Evolutionary rescue vs migration of a maladaptive genotype

A story from Florin Suter, Felix Rentschler and Balz Fuchs

Biological questions

- How does migration of a deleterious genotype influence extinction probability of a diploid population

- How big is the probability for a diploid population to be rescued with migration of a maladaptive genotype
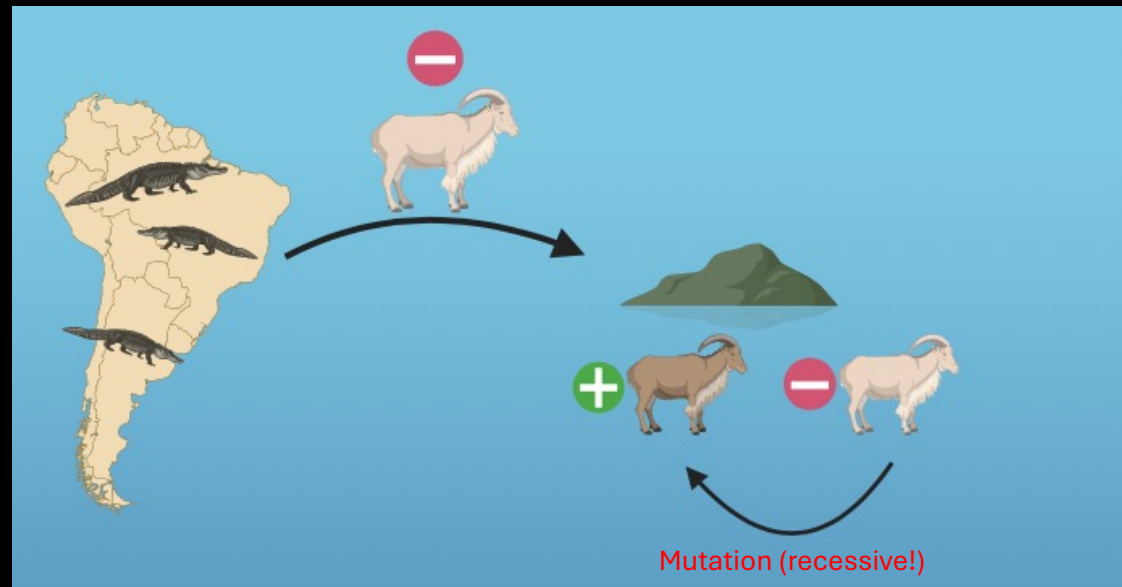
The story behind our model

Fixed parameters
- Starting-population Island: 1000 (wt)
- Heterozygotes: 0
- Homozygotes with mutation: 0
- Fitness wt: 0.9
- Fitness Aa: 0.9
- Fitness AA: 1.1
- Mutation rate: 0.005
- Maximal simulated generations: 10000

## Changing parameters
- Migrants/Generation: 0-10

Mutation (recessive!)

