

Supplemental Material: Base Diagnostics

Jose Guadalupe Hernandez

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Chapter 1

Introduction

This is the supplemental material for experiments breaking down nondominated sorting into its two main components: phenotypic fitness sharing and nondominated front ranking. We evaluated these components, along with standard nondominated sorting, on the contradictory objectives diagnostic to measure their contribution on the overall effectiveness of nondominated sorting.

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:

- Nondomintaed sorting breakdown (Section ??)

1.2 Contributing authors

- Jose Guadalupe Hernandez
- Alexander Lalejini
- Charles Ofria

1.3 Computer Setup

These analyses were conducted in the following computing environment:

```
print(version)
```

```
##
## platform      x86_64-pc-linux-gnu
## arch          x86_64
## os            linux-gnu
## system        x86_64, linux-gnu
## status
## major         4
## minor         3.1
## year          2023
## month         06
## day           16
## svn rev       84548
## language      R
## version.string R version 4.3.1 (2023-06-16)
## nickname      Beagle Scouts
```

1.4 Experimental setup

Setting up required variables.

```
# libraries we are using
```

```
library(ggplot2)
```

```
library(cowplot)
```

```
library(dplyr)
```

```
##
```

```
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':
```

```
##
```

```
##      filter, lag
```

```
## The following objects are masked from 'package:base':
```

```
##
```

```
##      intersect, setdiff, setequal, union
```

```
library(PupillometryR)
```

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

```
# data diractory for gh-pages
```

```
DATA_DIR = '/opt/ECJ-2023-Suite-Of-Diagnostic-Metrics-For-Characterizing-Selection-Sch
```

```
# data diractory for local testing
```

```
# DATA_DIR = '~/Desktop/Repositories/ECJ-2023-Suite-Of-Diagnostic-Metrics-For-Characte
```

```
# graph variables
```

```
SHAPE = c(5,3,1)
```

```

cb_palette <- c('#88CCEE', '#EE7733', '#EE3377')
TSIZE = 26
p_theme <- theme(
  text = element_text(size = 19),
  plot.title = element_text( face = "bold", size = 20, hjust=0.5),
  panel.border = element_blank(),
  panel.grid.minor = element_blank(),
  legend.title=element_text(size=13),
  legend.text=element_text(size=13),
  axis.title = element_text(size=19),
  axis.text = element_text(size=19),
  legend.position="bottom",
  panel.background = element_rect(fill = "#f1f2f5",
                                   colour = "white",
                                   linewidth = 0.5, linetype = "solid")
)

# default variables
DIMENSIONALITY = 100
GENERATIONS = 50000

# selection scheme related stuff
ACRO = c('nds', 'nfr', 'pfs')
NAMES = c('Nondominated sorting (nds)', 'Nondominated front ranking (nfr)', 'Phenotypic fitness sha

```


Chapter 2

Nondominated sorting breakdown

For these experiments we break down nondominated sorting into its two main components: phenotypic fitness sharing and nondominated front ranking. We evaluated these components, along with standard nondominated sorting, on the contradictory objectives diagnostic to measure their contribution on the overall effectiveness of nondominated sorting. Here we present the results for **activation gene coverage** and **satisfactory trait coverage** found by each selection scheme on the contradictory objectives diagnostic. 50 replicates are conducted for each scheme explored.

2.1 Data setup

```
over_time_df <- read.csv(paste(DATA_DIR, 'over-time.csv', sep = "", collapse = NULL), header = TRUE)
over_time_df$scheme <- factor(over_time_df$scheme, levels = NAMES)
over_time_df$acro <- factor(over_time_df$acro, levels = ACRO)
```

