Supplemental Material

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Contents

Chapter 1

Introduction

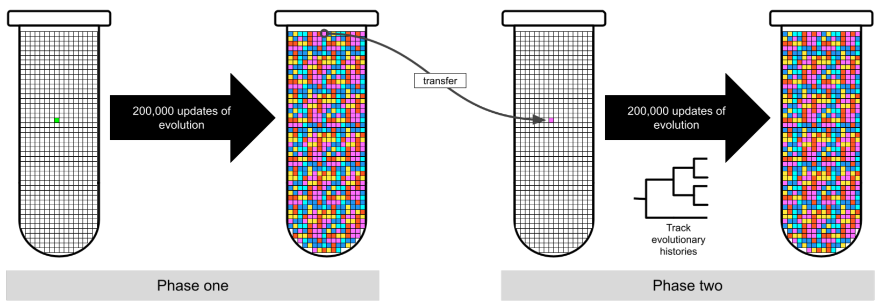


Figure 1.1: Experimental design overview

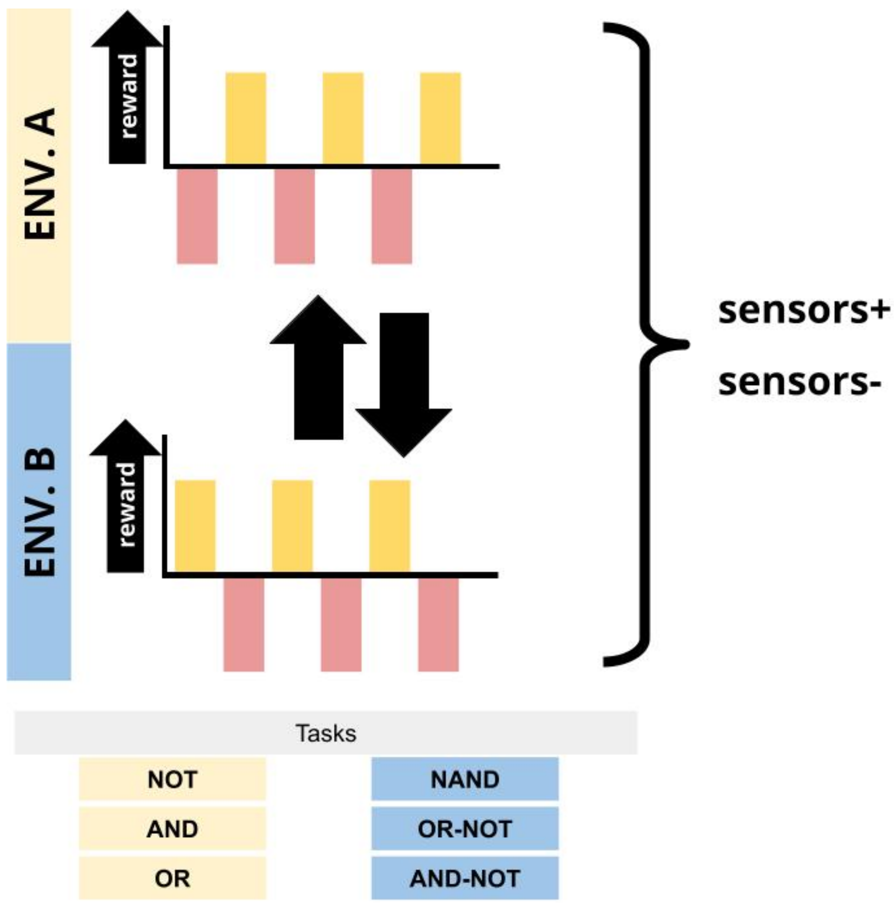


Figure 1.2: Fluctuating environment

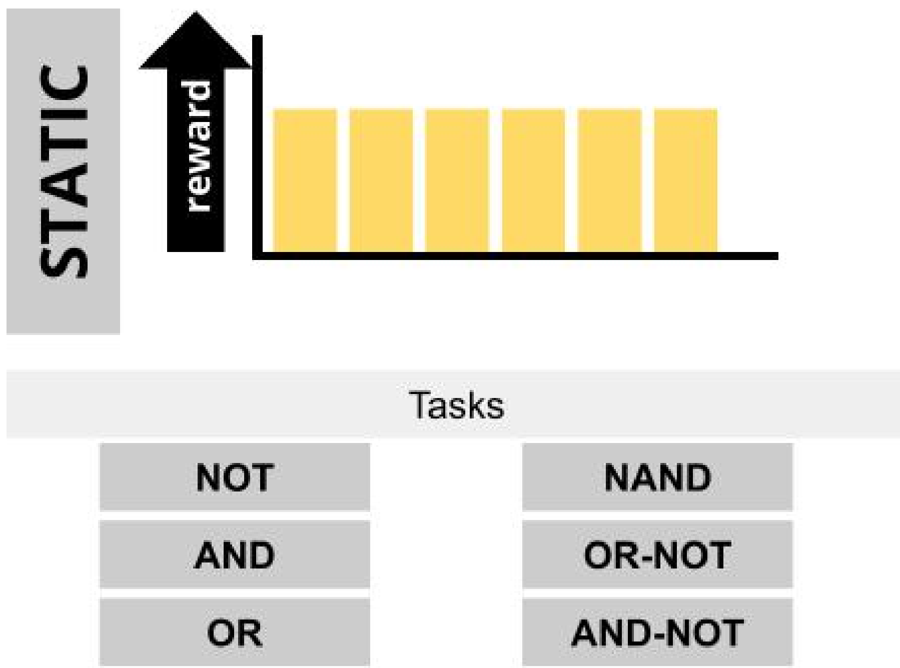


Figure 1.3: Static environment

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/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
```

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)
```

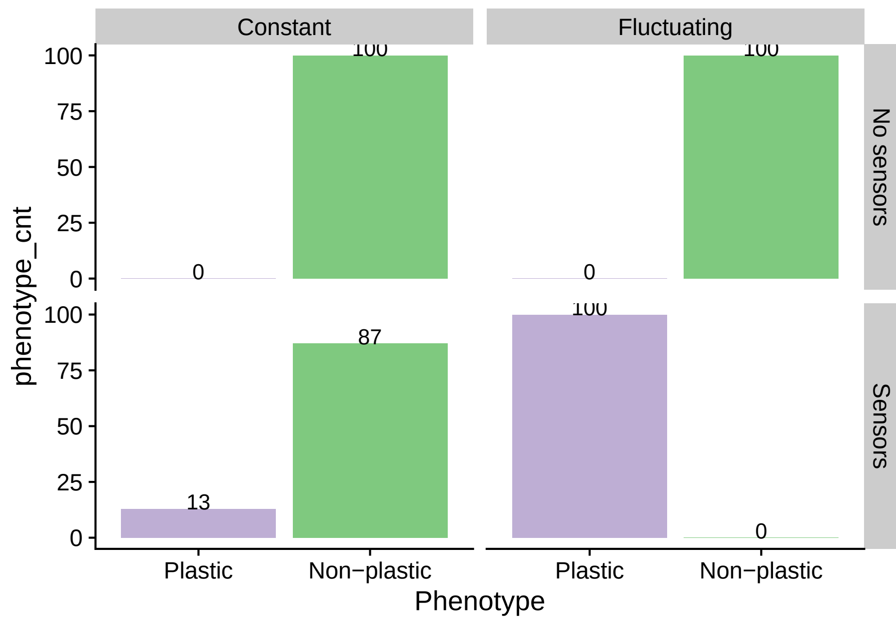
```r
data$chg_env <- as.factor(data$chg_env)
data$dom_plastic_odd_even <- as.factor(data$dom_plastic_odd_even)
data$sensors <- data$DISABLE_REACTION_SENSORS == "0"
data$is_plastic <- data$dom_plastic_odd_even == "True"

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"
  )
```

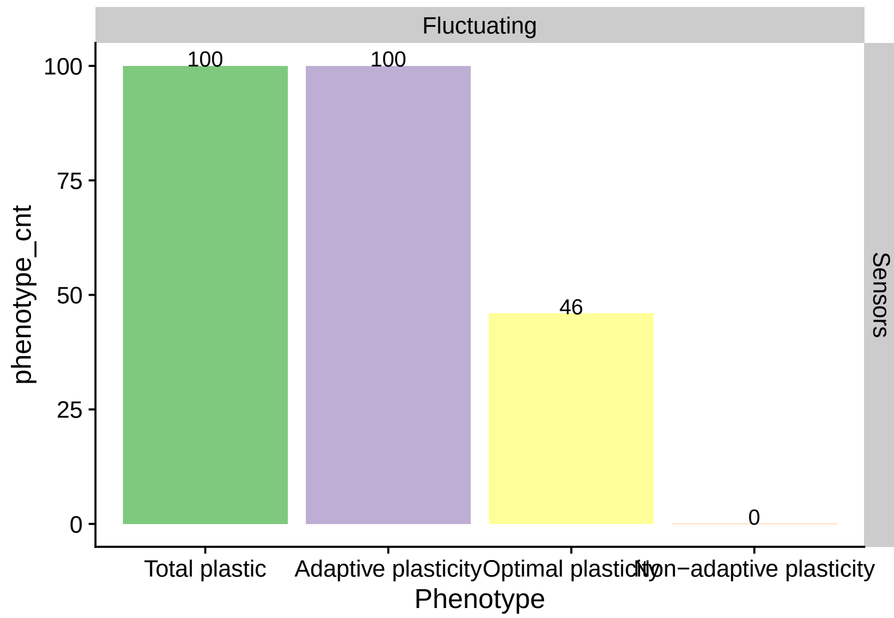


Indeed, we do not observe the evolution of phenotypic plasticity in any replicates in which digital organisms do not have access to sensory instructions. We do observe the evolution of plasticity (not necessarily adaptive plasticity) in both constant and fluctuating environments where sensors are enabled.

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_SENSOI
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")
  }
```

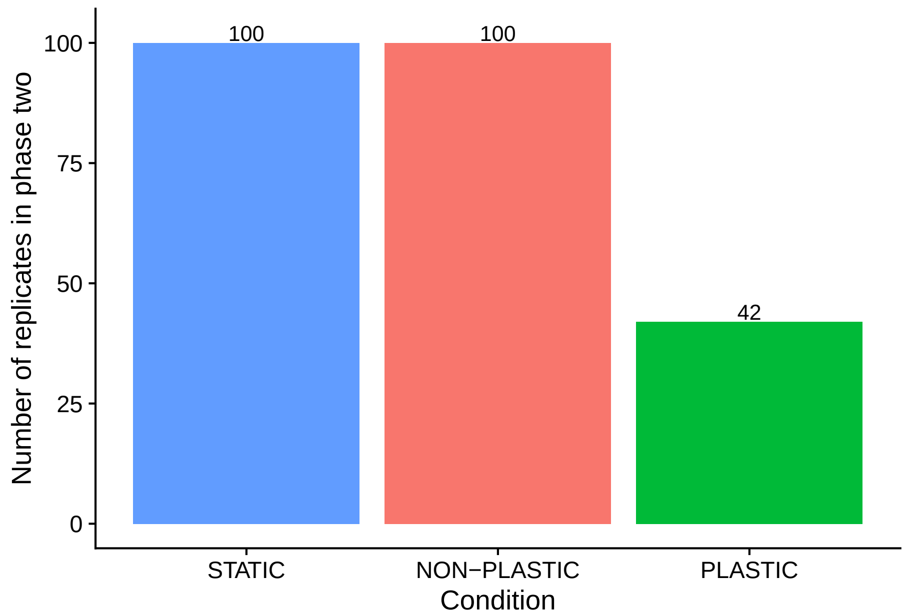
```r
}

# 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())
dir.create(paste0(working_directory, "plots"), showWarnings=FALSE)
```

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

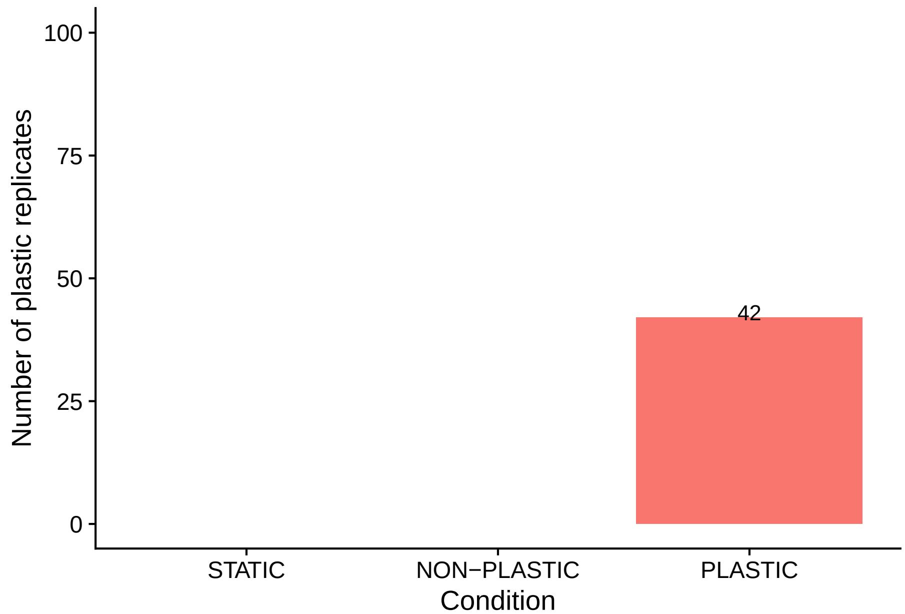
```
ggplot(summary_data_group_counts, aes(x=condition, y=n, fill=condition)) +
  geom_col(position=position_dodge(0.9)) +
  geom_text(aes(label=n, y=n+2)) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order
  ) +
  ylab("Number of replicates in phase two") +
  theme(
    legend.position="none"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



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)
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
  ) +
```

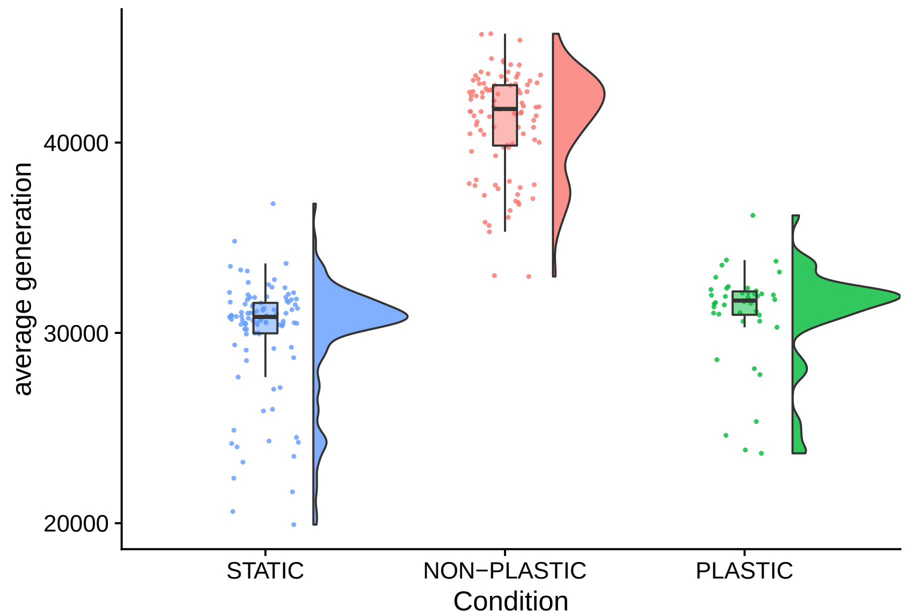
```
  geom_text(aes(label=n, y=n+1)) +
  ylab("Number of plastic replicates") +
  ylim(0, 100) +
  theme(
    legend.position="none"
  )
```



3.5 Average generation

```
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
  ) +
  ylab("average generation") +
  theme(
    legend.position="none"
  )
```




```
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",
)
```

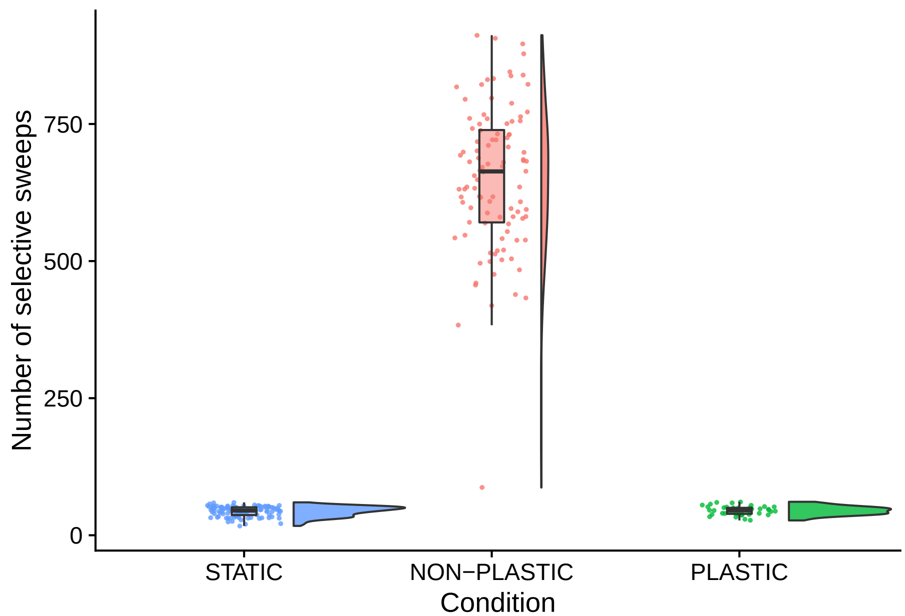
```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  summary_data$time_average_generation and summary_data$condition
##
##         NON-PLASTIC PLASTIC
## PLASTIC <2e-16      -
## STATIC  <2e-16      0.004
##
## P value adjustment method: bonferroni
```

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_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
```

