Supplemental Material for 'Hidden Lexicase Selection Parameters: Varying Population Size and Test Case Redundancy with Diagnostic Metrics'

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2024-05-06

Contents

```r
library(ggplot2)
library(cowplot)
library(dplyr)
library(PupillometryR)
library(scales) # to access break formatting functions


NAMES = c(50,100,500,1000,5000)
SHAPE <- c(25,21,22,23,24)
cb_palette <- c('#648FFF','#FE6100','#DC267F','#785EF0','#FFB000')
TSIZE <- 16

p_theme <- theme(
  plot.title = element_text( face = "bold", size = 16, hjust=0.5),
  panel.border = element_blank(),
  panel.grid.minor = element_blank(),
  legend.title=element_text(size=16),
  legend.text=element_text(size=16),
  axis.title = element_text(size=16),
  axis.text = element_text(size=16),
  legend.position="bottom",
  panel.background = element_rect(fill = "#f1f2f5",
                                  colour = "white",
                                  size = 0.5, linetype = "solid")
)
```

Chapter 1

Introduction

This is not intended as a stand-alone document, but as a companion to our manuscript.

1.1 About our supplemental material

As you may have noticed (unless you're reading a pdf version of this), our supplemental material is hosted using GitHub pages. We compiled our data analyses and supplemental documentation into this nifty web-accessible book using bookdown.

The code used for this supplemental material can be found in this GitHub repository.

Our supplemental material includes the following:

- Exploitation rate results (Section 2)
- Standard contradictory rates results (Section 3)
- Contradictory rates results w/ 50 redundant test cases (Section 4)
- Contradictory rates results w/ 100 redundant test cases (Section 5)
- Contradictory rates results w/ 200 redundant test cases (Section 6)
- Contradictory rates results w/ 400 redundant test cases (Section 7)

1.2 Contributing authors

- Jose Guadalupe Hernandez
- Anil Kumar Saini
- Jason H. Moore

Chapter 2

Exploitation rate results

Here we report the **performance** and evaluation a **satisfactory solution** was found on the exploitation rate diagnostic. 50 replicates were conducted for each population size explored. Performance is defined at the average trait performance, where we collect the best performing solution in each generation over time and the best performing solution evolved. A satisfactory solution is defined as a solution that has a phenotype with all traits greater than or equal to 99.0.

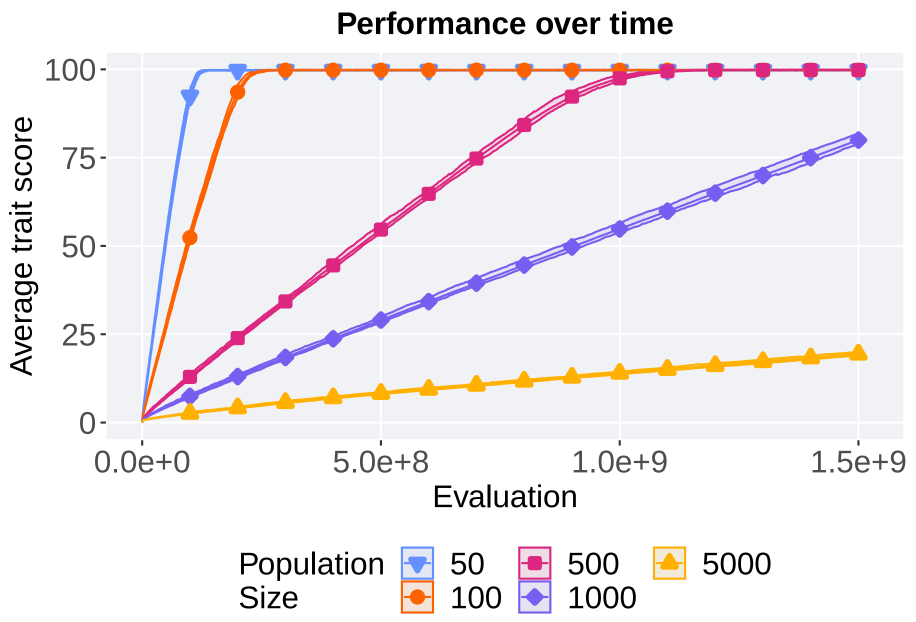
2.1 Analysis setup

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

# over time data
over_time <- read.csv("../Paper_Data/Exploitation/ot.csv", header = TRUE, stringsAsFactors = FALS
over_time$pop_size <- factor(over_time$pop_size, levels = NAMES)

# best performance data
best <- read.csv('../Paper_Data/Exploitation/best.csv', header = TRUE, stringsAsFactors = FALSE)
best$pop_size <- factor(best$pop_size, levels = NAMES)

# get the data
ssf <- read.csv('../Paper_Data/Exploitation/ssf.csv', header = TRUE, stringsAsFactors = FALSE)
ssf$pop_size <- factor(ssf$pop_size, levels = NAMES)
ssf <- filter(ssf, evaluation <= 1.5*10^9)
```

2.2 Performance over time

Performance of the best solution in the population at each generation over time.

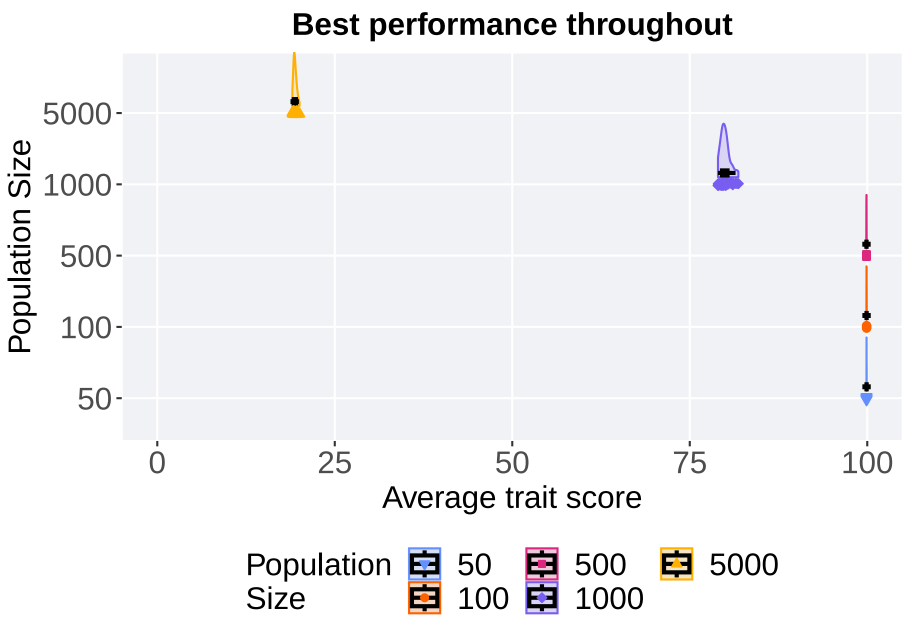
```r
# aggregate
lines = over_time %>%
  group_by(pop_size, eval) %>%
  dplyr::summarise(
    min = min(performance),
    mean = mean(performance),
    max = max(performance)
  )
lines$pop_size <- factor(lines$pop_size, levels = NAMES)

ggplot(lines, aes(x=eval, y=mean, group = pop_size, fill = pop_size, color = pop_size,
  geom_ribbon(aes(ymin = min, ymax = max), alpha = 0.1) +
  geom_line(linewidth = 0.5) +
  geom_point(data = filter(lines, eval %% 100000000 == 0 & eval != 0), size = 1.0, stro
  scale_y_continuous(
    name="Average trait score",
    limits=c(0, 100),
    breaks=seq(0,100, 25),
    labels=c("0", "25", "50", "75", "100")
  ) +
  scale_x_continuous(
    name="Evaluation",
    labels = c('0.0e+0', '5.0e+8','1.0e+9','1.5e+9'),
    limits = c(0,1520000000)

  ) +
  scale_shape_manual(values=SHAPE)+
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  ggtitle('Performance over time')+
  p_theme +
  guides(
    shape=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize'),
    color=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize'),
    fill=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize')
  )
```



2.3 Best performance evolved

Performance of the best solution found throughout the entire evolutionary run.