2.2 Activation gene coverage over time

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

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

```

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

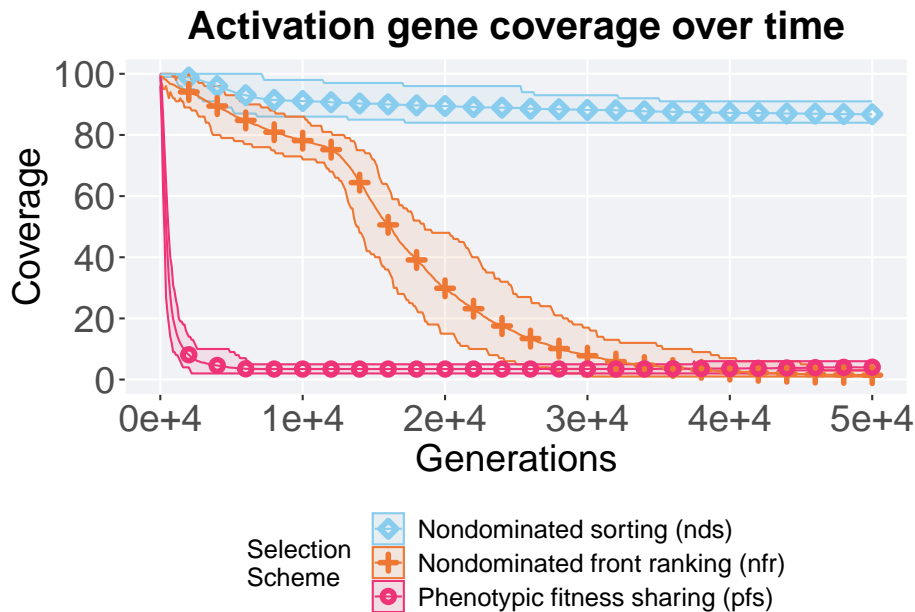
```

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

```

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

```



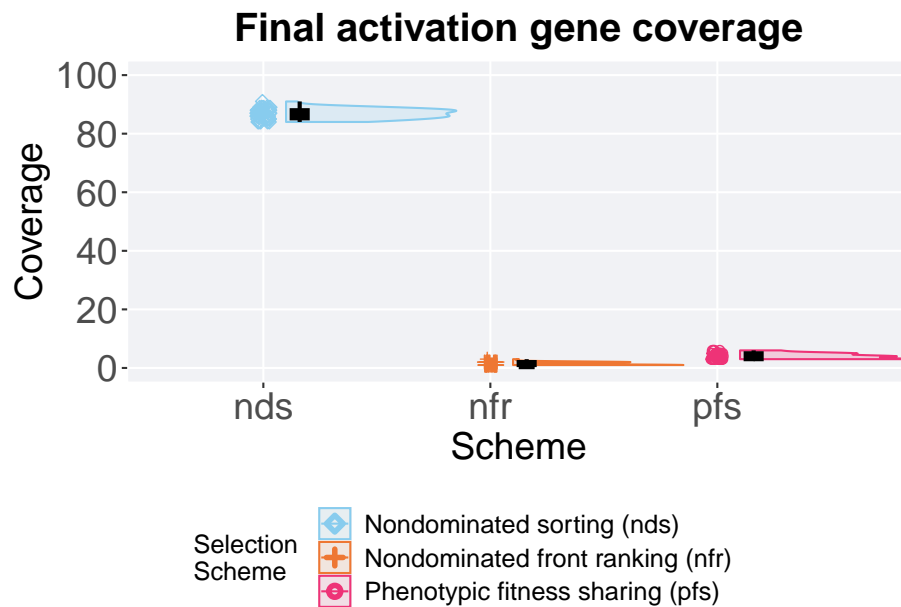
2.3 Final activation gene coverage

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

```
plot = filter(over_time_df, gen == 50000) %>%
  ggplot(., aes(x = acro, y = uni_str_pos, color = acro, fill = acro, shape = acro)) +
  geom_flat_violin(position = position_nudge(x = .1, y = 0), scale = 'width', alpha = 0.2, width
  geom_boxplot(color = 'black', width = .07, outlier.shape = NA, alpha = 0.0, size = 1.0, position
  geom_point(position = position_jitter(width = 0.03, height = 0.02), size = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Coverage",
    limits=c(0, 100),
    breaks=seq(0,100, 20),
    labels=c("0", "20", "40", "60", "80", "100")
  ) +
  scale_x_discrete(
    name="Scheme"
  ) +
  scale_shape_manual(values=SHAPE) +
  scale_colour_manual(values = cb_palette, ) +
  scale_fill_manual(values = cb_palette) +
  ggtitle('Final activation gene coverage') +
  p_theme
```

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

```
## Warning: Using the `size` aesthetic with geom_polygon was deprecated in ggplot2 3.4
## i Please use the `linewidth` aesthetic instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```



2.3.1 Stats

Summary statistics for the coverage found in the final population.