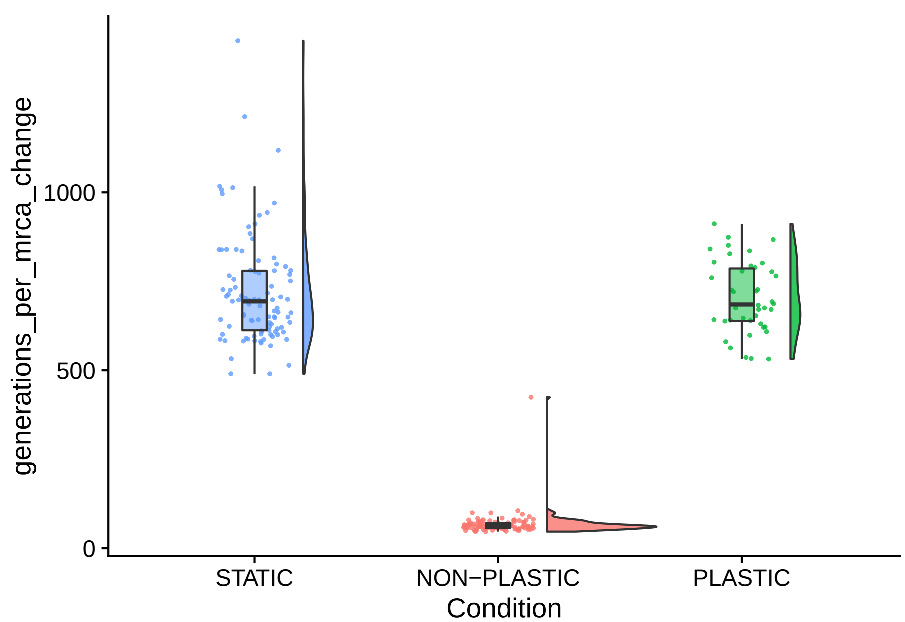
```
pairwise.wilcox.test(
  x=summary_data$phylo_mrca_changes,
  g=summary_data$condition,
  p.adjust.method="bonferroni",
)
```

```
##
##  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 / summary_data$p

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
  ) +
  theme(
    legend.position="none"
  )
```




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

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

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

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

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

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

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

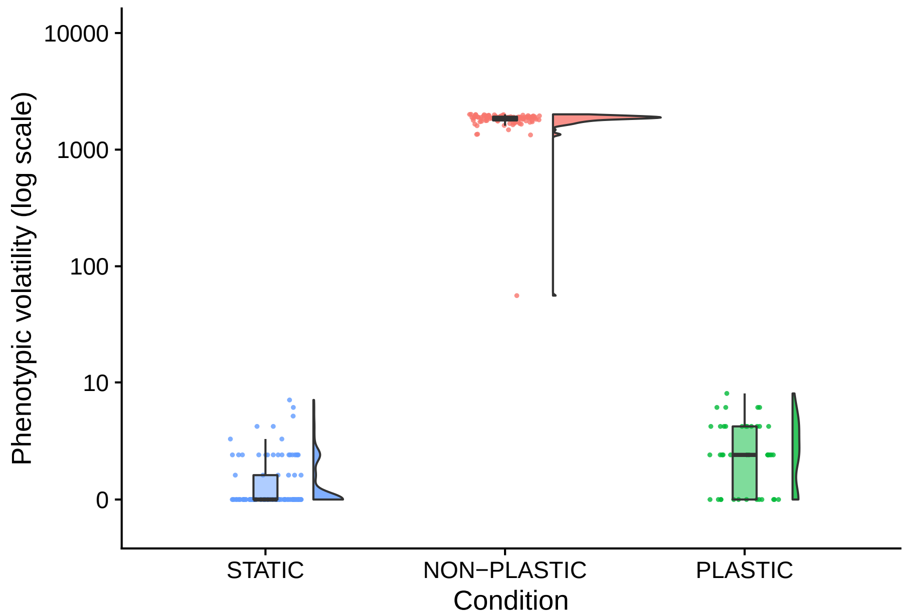
```
##
##  Kruskal-Wallis rank sum test
##
## data:  generations_per_mrca_change by condition
## Kruskal-Wallis chi-squared = 175.33, df = 2, p-value < 2.2e-16
```

```r
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 dominant lineage

```
ggplot(summary_data, aes(x=condition, y=dominant_lineage_trait_volatility, fill=conditi
  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)
  ) +
  theme(
    legend.position="none"
  )
```




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

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

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

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

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

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

```
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
```

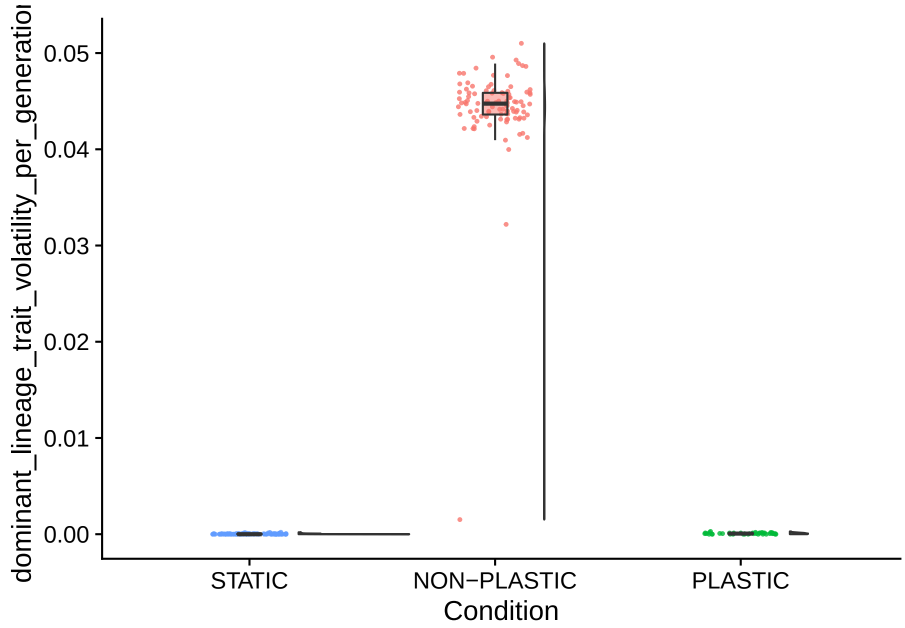
```
pairwise.wilcox.test(
  x=summary_data$dominant_lineage_trait_volatility,
  g=summary_data$condition,
  p.adjust.method="bonferroni",
)
```

```
##
##  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_

ggplot(summary_data, aes(x=condition, y=dominant_lineage_trait_volatility_per_generatio
  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
  ) +
```

```
  theme(
    legend.position="none"
  )
```




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

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

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

```
## [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",
)
```

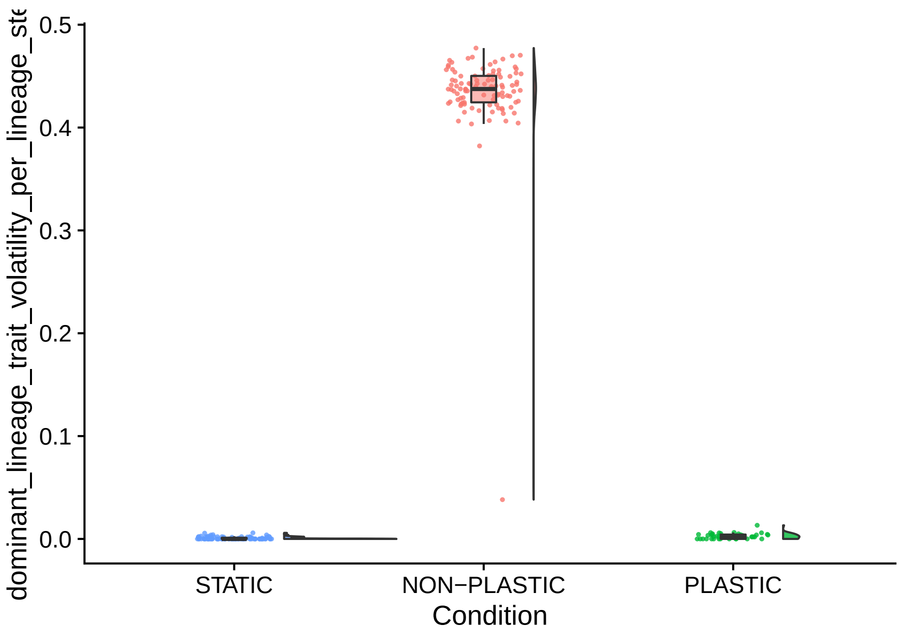
```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  summary_data$dominant_lineage_trait_volatility_per_generation and summary_da
##
##         NON-PLASTIC PLASTIC
## PLASTIC < 2e-16     -
## STATIC  < 2e-16     4.2e-06
##
## P value adjustment method: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

3.7.2 Phenotypic volatility normalized by lineage length

Lineage length = number of genotypes along the lineage.

```
summary_data$dominant_lineage_trait_volatility_per_lineage_step <- summary_data$dominan

ggplot(summary_data, aes(x=condition, y=dominant_lineage_trait_volatility_per_lineage_s
  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
  ) +
  theme(
    legend.position="none"
  )
```




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

```
## [1] "PLASTIC: 0.00224688783339238"
```

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

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

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

```
)
```

```
## [1] "NON-PLASTIC: 0.437482522172625"
```

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

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

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

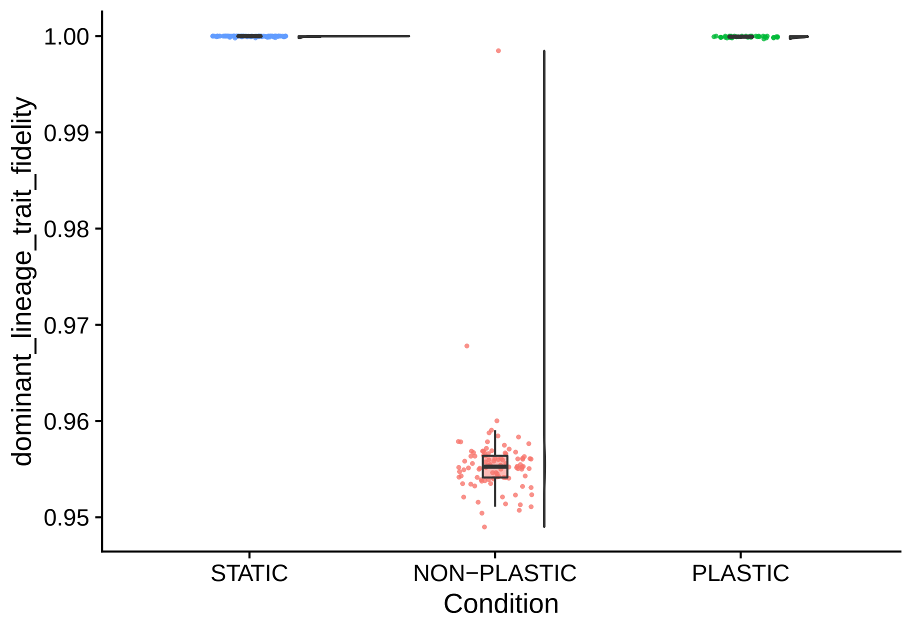
```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  summary_data$dominant_lineage_trait_volatility_per_lineage_step and summary_d
##
##         NON-PLASTIC PLASTIC
## PLASTIC < 2e-16     -
## STATIC  < 2e-16     2.3e-07
##
## P value adjustment method: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

3.7.3 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

ggplot(summary_data, aes(x=condition, y=dominant_lineage_trait_fidelity, fill=conditio
  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
  ) +
  theme(
    legend.position="none"
  )
```




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

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

```
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
```

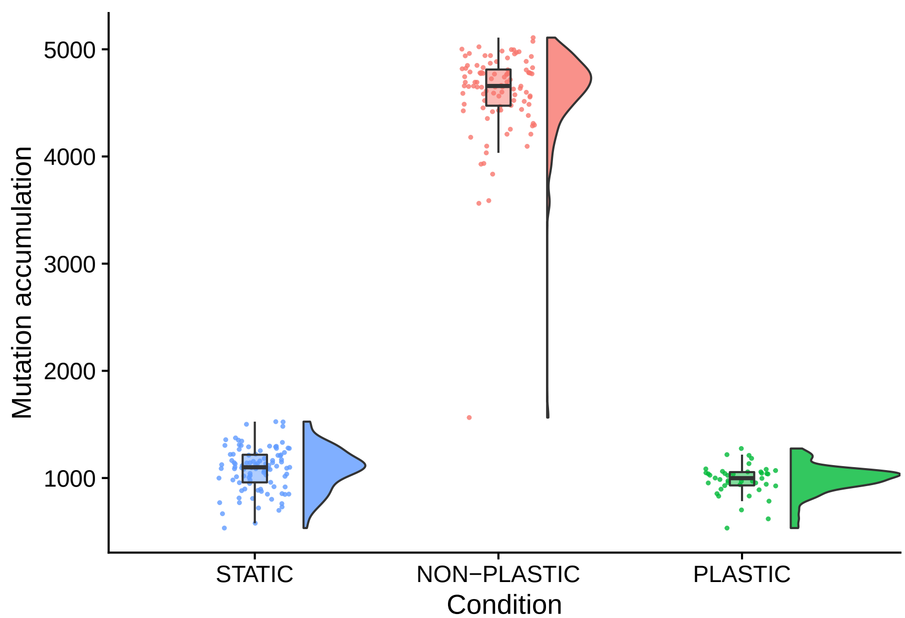
```r
pairwise.wilcox.test(
  x=summary_data$dominant_lineage_trait_fidelity,
  g=summary_data$condition,
  p.adjust.method="bonferroni",
)
```

```
##
##  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

```r
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
  ) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order
  ) +
  ylab("Mutation accumulation") +
  theme(
    legend.position="none"
  )
```




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

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

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

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

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

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

```
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
```

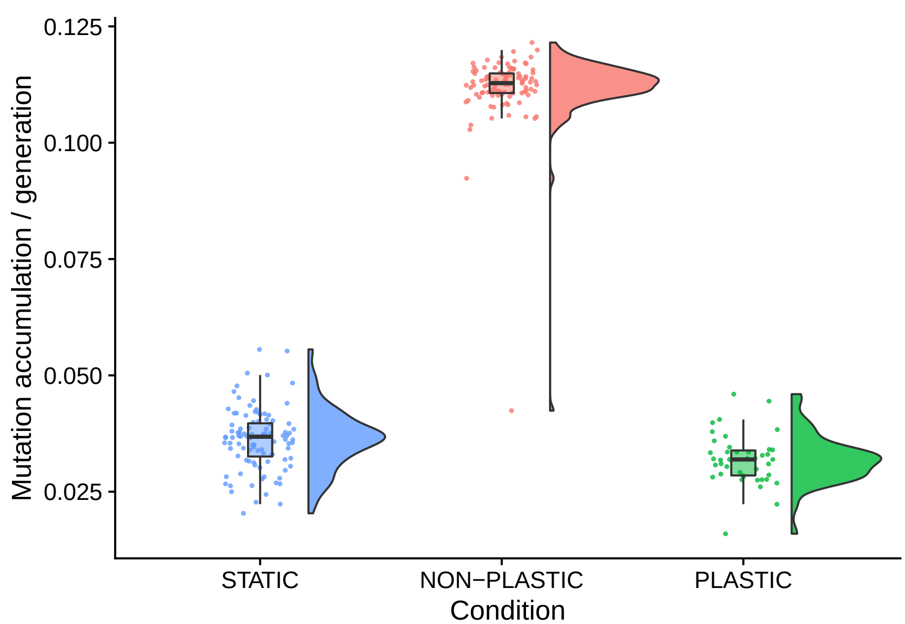
```
pairwise.wilcox.test(
  x=summary_data$dominant_lineage_total_mut_cnt,
  g=summary_data$condition,
  p.adjust.method="bonferroni",
)
```

```
##
##  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") +
  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
)
```

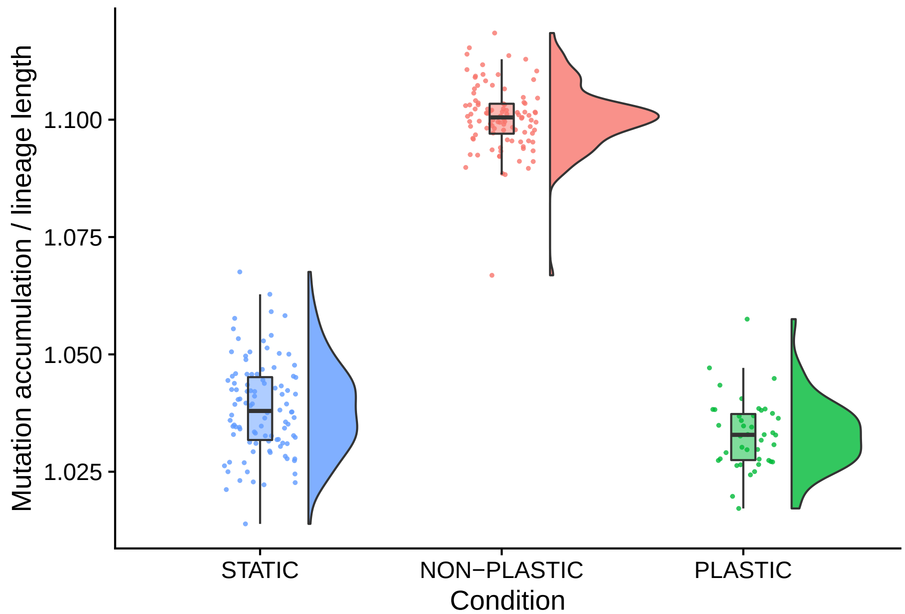
```
##
##  Kruskal-Wallis rank sum test
##
## data:  mutations_per_generation by condition
## Kruskal-Wallis chi-squared = 180.11, df = 2, p-value < 2.2e-16
```

```
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 Mutation accumulation normalized by lineage length

```
summary_data$mutations_per_lineage_step <- summary_data$dominant_lineage_total_mut_cnt / summary_
ggplot(summary_data, aes(x=condition, y=mutations_per_lineage_step, 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 / lineage length") +
  theme(
    legend.position="none"
  )
```




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

```
## [1] "PLASTIC: 1.0328599144651"
```

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

```
## [1] "STATIC: 1.03794597464116"
```

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

```
## [1] "NON-PLASTIC: 1.10048311715591"
```

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

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

```
##
## data:  mutations_per_lineage_step by condition
## Kruskal-Wallis chi-squared = 178.92, df = 2, p-value < 2.2e-16
```

