

# Testing disturploidy()

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This script tests:

- Selection on growth rate
- Disturbance
- Genome duplication

Using: `sim <- disturploidy(generations = 15)`

```
# trim to remove extinction
#sim <- sim[1:length(sim) - 1]
# convert sim output to dataframe
sim_df <- do.call("bind_rows", sim)
# add generations
gen <- NULL
for(pop in 1:length(sim)){
  this_gen <- rep(pop, nrow(sim[[pop]]))
  gen <- c(gen, this_gen)
}
sim_df$gen <- gen
# add growth rates
sim_df$growth_rate <- sapply(
  sim_df$genome, get_growth_rate
)
# add ploidy_lvl
sim_df$ploidy <- sim_df$genome %>%
  map("allelele") %>%
  sapply(nlevels)
# format and check data structure
sim_df$ID <- as.factor(sim_df$ID)
sim_df$life_stage <- as.factor(sim_df$life_stage)
summary(sim_df$life_stage)
```

```
##      0      1      2
## 2799 1410   218
```

```
summary(as.factor(sim_df$gen))
```

```
##      1      2      3      4      5      6
## 100  109  301  534 1167 2216
```

```
summary(sim_df$growth_rate)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##  1.207   1.420   1.484   1.477   1.534   1.797
```

```
summary(sim_df$ploidy)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##  2.000   2.000   2.000   2.013   2.000   3.000
```

```
str(sim_df, list.len = 10)
```

