

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
## 424    1
```

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

```
##    1    2    3    4    5    6    7    8    9   10   11   12   13
## 100   51   30   35   53   29   26    2   27   42    2   27    1
```

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

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##      5.33   10.29   11.85   16.59   19.26   64.69
```

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

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##      2.000   2.000   2.000   2.993   3.000  12.000
```

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

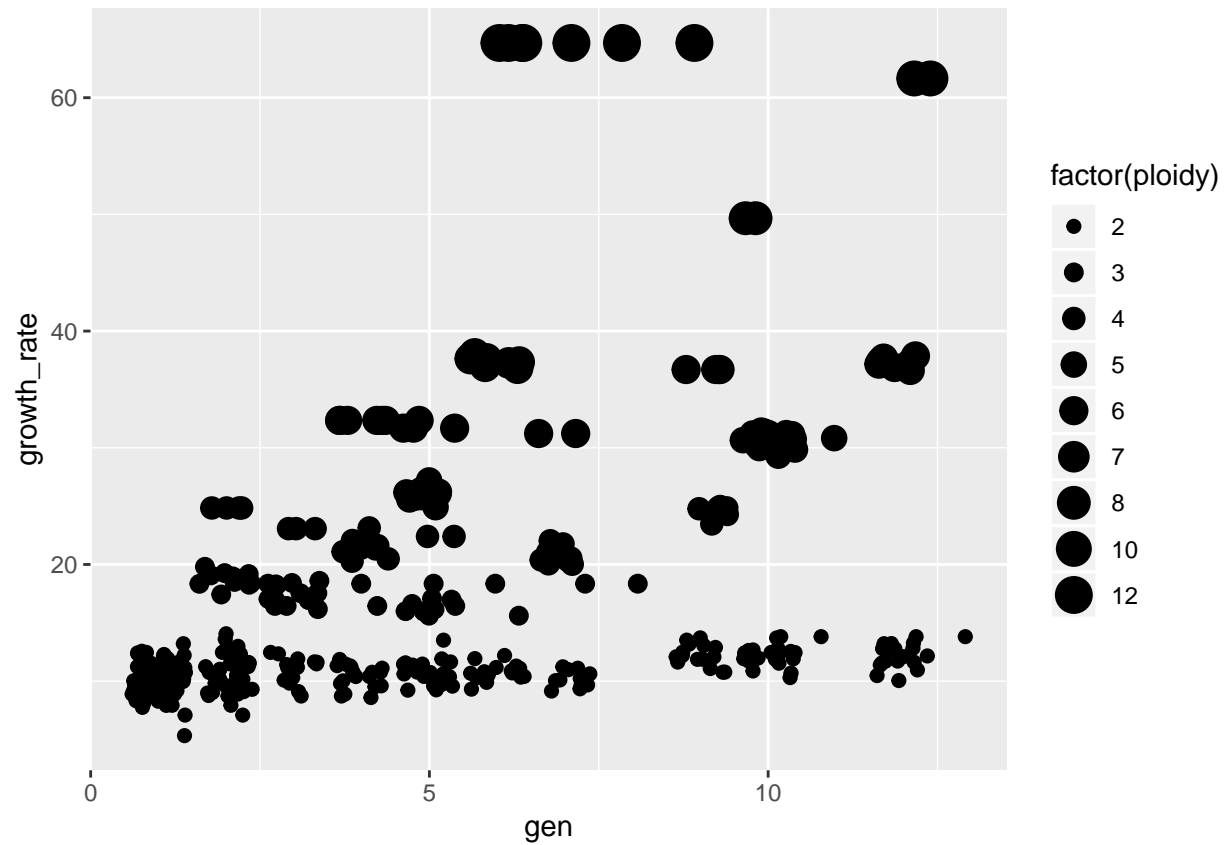
```
## Classes 'tbl_df', 'tbl' and 'data.frame': 425 obs. of 10 variables:
## $ X      : num  93 93 69 54 46 30 53 95 96 86 ...
## $ Y      : num  84 84 48 7 82 50 86 44 25 29 ...
## $ N      : int   2 2 1 1 1 1 1 1 1 1 ...
## $ ID      : Factor w/ 372 levels "0_1","0_10","0_100",...: 1 4 13 24 35 46 57 68 79 90 ...
## $ life_stage : Factor w/ 2 levels "0","1": 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 425
## ..$ :Classes 'tbl_df', 'tbl' and 'data.frame': 200 obs. of 3 variables:
## .. ..$ allele: Factor w/ 2 levels "1","2": 1 1 1 1 1 1 1 1 1 1 ...
## .. ..$ locus : Factor w/ 100 levels "1","2","3","4",...: 1 2 3 4 5 6 7 8 9 10 ...
## .. ..$ value : num  6.25 88.8 28.47 41.56 8.45 ...
## ..$ :Classes 'tbl_df', 'tbl' and 'data.frame': 200 obs. of 3 variables:
## .. ..$ allele: Factor w/ 2 levels "1","2": 1 1 1 1 1 1 1 1 1 1 ...
## .. ..$ locus : Factor w/ 100 levels "1","2","3","4",...: 1 2 3 4 5 6 7 8 9 10 ...
## .. ..$ value : num  24.9 52.2 31.5 58.9 74.3 ...
## ..$ :Classes 'tbl_df', 'tbl' and 'data.frame': 200 obs. of 3 variables:
## .. ..$ allele: Factor w/ 2 levels "1","2": 1 1 1 1 1 1 1 1 1 1 ...
## .. ..$ locus : Factor w/ 100 levels "1","2","3","4",...: 1 2 3 4 5 6 7 8 9 10 ...
## .. ..$ value : num  13.5 42.6 31.8 94.1 50.3 ...
## ..$ :Classes 'tbl_df', 'tbl' and 'data.frame': 200 obs. of 3 variables:
## .. ..