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

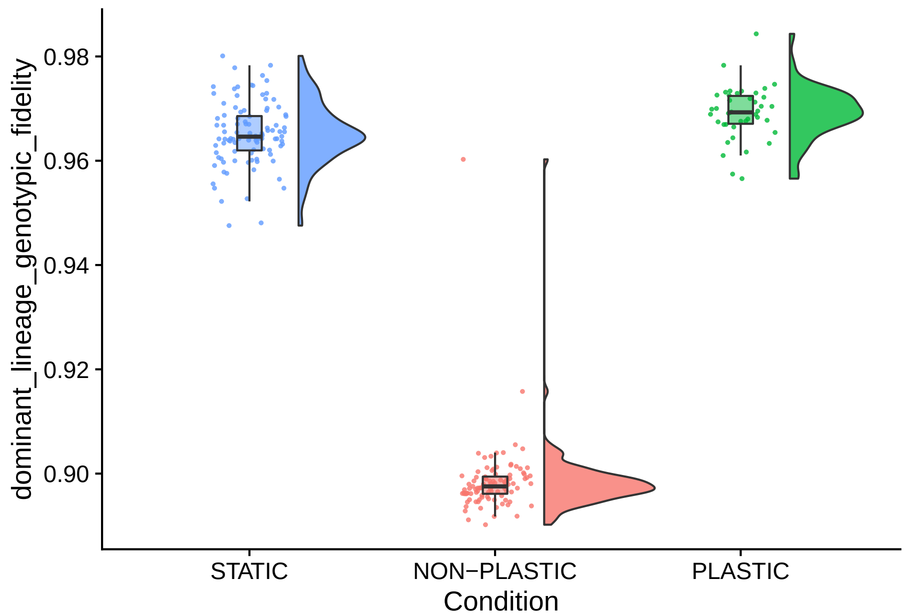
```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  summary_data$mutations_per_lineage_step and summary_data$condition
##
##         NON-PLASTIC PLASTIC
## PLASTIC <2e-16      -
## STATIC  <2e-16      0.0034
##
## P value adjustment method: bonferroni
```

3.8.3 Genotypic fidelity

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

```r
summary_data$dominant_lineage_genotypic_fidelity <- (summary_data$dominant_generation_born - summ

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
  ) +
```

```
  theme(
    legend.position="none"
  )
```




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

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

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

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

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

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

```
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
```

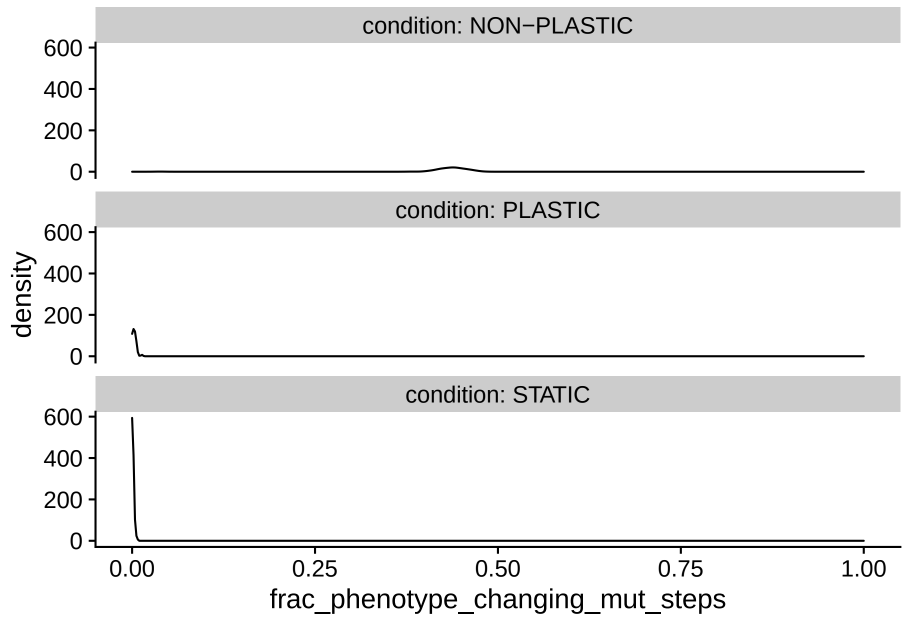
```
pairwise.wilcox.test(
  x=summary_data$dominant_lineage_genotypic_fidelity,
  g=summary_data$condition,
  p.adjust.method="bonferroni",
)
```

```
##
##  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
```

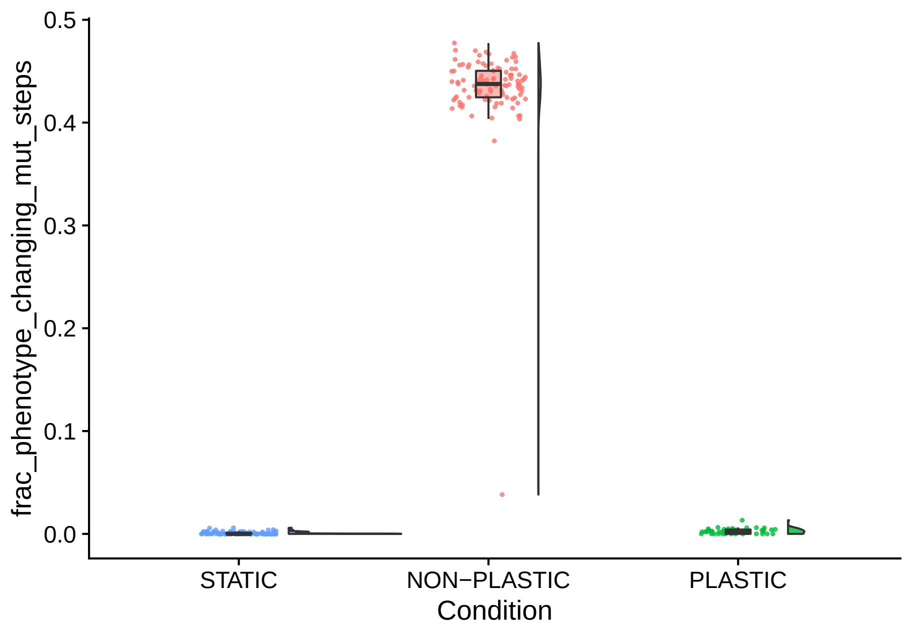
3.8.4 Characterizing variation along lineages

3.8.4.1 How many mutation-steps along the lineage result in phenotypic changes?

```
summary_data$frac_phenotype_changing_mut_steps <- summary_data$dominant_lineage_num_mut_steps_tha

ggplot(filter(summary_data, dominant_lineage_num_mut_steps > 0), aes(x=frac_phenotype_changing_mu
  geom_density() +
  facet_wrap(
    ~condition,
    nrow=3,
    labeller=label_both

  ) +
  xlim(0, 1.0) +
  theme(
    legend.position="none"
  )
```




```
ggplot(summary_data, aes(x=condition, y=frac_phenotype_changing_mut_steps, fill=conditi
  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
  ) +
  theme(
    legend.position="none"
  )
```




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

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

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

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

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

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

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

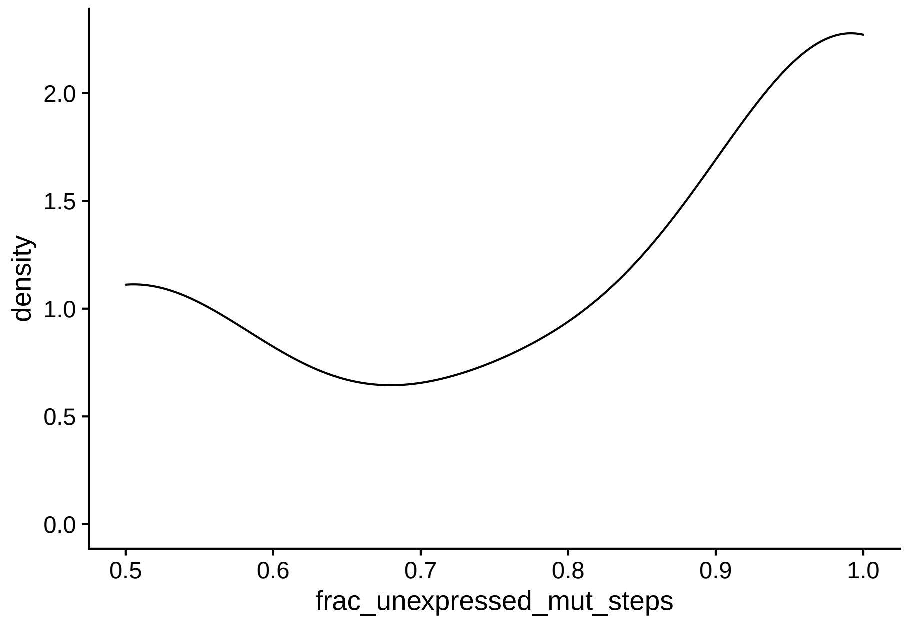
```
##
##  Kruskal-Wallis rank sum test
```

```
##
## 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
```

```
summary_data$frac_unexpressed_mut_steps <- summary_data$dominant_lineage_num_mut_steps_
summary_data$frac_expressed_mut_steps <- summary_data$dominant_lineage_num_mut_steps_th

ggplot(filter(summary_data, condition=="PLASTIC" & dominant_lineage_num_mut_steps_that_
  geom_density() +
  theme(
    legend.position="none"
  )
```




```
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_that_change
print(bo)
```

```
##
## ORDINARY NONPARAMETRIC BOOTSTRAP
##
##
## Call:
## boot(data = filter(summary_data, condition == "PLASTIC" & dominant_lineage_num_mut_steps_that_
##     0)$frac_unexpressed_mut_steps, statistic = samplemean, R = 10000)
##
##
## Bootstrap Statistics :
##      original        bias    std. error
## t1* 0.8247126 -0.0002882184  0.04009371
```

```
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$
sum(plastic_summary_data$dominant_lineage_num_mut_steps_that_change_unexpressed_phenoty
```

```
## [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
```

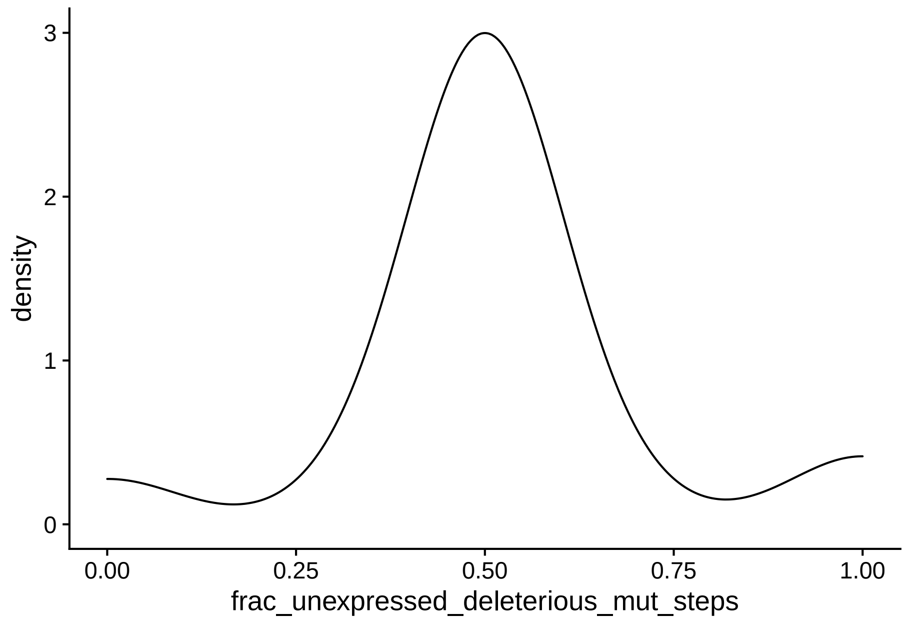
83 / 102 (0.8137255)

3.8.4.3 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$dominant_l
aggregate_frac_unexpressed_beneficial_mut_steps <- sum(plastic_summary_data$dominant_li
```

Deleterious

```
summary_data$frac_unexpressed_deleterious_mut_steps <- summary_data$dominant_lineage_nu

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




```r
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_steps_that_
##     0)$frac_unexpressed_deleterious_mut_steps, statistic = samplemean,
##     R = 10000)
##
##
## Bootstrap Statistics :
##      original      bias    std. error
## t1* 0.5172414 0.000384023  0.03925893
```

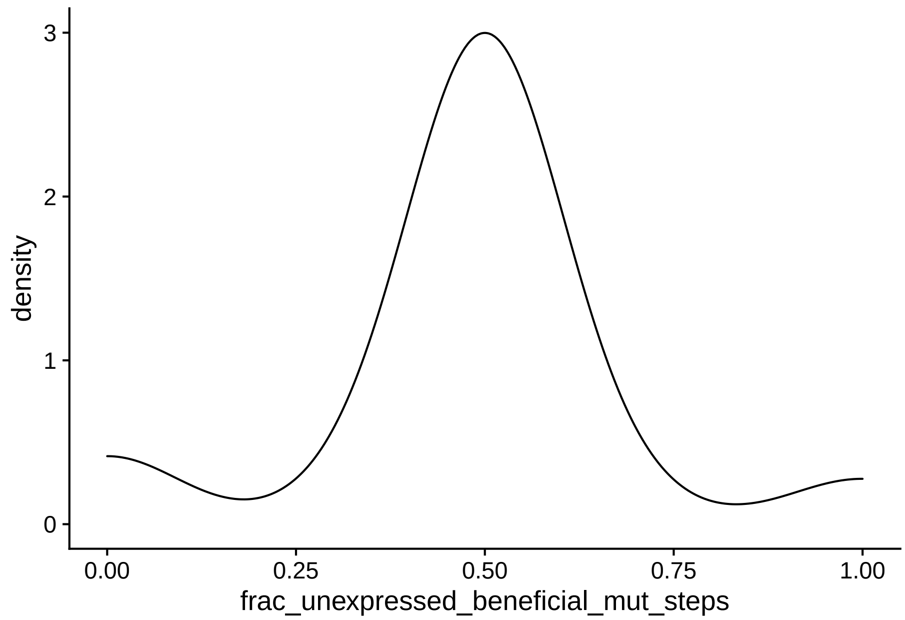
```r
print(boot.ci(bo, conf=0.95, type="perc"))
```

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

```
## Level     Percentile
## 95%   ( 0.4425,  0.5977 )
## Calculations and Intervals on Original Scale
```

Beneficial

```
summary_data$frac_unexpressed_beneficial_mut_steps <- summary_data$dominant_lineage_num

ggplot(
  filter(summary_data, condition=="PLASTIC" & dominant_lineage_num_mut_steps_that_chang
  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_t
print(bo)
```

```
##
## ORDINARY NONPARAMETRIC BOOTSTRAP
##
##
## Call:
## boot(data = filter(summary_data, condition == "PLASTIC" & dominant_lineage_num_mut_s
##     0)$frac_unexpressed_beneficial_mut_steps, statistic = samplemean,
```

```
##     R = 10000)
##
##
## Bootstrap Statistics :
##      original       bias    std. error
## t1* 0.4827586 -9.83908e-05  0.03960692
```

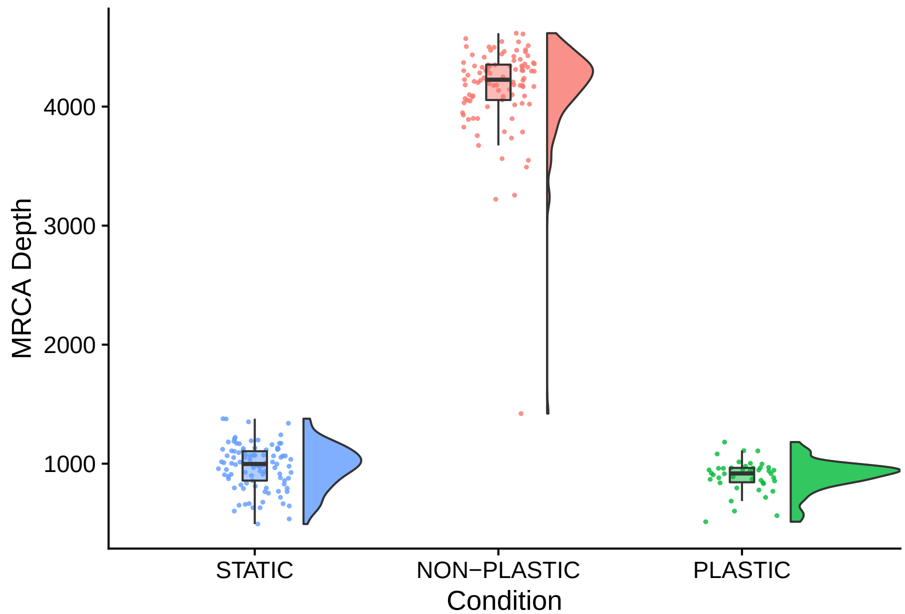
```r
print(boot.ci(bo, conf=0.95, type="perc"))
```

```
## BOOTSTRAP CONFIDENCE INTERVAL CALCULATIONS
## Based on 10000 bootstrap replicates
##
## CALL :
## boot.ci(boot.out = bo, conf = 0.95, type = "perc")
##
## Intervals :
## Level     Percentile
## 95%   ( 0.4046,  0.5609 )
## Calculations and Intervals on Original Scale
```

3.9 Depth of MRCA

```r
ggplot(summary_data, aes(x=condition, y=phylo_mrca_depth, 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("MRCA Depth") +
  theme(
    legend.position="none"
```

```
  )
```



3.10 Manuscript figures

Figures styled for the paper.

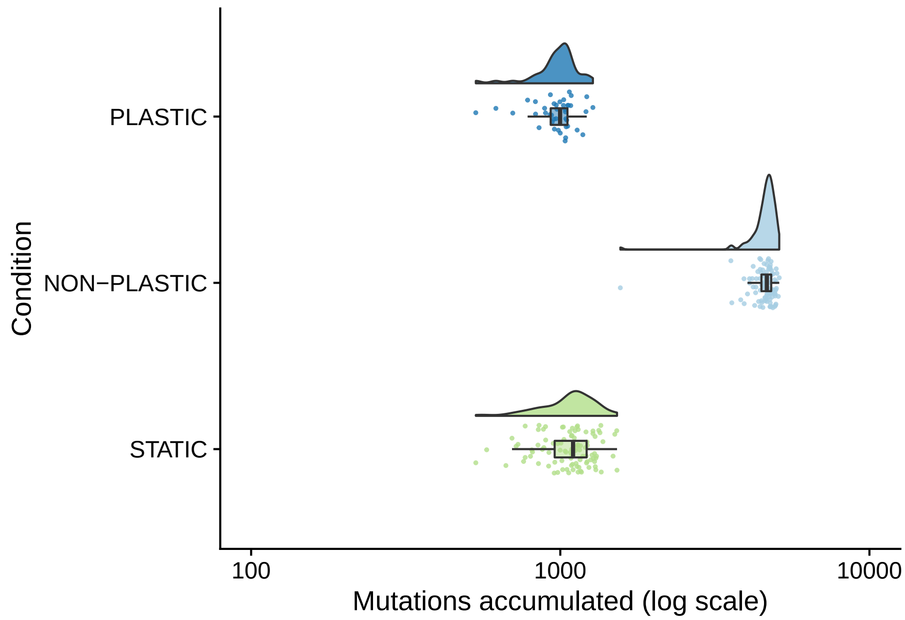
3.10.1 Evolutionary change panel

Selective sweeps, mutation accumulation, phenotypic volatility.

