

Plot Remi's Simulations

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Plotting Remi's simulations

```
## 'data.frame':   387840 obs. of  23 variables:
## $ Generation      : int  0 1 2 3 4 5 6 7 8 9 ...
## $ P0_meanFit      : num  1 1 0.931 0.925 0.932 ...
## $ P0_varFit       : num  0 0 0.0219 0.0186 0.0124 ...
## $ relFitness      : num  1 1 0.931 0.925 0.932 ...
## $ N               : int  10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 ...
## $ Patch_Number    : int  1 1 1 1 1 1 1 1 1 1 ...
## $ S_OD            : num  0.05 0.05 0.05 0.05 0.05 0.05 0.05 0.05 0.05 0.05 ...
## $ Unnamed..0      : int  1909 1909 1909 1909 1909 1909 1909 1909 1909 1909 ...
## $ cMperChrom       : int  100 100 100 100 100 100 100 100 100 100 ...
## $ fit_MAC         : Factor w/ 2 levels "0.9 0.95 1","0.98 0.99 1": 1 1 1 1 1 1 1 1 1 1 ...
## $ fit_PAC         : Factor w/ 2 levels "1 0.95 0.9","1 0.99 0.98": 1 1 1 1 1 1 1 1 1 1 ...
## $ migration_scenario : Factor w/ 8 levels "0.00025,0.00025,0.00025,0.00025,1,6,11,16",...: 8 8 8 8 8 8 8 8 8 8 ...
## $ mu              : int  0 0 0 0 0 0 0 0 0 0 ...
## $ nbChrom          : int  10 10 10 10 10 10 10 10 10 10 ...
## $ nbGenerations    : int  1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 ...
## $ nbLoci           : int  20 20 20 20 20 20 20 20 20 20 ...
## $ nbLoci_MAC       : int  0 0 0 0 0 0 0 0 0 0 ...
## $ nbLoci_OD        : int  20 20 20 20 20 20 20 20 20 20 ...
## $ nbLoci_PAC       : int  0 0 0 0 0 0 0 0 0 0 ...
## $ nbReplicates     : int  50 50 50 50 50 50 50 50 50 50 ...
## $ outputOptions    : Factor w/ 1 level "--fitnessStats_file NFN seqInt 0 1e3 1": 1 1 1 1 1 1 1 1 1 1 ...
## $ selectionOn      : Factor w/ 1 level "fertility": 1 1 1 1 1 1 1 1 1 1 ...
## $ simulationSuperSetID: Factor w/ 1 level "A.0.2": 1 1 1 1 1 1 1 1 1 1 ...
```

That's a whole lot of data, so let's slice it up a bit to make things quicker...

Let's ignore the Maladapted climate (MAC) alleles for the time being.

Let's also ignore pulsed migration for now.

