Supplemental Material

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2021-02-27

Contents

Chapter 1

Introduction

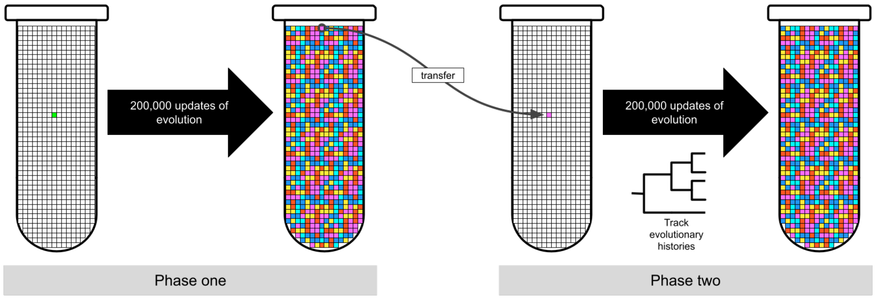

200,000 updates of evolution
transfer
200,000 updates of evolution
Track evolutionary histories
Phase one
Phase two

Figure 1.1: Experimental design overview

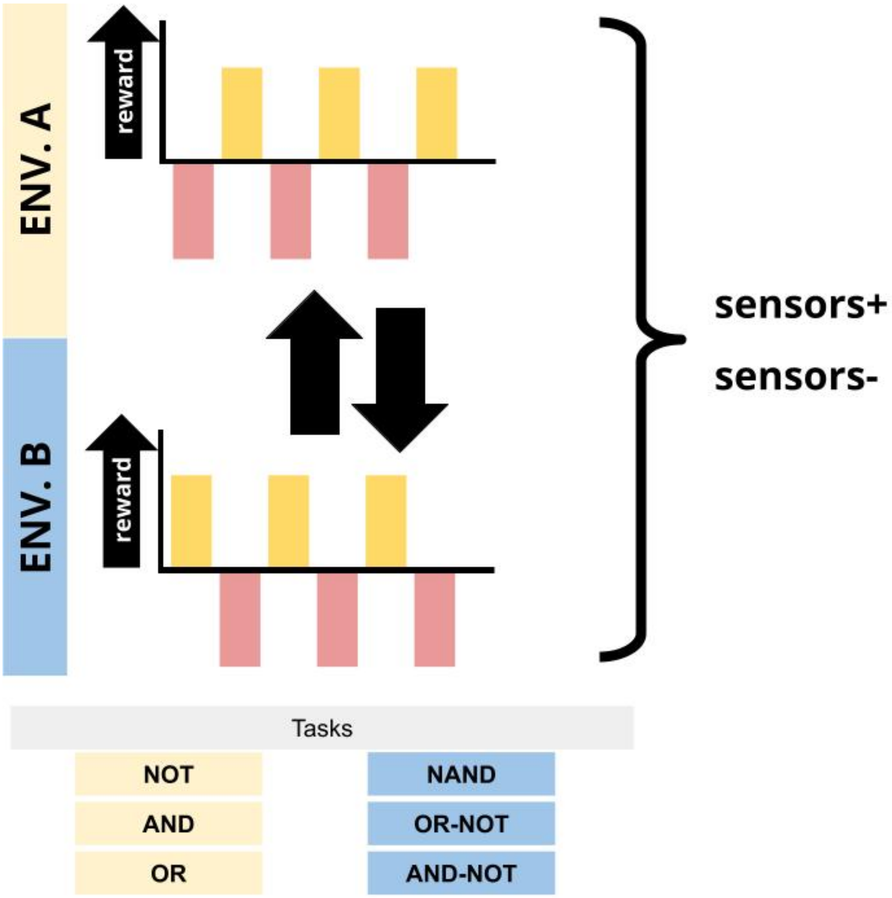


Figure 1.2: Fluctuating environment

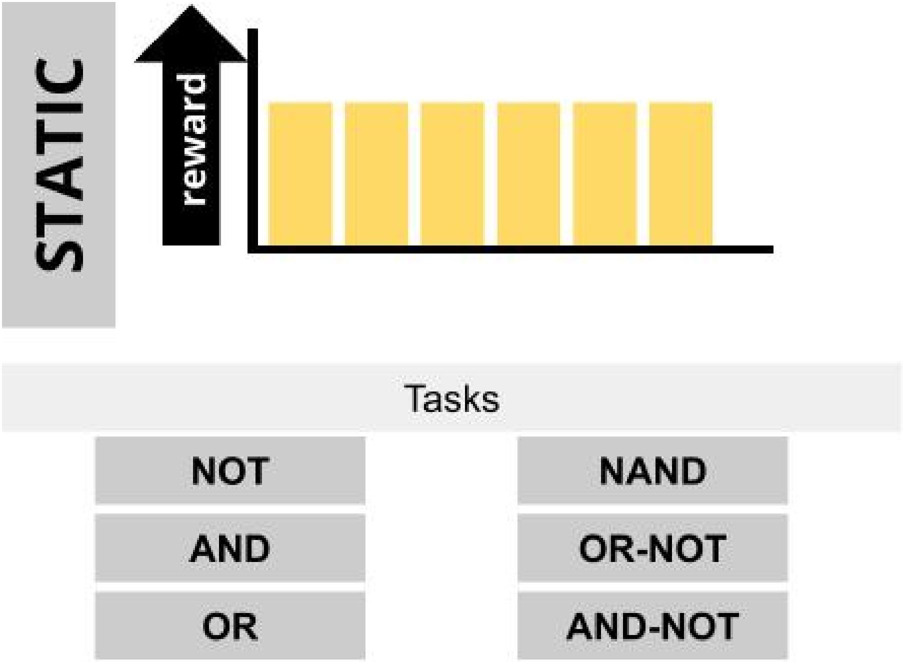


Figure 1.3: Static environment

Chapter 2

Validation experiment

In this experiment, we validate that (1) we observe the evolution of phenotypic plasticity in a changing environment when digital organisms have access to sensory instructions (capable of differentiating environmental states) and (2) that adaptive phenotypic plasticity does not evolve when populations lack access to sensory instructions.

2.1 Overview

```
total_updates <- 200000
replicates <- 100

all_traits <- c("not","nand","and","ornot","or","andnot")
traits_set_a <- c("not", "and", "or")
traits_set_b <- c("nand", "ornot", "andnot")

# Relative location of data.
working_directory <- "experiments/2021-01-07-validation/analysis/" # << For bookdown
# working_directory <- "./"                                              # << For local analysis
```

We evolved populations of digital organisms under four conditions:

1. A fluctuating environment with access to sensory instructions
2. A fluctuating environment without access to sensory instructions (i.e., sensory instructions are no-operations)
3. A constant environment with access to sensory instructions
4. A constant environment without access to sensory instructions

In fluctuating environments, we alternate between rewarding and punishing different sets of computational tasks. In one environment, we reward tasks not, and, or and punish tasks nand, ornot, andnot. In the alternative environment, we reward tasks nand, ornot, andnot and punish tasks not, and, or. In constant environments, we reward all tasks (not, nand, and, ornot, or, andnot).

For each replicate of each condition, we extract the dominant (i.e., most numerous) genotype at the end of the run to analyze further. We expect to observe the evolution of adaptive phenotypic plasticity in only the first experimental condition. In conditions without sensors, plasticity in any form should be unable to evolve.

2.2 Analysis dependencies

Load all required R libraries.

```
library(ggplot2)
library(tidyverse)
library(cowplot)
source("https://gist.githubusercontent.com/benmarwick/2a1bb0133ff568cbe28d/raw/fb53bd97
```

These analyses were conducted/knitted with 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          0.4
## year           2021
## month          02
## day            15
## svn rev        80002
## language       R
## version.string R version 4.0.4 (2021-02-15)
## nickname       Lost Library Book
```

2.3 Setup

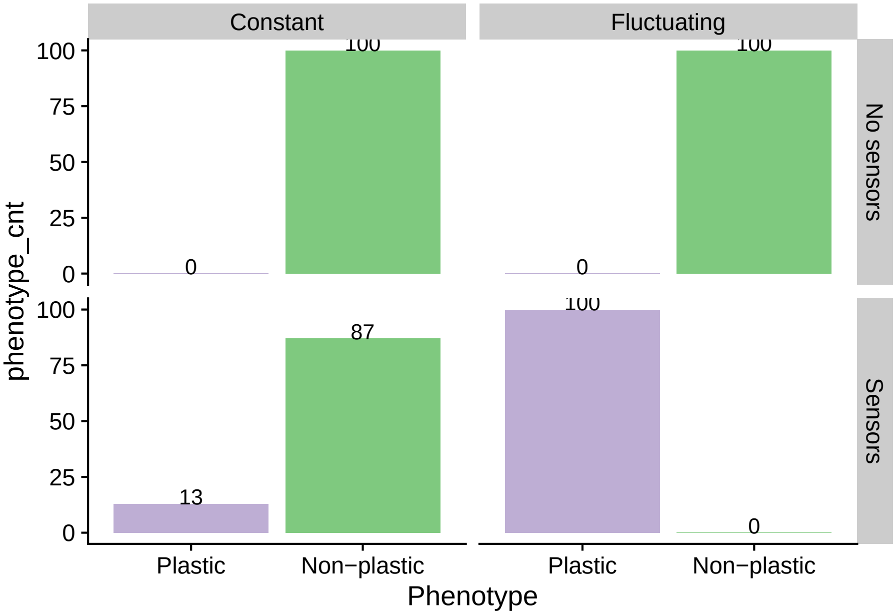
```
data_loc <- paste0(working_directory, "data/aggregate.csv")
data <- read.csv(data_loc, na.strings="NONE")

data$DISABLE_REACTION_SENSORS <- as.factor(data$DISABLE_REACTION_SENSORS)
```

```
data$chg_env <- as.factor(data$chg_env)
data$dom_plastic_odd_even <- as.factor(data$dom_plastic_odd_even)
data$sensors <- data$DISABLE_REACTION_SENSORS == "0"
data$is_plastic <- data$dom_plastic_odd_even == "True"

env_label_fun <- function(chg_env) {
  if (chg_env) {
    return("Fluctuating")
  } else {
    return("Constant")
  }
}

sensors_label_fun <- function(has_sensors) {
  if (has_sensors) {
    return("Sensors")
  } else {
    return("No sensors")
  }
}

# Count observed plasticity for each condition (I'm sure there's a 'tidier' way to do this..)
observed_plasticity <- data.frame(
  environment=character(),
  sensors=character(),
  plastic=integer(),
  nonplastic=integer(),
  plastic_adaptive=integer(),
  plastic_optimal=integer(),
  plastic_nonadaptive=integer()
)
for (env_chg in levels(data$chg_env)) {
  for (disabled_sensors in levels(data$DISABLE_REACTION_SENSORS)) {
    cond_data <- filter(data, chg_env == env_chg & data$DISABLE_REACTION_SENSORS == disabled_sens
    environment_label <- env_label_fun(env_chg)
    sensors_label <- sensors_label_fun(disabled_sensors == "0")

    observed_plasticity <- observed_plasticity %>% add_row(
      environment=environment_label,
      sensors=sensors_label,
      plastic=nrow(filter(cond_data, is_plastic==TRUE)),
      nonplastic=nrow(filter(cond_data, is_plastic==FALSE)),
      plastic_adaptive=nrow(filter(cond_data, dom_adaptive_plasticity=="True")),
      plastic_optimal=nrow(filter(cond_data, dom_optimal_plastic=="True")),
      plastic_nonadaptive=nrow(filter(cond_data, is_plastic==TRUE & dom_adaptive_plasticity=="Fal
    )
  }
}

observed_plasticity <- pivot_longer(
  observed_plasticity,
  cols=c("plastic", "plastic_adaptive", "plastic_optimal", "plastic_nonadaptive", "nonp
  names_to="phenotype",
  values_to="phenotype_cnt"
)

####### misc #######
# Configure our default graphing theme
theme_set(theme_cowplot())
```

2.4 Evolution of phenotypic plasticity

For each experimental condition, do we observe the evolution of phenotypic plasticity? To test for phenotypic plasticity, we culture digital organisms in both environments from the fluctuating condition (including organisms evolved in a constant environment). Any plasticity that we observe from digital organisms evolved under constant conditions is cryptic variation (as these organisms were never exposed to these culturing environments).

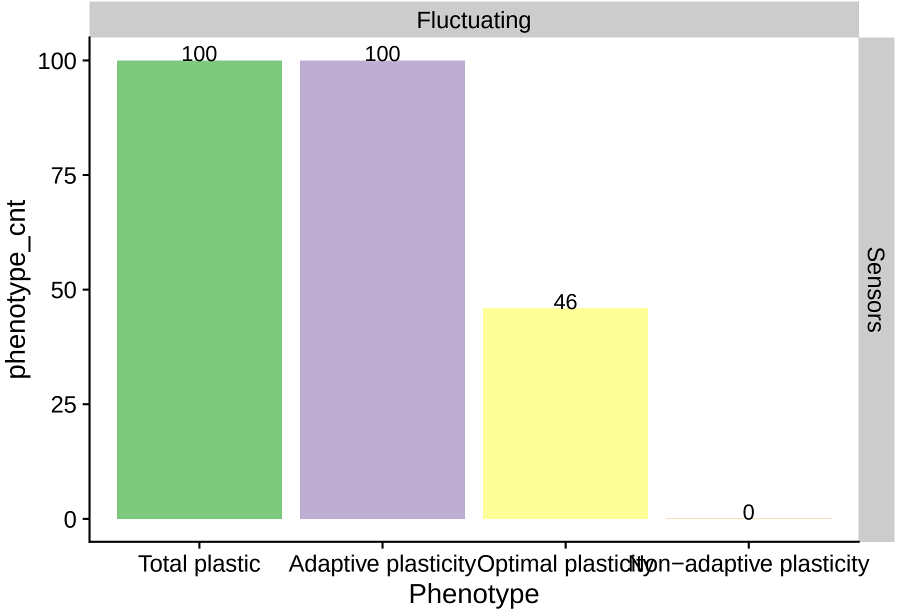
```
ggplot(filter(observed_plasticity, phenotype %in% c("plastic", "nonplastic")), aes(x=pl
  geom_bar(
    stat="identity",
    position=position_dodge(0.9)
  ) +
  geom_text(
    stat="identity",
    mapping=aes(label=phenotype_cnt),
    vjust=0.05
  ) +
  scale_fill_brewer(palette="Accent") +
  scale_x_discrete(
    name="Phenotype",
    limits=c("plastic", "nonplastic"),
    labels=c("Plastic", "Non-plastic")
  ) +
  facet_grid(sensors~environment) +
  theme(
    legend.position="none"
  )
```



Indeed, we do not observe the evolution of phenotypic plasticity in any replicates in which digital organisms do not have access to sensory instructions. We do observe the evolution of plasticity (not necessarily adaptive plasticity) in both constant and fluctuating environments where sensors are enabled.

To what extent is the observed phenotypic plasticity adaptive?

```
ggplot(filter(observed_plasticity, environment=="Fluctuating" & sensors == "Sensors" & phenotype
  geom_bar(
    stat="identity",
    position=position_dodge(0.9)
  ) +
  geom_text(
    stat="identity",
    mapping=aes(label=phenotype_cnt),
    vjust=0.05
  ) +
  scale_fill_brewer(palette="Accent") +
  scale_x_discrete(
    name="Phenotype",
    limits=c("plastic",  "plastic_adaptive", "plastic_optimal", "plastic_nonadaptive"),
    labels=c("Total plastic", "Adaptive plasticity", "Optimal plasticity", "Non-adaptive plastici
  ) +
  facet_grid(sensors~environment) +
  theme(
    legend.position="none"
)
```


Fluctuating
Sensors
phenotype_cnt
100
75
50
25
0
100
100
46
0
Total plastic
Adaptive plasticity
Optimal plasticity
Non−adaptive plasticity
Phenotype

Chapter 3

Evolutionary change

The effect of adaptive phenotypic plasticity on evolutionary change.

3.1 Overview

```
total_updates <- 200000
replicates <- 100

all_traits <- c("not","nand","and","ornot","or","andnot")
traits_set_a <- c("not", "and", "or")
traits_set_b <- c("nand", "ornot", "andnot")

# Relative location of data.
working_directory <- "experiments/2021-02-08-evo-dynamics/analysis/" # << For bookdown
# working_directory <- "./"                                               # << For local analysis
```

3.2 Analysis dependencies

Load all required R libraries.

```
library(ggplot2)
library(tidyverse)
library(cowplot)
library(RColorBrewer)
library(Hmisc)
library(boot)
source("https://gist.githubusercontent.com/benmarwick/2a1bb0133ff568cbe28d/raw/fb53bd97121f7f9ce9
```

These analyses were conducted/knitted with 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          0.4
## year           2021
## month          02
## day            15
## svn rev        80002
## language       R
## version.string R version 4.0.4 (2021-02-15)
## nickname       Lost Library Book
```

3.3 Setup

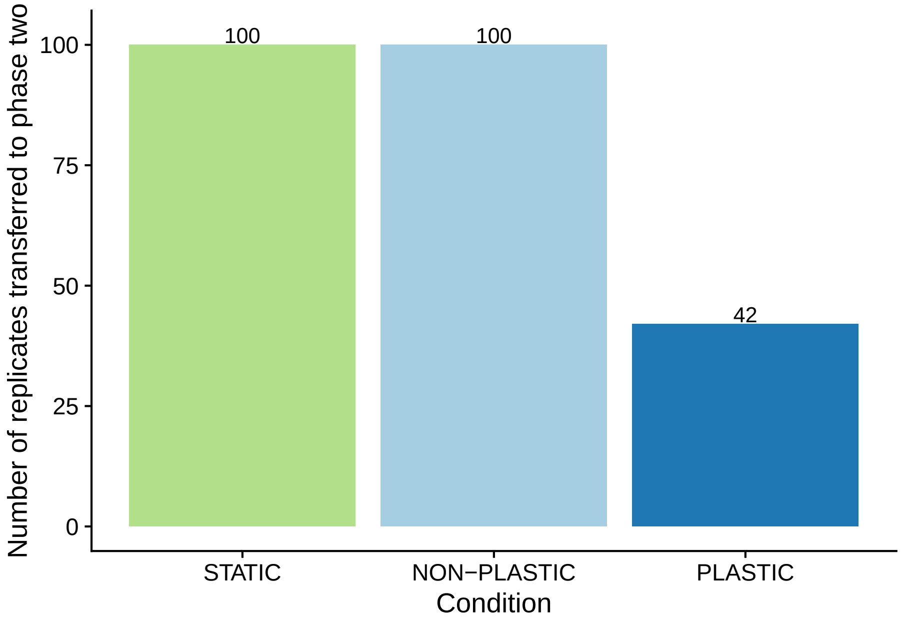
```
summary_data_loc <- paste0(working_directory, "data/aggregate.csv")
summary_data <- read.csv(summary_data_loc, na.strings="NONE")

summary_data$DISABLE_REACTION_SENSORS <- as.factor(summary_data$DISABLE_REACTION_SENSOR
summary_data$chg_env <- summary_data$chg_env == "True"
summary_data$dominant_plastic_odd_even <- as.factor(summary_data$dominant_plastic_odd_e
summary_data$sensors <- summary_data$DISABLE_REACTION_SENSORS == "0"
summary_data$is_plastic <- summary_data$dominant_plastic_odd_even == "True"

env_label_fun <- function(chg_env) {
  if (chg_env) {
    return("Fluctuating")
  } else {
    return("Constant")
  }
}

sensors_label_fun <- function(has_sensors) {
  if (has_sensors) {
    return("Sensors")
  } else {
    return("No sensors")
  }
```

```r
}

# note that this labeler makes assumptions about how we set up our experiment
condition_label_fun <- function(has_sensors, env_chg) {
  if (has_sensors && env_chg) {
    return("PLASTIC")
  } else if (env_chg) {
    return("NON-PLASTIC")
  } else {
    return("STATIC")
  }
}

summary_data$env_label <- mapply(
  env_label_fun,
  summary_data$chg_env
)
summary_data$sensors_label <- mapply(
  sensors_label_fun,
  summary_data$sensors
)
summary_data$condition <- mapply(
  condition_label_fun,
  summary_data$sensors,
  summary_data$chg_env
)

condition_order = c(
  "STATIC",
  "NON-PLASTIC",
  "PLASTIC"
)

####### misc #######
# Configure our default graphing theme
theme_set(theme_cowplot())
# Create a directory to store plots
dir.create(paste0(working_directory, "plots"), showWarnings=FALSE)
# Define sample mean function
samplemean <- function(x, d) {
  return(mean(x[d]))
}
```

3.4 The evolution of phenotypic plasticity

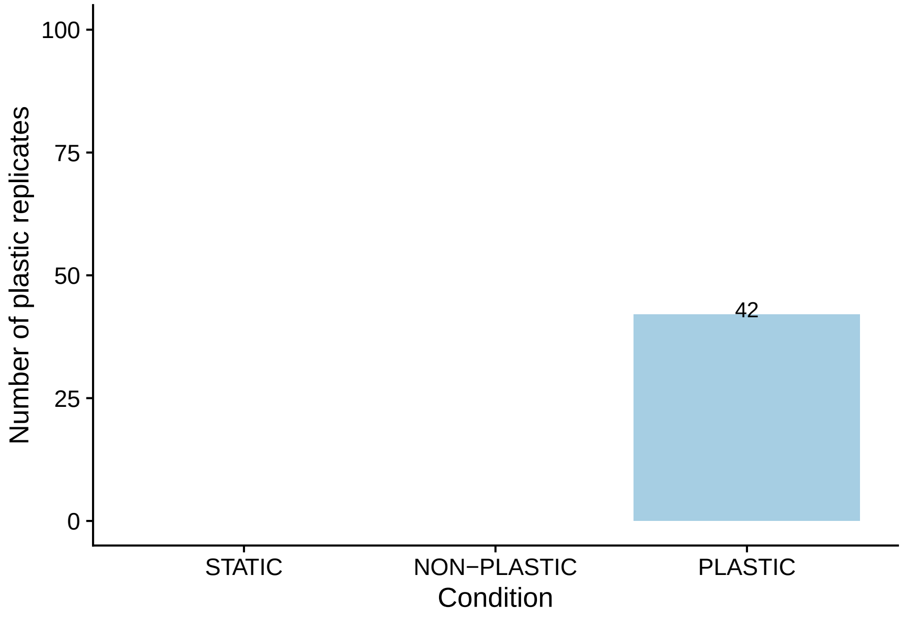
For sensor-enabled populations in fluctuating environments, we only transfered populations containing an optimally plastic genotype to phase-two.

```
summary_data_grouped = dplyr::group_by(summary_data, condition)
summary_data_group_counts = dplyr::summarize(summary_data_grouped, n=dplyr::n())

ggplot(summary_data_group_counts, aes(x=condition, y=n, fill=condition)) +
  geom_col(position=position_dodge(0.9)) +
  geom_text(aes(label=n, y=n+2)) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order
  ) +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  ylab("Number of replicates transferred to phase two") +
  theme(
    legend.position="none"
  )
```



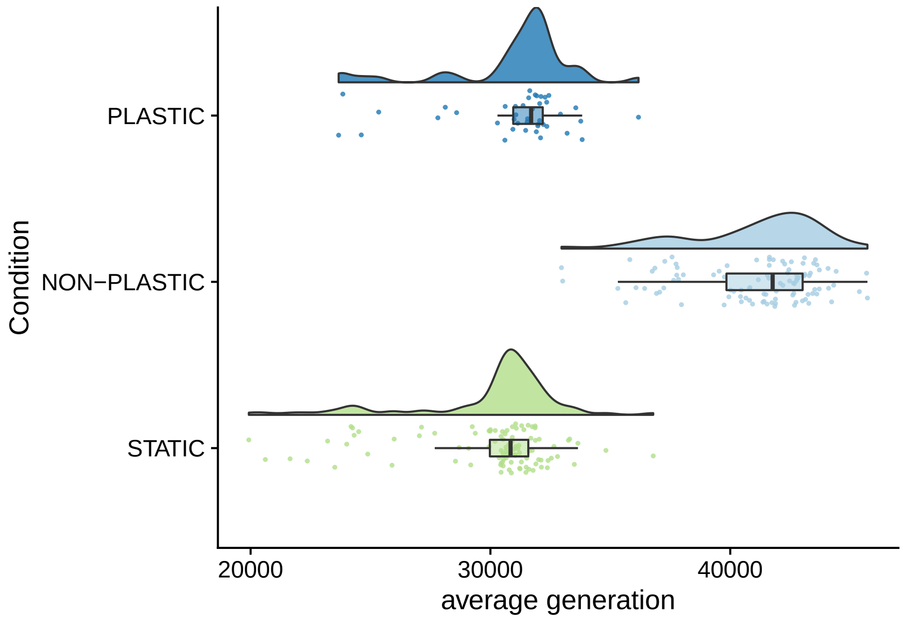
We can confirm our expectation that the dominant genotypes in non-plastic conditions are not phenotypically plastic.

```r
summary_data_grouped = dplyr::group_by(summary_data, condition, is_plastic)
summary_data_group_counts = dplyr::summarize(summary_data_grouped, n=dplyr::n())
ggplot(filter(summary_data_group_counts, is_plastic), aes(x=condition, y=n, fill=condition)) +
  geom_col(
    position=position_dodge(0.9)
  ) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order
  ) +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  geom_text(aes(label=n, y=n+1)) +
  ylab("Number of plastic replicates") +
  ylim(0, 100) +
  theme(
    legend.position="none"
  )
```



```r
ggplot(summary_data, aes(x=condition, y=time_average_generation, fill=condition)) +
  geom_flat_violin(
    position = position_nudge(x = .2, y = 0),
    alpha = .8
  ) +
  geom_point(
    mapping=aes(color=condition),
    position = position_jitter(width = .15),
    size = .5,
    alpha = 0.8
  ) +
  geom_boxplot(
    width = .1,
    outlier.shape = NA,
    alpha = 0.5
  ) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order
  ) +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  coord_flip() +
  ylab("average generation") +
  theme(
    legend.position="none"
  ) +
  ggsave(paste0(working_directory, "plots/", "average-generation.png"))
```

```
## Saving 6.5 x 4.5 in image
```



```
paste0(
  "PLASTIC median: ",
  median(filter(summary_data, condition=="PLASTIC")$time_average_generation)
)
```

```
## [1] "PLASTIC median: 31697.65"
```

```
paste0(
  "STATIC median: ",
  median(filter(summary_data, condition=="STATIC")$time_average_generation)
)
```

```
## [1] "STATIC median: 30839.75"
```

```
paste0(
  "NON-PLASTIC median: ",
  median(filter(summary_data, condition=="NON-PLASTIC")$time_average_generation)
)
```

```
## [1] "NON-PLASTIC median: 41768.65"
```

```
kruskal.test(
  formula=time_average_generation~condition,
  data=summary_data
)
```

```
##
##  Kruskal-Wallis rank sum test
```

```
##
## data:  time_average_generation by condition
## Kruskal-Wallis chi-squared = 177.33, df = 2, p-value < 2.2e-16
```

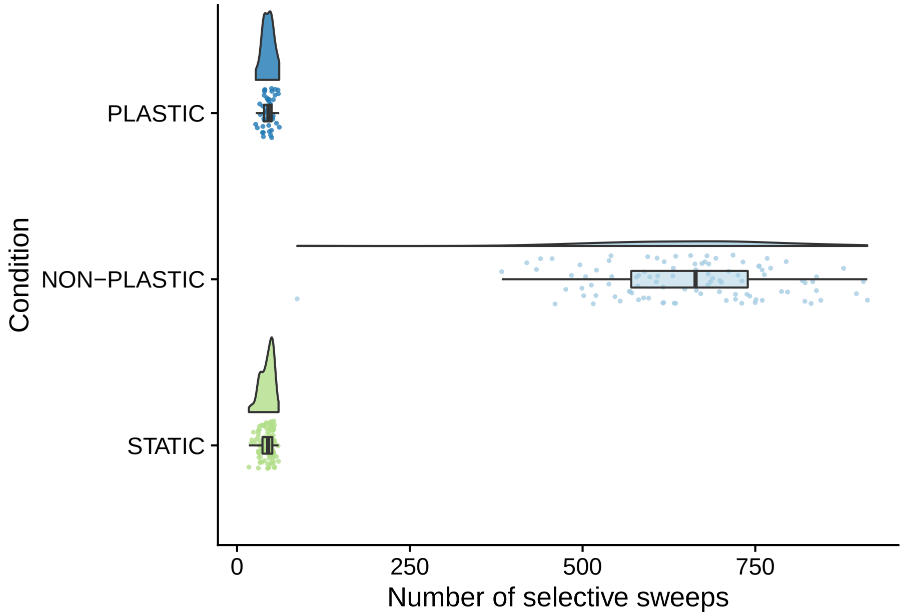
```
pairwise.wilcox.test(
  x=summary_data$time_average_generation,
  g=summary_data$condition,
  p.adjust.method="bonferroni",
)
```

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  summary_data$time_average_generation and summary_data$condition
##
##         NON-PLASTIC PLASTIC
## PLASTIC <2e-16      -
## STATIC  <2e-16      0.004
##
## P value adjustment method: bonferroni
```

3.6 Selective sweeps

The number of times the most recent common ancestor changes gives us the number of selective sweeps that occur during the experiment.