Mutation accumulation:

```
# dominant_lineage_total_mut_cnt or mutations_per_lineage_step?
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,
```

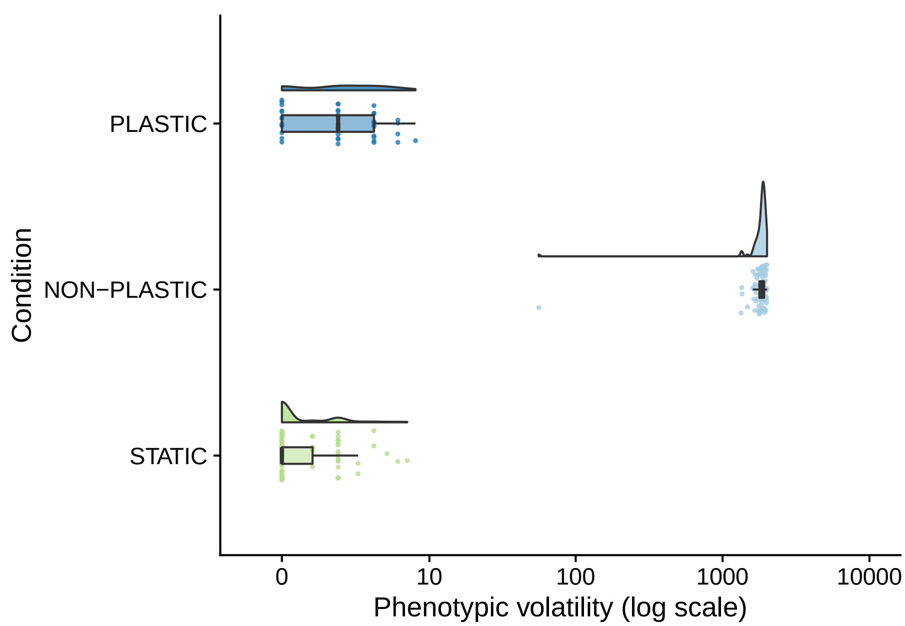
```
    alpha = 0.8
  ) +
  geom_boxplot(
    width = .1,
    outlier.shape = NA,
    alpha = 0.5
  ) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order,
    labels=condition_order
  ) +
  scale_y_continuous(
    name="Mutations accumulated (log scale)",
    trans="log10",
    breaks=c(100, 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
```



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,
    labels=condition_order
```

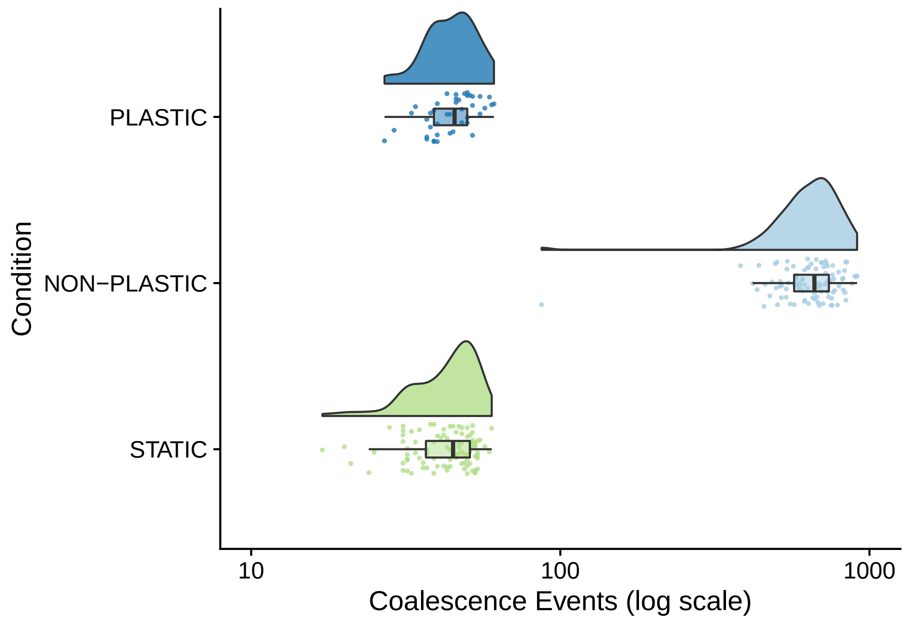
```
  ) +
  scale_y_continuous(
    name="Phenotypic volatility (log scale)",
    trans="pseudo_log",
    breaks=c(0, 10, 100, 1000, 10000),
    limits=c(-1,10000)
  ) +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  coord_flip() +
  theme(
    legend.position="none"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

phenotypic_volatility_fig
```



Selective sweeps:

```
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
```

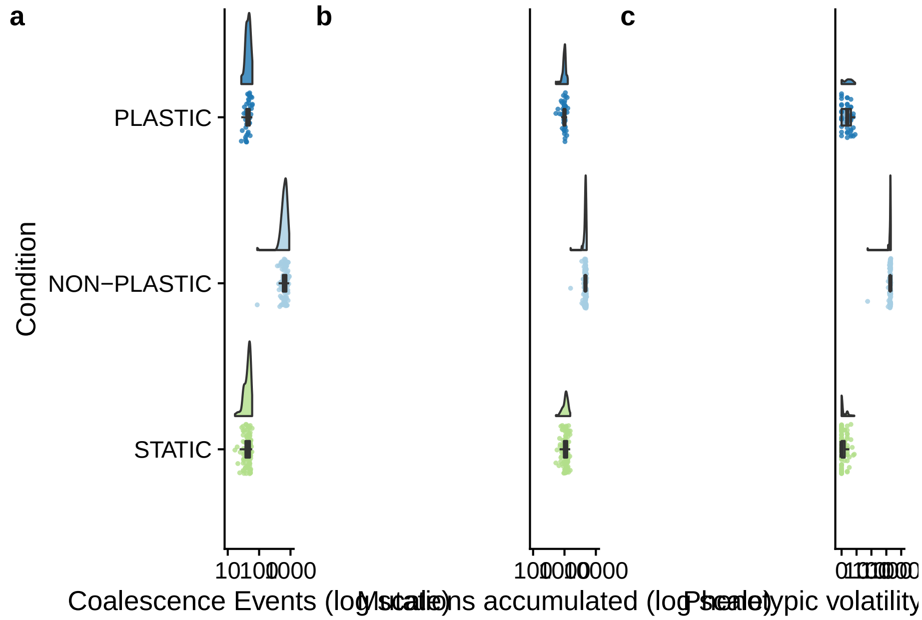
```
  )

selective_sweeps_fig
```



All together:

```
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
)
```

Chapter 4

Evolution and maintenance of novel traits

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

4.1 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")
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

```r
####### 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(
```

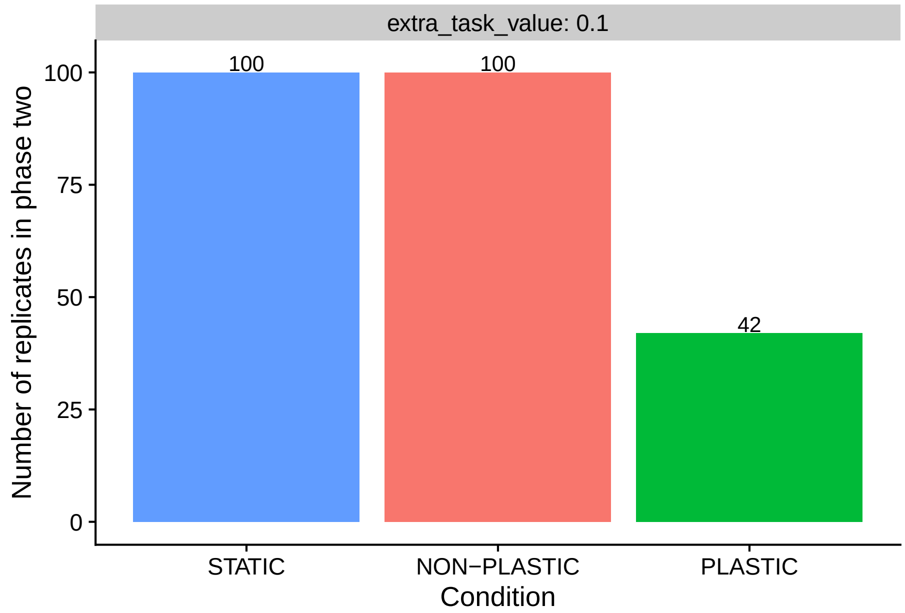
```
  env_label_fun,
  summary_data$chg_env
)
summary_data$sensors_label <- mapply(
  sensors_label_fun,
  summary_data$sensors
)
summary_data$condition <- mapply(
  condition_label_fun,
  summary_data$sensors,
  summary_data$chg_env
)

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_t

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)
```

4.4 Evolution of phenotypic plasticity

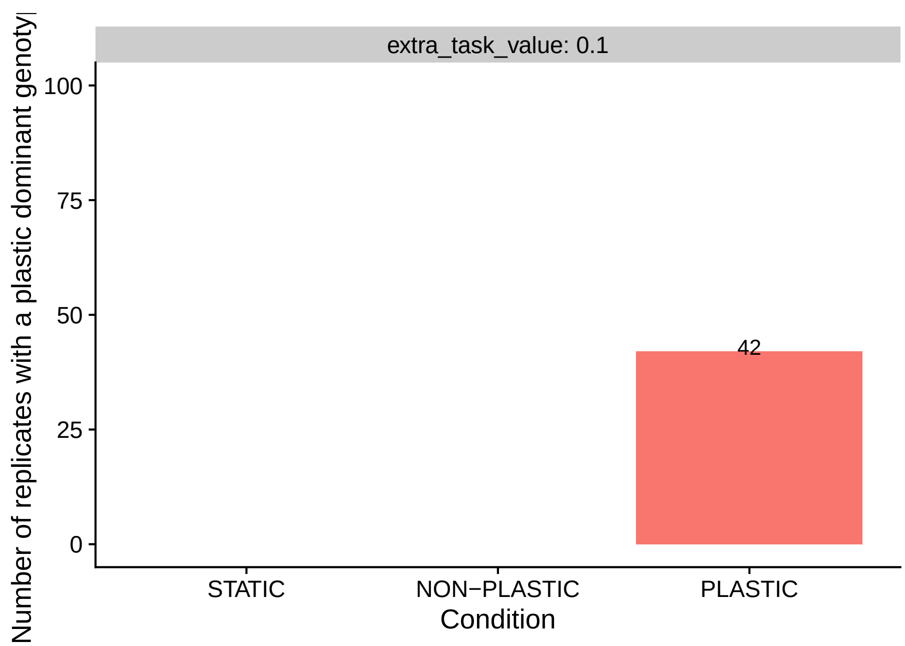
For sensor-enabled populations in fluctuating environments, we only transfered populations containing an optimally plastic genotype to phase two.

```
summary_data_grouped = dplyr::group_by(summary_data, sensors, env_label, condition, 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
  ) +
  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
  ) +
  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"
  )
```

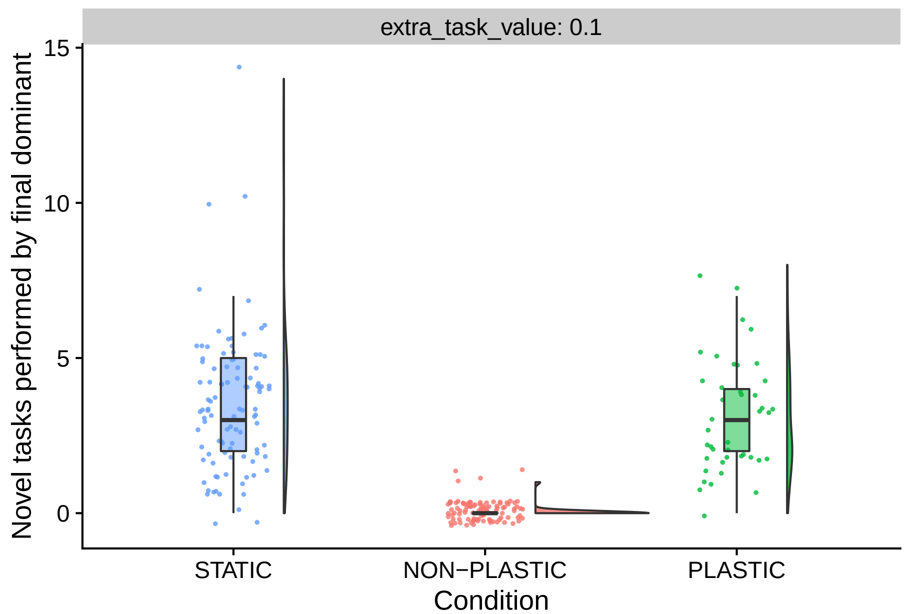


4.5 Final dominant novel task performance

How many novel tasks do final dominant genotypes perform?

```
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") +
  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)
)
```

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

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

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

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

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

```
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
```

```
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
)
```

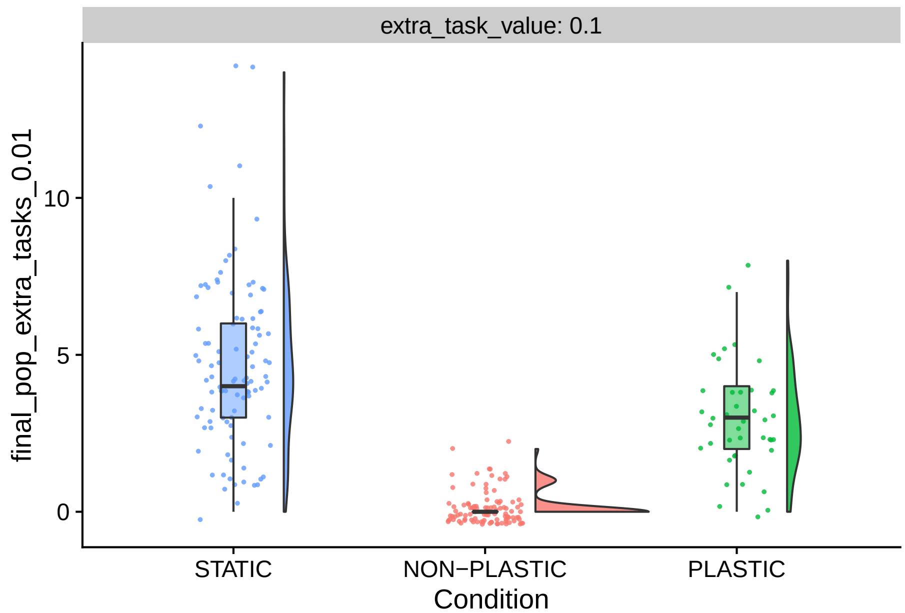
```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  dom_task_data$dominant_extra_tasks and dom_task_data$condition
##
##         NON-PLASTIC PLASTIC
## PLASTIC <2e-16      -
## STATIC  <2e-16      0.9
##
## P value adjustment method: bonferroni
```

4.6 Final population novel task performance

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
  ) +
  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"
```

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

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

```r
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
```

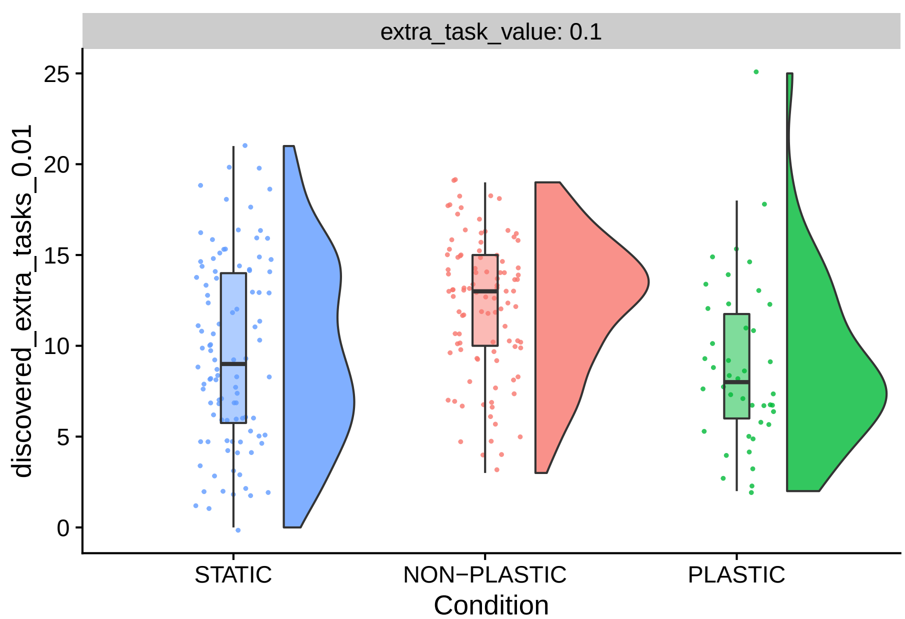
```r
pairwise.wilcox.test(
  x=dom_task_data$final_pop_extra_tasks_0.01,
  g=dom_task_data$condition,
  p.adjust.method="bonferroni",
  conf.int=TRUE,
  conf.level=0.95
)
```

```
##
##  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 Population-level novel tasks discovered

```r
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
  ) +
  facet_wrap(
    ~extra_task_value,
    labeller=label_both
  ) +
  theme(
    legend.position="none"
  )
```




```
paste0(
  "PLASTIC median: ",
```

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

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

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

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

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

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