R code

```r
12  simulate_one_gen_hardy_weinberg <- function(N_aa,N_Aa, N_AA, fitnessaa, fitnessAa, fitnessAA, avgmigrants, mut_rate) {
13      # calculate total pop size
14      tot_pop <- N_aa+N_Aa+N_AA
15      # calculate averag simulate_pop_HW <- function(N_init_aa, N_init_Aa, N_init_AA, fitr # Test the function and plot the result
16      avg_fit <- weighte   # Create the vector in which to save the results    # set t_max to a value to be used througout
17      # calculate determ   pop_vector <- c(N_init_aa, N_init_Aa, N_init_AA)        max_gen <- 1000
18      next_gen_tot_pop <   # initiate the variables                               # create your simulation data
19      # calculate the al   pop_new <- c(N_init_aa, N_init_Aa, N_init_AA)           output <- simulate_pop_HW(1000,0,0,0.9,0.9,1.1, 10,0.005,max_gen)
20      a_tot <- 2*N_aa+N_   v <- 0
21      A_tot <- 2*N_AA+N_   # run the simulation until generation t_max             # show the last few lines of the data table
22      a_to_A_mut <- rpoi   for (i in 1:t_max+1) {                                  print(output)
23      A_to_a_mut <- rpoi       #define fitness of a and A for each iteration       # plot the output - note that the plot range and the x axis have to be adjusted based on the length of the table
24      p <- (a_tot+A_to_a       # redefine the current population one generation later   # determine x axis range
25      q <- (A_tot+a_to_A       pop_new <- simulate_one_gen_hardy_weinberg(pop_new[1],pop_new   x_range <- 0:(length(output[,1])-1)
26      # Next generation        # add the new population sizes to the output vector # this plots the total population size
27      det_aa_next <- (p^       pop_vector <- rbind(pop_vector,pop_new)             plot(x_range,output[,1]+output[,2]+output[,3],type='l',ylim=c(0,max(output[,1]+output[,2]+output[,3])),xlab = "Generation",ylab =
28      det_Aa_next <- (2*       # condition to stop the simulation before t_max: either the p   "Population size")
29      det_AA_next <- (q^   extinct      if (pop_new[1]+pop_new[2]+pop_new[3]>=1.5*(N_init_aa+ N_init_ "Population size")
30                           }                                                      # add number of wild type individuals
31      #migrationrate                                                              lines(x_range,output[,1], col="blue")
32      aa_migrants <- rpo   # define the row and column names of the output vector  # add number of mutant individuals
33                           rownames(pop_vector) <- (0:t_max)[1:length(pop_vector[,1])] # r   lines(x_range,output[,2], col="red")
34      # draw offspring g   colnames(pop_vector) <- c("aa","Aa","AA")               lines(x_range,output[,3], col="green")
35      offsp_aa <- rpois(   # return the result
36      offsp_Aa <- rpois(   return(pop_vector)
37      offsp_AA <- rpois(   }
38
39
40      return(c(offsp_aa, offsp_Aa,offsp_AA))
41  }
42  # Test the function
43  print(simulate_one_gen_hardy_weinberg(100,0,0,0.9,0.9,1.1, 5, 0.01))
```
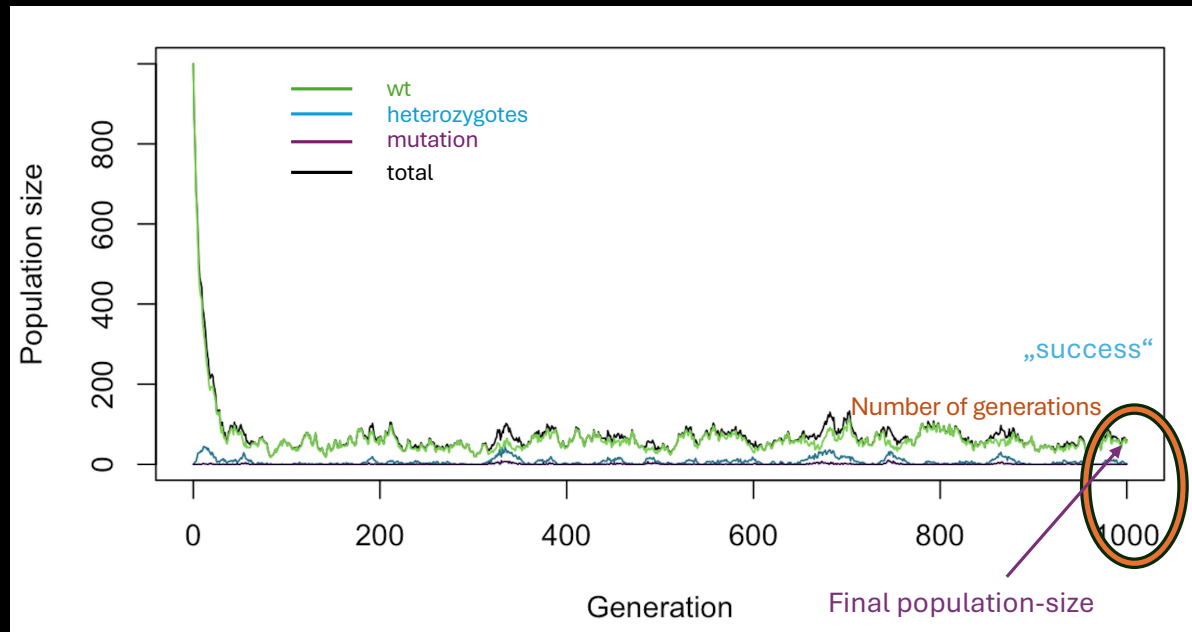
First graphs
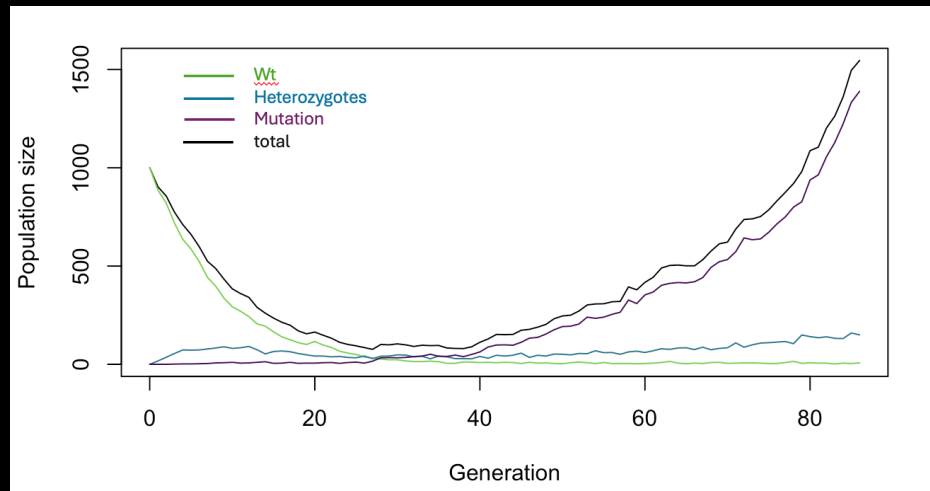
2 migrants/generation
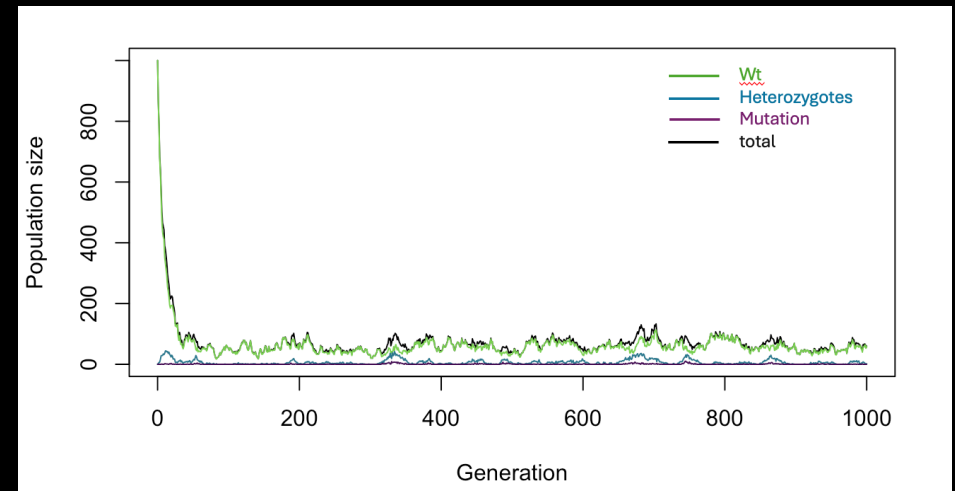
10 migrants/generation

