(legend.position = "none"),
  legend,
  nrow = 2,
  rel_heights = c(2, .3),
  label_size = TSIZE
)
```



#### 11.4.1.2.1 Stats

Summary statistics for the performance of the best performing solution found throughout 50,000 generations.

```
group_by(best, K) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(val)),
    min = min(val / TRAITS, na.rm = TRUE),
    median = median(val / TRAITS, na.rm = TRUE),
    mean = mean(val / TRAITS, na.rm = TRUE),
    max = max(val / TRAITS, na.rm = TRUE),
    IQR = IQR(val / TRAITS, na.rm = TRUE)
  )

## # A tibble: 6 x 8
##   K      count na_cnt   min median   mean   max   IQR
##   <fct> <int> <int> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 1        50     0  2.70  3.99  4.02  5.52 1.11
## 2 2        50     0  3.04  4.80  4.94  6.75 1.27
## 3 4        50     0  3.53  4.95  4.92  6.39 0.881
## 4 8        50     0  2.96  4.11  4.17  5.20 0.624
## 5 15       50     0  2.63  3.84  3.89  5.99 0.865
## 6 30       50     0  2.93  5.55  5.39  6.96 1.01
```

Kruskal–Wallis test provides evidence of statistical differences among the best performing solution found throughout 50,000 generations.

```
kruskal.test(val ~ K, data = best)

##
## Kruskal-Wallis rank sum test
##
## data: val by K
## Kruskal-Wallis chi-squared = 117.28, df = 5, p-value < 2.2e-16

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction on the best performing solution found throughout 50,000 generations.

pairwise.wilcox.test(x = best$val, g = best$K, p.adjust.method = "bonferroni",
                      paired = FALSE, conf.int = FALSE, alternative = 't')

##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: best$val and best$K
##
##    1      2      4      8     15
## 2 3.0e-05 -
## 4 2.2e-06 1.000 -
## 8 1.000 8.2e-05 1.2e-06 -
## 15 1.000 2.0e-07 2.2e-09 0.094 -
## 30 8.3e-11 0.070 0.011 2.8e-11 1.7e-12
##
## P value adjustment method: bonferroni
```

#### 11.4.1.3 End of 50,000 generations

Best performance in the population at the end of 50,000 generations.

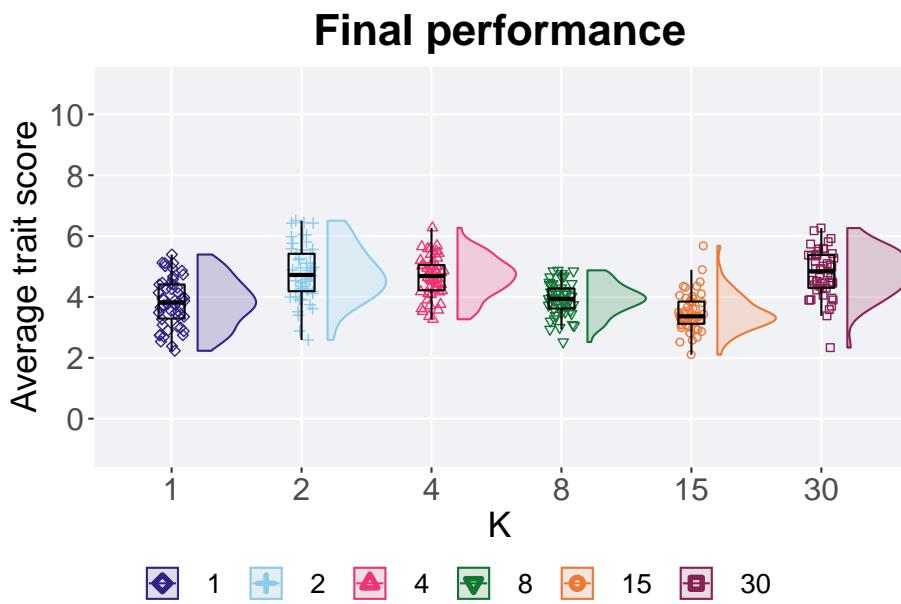
```
end = filter(nov_end, diagnostic == 'multipath_exploration')
plot = ggplot(end, aes(x = K, y = pop_fit_max / TRAITS, color = K, fill = K, shape = K))
  geom_flat_violin(position = position_nudge(x = .2, y = 0), scale = 'width', alpha = 0.5)
  geom_point(position = position_jitter(width = .1), size = 1.5, alpha = 1.0) +
  geom_boxplot(color = 'black', width = .2, outlier.shape = NA, alpha = 0.0) +
  scale_y_continuous(
    name = "Average trait score",
    limits = c(-1, 11),
    breaks = seq(0, 10, 2),
    labels = c("0", "2", "4", "6", "8", "10")
  ) +
  scale_x_discrete(
    name = "K"
```

```

) +
  scale_shape_manual(values=SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  p_theme

plot_grid(
  plot +
    ggtitle("Final performance") +
    theme(legend.position="none"),
  legend,
  nrow=2,
  rel_heights = c(2,.3),
  label_size = TSIZE
)

```



#### 11.4.1.3.1 Stats

Summary statistics for the best performance in the population at the end of 50,000 generations.