```
ggplot(summary_data, aes(x=condition, y=phylo_mrca_changes, fill=condition)) +
  geom_flat_violin(
    position = position_nudge(x = .2, y = 0),
    alpha = .8
  ) +
  geom_point(
    mapping=aes(color=condition),
    position = position_jitter(width = .15),
    size = .5,
    alpha = 0.8
  ) +
  geom_boxplot(
    width = .1,
    outlier.shape = NA,
    alpha = 0.5
  ) +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  coord_flip() +
  scale_x_discrete(
    name="Condition",
    limits=condition_order
  ) +
  ylab("Number of selective sweeps") +
  theme(
    legend.position="none"
  )
```



```
paste0(
  "PLASTIC: ",
  median(filter(summary_data, condition=="PLASTIC")$phylo_mrca_changes)
)
```

```
## [1] "PLASTIC: 45.5"
```

```
paste0(
  "STATIC: ",
  median(filter(summary_data, condition=="STATIC")$phylo_mrca_changes)
)
```

```
## [1] "STATIC: 45"
```

```
paste0(
  "NON-PLASTIC: ",
  median(filter(summary_data, condition=="NON-PLASTIC")$phylo_mrca_changes)
)
```

```
## [1] "NON-PLASTIC: 663.5"
```

```
kruskal.test(
  formula=phylo_mrca_changes~condition,
  data=summary_data
)
```

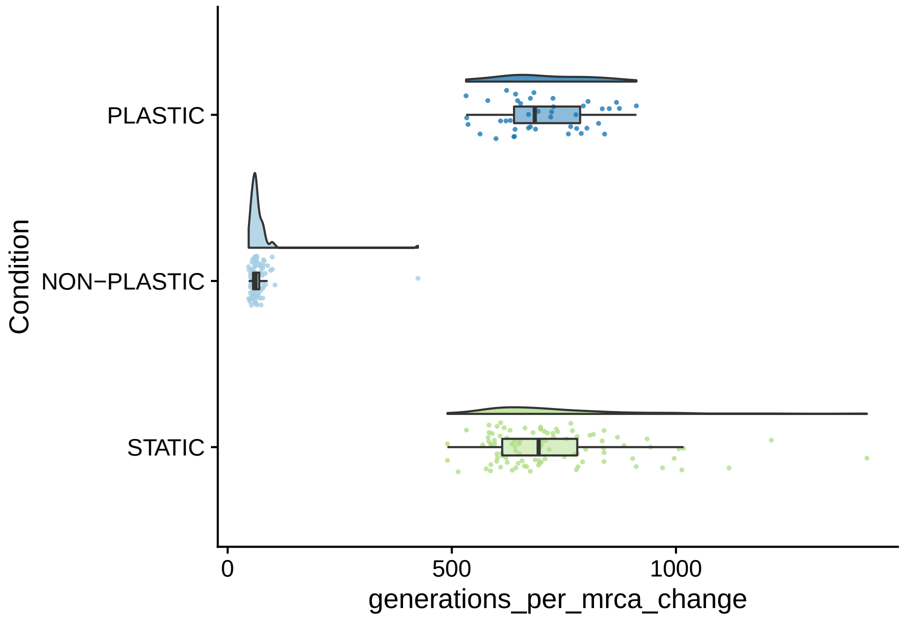
```
##
##  Kruskal-Wallis rank sum test
##
## data:  phylo_mrca_changes by condition
## Kruskal-Wallis chi-squared = 175.46, df = 2, p-value < 2.2e-16
```

```
pairwise.wilcox.test(
  x=summary_data$phylo_mrca_changes,
  g=summary_data$condition,
  p.adjust.method="bonferroni",
)
```

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  summary_data$phylo_mrca_changes and summary_data$condition
##
##         NON-PLASTIC PLASTIC
## PLASTIC <2e-16      -
## STATIC  <2e-16      1
##
## P value adjustment method: bonferroni
```

3.6.1 Average number of generations between selective sweeps

```
summary_data$generations_per_mrca_change <- summary_data$time_average_generation / summ

ggplot(summary_data, aes(x=condition, y=generations_per_mrca_change, fill=condition)) +
  geom_flat_violin(
    position = position_nudge(x = .2, y = 0),
    alpha = .8
  ) +
  geom_point(
    mapping=aes(color=condition),
    position = position_jitter(width = .15),
    size = .5,
    alpha = 0.8
  ) +
  geom_boxplot(
    width = .1,
    outlier.shape = NA,
    alpha = 0.5
  ) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order
  ) +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  coord_flip() +
  theme(
    legend.position="none"
  )
```



```
paste0(
  "PLASTIC: ",
  median(filter(summary_data, condition=="PLASTIC")$generations_per_mrca_change)
)
```

```
## [1] "PLASTIC: 685.001780758557"
```

```
paste0(
  "STATIC: ",
  median(filter(summary_data, condition=="STATIC")$generations_per_mrca_change)
)
```

```
## [1] "STATIC: 693.676265008576"
```

```
paste0(
  "NON-PLASTIC: ",
  median(filter(summary_data, condition=="NON-PLASTIC")$generations_per_mrca_change)
)
```

```
## [1] "NON-PLASTIC: 62.0184902295191"
```

```
kruskal.test(
  formula=generations_per_mrca_change~condition,
  data=summary_data
)
```

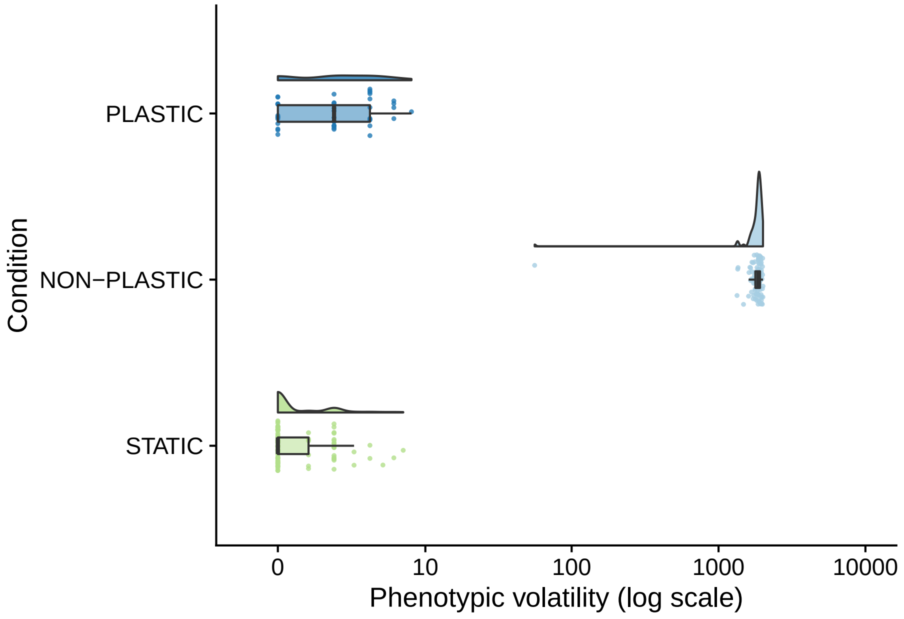
```
##
##  Kruskal-Wallis rank sum test
##
## data:  generations_per_mrca_change by condition
## Kruskal-Wallis chi-squared = 175.33, df = 2, p-value < 2.2e-16
```

```
pairwise.wilcox.test(
  x=summary_data$generations_per_mrca_change,
  g=summary_data$condition,
  p.adjust.method="bonferroni",
)
```

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  summary_data$generations_per_mrca_change and summary_data$condition
##
##         NON-PLASTIC PLASTIC
## PLASTIC <2e-16      -
## STATIC  <2e-16      1
##
## P value adjustment method: bonferroni
```

3.7 Phenotypic volatility along the dominant lineage

```
ggplot(summary_data, aes(x=condition, y=dominant_lineage_trait_volatility, fill=condition)) +
  geom_flat_violin(
    position = position_nudge(x = .2, y = 0),
    alpha = .8
  ) +
  geom_point(
    mapping=aes(color=condition),
    position = position_jitter(width = .15),
    size = .5,
    alpha = 0.8
  ) +
  geom_boxplot(
    width = .1,
    outlier.shape = NA,
    alpha = 0.5
  ) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order
  ) +
  scale_y_continuous(
    name="Phenotypic volatility (log scale)",
    trans="pseudo_log",
    breaks=c(0, 10, 100, 1000, 10000),
    limits=c(-1,10000)
  ) +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  coord_flip() +
  theme(
    legend.position="none"
  )
```



```r
paste0(
  "PLASTIC: ",
  median(filter(summary_data, condition=="PLASTIC")$dominant_lineage_trait_volatility)
)
```

```
## [1] "PLASTIC: 2"
```

```r
paste0(
  "STATIC: ",
  median(filter(summary_data, condition=="STATIC")$dominant_lineage_trait_volatility)
)
```

```
## [1] "STATIC: 0"
```

```r
paste0(
  "NON-PLASTIC: ",
  median(filter(summary_data, condition=="NON-PLASTIC")$dominant_lineage_trait_volatil
)
```

```
## [1] "NON-PLASTIC: 1868"
```

```r
kruskal.test(
  formula=dominant_lineage_trait_volatility~condition,
  data=summary_data
)
```

```
##
##  Kruskal-Wallis rank sum test
```

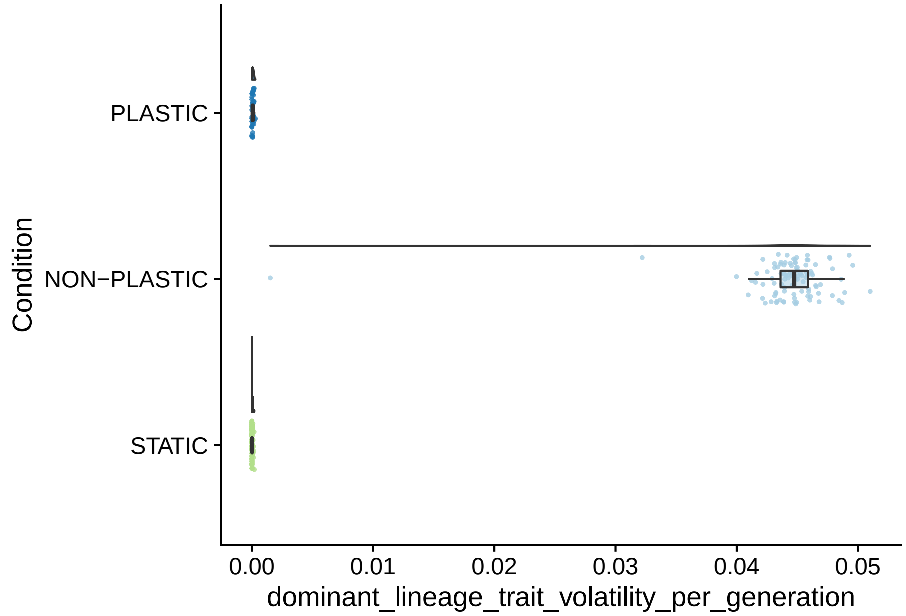
```
##
## data:  dominant_lineage_trait_volatility by condition
## Kruskal-Wallis chi-squared = 190.78, df = 2, p-value < 2.2e-16
```

```
pairwise.wilcox.test(
  x=summary_data$dominant_lineage_trait_volatility,
  g=summary_data$condition,
  p.adjust.method="bonferroni",
)
```

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  summary_data$dominant_lineage_trait_volatility and summary_data$condition
##
##         NON-PLASTIC PLASTIC
## PLASTIC < 2e-16     -
## STATIC  < 2e-16     8.7e-07
##
## P value adjustment method: bonferroni
```

3.7.1 Phenotypic volatility normalized by generations elapsed

```
summary_data$dominant_lineage_trait_volatility_per_generation <- summary_data$dominant_lineage_tr

ggplot(summary_data, aes(x=condition, y=dominant_lineage_trait_volatility_per_generation, fill=co
  geom_flat_violin(
    position = position_nudge(x = .2, y = 0),
    alpha = .8
  ) +
  geom_point(
    mapping=aes(color=condition),
    position = position_jitter(width = .15),
    size = .5,
    alpha = 0.8
  ) +
  geom_boxplot(
    width = .1,
    outlier.shape = NA,
    alpha = 0.5
  ) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order
  ) +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  coord_flip() +
  theme(
    legend.position="none"
  )
```



```
paste0(
  "PLASTIC: ",
  median(filter(summary_data, condition=="PLASTIC")$dominant_lineage_trait_volatility_p
)
```

```
## [1] "PLASTIC: 6.33339279717772e-05"
```

```
paste0(
  "STATIC: ",
  median(filter(summary_data, condition=="STATIC")$dominant_lineage_trait_volatility_pe
)
```

```
## [1] "STATIC: 0"
```

```
paste0(
  "NON-PLASTIC: ",
  median(filter(summary_data, condition=="NON-PLASTIC")$dominant_lineage_trait_volatility_per_gen
)
```

```
## [1] "NON-PLASTIC: 0.0447440145638177"
```

```
kruskal.test(
  formula=dominant_lineage_trait_volatility_per_generation~condition,
  data=summary_data
)
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  dominant_lineage_trait_volatility_per_generation by condition
## Kruskal-Wallis chi-squared = 189.62, df = 2, p-value < 2.2e-16
```

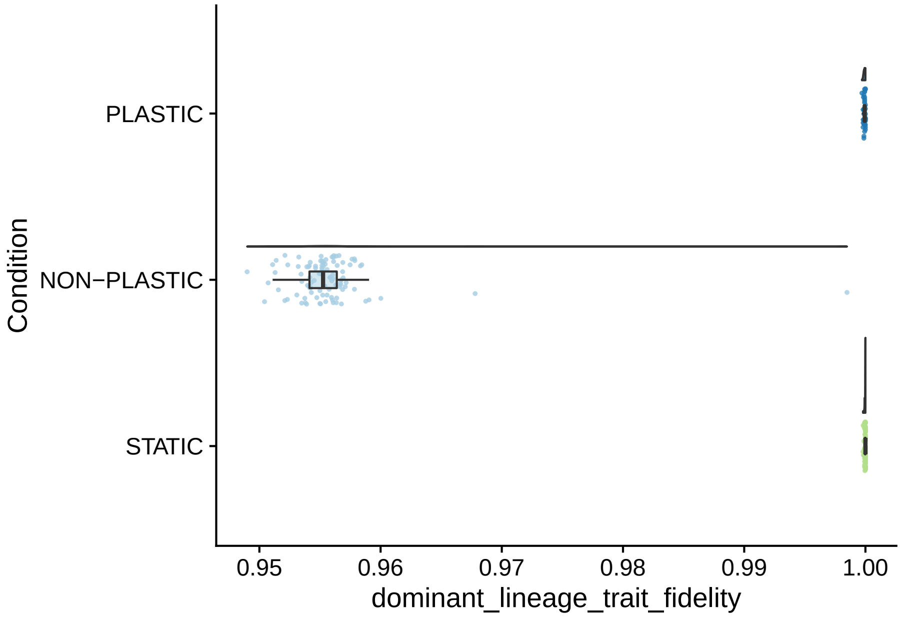
```
pairwise.wilcox.test(
  x=summary_data$dominant_lineage_trait_volatility_per_generation,
  g=summary_data$condition,
  p.adjust.method="bonferroni",
)
```

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  summary_data$dominant_lineage_trait_volatility_per_generation and summary_data$conditio
##
##         NON-PLASTIC PLASTIC
## PLASTIC < 2e-16     -
## STATIC  < 2e-16     4.2e-06
##
## P value adjustment method: bonferroni
```

3.7.2 Phenotypic fidelity

Frequency that an offspring's genotype is identical to a parent genotype (along the dominant lineage).

```
summary_data$dominant_lineage_trait_fidelity <- (summary_data$dominant_generation_born - summary_

ggplot(summary_data, aes(x=condition, y=dominant_lineage_trait_fidelity, fill=condition)) +
  geom_flat_violin(
    position = position_nudge(x = .2, y = 0),
    alpha = .8
  ) +
  geom_point(
    mapping=aes(color=condition),
    position = position_jitter(width = .15),
    size = .5,
    alpha = 0.8
  ) +
  geom_boxplot(
    width = .1,
    outlier.shape = NA,
    alpha = 0.5
  ) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order
  ) +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  coord_flip() +
  theme(
    legend.position="none"
  )
```



```r
paste0(
  "PLASTIC: ",
  median(filter(summary_data, condition=="PLASTIC")$dominant_lineage_trait_fidelity)
)
```

```
## [1] "PLASTIC: 0.999936666072028"
```

```r
paste0(
  "STATIC: ",
  median(filter(summary_data, condition=="STATIC")$dominant_lineage_trait_fidelity)
)
```

```
## [1] "STATIC: 1"
```

```r
paste0(
  "NON-PLASTIC: ",
  median(filter(summary_data, condition=="NON-PLASTIC")$dominant_lineage_trait_fidelity)
)
```

```
## [1] "NON-PLASTIC: 0.955255985436182"
```

```r
kruskal.test(
  formula=dominant_lineage_trait_fidelity~condition,
  data=summary_data
)
```

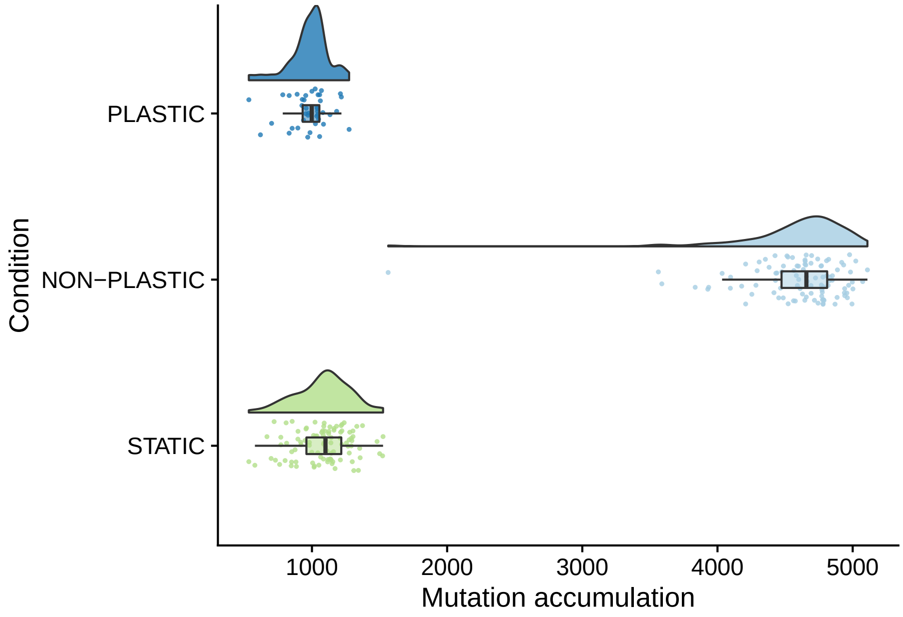
```
##
##  Kruskal-Wallis rank sum test
##
## data:  dominant_lineage_trait_fidelity by condition
## Kruskal-Wallis chi-squared = 189.62, df = 2, p-value < 2.2e-16
```

```r
pairwise.wilcox.test(
  x=summary_data$dominant_lineage_trait_fidelity,
  g=summary_data$condition,
  p.adjust.method="bonferroni",
)
```

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  summary_data$dominant_lineage_trait_fidelity and summary_data$condition
##
##         NON-PLASTIC PLASTIC
## PLASTIC < 2e-16     -
## STATIC  < 2e-16     4.2e-06
##
## P value adjustment method: bonferroni
```

3.8 Mutation accumulation along the dominant lineage

```
ggplot(summary_data, aes(x=condition, y=dominant_lineage_total_mut_cnt, fill=condition)
  geom_flat_violin(
    position = position_nudge(x = .2, y = 0),
    alpha = .8
  ) +
  geom_point(
    mapping=aes(color=condition),
    position = position_jitter(width = .15),
    size = .5,
    alpha = 0.8
  ) +
  geom_boxplot(
    width = .1,
    outlier.shape = NA,
    alpha = 0.5
  ) +
  ylab("Mutation accumulation") +
  scale_x_discrete(
    name="Condition",
    limits=condition_order
  ) +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  coord_flip() +
  theme(
    legend.position="none"
  )
```



```r
paste0(
  "PLASTIC: ",
  median(filter(summary_data, condition=="PLASTIC")$dominant_lineage_total_mut_cnt)
)
```

```
## [1] "PLASTIC: 998.5"
```

```r
paste0(
  "STATIC: ",
  median(filter(summary_data, condition=="STATIC")$dominant_lineage_total_mut_cnt)
)
```

```
## [1] "STATIC: 1100"
```

```r
paste0(
  "NON-PLASTIC: ",
  median(filter(summary_data, condition=="NON-PLASTIC")$dominant_lineage_total_mut_cnt)
)
```

```
## [1] "NON-PLASTIC: 4657.5"
```

```r
kruskal.test(
  formula=dominant_lineage_total_mut_cnt~condition,
  data=summary_data
)
```

```
##
##  Kruskal-Wallis rank sum test
```

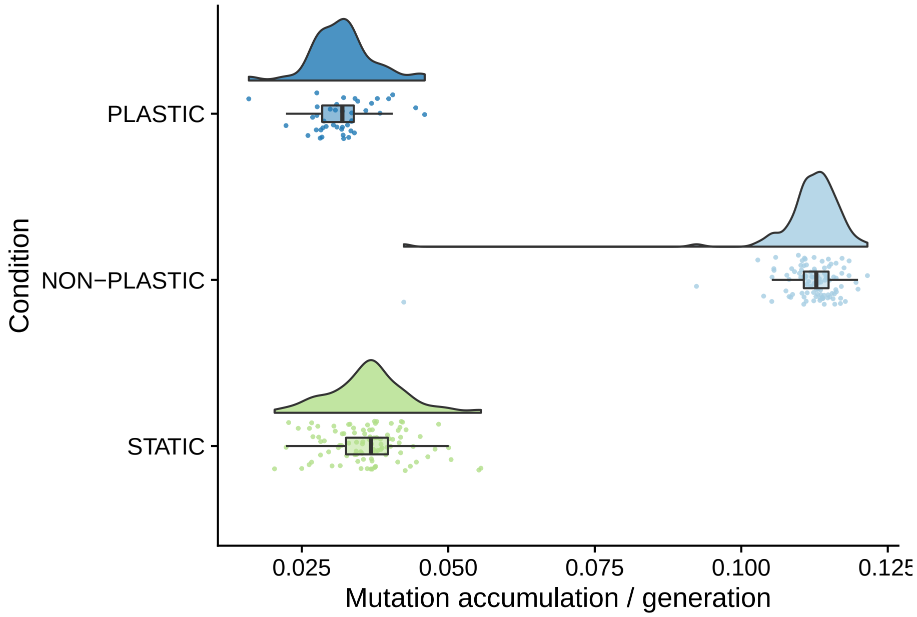
```
##
## data:  dominant_lineage_total_mut_cnt by condition
## Kruskal-Wallis chi-squared = 179.33, df = 2, p-value < 2.2e-16
```

```
pairwise.wilcox.test(
  x=summary_data$dominant_lineage_total_mut_cnt,
  g=summary_data$condition,
  p.adjust.method="bonferroni",
)
```

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  summary_data$dominant_lineage_total_mut_cnt and summary_data$condition
##
##         NON-PLASTIC PLASTIC
## PLASTIC <2e-16      -
## STATIC  <2e-16      0.0019
##
## P value adjustment method: bonferroni
```

3.8.1 Mutation accumulation normalized by generations elapsed

```
summary_data$mutations_per_generation <- summary_data$dominant_lineage_total_mut_cnt /

ggplot(summary_data, aes(x=condition, y=mutations_per_generation, fill=condition)) +
  geom_flat_violin(
    position = position_nudge(x = .2, y = 0),
    alpha = .8
  ) +
  geom_point(
    mapping=aes(color=condition),
    position = position_jitter(width = .15),
    size = .5,
    alpha = 0.8
  ) +
  geom_boxplot(
    width = .1,
    outlier.shape = NA,
    alpha = 0.5
  ) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order
  ) +
  ylab("Mutation accumulation / generation") +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  coord_flip() +
  theme(
    legend.position="none"
  )
```



```
paste0(
  "PLASTIC: ",
  median(filter(summary_data, condition=="PLASTIC")$mutations_per_generation)
)
```

```
## [1] "PLASTIC: 0.0319267181456982"
```

```
paste0(
  "STATIC: ",
  median(filter(summary_data, condition=="STATIC")$mutations_per_generation)
)
```

```
## [1] "STATIC: 0.0368157192941933"
```

```
paste0(
  "NON-PLASTIC: ",
  median(filter(summary_data, condition=="NON-PLASTIC")$mutations_per_generation)
)
```

```
## [1] "NON-PLASTIC: 0.112804526786948"
```

```
kruskal.test(
  formula=mutations_per_generation~condition,
  data=summary_data
)
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  mutations_per_generation by condition
## Kruskal-Wallis chi-squared = 180.11, df = 2, p-value < 2.2e-16
```

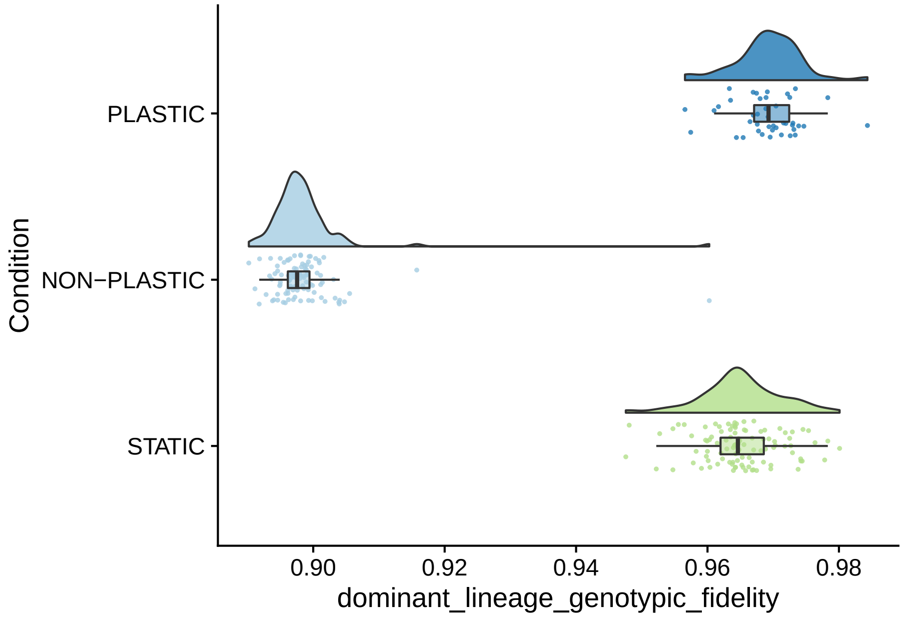
```
pairwise.wilcox.test(
  x=summary_data$mutations_per_generation,
  g=summary_data$condition,
  p.adjust.method="bonferroni",
)
```

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  summary_data$mutations_per_generation and summary_data$condition
##
##         NON-PLASTIC PLASTIC
## PLASTIC <2e-16      -
## STATIC  <2e-16      2e-04
##
## P value adjustment method: bonferroni
```