```
ggplot(best, aes(x = pop_size, y = performance, color = pop_size, fill = pop_size, shape = pop_si
  geom_flat_violin(position = position_nudge(x = .1, y = 0), scale = 'width', alpha = 0.2, width
  geom_boxplot(color = 'black', width = .07, outlier.shape = NA, alpha = 0.0, size = 1.0, positic
  geom_point(position = position_jitter(width = 0.02, height = 0.0001), size = 1.5, alpha = 1.0)
  scale_y_continuous(
    name="Average trait score",
    limits=c(0, 100),
    breaks=seq(0,100, 25),
    labels=c("0", "25", "50", "75", "100")
  ) +
  scale_x_discrete(
    name="Population Size"
  )+
  scale_shape_manual(values=SHAPE)+
  scale_colour_manual(values = cb_palette, ) +
  scale_fill_manual(values = cb_palette) +
  ggtitle('Best performance throughout')+
  p_theme+ coord_flip() +
  guides(
    shape=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize'),
    color=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize'),
    fill=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize')
  )
```



2.3.1 Summary statistics

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

```
## # A tibble: 5 x 8
##   pop_size count na_cnt   min median  mean   max    IQR
##   <fct>    <int>  <int> <dbl>  <dbl> <dbl> <dbl>  <dbl>
## 1 50         50      0  99.9   99.9  99.9  99.9 0.0149
## 2 100        50      0  99.9   99.9  99.9  99.9 0.0166
## 3 500        50      0  99.9   99.9  99.9  99.9 0.0235
## 4 1000       50      0  79.0   79.9  80.0  81.8 0.779
## 5 5000       50      0  19.0   19.4  19.4  20.0 0.299
```

2.3.2 Kruskal-Wallis test

```
kruskal.test(performance ~ pop_size, data = best)
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  performance by pop_size
## Kruskal-Wallis chi-squared = 198.29, df = 4,
## p-value < 2.2e-16
```

2.3.3 Pairwise wilcoxon test

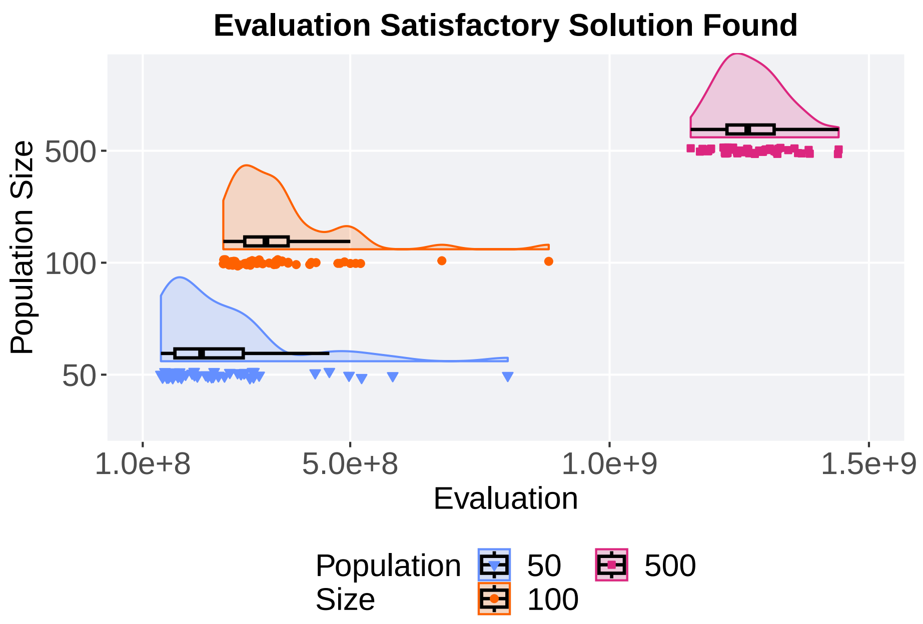
```
pairwise.wilcox.test(x = best$performance, g = best$pop_size, p.adjust.method = "bonferroni",
                     paired = FALSE, conf.int = FALSE, alternative = 'l')
```

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  best$performance and best$pop_size
##
##      50      100     500     1000
## 100  1.00000 -       -       -
## 500  0.00078 0.00059 -       -
## 1000 < 2e-16 < 2e-16 < 2e-16 -
## 5000 < 2e-16 < 2e-16 < 2e-16 < 2e-16
##
## P value adjustment method: bonferroni
```

2.4 Evaluation satisfactory solution if found

Evaluation a satisfactory solution is found for each population size.

```
ggplot(ssf, aes(x = pop_size, y = evaluation, color = pop_size, fill = pop_size, shape
  geom_flat_violin(position = position_nudge(x = 0.12, y = 0), scale = 'width', alpha =
  geom_boxplot(color = 'black', width = .08, outlier.shape = NA, alpha = 0.0, size = 0
  geom_point(position = position_jitter(width = 0.03, height = 0.000001), size = 1.5, a
  scale_y_continuous(
    name = 'Evaluation',
    breaks = c(100000000,500000000,1000000000,1500000000),
    labels = c('1.0e+8', '5.0e+8','1.0e+9','1.5e+9'),
    limits = c(100000000,1500000000)
    ) +
  scale_x_discrete(
    name="Population Size",
  )+
  scale_shape_manual(values=SHAPE, )+
  scale_colour_manual(values = cb_palette, ) +
  scale_fill_manual(values = cb_palette) +
  ggtitle(bquote('Evaluation Satisfactory Solution Found'))+
  p_theme + coord_flip() +
  guides(
    shape=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize'),
    color=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize'),
    fill=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize')
  )
```



2.4.1 Summary statistics

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

```
## # A tibble: 3 x 8
##   pop_size count na_cnt    min median   mean    max    IQR
##   <fct>    <int>  <int>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>
## 1 50          50      0 1.35e8 2.13e8 2.52e8 8.04e8 1.32e8
## 2 100         50      0 2.55e8 3.38e8 3.65e8 8.83e8 8.37e7
## 3 500         50      0 1.16e9 1.27e9 1.28e9 1.44e9 9.10e7
```

2.4.2 Kruskal-Wallis test

```
kruskal.test(evaluation ~ pop_size, data = ssf)
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  evaluation by pop_size
## Kruskal-Wallis chi-squared = 113.38, df = 2,
## p-value < 2.2e-16
```

2.4.3 Pairwise wilcoxon test

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

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

```
##
## data:  ssf$evaluation and ssf$pop_size
##
##     50      100
## 100 3.1e-08 -
## 500 < 2e-16 < 2e-16
##
## P value adjustment method: bonferroni
```

Chapter 3

Contradictory objectives 100 results

Here we report the **activation gene coverage** and **satisfactory trait coverage** was found on the contradictory objectives diagnostic. 50 replicates were conducted for each population size explored. Activation gene coverage is calculated by finding all the unique activation genes found within a given population. Satisfactory trait coverage is calculated by finding all the unique satisfactory traits found within a given population.

3.1 Analysis setup

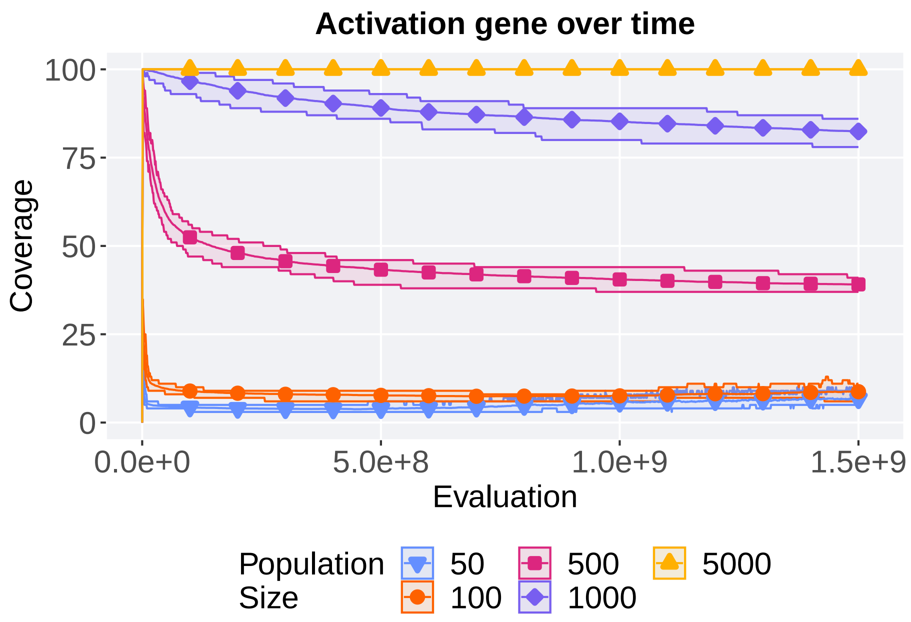
```
library(ggplot2)
library(cowplot)
library(dplyr)
library(PupillometryR)

# over time data
over_time <- read.csv("../Paper_Data/Contradictory-100/ot.csv", header = TRUE, stringsAsFactors =
over_time$pop_size <- factor(over_time$pop_size, levels = NAMES)

# best performance data
best <- read.csv('../Paper_Data/Contradictory-100/best.csv', header = TRUE, stringsAsFactors = FA
best$pop_size <- factor(best$pop_size, levels = NAMES)
```

3.2 Activation gene coverage

3.2.1 Coverage over time

Performance of the best solution in the population at each generation over time.

```
# aggregate
lines = over_time %>%
  group_by(pop_size, eval) %>%
  dplyr::summarise(
    min = min(activation_coverage),
    mean = mean(activation_coverage),
    max = max(activation_coverage)
  )
lines$pop_size <- factor(lines$pop_size, levels = NAMES)

ggplot(lines, aes(x=eval, y=mean, group = pop_size, fill = pop_size, color = pop_size,
  geom_ribbon(aes(ymin = min, ymax = max), alpha = 0.1) +
  geom_line(linewidth = 0.5) +
  geom_point(data = filter(lines, eval %% 100000000 == 0 & eval != 0), size = 1.0, stro
  scale_y_continuous(
    name="Coverage",
    limits=c(0, 100),
    breaks=seq(0,100, 25),
    labels=c("0", "25", "50", "75", "100")
  ) +
  scale_x_continuous(
    name="Evaluation",
    labels = c('0.0e+0', '5.0e+8','1.0e+9','1.5e+9'),
    limits = c(0,1520000000)

  ) +
  scale_shape_manual(values=SHAPE)+
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  ggtitle('Activation gene over time')+
  p_theme +
  guides(
    shape=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize'),
    color=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize'),
    fill=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize')
  )
```