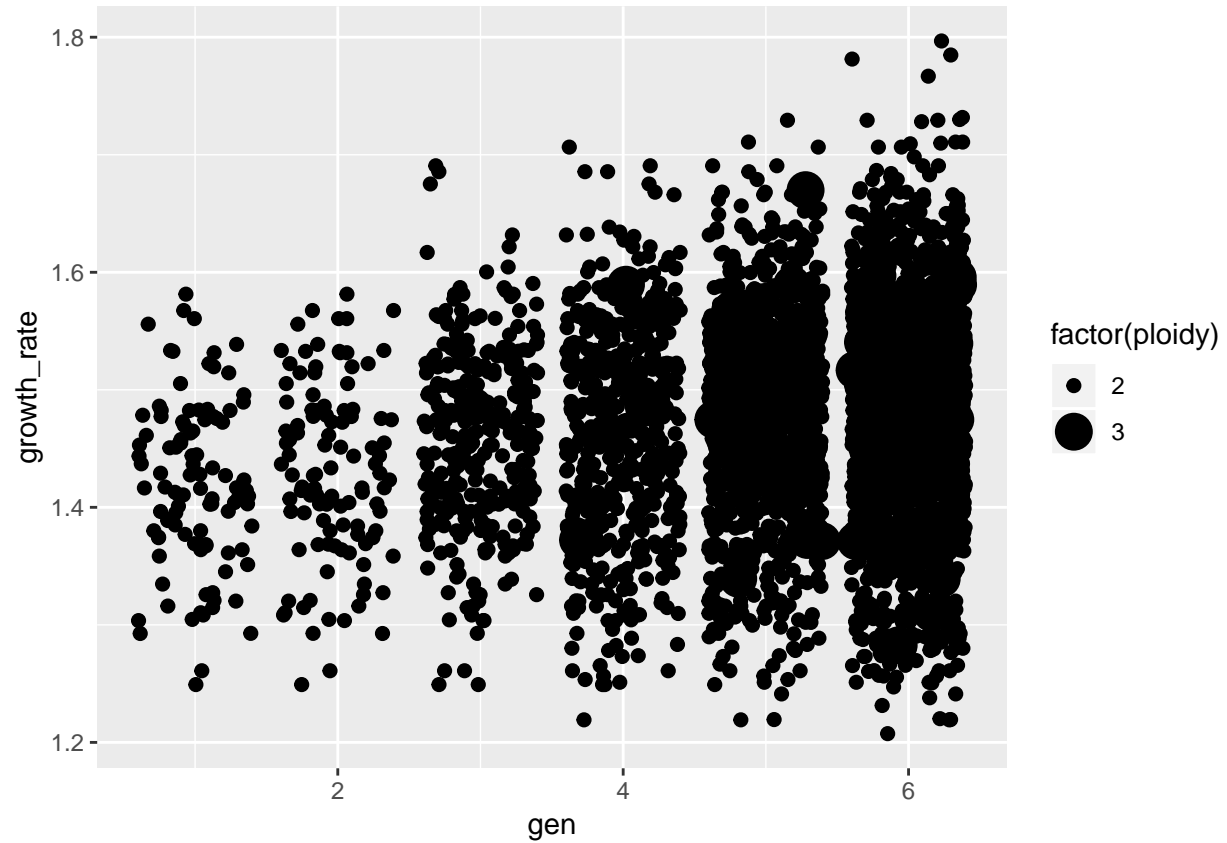
```
## Classes 'tbl_df', 'tbl' and 'data.frame': 4427 obs. of 10 variables:
## $ X      : num  66 66 88 40 100 98 80 54 89 10 ...
## $ Y      : num  38 38 67 65 28 20 85 53 72 64 ...
## $ N      : int   2 2 1 1 1 1 1 1 1 1 ...
## $ ID      : Factor w/ 2248 levels "0_1","0_10","0_100",...: 12 14 1 13 24 35 46 57 68 79 ...
## $ life_stage : Factor w/ 3 levels "0","1","2": 1 1 1 1 1 1 1 1 1 1 ...
## $ size     : num   0 0 0 0 0 0 0 0 0 0 ...
## $ genome   :List of 4427
## ..$ :Classes 'tbl_df', 'tbl' and 'data.frame': 20 obs. of 3 variables:
## .. ..$ allele: Factor w/ 2 levels "1","2": 1 1 1 1 1 1 1 1 1 1 ...
## .. ..$ locus : Factor w/ 10 levels "1","2","3","4",...: 1 2 3 4 5 6 7 8 9 10 ...
## .. ..$ value : num  89.9 67.78 45.76 12.5 1.34 ...
## ..$ :Classes 'tbl_df', 'tbl' and 'data.frame': 20 obs. of 3 variables:
## .. ..$ allele: Factor w/ 2 levels "1","2": 1 1 1 1 1 1 1 1 1 1 ...
## .. ..$ locus : Factor w/ 10 levels "1","2","3","4",...: 1 2 3 4 5 6 7 8 9 10 ...
## .. ..$ value : num  48.4 83.1 60.2 94.1 96 ...
## ..$ :Classes 'tbl_df', 'tbl' and 'data.frame': 20 obs. of 3 variables:
## .. ..$ allele: Factor w/ 2 levels "1","2": 1 1 1 1 1 1 1 1 1 1 ...
## .. ..$ locus : Factor w/ 10 levels "1","2","3","4",...: 1 2 3 4 5 6 7 8 9 10 ...
## .. ..$ value : num  20.9 77.3 27.3 29.3 85.4 ...
## ..$ :Classes 'tbl_df', 'tbl' and 'data.frame': 20 obs. of 3 variables:
## .. ..$ allele: Factor w/ 2 levels "1","2": 1 1 1 1 1 1 1 1 1 1 ...
## .. ..$ locus : Factor w/ 10 levels "1","2","3","4",...: 1 2 3 4 5 6 7 8 9 10 ...
## .. ..$ value : num   1.35 89.01 39.11 36.31 89.64 ...
## ..$ :Classes 'tbl_df', 'tbl' and 'data.frame': 20 obs. of 3 variables:
## .. ..$ allele: Factor w/ 2 levels "1","2": 1 1 1 1 1 1 1 1 1 1 ...
## .. ..$ locus : Factor w/ 10 levels "1","2","3","4",...: 1 2 3 4 5 6 7 8 9 10 ...
## .. ..$ value : num  7.0378 23.8837 55.3548 0.0707 1.7314 ...
## ..$ :Classes 'tbl_df', 'tbl' and 'data.frame': 20 obs. of 3 variables:
## .. ..$ allele: Factor w/ 2 levels "1","2": 1 1 1 1 1 1 1 1 1 1 ...
## .. ..$ locus : Factor w/ 10 levels "1","2","3","4",...: 1 2 3 4 5 6 7 8 9 10 ...
## .. ..$ value : num  89.19 10.26 93.34 4.77 78.13 ...
## ..$ :Classes 'tbl_df', 'tbl' and 'data.frame': 20 obs. of 3 variables:
## .. ..$ allele: Factor w/ 2 levels "1","2": 1 1 1 1 1 1 1 1 1 1 ...
## .. ..$ locus : Factor w/ 10 levels "1","2","3","4",...: 1 2 3 4 5 6 7 8 9 10 ...
## .. ..$ value : num  56.8 75.7 14.8 57.5 52.4 ...
## ..$ :Classes 'tbl_df', 'tbl' and 'data.frame': 20 obs. of 3 variables:
## .. ..$ allele: Factor w/ 2 levels "1","2": 1 1 1 1 1 1 1 1 1 1 ...
## .. ..$ locus : Factor w/ 10 levels "1","2","3","4",...: 1 2 3 4 5 6 7 8 9 10 ...
## .. ..$ value : num   2.73 18.16 31.83 99.11 43.19 ...
## ..$ :Classes 'tbl_df', 'tbl' and 'data.frame': 20 obs. of 3 variables:
## .. ..$ allele: Factor w/ 2 levels "1","2": 1 1 1 1 1 1 1 1 1 1 ...
## .. ..$ locus : Factor w/ 10 levels "1","2","3","4",...: 1 2 3 4 5 6 7 8 9 10 ...
## .. ..$ value : num  86.9 62.8 94.5 77.6 49.7 ...
## ..$ :Classes 'tbl_df', 'tbl' and 'data.frame': 20 obs. of 3 variables:
## .. ..$ allele: Factor w/ 2 levels "1","2": 1 1 1 1 1 1 1 1 1 1 ...
## .. ..$ locus : Factor w/ 10 levels "1","2","3","4",...: 1 2 3 4 5 6 7 8 9 10 ...
## .. ..$ value : num  92.5 32.9 92.9 33.1 84.8 ...
## .. [list output truncated]
## $ gen      : int   1 1 1 1 1 1 1 1 1 1 ...
## $ growth_rate: num   1.37 1.53 1.36 1.44 1.32 ...
## $ ploidy    : int   2 2 2 2 2 2 2 2 2 2 ...
```

```

# quick plot selection
# looks less clear since distrubance added
qplot(
  gen,
  growth_rate,
  data = sim_df,
  geom = "jitter",
  size = factor(ploidy)
)