3.8.2 Genotypic fidelity

The frequency that an offspring's genotype is the same as a parent's genotype.

```
summary_data$dominant_lineage_genotypic_fidelity <- (summary_data$dominant_generation_l

ggplot(summary_data, aes(x=condition, y=dominant_lineage_genotypic_fidelity, fill=condi
  geom_flat_violin(
    position = position_nudge(x = .2, y = 0),
    alpha = .8
  ) +
  geom_point(
    mapping=aes(color=condition),
    position = position_jitter(width = .15),
    size = .5,
    alpha = 0.8
  ) +
  geom_boxplot(
    width = .1,
    outlier.shape = NA,
    alpha = 0.5
  ) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order
  ) +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  coord_flip() +
  theme(
    legend.position="none"
  )
```



```r
paste0(
  "PLASTIC: ",
  median(filter(summary_data, condition=="PLASTIC")$dominant_lineage_genotypic_fidelity
)
```

```
## [1] "PLASTIC: 0.969286906891951"
```

```r
paste0(
  "STATIC: ",
  median(filter(summary_data, condition=="STATIC")$dominant_lineage_genotypic_fidelity)
)
```

```
## [1] "STATIC: 0.964620594632577"
```

```r
paste0(
  "NON-PLASTIC: ",
  median(filter(summary_data, condition=="NON-PLASTIC")$dominant_lineage_genotypic_fide
)
```

```
## [1] "NON-PLASTIC: 0.89754902563783"
```

```r
kruskal.test(
  formula=dominant_lineage_genotypic_fidelity~condition,
  data=summary_data
)
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  dominant_lineage_genotypic_fidelity by condition
## Kruskal-Wallis chi-squared = 179.86, df = 2, p-value < 2.2e-16
```

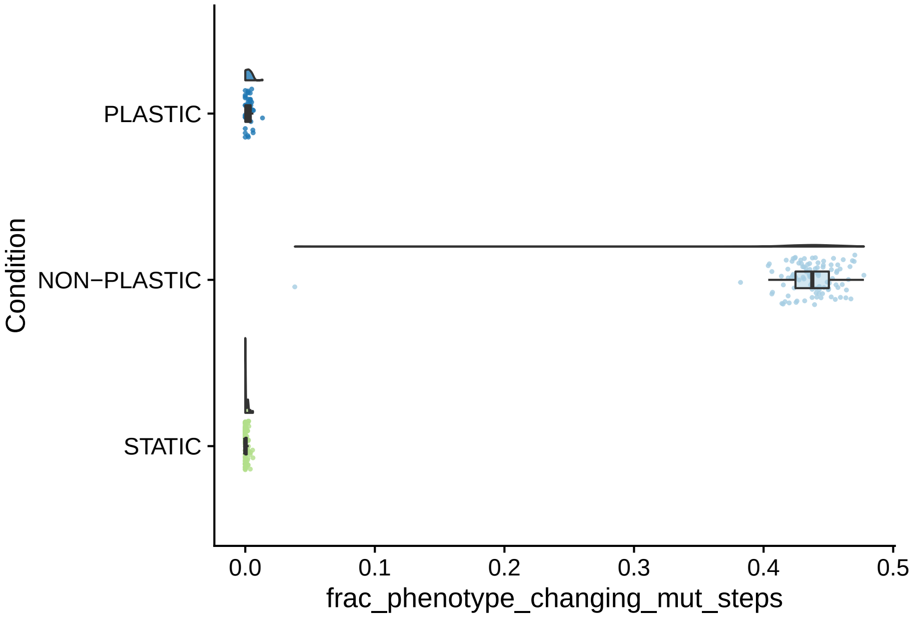
```r
pairwise.wilcox.test(
  x=summary_data$dominant_lineage_genotypic_fidelity,
  g=summary_data$condition,
  p.adjust.method="bonferroni",
)
```

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  summary_data$dominant_lineage_genotypic_fidelity and summary_data$condition
##
##         NON-PLASTIC PLASTIC
## PLASTIC <2e-16      -
## STATIC  <2e-16      2e-04
##
## P value adjustment method: bonferroni
```

3.9 Characterizing variation along dominant lineages

```
summary_data$frac_phenotype_changing_mut_steps <- summary_data$dominant_lineage_num_mut_steps_tha
ggplot(summary_data, aes(x=condition, y=frac_phenotype_changing_mut_steps, fill=condition)) +
  geom_flat_violin(
    position = position_nudge(x = .2, y = 0),
    alpha = .8
  ) +
  geom_point(
    mapping=aes(color=condition),
    position = position_jitter(width = .15),
    size = .5,
    alpha = 0.8
  ) +
  geom_boxplot(
    width = .1,
    outlier.shape = NA,
    alpha = 0.5
  ) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order
  ) +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  coord_flip() +
  theme(
    legend.position="none"
  ) +
  ggsave(paste0(working_directory, "plots/", "frac_phenotype_changing_mutational_steps.png"))
```

```
## Saving 6.5 x 4.5 in image
```



```
paste0(
  "PLASTIC: ",
  median(filter(summary_data, condition=="PLASTIC")$frac_phenotype_changing_mut_steps)
)
```

```
## [1] "PLASTIC: 0.00224941742616098"
```

```
paste0(
  "STATIC: ",
  median(filter(summary_data, condition=="STATIC")$frac_phenotype_changing_mut_steps)
)
```

```
## [1] "STATIC: 0"
```

```
paste0(
  "NON-PLASTIC: ",
  median(filter(summary_data, condition=="NON-PLASTIC")$frac_phenotype_changing_mut_ste
)
```

```
## [1] "NON-PLASTIC: 0.437583018324547"
```

```
kruskal.test(
  formula=frac_phenotype_changing_mut_steps~condition,
  data=summary_data
)
```

```
##
##  Kruskal-Wallis rank sum test
```

```
##
## data:  frac_phenotype_changing_mut_steps by condition
## Kruskal-Wallis chi-squared = 191.23, df = 2, p-value < 2.2e-16
```

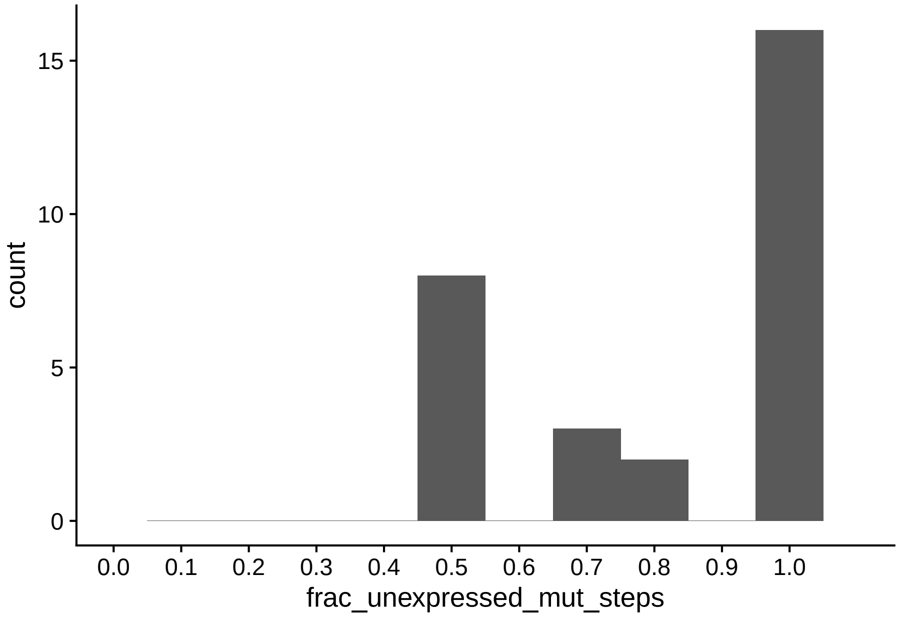
```
pairwise.wilcox.test(
  x=summary_data$frac_phenotype_changing_mut_steps,
  g=summary_data$condition,
  p.adjust.method="bonferroni",
)
```

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  summary_data$frac_phenotype_changing_mut_steps and summary_data$condition
##
##         NON-PLASTIC PLASTIC
## PLASTIC < 2e-16     -
## STATIC  < 2e-16     2.3e-07
##
## P value adjustment method: bonferroni
```

3.9.2 For PLASTIC populations, what fraction of phenotype-altering mutations occurred in the

```
summary_data$frac_unexpressed_mut_steps <- summary_data$dominant_lineage_num_mut_steps_that_chang
summary_data$frac_expressed_mut_steps <- summary_data$dominant_lineage_num_mut_steps_that_change_

ggplot(filter(summary_data, condition=="PLASTIC" & dominant_lineage_num_mut_steps_that_change_agg
  geom_histogram(binwidth=0.1) +
  scale_x_continuous(
    limits=c(0, 1.1),
    breaks=seq(0, 1.0, 0.1)
  ) +
  theme(
    legend.position="none"
  )
```

```
## Warning: Removed 2 rows containing missing values (geom_bar).
```



```
print(paste0("PLASTIC - Mean with bootstrapped 95% CI"))
```

```
## [1] "PLASTIC - Mean with bootstrapped 95% CI"
```

```
bo <- boot(filter(summary_data, condition=="PLASTIC" & dominant_lineage_num_mut_steps_
print(bo)
```

```
##
## ORDINARY NONPARAMETRIC BOOTSTRAP
##
##
## Call:
## boot(data = filter(summary_data, condition == "PLASTIC" & dominant_lineage_num_mut_
##     0)$frac_unexpressed_mut_steps, statistic = samplemean, R = 10000)
##
##
## Bootstrap Statistics :
##      original      bias    std. error
## t1* 0.8247126 0.000641954  0.04028272
```

```
print(boot.ci(bo, conf=0.95, type="perc"))
```

```
## BOOTSTRAP CONFIDENCE INTERVAL CALCULATIONS
## Based on 10000 bootstrap replicates
##
## CALL :
## boot.ci(boot.out = bo, conf = 0.95, type = "perc")
```

```
##
## Intervals :
## Level     Percentile
## 95%   ( 0.7443,  0.9023 )
## Calculations and Intervals on Original Scale
```

```
plastic_summary_data <- filter(summary_data, condition=="PLASTIC")
aggregate_frac_mut_steps_that_change_unexpressed_phenotype <- sum(plastic_summary_data$dominant_l
sum(plastic_summary_data$dominant_lineage_num_mut_steps_that_change_unexpressed_phenotype)
```

```
## [1] 83
```

```
sum(plastic_summary_data$dominant_lineage_num_mut_steps_that_change_aggregate_phenotype)
```

```
## [1] 102
```

```
aggregate_frac_mut_steps_that_change_unexpressed_phenotype
```

```
## [1] 0.8137255
```

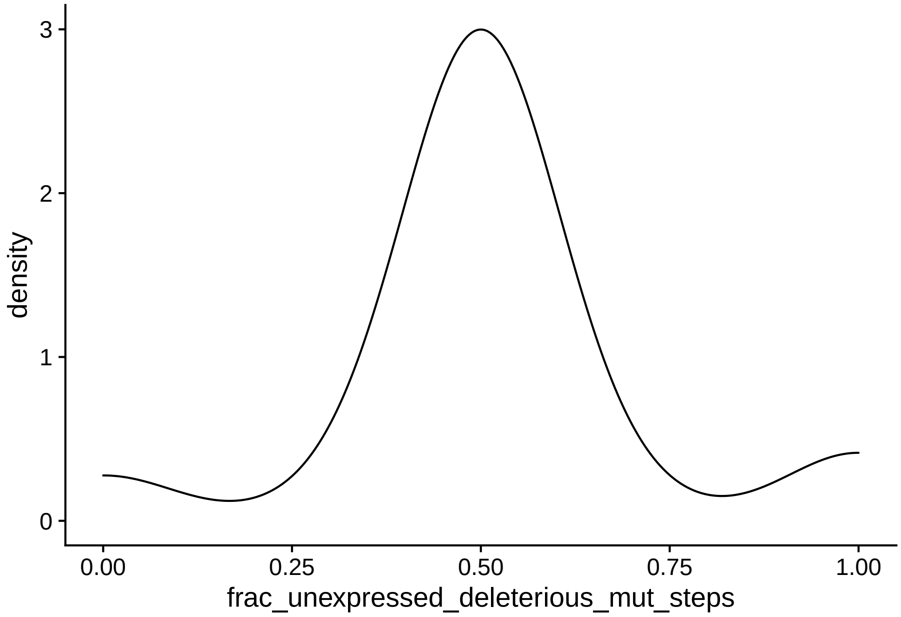
83 / 102 (0.8137255)

3.9.3 For PLASTIC populations, what fraction of mutations that affect the unexpressed phenotype are deleterious versus beneficial?

```
aggregate_frac_unexpressed_deleterious_mut_steps <- sum(plastic_summary_data$dominant_lineage_num
aggregate_frac_unexpressed_beneficial_mut_steps <- sum(plastic_summary_data$dominant_lineage_num_
```

3.9.3.1 Deleterious mutations

```
summary_data$frac_unexpressed_deleterious_mut_steps <- summary_data$dominant_lineage_num_mut_step
ggplot(
  filter(summary_data, condition=="PLASTIC" & dominant_lineage_num_mut_steps_that_change_unexpres
  aes(x=frac_unexpressed_deleterious_mut_steps)
  ) +
  geom_density() +
  theme(
    legend.position="none"
  )
```



```
bo <- boot(filter(summary_data, condition=="PLASTIC" & dominant_lineage_num_mut_steps_
print(bo)
```

```
##
## ORDINARY NONPARAMETRIC BOOTSTRAP
##
##
## Call:
## boot(data = filter(summary_data, condition == "PLASTIC" & dominant_lineage_num_mut_s
##     0)$frac_unexpressed_deleterious_mut_steps, statistic = samplemean,
##     R = 10000)
##
##
## Bootstrap Statistics :
##      original      bias    std. error
## t1* 0.5172414 0.000305977  0.03987936
```

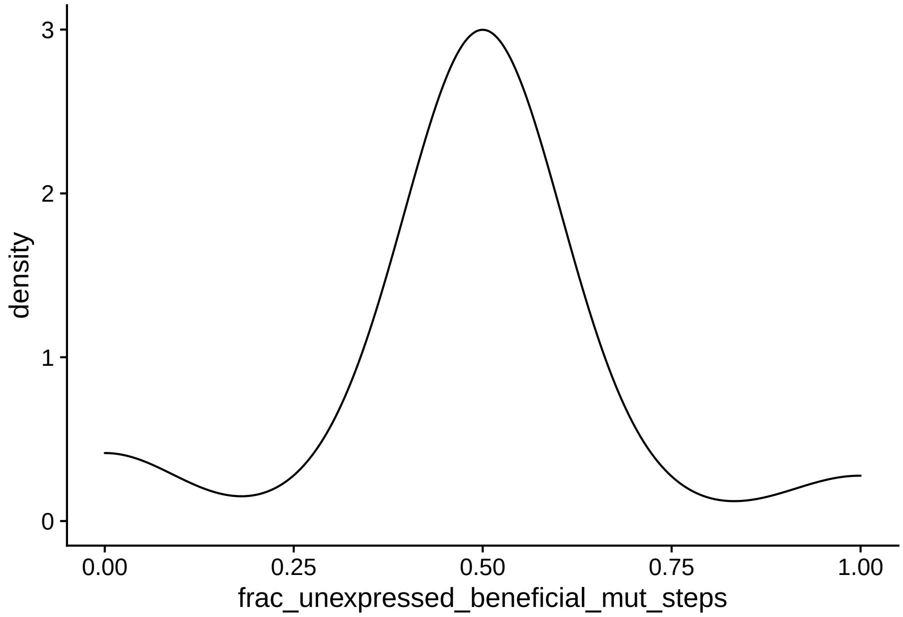
```
print(boot.ci(bo, conf=0.95, type="perc"))
```

```
## BOOTSTRAP CONFIDENCE INTERVAL CALCULATIONS
## Based on 10000 bootstrap replicates
##
## CALL :
## boot.ci(boot.out = bo, conf = 0.95, type = "perc")
##
## Intervals :
```

```
## Level     Percentile
## 95%   ( 0.4402,  0.5966 )
## Calculations and Intervals on Original Scale
```

3.9.3.2 Beneficial mutations

```
summary_data$frac_unexpressed_beneficial_mut_steps <- summary_data$dominant_lineage_num_mut_steps

ggplot(
  filter(summary_data, condition=="PLASTIC" & dominant_lineage_num_mut_steps_that_change_unexpres
  aes(x=frac_unexpressed_beneficial_mut_steps)
  ) +
  geom_density() +
  theme(
    legend.position="none"
  )
```



```
bo <- boot(filter(summary_data, condition=="PLASTIC" & dominant_lineage_num_mut_steps_that_change
print(bo)
```

```
##
## ORDINARY NONPARAMETRIC BOOTSTRAP
##
##
## Call:
```

```
## boot(data = filter(summary_data, condition == "PLASTIC" & dominant_lineage_num_mut_
##     0)$frac_unexpressed_beneficial_mut_steps, statistic = samplemean,
##     R = 10000)
##
##
## Bootstrap Statistics :
##      original       bias    std. error
## t1* 0.4827586 0.0002496552  0.03981286
```

```
print(boot.ci(bo, conf=0.95, type="perc"))
```

```
## BOOTSTRAP CONFIDENCE INTERVAL CALCULATIONS
## Based on 10000 bootstrap replicates
##
## CALL :
## boot.ci(boot.out = bo, conf = 0.95, type = "perc")
##
## Intervals :
## Level     Percentile
## 95%   ( 0.4034,  0.5609 )
## Calculations and Intervals on Original Scale
```

3.10 Manuscript figures

Figures styled for the paper.

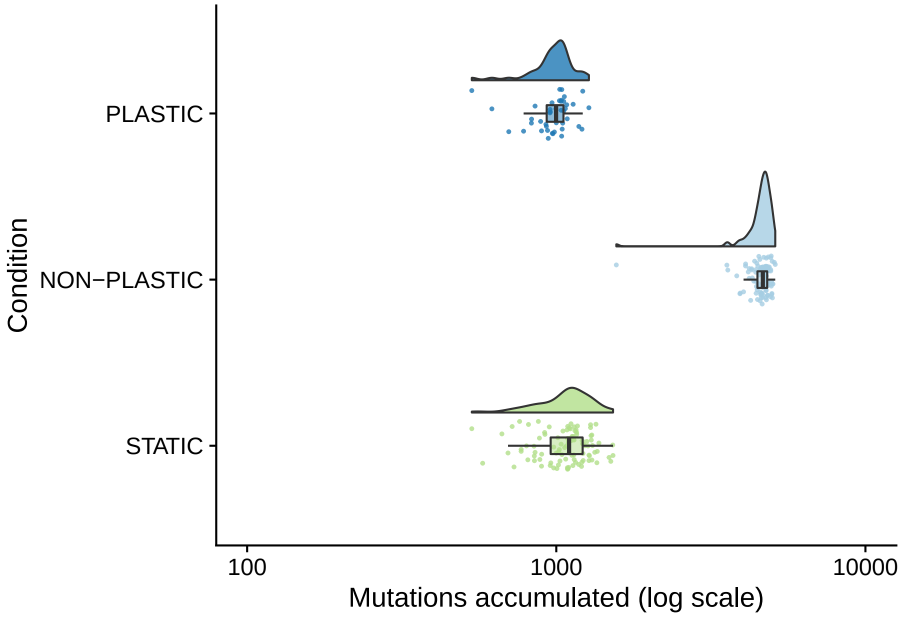
3.10.1 Total evolutionary change

Selective sweeps, mutation accumulation, phenotypic volatility.

3.10.1.1 Total mutation accumulation

```
mutation_count_fig <- ggplot(
    summary_data,
    aes(x=condition, y=dominant_lineage_total_mut_cnt, fill=condition)
  ) +
  geom_flat_violin(
    position = position_nudge(x = .2, y = 0),
    alpha = .8
  ) +
  geom_point(
    mapping=aes(color=condition),
    position = position_jitter(width = .15),
    size = .5,
    alpha = 0.8
  ) +
```

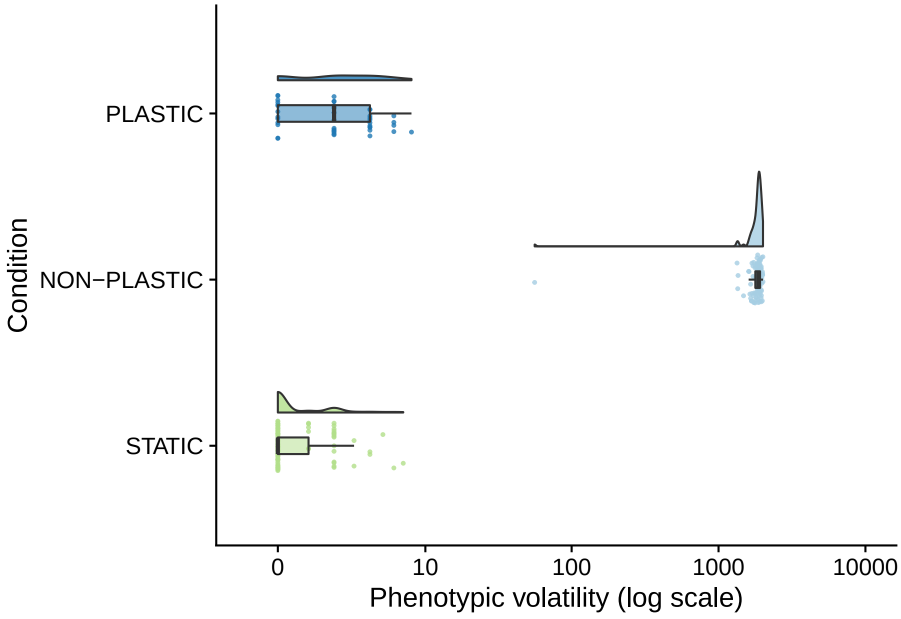
```r
  geom_boxplot(
    width = .1,
    outlier.shape = NA,
    alpha = 0.5
  ) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order,
    labels=condition_order
  ) +
  scale_y_continuous(
    name="Mutations accumulated (log scale)",
    trans="log10",
    breaks=c(100, 1000, 10000),
    limits=c(100, 10000)
  ) +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  coord_flip() +
  theme(
    legend.position="none"
  ) +
  ggsave(
    paste0(working_directory, "plots/", "mutation-accumulation.pdf"),
    width=5,
    height=4
  )
mutation_count_fig
```



3.10.1.2 Phenotypic volatility

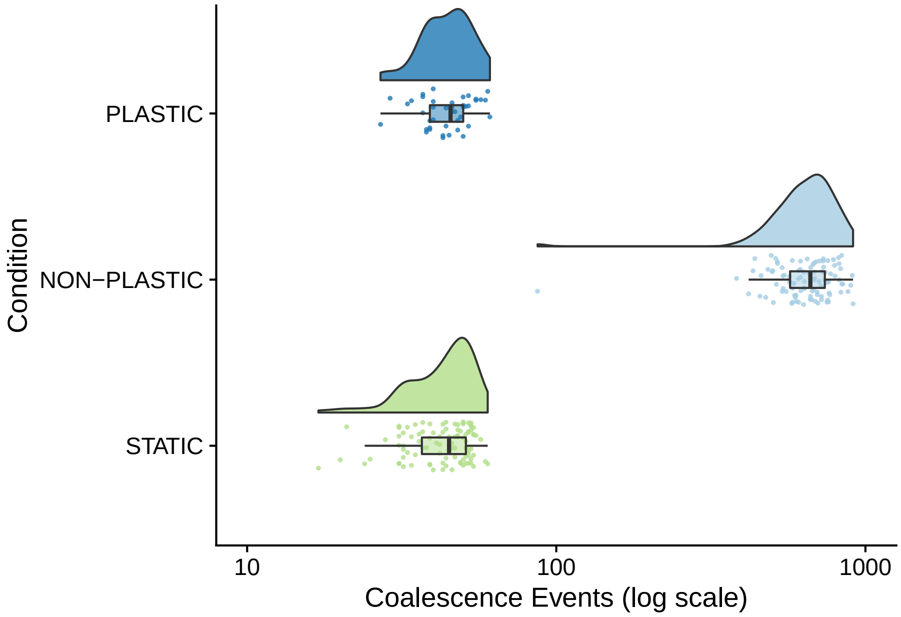
```
phenotypic_volatility_fig <- ggplot(
    summary_data,
    aes(x=condition, y=dominant_lineage_trait_volatility, fill=condition)
  ) +
  geom_flat_violin(
    position = position_nudge(x = .2, y = 0),
    alpha = .8
  ) +
  geom_point(
    mapping=aes(color=condition),
    position = position_jitter(width = .15),
    size = .5,
    alpha = 0.8
  ) +
  geom_boxplot(
    width = .1,
    outlier.shape = NA,
    alpha = 0.5
  ) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order,
```

```r
    labels=condition_order
  ) +
  scale_y_continuous(
    name="Phenotypic volatility (log scale)",
    trans="pseudo_log",
    breaks=c(0, 10, 100, 1000, 10000),
    limits=c(-1,10000)
  ) +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  coord_flip() +
  theme(
    legend.position="none"
  ) +
  ggsave(
    paste0(working_directory, "plots/", "phenotypic-volatility.pdf"),
    width=4,
    height=4
  )

phenotypic_volatility_fig
```



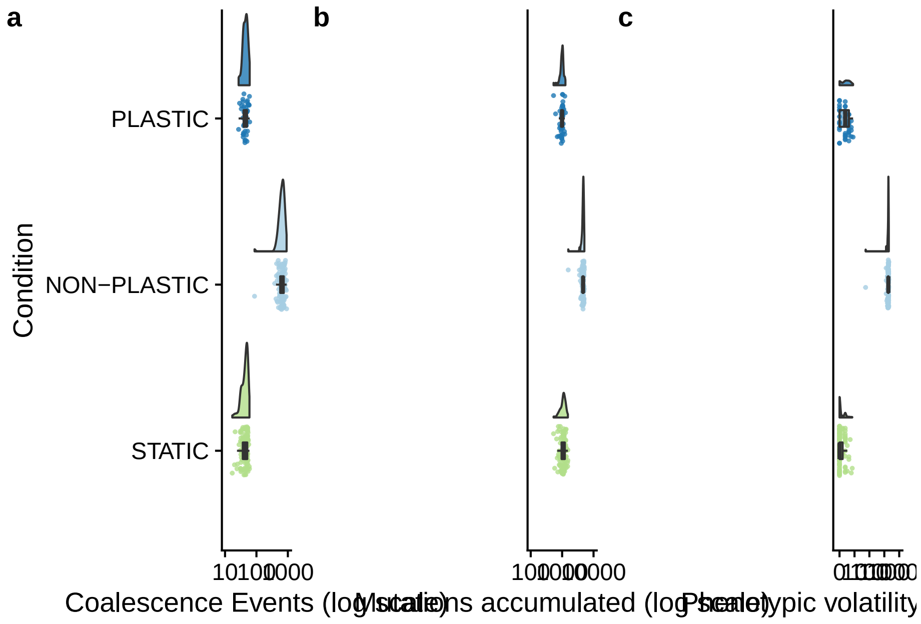
3.10.1.3 Coalescence events

```
selective_sweeps_fig <- ggplot(
    summary_data,
    aes(x=condition, y=phylo_mrca_changes, fill=condition)
  ) +
  geom_flat_violin(
    position = position_nudge(x = .2, y = 0),
    alpha = .8
  ) +
  geom_point(
    mapping=aes(color=condition),
    position = position_jitter(width = .15),
    size = .5,
    alpha = 0.8
  ) +
  geom_boxplot(
    width = .1,
    outlier.shape = NA,
    alpha = 0.5
  ) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order,
    labels=condition_order
  ) +
  scale_y_continuous(
    name="Coalescence Events (log scale)",
    trans="log10",
    breaks=c(10, 100, 1000),
    limits=c(10, 1000)
  ) +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  coord_flip() +
  theme(
    legend.position="none"
  ) +
  ggsave(
    paste0(working_directory, "plots/", "selective-sweeps.pdf"),
    width=4,
    height=4
  )

selective_sweeps_fig
```



3.10.1.4 Combined

```
grid <- plot_grid(
  selective_sweeps_fig + theme(
    legend.position="none"
  ),
  mutation_count_fig + theme(
    legend.position="none",
    axis.ticks.y=element_blank(),
    axis.text.y=element_blank(),
    axis.title.y=element_blank()
  ),
  phenotypic_volatility_fig + theme(
    legend.position="none",
    axis.ticks.y=element_blank(),
    axis.text.y=element_blank(),
    axis.title.y=element_blank()
  ),
  nrow=1,
  align="v",
  labels="auto"
)
grid
```