```

group_by(end, K) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(pop_fit_max / TRAITS)),

```

```

min = min(pop_fit_max / TRAITS, na.rm = TRUE),
median = median(pop_fit_max / TRAITS, na.rm = TRUE),
mean = mean(pop_fit_max / TRAITS, na.rm = TRUE),
max = max(pop_fit_max / TRAITS, na.rm = TRUE),
IQR = IQR(pop_fit_max / TRAITS, na.rm = TRUE)
)

## # A tibble: 6 x 8
##   K     count na_cnt   min median   mean   max   IQR
##   <fct> <int> <int> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 1      50     0  2.23  3.82  3.82  5.39 1.12
## 2 2      50     0  2.59  4.72  4.77  6.51 1.23
## 3 4      50     0  3.27  4.69  4.66  6.27 0.828
## 4 8      50     0  2.52  3.94  3.93  4.87 0.654
## 5 15     50     0  2.10  3.36  3.49  5.68 0.730
## 6 30     50     0  2.34  4.84  4.78  6.26 1.08

```

Kruskal–Wallis test provides evidence of statistical differences among best performance in the population at the end of 50,000 generations.

```
kruskal.test(pop_fit_max ~ K, data = end)
```

```

##
## Kruskal-Wallis rank sum test
##
## data: pop_fit_max by K
## Kruskal-Wallis chi-squared = 105.39, df = 5, p-value < 2.2e-16

```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction on the best performance in the population at the end of 50,000 generations.

```

pairwise.wilcox.test(x = end$pop_fit_max, g = end$K , p.adjust.method = "bonferroni",
                      paired = FALSE, conf.int = FALSE, alternative = 't')

##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: end$pop_fit_max and end$K
##
##   1     2     4     8     15
## 2 2.3e-05 -     -     -     -
## 4 2.3e-05 1.0000 -     -     -
## 8 1.0000  1.0e-05 4.3e-06 -     -
## 15 0.2784 6.4e-10 9.2e-11 0.0012 - 
## 30 2.3e-06 1.0000  1.0000 5.3e-07 4.0e-11
##
## P value adjustment method: bonferroni

```

### 11.4.2 Activation gene coverage

Here we analyze the activation gene coverage for each parameter replicate on the multi-path exploration diagnostic.

#### 11.4.2.1 Coverage over time

Activation gene coverage over time.

```
problem <- filter(nov_ot, diagnostic == 'multipath_exploration')
lines = problem %>%
  group_by(K, gen) %>%
  dplyr::summarise(
    min = min(uni_str_pos),
    mean = mean(uni_str_pos),
    max = max(uni_str_pos)
  )

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

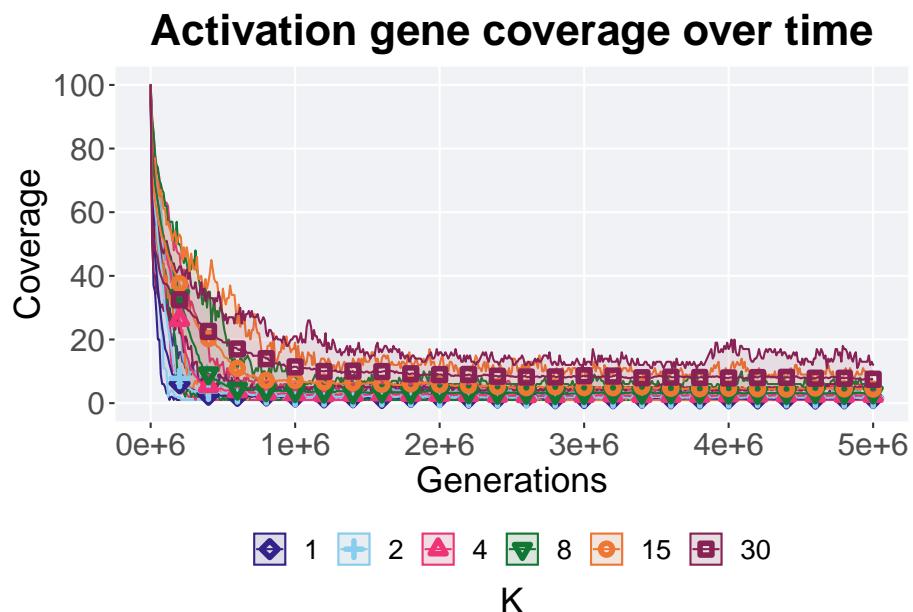
points = filter(lines, gen %% 2000 == 0 & gen != 0)

ot = ggplot(lines, aes(x=gen, y=mean, group = K, fill = K, color = K, shape = K)) +
  geom_ribbon(aes(ymin = min, ymax = max), alpha = 0.1) +
  geom_line(size = 0.5) +
  geom_point(data = points, size = 1.5, stroke = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Coverage",
    limits=c(-1, 101),
    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+6", "1e+6", "2e+6", "3e+6", "4e+6", "5e+6")
  ) +
  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 +
  guides(
    shape=guide_legend(nrow=1, title.position = "bottom"),
    color=guide_legend(nrow=1, title.position = "bottom"),
    fill=guide_legend(nrow=1, title.position = "bottom")
  )
```

```

    fill=guide_legend(nrow=1, title.position = "bottom")
) +
theme(
  legend.position = "bottom",
  legend.box="vertical",
  legend.justification="center",
  legend.title.align=0.5
)
ot

```



#### 11.4.2.2 End of 50,000 generations

Activation gene coverage in the population at the end of 50,000 generations.