Accumulating data:

1000 replicates of 10000 Generations for all the migration-rates from 0-10

Results in dataframe:
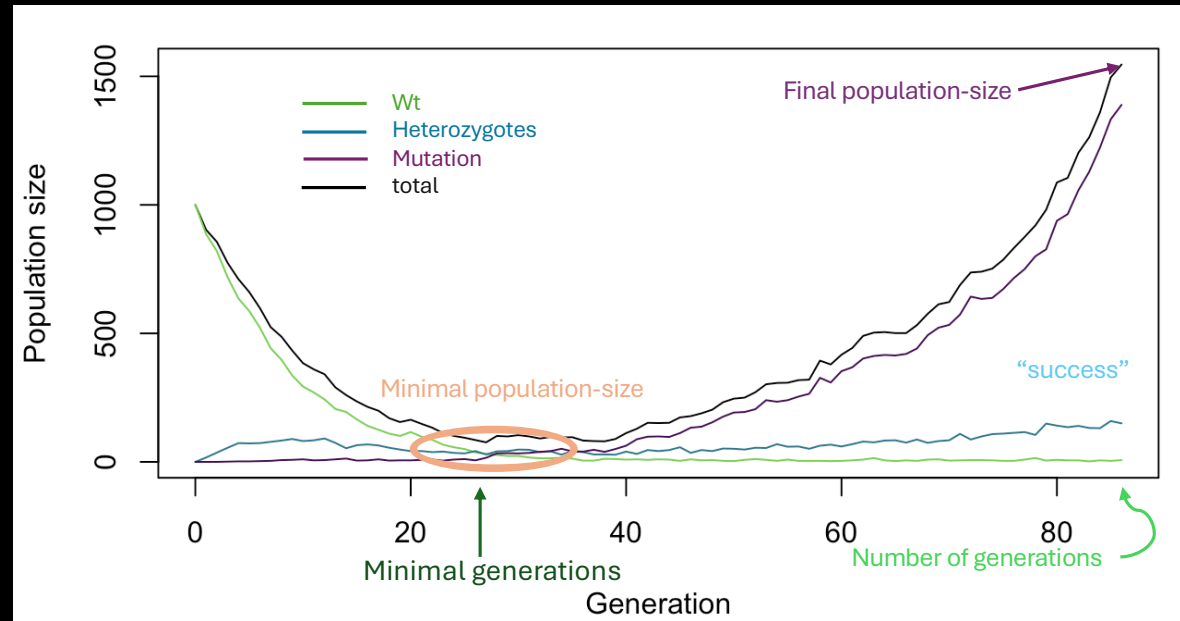Number of generations
Minimal population-size
Minimal generations
Final population-size
p_final
"success" (extinction, rescue, persistence)

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Results

How does migration of a deleterious genotype influence extinction probability of a diploid population?