```

## Warning: Using size for a discrete variable is not advised.

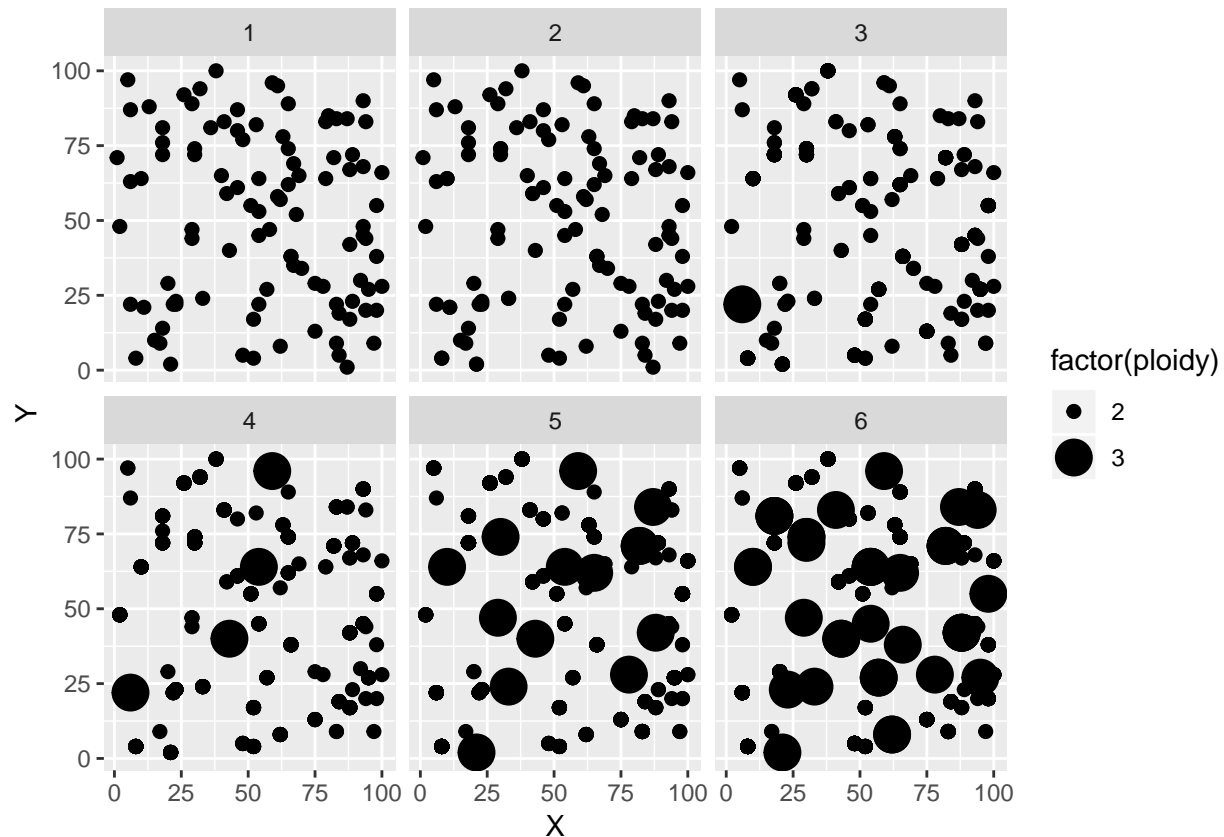


```

# quick plot disturbance
# should see disturbance reducing plants on right
qplot(
  X, Y,
  data = sim_df,
  xlim = c(1, 100),
  size = factor(ploidy),
  facets = ~gen
)

```

## Warning: Using size for a discrete variable is not advised.



```
# quick histogram of ploidy levels
qplot(
  factor(ploidy),
  data = sim_df,
  facets = ~gen
)
```