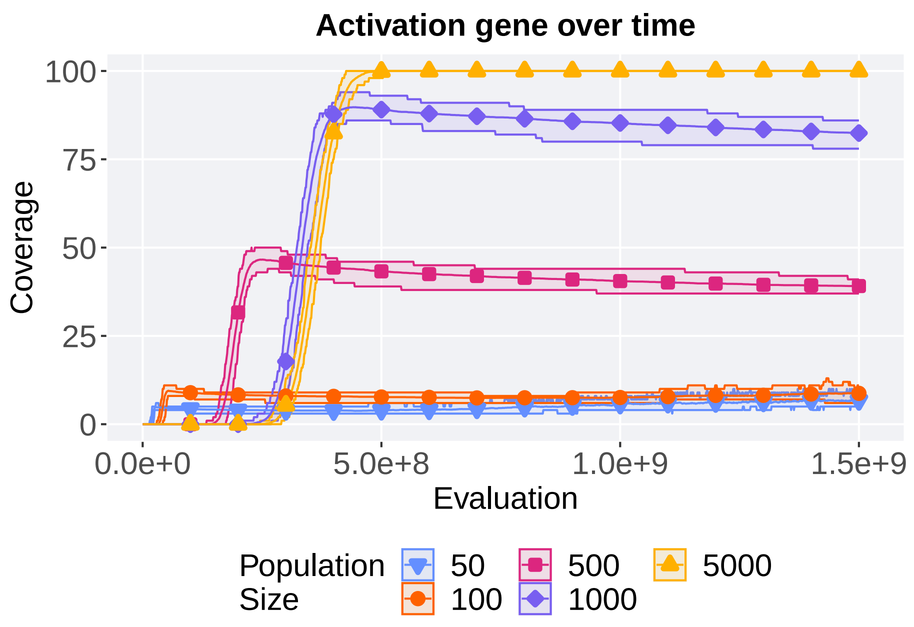


3.3 Satisfactory trait coverage

3.3.1 Coverage over time

Satisfactory trait coverage over time.

```
# aggregate
lines = over_time %>%
  group_by(pop_size, eval) %>%
  dplyr::summarise(
    min = min(satisfactory_coverage),
    mean = mean(satisfactory_coverage),
    max = max(satisfactory_coverage)
  )
lines$pop_size <- factor(lines$pop_size, levels = NAMES)

ggplot(lines, aes(x=eval, y=mean, group = pop_size, fill = pop_size, color = pop_size, shape = po
  geom_ribbon(aes(ymin = min, ymax = max), alpha = 0.1) +
  geom_line(linewidth = 0.5) +
  geom_point(data = filter(lines, eval %% 100000000 == 0 & eval != 0), size = 1.0, stroke = 2.0,
  scale_y_continuous(
    name="Coverage",
    limits=c(0, 100),
    breaks=seq(0,100, 25),
    labels=c("0", "25", "50", "75", "100")
  ) +
  scale_x_continuous(
    name="Evaluation",
    labels = c('0.0e+0', '5.0e+8','1.0e+9','1.5e+9'),
    limits = c(0,1520000000)

  ) +
  scale_shape_manual(values=SHAPE)+
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  ggtitle('Activation gene over time')+
  p_theme +
  guides(
    shape=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize'),
    color=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize'),
    fill=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize')
  )
```

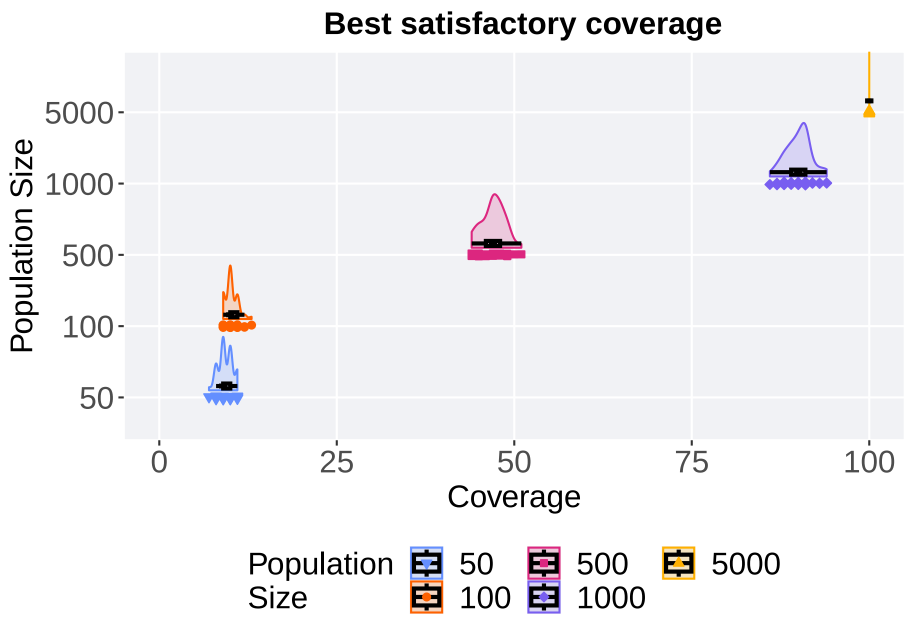


3.3.2 Best satisfactory trait coverage found throughout run

Satisfactory trait coverage of the best population found throughout an evolutionary run.

```
ggplot(best, aes(x = pop_size, y = coverage, color = pop_size, fill = pop_size, shape = pop_size)
  geom_flat_violin(position = position_nudge(x = .1, y = 0), scale = 'width', alpha = 0.2, width
  geom_boxplot(color = 'black', width = .07, outlier.shape = NA, alpha = 0.0, size = 1.0, positio
  geom_point(position = position_jitter(width = 0.02, height = 0.0001), size = 1.5, alpha = 1.0)
  scale_y_continuous(
    name="Coverage",
    limits=c(0, 100),
    breaks=seq(0,100, 25),
    labels=c("0", "25", "50", "75", "100"),
  ) +
  scale_x_discrete(
    name="Population Size"
  )+
  scale_shape_manual(values=SHAPE)+
  scale_colour_manual(values = cb_palette, ) +
  scale_fill_manual(values = cb_palette) +
  ggtitle('  Best satisfactory coverage')+
  p_theme + coord_flip() +
  guides(
    shape=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize'),
    color=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize'),
    fill=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize')
  )
```

```
## Warning: Removed 27 rows containing missing values
## (‘geom_point()‘).
```



3.3.2.1 Summary statistics

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

```
## # A tibble: 5 x 8
##   pop_size count na_cnt   min median  mean   max   IQR
##   <fct>    <int>  <int> <int>  <dbl> <dbl> <int> <dbl>
## 1 50          50      0     7      9  9.36    11     1
## 2 100         50      0     9     10  10.1    13     1
## 3 500         50      0    44     47  47.0    51     2
## 4 1000        50      0    86     90  90.0    94     2
## 5 5000        50      0   100    100 100     100     0
```

3.3.2.2 Kruskal-Wallis test

```
kruskal.test(coverage ~ pop_size, data = best)
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  coverage by pop_size
## Kruskal-Wallis chi-squared = 232.33, df = 4,
## p-value < 2.2e-16
```

3.3.2.3 Pairwise wilcoxon test

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

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  best$coverage and best$pop_size
##
##      50     100    500    1000
## 100  0.0019 -      -      -
## 500  <2e-16 <2e-16 -      -
## 1000 <2e-16 <2e-16 <2e-16 -
## 5000 <2e-16 <2e-16 <2e-16 <2e-16
##
## P value adjustment method: bonferroni
```

Chapter 4

Contradictory objectives 150 results

Here we report the **activation gene coverage** and **satisfactory trait coverage** was found on the contradictory objectives diagnostic. 50 replicates were conducted for each population size explored. Activation gene coverage is calculated by finding all the unique activation genes found within a given population. Satisfactory trait coverage is calculated by finding all the unique satisfactory traits found within a given population.

4.1 Analysis setup

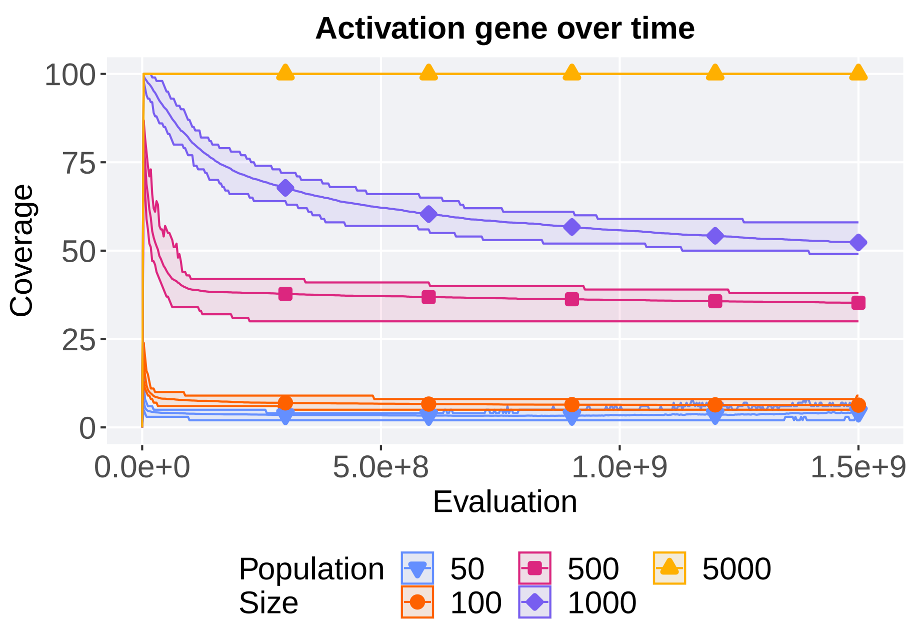
```
library(ggplot2)
library(cowplot)
library(dplyr)
library(PupillometryR)