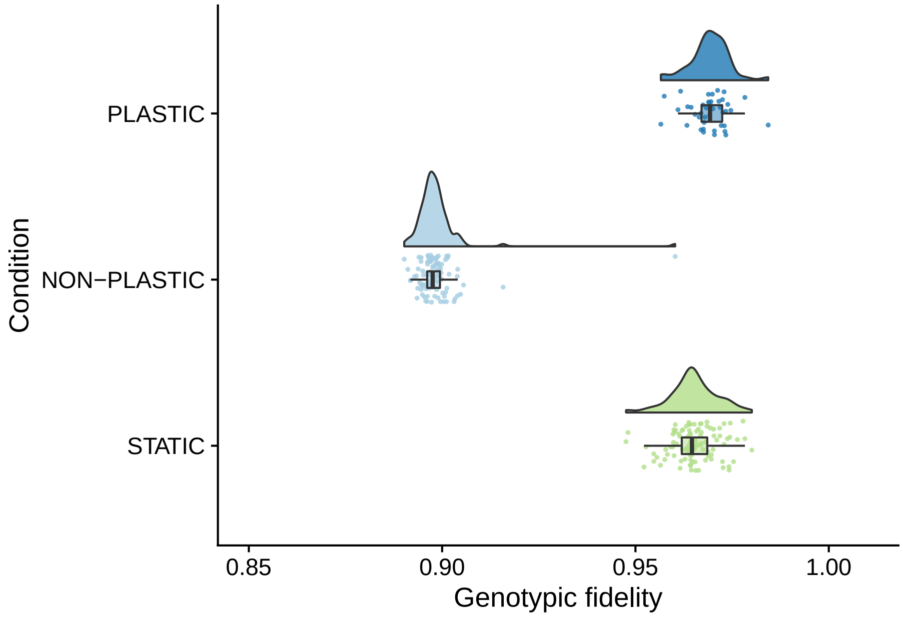


```
save_plot(
   paste0(working_directory, "plots/", "evolutionary-dynamics.pdf"),
   grid,
   base_height=6,
   base_asp=2.5
)
save_plot(
   paste0(working_directory, "plots/", "evolutionary-dynamics.png"),
   grid,
   base_height=6,
   base_asp=2.5
)
```

3.10.2 Rate of evolutionary change

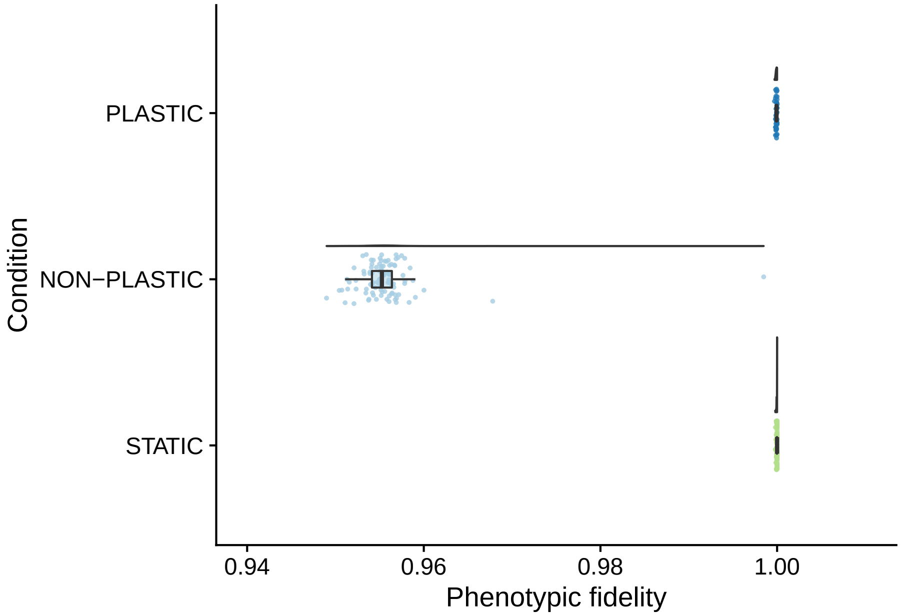
3.10.2.1 Genotypic fidelity

```
genotypic_fidelity_fig <- ggplot(
    summary_data,
    aes(x=condition, y=dominant_lineage_genotypic_fidelity, fill=condition)
  ) +
  geom_flat_violin(
    position = position_nudge(x = .2, y = 0),
    alpha = .8
  ) +
  geom_point(
    mapping=aes(color=condition),
    position = position_jitter(width = .15),
    size = .5,
    alpha = 0.8
  ) +
  geom_boxplot(
    width = .1,
    outlier.shape = NA,
    alpha = 0.5
  ) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order,
    labels=condition_order
  ) +
  scale_y_continuous(
    name="Genotypic fidelity",
    limits=c(0.85, 1.01),
    breaks=c(0.85, 0.90, 0.95, 1.0) #seq(0.85, 1.0, 0.02)
  ) +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  coord_flip() +
  theme(
    legend.position="none"
  ) +
  ggsave(
    paste0(working_directory, "plots/", "genotypic-fidelity.png"),
    width=5,
    height=4
  )
genotypic_fidelity_fig
```



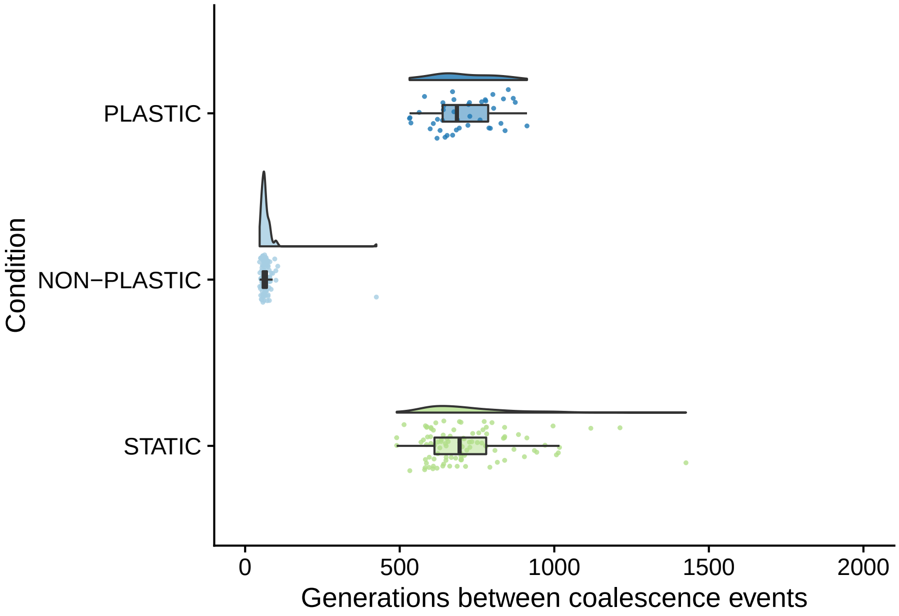
3.10.2.2 Phenotypic fidelity

```
phenotypic_fidelity_fig <- ggplot(
    summary_data,
    aes(x=condition, y=dominant_lineage_trait_fidelity, fill=condition)
  ) +
  geom_flat_violin(
    position = position_nudge(x = .2, y = 0),
    alpha = .8
  ) +
  geom_point(
    mapping=aes(color=condition),
    position = position_jitter(width = .15),
    size = .5,
    alpha = 0.8
  ) +
  geom_boxplot(
    width = .1,
    outlier.shape = NA,
    alpha = 0.5
  ) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order,
    labels=condition_order
  ) +
  scale_y_continuous(
    name="Phenotypic fidelity",
    limits=c(0.94, 1.01),
    breaks=c(0.94, 0.96, 0.98, 1.0) #seq(0.94, 1.0, 0.01)
  ) +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  coord_flip() +
  theme(
    legend.position="none"
  ) +
  ggsave(
    paste0(working_directory, "plots/", "phenotypic-fidelity.png"),
    width=4,
    height=4
  )

phenotypic_fidelity_fig
```



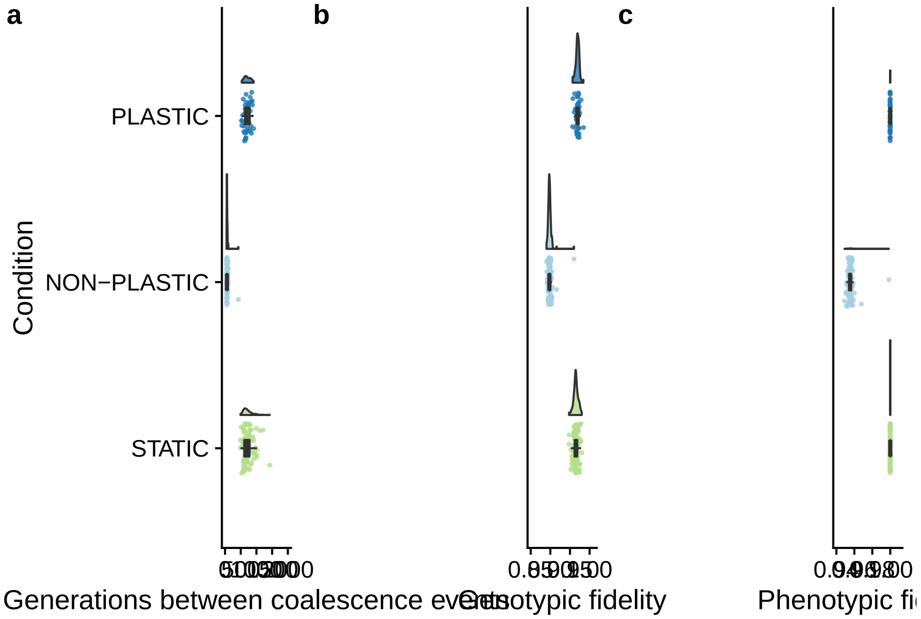
3.10.2.3 Generations per selective sweep

```
selective_sweeps_rate_fig <- ggplot(
    summary_data,
    aes(x=condition, y=generations_per_mrca_change, fill=condition)
  ) +
  geom_flat_violin(
    position = position_nudge(x = .2, y = 0),
    alpha = .8
  ) +
  geom_point(
    mapping=aes(color=condition),
    position = position_jitter(width = .15),
    size = .5,
    alpha = 0.8
  ) +
  geom_boxplot(
    width = .1,
    outlier.shape = NA,
    alpha = 0.5
  ) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order,
    labels=condition_order
  ) +
  scale_y_continuous(
    name="Generations between coalescence events",
    limits=c(0, 2000),
    breaks=seq(0, 2000, 500)
  ) +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  coord_flip() +
  theme(
    legend.position="none"
  ) +
  ggsave(
    paste0(working_directory, "plots/", "generations-between-selective-sweeps.png"),
    width=4,
    height=4
  )

selective_sweeps_rate_fig
```



3.10.2.4 Combined

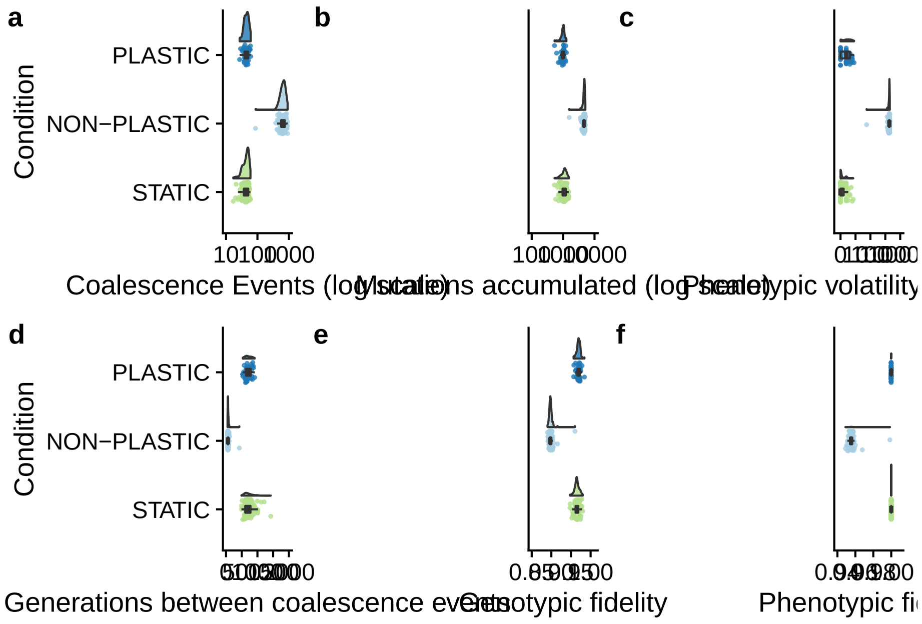
```
grid <- plot_grid(
  selective_sweeps_rate_fig + theme(
    legend.position="none"
  ),
  genotypic_fidelity_fig + theme(
    legend.position="none",
    axis.ticks.y=element_blank(),
    axis.text.y=element_blank(),
    axis.title.y=element_blank()
  ),
  phenotypic_fidelity_fig + theme(
    legend.position="none",
    axis.ticks.y=element_blank(),
    axis.text.y=element_blank(),
    axis.title.y=element_blank()
  ),
  nrow=1,
  align="v",
  labels="auto"
)
grid
```



```
save_plot(
   paste0(working_directory, "plots/", "rate-evolutionary-dynamics.png"),
   grid,
   base_height=6,
   base_asp=2.5
)
```

3.10.3 Full panel

```
grid <- plot_grid(
  selective_sweeps_fig + theme(
    legend.position="none"
  ),
  mutation_count_fig + theme(
    legend.position="none",
    axis.ticks.y=element_blank(),
    axis.text.y=element_blank(),
    axis.title.y=element_blank()
  ),
  phenotypic_volatility_fig + theme(
    legend.position="none",
    axis.ticks.y=element_blank(),
    axis.text.y=element_blank(),
    axis.title.y=element_blank()
  ),
  selective_sweeps_rate_fig + theme(
    legend.position="none"
  ),
  genotypic_fidelity_fig + theme(
    legend.position="none",
    axis.ticks.y=element_blank(),
    axis.text.y=element_blank(),
    axis.title.y=element_blank()
  ),
  phenotypic_fidelity_fig + theme(
    legend.position="none",
    axis.ticks.y=element_blank(),
    axis.text.y=element_blank(),
    axis.title.y=element_blank()
  ),
  nrow=2,
  ncol=3,
  align="v",
  labels="auto"
)
grid
```



```
save_plot(
   paste0(working_directory, "plots/", "evolutionary-change-full-panel.pdf"),
   grid,
   base_height=12,
   base_asp=3/2
)
```

Chapter 4

Evolution and maintenance of novel traits

The effect of adaptive phenotypic plasticity on the evolution and maintenance of novel tasks.

4.1 Overview

```r
total_updates <- 200000
replicates <- 100

focal_traits <- c("not","nand","and","ornot","or","andnot")
traits_set_a <- c("not", "and", "or")
traits_set_b <- c("nand", "ornot", "andnot")
extra_traits <- c(
  "nor","xor","equals",
  "logic_3aa","logic_3ab","logic_3ac",
  "logic_3ad","logic_3ae","logic_3af",
  "logic_3ag","logic_3ah","logic_3ai",
  "logic_3aj","logic_3ak","logic_3al",
  "logic_3am","logic_3an","logic_3ao",
  "logic_3ap","logic_3aq","logic_3ar",
  "logic_3as","logic_3at","logic_3au",
  "logic_3av","logic_3aw","logic_3ax",
  "logic_3ay","logic_3az","logic_3ba",
  "logic_3bb","logic_3bc","logic_3bd",
  "logic_3be","logic_3bf","logic_3bg",
  "logic_3bh","logic_3bi","logic_3bj",
  "logic_3bk","logic_3bl","logic_3bm",
  "logic_3bn","logic_3bo","logic_3bp",
  "logic_3bq","logic_3br","logic_3bs",
  "logic_3bt","logic_3bu","logic_3bv",
  "logic_3bw","logic_3bx","logic_3by",
  "logic_3bz","logic_3ca","logic_3cb",
  "logic_3cc","logic_3cd","logic_3ce",
  "logic_3cf","logic_3cg","logic_3ch",
  "logic_3ci","logic_3cj","logic_3ck",
  "logic_3cl","logic_3cm","logic_3cn",
  "logic_3co","logic_3cp"
)

# Relative location of data.
working_directory <- "experiments/2021-01-31-complex-features/analysis/" # << For book
# working_directory <- "./"
```

4.2 Analysis dependencies

Load all required R libraries.

```
library(ggplot2)
library(tidyverse)
library(cowplot)
library(RColorBrewer)
library(Hmisc)
library(boot)
source("https://gist.githubusercontent.com/benmarwick/2a1bb0133ff568cbe28d/raw/fb53bd9
```

These analyses were conducted/knitted with 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          0.4
## year           2021
## month          02
## day            15
## svn rev        80002
## language       R
## version.string R version 4.0.4 (2021-02-15)
## nickname       Lost Library Book
```

4.3 Setup

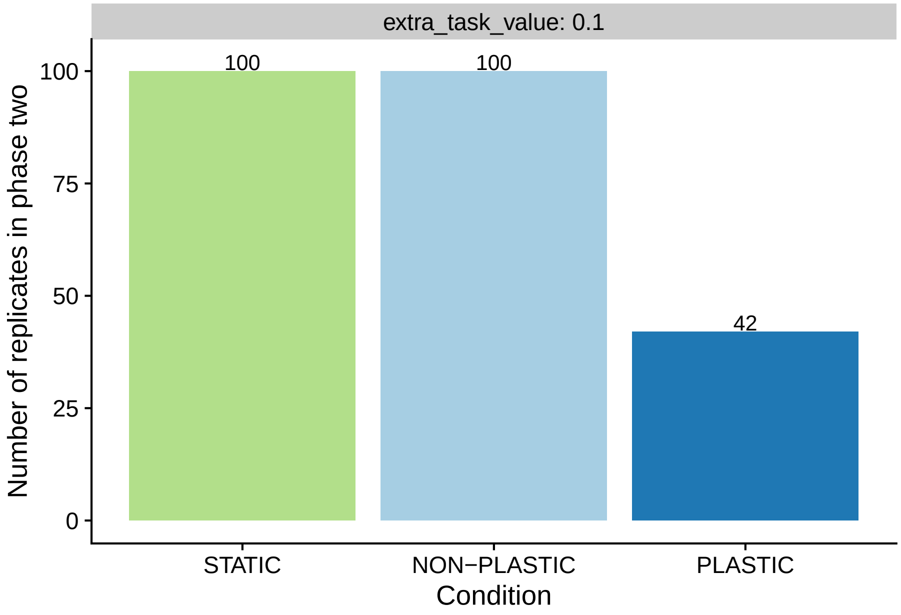
```
####### summary data #######
summary_data_loc <- paste0(working_directory, "data/aggregate.csv")
summary_data <- read.csv(summary_data_loc, na.strings="NONE")

summary_data$DISABLE_REACTION_SENSORS <- as.factor(summary_data$DISABLE_REACTION_SENSORS)
summary_data$chg_env <- summary_data$chg_env == "True"
summary_data$dominant_plastic_odd_even <- as.factor(summary_data$dominant_plastic_odd_even)
summary_data$sensors <- summary_data$DISABLE_REACTION_SENSORS == "0"
summary_data$is_plastic <- summary_data$dominant_plastic_odd_even == "True"
summary_data$extra_task_value <- as.factor(summary_data$extra_task_value)
summary_data <- filter(summary_data, extra_task_value == 0.1)

env_label_fun <- function(chg_env) {
  if (chg_env) {
    return("Fluctuating")
  } else {
    return("Constant")
  }
}

sensors_label_fun <- function(has_sensors) {
  if (has_sensors) {
    return("Sensors")
  } else {
    return("No sensors")
  }
}

condition_label_fun <- function(has_sensors, env_chg) {
  if (has_sensors && env_chg) {
    return("PLASTIC")
  } else if (env_chg) {
    return("NON-PLASTIC")
  } else {
    return("STATIC")
  }
}

summary_data$env_label <- mapply(
  env_label_fun,
  summary_data$chg_env
)
summary_data$sensors_label <- mapply(
  sensors_label_fun,
  summary_data$sensors
)
summary_data$condition <- mapply(
  condition_label_fun,
  summary_data$sensors,
  summary_data$chg_env
)

condition_order = c(
  "STATIC",
  "NON-PLASTIC",
  "PLASTIC"
)

###### time series #####
lineage_time_series_data_loc <- paste0(working_directory, "data/lineage_series.csv")
lineage_time_series_data <- read.csv(lineage_time_series_data_loc)

lineage_time_series_data$DISABLE_REACTION_SENSORS <- as.factor(lineage_time_series_data
lineage_time_series_data$chg_env <- lineage_time_series_data$chg_env == "True"
lineage_time_series_data$sensors <- lineage_time_series_data$DISABLE_REACTION_SENSORS =
lineage_time_series_data$extra_task_value <- as.factor(lineage_time_series_data$extra_

lineage_time_series_data$env_label <- mapply(
  env_label_fun,
  lineage_time_series_data$chg_env
)
lineage_time_series_data$sensors_label <- mapply(
  sensors_label_fun,
  lineage_time_series_data$sensors
)
lineage_time_series_data$condition <- mapply(
  condition_label_fun,
  lineage_time_series_data$sensors,
  lineage_time_series_data$chg_env
)

####### misc #######
# Configure our default graphing theme
theme_set(theme_cowplot())
```

```r
# Create directory to dump plots
dir.create(paste0(working_directory, "plots"), showWarnings=FALSE)
# Sample mean function
samplemean <- function(x, d) {
  return(mean(x[d]))
}
```

4.4 The evolution of phenotypic plasticity

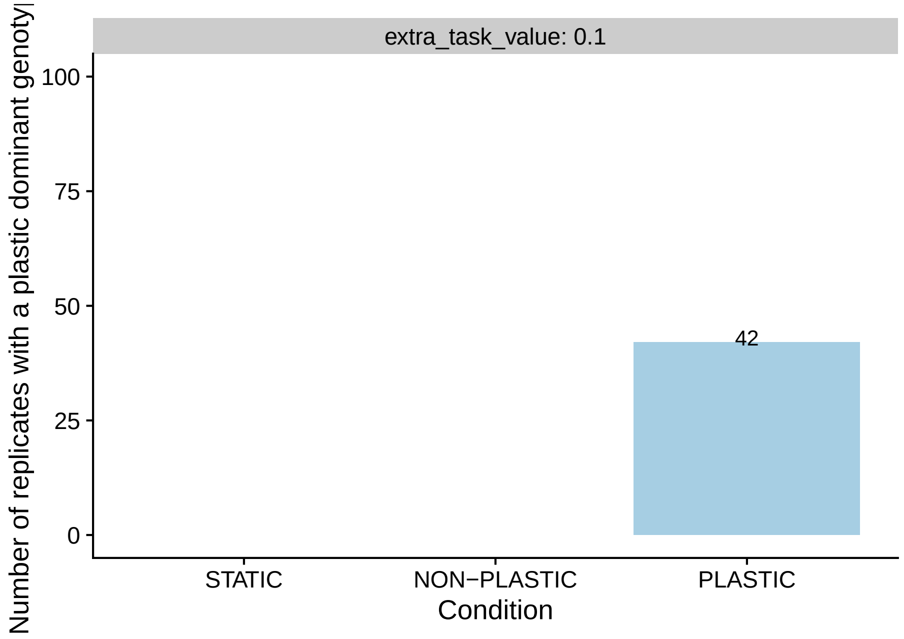
For sensor-enabled populations in fluctuating environments, we only transfered populations containing an optimally plastic genotype to phase two.

```r
summary_data_grouped = dplyr::group_by(summary_data, sensors, env_label, condition, extra_task_va
summary_data_group_counts = dplyr::summarize(summary_data_grouped, n=dplyr::n())

ggplot(summary_data_group_counts, aes(x=condition, y=n, fill=condition)) +
  geom_col(position=position_dodge(0.9)) +
  geom_text(aes(label=n, y=n+2)) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order
  ) +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  ylab("Number of replicates in phase two") +
  facet_wrap(~extra_task_value, labeller=label_both) +
  theme(
    legend.position="none"
  )
```



We can confirm our expectation that the dominant genotypes in non-plastic conditions are not phenotypically plastic.

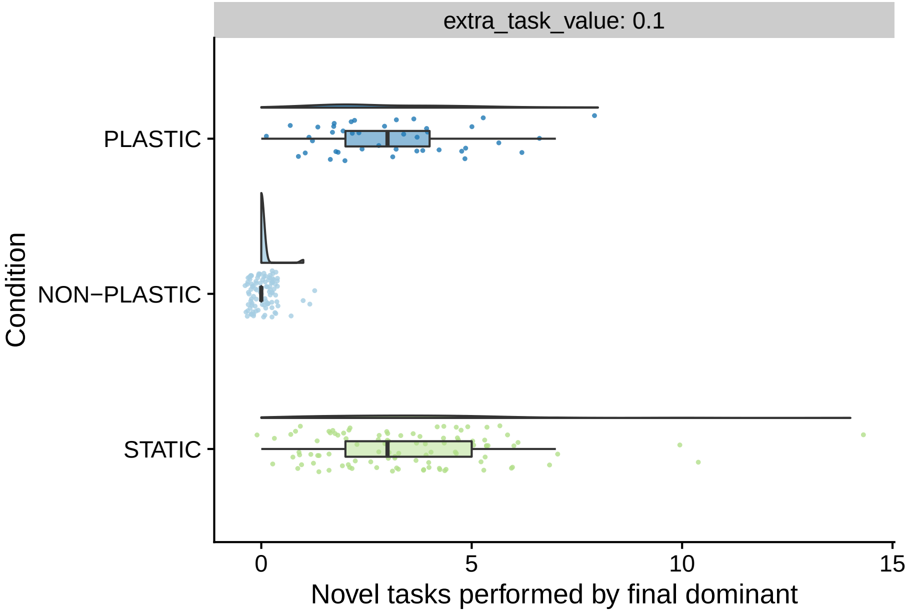
```
summary_data_grouped = dplyr::group_by(summary_data, condition, is_plastic, extra_task_
summary_data_group_counts = dplyr::summarize(summary_data_grouped, n=dplyr::n())
ggplot(filter(summary_data_group_counts, is_plastic), aes(x=condition, y=n, fill=condi
  geom_col(position=position_dodge(0.9)) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order
  ) +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  ylim(0, 100) +
  geom_text(aes(label=n, y=n+1)) +
  ylab("Number of replicates with a plastic dominant genotype") +
  facet_wrap(~extra_task_value, labeller=label_both) +
  theme(
    legend.position="none"
  )
```



4.5 Novel task performance - final dominant genotype

How many novel tasks do final dominant genotypes perform?