```
act_coverage = filter(over_time_df, gen == 50000)
act_coverage$acro = factor(act_coverage$acro, levels = c('nds', 'pfs', 'nfr'))
act_coverage %>%
  group_by(acro) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(uni_str_pos)),
```

```

    min = min(uni_str_pos, na.rm = TRUE),
    median = median(uni_str_pos, na.rm = TRUE),
    mean = mean(uni_str_pos, na.rm = TRUE),
    max = max(uni_str_pos, na.rm = TRUE),
    IQR = IQR(uni_str_pos, na.rm = TRUE)
  )

```

```

## # A tibble: 3 x 8
##   acro count na_cnt   min median   mean   max   IQR
##   <fct> <int>   <int> <int>   <dbl> <dbl> <int> <dbl>
## 1 nds     50     0    84    87 86.8    91  2.75
## 2 pfs     50     0     3     4  4.04     6   2
## 3 nfr     50     0     1     1  1.44     3   1

```

Kruskal–Wallis test illustrates evidence of statistical differences.

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

```

##
## Kruskal-Wallis rank sum test
##
## data: uni_str_pos by acro
## Kruskal-Wallis chi-squared = 133.91, df = 2, p-value < 2.2e-16

```

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

```

pairwise.wilcox.test(x = act_coverage$uni_str_pos, g = act_coverage$acro, p.adjust.method = "bonf",
                     paired = FALSE, conf.int = FALSE, alternative = 'l')

```

```

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

```

2.4 Satisfactory trait coverage over time

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

```

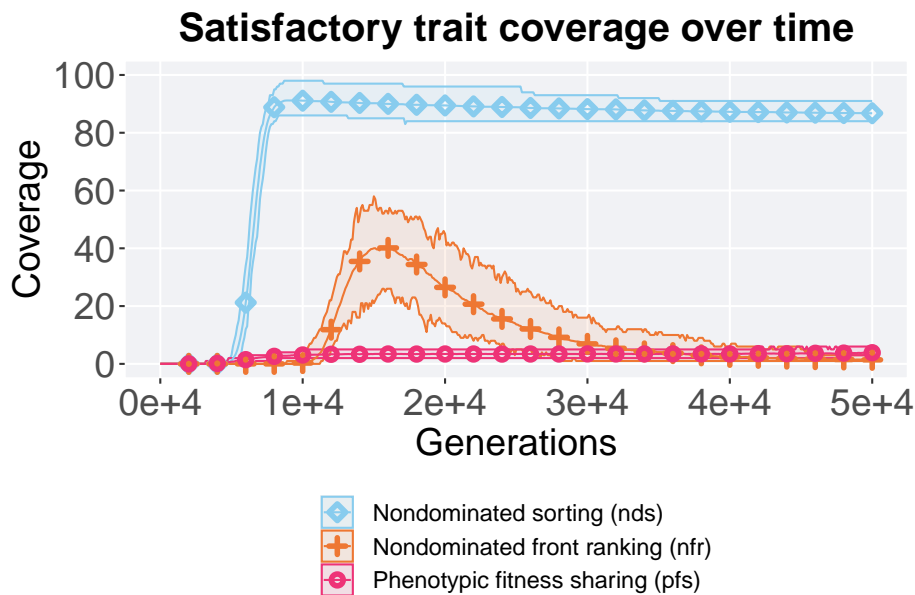
lines = over_time_df %>%
  group_by(scheme, gen) %>%

```