$ allele: Factor w/ 2 levels "1","2": 1 1 1 1 1 1 1 1 1 1 ...
## .. ..$ locus : Factor w/ 100 levels "1","2","3","4",...: 1 2 3 4 5 6 7 8 9 10 ...
## .. ..$ value : num  57.1 72.7 40.5 23.9 76.6 ...
## ..$ :Classes 'tbl_df', 'tbl' and 'data.frame': 200 obs. of 3 variables:
## .. ..$ allele: Factor w/ 2 levels "1","2": 1 1 1 1 1 1 1 1 1 1 ...
## .. ..$ locus : Factor w/ 100 levels "1","2","3","4",...: 1 2 3 4 5 6 7 8 9 10 ...
## .. ..$ value : num  28.9 93.1 51.3 93.8 60.8 ...
## ..$ :Classes 'tbl_df', 'tbl' and 'data.frame': 200 obs. of 3 variables:
## .. ..$ allele: Factor w/ 2 levels "1","2": 1 1 1 1 1 1 1 1 1 1 ...
## .. ..$ locus : Factor w/ 100 levels "1","2","3","4",...: 1 2 3 4 5 6 7 8 9 10 ...
## .. ..$ value : num  72.82 4.09 39.68 66.58 49.24 ...
## ..$ :Classes 'tbl_df', 'tbl' and 'data.frame': 200 obs. of 3 variables:
## .. ..$ allele: Factor w/ 2 levels "1","2": 1 1 1 1 1 1 1 1 1 1 ...
## .. ..$ locus : Factor w/ 100 levels "1","2","3","4",...: 1 2 3 4 5 6 7 8 9 10 ...
## .. ..$ value : num  73.86 32.22 23.05 4.07 77.99 ...
## ..$ :Classes 'tbl_df', 'tbl' and 'data.frame': 200 obs. of 3 variables:
## .. ..$ allele: Factor w/ 2 levels "1","2": 1 1 1 1 1 1 1 1 1 1 ...
## .. ..$ locus : Factor w/ 100 levels "1","2","3","4",...: 1 2 3 4 5 6 7 8 9 10 ...
## .. ..$ value : num  26.3 44.4 58.2 37.5 85.8 ...
## ..$ :Classes 'tbl_df', 'tbl' and 'data.frame': 200 obs. of 3 variables:
## .. ..$ allele: Factor w/ 2 levels "1","2": 1 1 1 1 1 1 1 1 1 1 ...
## .. ..$ locus : Factor w/ 100 levels "1","2","3","4",...: 1 2 3 4 5 6 7 8 9 10 ...
## .. ..$ value : num  29.995 23.052 0.724 61.162 36.766 ...
## ..$ :Classes 'tbl_df', 'tbl' and 'data.frame': 200 obs. of 3 variables:
## .. ..$ allele: Factor w/ 2 levels "1","2": 1 1 1 1 1 1 1 1 1 1 ...
## .. ..$ locus : Factor w/ 100 levels "1","2","3","4",...: 1 2 3 4 5 6 7 8 9 10 ...
## .. ..$ value : num  40.63 72.87 62.44 70.76 4.05 ...
## .. [list output truncated]
## $ gen      : int   1 1 1 1 1 1 1 1 1 1 ...
## $ growth_rate: num   9.6 9.03 9.19 10.54 10.3 ...
## $ 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.