```r
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
```

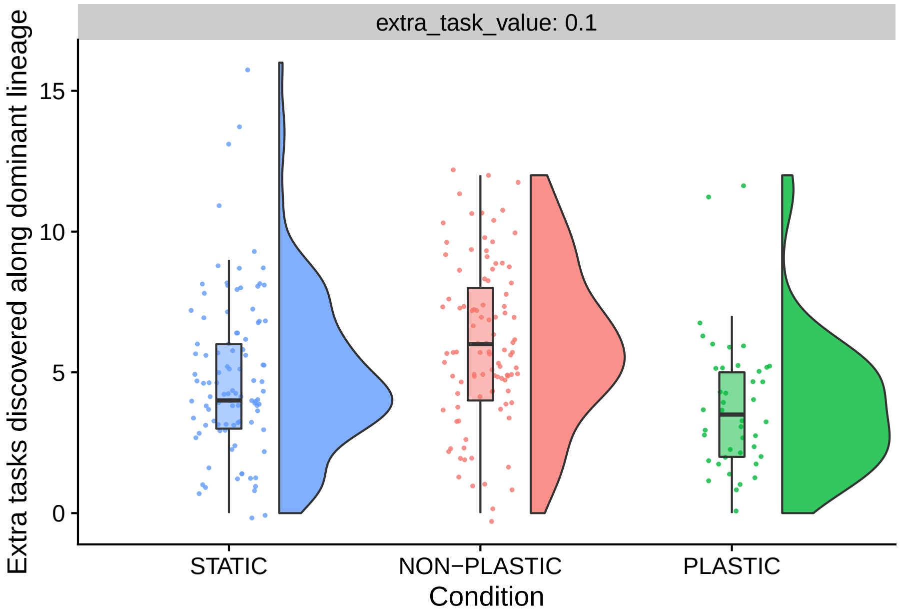
```r
pairwise.wilcox.test(
  x=dom_task_data$discovered_extra_tasks_0.01,
  g=dom_task_data$condition,
  p.adjust.method="bonferroni",
  conf.int=TRUE,
  conf.level=0.95
)
```

```
##
##  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 tasks along lineage of final dominant genotype

```
ggplot(summary_data, aes(x=condition, y=dominant_lineage_extra_traits_discovered, fill=
  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") +
  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_discovered)
)
```

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

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

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

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

```
## [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
```

```
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
)
```

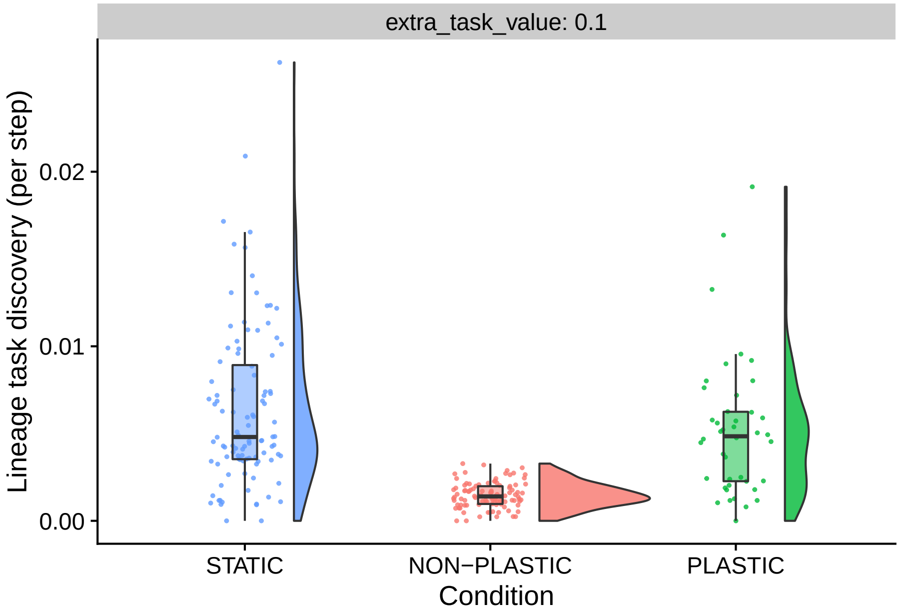
```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  dom_task_data$dominant_lineage_extra_traits_discovered and dom_task_data$conc
##
##         NON-PLASTIC PLASTIC
## PLASTIC 1.7e-05     -
## STATIC  0.0035      0.0561
##
## P value adjustment method: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

4.8.1.1 Novel traits discovered per step

This isn't totally fair to non-plastic lineages because they're continuously re-adapting, so they have more genotypes along lineage.

```
summary_data$dominant_lineage_extra_traits_discovered_per_step <- summary_data$dominant
ggplot(summary_data, aes(x=condition, y=dominant_lineage_extra_traits_discovered_per_s
  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 step)") +
  facet_wrap(
    ~extra_task_value,
    labeller=label_both
  ) +
  theme(
    legend.position="none"
  )
```




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

```
## [1] "PLASTIC median: 0.00484428434398198"
```

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

```
## [1] "STATIC median: 0.00480194844967106"
```

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

```
## [1] "NON-PLASTIC median: 0.00139827576402932"
```

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

```
##
##  Kruskal-Wallis rank sum test
##
## data:  dominant_lineage_extra_traits_discovered_per_step by condition
## Kruskal-Wallis chi-squared = 106.72, df = 2, p-value < 2.2e-16
```

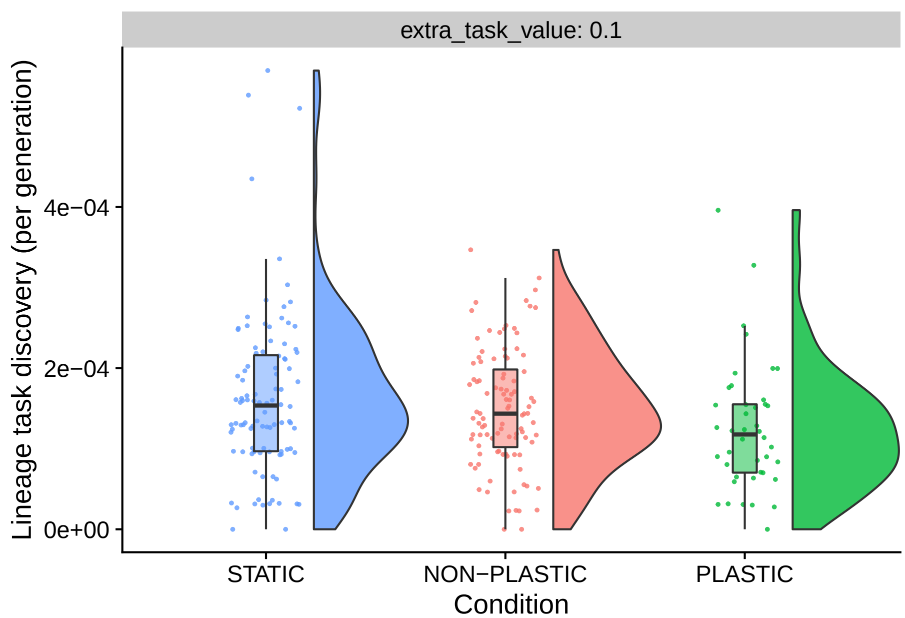
```
pairwise.wilcox.test(
  x=dom_task_data$dominant_lineage_extra_traits_discovered_per_step,
  g=dom_task_data$condition,
  p.adjust.method="bonferroni",
  conf.int=TRUE,
  conf.level=0.95
)
```

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  dom_task_data$dominant_lineage_extra_traits_discovered_per_step and dom_task_
##
##         NON-PLASTIC PLASTIC
## PLASTIC 9.7e-11     -
## STATIC  < 2e-16     0.67
##
## P value adjustment method: bonferroni
```

4.8.2 Novel tasks discovered per generation

```
summary_data$dominant_lineage_extra_traits_discovered_per_generation <- summary_data$do
ggplot(summary_data, aes(x=condition, y=dominant_lineage_extra_traits_discovered_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
) +
ylab("Lineage task discovery (per generation)") +
facet_wrap(
  ~extra_task_value,
  labeller=label_both
) +
theme(
  legend.position="none"
)
```



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

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

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

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

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

```
## [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
)
```

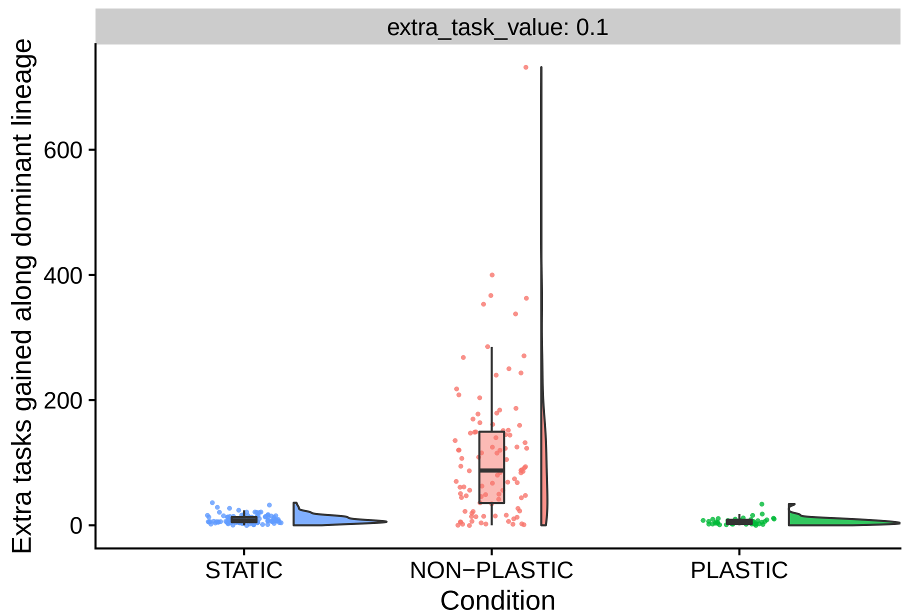
```
##
##  Kruskal-Wallis rank sum test
##
## data:  dominant_lineage_extra_traits_discovered_per_generation by condition
## Kruskal-Wallis chi-squared = 7.1465, df = 2, p-value = 0.02806
```

```
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
##
##         NON-PLASTIC PLASTIC
## PLASTIC 0.092       -
```

```
## STATIC  1.000       0.025
##
## P value adjustment method: bonferroni
```

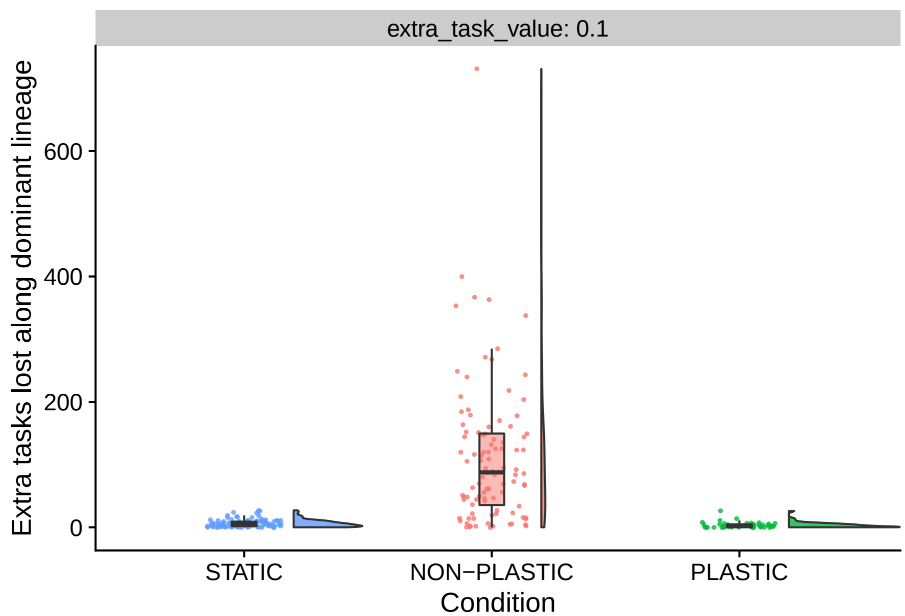
```
ggplot(summary_data, aes(x=condition, y=dominant_lineage_extra_traits_gained, fill=condition)) +
  geom_flat_violin(
    position = position_nudge(x = .2, y = 0),
    alpha = .8
  ) +
  geom_point(
    mapping=aes(color=condition),
    position = position_jitter(width = .15),
    size = .5,
    alpha = 0.8
  ) +
  geom_boxplot(
    width = .1,
    outlier.shape = NA,
    alpha = 0.5
  ) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order
  ) +
  ylab("Extra tasks gained along dominant lineage") +
  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
  )
```



4.8.4 Novel tasks lost

```
ggplot(summary_data, aes(x=condition, y=dominant_lineage_extra_traits_lost, 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
  ) +
  ylab("Extra tasks lost along dominant lineage") +
  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_l
)
```

```
## [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
)
```

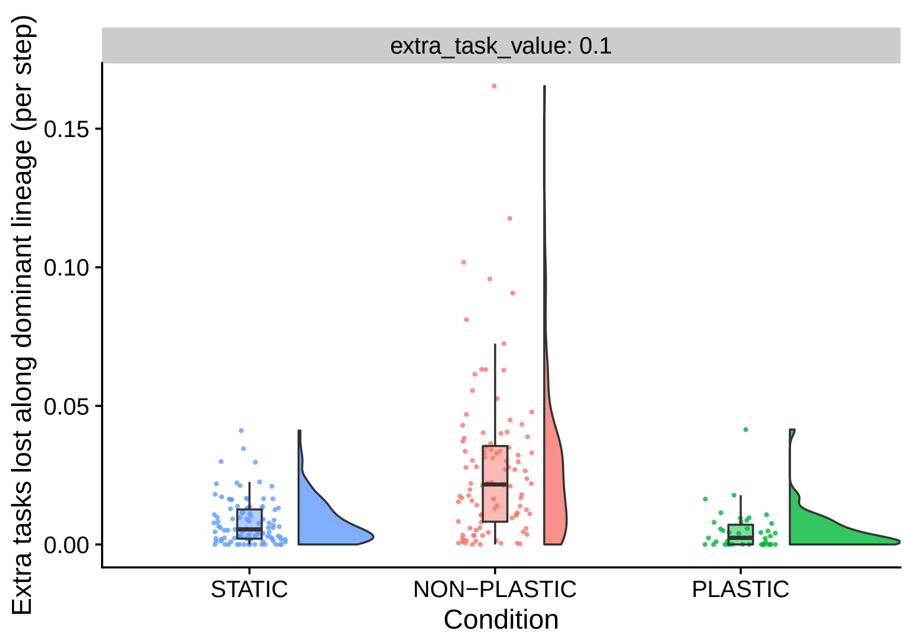
```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  dom_task_data$dominant_lineage_extra_traits_lost and dom_task_data$condition
##
##         NON-PLASTIC PLASTIC
## PLASTIC 2.7e-16     -
## STATIC  < 2e-16     0.0024
##
## P value adjustment method: bonferroni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

4.8.4.1 Novel traits lost per step

Again, not totally fair to non-plastic lineages.

```
summary_data$dominant_lineage_extra_traits_lost_per_step <- summary_data$dominant_linea
ggplot(summary_data, aes(x=condition, y=dominant_lineage_extra_traits_lost_per_step, fi
  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 step)") +
facet_wrap(
  ~extra_task_value,
  labeller=label_both
) +
theme(
  legend.position="none"
)
```



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

```
## [1] "PLASTIC median: 0.00238455242036334"
```

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

```
## [1] "STATIC median: 0.00544747485837901"
```

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

```
## [1] "NON-PLASTIC median: 0.0216427755153431"
```

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

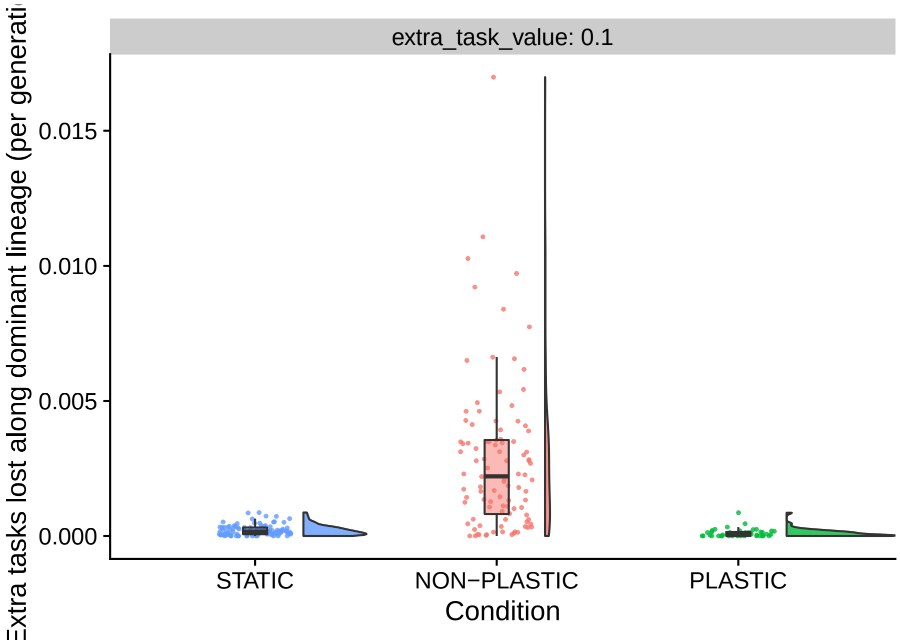
```
##
##  Kruskal-Wallis rank sum test
##
## data:  dominant_lineage_extra_traits_lost_per_step by condition
## Kruskal-Wallis chi-squared = 65.779, df = 2, p-value = 5.204e-15
```

```
pairwise.wilcox.test(
  x=dom_task_data$dominant_lineage_extra_traits_lost_per_step,
  g=dom_task_data$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$dominant_lineage_extra_traits_lost_per_step and dom_task_data$c
##
##         NON-PLASTIC PLASTIC
## PLASTIC 1.3e-10     -
```

```
## STATIC  1.7e-10     0.0092
##
## P value adjustment method: bonferroni
```

```
summary_data$dominant_lineage_extra_traits_lost_per_generation <- summary_data$dominant_lineage_e
ggplot(summary_data, aes(x=condition, y=dominant_lineage_extra_traits_lost_per_generation, 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
  ) +
  ylab("Extra tasks lost along dominant lineage (per generation)") +
  facet_wrap(
    ~extra_task_value,
    labeller=label_both
  ) +
  theme(
    legend.position="none"
  )
```




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

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

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

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

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