```r
ggplot(summary_data, aes(x=condition, y=dominant_extra_tasks, fill=condition)) +
  geom_flat_violin(
    position = position_nudge(x = .2, y = 0),
    alpha = .8
  ) +
  geom_point(
    mapping=aes(color=condition),
    position = position_jitter(width = .15),
    size = .5,
    alpha = 0.8
  ) +
  geom_boxplot(
    width = .1,
    outlier.shape = NA,
    alpha = 0.5
  ) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order
  ) +
  ylab("Novel tasks performed by final dominant") +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  coord_flip() +
  facet_wrap(
    ~extra_task_value,
    labeller=label_both
  ) +
  theme(
    legend.position="none"
  ) +
  ggsave(
    paste0(working_directory, "plots/dominant-extra-tasks.pdf"),
    width=15,
    height=10
  )
```



```
paste0(
  "PLASTIC median: ",
  median(filter(summary_data, condition=="PLASTIC")$dominant_extra_tasks)
```

```r
)
```

```
## [1] "PLASTIC median: 3"
```

```r
paste0(
  "STATIC median: ",
  median(filter(summary_data, condition=="STATIC")$dominant_extra_tasks)
)
```

```
## [1] "STATIC median: 3"
```

```r
paste0(
  "NON-PLASTIC median: ",
  median(filter(summary_data, condition=="NON-PLASTIC")$dominant_extra_tasks)
)
```

```
## [1] "NON-PLASTIC median: 0"
```

```r
reward_level <- 0.1
dom_task_data <- filter(summary_data, extra_task_value==reward_level)
kruskal.test(
  formula=dominant_extra_tasks~condition,
  data=dom_task_data
)
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  dominant_extra_tasks by condition
## Kruskal-Wallis chi-squared = 177.17, df = 2, p-value < 2.2e-16
```

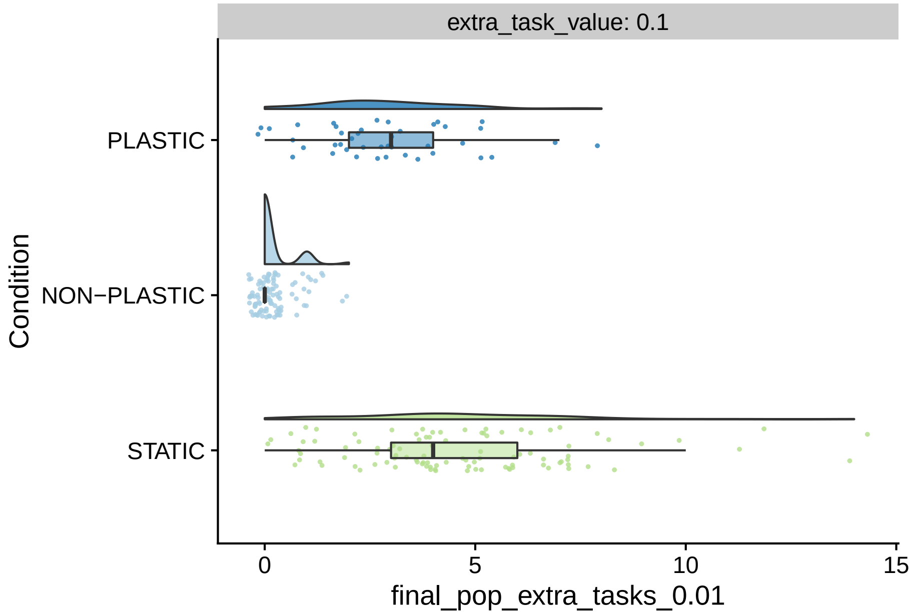
```r
pairwise.wilcox.test(
  x=dom_task_data$dominant_extra_tasks,
  g=dom_task_data$condition,
  p.adjust.method="bonferroni",
  conf.int=TRUE,
  conf.level=0.95
)
```

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  dom_task_data$dominant_extra_tasks and dom_task_data$condition
##
##         NON-PLASTIC PLASTIC
## PLASTIC <2e-16      -
## STATIC  <2e-16      0.9
##
## P value adjustment method: bonferroni
```

4.6 Novel task performance - final population

How many novel tasks are performed across the final population (1% of organisms must perform to count)?

```
ggplot(summary_data, aes(x=condition, y=final_pop_extra_tasks_0.01, fill=condition)) +
  geom_flat_violin(
    position = position_nudge(x = .2, y = 0),
    alpha = .8
  ) +
  geom_point(
    mapping=aes(color=condition),
    position = position_jitter(width = .15),
    size = .5,
    alpha = 0.8
  ) +
  geom_boxplot(
    width = .1,
    outlier.shape = NA,
    alpha = 0.5
  ) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order
  ) +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  coord_flip() +
  facet_wrap(
    ~extra_task_value,
    labeller=label_both
  ) +
  theme(
    legend.position="none"
  )
```



```
paste0(
  "PLASTIC median: ",
  median(filter(summary_data, condition=="PLASTIC")$final_pop_extra_tasks_0.01)
)
```

```
## [1] "PLASTIC median: 3"
```

```
paste0(
  "STATIC median: ",
  median(filter(summary_data, condition=="STATIC")$final_pop_extra_tasks_0.01)
)
```

```
## [1] "STATIC median: 4"
```

```
paste0(
  "NON-PLASTIC median: ",
  median(filter(summary_data, condition=="NON-PLASTIC")$final_pop_extra_tasks_0.01)
)
```

```
## [1] "NON-PLASTIC median: 0"
```

```
reward_level <- 0.1
dom_task_data <- filter(summary_data, extra_task_value==reward_level)
kruskal.test(
  formula=final_pop_extra_tasks_0.01~condition,
  data=dom_task_data
)
```

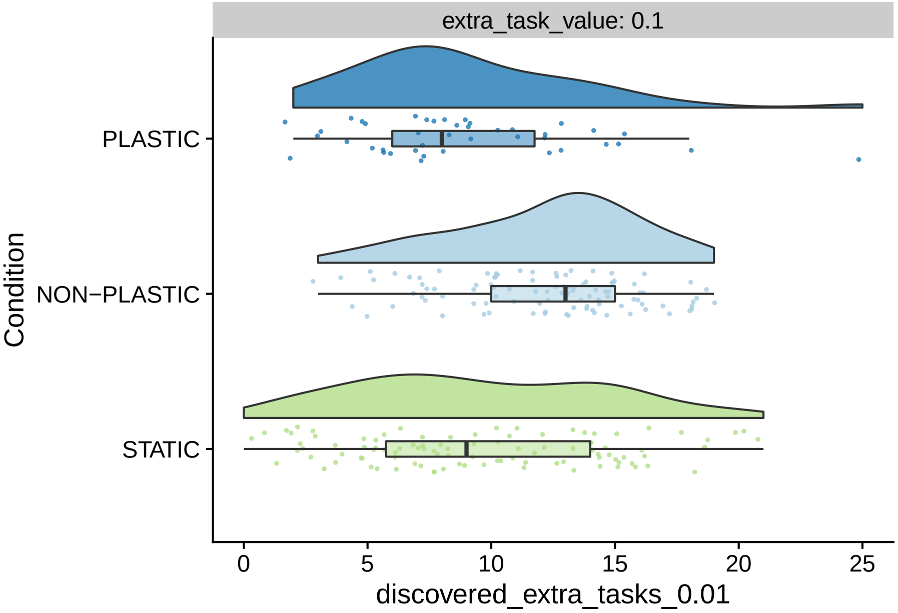
```
##
##  Kruskal-Wallis rank sum test
##
## data:  final_pop_extra_tasks_0.01 by condition
## Kruskal-Wallis chi-squared = 169.47, df = 2, p-value < 2.2e-16
```

```
pairwise.wilcox.test(
  x=dom_task_data$final_pop_extra_tasks_0.01,
  g=dom_task_data$condition,
  p.adjust.method="bonferroni",
  conf.int=TRUE,
  conf.level=0.95
)
```

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  dom_task_data$final_pop_extra_tasks_0.01 and dom_task_data$condition
##
##         NON-PLASTIC PLASTIC
## PLASTIC < 2e-16     -
## STATIC  < 2e-16     0.00016
##
## P value adjustment method: bonferroni
```

4.7 Novel task discovery - population

```
ggplot(summary_data, aes(x=condition, y=discovered_extra_tasks_0.01, fill=condition)) +
  geom_flat_violin(
    position = position_nudge(x = .2, y = 0),
    alpha = .8
  ) +
  geom_point(
    mapping=aes(color=condition),
    position = position_jitter(width = .15),
    size = .5,
    alpha = 0.8
  ) +
  geom_boxplot(
    width = .1,
    outlier.shape = NA,
    alpha = 0.5
  ) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order
  ) +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  coord_flip() +
  facet_wrap(
    ~extra_task_value,
    labeller=label_both
  ) +
  theme(
    legend.position="none"
  )
```



```
paste0(
  "PLASTIC median: ",
  median(filter(summary_data, condition=="PLASTIC")$discovered_extra_tasks_0.01)
)
```

```
## [1] "PLASTIC median: 8"
```

```
paste0(
  "STATIC median: ",
  median(filter(summary_data, condition=="STATIC")$discovered_extra_tasks_0.01)
)
```

```
## [1] "STATIC median: 9"
```

```
paste0(
  "NON-PLASTIC median: ",
  median(filter(summary_data, condition=="NON-PLASTIC")$discovered_extra_tasks_0.01)
)
```

```
## [1] "NON-PLASTIC median: 13"
```

```
reward_level <- 0.1
dom_task_data <- filter(summary_data, extra_task_value==reward_level)
kruskal.test(
  formula=discovered_extra_tasks_0.01~condition,
  data=dom_task_data
)
```

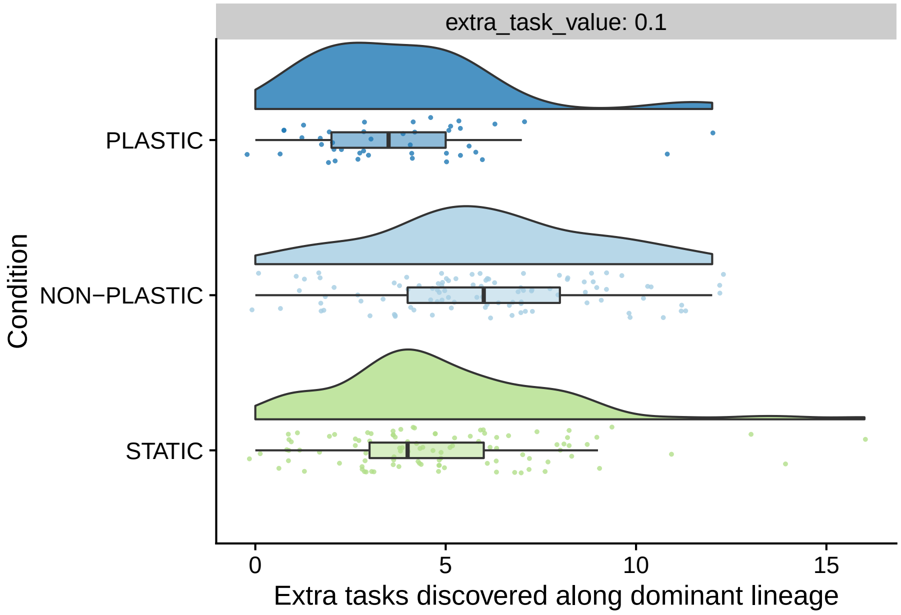
```
##
##  Kruskal-Wallis rank sum test
##
## data:  discovered_extra_tasks_0.01 by condition
## Kruskal-Wallis chi-squared = 24.271, df = 2, p-value = 5.365e-06
```

```
pairwise.wilcox.test(
  x=dom_task_data$discovered_extra_tasks_0.01,
  g=dom_task_data$condition,
  p.adjust.method="bonferroni",
  conf.int=TRUE,
  conf.level=0.95
)
```

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  dom_task_data$discovered_extra_tasks_0.01 and dom_task_data$condition
##
##         NON-PLASTIC PLASTIC
## PLASTIC 2.4e-05     -
## STATIC  0.00035     1.00000
##
## P value adjustment method: bonferroni
```

4.8 Novel task discovery - lineage of final dominant genotype

```
ggplot(summary_data, aes(x=condition, y=dominant_lineage_extra_traits_discovered, fill=condition)
  geom_flat_violin(
    position = position_nudge(x = .2, y = 0),
    alpha = .8
  ) +
  geom_point(
    mapping=aes(color=condition),
    position = position_jitter(width = .15),
    size = .5,
    alpha = 0.8
  ) +
  geom_boxplot(
    width = .1,
    outlier.shape = NA,
    alpha = 0.5
  ) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order
  ) +
  ylab("Extra tasks discovered along dominant lineage") +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  coord_flip() +
  facet_wrap(
    ~extra_task_value,
    labeller=label_both
  ) +
  theme(
    legend.position="none"
  ) +
  ggsave(
    paste0(working_directory, "plots/dominant-lineage-extra-tasks-discovered.pdf"),
    width=15,
    height=10
  )
```



```
paste0(
  "PLASTIC median: ",
  median(filter(summary_data, condition=="PLASTIC")$dominant_lineage_extra_traits_disco
)
```

```
## [1] "PLASTIC median: 3.5"
```

```
paste0(
  "STATIC median: ",
  median(filter(summary_data, condition=="STATIC")$dominant_lineage_extra_traits_disco
)
```

```
## [1] "STATIC median: 4"
```

```
paste0(
  "NON-PLASTIC median: ",
  median(filter(summary_data, condition=="NON-PLASTIC")$dominant_lineage_extra_traits_d
)
```

```
## [1] "NON-PLASTIC median: 6"
```

```
reward_level <- 0.1
dom_task_data <- filter(summary_data, extra_task_value==reward_level)
kruskal.test(
  formula=dominant_lineage_extra_traits_discovered~condition,
  data=dom_task_data
)
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  dominant_lineage_extra_traits_discovered by condition
## Kruskal-Wallis chi-squared = 24.099, df = 2, p-value = 5.846e-06
```

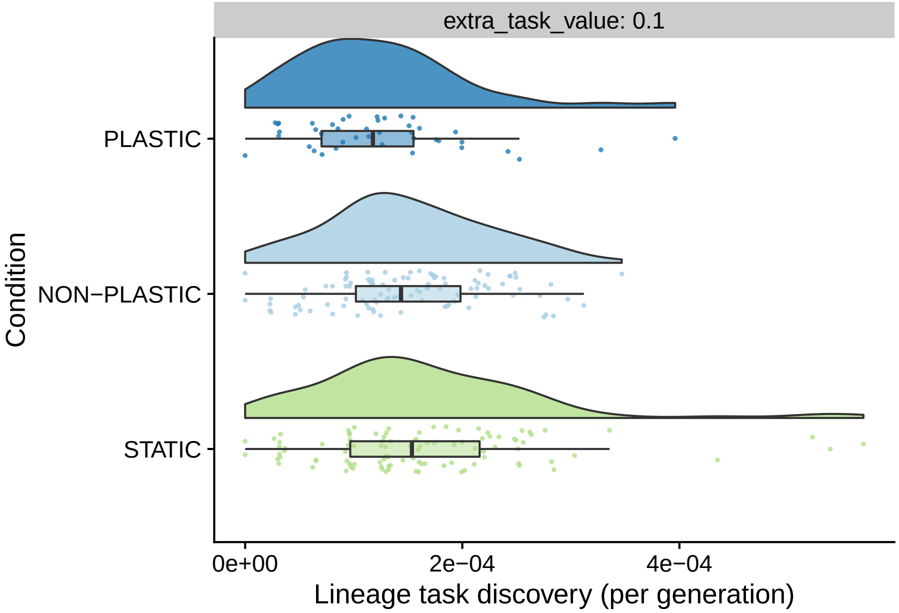
```r
pairwise.wilcox.test(
  x=dom_task_data$dominant_lineage_extra_traits_discovered,
  g=dom_task_data$condition,
  p.adjust.method="bonferroni",
  conf.int=TRUE,
  conf.level=0.95
)
```

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  dom_task_data$dominant_lineage_extra_traits_discovered and dom_task_data$condition
##
##         NON-PLASTIC PLASTIC
## PLASTIC 1.7e-05     -
## STATIC  0.0035      0.0561
##
## P value adjustment method: bonferroni
```

4.8.1 Per-generation novel task discovery - lineage of final dominant genotype

```r
summary_data$dominant_lineage_extra_traits_discovered_per_generation <- summary_data$dominant_lin
ggplot(summary_data, aes(x=condition, y=dominant_lineage_extra_traits_discovered_per_generation,
  geom_flat_violin(
    position = position_nudge(x = .2, y = 0),
    alpha = .8
  ) +
  geom_point(
    mapping=aes(color=condition),
    position = position_jitter(width = .15),
    size = .5,
    alpha = 0.8
  ) +
  geom_boxplot(
    width = .1,
    outlier.shape = NA,
    alpha = 0.5
  ) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order
  ) +
  ylab("Lineage task discovery (per generation)") +
  facet_wrap(
    ~extra_task_value,
    labeller=label_both
  ) +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  coord_flip() +
  theme(
    legend.position="none"
  ) +
  ggsave(paste0(working_directory, "plots/", "discovery-per-generation.png"))
```

```
## Saving 6.5 x 4.5 in image
```



```
paste0(
  "PLASTIC median: ",
  median(filter(summary_data, condition=="PLASTIC")$dominant_lineage_extra_traits_disc
)
```

```
## [1] "PLASTIC median: 0.000117695011124939"
```

```
paste0(
  "STATIC median: ",
  median(filter(summary_data, condition=="STATIC")$dominant_lineage_extra_traits_discovered_per_g
)
```

```
## [1] "STATIC median: 0.00015363220504867"
```

```
paste0(
  "NON-PLASTIC median: ",
  median(filter(summary_data, condition=="NON-PLASTIC")$dominant_lineage_extra_traits_discovered_
)
```

```
## [1] "NON-PLASTIC median: 0.00014358046266055"
```

```
reward_level <- 0.1
dom_task_data <- filter(summary_data, extra_task_value==reward_level)
kruskal.test(
  formula=dominant_lineage_extra_traits_discovered_per_generation~condition,
  data=dom_task_data
)
```

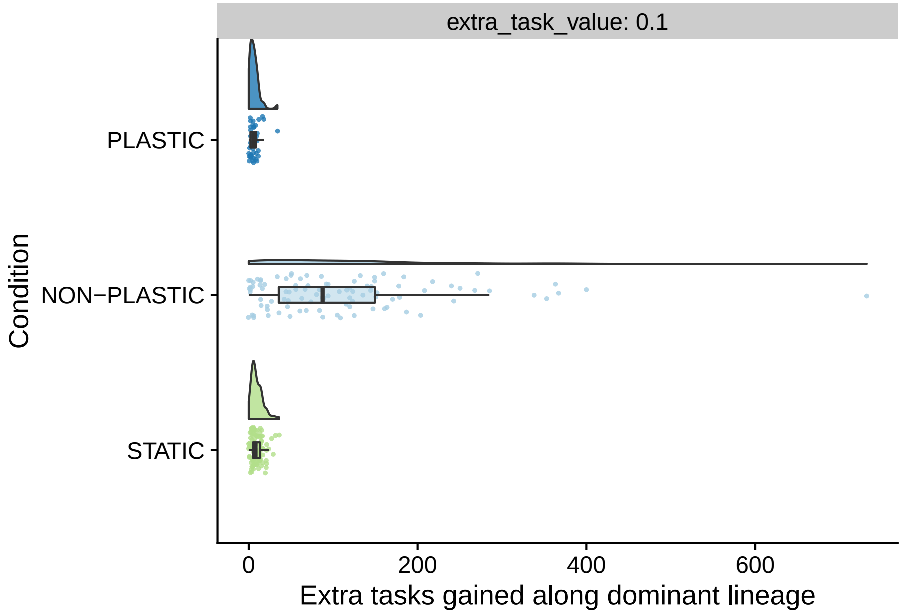
```
##
##  Kruskal-Wallis rank sum test
##
## data:  dominant_lineage_extra_traits_discovered_per_generation by condition
## Kruskal-Wallis chi-squared = 7.1465, df = 2, p-value = 0.02806
```

```
pairwise.wilcox.test(
  x=dom_task_data$dominant_lineage_extra_traits_discovered_per_generation,
  g=dom_task_data$condition,
  p.adjust.method="bonferroni",
  conf.int=TRUE,
  conf.level=0.95
)
```

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  dom_task_data$dominant_lineage_extra_traits_discovered_per_generation and dom_task_data
##
##         NON-PLASTIC PLASTIC
## PLASTIC 0.092       -
## STATIC  1.000       0.025
##
## P value adjustment method: bonferroni
```

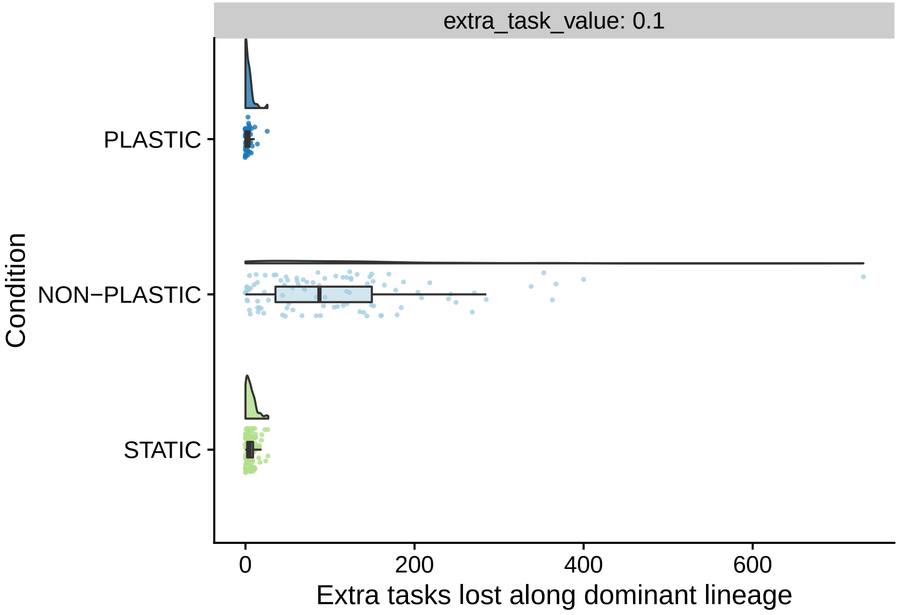
4.9 Novel tasks gained along final dominant lineages

```
ggplot(summary_data, aes(x=condition, y=dominant_lineage_extra_traits_gained, fill=cond
  geom_flat_violin(
    position = position_nudge(x = .2, y = 0),
    alpha = .8
  ) +
  geom_point(
    mapping=aes(color=condition),
    position = position_jitter(width = .15),
    size = .5,
    alpha = 0.8
  ) +
  geom_boxplot(
    width = .1,
    outlier.shape = NA,
    alpha = 0.5
  ) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order
  ) +
  ylab("Extra tasks gained along dominant lineage") +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  coord_flip() +
  facet_wrap(
    ~extra_task_value,
    labeller=label_both
  ) +
  theme(
    legend.position="none"
  ) +
  ggsave(
    paste0(working_directory, "plots/dominant-lineage-extra-tasks-gained.pdf"),
    width=15,
    height=10
  )
```



4.10 Novel task loss along final dominant lineages

```
ggplot(summary_data, aes(x=condition, y=dominant_lineage_extra_traits_lost, fill=condition)) +
  geom_flat_violin(
    position = position_nudge(x = .2, y = 0),
    alpha = .8
  ) +
  geom_point(
    mapping=aes(color=condition),
    position = position_jitter(width = .15),
    size = .5,
    alpha = 0.8
  ) +
  geom_boxplot(
    width = .1,
    outlier.shape = NA,
    alpha = 0.5
  ) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order
  ) +
  ylab("Extra tasks lost along dominant lineage") +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  coord_flip() +
  facet_wrap(
    ~extra_task_value,
    labeller=label_both
  ) +
  theme(
    legend.position="none"
  ) +
  ggsave(
    paste0(working_directory, "plots/dominant-lineage-extra-tasks-lost.pdf"),
    width=15,
    height=10
  )
```



```
paste0(
  "PLASTIC median: ",
  median(filter(summary_data, condition=="PLASTIC")$dominant_lineage_extra_traits_lost
)
```

```
## [1] "PLASTIC median: 2"
```

```
paste0(
  "STATIC median: ",
  median(filter(summary_data, condition=="STATIC")$dominant_lineage_extra_traits_lost)
)
```

```
## [1] "STATIC median: 5"
```

```
paste0(
  "NON-PLASTIC median: ",
  median(filter(summary_data, condition=="NON-PLASTIC")$dominant_lineage_extra_traits_lost)
)
```

```
## [1] "NON-PLASTIC median: 87.5"
```

```
reward_level <- 0.1
dom_task_data <- filter(summary_data, extra_task_value==reward_level)
kruskal.test(
  formula=dominant_lineage_extra_traits_lost~condition,
  data=dom_task_data
)
```

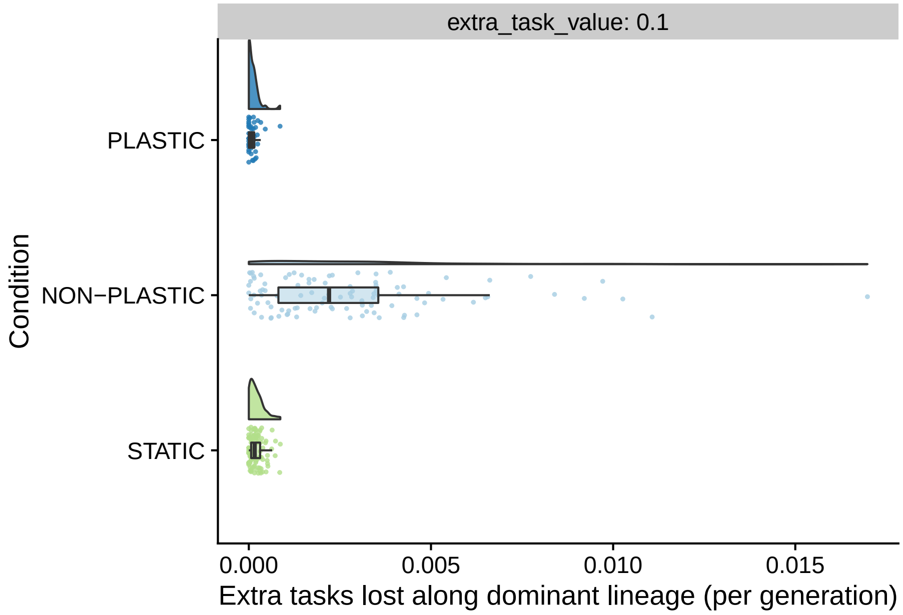
```
## 
##  Kruskal-Wallis rank sum test
## 
## data:  dominant_lineage_extra_traits_lost by condition
## Kruskal-Wallis chi-squared = 129.06, df = 2, p-value < 2.2e-16
```

```
pairwise.wilcox.test(
  x=dom_task_data$dominant_lineage_extra_traits_lost,
  g=dom_task_data$condition,
  p.adjust.method="bonferroni",
  conf.int=TRUE,
  conf.level=0.95
)
```

```
## 
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction 
## 
## data:  dom_task_data$dominant_lineage_extra_traits_lost and dom_task_data$condition 
## 
##         NON-PLASTIC PLASTIC
## PLASTIC 2.7e-16     -      
## STATIC  < 2e-16     0.0024 
## 
## P value adjustment method: bonferroni
```

```
summary_data$dominant_lineage_extra_traits_lost_per_generation <- summary_data$dominant
ggplot(summary_data, aes(x=condition, y=dominant_lineage_extra_traits_lost_per_generati
  geom_flat_violin(
    position = position_nudge(x = .2, y = 0),
    alpha = .8
  ) +
  geom_point(
    mapping=aes(color=condition),
    position = position_jitter(width = .15),
    size = .5,
    alpha = 0.8
  ) +
  geom_boxplot(
    width = .1,
    outlier.shape = NA,
    alpha = 0.5
  ) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order
  ) +
  ylab("Extra tasks lost along dominant lineage (per generation)") +
  facet_wrap(
    ~extra_task_value,
    labeller=label_both
  ) +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  coord_flip() +
  theme(
    legend.position="none"
  ) +
  ggsave(paste0(working_directory, "plots/", "tasks-lost-per-generation.png"))
```

```
## Saving 6.5 x 4.5 in image
```



```
paste0(
  "PLASTIC median: ",
  median(filter(summary_data, condition=="PLASTIC")$dominant_lineage_extra_traits_lost_per_genera
)
```

```
## [1] "PLASTIC median: 6.25141973661864e-05"
```

```
paste0(
  "STATIC median: ",
  median(filter(summary_data, condition=="STATIC")$dominant_lineage_extra_traits_lost_per_generat
)
```

```
## [1] "STATIC median: 0.000161396283669756"
```

```
paste0(
  "NON-PLASTIC median: ",
  median(filter(summary_data, condition=="NON-PLASTIC")$dominant_lineage_extra_traits_lost_per_ge
)
```

```
## [1] "NON-PLASTIC median: 0.0022026054610079"
```

```
reward_level <- 0.1
dom_task_data <- filter(summary_data, extra_task_value==reward_level)
kruskal.test(
  formula=dominant_lineage_extra_traits_lost_per_generation~condition,
  data=dom_task_data
)
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  dominant_lineage_extra_traits_lost_per_generation by condition
## Kruskal-Wallis chi-squared = 121.41, df = 2, p-value < 2.2e-16
```

```
pairwise.wilcox.test(
  x=dom_task_data$dominant_lineage_extra_traits_lost_per_generation,
  g=dom_task_data$condition,
  p.adjust.method="bonferroni",
  conf.int=TRUE,
  conf.level=0.95
)
```