# over time data
over_time <- read.csv("../Paper_Data/Contradictory-150/ot.csv", header = TRUE, stringsAsFactors =
over_time$pop_size <- factor(over_time$pop_size, levels = NAMES)

# best performance data
best <- read.csv('../Paper_Data/Contradictory-150/best.csv', header = TRUE, stringsAsFactors = FA
best$pop_size <- factor(best$pop_size, levels = NAMES)
```

4.2 Activation gene coverage

4.2.1 Coverage over time

Performance of the best solution in the population at each generation over time.

```
# aggregate
lines = over_time %>%
  group_by(pop_size, eval) %>%
  dplyr::summarise(
    min = min(activation_coverage),
    mean = mean(activation_coverage),
    max = max(activation_coverage)
  )
lines$pop_size <- factor(lines$pop_size, levels = NAMES)

ggplot(lines, aes(x=eval, y=mean, group = pop_size, fill = pop_size, color = pop_size,
  geom_ribbon(aes(ymin = min, ymax = max), alpha = 0.1) +
  geom_line(linewidth = 0.5) +
  geom_point(data = filter(lines, eval %% 100000000 == 0 & eval != 0), size = 1.0, str
  scale_y_continuous(
    name="Coverage",
    limits=c(0, 100),
    breaks=seq(0,100, 25),
    labels=c("0", "25", "50", "75", "100")
  ) +
  scale_x_continuous(
    name="Evaluation",
    labels = c('0.0e+0', '5.0e+8','1.0e+9','1.5e+9'),
    limits = c(0,1520000000)

  ) +
  scale_shape_manual(values=SHAPE)+
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  ggtitle('Activation gene over time')+
  p_theme +
  guides(
    shape=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize'),
    color=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize'),
    fill=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize')
  )
```

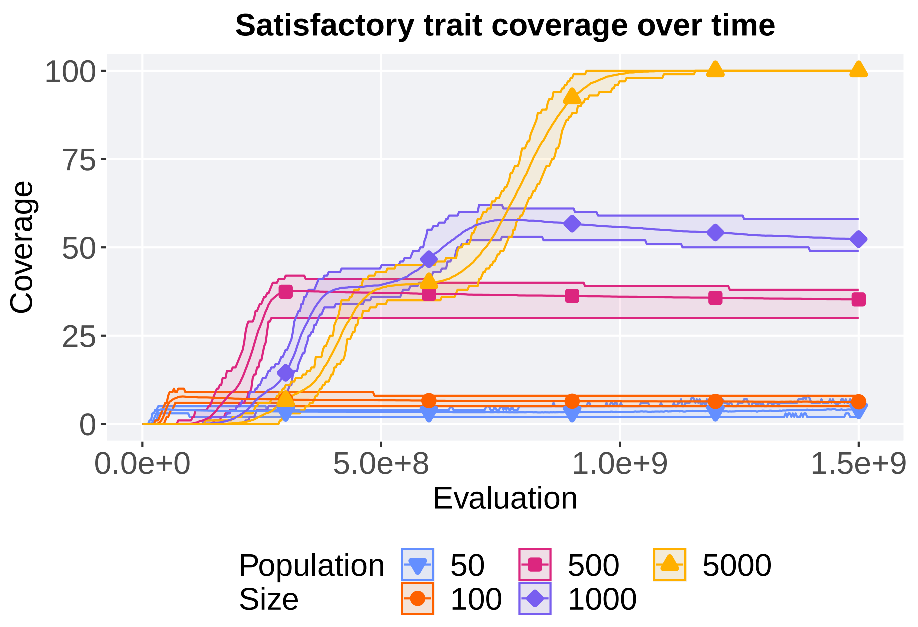


4.3 Satisfactory trait coverage

4.3.1 Coverage over time

Satisfactory trait coverage over time.

```
# aggregate
lines = over_time %>%
  group_by(pop_size, eval) %>%
  dplyr::summarise(
    min = min(satisfactory_coverage),
    mean = mean(satisfactory_coverage),
    max = max(satisfactory_coverage)
  )
lines$pop_size <- factor(lines$pop_size, levels = NAMES)

ggplot(lines, aes(x=eval, y=mean, group = pop_size, fill = pop_size, color = pop_size, shape = po
  geom_ribbon(aes(ymin = min, ymax = max), alpha = 0.1) +
  geom_line(linewidth = 0.5) +
  geom_point(data = filter(lines, eval %% 100000000 == 0 & eval != 0), size = 1.0, stroke = 2.0,
  scale_y_continuous(
    name="Coverage",
    limits=c(0, 100),
    breaks=seq(0,100, 25),
    labels=c("0", "25", "50", "75", "100")
  ) +
  scale_x_continuous(
    name="Evaluation",
    labels = c('0.0e+0', '5.0e+8','1.0e+9','1.5e+9'),
    limits = c(0,1520000000)

  ) +
  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=2, title.position = "left", title = 'Population\nSize'),
    color=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize'),
    fill=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize')
  )
```

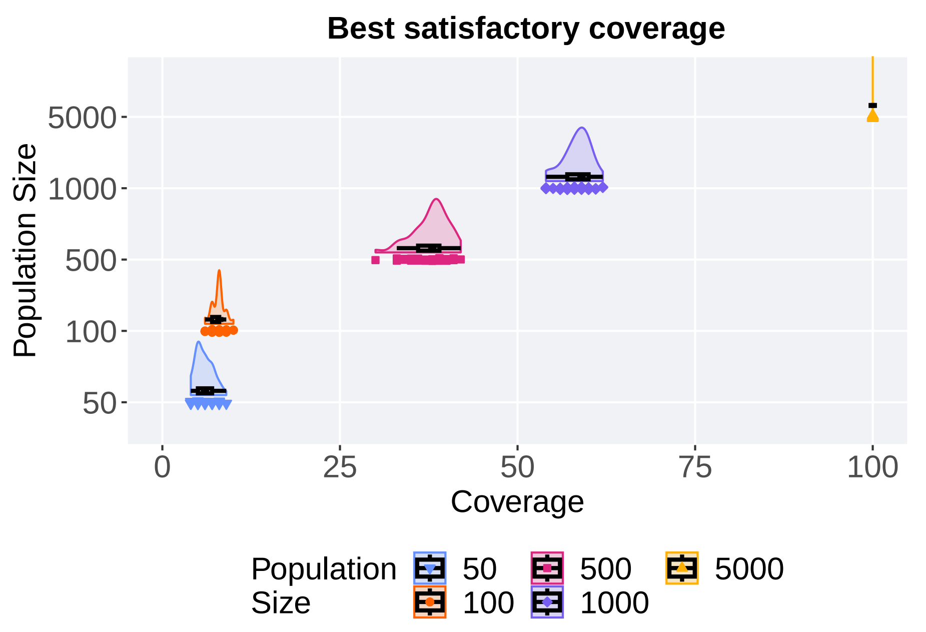


4.3.2 Best satisfactory trait coverage found throughout run

Satisfactory trait coverage of the best population found throughout an evolutionary run.