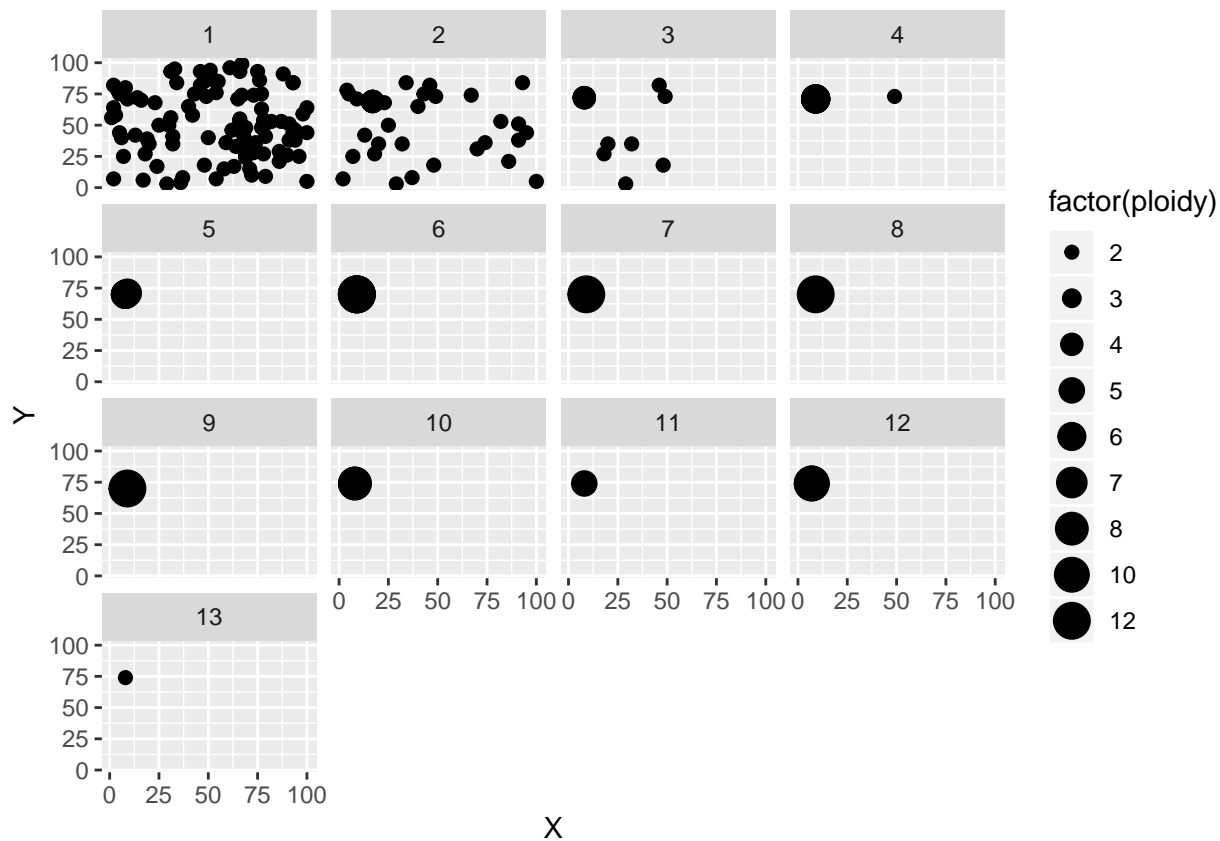


```

# 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
)
```