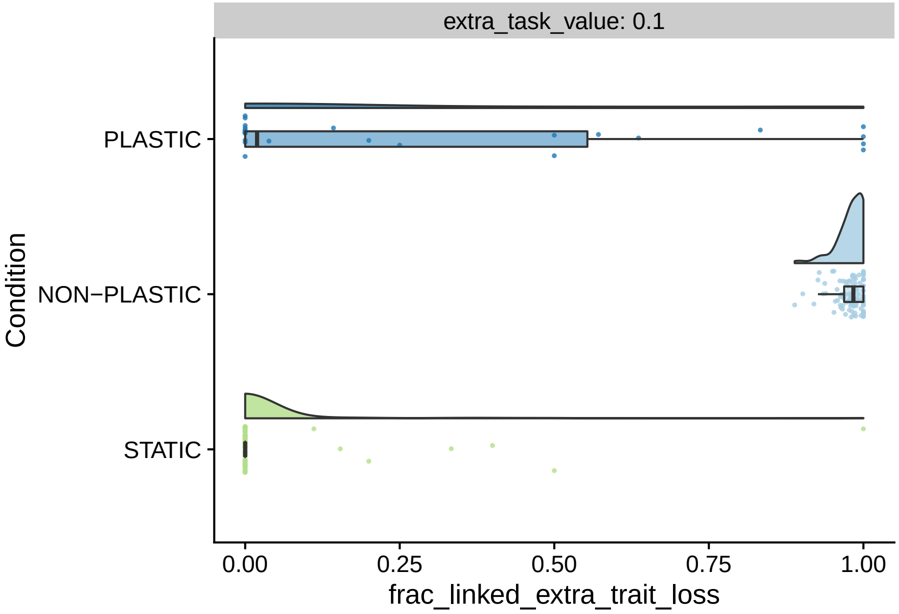
```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  dom_task_data$dominant_lineage_extra_traits_lost_per_generation and dom_task_
##
##         NON-PLASTIC PLASTIC
## PLASTIC 1.1e-15     -
## STATIC  < 2e-16     0.0012
##
## P value adjustment method: bonferroni
```

4.11 How many instances of novel trait loss co-occurred with changes in base phenotype?

Task loss linked with primary trait changes.

```
lost_traits_summary_data <- filter(summary_data, extra_task_value==0.1 & dominant_linea
lost_traits_summary_data$frac_linked_extra_trait_loss <- lost_traits_summary_data$domin

# ggplot(lost_traits_summary_data, aes(x=frac_linked_extra_trait_loss, fill=condition),
#   geom_density() +
#   facet_grid(
#     condition~extra_task_value,
#     labeller=label_both
#   ) +
#   theme(
#     legend.position="none"
#   ) +
#   scale_fill_brewer(
#     palette="Paired"
#   ) +
#   scale_color_brewer(
#     palette="Paired"
#   ) +
#   ggsave(
#     paste0(working_directory, "plots/dominant-lineage-extra-tasks-lost-linkage.png"),
#     width=15,
#     height=10
#   )
```

```
ggplot(lost_traits_summary_data, aes(x=condition, y=frac_linked_extra_trait_loss, fill=condition)
  geom_flat_violin(
    position = position_nudge(x = .2, y = 0),
    alpha = .8
  ) +
  geom_point(
    mapping=aes(color=condition),
    position = position_jitter(width = .15),
    size = .5,
    alpha = 0.8
  ) +
  geom_boxplot(
    width = .1,
    outlier.shape = NA,
    alpha = 0.5
  ) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order
  ) +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  coord_flip() +
  facet_wrap(
    ~extra_task_value,
    labeller=label_both
  ) +
  theme(
    legend.position="none"
  )
```



```
paste0(
  "PLASTIC median: ",
  median(filter(lost_traits_summary_data, condition=="PLASTIC")$frac_linked_extra_trai
)
```

```
## [1] "PLASTIC median: 0.0192307692307692"
```

```
paste0(
  "STATIC median: ",
  median(filter(lost_traits_summary_data, condition=="STATIC")$frac_linked_extra_trait_
)
```

```
## [1] "STATIC median: 0"
```

```
paste0(
  "NON-PLASTIC median: ",
  median(filter(lost_traits_summary_data, condition=="NON-PLASTIC")$frac_linked_extra_
)
```

```
## [1] "NON-PLASTIC median: 0.983803278688525"
```

```
kruskal.test(
  formula=frac_linked_extra_trait_loss~condition,
  data=lost_traits_summary_data
)
```

```
## 
##  Kruskal-Wallis rank sum test
```

```
##
## data:  frac_linked_extra_trait_loss by condition
## Kruskal-Wallis chi-squared = 153.68, df = 2, p-value < 2.2e-16
```

```
pairwise.wilcox.test(
  x=lost_traits_summary_data$frac_linked_extra_trait_loss,
  g=lost_traits_summary_data$condition,
  p.adjust.method="bonferroni",
  conf.int=TRUE,
  conf.level=0.95
)
```

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  lost_traits_summary_data$frac_linked_extra_trait_loss and lost_traits_summary_data$cond
##
##         NON-PLASTIC PLASTIC
## PLASTIC 1.9e-08     -
## STATIC  < 2e-16     1.8e-06
##
## P value adjustment method: bonferroni
```

```
sum(filter(lost_traits_summary_data, condition=="NON-PLASTIC")$dominant_lineage_extra_traits_lost
```

```
## [1] 10998
```

```
sum(filter(lost_traits_summary_data, condition=="NON-PLASTIC")$dominant_lineage_extra_traits_lost
```

```
## [1] 11229
```

```
aggregate_frac_linked_extra_trait_loss_nonplastic <- sum(filter(lost_traits_summary_data, conditi
aggregate_frac_linked_extra_trait_loss_nonplastic
```

```
## [1] 0.9794283
```

```
sum(filter(lost_traits_summary_data, condition=="PLASTIC")$dominant_lineage_extra_traits_lost_lin
```

```
## [1] 29
```

```
sum(filter(lost_traits_summary_data, condition=="PLASTIC")$dominant_lineage_extra_traits_lost)
```

```
## [1] 142
```

```
aggregate_frac_linked_extra_trait_loss_plastic <- sum(filter(lost_traits_summary_data, condition=
aggregate_frac_linked_extra_trait_loss_plastic
```

```
## [1] 0.2042254
```

```
sum(filter(lost_traits_summary_data, condition=="STATIC")$dominant_lineage_extra_traits_lost_link
```

```
## [1] 13
```

```
sum(filter(lost_traits_summary_data, condition=="STATIC")$dominant_lineage_extra_traits
```

```
## [1] 631
```

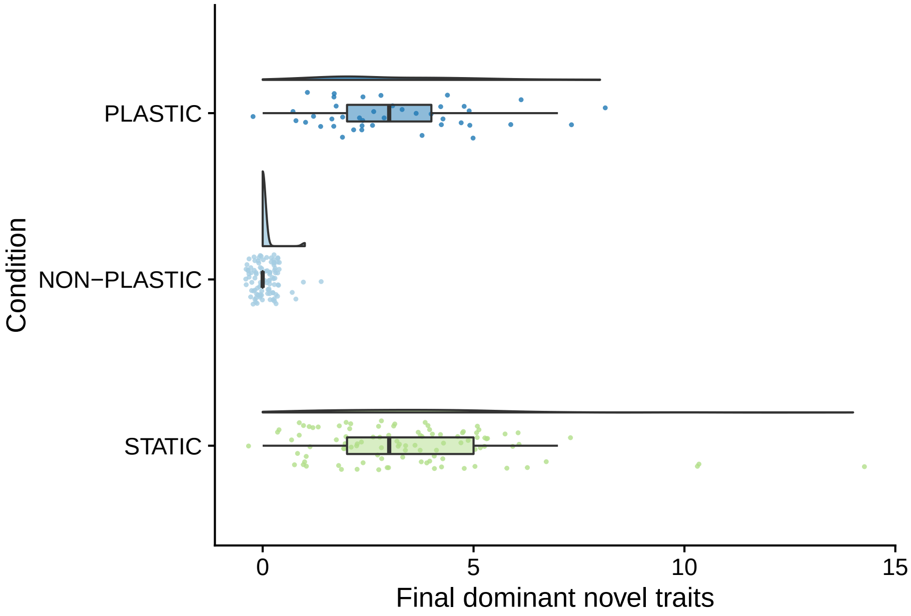
```
aggregate_frac_linked_extra_trait_loss_nonplastic <- sum(filter(lost_traits_summary_da
aggregate_frac_linked_extra_trait_loss_nonplastic
```

```
## [1] 0.02060222
```

4.12 Manuscript figures

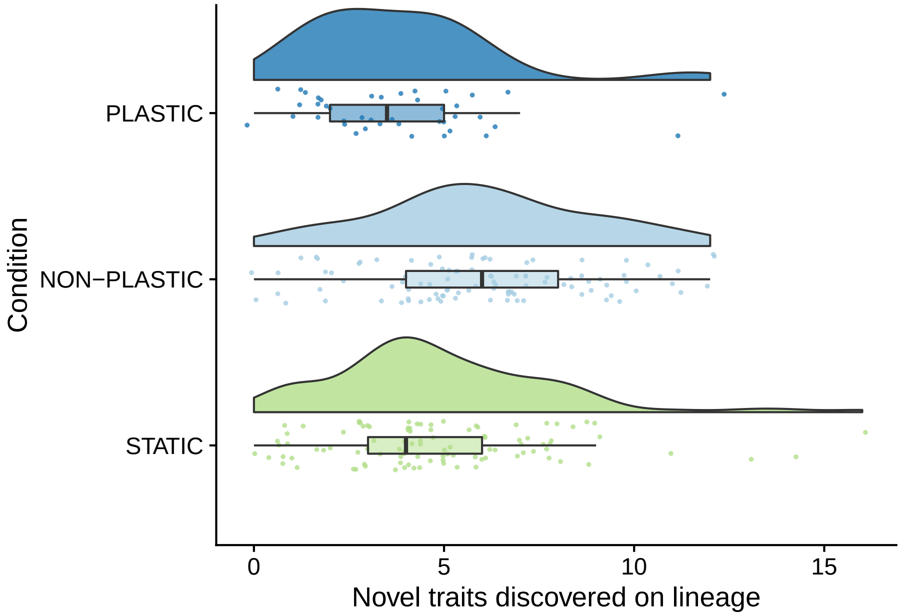
4.12.1 Overall task performance

```
extra_task_reward_value=0.1
dominant_extra_tasks_fig <- ggplot(
    filter(summary_data, extra_task_value==extra_task_reward_value),
    aes(x=condition, y=dominant_extra_tasks, fill=condition)
  ) +
  geom_flat_violin(
    position = position_nudge(x = .2, y = 0),
    alpha = .8
  ) +
  geom_point(
    mapping=aes(color=condition),
    position = position_jitter(width = .15),
    size = .5,
    alpha = 0.8
  ) +
  geom_boxplot(
    width = .1,
    outlier.shape = NA,
    alpha = 0.5
  ) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order,
    labels=condition_order
  ) +
  scale_y_continuous(
    name="Final dominant novel traits"
  ) +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  theme(
    legend.position="none"
  ) +
  coord_flip()
dominant_extra_tasks_fig
```



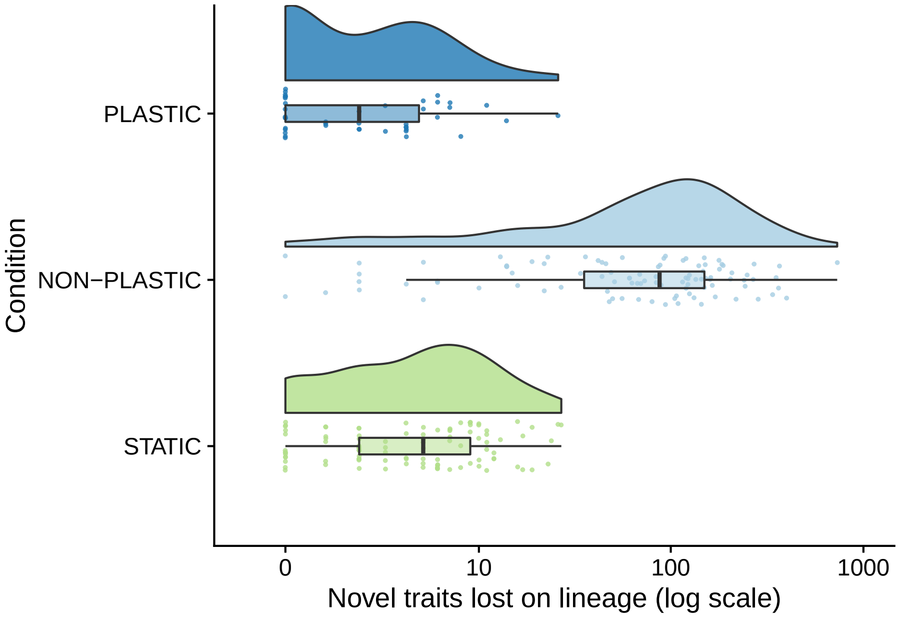
4.12.2 Overall task discovery

```
lineage_extra_tasks_discovered_fig <- ggplot(
    filter(summary_data, extra_task_value==extra_task_reward_value),
    aes(x=condition, y=dominant_lineage_extra_traits_discovered, fill=condition)
  ) +
  geom_flat_violin(
    position = position_nudge(x = .2, y = 0),
    alpha = .8
  ) +
  geom_point(
    mapping=aes(color=condition),
    position = position_jitter(width = .15),
    size = .5,
    alpha = 0.8
  ) +
  geom_boxplot(
    width = .1,
    outlier.shape = NA,
    alpha = 0.5
  ) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order,
    labels=condition_order
  ) +
  scale_y_continuous(
    name="Novel traits discovered on lineage"
  ) +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  theme(
    legend.position="none"
  ) +
  coord_flip()
lineage_extra_tasks_discovered_fig
```



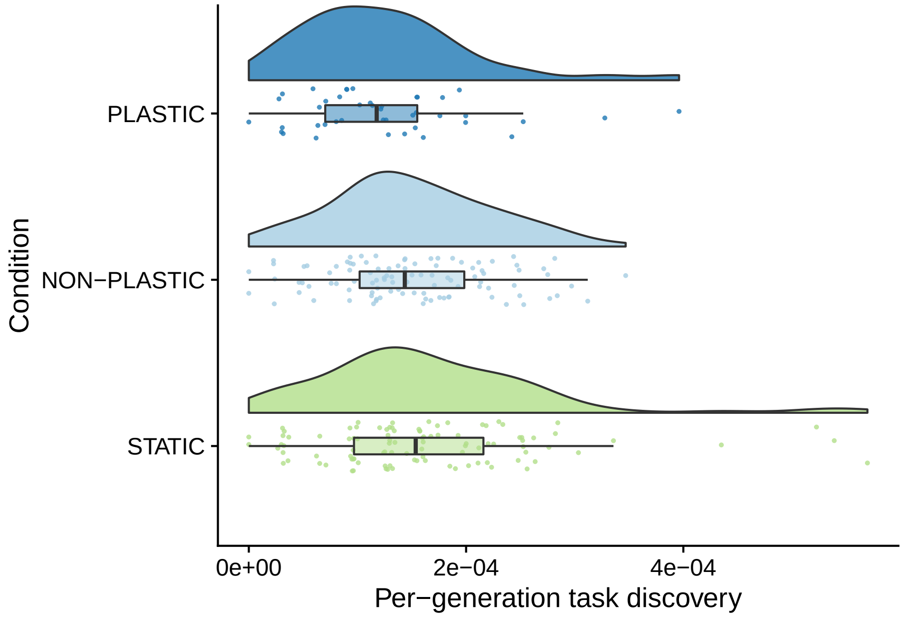
4.12.3 Overall task loss

```r
lineage_extra_tasks_lost_fig <- ggplot(
    filter(summary_data, extra_task_value==extra_task_reward_value),
    aes(x=condition, y=dominant_lineage_extra_traits_lost, fill=condition)
  ) +
  geom_flat_violin(
    position = position_nudge(x = .2, y = 0),
    alpha = .8
  ) +
  geom_point(
    mapping=aes(color=condition),
    position = position_jitter(width = .15),
    size = .5,
    alpha = 0.8
  ) +
  geom_boxplot(
    width = .1,
    outlier.shape = NA,
    alpha = 0.5
  ) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order,
    labels=condition_order
  ) +
  scale_y_continuous(
    name="Novel traits lost on lineage (log scale)",
    trans="pseudo_log",
    breaks=c(0,10,100,1000),
    limits=c(-1,1000)
  ) +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  theme(
    legend.position="none"
  ) +
  coord_flip()

lineage_extra_tasks_lost_fig
```



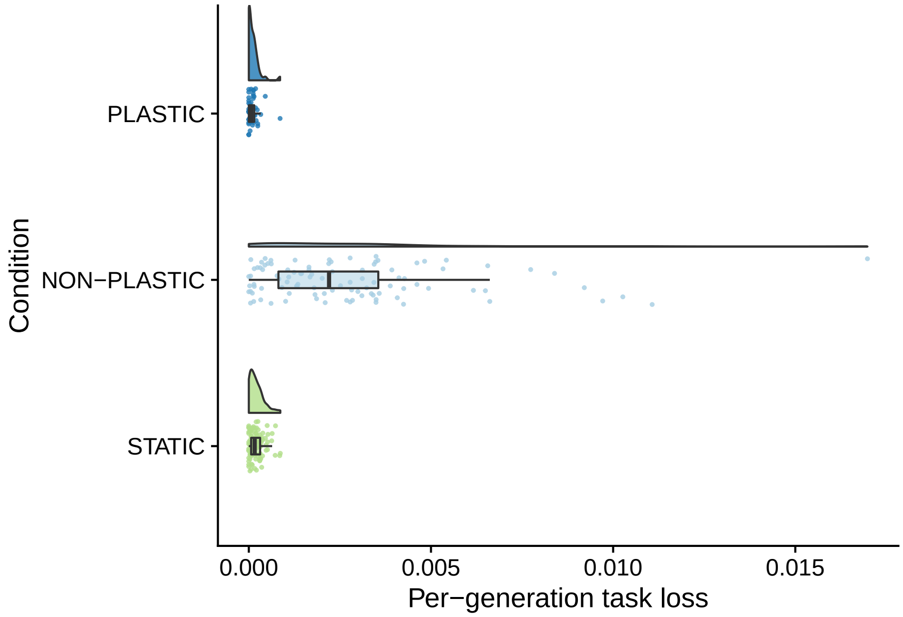
4.12.4 Per-generation task discovery

```
lineage_per_gen_task_discovery <- ggplot(
    summary_data,
    aes(x=condition, y=dominant_lineage_extra_traits_discovered_per_generation, fill=co
  ) +
  geom_flat_violin(
    position = position_nudge(x = .2, y = 0),
    alpha = .8
  ) +
  geom_point(
    mapping=aes(color=condition),
    position = position_jitter(width = .15),
    size = .5,
    alpha = 0.8
  ) +
  geom_boxplot(
    width = .1,
    outlier.shape = NA,
    alpha = 0.5
  ) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order
  ) +
  ylab("Per-generation task discovery") +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  coord_flip() +
  theme(
    legend.position="none"
  )
lineage_per_gen_task_discovery
```



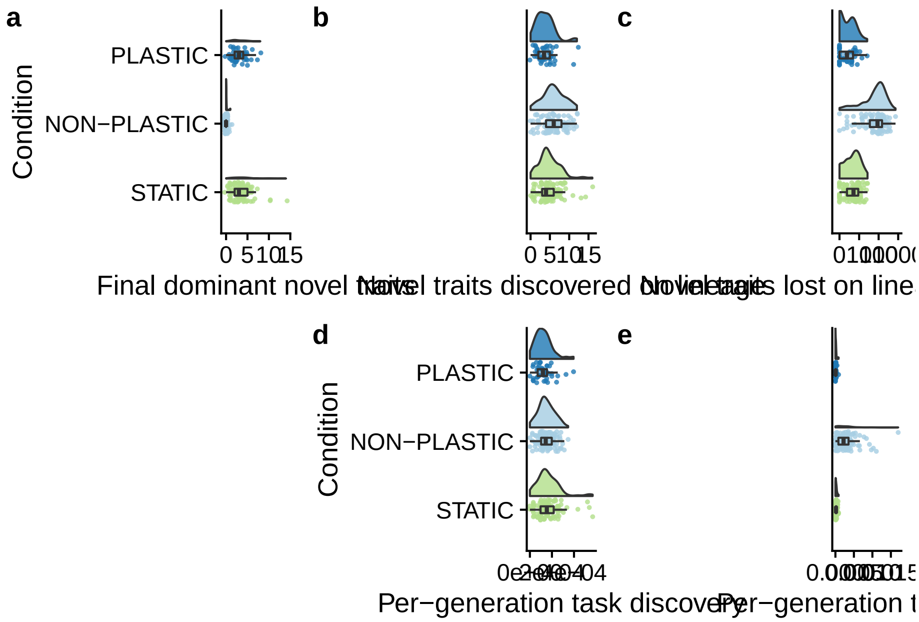
4.12.5 Per-generation task loss

```
lineage_per_gen_task_loss <- ggplot(
    summary_data,
    aes(x=condition, y=dominant_lineage_extra_traits_lost_per_generation, fill=condition)
  ) +
  geom_flat_violin(
    position = position_nudge(x = .2, y = 0),
    alpha = .8
  ) +
  geom_point(
    mapping=aes(color=condition),
    position = position_jitter(width = .15),
    size = .5,
    alpha = 0.8
  ) +
  geom_boxplot(
    width = .1,
    outlier.shape = NA,
    alpha = 0.5
  ) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order
  ) +
  ylab("Per-generation task loss") +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  coord_flip() +
  theme(
    legend.position="none"
  )
lineage_per_gen_task_loss
```



4.13 Combined panel

```
grid <- plot_grid(
  dominant_extra_tasks_fig,
  lineage_extra_tasks_discovered_fig + theme(axis.ticks.y=element_blank(),axis.text.y=element_bla
  lineage_extra_tasks_lost_fig + theme(axis.ticks.y=element_blank(),axis.text.y=element_blank(),a
  NULL,
  lineage_per_gen_task_discovery,
  lineage_per_gen_task_loss + theme(axis.ticks.y=element_blank(),axis.text.y=element_blank(),axis
  nrow=2,
  align="v",
  # labels="auto"
  labels=c("a", "b","c","", "d","e")
)
save_plot(
   paste0(working_directory, "plots/", "complex-traits-panel.pdf"),
   grid,
   base_height=12,
   base_asp=3/2
)
grid
```



```
# save_plot(
#    paste0(working_directory, "plots/", "complex-traits-panel.png"),
#    grid,
#    base_height=6,
#    base_asp=2.5
# )
```

Chapter 5

Accumulation of deleterious instructions

The effect of adaptive phenotypic plasticity on the accumulation of deleterious genes.

5.1 Overview

```
total_updates <- 200000
replicates <- 100

focal_traits <- c("not","nand","and","ornot","or","andnot")
traits_set_a <- c("not", "and", "or")
traits_set_b <- c("nand", "ornot", "andnot")

# Relative location of data.
working_directory <- "experiments/2021-02-05-hitchhiking/analysis/" # << For bookdown
# working_directory <- "./"
```

5.2 Analysis dependencies

Load all required R libraries.

```
library(RColorBrewer)
library(ggplot2)
library(tidyverse)
library(cowplot)
library(Hmisc)
library(boot)
library(fmsb)
library(knitr)
source("https://gist.githubusercontent.com/benmarwick/2a1bb0133ff568cbe28d/raw/fb53bd9
```

These analyses were conducted/knitted with 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          0.4
## year           2021
## month          02
## day            15
## svn rev        80002
## language       R
## version.string R version 4.0.4 (2021-02-15)
## nickname       Lost Library Book
```

5.3 Setup

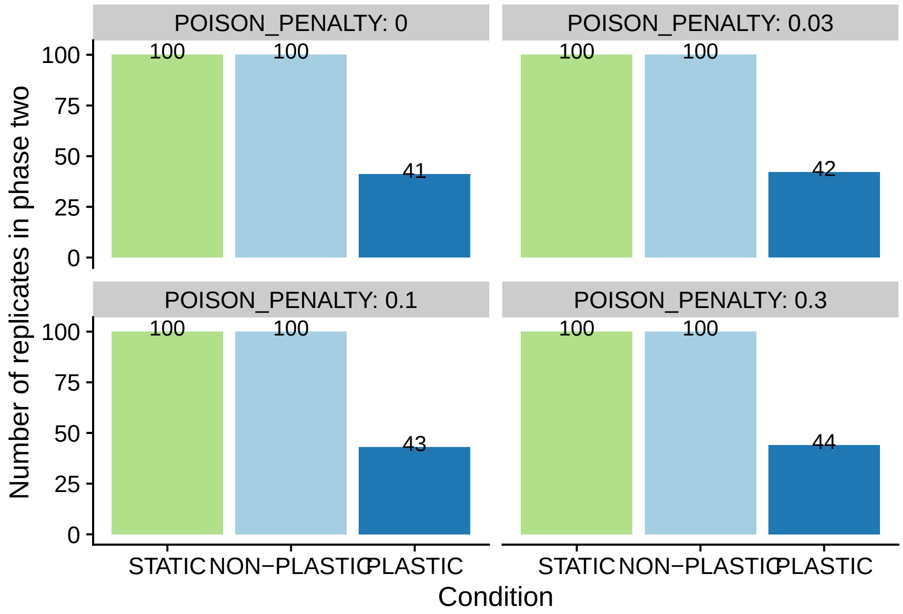
```
####### summary data #######
summary_data_loc <- paste0(working_directory, "data/aggregate.csv")
summary_data <- read.csv(summary_data_loc, na.strings="NONE")

summary_data$DISABLE_REACTION_SENSORS <- as.factor(summary_data$DISABLE_REACTION_SENSO
summary_data$chg_env <- summary_data$chg_env == "True"
summary_data$dominant_plastic_odd_even <- as.factor(summary_data$dominant_plastic_odd_
summary_data$sensors <- summary_data$DISABLE_REACTION_SENSORS == "0"
summary_data$is_plastic <- summary_data$dominant_plastic_odd_even == "True"
summary_data$POISON_PENALTY <- as.factor(summary_data$POISON_PENALTY)

env_label_fun <- function(chg_env) {
  if (chg_env) {
    return("Fluctuating")
  } else {
    return("Constant")
  }
```

```
}

sensors_label_fun <- function(has_sensors) {
  if (has_sensors) {
    return("Sensors")
  } else {
    return("No sensors")
  }
}

condition_label_fun <- function(has_sensors, env_chg) {
  if (has_sensors && env_chg) {
    return("PLASTIC")
  } else if (env_chg) {
    return("NON-PLASTIC")
  } else {
    return("STATIC")
  }
}

summary_data$env_label <- mapply(
  env_label_fun,
  summary_data$chg_env
)
summary_data$sensors_label <- mapply(
  sensors_label_fun,
  summary_data$sensors
)
summary_data$condition <- mapply(
  condition_label_fun,
  summary_data$sensors,
  summary_data$chg_env
)

condition_order = c(
  "STATIC",
  "NON-PLASTIC",
  "PLASTIC"
)

###### time series #####
lineage_time_series_data_loc <- paste0(working_directory, "data/lineage_series.csv")
lineage_time_series_data <- read.csv(lineage_time_series_data_loc)

lineage_time_series_data$DISABLE_REACTION_SENSORS <- as.factor(lineage_time_series_data$DISABLE_F
lineage_time_series_data$chg_env <- lineage_time_series_data$chg_env == "True"
lineage_time_series_data$sensors <- lineage_time_series_data$DISABLE_REACTION_SENSORS =
lineage_time_series_data$POISON_PENALTY <- as.factor(lineage_time_series_data$POISON_VA

lineage_time_series_data$env_label <- mapply(
  env_label_fun,
  lineage_time_series_data$chg_env
)
lineage_time_series_data$sensors_label <- mapply(
  sensors_label_fun,
  lineage_time_series_data$sensors
)
lineage_time_series_data$condition <- mapply(
  condition_label_fun,
  lineage_time_series_data$sensors,
  lineage_time_series_data$chg_env
)

####### misc #######
# Configure our default graphing theme
theme_set(theme_cowplot())
dir.create(paste0(working_directory, "plots"), showWarnings=FALSE)
samplemean <- function(x, d) {
  return(mean(x[d]))
}
```

5.4 Evolution of phenotypic plasticity

For sensor-enabled populations in fluctuating environments, we only transfered populations containing an optimally plastic genotype to phase-two.

```
summary_data_grouped = dplyr::group_by(summary_data, sensors, env_label, condition, POI
summary_data_group_counts = dplyr::summarize(summary_data_grouped, n=dplyr::n())

ggplot(summary_data_group_counts, aes(x=condition, y=n, fill=condition)) +
  geom_col(position=position_dodge(0.9)) +
  geom_text(aes(label=n, y=n+2)) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order
  ) +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  ylab("Number of replicates in phase two") +
  facet_wrap(~POISON_PENALTY, labeller=label_both) +
  theme(
    legend.position="none"
  )
```