```
ggplot(best, aes(x = pop_size, y = coverage, color = pop_size, fill = pop_size, shape = pop_size)
  geom_flat_violin(position = position_nudge(x = .1, y = 0), scale = 'width', alpha = 0.2, width
  geom_boxplot(color = 'black', width = .07, outlier.shape = NA, alpha = 0.0, size = 1.0, positic
  geom_point(position = position_jitter(width = 0.02, height = 0.0001), size = 1.5, alpha = 1.0)
  scale_y_continuous(
    name="Coverage",
    limits=c(0, 100),
    breaks=seq(0,100, 25),
    labels=c("0", "25", "50", "75", "100"),
  ) +
  scale_x_discrete(
    name="Population Size"
  )+
  scale_shape_manual(values=SHAPE)+
  scale_colour_manual(values = cb_palette, ) +
  scale_fill_manual(values = cb_palette) +
  ggtitle('  Best satisfactory coverage')+
  p_theme + coord_flip() +
  guides(
    shape=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize'),
    color=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize'),
    fill=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize')
  )
```

```
## Warning: Removed 24 rows containing missing values
## (‘geom_point()‘).
```



4.3.2.1 Summary statistics

```r
best %>%
  group_by(pop_size) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(coverage)),
    min = min(coverage, na.rm = TRUE),
    median = median(coverage, na.rm = TRUE),
    mean = mean(coverage, na.rm = TRUE),
    max = max(coverage, na.rm = TRUE),
    IQR = IQR(coverage, na.rm = TRUE)
  )
```

```
## # A tibble: 5 x 8
##   pop_size count na_cnt   min median  mean   max   IQR
##   <fct>    <int>  <int> <int>  <dbl> <dbl> <int> <dbl>
## 1 50          50      0     4      6  5.86     9     2
## 2 100         50      0     6      8  7.88    10     1
## 3 500         50      0    30     38 37.8     42     3
## 4 1000        50      0    54     59 58.4     62     3
## 5 5000        50      0   100    100 100     100     0
```

4.3.2.2 Kruskal-Wallis test

```r
kruskal.test(coverage ~ pop_size, data = best)
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  coverage by pop_size
## Kruskal-Wallis chi-squared = 237.37, df = 4,
## p-value < 2.2e-16
```

4.3.2.3 Pairwise wilcoxon test

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

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  best$coverage and best$pop_size
##
##      50      100     500     1000
## 100  1.2e-11 -       -       -
## 500  < 2e-16 < 2e-16 -       -
## 1000 < 2e-16 < 2e-16 < 2e-16 -
## 5000 < 2e-16 < 2e-16 < 2e-16 < 2e-16
##
## P value adjustment method: bonferroni
```

Chapter 5

Contradictory objectives 200 results

Here we report the **activation gene coverage** and **satisfactory trait coverage** was found on the contradictory objectives diagnostic. 50 replicates were conducted for each population size explored. Activation gene coverage is calculated by finding all the unique activation genes found within a given population. Satisfactory trait coverage is calculated by finding all the unique satisfactory traits found within a given population.

5.1 Analysis setup

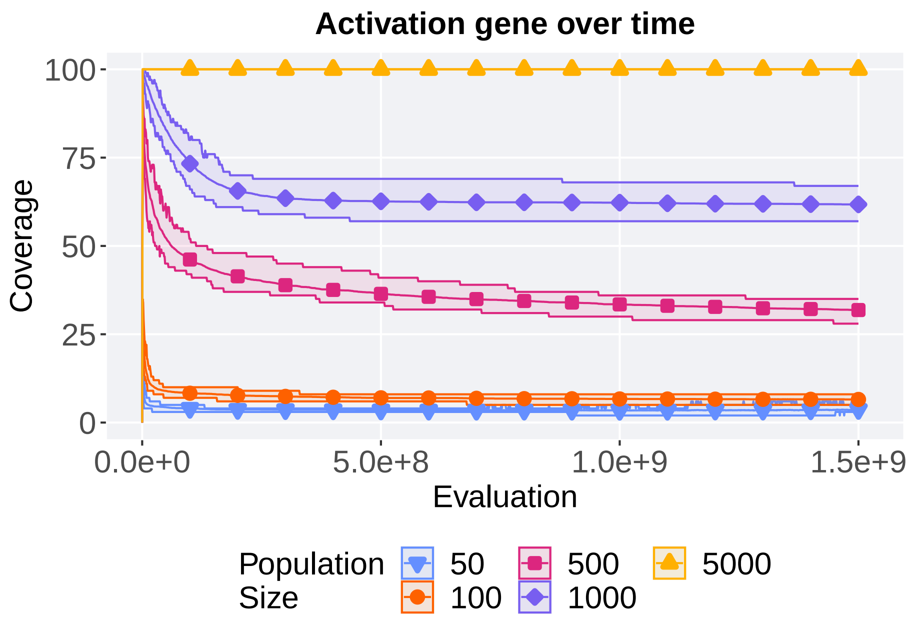
```
library(ggplot2)
library(cowplot)
library(dplyr)
library(PupillometryR)

# over time data
over_time <- read.csv("../Paper_Data/Contradictory-200/ot.csv", header = TRUE, stringsAsFactors =
over_time$pop_size <- factor(over_time$pop_size, levels = NAMES)

# best performance data
best <- read.csv('../Paper_Data/Contradictory-200/best.csv', header = TRUE, stringsAsFactors = FA
best$pop_size <- factor(best$pop_size, levels = NAMES)
```

5.2 Activation gene coverage

5.2.1 Coverage over time

Performance of the best solution in the population at each generation over time.

```
# aggregate
lines = over_time %>%
  group_by(pop_size, eval) %>%
  dplyr::summarise(
    min = min(activation_coverage),
    mean = mean(activation_coverage),
    max = max(activation_coverage)
  )
lines$pop_size <- factor(lines$pop_size, levels = NAMES)

ggplot(lines, aes(x=eval, y=mean, group = pop_size, fill = pop_size, color = pop_size,
  geom_ribbon(aes(ymin = min, ymax = max), alpha = 0.1) +
  geom_line(linewidth = 0.5) +
  geom_point(data = filter(lines, eval %% 100000000 == 0 & eval != 0), size = 1.0, str
  scale_y_continuous(
    name="Coverage",
    limits=c(0, 100),
    breaks=seq(0,100, 25),
    labels=c("0", "25", "50", "75", "100")
  ) +
  scale_x_continuous(
    name="Evaluation",
    labels = c('0.0e+0', '5.0e+8','1.0e+9','1.5e+9'),
    limits = c(0,1520000000)

  ) +
  scale_shape_manual(values=SHAPE)+
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  ggtitle('Activation gene over time')+
  p_theme +
  guides(
    shape=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize'),
    color=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize'),
    fill=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize')
  )
```

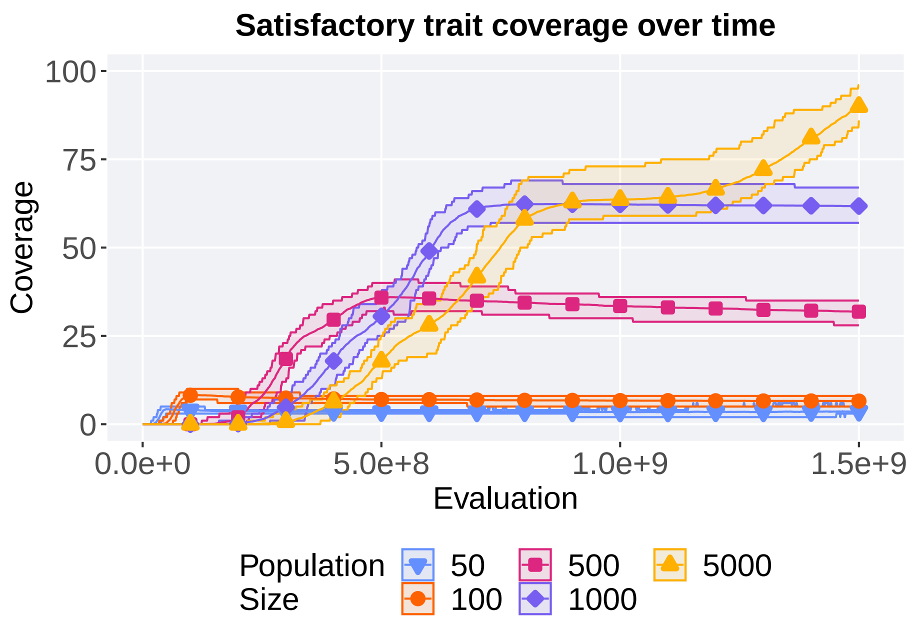


5.3 Satisfactory trait coverage

5.3.1 Coverage over time

Satisfactory trait coverage over time.