How big is the probability for a diploid population to be rescued with migration of a maladaptive genotype?

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Distribution of Final Population Size by Migration per Generation
(fitnessAa = 0.9)
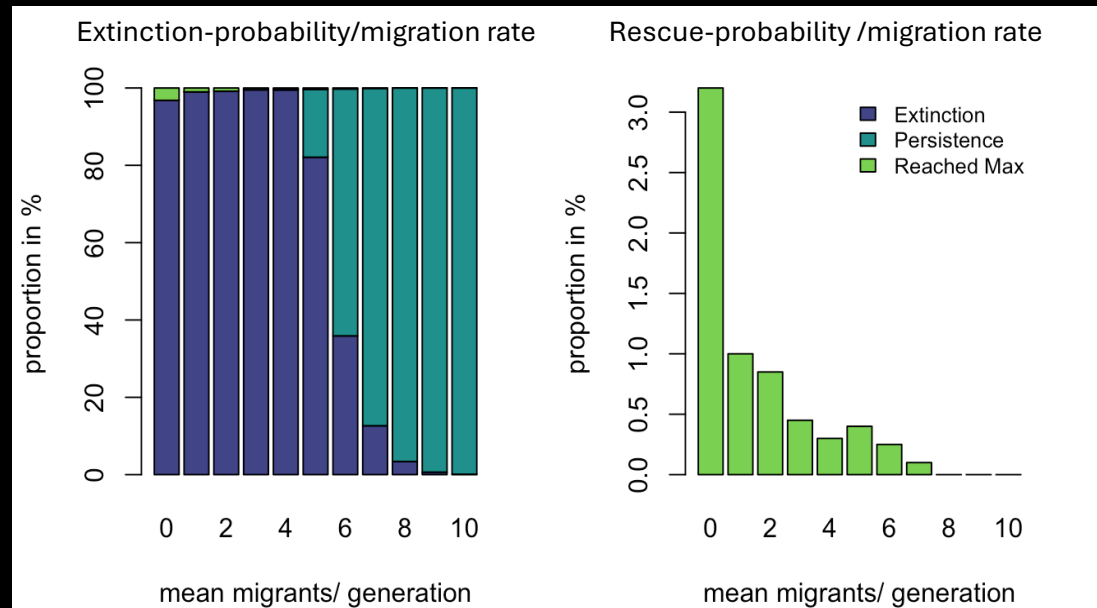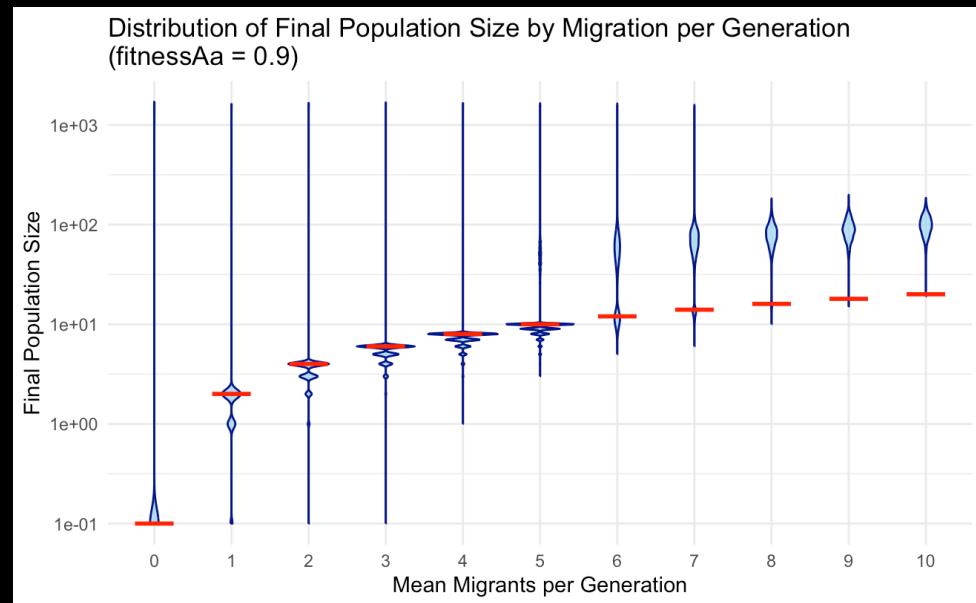
With increasing migration, the populations were not extinct anymore
→ stabilization

Fazit

- How does migration of a deleterious genotype influence extinction probability of a diploid population?