```

end = filter(nov_end, diagnostic == 'multipath_exploration')
plot = ggplot(end, aes(x = K, y = uni_str_pos, color = K, fill = K, shape = K)) +
  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(-1, 21),
    breaks=seq(0,20, 5),
    labels=c("0", "5", "10", "15", "20"))

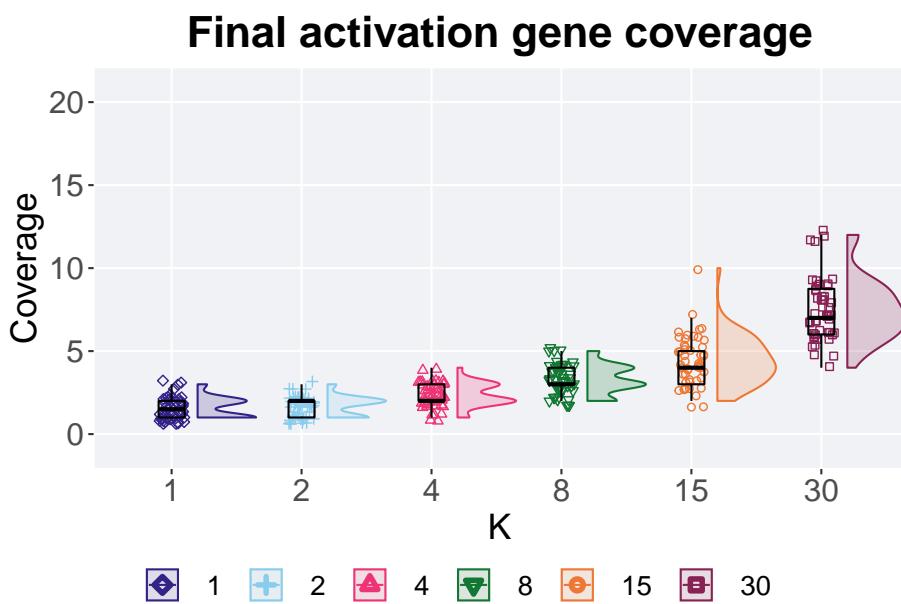
```

```

) +
  scale_x_discrete(
    name="K"
) +
  scale_shape_manual(values=SHAPE) +
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  p_theme

plot_grid(
  plot +
    ggtitle("Final activation gene coverage") +
    theme(legend.position="none"),
  legend,
  nrow=2,
  rel_heights = c(2,.3),
  label_size = TSIZE
)

```



#### 11.4.2.2.1 Stats

Summary statistics for the activation gene coverage in the population at the end of 50,000 generations.

```

group_by(end, K) %>%
  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: 6 x 8
##   K      count na_cnt  min median  mean   max   IQR
##   <fct> <int>   <int> <dbl> <dbl> <int> <dbl>
## 1 1        50     0     1    1.5  1.58     3    1
## 2 2        50     0     1    2    1.7     3    1
## 3 4        50     0     1    2    2.34     4    1
## 4 8        50     0     2    3    3.28     5    1
## 5 15       50     0     2    4    4.42    10    2
## 6 30       50     0     4    7    7.5    12   2.75

```

Kruskal–Wallis test provides evidence of statistical differences among activation gene coverage in the population at the end of 50,000 generations.

```
kruskal.test(uni_str_pos ~ K, data = end)
```

```

##
## Kruskal-Wallis rank sum test
##
## data: uni_str_pos by K
## Kruskal-Wallis chi-squared = 227.47, df = 5, p-value < 2.2e-16

```

Results for post-hoc Wilcoxon rank-sum test with a Bonferroni correction on the activation gene coverage in the population at the end of 50,000 generations.

```

pairwise.wilcox.test(x = end$uni_str_pos, g = end$K , p.adjust.method = "bonferroni",
                      paired = FALSE, conf.int = FALSE, alternative = 't')

##
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data: end$uni_str_pos and end$K
##
##      1      2      4      8      15
## 2  1.00000 -      -      -      -
## 4  1.3e-05 0.00023 -      -      -
## 8  5.1e-13 1.8e-12 8.0e-06 -      -
## 15 1.3e-15 1.9e-15 8.9e-12 0.00034 -

```

```
## 30 < 2e-16 < 2e-16 < 2e-16 < 2e-16 4.6e-12
##
## P value adjustment method: bonferroni
```