```
## [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
```

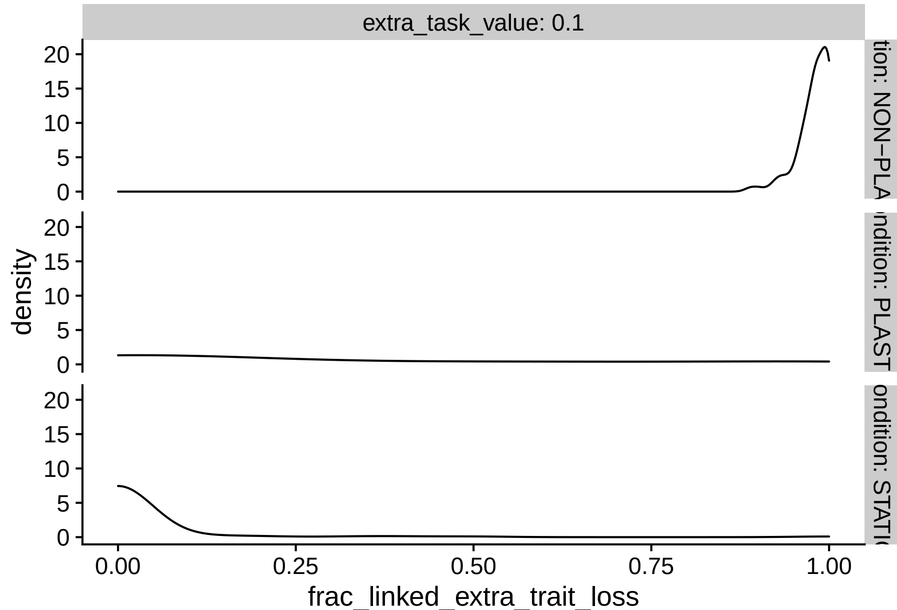
```
pairwise.wilcox.test(
  x=dom_task_data$dominant_lineage_extra_traits_lost_per_generation,
  g=dom_task_data$condition,
  p.adjust.method="bonferroni",
  conf.int=TRUE,
  conf.level=0.95
)
```

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

4.8.4.3 How many instances of novel trait loss co-occur with changes in base phenotype?

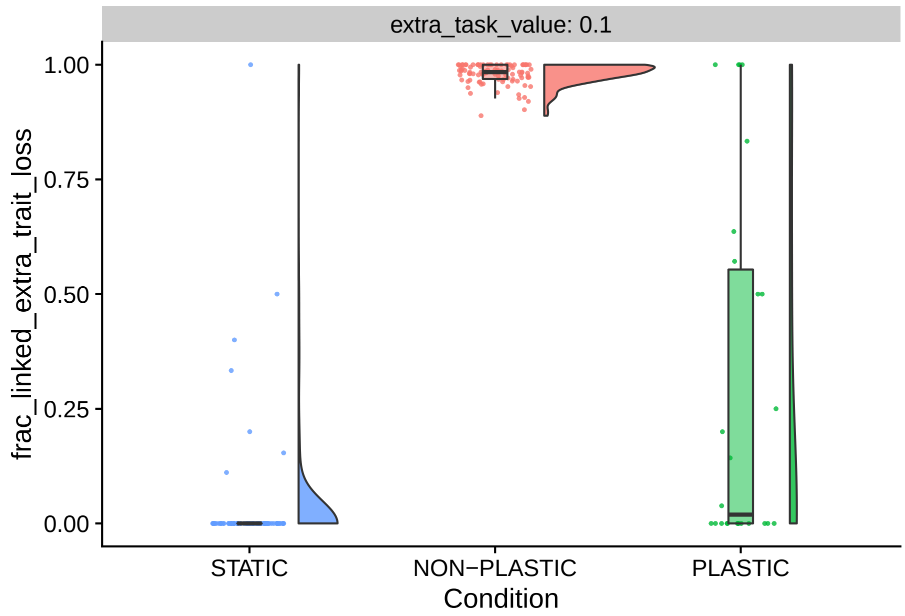
Task loss linked with primary trait changes.

```
lost_traits_summary_data <- filter(summary_data, extra_task_value==0.1 & dominant_lineage_extra_t
lost_traits_summary_data$frac_linked_extra_trait_loss <- lost_traits_summary_data$dominant_lineag

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




```
ggplot(lost_traits_summary_data, aes(x=condition, y=frac_linked_extra_trait_loss, fill=
  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
  ) +
  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_trait_loss)
)
```

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

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

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

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

```
## [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_summar
##
##         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_
```

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

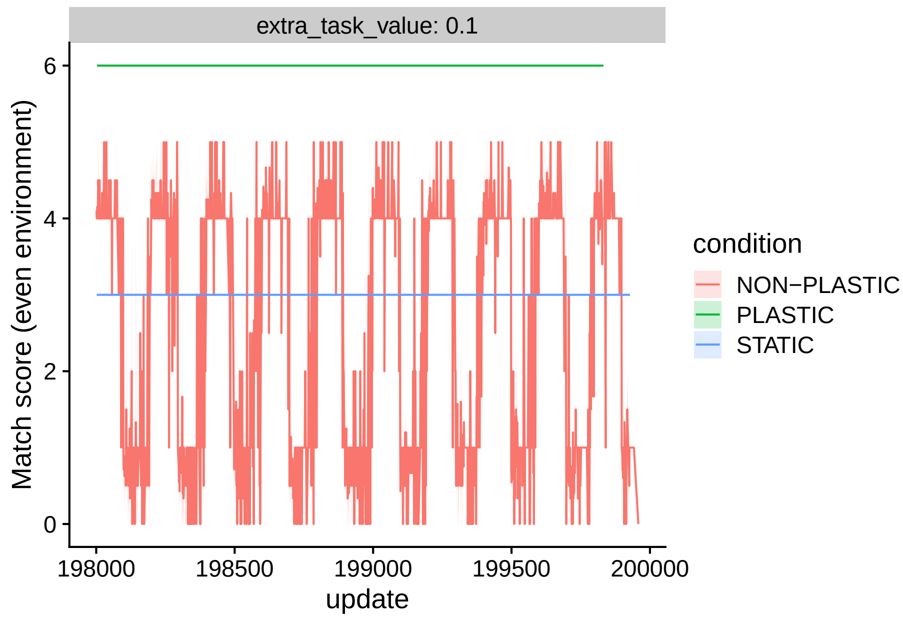
```r
aggregate_frac_linked_extra_trait_loss_nonplastic <- sum(filter(lost_traits_summary_data, conditi
aggregate_frac_linked_extra_trait_loss_nonplastic
```

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

4.9 Extra task performance over time

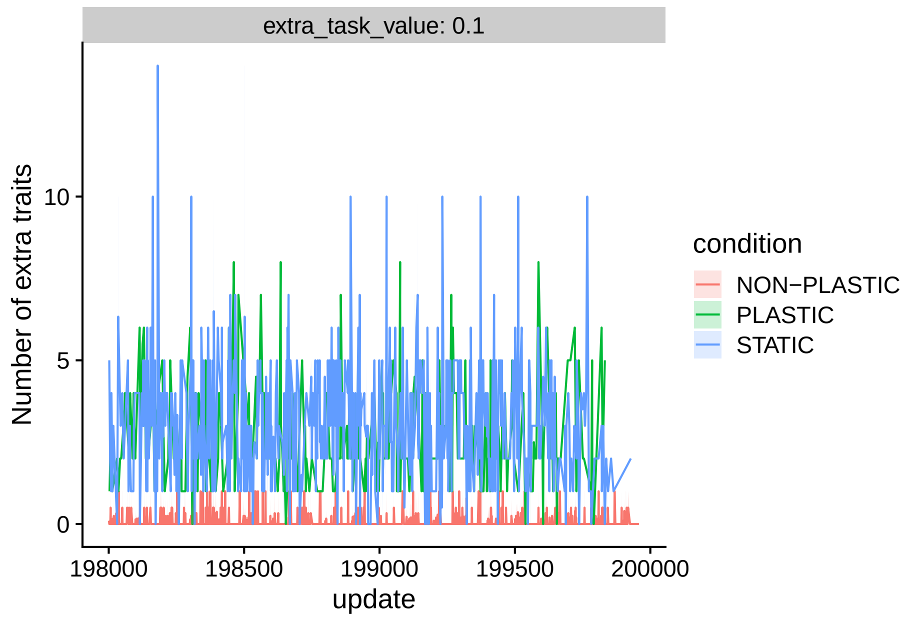
Match score over time

```r
lineage_reward10 <- filter(lineage_time_series_data, extra_task_value=="0.1")

ggplot(filter(lineage_reward10, update>198000 & update<=200000), aes(x=update, y=match_score_even
  stat_summary(fun="mean", geom="line") +
  stat_summary(
    fun.data="mean_cl_boot",
    fun.args=list(conf.int=0.95),
    geom="ribbon",
    alpha=0.2,
    linetype=0
  ) +
  ylab("Match score (even environment)") +
  facet_wrap(
    ~extra_task_value,
    labeller=label_both
  ) +
  ggsave(
    paste0(working_directory, "plots/dominant-lineage-match-score-even-val10.png"),
    width=15,
    height=10
  )
```



Extra tasks over time

```
ggplot(filter(lineage_reward10, update>198000 & update<=200000), aes(x=update, y=extra_
  stat_summary(fun="mean", geom="line") +
  stat_summary(
    fun.data="mean_cl_boot",
    fun.args=list(conf.int=0.95),
    geom="ribbon",
    alpha=0.2,
    linetype=0
  ) +
  ylab("Number of extra traits") +
  facet_wrap(
    ~extra_task_value,
    labeller=label_both
  ) +
  ggsave(
    paste0(working_directory, "plots/dominant-lineage-extra-traits-val10.png"),
    width=15,
    height=10
  )
```

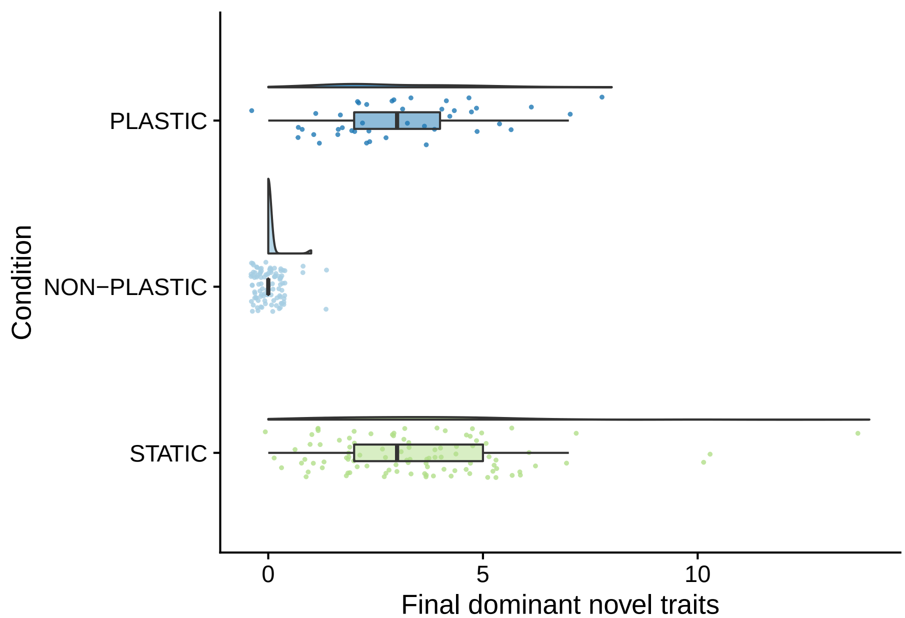


4.10 Manuscript figures

Final dominant extra tasks.

```
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
  ) +
```

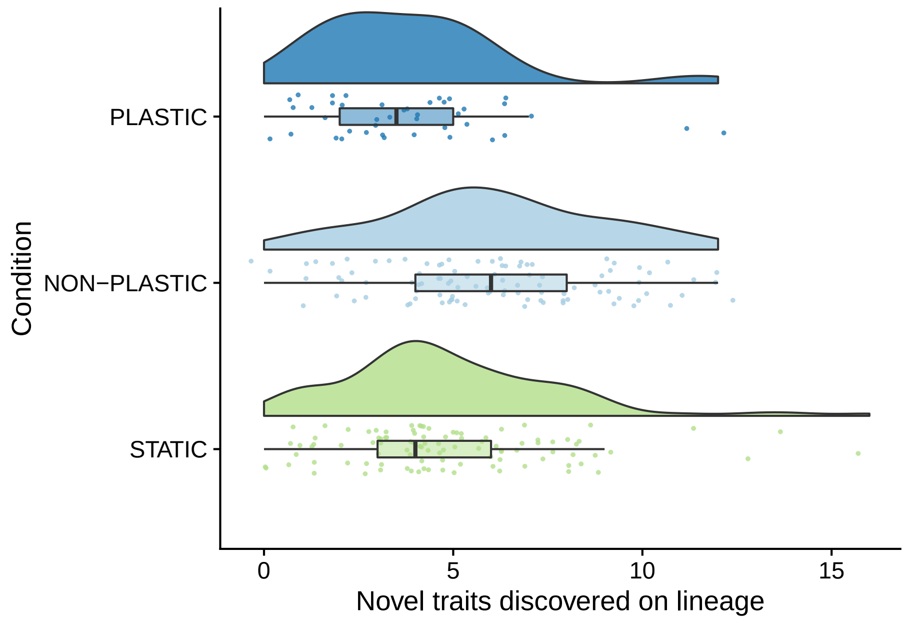
```
  scale_x_discrete(
    name="Condition",
    limits=condition_order,
    labels=condition_order
  ) +
  scale_y_continuous(
    name="Final dominant novel traits"
  ) +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  theme(
    legend.position="none"
  ) +
  coord_flip()
dominant_extra_tasks_fig
```



Final dominant lineage tasks discovered.

```
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)
```

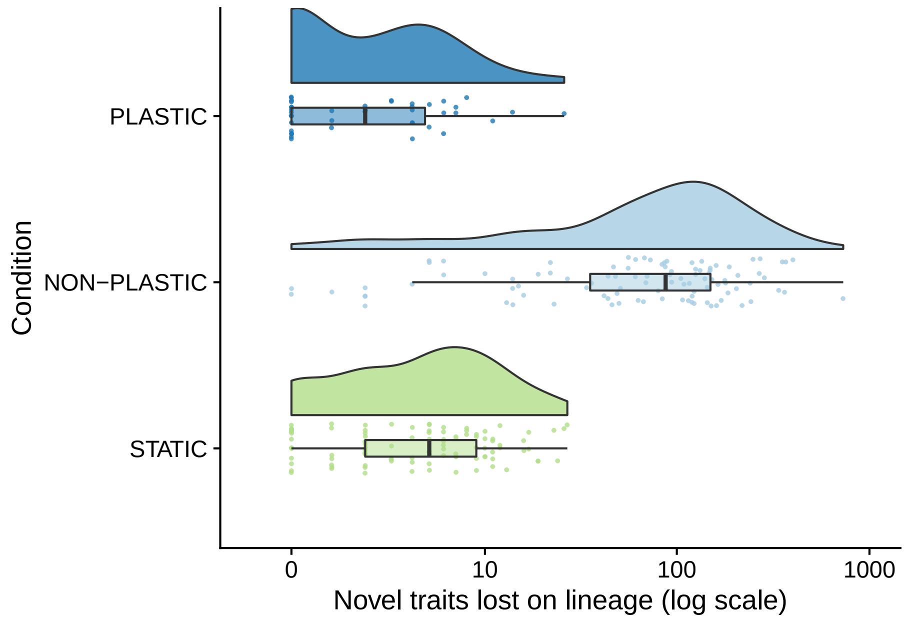
```
  ) +
  geom_flat_violin(
    position = position_nudge(x = .2, y = 0),
    alpha = .8
  ) +
  geom_point(
    mapping=aes(color=condition),
    position = position_jitter(width = .15),
    size = .5,
    alpha = 0.8
  ) +
  geom_boxplot(
    width = .1,
    outlier.shape = NA,
    alpha = 0.5
  ) +
  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
```



Final dominant lineage tasks lost.

```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
```

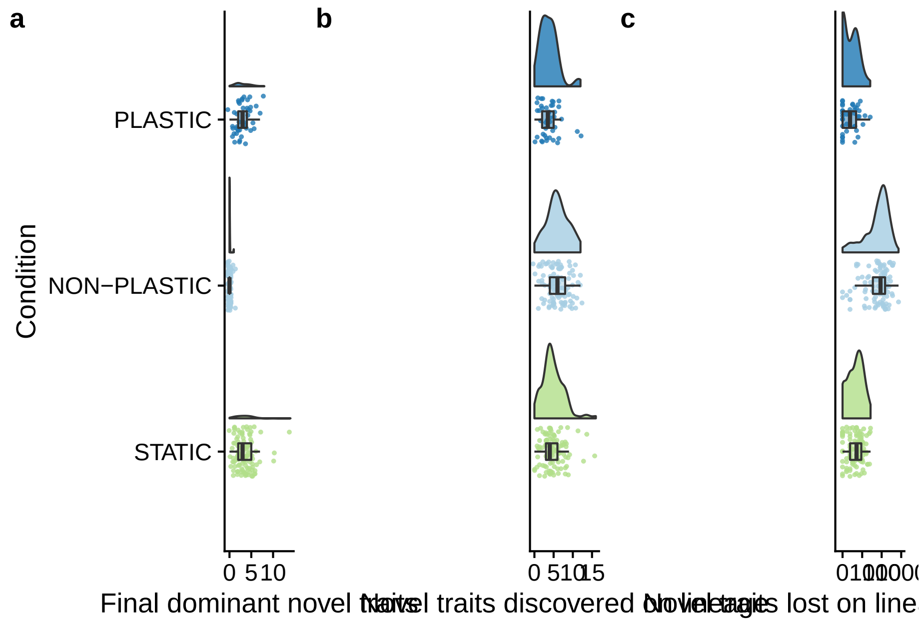
```
  ) +
  scale_y_continuous(
    name="Novel traits lost on lineage (log scale)",
    trans="pseudo_log",
    breaks=c(0,10,100,1000),
    limits=c(-1,1000)
  ) +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  theme(
    legend.position="none"
  ) +
  coord_flip()

lineage_extra_tasks_lost_fig
```



Pull it all together.

```
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
  nrow=1,
  align="v",
  labels="auto"
)
save_plot(
   paste0(working_directory, "plots/", "complex-traits-panel.pdf"),
   grid,
   base_height=6,
   base_asp=2.5
)
grid
```



Chapter 5

Genetic hitchhiking

The effect of adaptive phenotypic plasticity on (deleterious) genetic hitchhiking.