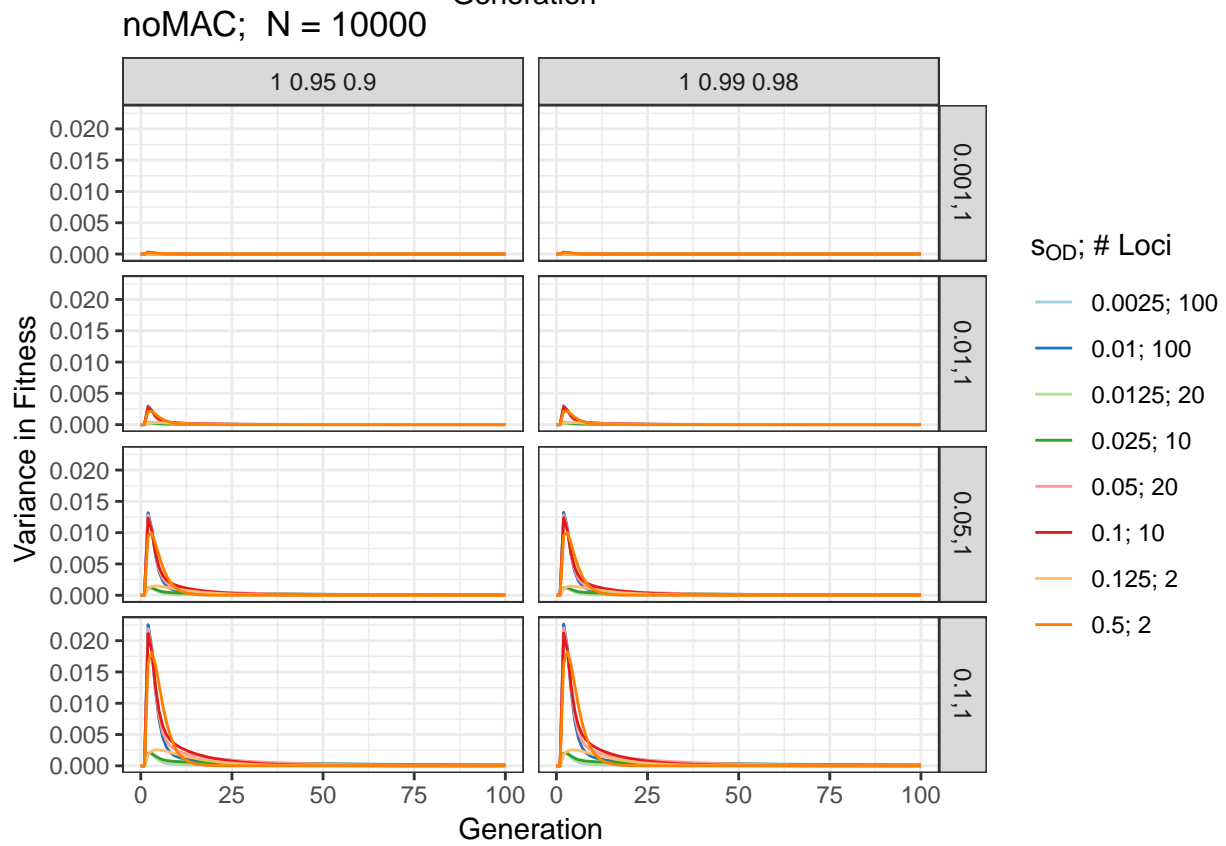
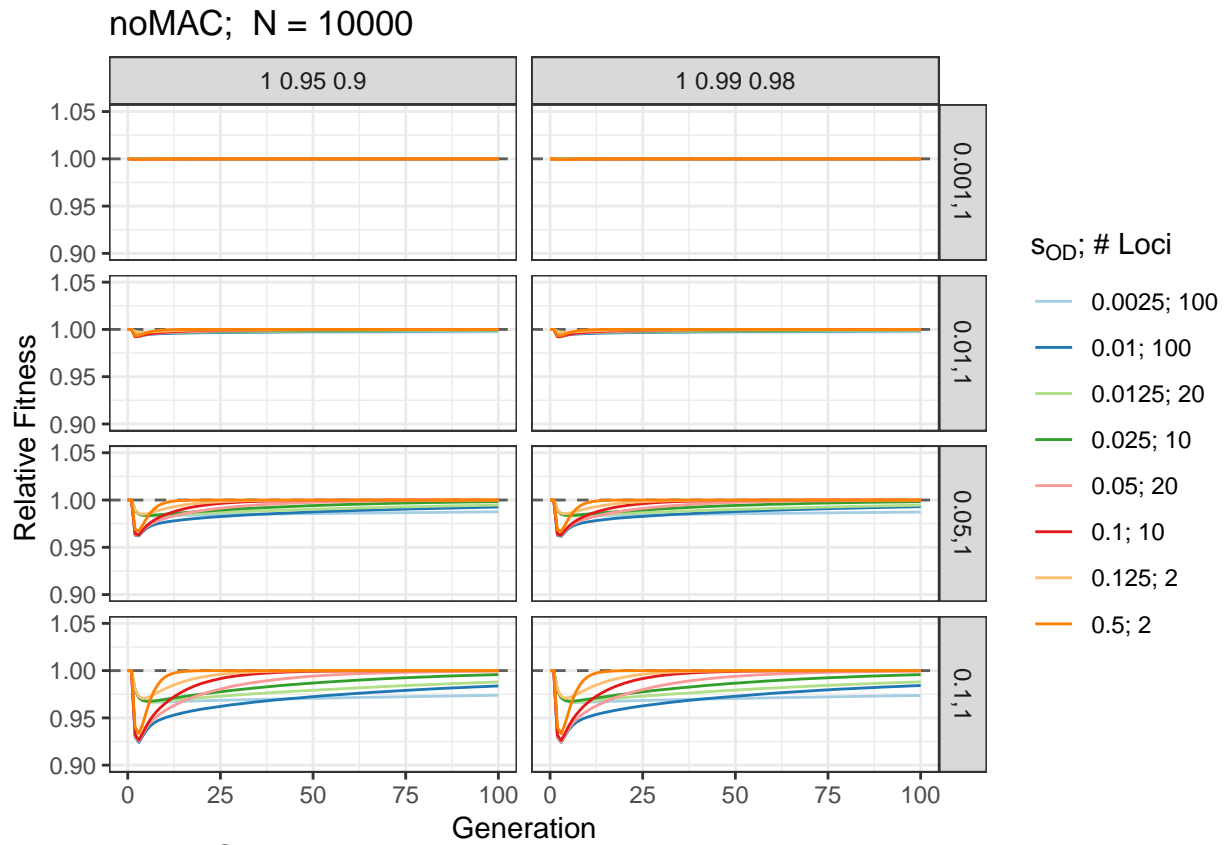
Let's plot the $N_e = 10000$ simulations.