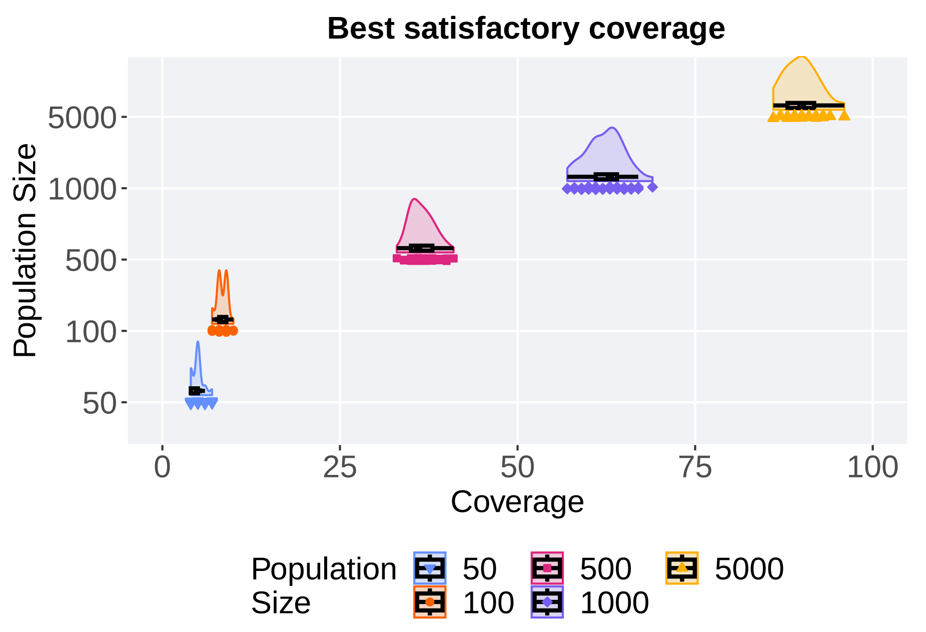
```
# aggregate
lines = over_time %>%
  group_by(pop_size, eval) %>%
  dplyr::summarise(
    min = min(satisfactory_coverage),
    mean = mean(satisfactory_coverage),
    max = max(satisfactory_coverage)
  )
lines$pop_size <- factor(lines$pop_size, levels = NAMES)

ggplot(lines, aes(x=eval, y=mean, group = pop_size, fill = pop_size, color = pop_size, shape = po
  geom_ribbon(aes(ymin = min, ymax = max), alpha = 0.1) +
  geom_line(linewidth = 0.5) +
  geom_point(data = filter(lines, eval %% 100000000 == 0 & eval != 0), size = 1.0, stroke = 2.0,
  scale_y_continuous(
    name="Coverage",
    limits=c(0, 100),
    breaks=seq(0,100, 25),
    labels=c("0", "25", "50", "75", "100")
  ) +
  scale_x_continuous(
    name="Evaluation",
    labels = c('0.0e+0', '5.0e+8','1.0e+9','1.5e+9'),
    limits = c(0,1520000000)

  ) +
  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=2, title.position = "left", title = 'Population\nSize'),
    color=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize'),
    fill=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize')
  )
```



5.3.2 Best satisfactory trait coverage found throughout run

Satisfactory trait coverage of the best population found throughout an evolutionary run.

```
ggplot(best, aes(x = pop_size, y = coverage, color = pop_size, fill = pop_size, shape = pop_size)
  geom_flat_violin(position = position_nudge(x = .1, y = 0), scale = 'width', alpha = 0.2, width
  geom_boxplot(color = 'black', width = .07, outlier.shape = NA, alpha = 0.0, size = 1.0, positio
  geom_point(position = position_jitter(width = 0.02, height = 0.0001), size = 1.5, alpha = 1.0)
  scale_y_continuous(
    name="Coverage",
    limits=c(0, 100),
    breaks=seq(0,100, 25),
    labels=c("0", "25", "50", "75", "100"),
  ) +
  scale_x_discrete(
    name="Population Size"
  )+
  scale_shape_manual(values=SHAPE)+
  scale_colour_manual(values = cb_palette, ) +
  scale_fill_manual(values = cb_palette) +
  ggtitle('  Best satisfactory coverage')+
  p_theme + coord_flip() +
  guides(
    shape=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize'),
    color=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize'),
    fill=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize')
  )
```



5.3.2.1 Summary statistics

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

```
## # A tibble: 5 x 8
##   pop_size count na_cnt   min median  mean   max   IQR
##   <fct>    <int>  <int> <int>  <dbl> <dbl> <int> <dbl>
## 1 50          50      0     4      5  4.94     7  1
## 2 100         50      0     7      8  8.38    10  1
## 3 500         50      0    33     36 36.5     41  3
## 4 1000        50      0    57     63 62.3     69  3
## 5 5000        50      0    86     90 90.0     96  3.75
```

5.3.2.2 Kruskal-Wallis test

```
kruskal.test(coverage ~ pop_size, data = best)
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  coverage by pop_size
## Kruskal-Wallis chi-squared = 239.68, df = 4,
## p-value < 2.2e-16
```

5.3.2.3 Pairwise wilcoxon test

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

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  best$coverage and best$pop_size
##
##      50     100    500    1000
## 100  <2e-16 -      -      -
## 500  <2e-16 <2e-16 -      -
## 1000 <2e-16 <2e-16 <2e-16 -
## 5000 <2e-16 <2e-16 <2e-16 <2e-16
##
## P value adjustment method: bonferroni
```

Chapter 6

Contradictory objectives 300 results

Here we report the **activation gene coverage** and **satisfactory trait coverage** was found on the contradictory objectives diagnostic. 50 replicates were conducted for each population size explored. Activation gene coverage is calculated by finding all the unique activation genes found within a given population. Satisfactory trait coverage is calculated by finding all the unique satisfactory traits found within a given population.

6.1 Analysis setup

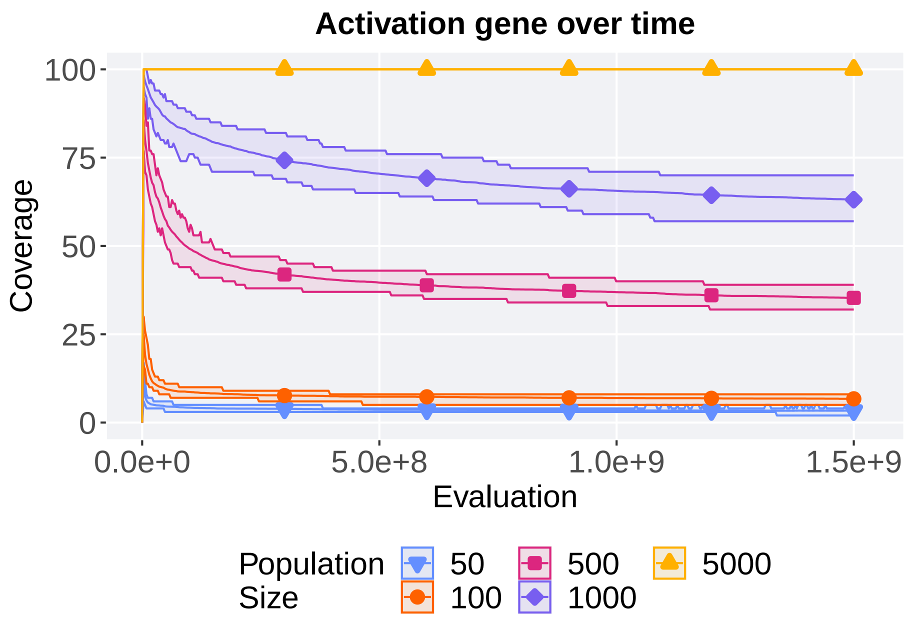
```
library(ggplot2)
library(cowplot)
library(dplyr)
library(PupillometryR)

# over time data
over_time <- read.csv("../Paper_Data/Contradictory-300/ot.csv", header = TRUE, stringsAsFactors =
over_time$pop_size <- factor(over_time$pop_size, levels = NAMES)

# best performance data
best <- read.csv('../Paper_Data/Contradictory-300/best.csv', header = TRUE, stringsAsFactors = FA
best$pop_size <- factor(best$pop_size, levels = NAMES)
```

6.2 Activation gene coverage

6.2.1 Coverage over time

Performance of the best solution in the population at each generation over time.

```
# aggregate
lines = over_time %>%
  group_by(pop_size, eval) %>%
  dplyr::summarise(
    min = min(activation_coverage),
    mean = mean(activation_coverage),
    max = max(activation_coverage)
  )
lines$pop_size <- factor(lines$pop_size, levels = NAMES)

ggplot(lines, aes(x=eval, y=mean, group = pop_size, fill = pop_size, color = pop_size,
  geom_ribbon(aes(ymin = min, ymax = max), alpha = 0.1) +
  geom_line(linewidth = 0.5) +
  geom_point(data = filter(lines, eval %% 100000000 == 0 & eval != 0), size = 1.0, stro
  scale_y_continuous(
    name="Coverage",
    limits=c(0, 100),
    breaks=seq(0,100, 25),
    labels=c("0", "25", "50", "75", "100")
  ) +
  scale_x_continuous(
    name="Evaluation",
    labels = c('0.0e+0', '5.0e+8','1.0e+9','1.5e+9'),
    limits = c(0,1530000000)