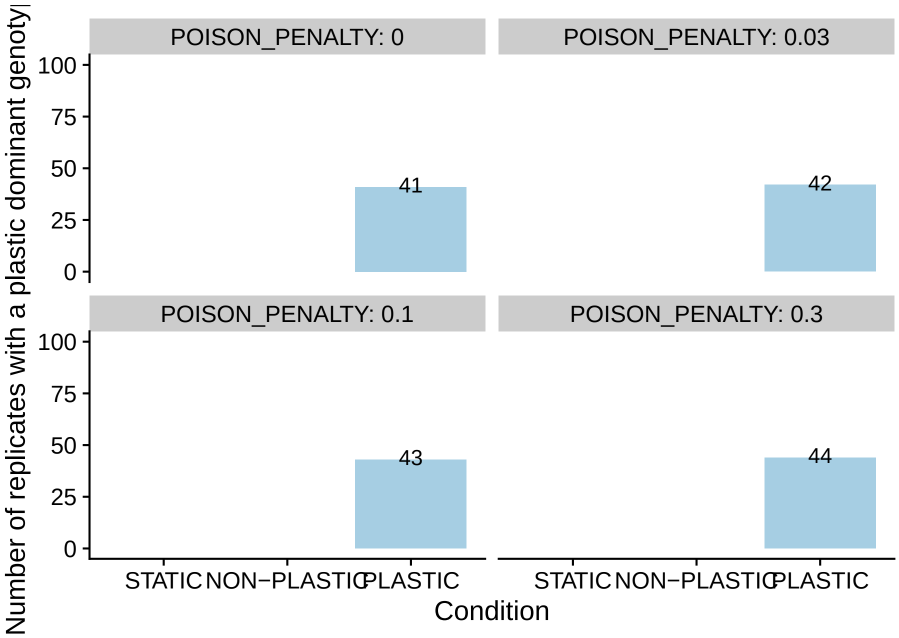


We can confirm our expectation that the dominant genotypes in non-plastic conditions are not phenotypically plastic.

```
summary_data_grouped = dplyr::group_by(summary_data, condition, is_plastic, POISON_PENALTY)
summary_data_group_counts = dplyr::summarize(summary_data_grouped, n=dplyr::n())
```

```
## `summarise()` has grouped output by 'condition', 'is_plastic'. You can override using the `.gr
```

```
ggplot(filter(summary_data_group_counts, is_plastic), aes(x=condition, y=n, fill=condition)) +
  geom_col(position=position_dodge(0.9)) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order
  ) +
  geom_text(aes(label=n, y=n+1)) +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  ylab("Number of replicates with a plastic dominant genotype") +
  ylim(0, 100) +
  facet_wrap(~POISON_PENALTY, labeller=label_both) +
  theme(
    legend.position="none"
  )
```



5.5 Poison instruction execution

5.5.1 Number of replicates where final dominant genotype executes the poison instruction

```
poison_penalty <- 0.1
```

```
occurrences <- c(
  length(filter(summary_data, POISON_PENALTY==poison_penalty & condition=="NON-PLASTIC"
  length(filter(summary_data, POISON_PENALTY==poison_penalty & condition=="PLASTIC" & c
  length(filter(summary_data, POISON_PENALTY==poison_penalty & condition=="STATIC" & do
)
trials <- c(
  length(filter(summary_data, POISON_PENALTY==poison_penalty & condition=="NON-PLASTIC"
  length(filter(summary_data, POISON_PENALTY==poison_penalty & condition=="PLASTIC")$RANDOM_SEED)
  length(filter(summary_data, POISON_PENALTY==poison_penalty & condition=="STATIC" )$RANDOM_SEED)
)
names(trials) <- c(
  "NON-PLASTIC",
  "PLASTIC",
  "STATIC"
)
names(occurrences) <- c(
  "NON-PLASTIC",
  "PLASTIC",
  "STATIC"
)

poison_exec_table <- data.frame(
  executes.poison=occurrences,
  replicates=trials
)
kable(poison_exec_table)
```

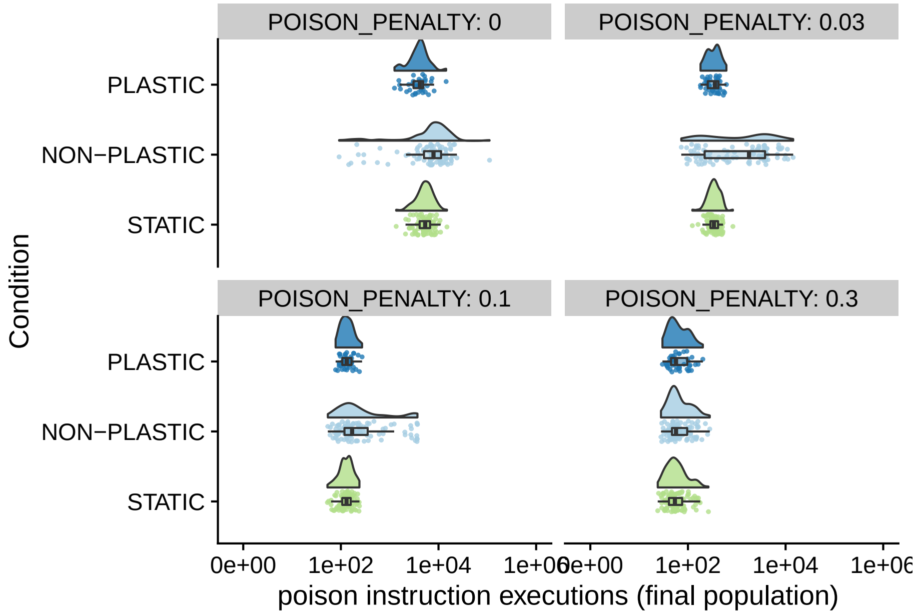
	executes.poison	replicates
NON-PLASTIC	14	100
PLASTIC	0	43
STATIC	0	100

```
pairwise.fisher.test(x=occurrences, n=trials, p.adjust.method="bonferroni")
```

```
##
##  Pairwise comparisons using Pairwise comparison of proportions (Fisher)
##
## data:  occurrences out of trials
##
##         NON-PLASTIC PLASTIC
## PLASTIC 0.03212     -
## STATIC  0.00022     1.00000
##
## P value adjustment method: bonferroni
```

5.5.2 Poison instruction execution in final population

```
ggplot(summary_data, aes(x=condition, y=final_population_poison, fill=condition)) +
  geom_flat_violin(
    position = position_nudge(x = .2, y = 0),
    alpha = .8
  ) +
  geom_point(
    mapping=aes(color=condition),
    position = position_jitter(width = .15),
    size = .5,
    alpha = 0.8
  ) +
  geom_boxplot(
    width = .1,
    outlier.shape = NA,
    alpha = 0.5
  ) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order
  ) +
  scale_y_continuous(
    name="poison instruction executions (final population)",
    trans="pseudo_log",
    breaks=c(0,100,10000,1000000),
    limits=c(-1,1000000)
  ) +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  facet_wrap(
    ~POISON_PENALTY,
    labeller=label_both
  ) +
  coord_flip() +
  theme(
    legend.position="none"
  ) +
  ggsave(
    paste0(working_directory, "plots/final-population-poison-log.pdf"),
    width=15,
    height=10
  )
```



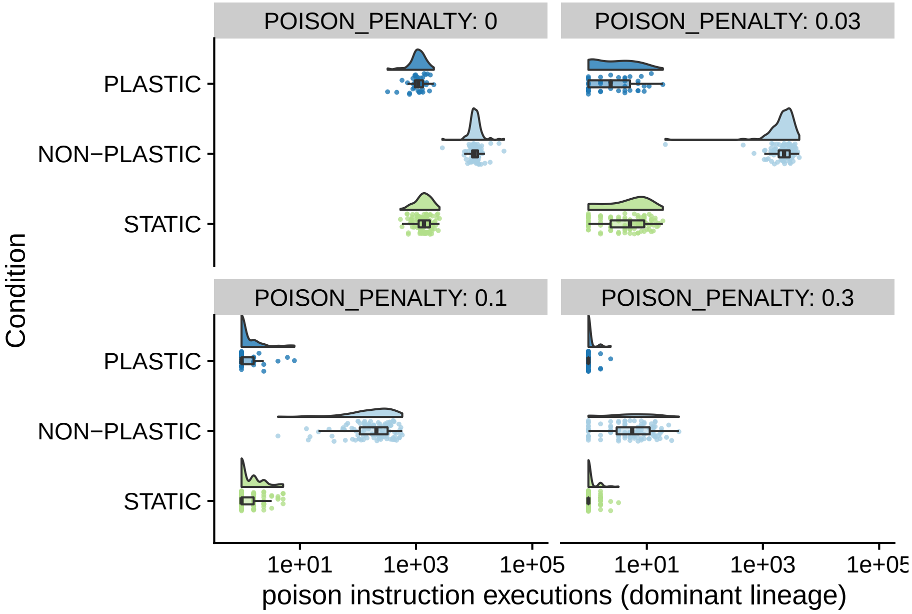
```
penalties <- levels(summary_data$POISON_PENALTY)
for (penalty in penalties) {
  stat_data <- filter(summary_data, POISON_PENALTY==penalty)
  print(
    paste0(
      "PENALTY: ", penalty
    )
  )
  kt <- kruskal.test(
      formula=final_population_poison~condition,
      data=stat_data
    )
  print(
    kt
  )
  if (is.na(kt$p.value)) { next }
  if (kt$p.value > 0.05) { next }
  print(
    pairwise.wilcox.test(
      x=stat_data$final_population_poison,
      g=stat_data$condition,
      p.adjust.method="bonferroni"
    )
  )
}
```

```
## [1] "PENALTY: 0"
##
##  Kruskal-Wallis rank sum test
##
## data:  final_population_poison by condition
## Kruskal-Wallis chi-squared = 43.589, df = 2, p-value = 3.426e-10
##
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  stat_data$final_population_poison and stat_data$condition
##
##         NON-PLASTIC PLASTIC
## PLASTIC 8.7e-07     -
## STATIC  9.8e-07     0.00074
##
## P value adjustment method: bonferroni
## [1] "PENALTY: 0.03"
##
##  Kruskal-Wallis rank sum test
##
## data:  final_population_poison by condition
## Kruskal-Wallis chi-squared = 20.74, df = 2, p-value = 3.136e-05
##
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  stat_data$final_population_poison and stat_data$condition
##
##         NON-PLASTIC PLASTIC
## PLASTIC 0.003       -
## STATIC  1e-04       1.000
##
## P value adjustment method: bonferroni
## [1] "PENALTY: 0.1"
##
##  Kruskal-Wallis rank sum test
##
## data:  final_population_poison by condition
## Kruskal-Wallis chi-squared = 20.608, df = 2, p-value = 3.35e-05
##
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  stat_data$final_population_poison and stat_data$condition
##
```

```
##         NON-PLASTIC PLASTIC
## PLASTIC 0.0093      -
## STATIC  4.9e-05     1.0000
##
## P value adjustment method: bonferroni
## [1] "PENALTY: 0.3"
##
##  Kruskal-Wallis rank sum test
##
## data:  final_population_poison by condition
## Kruskal-Wallis chi-squared = 3.3994, df = 2, p-value = 0.1827
```

5.5.3 Poison instruction execution along final dominant lineage (cummulative)

```r
ggplot(summary_data, aes(x=condition, y=dominant_lineage_times_poison_executed, fill=condition))
  geom_flat_violin(
    position = position_nudge(x = .2, y = 0),
    alpha = .8
  ) +
  geom_point(
    mapping=aes(color=condition),
    position = position_jitter(width = .15),
    size = .5,
    alpha = 0.8
  ) +
  geom_boxplot(
    width = .1,
    outlier.shape = NA,
    alpha = 0.5
  ) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order
  ) +
  scale_y_continuous(
    name="poison instruction executions (dominant lineage)",
    trans="pseudo_log",
    breaks=c(10,1000,100000),
    limits=c(-1,100000)
  ) +
  facet_wrap(
    ~POISON_PENALTY,
    labeller=label_both
  ) +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  coord_flip() +
  theme(
    legend.position="none"
  ) +
  ggsave(
    paste0(working_directory, "plots/final-dominant-lineage-poison-log.pdf"),
    width=15,
    height=10
  )
```



```
penalties <- levels(summary_data$POISON_PENALTY)
for (penalty in penalties) {
  stat_data <- filter(summary_data, POISON_PENALTY==penalty)
  print(
    paste0(
      "PENALTY: ", penalty
    )
  )
  kt <- kruskal.test(
      formula=dominant_lineage_times_poison_executed~condition,
      data=stat_data
    )
  print(
    kt
  )
  if (is.na(kt$p.value)) { next }
  if (kt$p.value > 0.05) { next }
  print(
    pairwise.wilcox.test(
      x=stat_data$dominant_lineage_times_poison_executed,
      g=stat_data$condition,
      p.adjust.method="bonferroni"
    )
  )
}
```

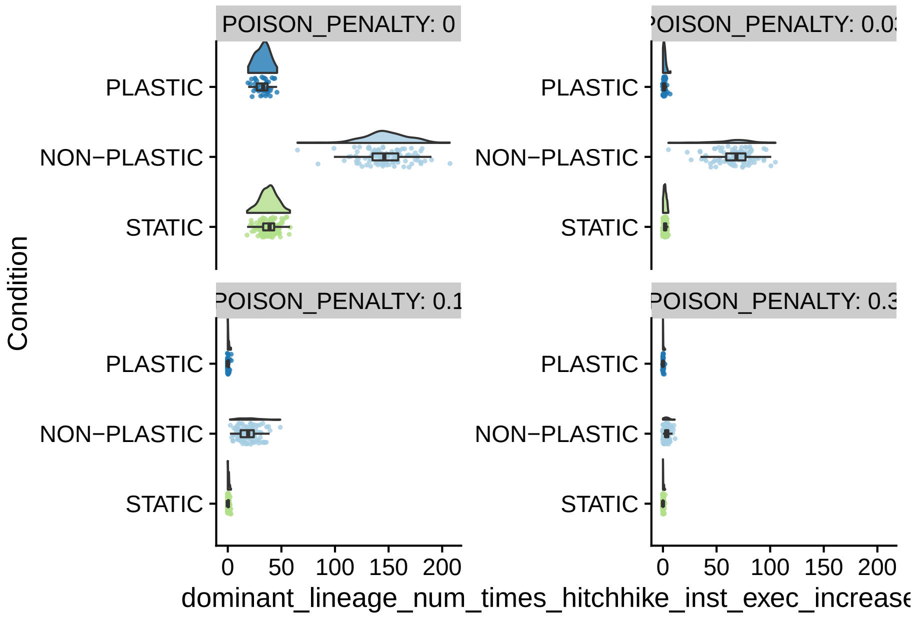
```
## [1] "PENALTY: 0"
##
##  Kruskal-Wallis rank sum test
##
## data:  dominant_lineage_times_poison_executed by condition
## Kruskal-Wallis chi-squared = 178.84, df = 2, p-value < 2.2e-16
##
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  stat_data$dominant_lineage_times_poison_executed and stat_data$condition
##
##         NON-PLASTIC PLASTIC
## PLASTIC <2e-16      -
## STATIC  <2e-16      0.0018
##
## P value adjustment method: bonferroni
## [1] "PENALTY: 0.03"
##
##  Kruskal-Wallis rank sum test
##
## data:  dominant_lineage_times_poison_executed by condition
## Kruskal-Wallis chi-squared = 178.62, df = 2, p-value < 2.2e-16
##
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  stat_data$dominant_lineage_times_poison_executed and stat_data$condition
```

```
##
##         NON-PLASTIC PLASTIC
## PLASTIC <2e-16      -
## STATIC  <2e-16      0.011
##
## P value adjustment method: bonferroni
## [1] "PENALTY: 0.1"
##
##  Kruskal-Wallis rank sum test
##
## data:  dominant_lineage_times_poison_executed by condition
## Kruskal-Wallis chi-squared = 184.83, df = 2, p-value < 2.2e-16
##
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  stat_data$dominant_lineage_times_poison_executed and stat_data$condition
##
##         NON-PLASTIC PLASTIC
## PLASTIC <2e-16      -
## STATIC  <2e-16      0.21
##
## P value adjustment method: bonferroni
## [1] "PENALTY: 0.3"
##
##  Kruskal-Wallis rank sum test
##
## data:  dominant_lineage_times_poison_executed by condition
## Kruskal-Wallis chi-squared = 149.48, df = 2, p-value < 2.2e-16
##
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  stat_data$dominant_lineage_times_poison_executed and stat_data$condition
##
##         NON-PLASTIC PLASTIC
## PLASTIC 4.4e-16     -
## STATIC  < 2e-16     0.84
##
## P value adjustment method: bonferroni
```

5.6 Characterizing mutations that increase poison instruction execution

5.6.1 Number of offspring along dominant lineage with increase in poison instruction execution

```
ggplot(summary_data, aes(x=condition, y=dominant_lineage_num_times_hitchhike_inst_exec_increases,
  geom_flat_violin(
    position = position_nudge(x = .2, y = 0),
    alpha = .8
  ) +
  geom_point(
    mapping=aes(color=condition),
    position = position_jitter(width = .15),
    size = .5,
    alpha = 0.8
  ) +
  geom_boxplot(
    width = .1,
    outlier.shape = NA,
    alpha = 0.5
  ) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order
  ) +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  coord_flip() +
  facet_wrap(
    ~POISON_PENALTY,
    labeller=label_both,
    scales="free_y"
  ) +
  theme(
    legend.position="none"
  ) +
  ggsave(
    paste0(working_directory, "plots/final-dominant-lineage-poison-increase-num-mutants-log.png")
    width=15,
    height=10
  )
```



```
penalties <- levels(summary_data$POISON_PENALTY)
for (penalty in penalties) {
  stat_data <- filter(summary_data, POISON_PENALTY==penalty)
  print(
    paste0(
      "PENALTY: ", penalty
    )
  )
  kt <- kruskal.test(
      formula=dominant_lineage_num_times_hitchhike_inst_exec_increases~condition,
      data=stat_data
    )
  print(
    kt
  )
  if (is.na(kt$p.value)) { next }
  if (kt$p.value > 0.05) { next }
  print(
    pairwise.wilcox.test(
      x=stat_data$dominant_lineage_num_times_hitchhike_inst_exec_increases,
      g=stat_data$condition,
      p.adjust.method="bonferroni"
    )
  )
}
```

```
## [1] "PENALTY: 0"
##
##  Kruskal-Wallis rank sum test
##
## data:  dominant_lineage_num_times_hitchhike_inst_exec_increases by condition
## Kruskal-Wallis chi-squared = 179.79, df = 2, p-value < 2.2e-16
##
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  stat_data$dominant_lineage_num_times_hitchhike_inst_exec_increases and stat_data$condit
##
##         NON-PLASTIC PLASTIC
## PLASTIC < 2e-16     -
## STATIC  < 2e-16     0.00046
##
## P value adjustment method: bonferroni
## [1] "PENALTY: 0.03"
##
##  Kruskal-Wallis rank sum test
##
## data:  dominant_lineage_num_times_hitchhike_inst_exec_increases by condition
## Kruskal-Wallis chi-squared = 179.35, df = 2, p-value < 2.2e-16
##
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  stat_data$dominant_lineage_num_times_hitchhike_inst_exec_increases and stat_data$condit
##
##         NON-PLASTIC PLASTIC
## PLASTIC <2e-16      -
## STATIC  <2e-16      0.03
##
## P value adjustment method: bonferroni
## [1] "PENALTY: 0.1"
##
##  Kruskal-Wallis rank sum test
##
## data:  dominant_lineage_num_times_hitchhike_inst_exec_increases by condition
## Kruskal-Wallis chi-squared = 185.34, df = 2, p-value < 2.2e-16
##
##
```

```
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  stat_data$dominant_lineage_num_times_hitchhike_inst_exec_increases and stat_c
##
##         NON-PLASTIC PLASTIC
## PLASTIC <2e-16      -
## STATIC  <2e-16      0.27
##
## P value adjustment method: bonferroni
## [1] "PENALTY: 0.3"
##
##  Kruskal-Wallis rank sum test
##
## data:  dominant_lineage_num_times_hitchhike_inst_exec_increases by condition
## Kruskal-Wallis chi-squared = 146.35, df = 2, p-value < 2.2e-16
##
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  stat_data$dominant_lineage_num_times_hitchhike_inst_exec_increases and stat_c
##
##         NON-PLASTIC PLASTIC
## PLASTIC 7.8e-16     -
## STATIC  < 2e-16     0.86
##
## P value adjustment method: bonferroni
```

```
sum(filter(summary_data, condition=="NON-PLASTIC" & POISON_PENALTY==0.1)$dominant_linea
```

```
## [1] 1916
```

```
sum(filter(summary_data, condition=="PLASTIC" & POISON_PENALTY==0.1)$dominant_lineage_n
```

```
## [1] 18
```

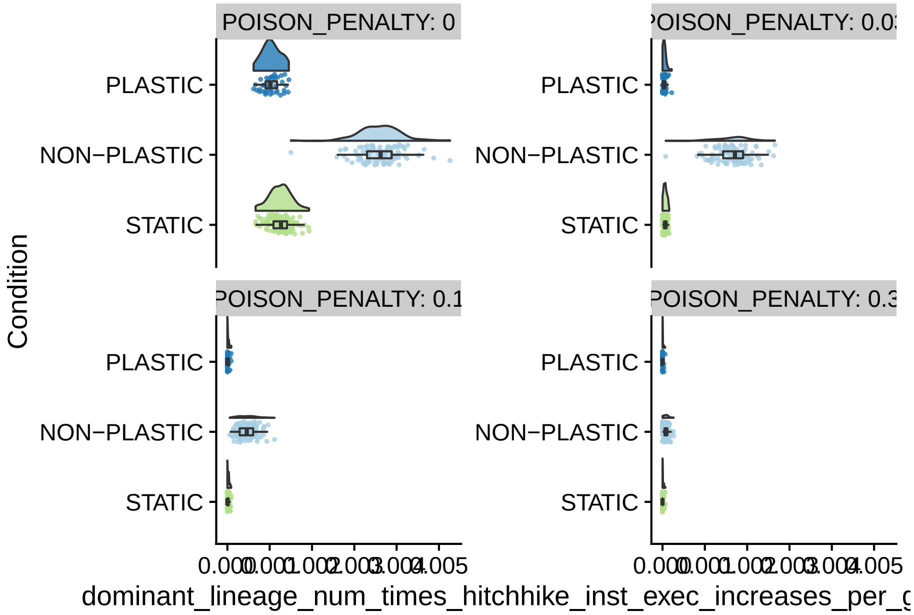
```
sum(filter(summary_data, condition=="STATIC" & POISON_PENALTY==0.1)$dominant_lineage_nu
```

```
## [1] 58
```

```
# sum(filter(summary_data, condition=="NON-PLASTIC" & POISON_PENALTY==0.1)$dominant_li
# sum(filter(summary_data, condition=="PLASTIC" & POISON_PENALTY==0.1)$dominant_lineag
# sum(filter(summary_data, condition=="STATIC" & POISON_PENALTY==0.1)$dominant_lineage_
```

5.6.2 Per-generation increases in poison instruction execution

```
summary_data$dominant_lineage_num_times_hitchhike_inst_exec_increases_per_generation <- summary_d
ggplot(summary_data, aes(x=condition, y=dominant_lineage_num_times_hitchhike_inst_exec_increases_
  geom_flat_violin(
    position = position_nudge(x = .2, y = 0),
    alpha = .8
  ) +
  geom_point(
    mapping=aes(color=condition),
    position = position_jitter(width = .15),
    size = .5,
    alpha = 0.8
  ) +
  geom_boxplot(
    width = .1,
    outlier.shape = NA,
    alpha = 0.5
  ) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order
  ) +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  facet_wrap(
    ~POISON_PENALTY,
    labeller=label_both,
    scales="free_y"
  ) +
  coord_flip() +
  theme(
    legend.position="none"
  ) +
  ggsave(
    paste0(working_directory, "plots/final-dominant-lineage-poison-increase-per-generation.png"),
    width=15,
    height=10
  )
```



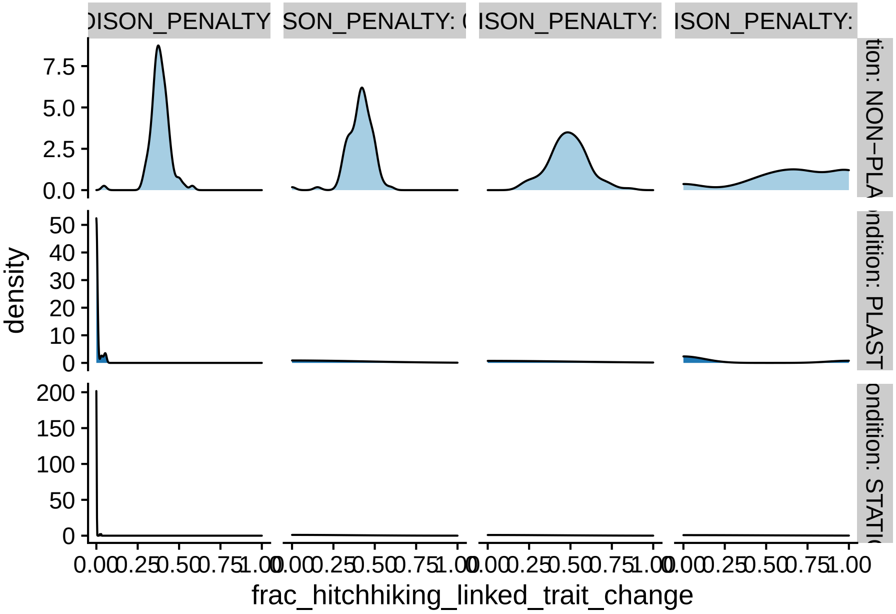
```
penalties <- levels(summary_data$POISON_PENALTY)
for (penalty in penalties) {
  stat_data <- filter(summary_data, POISON_PENALTY==penalty)
  print(
    paste0(
      "PENALTY: ", penalty
    )
  )
  kt <- kruskal.test(
      formula=dominant_lineage_num_times_hitchhike_inst_exec_increases_per_generation~
      data=stat_data
    )
  print(
    kt
  )
  if (is.na(kt$p.value)) { next }
  if (kt$p.value > 0.05) { next }
  print(
    pairwise.wilcox.test(
      x=stat_data$dominant_lineage_num_times_hitchhike_inst_exec_increases_per_generati
      g=stat_data$condition,
      p.adjust.method="bonferroni"
    )
  )
}
```

```
## [1] "PENALTY: 0"
##
##  Kruskal-Wallis rank sum test
##
## data:  dominant_lineage_num_times_hitchhike_inst_exec_increases_per_generation by condition
## Kruskal-Wallis chi-squared = 180.05, df = 2, p-value < 2.2e-16
##
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  stat_data$dominant_lineage_num_times_hitchhike_inst_exec_increases_per_generation and s
##
##         NON-PLASTIC PLASTIC
## PLASTIC < 2e-16     -
## STATIC  < 2e-16     7.8e-05
##
## P value adjustment method: bonferroni
## [1] "PENALTY: 0.03"
##
##  Kruskal-Wallis rank sum test
##
## data:  dominant_lineage_num_times_hitchhike_inst_exec_increases_per_generation by condition
## Kruskal-Wallis chi-squared = 176.25, df = 2, p-value < 2.2e-16
##
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  stat_data$dominant_lineage_num_times_hitchhike_inst_exec_increases_per_generation and s
##
##         NON-PLASTIC PLASTIC
## PLASTIC <2e-16      -
## STATIC  <2e-16      0.019
##
## P value adjustment method: bonferroni
## [1] "PENALTY: 0.1"
##
##  Kruskal-Wallis rank sum test
##
## data:  dominant_lineage_num_times_hitchhike_inst_exec_increases_per_generation by condition
## Kruskal-Wallis chi-squared = 184.17, df = 2, p-value < 2.2e-16
##
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  stat_data$dominant_lineage_num_times_hitchhike_inst_exec_increases_per_generation and s
##
```