No pre-adapted climate (PAC) alleles

```
## [1] "0"   "2"   "10"  "20"  "100"

## pdf
## 2

## pdf
## 2
```



scale_colour_brewer(palette = "Paired")

5 pre-adapted climate (PAC) alleles

```
## [1] "0"  "2"  "10" "20" "100"
```

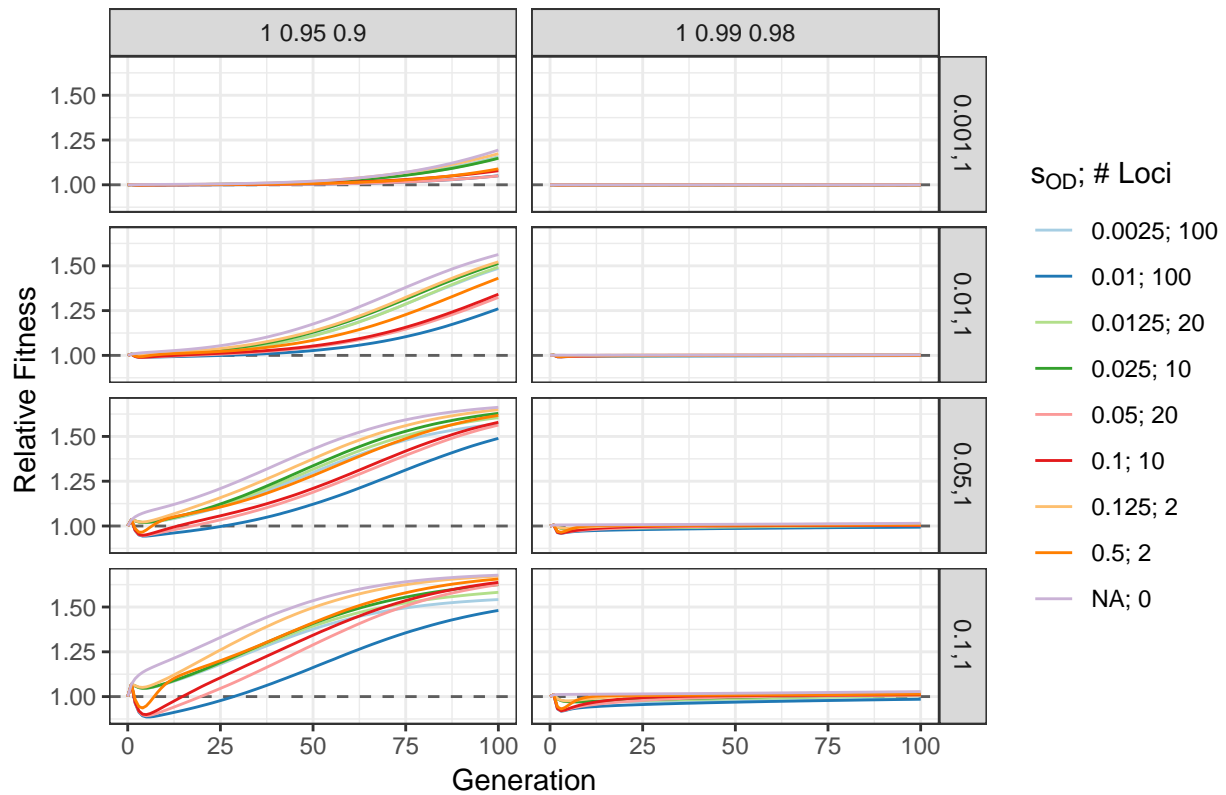
```
## pdf
```

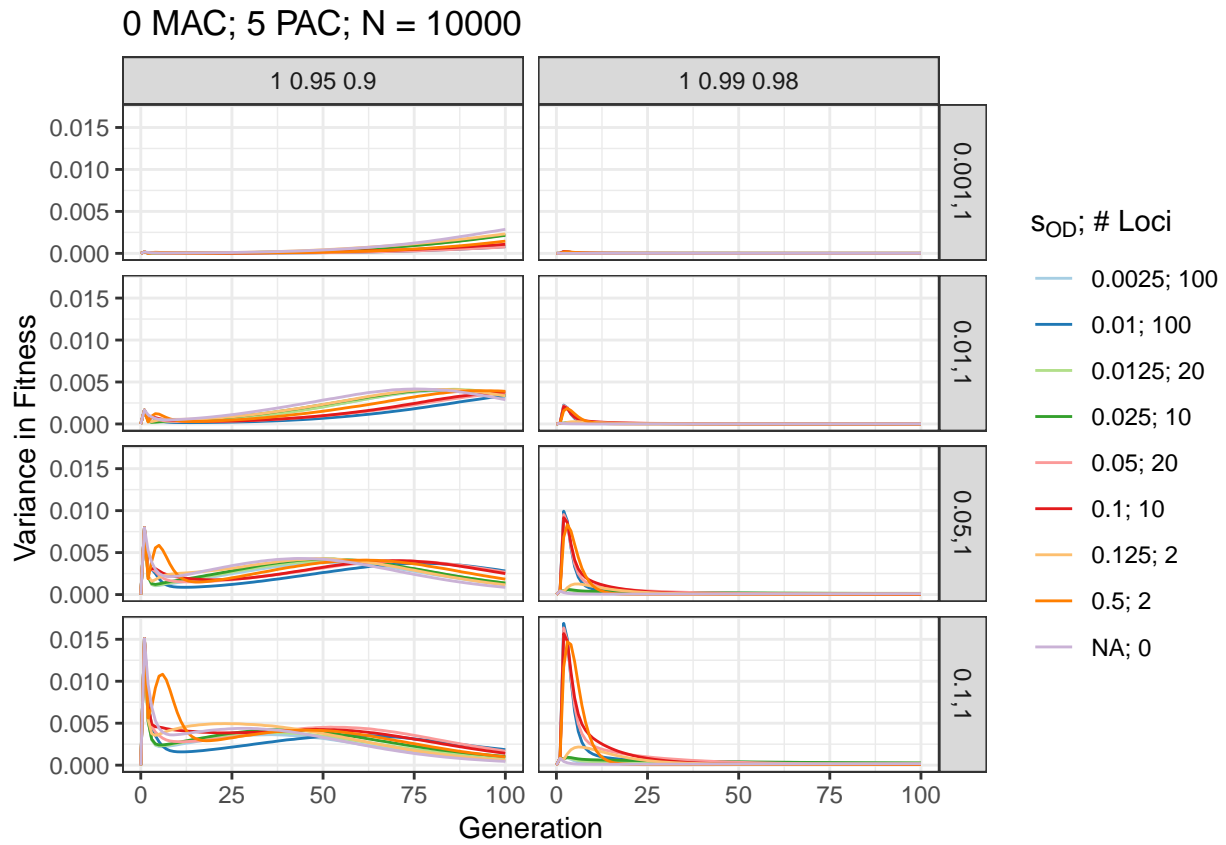
```
## 2
```

```
## pdf
```

```
## 2
```