  ) +
  scale_shape_manual(values=SHAPE)+
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  ggtitle('Activation gene over time')+
  p_theme +
  guides(
    shape=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize'),
    color=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize'),
    fill=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize')
  )
```

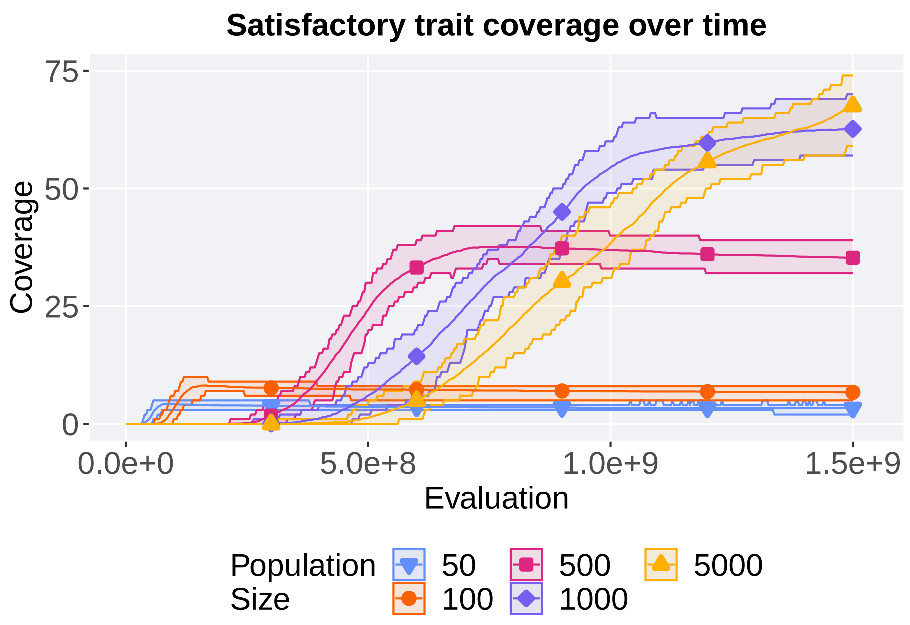


6.3 Satisfactory trait coverage

6.3.1 Coverage over time

Satisfactory trait coverage over time.

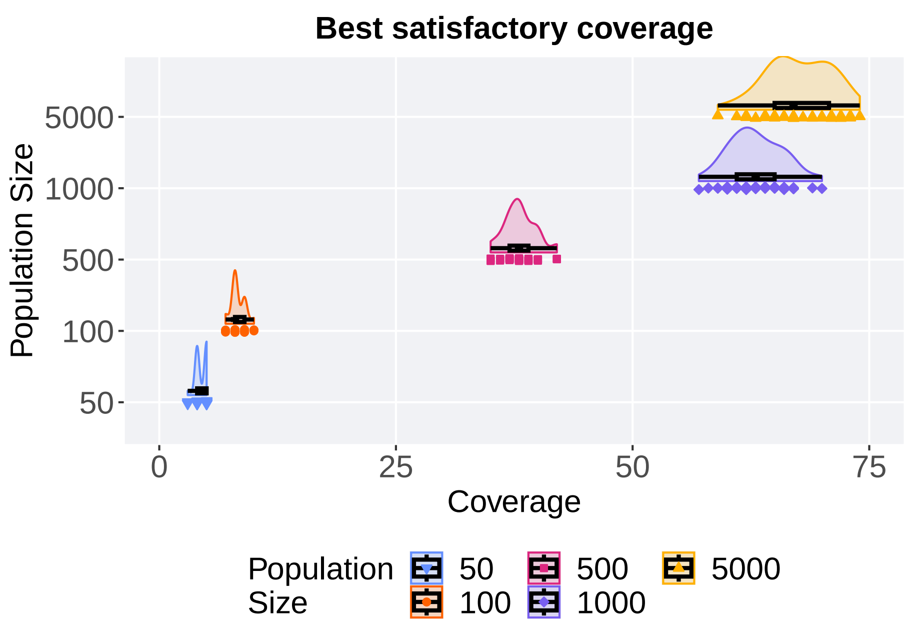
```
# aggregate
lines = over_time %>%
  group_by(pop_size, eval) %>%
  dplyr::summarise(
    min = min(satisfactory_coverage),
    mean = mean(satisfactory_coverage),
    max = max(satisfactory_coverage)
  )
lines$pop_size <- factor(lines$pop_size, levels = NAMES)

ggplot(lines, aes(x=eval, y=mean, group = pop_size, fill = pop_size, color = pop_size, shape = po
  geom_ribbon(aes(ymin = min, ymax = max), alpha = 0.1) +
  geom_line(linewidth = 0.5) +
  geom_point(data = filter(lines, eval %% 100000000 == 0 & eval != 0), size = 1.0, stroke = 2.0,
  scale_y_continuous(
    name="Coverage",
    limits=c(0, 75),
    breaks=seq(0,75, 25),
    labels=c("0", "25", "50", "75")
  ) +
  scale_x_continuous(
    name="Evaluation",
    labels = c('0.0e+0', '5.0e+8','1.0e+9','1.5e+9'),
    limits = c(0,1530000000)

  ) +
  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=2, title.position = "left", title = 'Population\nSize'),
    color=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize'),
    fill=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize')
  )
```



6.3.2 Best satisfactory trait coverage found throughout run

Satisfactory trait coverage of the best population found throughout an evolutionary run.

```r
ggplot(best, aes(x = pop_size, y = coverage, color = pop_size, fill = pop_size, shape = pop_size)
  geom_flat_violin(position = position_nudge(x = .1, y = 0), scale = 'width', alpha = 0.2, width
  geom_boxplot(color = 'black', width = .07, outlier.shape = NA, alpha = 0.0, size = 1.0, positio
  geom_point(position = position_jitter(width = 0.02, height = 0.0001), size = 1.5, alpha = 1.0)
  scale_y_continuous(
    name="Coverage",
    limits=c(0, 75),
    breaks=seq(0,75, 25),
    labels=c("0", "25", "50", "75")
  ) +
  scale_x_discrete(
    name="Population Size"
  )+
  scale_shape_manual(values=SHAPE)+
  scale_colour_manual(values = cb_palette, ) +
  scale_fill_manual(values = cb_palette) +
  ggtitle('Best satisfactory coverage')+
  p_theme + coord_flip() +
  guides(
    shape=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize'),
    color=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize'),
    fill=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize')
  )
```



6.3.2.1 Summary statistics

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

```
## # A tibble: 5 x 8
##   pop_size count na_cnt   min median  mean   max   IQR
##   <fct>    <int>  <int> <int>  <dbl> <dbl> <int> <dbl>
## 1 50          50      0     3    4.5  4.46     5  1
## 2 100         50      0     7    8     8.3    10  1
## 3 500         50      0    35   38    38.1    42  2
## 4 1000        50      0    57   63    63.0    70  4
## 5 5000        50      0    59   67    67.5    74  5.75
```

6.3.2.2 Kruskal-Wallis test

```
kruskal.test(coverage ~ pop_size, data = best)
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  coverage by pop_size
## Kruskal-Wallis chi-squared = 233.56, df = 4,
## p-value < 2.2e-16
```

6.3.2.3 Pairwise wilcoxon test

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

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  best$coverage and best$pop_size
##
##      50      100     500     1000
## 100  < 2e-16 -       -       -
## 500  < 2e-16 < 2e-16 -       -
## 1000 < 2e-16 < 2e-16 < 2e-16 -
## 5000 < 2e-16 < 2e-16 < 2e-16 2.3e-08
##
## P value adjustment method: bonferroni
```

Chapter 7

Contradictory objectives 500 results

Here we report the **activation gene coverage** and **satisfactory trait coverage** was found on the contradictory objectives diagnostic. 50 replicates were conducted for each population size explored. Activation gene coverage is calculated by finding all the unique activation genes found within a given population. Satisfactory trait coverage is calculated by finding all the unique satisfactory traits found within a given population.

7.1 Analysis setup

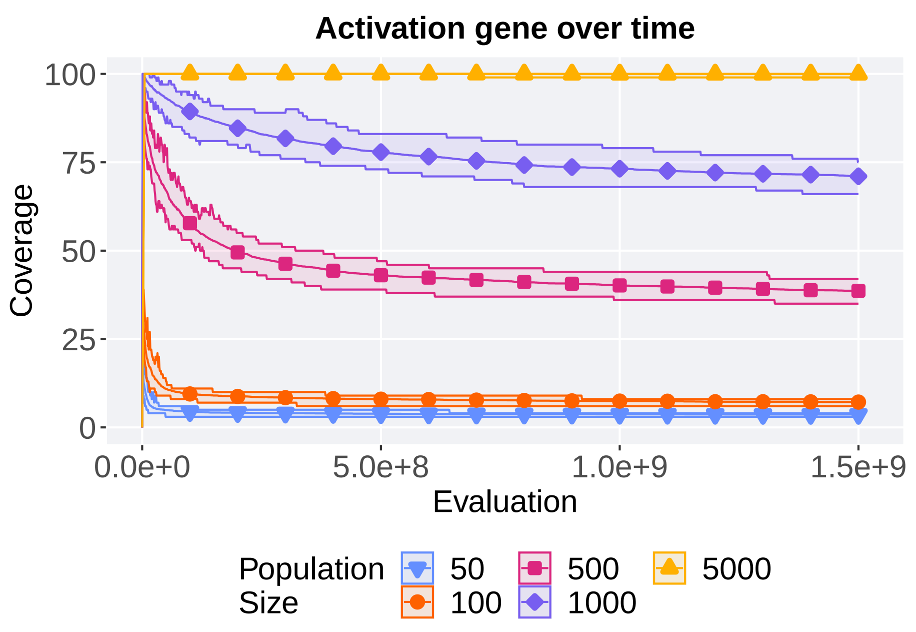
```
library(ggplot2)
library(cowplot)
library(dplyr)
library(PupillometryR)

# over time data
over_time <- read.csv("../Paper_Data/Contradictory-500/ot.csv", header = TRUE, stringsAsFactors =
over_time$pop_size <- factor(over_time$pop_size, levels = NAMES)

# best performance data
best <- read.csv('../Paper_Data/Contradictory-500/best.csv', header = TRUE, stringsAsFactors = FA
best$pop_size <- factor(best$pop_size, levels = NAMES)
```