➢ "The probability of extinction initially increases with the number of generations but decreases rapidly from the 5th generation and reaches zero at 10 generations, which leads to population stability."

Fazit

- How big is the probability for a diploid population to be rescued with migration of a maladaptive genotype?

➤ "The probability of rescue falls rapidly from 3% at 0 migration to 1% at 1 migrant/generation and then continuously to 0.2% at 7 migrants/generation, remaining at 0% from 8 migrants."
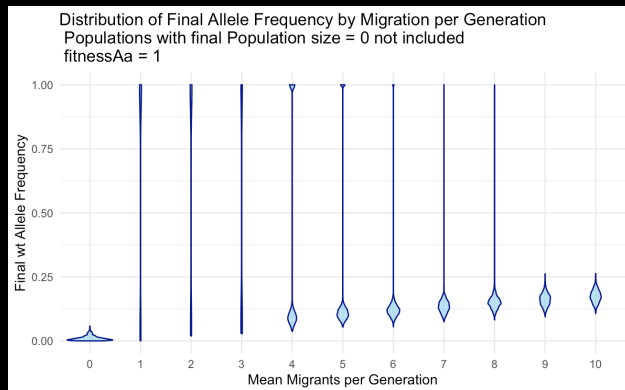
Thank you

- research group:

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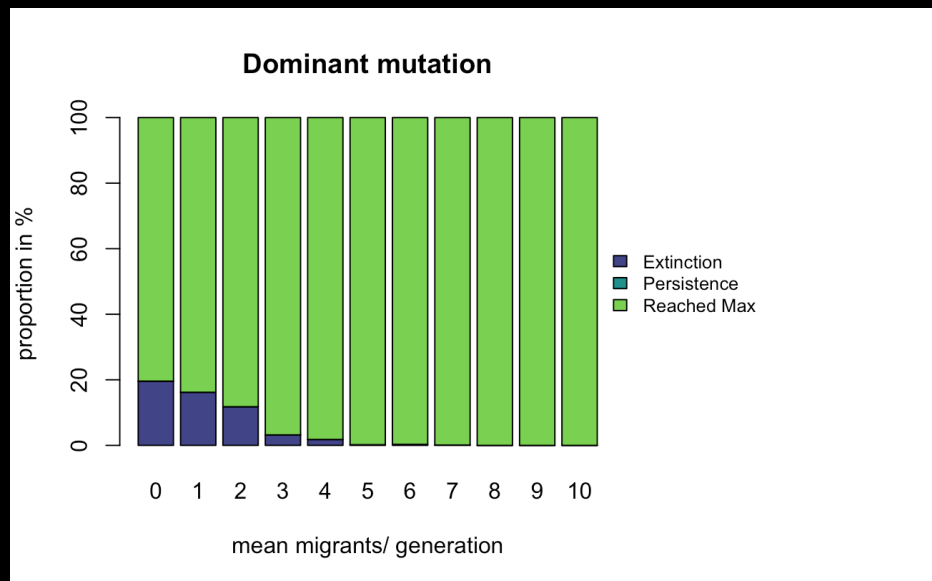
seit 1866
RUGEN BRÄU
INTERLAKEN
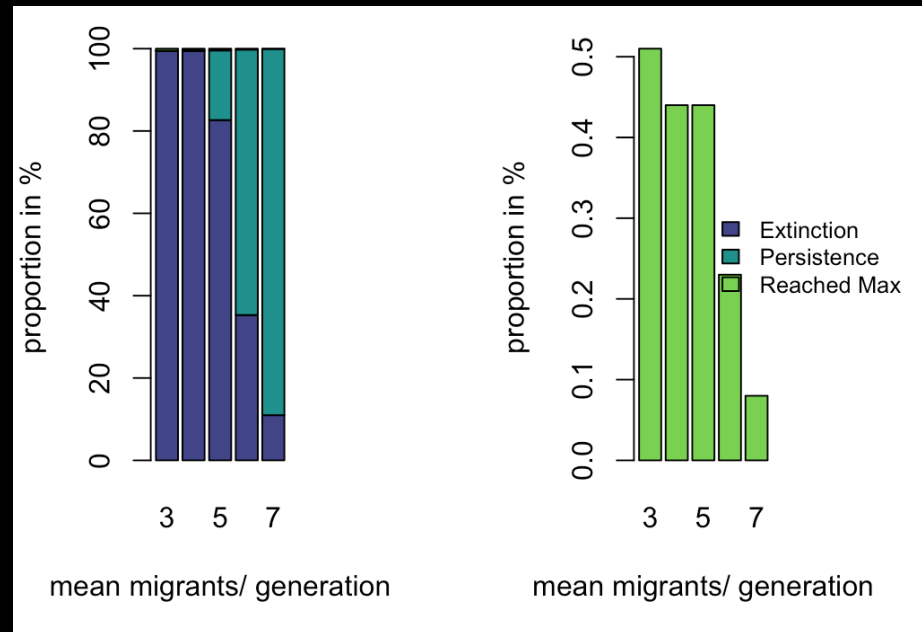
Additional slides