0 MAC; 5 PAC; N = 10000





50 pre-adapted climate (PAC) alleles

```
## [1] "0" "2" "10" "20" "100"
```

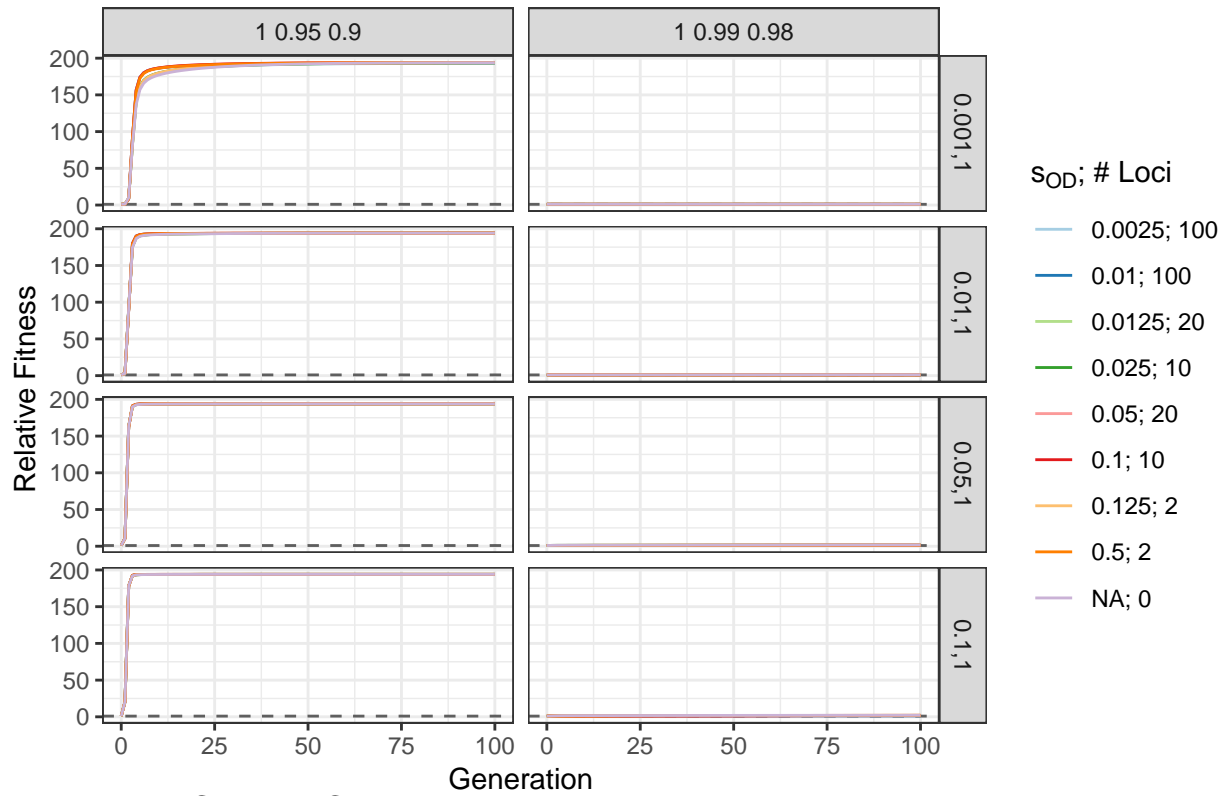
```
## pdf
```

```
## 2
```

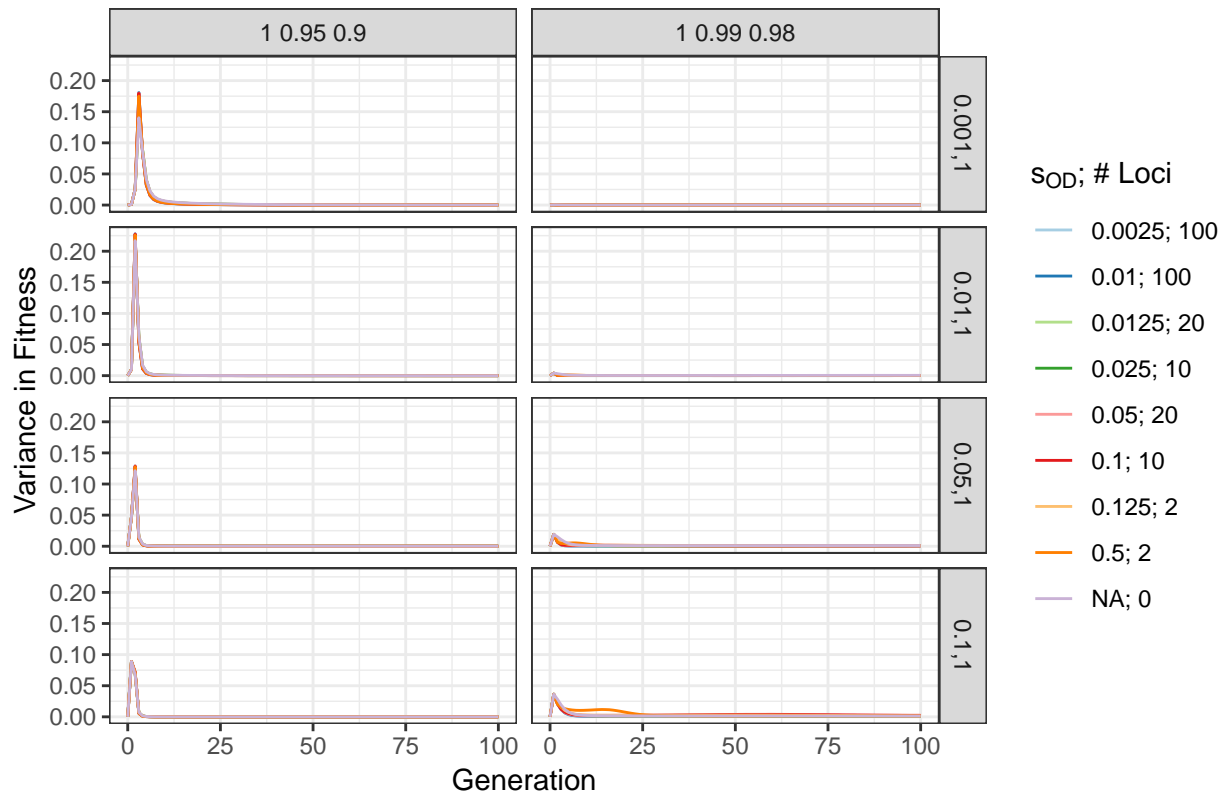
```
## pdf
```

```
## 2
```