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)
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
```

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")
```

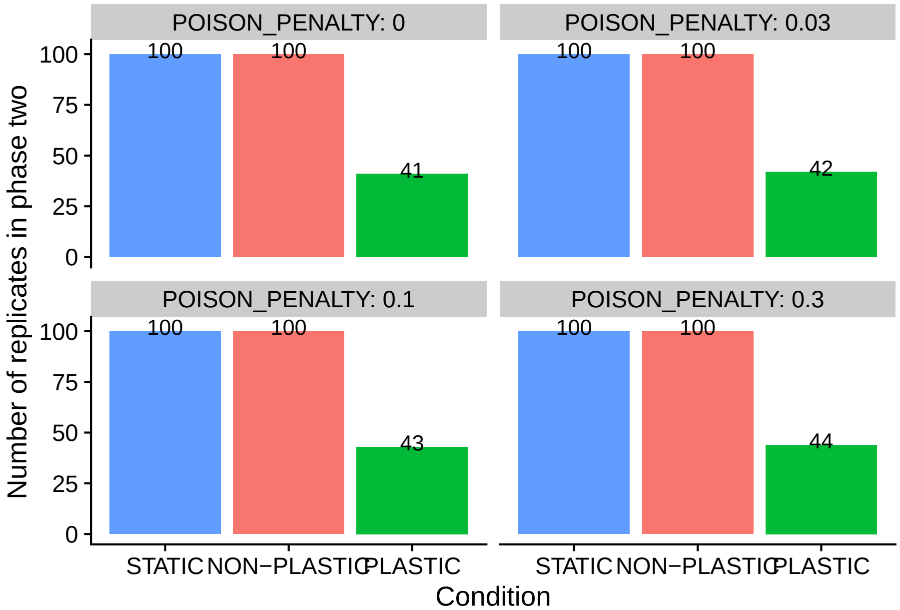
```
  } else {
    return("No sensors")
  }
}

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_R
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 == "0"
lineage_time_series_data$POISON_PENALTY <- as.factor(lineage_time_series_data$POISON_VALUE)

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)
```

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
  ) +
  ylab("Number of replicates in phase two") +
  facet_wrap(~POISON_PENALTY, labeller=label_both) +
  theme(
    legend.position="none"
  )
```

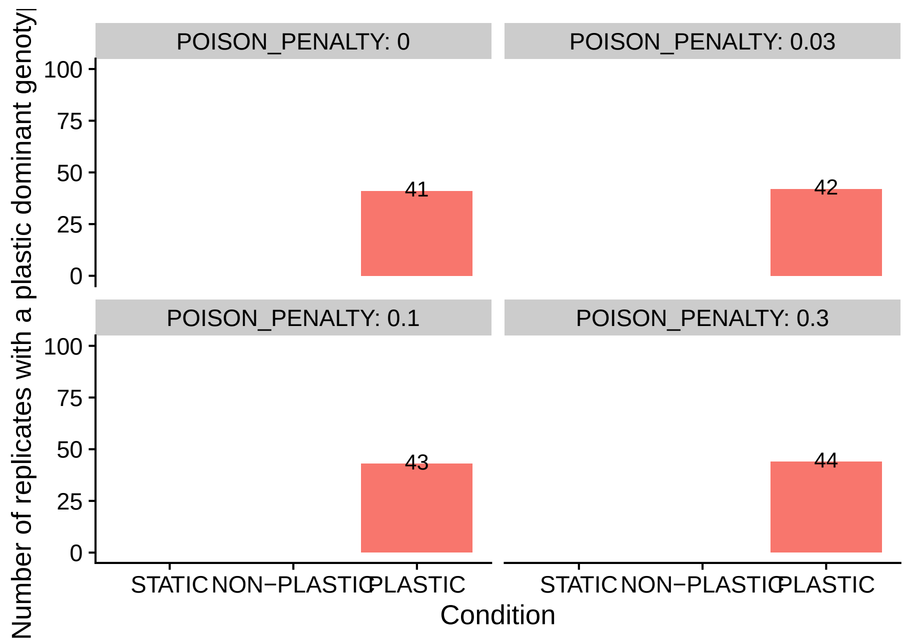


We can confirm our expectation that the dominant genotypes in non-plastic conditions are not phenotypically plastic.

```
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)) +
  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 Hitchhiking instruction execution

5.5.1 Number of replicates where final dominant genotype executes hitchhiker instruction

```
hitchiker_penalty <- 0.1
```

```
occurrences <- c(
  length(filter(summary_data, POISON_PENALTY==hitchiker_penalty & condition=="NON-PLAS
  length(filter(summary_data, POISON_PENALTY==hitchiker_penalty & condition=="PLASTIC"
  length(filter(summary_data, POISON_PENALTY==hitchiker_penalty & condition=="STATIC" &
)
trials <- c(
  length(filter(summary_data, POISON_PENALTY==hitchiker_penalty & condition=="NON-PLAS
  length(filter(summary_data, POISON_PENALTY==hitchiker_penalty & condition=="PLASTIC")
  length(filter(summary_data, POISON_PENALTY==hitchiker_penalty & condition=="STATIC" )
)
names(trials) <- c(
  "NON-PLASTIC",
  "PLASTIC",
  "STATIC"
)
names(occurrences) <- c(
  "NON-PLASTIC",
```

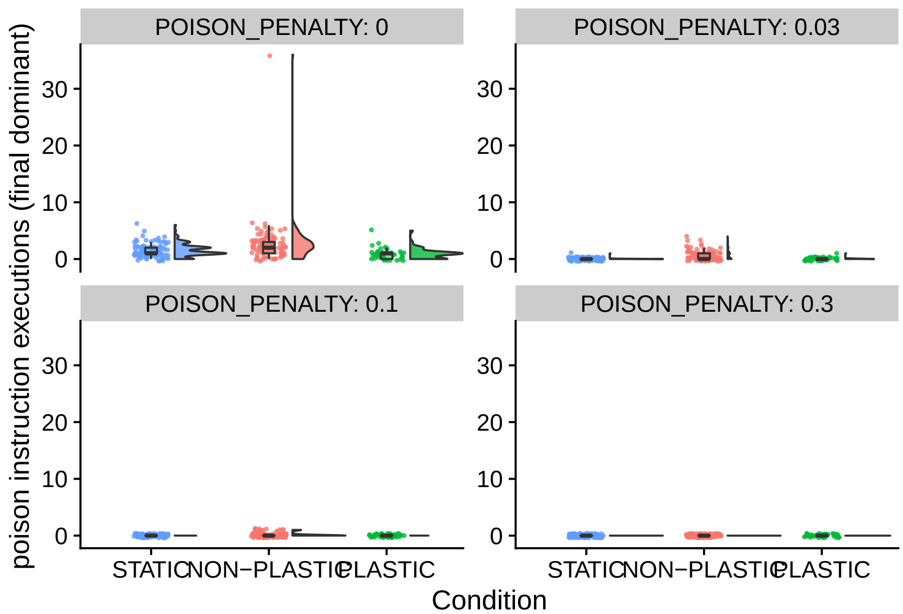
```
  "PLASTIC",
  "STATIC"
)

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 Final dominant genotype hitchhiker execution

```
ggplot(summary_data, aes(x=condition, y=dominant_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
  ) +
  ylab("poison instruction executions (final dominant)") +
  facet_wrap(
    ~POISON_PENALTY,
    labeller=label_both,
    scale="free_y"
  ) +
```

```
  theme(
    legend.position="none"
  ) +
  ggsave(
    paste0(working_directory, "plots/dominant-poison.pdf"),
    width=15,
    height=10
  )
```




```
penalties <- levels(summary_data$POISON_PENALTY)
for (penalty in penalties) {
  stat_data <- filter(summary_data, POISON_PENALTY==penalty)
  print(
    paste0(
      "PENALTY: ", penalty
    )
  )
  kt <- kruskal.test(
      formula=dominant_times_poison_executed~condition,
      data=stat_data
    )
  print(
    kt
  )
  if (is.na(kt$p.value)) { next }
```

```
  if (kt$p.value > 0.05) { next }
  print(
    pairwise.wilcox.test(
      x=stat_data$dominant_times_poison_executed,
      g=stat_data$condition,
      p.adjust.method="bonferroni"
    )
  )
}
```

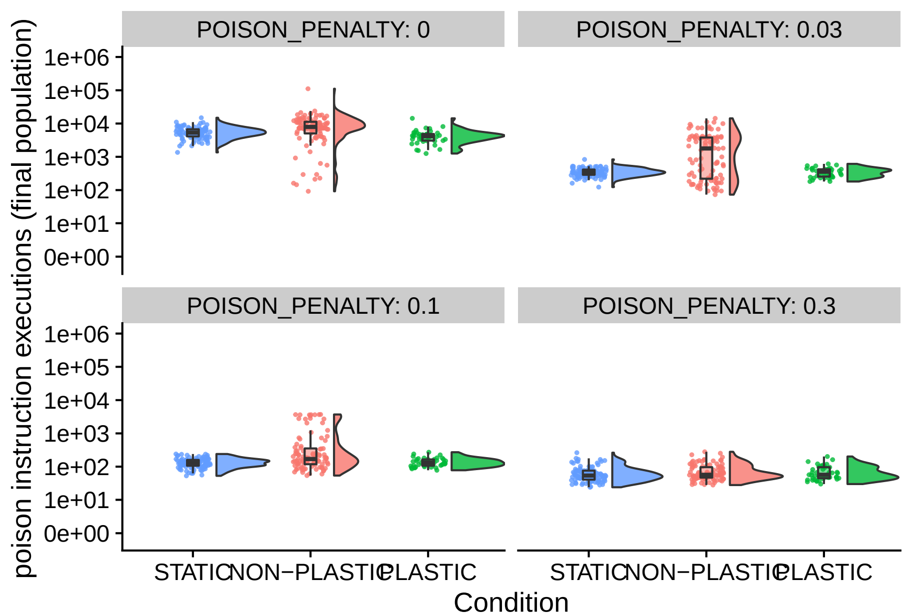
```
## [1] "PENALTY: 0"
##
##  Kruskal-Wallis rank sum test
##
## data:  dominant_times_poison_executed by condition
## Kruskal-Wallis chi-squared = 36.988, df = 2, p-value = 9.294e-09
##
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  stat_data$dominant_times_poison_executed and stat_data$condition
##
##         NON-PLASTIC PLASTIC
## PLASTIC 2.8e-07     -
## STATIC  0.00015     0.00198
##
## P value adjustment method: bonferroni
## [1] "PENALTY: 0.03"
##
##  Kruskal-Wallis rank sum test
##
## data:  dominant_times_poison_executed by condition
## Kruskal-Wallis chi-squared = 72.995, df = 2, p-value < 2.2e-16
##
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  stat_data$dominant_times_poison_executed and stat_data$condition
##
##         NON-PLASTIC PLASTIC
## PLASTIC 2.0e-06     -
## STATIC  2.8e-13     1
##
## P value adjustment method: bonferroni
## [1] "PENALTY: 0.1"
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  dominant_times_poison_executed by condition
## Kruskal-Wallis chi-squared = 21.157, df = 2, p-value = 2.546e-05
##
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  stat_data$dominant_times_poison_executed and stat_data$condition
##
##         NON-PLASTIC PLASTIC
## PLASTIC 0.02034     -
## STATIC  0.00022     -
##
## P value adjustment method: bonferroni
## [1] "PENALTY: 0.3"
##
##  Kruskal-Wallis rank sum test
##
## data:  dominant_times_poison_executed by condition
## Kruskal-Wallis chi-squared = NaN, df = 2, p-value = NA
```

5.5.3 Hitchhiker 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(0,10,100,1000, 10000, 100000, 1000000),
    limits=c(-1,1000000)
  ) +
  facet_wrap(
    ~POISON_PENALTY,
    labeller=label_both
  ) +
  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"
    )
  )
}
```

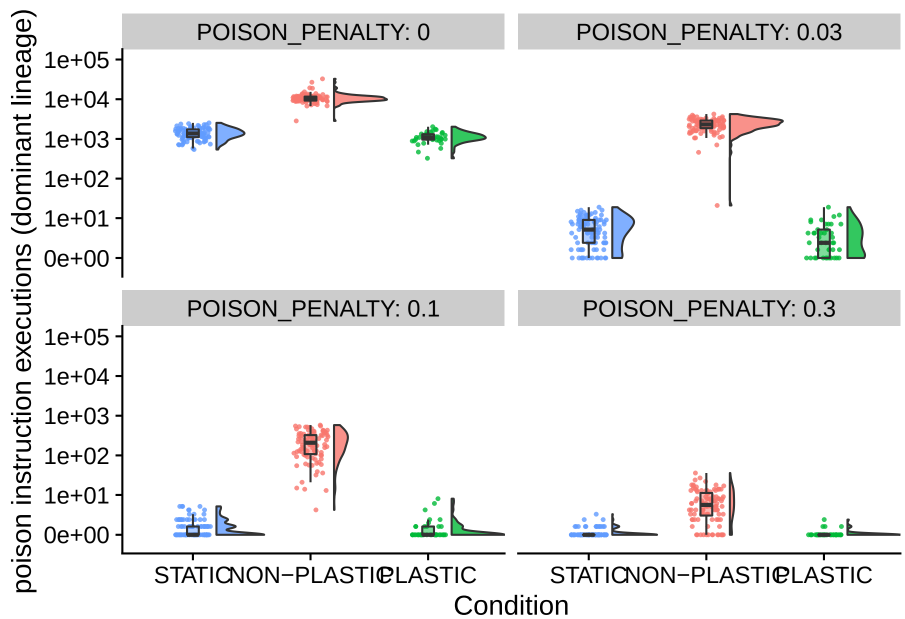
```
## [1] "PENALTY: 0"
##
##  Kruskal-Wallis rank sum test
##
## data:  final_population_poison by condition
## Kruskal-Wallis chi-squared = 43.589, df = 2, p-value = 3.426e-10
##
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  stat_data$final_population_poison and stat_data$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
```

5.5.4 Hitchhiker instruction execution along final dominant lineage (cummulative)

```
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(0,10,100,1000,10000,100000),
    limits=c(-1,100000)
  ) +
  facet_wrap(
    ~POISON_PENALTY,
    labeller=label_both
  ) +
  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
##
```

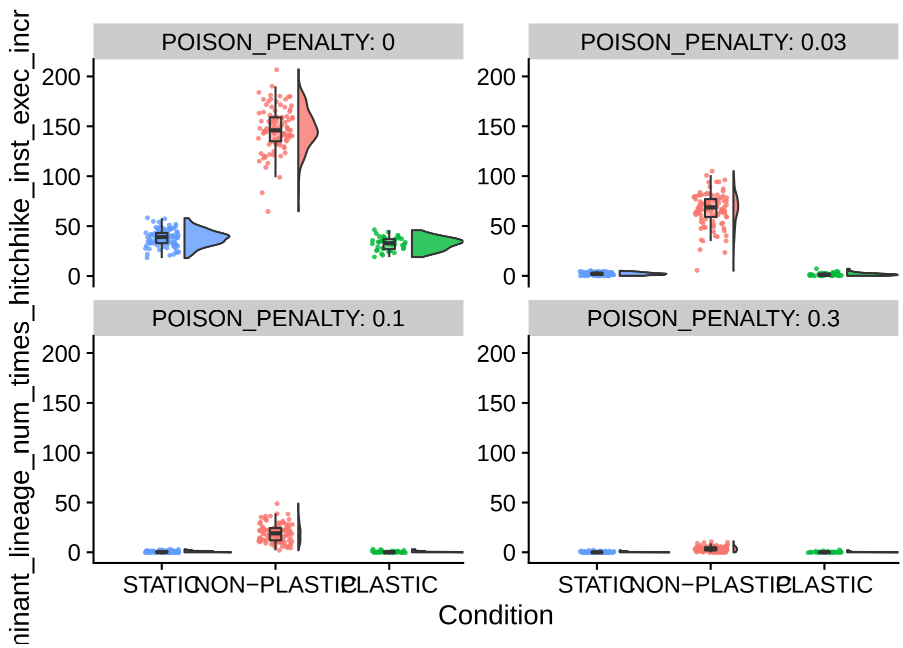
```
##         NON-PLASTIC PLASTIC
## PLASTIC <2e-16      -
## STATIC  <2e-16      0.21
##
## P value adjustment method: bonferroni
## [1] "PENALTY: 0.3"
##
##  Kruskal-Wallis rank sum test
##
## data:  dominant_lineage_times_poison_executed by condition
## Kruskal-Wallis chi-squared = 149.48, df = 2, 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 hitchhiker instruction execution

5.6.1 Number of offspring along dominant lineage with increase in hitchiker 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
  ) +
  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
    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$dominant_lineage_num_times_hitchhike_inst_exec_increases and stat_c
##
##         NON-PLASTIC PLASTIC
## PLASTIC <2e-16      -
## STATIC  <2e-16      0.03
##
## P value adjustment method: bonferroni
## [1] "PENALTY: 0.1"
##
##  Kruskal-Wallis rank sum test
##
## data:  dominant_lineage_num_times_hitchhike_inst_exec_increases by condition
## Kruskal-Wallis chi-squared = 185.34, df = 2, p-value < 2.2e-16
##
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  stat_data$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
```

```r
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_num_times_h
```

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

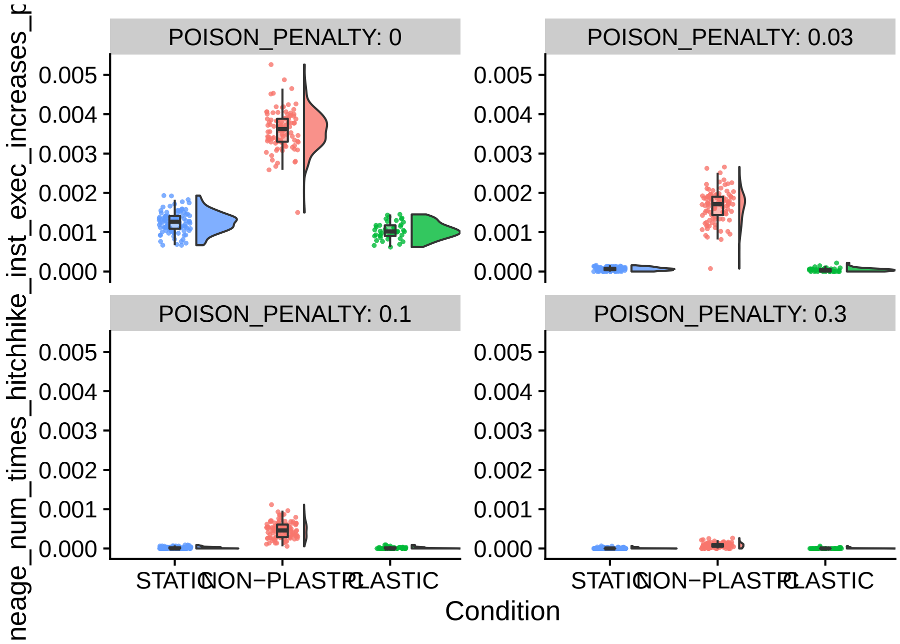
```
sum(filter(summary_data, condition=="STATIC" & POISON_PENALTY==0.1)$dominant_lineage_num_times_hi
```