Additional slides

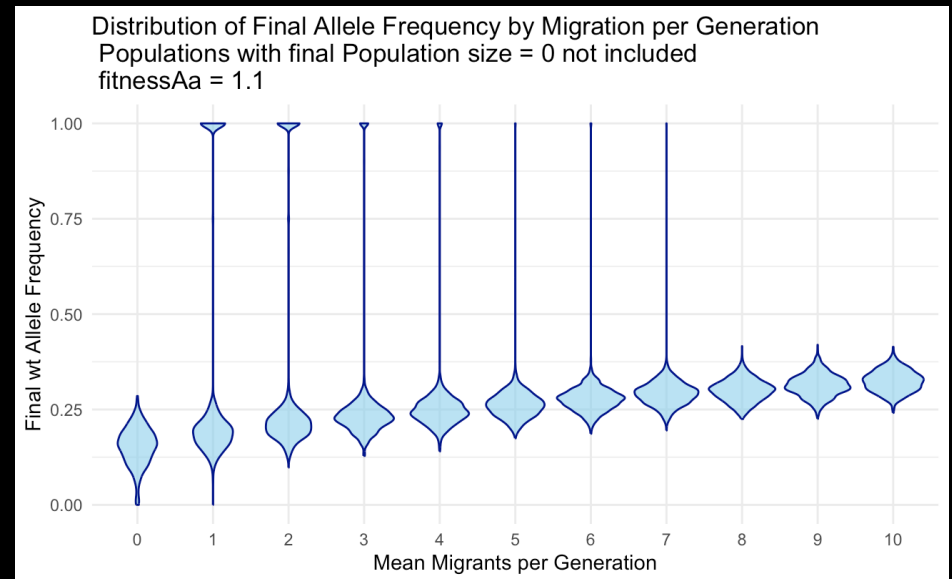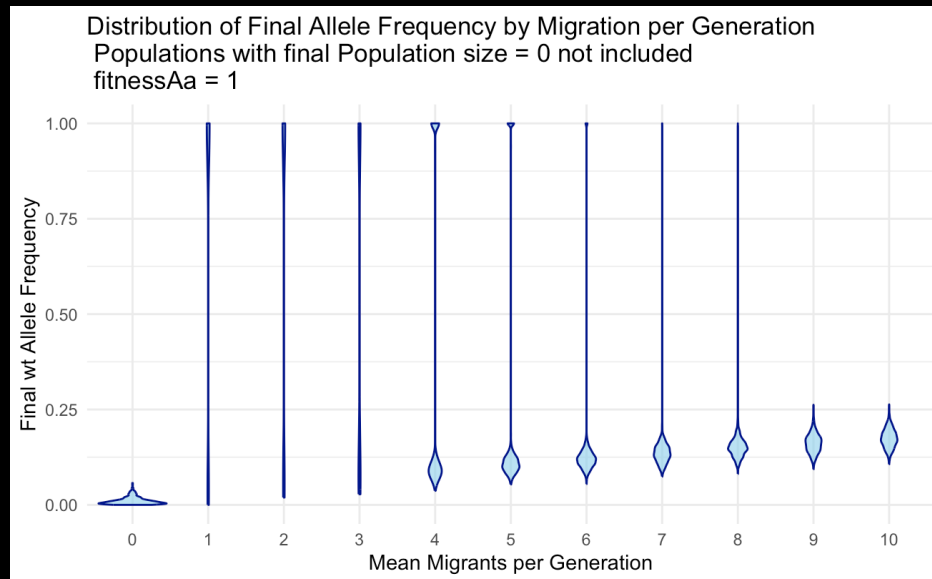Allele-frequencies of heterozygotes with intermediate fitness
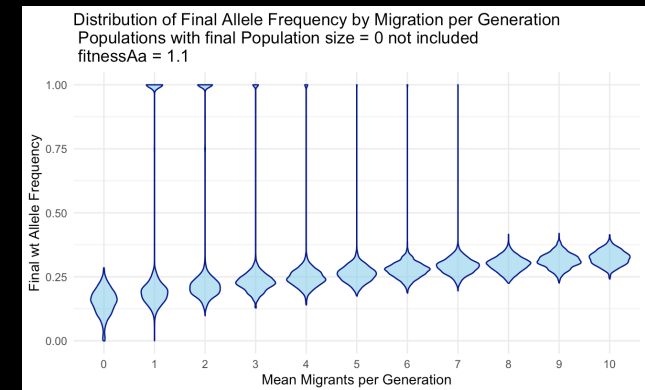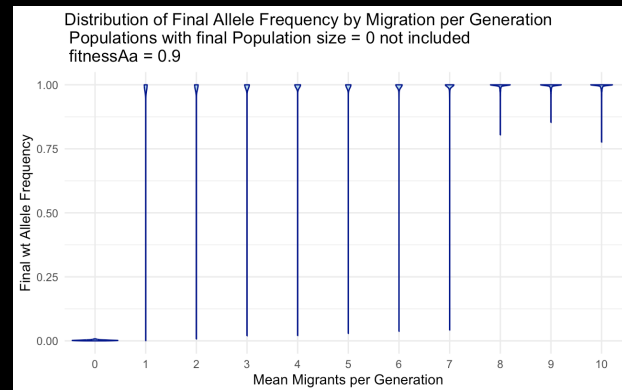
Additional slides