0 MAC; 50 PAC; N = 10000



0 MAC; 50 PAC; N = 10000



5 Maladapted climate alleles; 0 PAC alleles

```
## [1] "0"  "2"  "10" "20" "100"
```

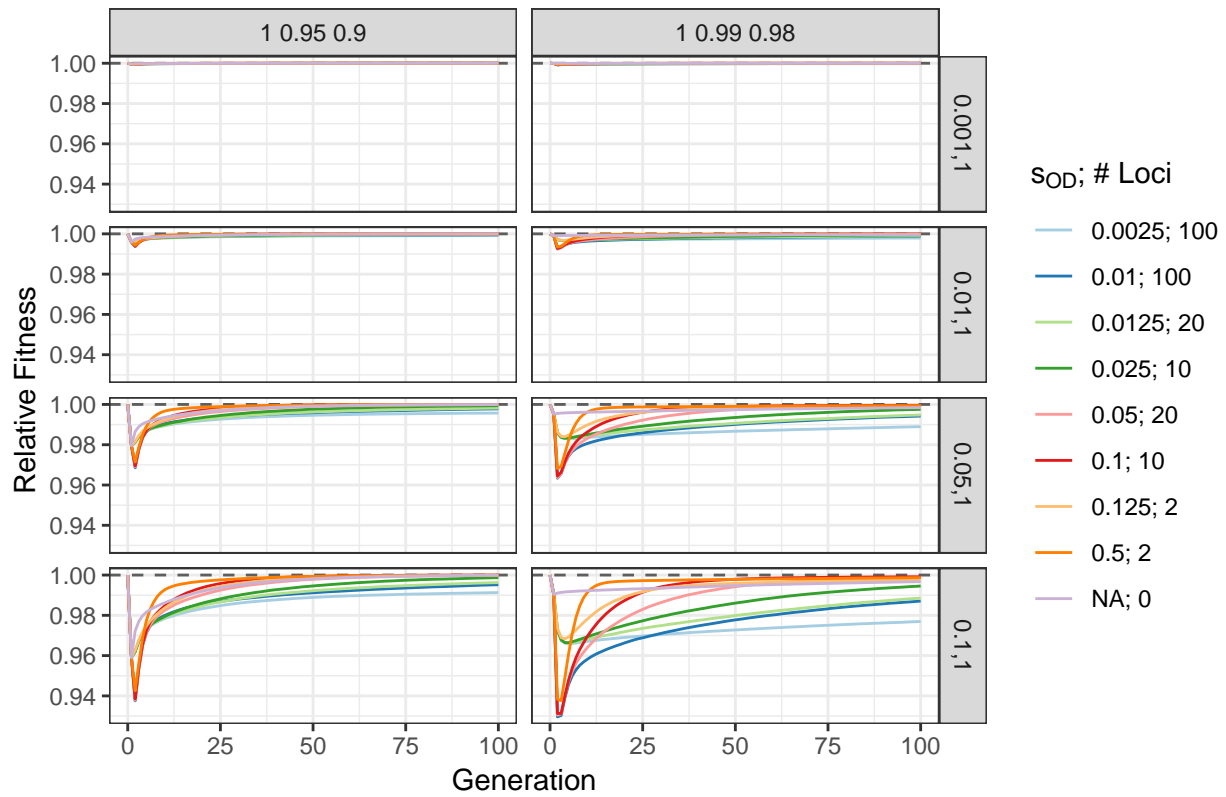
```
## pdf
```

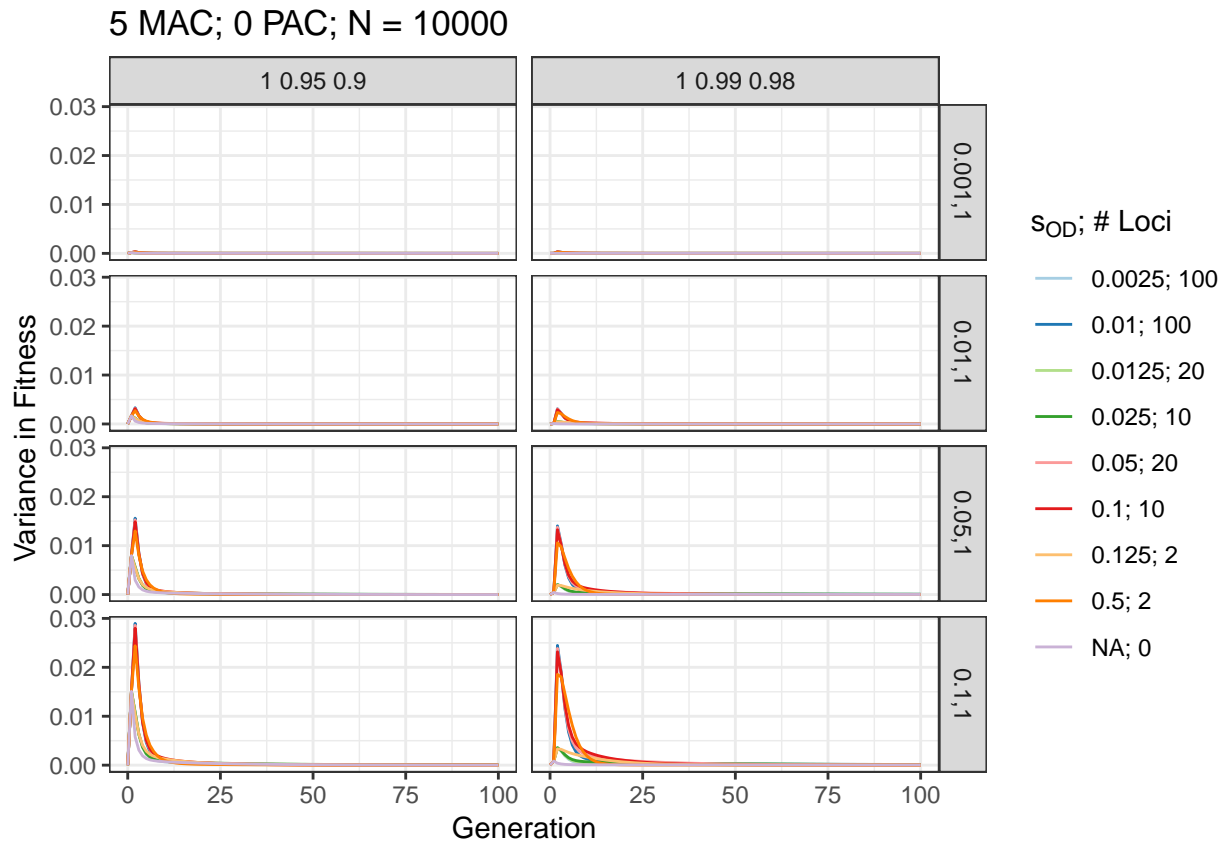
```
## 2
```

```
## pdf
```

```
## 2
```

5 MAC; 0 PAC; N = 10000





5 Maladapted climate alleles; 5 PAC alleles

```
## [1] "0"    "2"    "10"   "20"   "100"
```

```
## pdf
```

```
## 2
```

```
## pdf
```

```
## 2
```

5 MAC; 5 PAC; PAC = 0.05; N = 10000