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

```
# sum(filter(summary_data, condition=="NON-PLASTIC" & POISON_PENALTY==0.1)$dominant_lineage_trai
# sum(filter(summary_data, condition=="PLASTIC" & POISON_PENALTY==0.1)$dominant_lineage_trait_vol
# sum(filter(summary_data, condition=="STATIC" & POISON_PENALTY==0.1)$dominant_lineage_trait_vola
```

5.6.1.1 Normalized by generations

```
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
  ) +
  facet_wrap(
    ~POISON_PENALTY,
    labeller=label_both,
    scales="free_y"
  ) +
  theme(
    legend.position="none"
  )
```



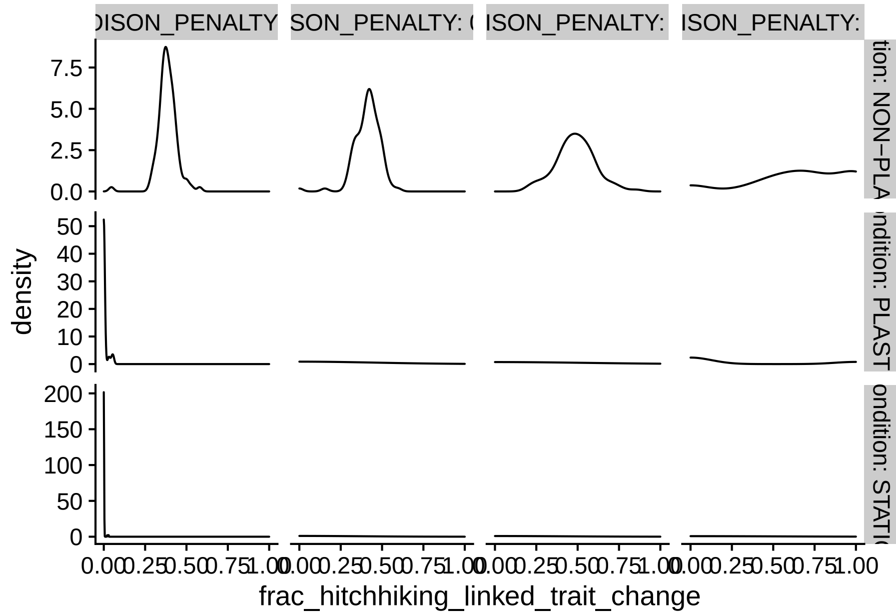

```
penalties <- levels(summary_data$POISON_PENALTY)
for (penalty in penalties) {
  stat_data <- filter(summary_data, POISON_PENALTY==penalty)
  print(
    paste0(
      "PENALTY: ", penalty
    )
  )
  kt <- kruskal.test(
      formula=dominant_lineage_num_times_hitchhike_inst_exec_increases_per_generation~c
      data=stat_data
    )
  print(
    kt
  )
  if (is.na(kt$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
```

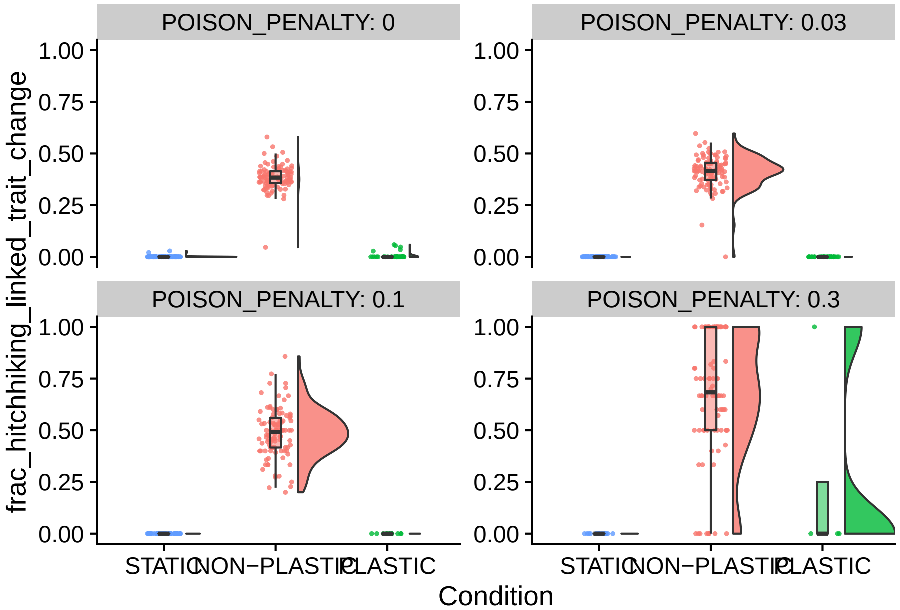
5.6.2 What fraction of mutations that increase hitchhiker instruction execution co-occur with base trait changes?

```
# Fraction of unexpressed vs expressed increases in hitchhiker instructions
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"
  ) +
  theme(
    legend.position="none"
  ) +
  ggsave(
    paste0(working_directory, "plots/dominant-lineage-frac_hitchhiking_linked_trait_cha
    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
  ) +
  facet_wrap(
    ~POISON_PENALTY,
    labeller=label_both,
    scales="free_y"
  ) +
```

```
  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
```

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

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

```r
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, ")")
```

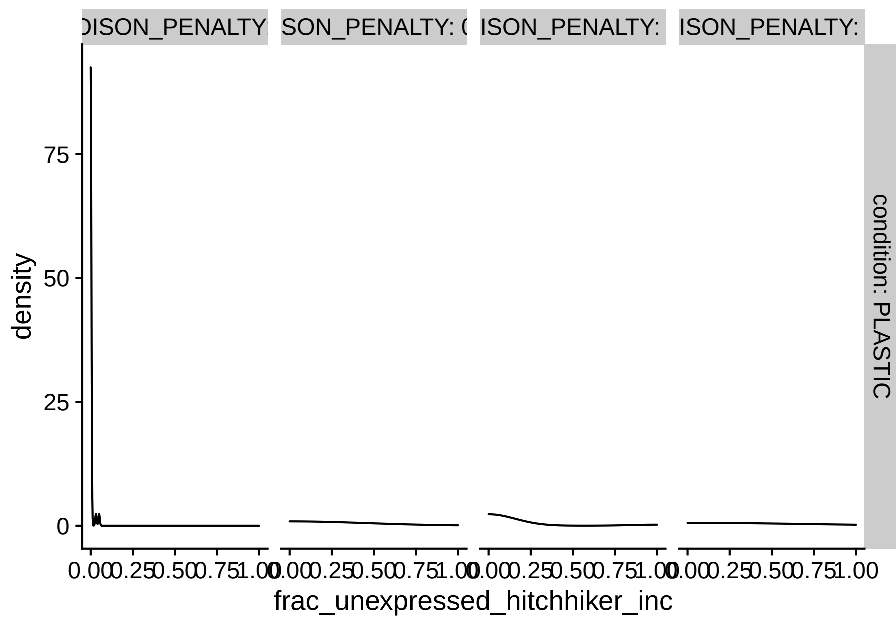
```
## [1] "PLASTIC: 0 (0/18)"
```

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

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

5.6.3 What about unexpressed vs expressed trait changes in plastic populations?

```
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 & conditio
  geom_density() +
  facet_grid(
    condition~POISON_PENALTY,
    labeller=label_both,
    scales="free_y"
  ) +
  theme(
    legend.position="none"
  )
```



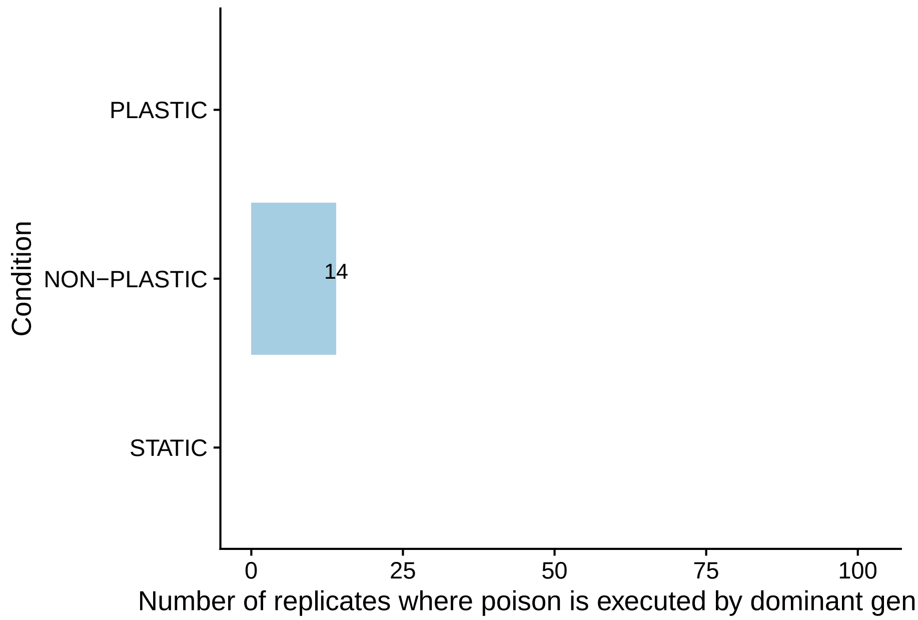

```
# ggplot(filter(summary_data, dominant_lineage_num_times_hitchhike_inst_exec_increases>0 & condi
#   geom_density() +
#   facet_grid(
#     condition~POISON_PENALTY,
#     labeller=label_both,
#     scales="free_y"
#   ) +
#   theme(
```

```
#     legend.position="none"
#   )
```

```
hitchiker_penalty <- 0.1
```

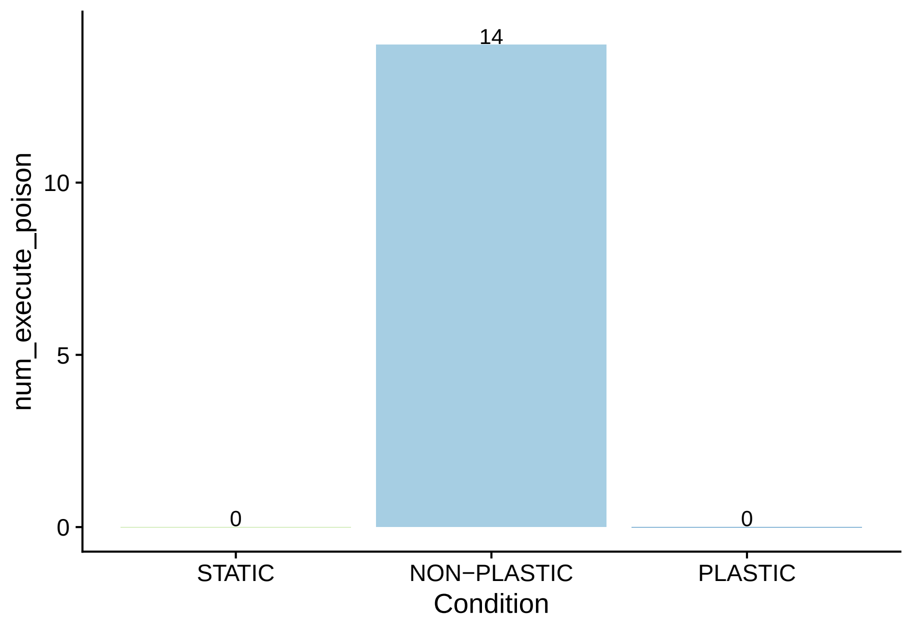
5.7 Manuscript figures

```
ggplot(filter(summary_data, POISON_PENALTY==hitchiker_penalty & condition=="NON-PLASTI
  geom_bar() +
  geom_text(
    stat="count",
    mapping=aes(label=..count..),
    position=position_dodge(0.9),
    vjust=0
  ) +
  scale_y_continuous(
    name="Number of replicates where poison is executed by dominant genotype",
    limits=c(0, replicates+2)
  ) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order,
    labels=condition_order,
    breaks=condition_order
  ) +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  coord_flip() +
  theme(
    legend.position="none"
  )
```




```
fig_data <- data.frame(
  num_execute_poison=c(
    length(filter(summary_data, POISON_PENALTY==hitchiker_penalty & condition=="NON-PLASTIC" & do
    length(filter(summary_data, POISON_PENALTY==hitchiker_penalty & condition=="PLASTIC" & domina
    length(filter(summary_data, POISON_PENALTY==hitchiker_penalty & condition=="STATIC" & dominar
  ),
  num_execute_no_poison=c(
    length(filter(summary_data, POISON_PENALTY==hitchiker_penalty & condition=="NON-PLASTIC" & do
    length(filter(summary_data, POISON_PENALTY==hitchiker_penalty & condition=="PLASTIC" & domina
    length(filter(summary_data, POISON_PENALTY==hitchiker_penalty & condition=="STATIC" & dominar
  ),
  total=c(
    length(filter(summary_data, POISON_PENALTY==hitchiker_penalty & condition=="NON-PLASTIC")$RAN
    length(filter(summary_data, POISON_PENALTY==hitchiker_penalty & condition=="PLASTIC")$RANDOM_
    length(filter(summary_data, POISON_PENALTY==hitchiker_penalty & condition=="STATIC" )$RANDOM_
  ),
  condition=c(
    "NON-PLASTIC",
    "PLASTIC",
    "STATIC"
  )
)

ggplot(fig_data, aes(x=condition, y=num_execute_poison, fill=condition)) +
  geom_col(position=position_dodge(0.9)) +
```

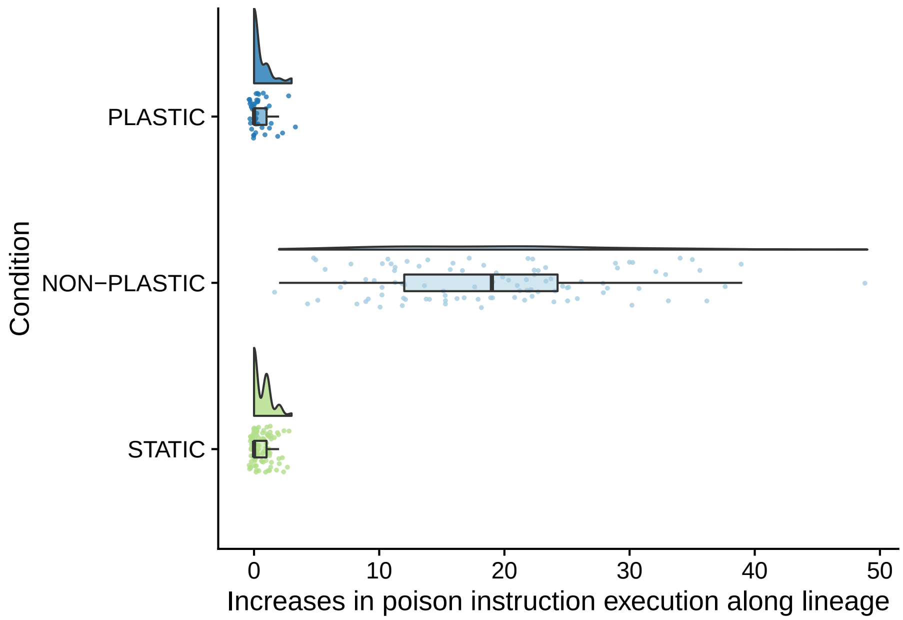
```
  geom_text(aes(label=num_execute_poison, y=num_execute_poison+0.25)) +
  scale_x_discrete(
    name="Condition",
    limits=condition_order
  ) +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  theme(
    legend.position="none"
  )
```



Number of poison increases along lineage.

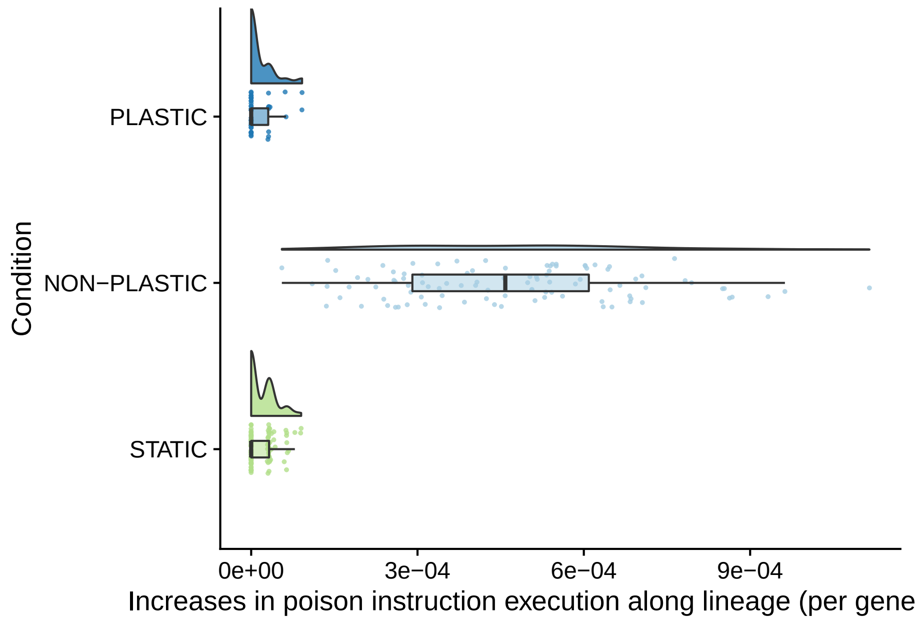
```
poison_increases_fig <- ggplot(
    filter(summary_data, POISON_PENALTY==hitchiker_penalty),
    aes(x=condition, y=dominant_lineage_num_times_hitchhike_inst_exec_increases, fill=c
  ) +
  geom_flat_violin(
    position = position_nudge(x = .2, y = 0),
    alpha = .8
  ) +
```

```
  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 instruction execution along lineage",
  ) +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  theme(
    legend.position="none"
  ) +
  coord_flip()

poison_increases_fig
```




```
poison_increases_per_gen_fig <- ggplot(
    filter(summary_data, POISON_PENALTY==hitchiker_penalty),
    aes(x=condition, y=dominant_lineage_num_times_hitchhike_inst_exec_increases_per_ger
  ) +
  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 instruction execution along lineage (per generation)",
  ) +
  scale_fill_brewer(
    palette="Paired"
  ) +
  scale_color_brewer(
    palette="Paired"
  ) +
  theme(
    legend.position="none"
  ) +
  coord_flip()

poison_increases_per_gen_fig
```



Pull it all together.

```
# grid <- plot_grid(
#   dominant_extra_tasks_fig,
#   lineage_extra_tasks_discovered_fig + theme(axis.ticks.y=element_blank(),axis.text.y=element_b
#   lineage_extra_tasks_lost_fig + theme(axis.ticks.y=element_blank(),axis.text.y=element_blank()
#   nrow=1,
#   align="v",
#   labels="auto"
# )
```

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