Extinction-probabilities with a dominant mutation and heterozygotes with intermediate fitness
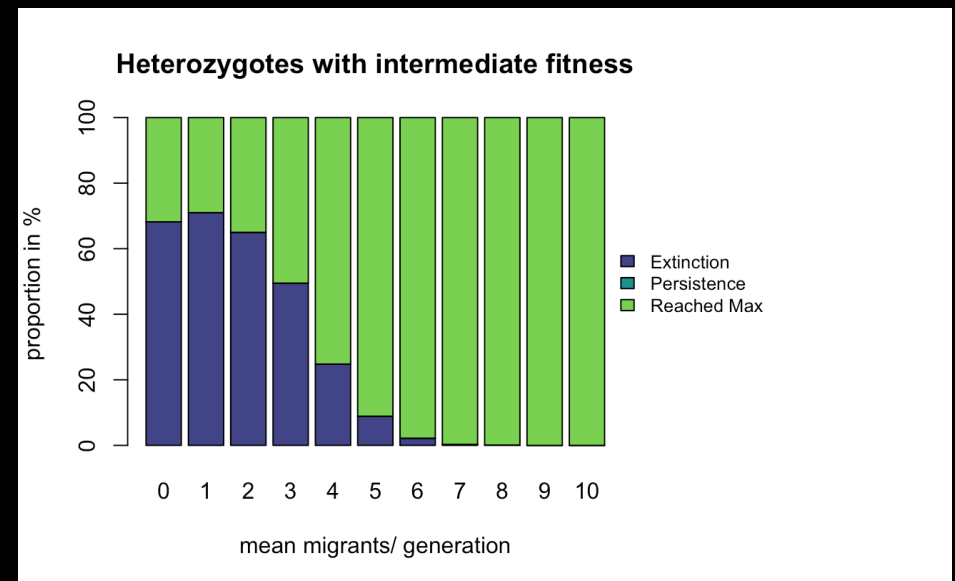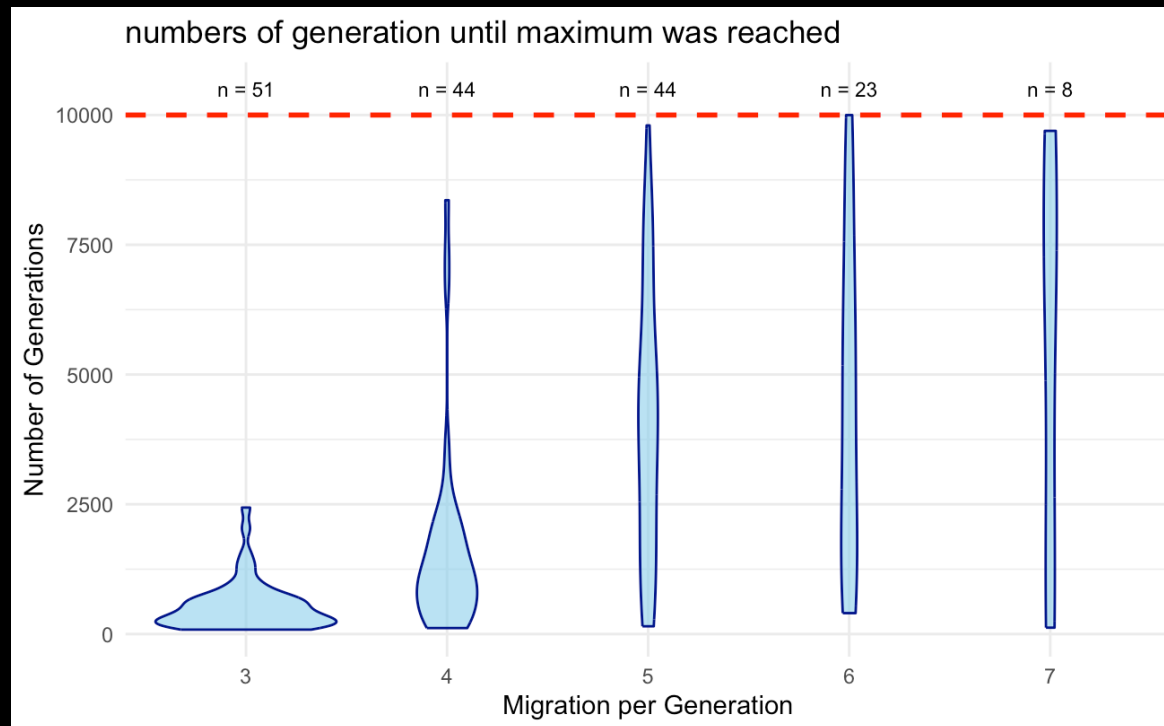
Additional slides