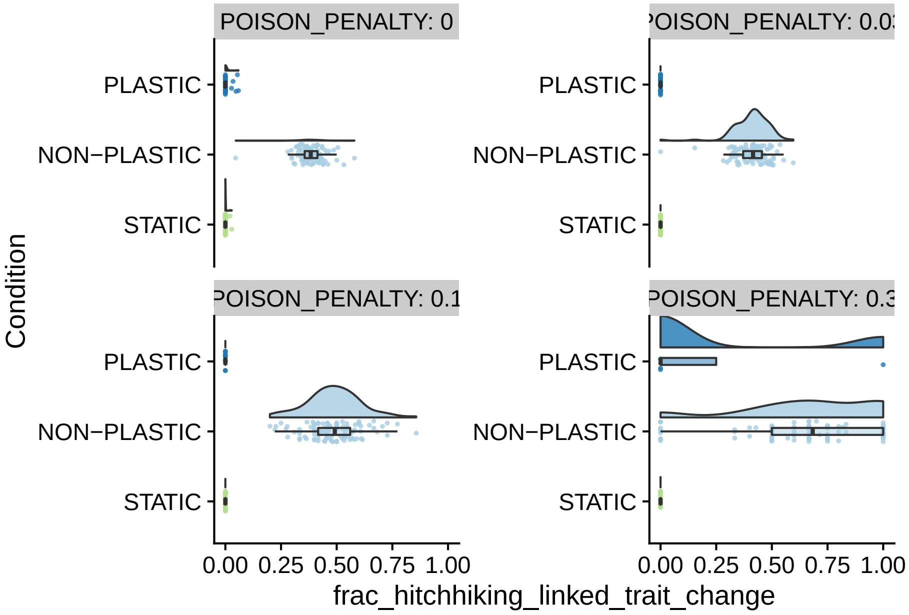
```
##         NON-PLASTIC PLASTIC
## PLASTIC <2e-16      -
## STATIC  <2e-16      0.2
##
## P value adjustment method: bonferroni
## [1] "PENALTY: 0.3"
##
##  Kruskal-Wallis rank sum test
##
## data:  dominant_lineage_num_times_hitchhike_inst_exec_increases_per_generation by co
## Kruskal-Wallis chi-squared = 140.99, df = 2, p-value < 2.2e-16
##
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  stat_data$dominant_lineage_num_times_hitchhike_inst_exec_increases_per_genera
##
##         NON-PLASTIC PLASTIC
## PLASTIC 2.2e-15     -
## STATIC  < 2e-16     0.79
##
## P value adjustment method: bonferroni
```

5.6.3 What fraction of mutations that increase poison instruction execution co-occur with base trait changes?

```
summary_data$frac_hitchhiking_linked_trait_change <- summary_data$dominant_lineage_num_

ggplot(filter(summary_data, dominant_lineage_num_times_hitchhike_inst_exec_increases>0)
  geom_density() +
  facet_grid(
    condition~POISON_PENALTY,
    labeller=label_both,
    scales="free_y"
  ) +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  theme(
    legend.position="none"
  ) +
  ggsave(
    paste0(working_directory, "plots/dominant-lineage-frac_hitchhiking_linked_trait_change.png"),
    width=15,
    height=10
  )
```



```
ggplot(filter(summary_data, dominant_lineage_num_times_hitchhike_inst_exec_increases>0 ), aes(x=c
  geom_flat_violin(
    position = position_nudge(x = .2, y = 0),
    alpha = .8
  ) +
  geom_point(
    mapping=aes(color=condition),
    position = position_jitter(width = .15),
    size = .5,
    alpha = 0.8
  ) +
  geom_boxplot(
    width = .1,
    outlier.shape = NA,
    alpha = 0.5
  ) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order
  ) +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  facet_wrap(
    ~POISON_PENALTY,
    labeller=label_both,
    scales="free_y"
  ) +
  coord_flip() +
  theme(
    legend.position="none"
  )
```



```
penalties <- levels(summary_data$POISON_PENALTY)
for (penalty in penalties) {
  stat_data <- filter(summary_data, POISON_PENALTY==penalty & dominant_lineage_num_time
  print(
    paste0(
      "PENALTY: ", penalty
    )
  )
  kt <- kruskal.test(
      formula=frac_hitchhiking_linked_trait_change~condition,
      data=stat_data
    )
  print(
    kt
  )
  if (is.na(kt$p.value)) { next }
  if (kt$p.value > 0.05) { next }
  print(
    pairwise.wilcox.test(
      x=stat_data$frac_hitchhiking_linked_trait_change,
      g=stat_data$condition,
      p.adjust.method="bonferroni",
      exact=FALSE
    )
  )
}
```

```
## [1] "PENALTY: 0"
##
##  Kruskal-Wallis rank sum test
##
## data:  frac_hitchhiking_linked_trait_change by condition
## Kruskal-Wallis chi-squared = 211.29, df = 2, p-value < 2.2e-16
##
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  stat_data$frac_hitchhiking_linked_trait_change and stat_data$condition
##
##         NON-PLASTIC PLASTIC
## PLASTIC <2e-16      -
## STATIC  <2e-16      0.031
##
## P value adjustment method: bonferroni
## [1] "PENALTY: 0.03"
##
##  Kruskal-Wallis rank sum test
##
## data:  frac_hitchhiking_linked_trait_change by condition
## Kruskal-Wallis chi-squared = 186.88, df = 2, p-value < 2.2e-16
##
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
```

```
##
## data:  stat_data$frac_hitchhiking_linked_trait_change and stat_data$condition
##
##         NON-PLASTIC PLASTIC
## PLASTIC 2.9e-16     -
## STATIC  < 2e-16     -
##
## P value adjustment method: bonferroni
## [1] "PENALTY: 0.1"
##
##  Kruskal-Wallis rank sum test
##
## data:  frac_hitchhiking_linked_trait_change by condition
## Kruskal-Wallis chi-squared = 113.72, df = 2, p-value < 2.2e-16
##
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  stat_data$frac_hitchhiking_linked_trait_change and stat_data$condition
##
##         NON-PLASTIC PLASTIC
## PLASTIC 3.3e-08     -
## STATIC  < 2e-16     -
##
## P value adjustment method: bonferroni
## [1] "PENALTY: 0.3"
##
##  Kruskal-Wallis rank sum test
##
## data:  frac_hitchhiking_linked_trait_change by condition
## Kruskal-Wallis chi-squared = 34.791, df = 2, p-value = 2.788e-08
##
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  stat_data$frac_hitchhiking_linked_trait_change and stat_data$condition
##
##         NON-PLASTIC PLASTIC
## PLASTIC 0.26        -
## STATIC  2.4e-08     0.18
##
## P value adjustment method: bonferroni
```

```
denom <- sum(filter(summary_data, condition=="NON-PLASTIC" & POISON_PENALTY==0.1)$domi
num <- sum(filter(summary_data, condition=="NON-PLASTIC" & POISON_PENALTY==0.1)$dominan
paste0("NON-PLASTIC: ", num/denom, "(", num, "/", denom, ")")
```

```
## [1] "NON-PLASTIC: 0.498956158663883(956/1916)"
```

```
denom <- sum(filter(summary_data, condition=="PLASTIC" & POISON_PENALTY==0.1)$dominant_lineage_nu
num <- sum(filter(summary_data, condition=="PLASTIC" & POISON_PENALTY==0.1)$dominant_lineage_num_
paste0("PLASTIC: ", num/denom, " (", num, "/", denom, ")")
```

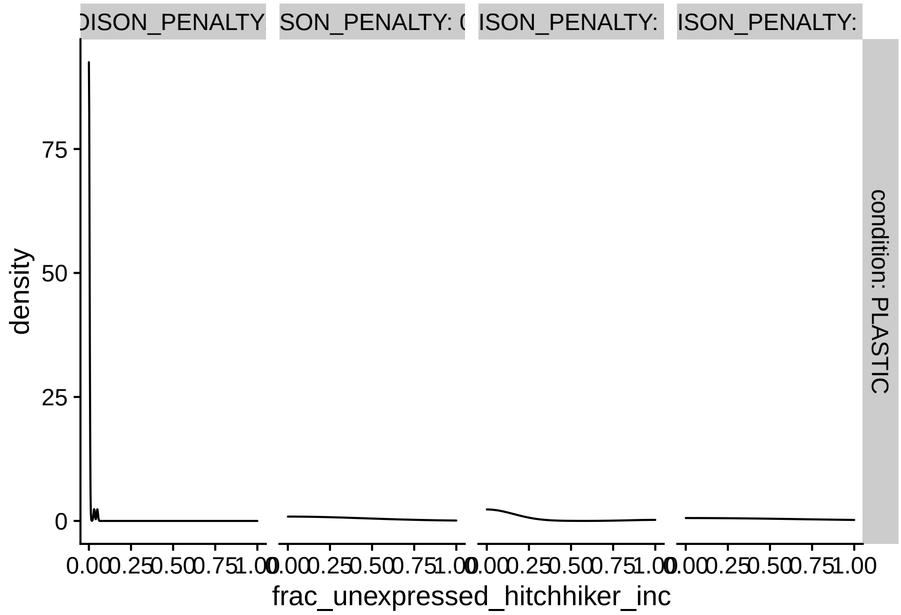
```
## [1] "PLASTIC: 0 (0/18)"
```

```
denom <- sum(filter(summary_data, condition=="STATIC" & POISON_PENALTY==0.1)$dominant_lineage_num
num <- sum(filter(summary_data, condition=="STATIC" & POISON_PENALTY==0.1)$dominant_lineage_num_t
paste0("STATIC: ", num/denom, " (", num, "/", denom, ")")
```

```
## [1] "STATIC: 0 (0/58)"
```

5.7 What fraction of poison execution increases occur in unexpressed phenotype (as cryptic

```
summary_data$frac_unexpressed_hitchhiker_inc <- summary_data$dominant_lineage_num_times_hitchhike
summary_data$frac_expressed_hitchiker_inc <- summary_data$dominant_lineage_num_times_hitchhike_in

ggplot(filter(summary_data, dominant_lineage_num_times_hitchhike_inst_exec_increases>0 & conditic
  geom_density() +
  facet_grid(
    condition~POISON_PENALTY,
    labeller=label_both,
    scales="free_y"
  ) +
  theme(
    legend.position="none"
  )
```



```
denom <- sum(filter(summary_data, condition=="PLASTIC" & POISON_PENALTY==0.1)$dominant_
num <- sum(filter(summary_data, condition=="PLASTIC" & POISON_PENALTY==0.1)$dominant_li
paste0("PLASTIC: ", num/denom, " (", num, "/", denom, ")")
```

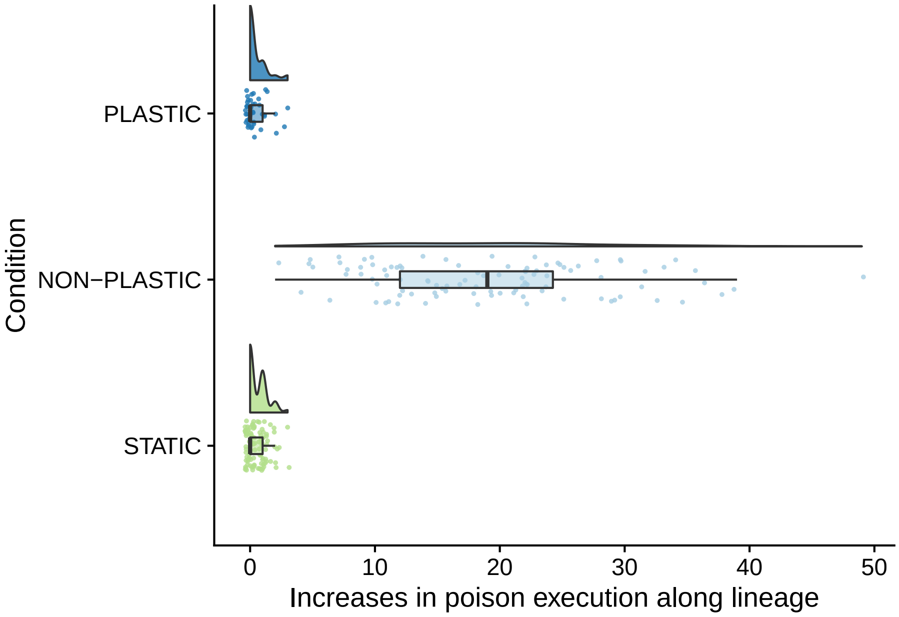
```
## [1] "PLASTIC: 0.0555555555555556 (1/18)"
```

5.8 Manuscript figures

```
poison_penalty <- 0.1
```

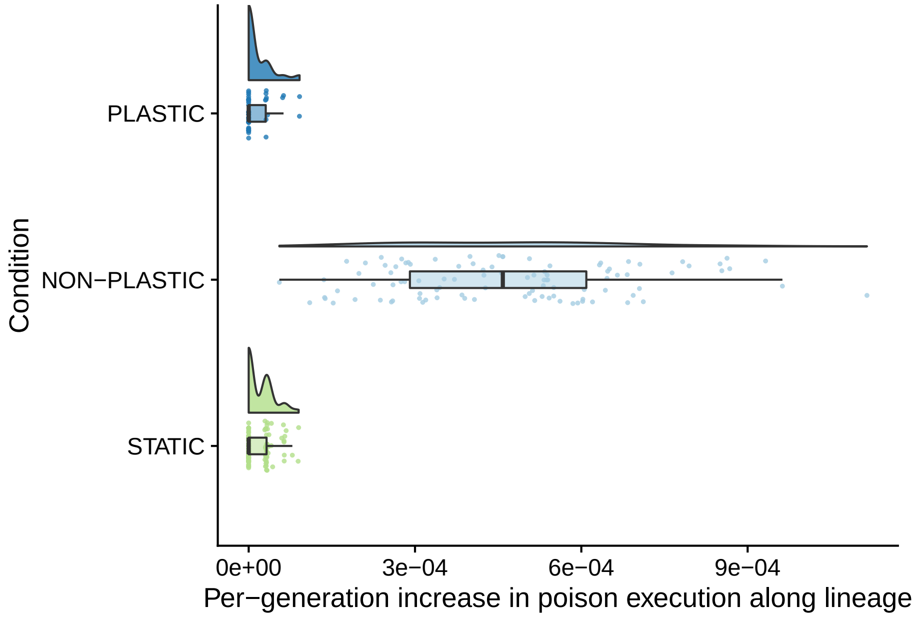
5.8.1 Total poison execution increases along lineage.

```
poison_increases_fig <- ggplot(
    filter(summary_data, POISON_PENALTY==poison_penalty),
    aes(x=condition, y=dominant_lineage_num_times_hitchhike_inst_exec_increases, fill=c
  ) +
  geom_flat_violin(
    position = position_nudge(x = .2, y = 0),
    alpha = .8
  ) +
  geom_point(
    mapping=aes(color=condition),
    position = position_jitter(width = .15),
    size = .5,
    alpha = 0.8
  ) +
  geom_boxplot(
    width = .1,
    outlier.shape = NA,
    alpha = 0.5
  ) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order,
    labels=condition_order
  ) +
  scale_y_continuous(
    name="Increases in poison execution along lineage",
  ) +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  theme(
    legend.position="none"
  ) +
  coord_flip()

poison_increases_fig
```



5.8.2 Per-generation poison execution increases along lineage

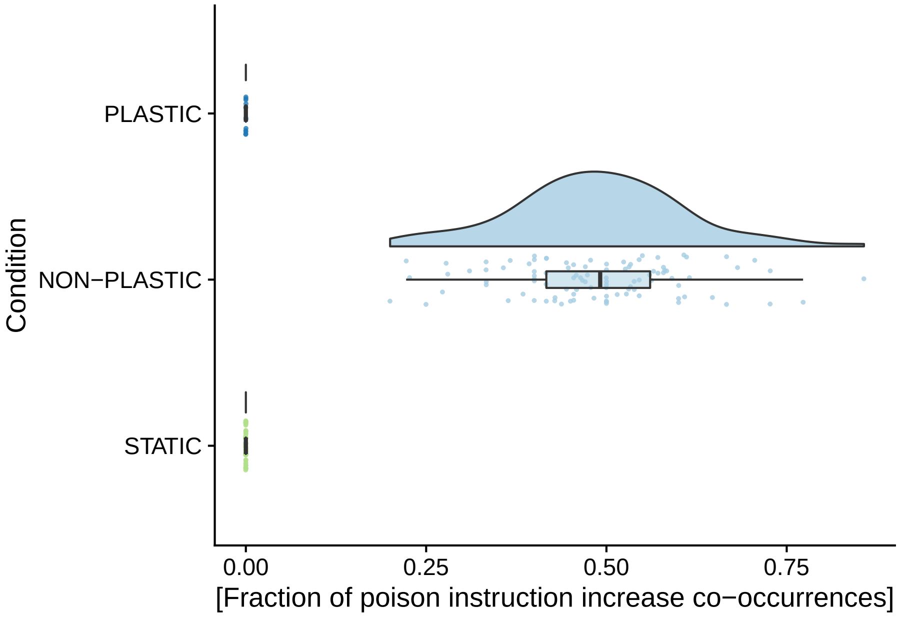
```
poison_increases_per_gen_fig <- ggplot(
    filter(summary_data, POISON_PENALTY==poison_penalty),
    aes(x=condition, y=dominant_lineage_num_times_hitchhike_inst_exec_increases_per_ge
  ) +
  geom_flat_violin(
    position = position_nudge(x = .2, y = 0),
    alpha = .8
  ) +
  geom_point(
    mapping=aes(color=condition),
    position = position_jitter(width = .15),
    size = .5,
    alpha = 0.8
  ) +
  geom_boxplot(
    width = .1,
    outlier.shape = NA,
    alpha = 0.5
  ) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order,
    labels=condition_order
  ) +
  scale_y_continuous(
    name="Per-generation increase in poison execution along lineage",
  ) +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  theme(
    legend.position="none"
  ) +
  coord_flip()

poison_increases_per_gen_fig
```



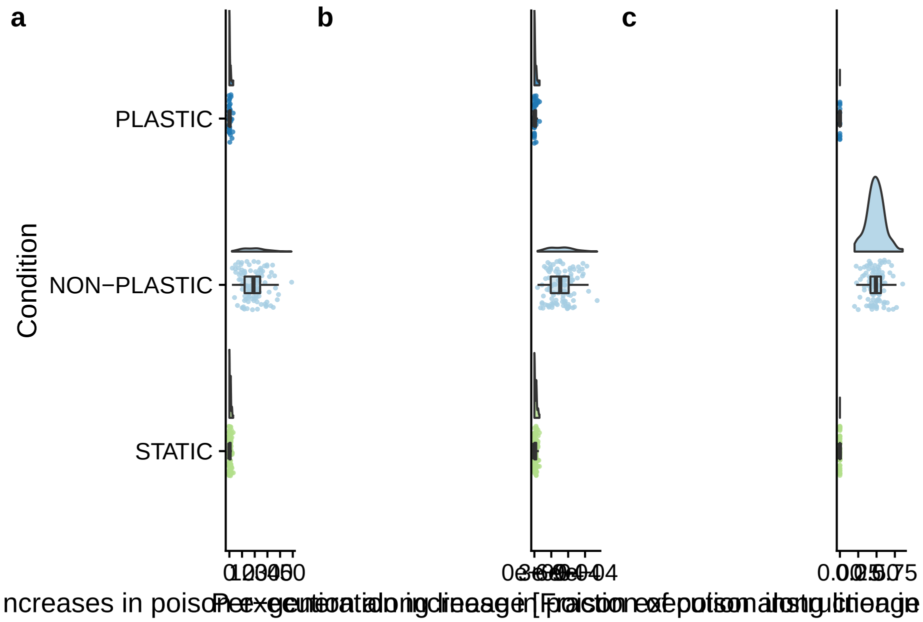
5.8.3 Co-occurrence

```
linked_trait_change_fig <- ggplot(
    filter(summary_data, POISON_PENALTY==poison_penalty & dominant_lineage_num_times_hitchhike_in
    aes(x=condition, y=frac_hitchhiking_linked_trait_change, fill=condition)
```

```
  ) +
  geom_flat_violin(
    position = position_nudge(x = .2, y = 0),
    alpha = .8
  ) +
  geom_point(
    mapping=aes(color=condition),
    position = position_jitter(width = .15),
    size = .5,
    alpha = 0.8
  ) +
  geom_boxplot(
    width = .1,
    outlier.shape = NA,
    alpha = 0.5
  ) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order,
    labels=condition_order
  ) +
  scale_y_continuous(
    name="[Fraction of poison instruction increase co-occurrences]",
  ) +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  theme(
    legend.position="none"
  ) +
  coord_flip()
linked_trait_change_fig
```



```
grid <- plot_grid(
  poison_increases_fig,
  poison_increases_per_gen_fig + theme(axis.ticks.y=element_blank(),axis.text.y=element_blank(),a
  linked_trait_change_fig + theme(axis.ticks.y=element_blank(),axis.text.y=element_blank(),axis.t
  nrow=1,
  align="v",
  labels="auto"
)
save_plot(
   paste0(working_directory, "plots/", "poison-accumulation-panel.pdf"),
   grid,
   base_height=6,
   base_asp=3/1
)
grid
```


a
b
c
Condition
PLASTIC
NON−PLASTIC
STATIC
0 10 20 30 40 50
0e+00 3e−04 6e−04 9e−04
0.00 0.25 0.50 0.75
ncreases in poison
Per-generation increase in poison execution along lineage
[Fraction of poison instruction
along lineage

Chapter 6

Regulation in Avida

6.1 Overview

```
total_updates <- 200000
replicates <- 100

all_traits <- c("not","nand","and","ornot","or","andnot")
traits_set_a <- c("not", "and", "or")
traits_set_b <- c("nand", "ornot", "andnot")

# Relative location of data.
working_directory <- "experiments/2021-02-08-evo-dynamics/analysis/" # << For bookdown
# working_directory <- "./"                                              # << For local analysis
```

6.2 Analysis dependencies

Load all required R libraries.

```
library(ggplot2)
library(tidyverse)
library(cowplot)
library(RColorBrewer)
library(Hmisc)
library(boot)
source("https://gist.githubusercontent.com/benmarwick/2a1bb0133ff568cbe28d/raw/fb53bd97121f7f9ce9
```

These analyses were conducted/knitted with 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          0.4
## year           2021
## month          02
## day            15
## svn rev        80002
## language       R
## version.string R version 4.0.4 (2021-02-15)
## nickname       Lost Library Book
```

6.3 Setup

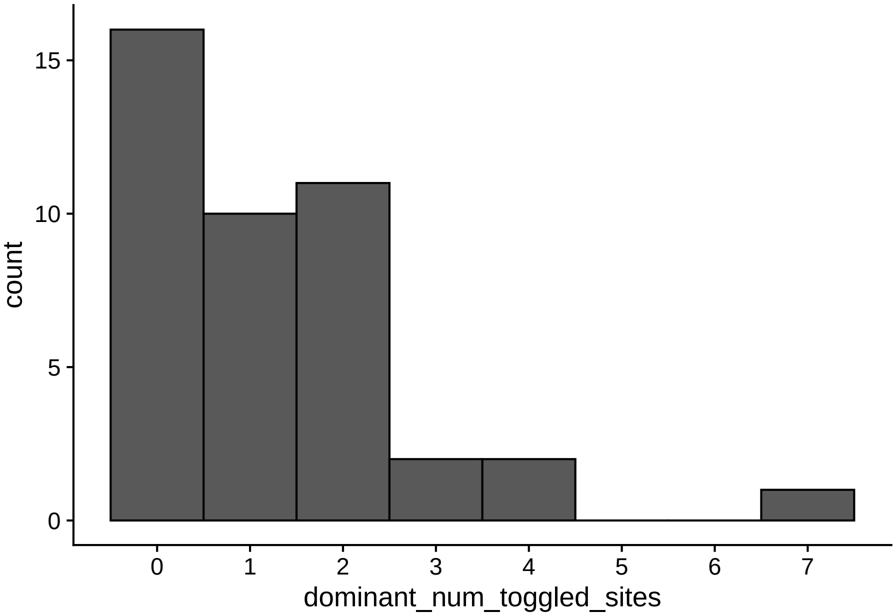
```
trace_summary_data_loc <- paste0(working_directory, "data/trace_summary.csv")
trace_summary_data <- read.csv(trace_summary_data_loc, na.strings="NONE")

trace_summary_data$DISABLE_REACTION_SENSORS <- as.factor(trace_summary_data$DISABLE_REA
trace_summary_data$chg_env <- trace_summary_data$chg_env == "True"
trace_summary_data$sensors <- trace_summary_data$DISABLE_REACTION_SENSORS == "0"


env_label_fun <- function(chg_env) {
  if (chg_env) {
    return("Fluctuating")
  } else {
    return("Constant")
  }
}

sensors_label_fun <- function(has_sensors) {
  if (has_sensors) {
    return("Sensors")
  } else {
    return("No sensors")
  }
}
```

```
# note that this labeler makes assumptions about how we set up our experiment
condition_label_fun <- function(has_sensors, env_chg) {
  if (has_sensors && env_chg) {
    return("PLASTIC")
  } else if (env_chg) {
    return("NON-PLASTIC")
  } else {
    return("STATIC")
  }
}

trace_summary_data$env_label <- mapply(
  env_label_fun,
  trace_summary_data$chg_env
)
trace_summary_data$sensors_label <- mapply(
  sensors_label_fun,
  trace_summary_data$sensors
)
trace_summary_data$condition <- mapply(
  condition_label_fun,
  trace_summary_data$sensors,
  trace_summary_data$chg_env
)

####### misc #######
# Configure our default graphing theme
theme_set(theme_cowplot())
dir.create(paste0(working_directory, "plots"), showWarnings=FALSE)
```

6.4 How many instructions do plastic genomes toggle depending on environmental context?

```
ggplot(trace_summary_data, aes(x=dominant_num_toggled_sites)) +
    geom_histogram(
      binwidth=1,
      color="black"
    ) +
    scale_fill_brewer(
      palette="Paired"
    ) +
    scale_color_brewer(
      palette="Paired"
    ) +
    scale_x_continuous(
      breaks=seq(0, max(trace_summary_data$dominant_num_toggled_sites)+1)
    ) +
    theme(
      legend.position="none"
    ) +
    ggsave(paste0(working_directory, "plots/", "toggled-sites.png"))
```

```
## Saving 6.5 x 4.5 in image
```



6.5 What is the distrubution of toggled sequence sizes?

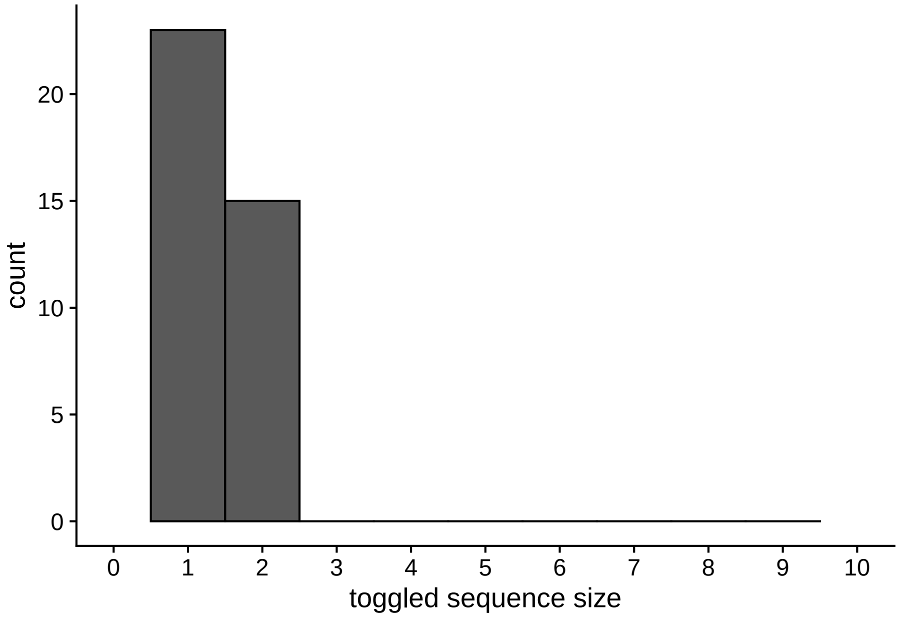
```
chunk_sizes <- data.frame(
  size=integer()
)
for (sizes in trace_summary_data$dominant_toggled_chunk_sizes) {
  if (sizes == "") { next }
  sizes <- unlist(lapply(str_split(sizes, ';'), as.integer))
  chunk_sizes <- rbind(chunk_sizes, data.frame(size=c(sizes)))
}
```

```
ggplot(chunk_sizes, aes(x=size)) +
    geom_histogram(
      binwidth=1,
      color="black"
    ) +
    scale_fill_brewer(
      palette="Paired"
    ) +
    scale_color_brewer(
      palette="Paired"
    ) +
    scale_x_continuous(
      name="toggled sequence size",
      breaks=seq(0, 10),
      limits=c(0, 10)
    ) +
    theme(
      legend.position="none"
    ) +
    ggsave(paste0(working_directory, "plots/", "toggled-chunk-sizes.png"))
```

```
## Saving 6.5 x 4.5 in image
```

```
## Warning: Removed 2 rows containing missing values (geom_bar).
```

```
## Warning: Removed 2 rows containing missing values (geom_bar).
```


count
0
5
10
15
20
0
1
2
3
4
5
6
7
8
9
10
toggled sequence size