7.2 Activation gene coverage

7.2.1 Coverage over time

Performance of the best solution in the population at each generation over time.

```
# aggregate
lines = over_time %>%
  group_by(pop_size, eval) %>%
  dplyr::summarise(
    min = min(activation_coverage),
    mean = mean(activation_coverage),
    max = max(activation_coverage)
  )
lines$pop_size <- factor(lines$pop_size, levels = NAMES)

ggplot(lines, aes(x=eval, y=mean, group = pop_size, fill = pop_size, color = pop_size,
  geom_ribbon(aes(ymin = min, ymax = max), alpha = 0.1) +
  geom_line(linewidth = 0.5) +
  geom_point(data = filter(lines, eval %% 100000000 == 0 & eval != 0), size = 1.0, stro
  scale_y_continuous(
    name="Coverage",
    limits=c(0, 100),
    breaks=seq(0,100, 25),
    labels=c("0", "25", "50", "75", "100")
  ) +
  scale_x_continuous(
    name="Evaluation",
    labels = c('0.0e+0', '5.0e+8','1.0e+9','1.5e+9'),
    limits = c(0,1520000000)

  ) +
  scale_shape_manual(values=SHAPE)+
  scale_colour_manual(values = cb_palette) +
  scale_fill_manual(values = cb_palette) +
  ggtitle('Activation gene over time')+
  p_theme +
  guides(
    shape=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize'),
    color=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize'),
    fill=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize')
  )
```

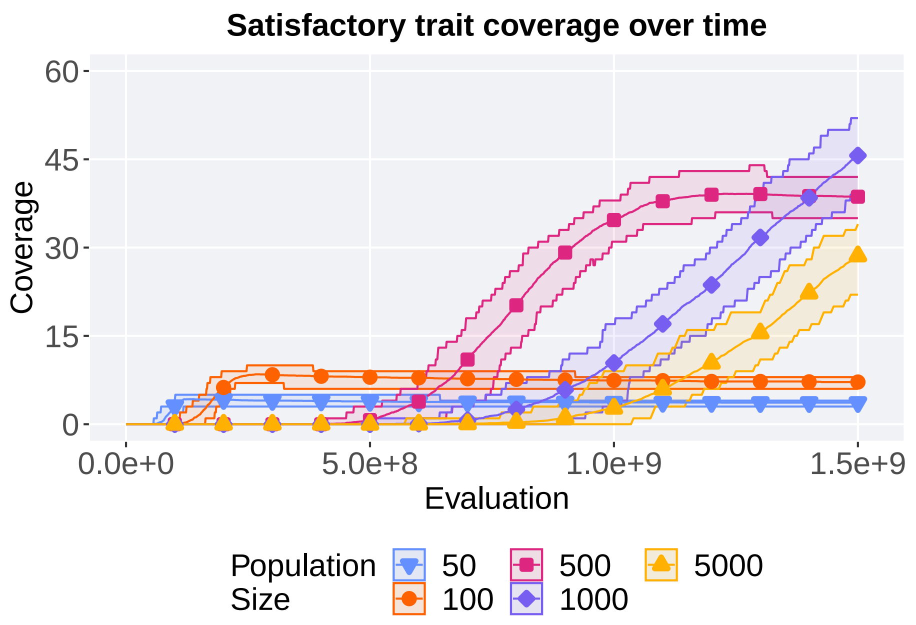


7.3 Satisfactory trait coverage

7.3.1 Coverage over time

Satisfactory trait coverage over time.

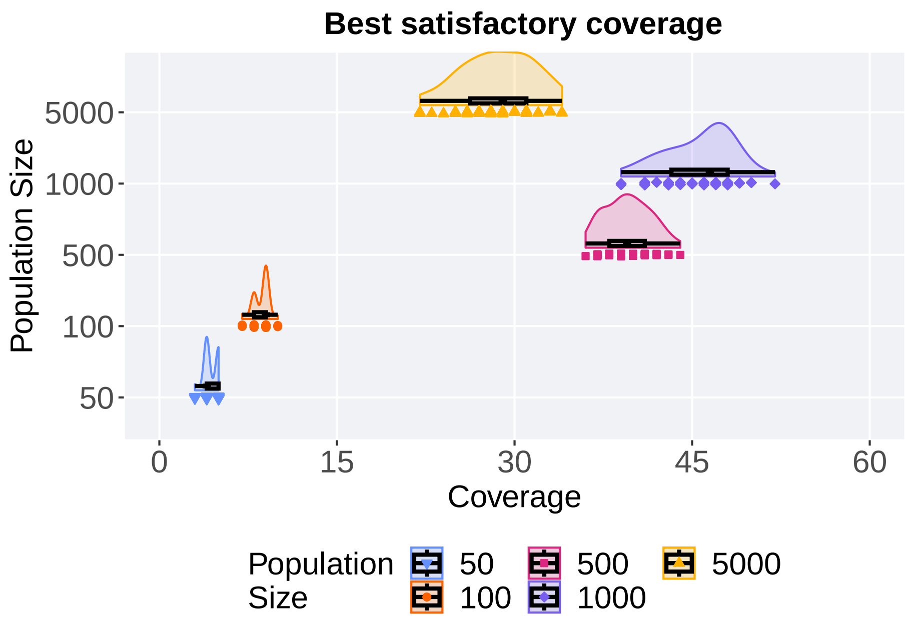
```
# aggregate
lines = over_time %>%
  group_by(pop_size, eval) %>%
  dplyr::summarise(
    min = min(satisfactory_coverage),
    mean = mean(satisfactory_coverage),
    max = max(satisfactory_coverage)
  )
lines$pop_size <- factor(lines$pop_size, levels = NAMES)

ggplot(lines, aes(x=eval, y=mean, group = pop_size, fill = pop_size, color = pop_size, shape = po
  geom_ribbon(aes(ymin = min, ymax = max), alpha = 0.1) +
  geom_line(linewidth = 0.5) +
  geom_point(data = filter(lines, eval %% 100000000 == 0 & eval != 0), size = 1.0, stroke = 2.0,
  scale_y_continuous(
    name="Coverage",
    limits=c(0, 60),
    breaks=seq(0,60, 15),
    labels=c("0", "15", "30", "45", "60")
  ) +
  scale_x_continuous(
    name="Evaluation",
    labels = c('0.0e+0', '5.0e+8','1.0e+9','1.5e+9'),
    limits = c(0,1520000000)

  ) +
  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=2, title.position = "left", title = 'Population\nSize'),
    color=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize'),
    fill=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize')
  )
```



7.3.2 Best satisfactory trait coverage found throughout run

Satisfactory trait coverage of the best population found throughout an evolutionary run.

```r
ggplot(best, aes(x = pop_size, y = coverage, color = pop_size, fill = pop_size, shape = pop_size)
  geom_flat_violin(position = position_nudge(x = .1, y = 0), scale = 'width', alpha = 0.2, width
  geom_boxplot(color = 'black', width = .07, outlier.shape = NA, alpha = 0.0, size = 1.0, positio
  geom_point(position = position_jitter(width = 0.02, height = 0.0001), size = 1.5, alpha = 1.0)
  scale_y_continuous(
    name="Coverage",
    limits=c(0, 60),
    breaks=seq(0,60, 15),
    labels=c("0", "15", "30", "45", "60")
  ) +
  scale_x_discrete(
    name="Population Size"
  )+
  scale_shape_manual(values=SHAPE)+
  scale_colour_manual(values = cb_palette, ) +
  scale_fill_manual(values = cb_palette) +
  ggtitle('  Best satisfactory coverage')+
  p_theme + coord_flip() +
  guides(
    shape=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize'),
    color=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize'),
    fill=guide_legend(nrow=2, title.position = "left", title = 'Population\nSize')
  )
```



7.3.2.1 Summary statistics

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

```
## # A tibble: 5 x 8
##   pop_size count na_cnt   min median  mean   max   IQR
##   <fct>    <int>  <int> <int>  <dbl> <dbl> <int> <dbl>
## 1 50          50      0     3    4    4.36     5  1
## 2 100         50      0     7    9    8.62    10  1
## 3 500         50      0    36   39.5 39.6     44  3
## 4 1000        50      0    39   46.5 45.7     52  4.75
## 5 5000        50      0    22   29   28.6     34  4.75
```

7.3.2.2 Kruskal-Wallis test

```
kruskal.test(coverage ~ pop_size, data = best)
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  coverage by pop_size
## Kruskal-Wallis chi-squared = 237.63, df = 4,
## p-value < 2.2e-16
```

7.3.2.3 Pairwise wilcoxon test

```
best$pop_size <- factor(best$pop_size, levels = c(1000,500,5000,100,50))
pairwise.wilcox.test(x = best$coverage, g = best$pop_size, p.adjust.method = "bonferroni",
                     paired = FALSE, conf.int = FALSE, alternative = 'l')
```

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  best$coverage and best$pop_size
##
##      1000    500     5000    100
## 500  5.7e-14 -       -       -
## 5000 < 2e-16 < 2e-16 -       -
## 100  < 2e-16 < 2e-16 < 2e-16 -
## 50   < 2e-16 < 2e-16 < 2e-16 < 2e-16
##
## P value adjustment method: bonferroni
```