```
dplyr::summarise(
  min = min(pop_uni_obj),
  mean = mean(pop_uni_obj),
  max = max(pop_uni_obj)
)
```

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

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

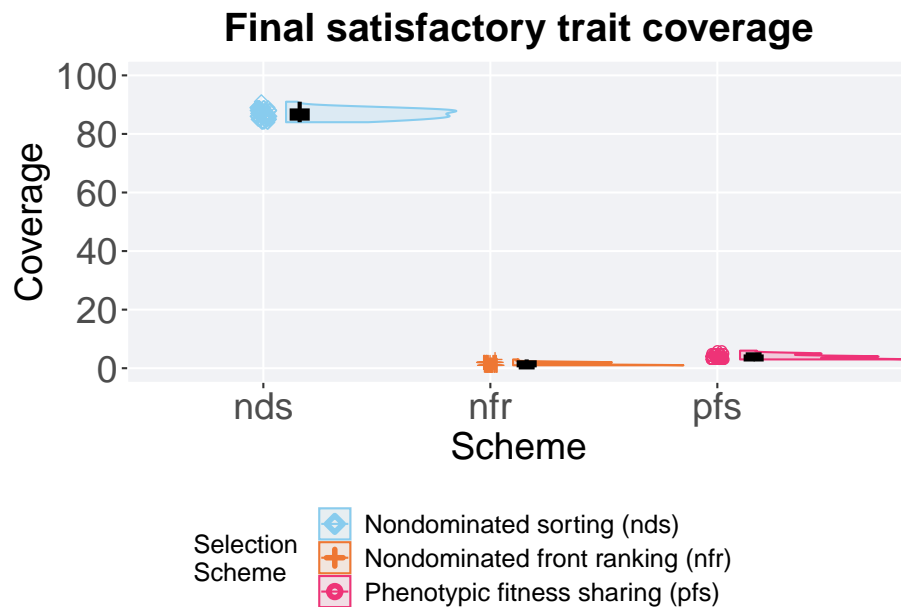


2.5 Final satisfactory trait coverage

Satisfactory trait coverage found in the final population at 50,000 generations.

```
plot = filter(over_time_df, gen == 50000) %>%
  ggplot(., aes(x = acro, y = pop_uni_obj, color = acro, fill = acro, shape = acro)) +
  geom_flat_violin(position = position_nudge(x = .1, y = 0), scale = 'width', alpha = 0.2, width
  geom_boxplot(color = 'black', width = .07, outlier.shape = NA, alpha = 0.0, size = 1.0, position
  geom_point(position = position_jitter(width = 0.03, height = 0.02), size = 2.0, alpha = 1.0) +
  scale_y_continuous(
    name="Coverage",
    limits=c(0, 100),
    breaks=seq(0,100, 20),
    labels=c("0", "20", "40", "60", "80", "100")
  ) +
  scale_x_discrete(
    name="Scheme"
  ) +
  scale_shape_manual(values=SHAPE) +
  scale_colour_manual(values = cb_palette, ) +
  scale_fill_manual(values = cb_palette) +
  ggtitle('Final satisfactory trait coverage') +
  p_theme
```

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



2.5.1 Stats

Summary statistics for the coverage found in the final population.

```
sat_coverage = filter(over_time_df, gen == 50000)
sat_coverage$acro = factor(sat_coverage$acro, levels = c('nds', 'pfs', 'nfr'))
sat_coverage %>%
  group_by(acro) %>%
  dplyr::summarise(
    count = n(),
    na_cnt = sum(is.na(pop_uni_obj)),
    min = min(pop_uni_obj, na.rm = TRUE),
    median = median(pop_uni_obj, na.rm = TRUE),
    mean = mean(pop_uni_obj, na.rm = TRUE),
    max = max(pop_uni_obj, na.rm = TRUE),
    IQR = IQR(pop_uni_obj, na.rm = TRUE)
  )
```



```
## # A tibble: 3 x 8
##   acro count na_cnt min median mean max IQR
##   <fct> <int> <int> <int> <dbl> <dbl> <int> <dbl>
## 1 nds     50      0    84     87 86.8    91  2.75
## 2 pfs     50      0      3      4  3.86     6   1
## 3 nfr     50      0      1      1  1.4      3   1
```

Kruskal-Wallis test illustrates evidence of statistical differences.

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

```
##
## Kruskal-Wallis rank sum test
##
## data: pop_uni_obj by acro
## Kruskal-Wallis chi-squared = 134.12, df = 2, p-value < 2.2e-16
```

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

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

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