Distribution of Final Allele Frequency by Migration per Generation
Populations with final Population size = 0 not included
fitnessAa = 1

Distribution of Final Allele Frequency by Migration per Generation
Populations with final Population size = 0 not included
fitnessAa = 1.1

Additional slides

Additional slides

numbers of generation until maximum was reached, fitnessAa = 0.9

numbers of generation until maximum was reached, fitnessAa = 1

numbers of generation until maximum was reached, fitnessAa = 1.1
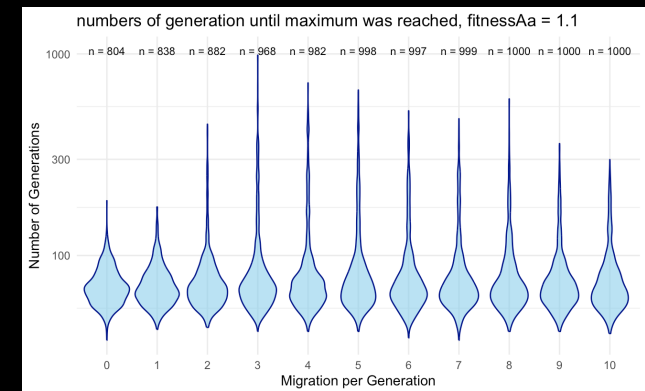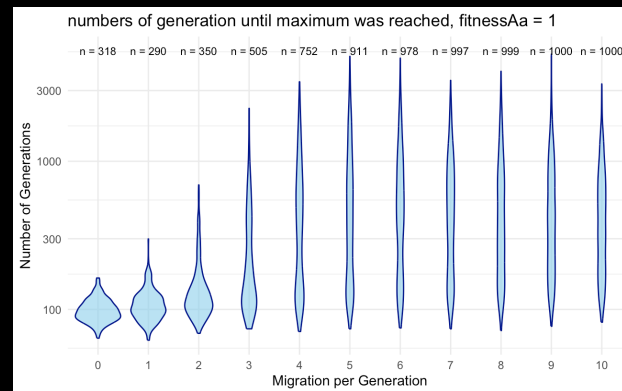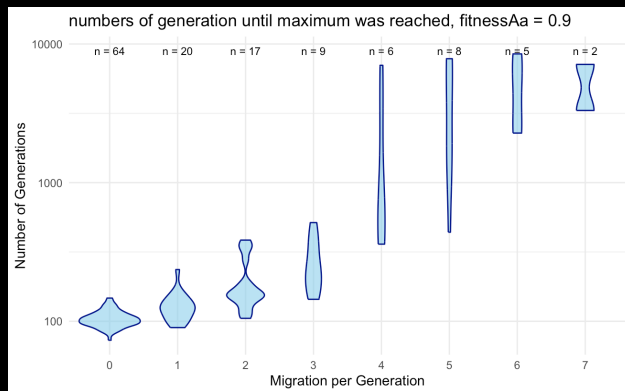
Additional slides

Extinction-probability with a higher mutation-rate (0.01)