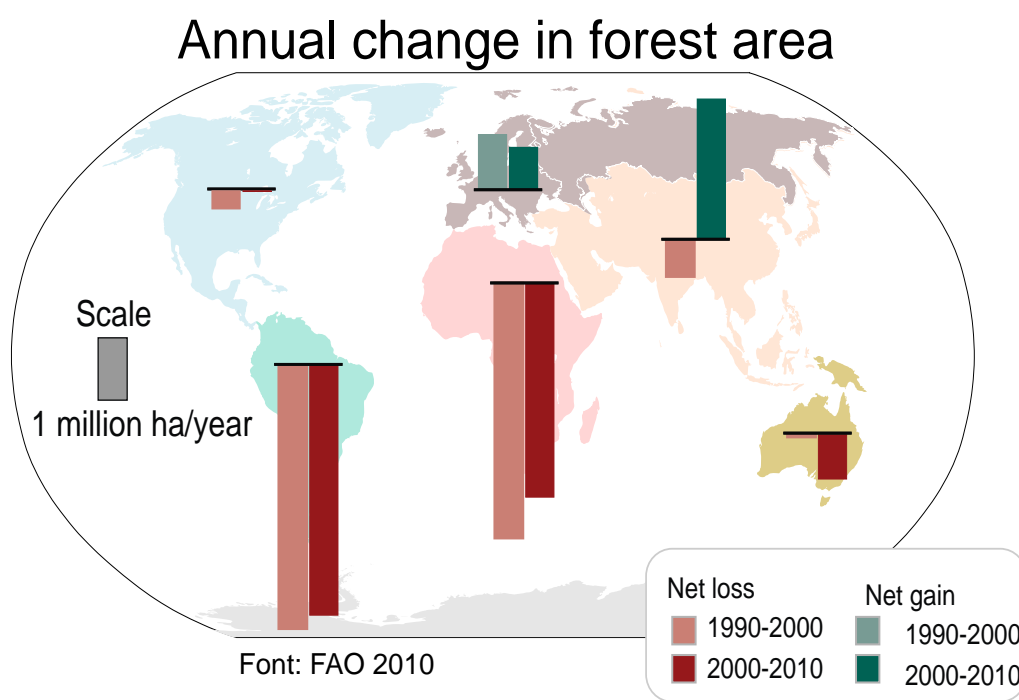# Using spatial population genetics to simulate the efficacy of tropical forest restoration efforts

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Introduction

Deforestation

Annual change in forest area

850 million hectares of tropical forests were degraded or deforested in the last century

Scale
1 million ha/year

Net loss   Net gain
1990-2000   1990-2000
2000-2010   2000-2010

Font: FAO 2010

Conservation + Restoration

Conservation of remnant areas is one solution for the intense forest and biodiversity loss. Ecological restoration is also required to speed ecosystem recovery [1]. Over the past 30 years, riparian forest formations have received special attention, due to their importance to river protection [2].

High genetic diversity
Potential to adapt to environmental change

To maintain viability and evolutionary potential, it is important to retain the maximal allelic diversity at all loci within a population, which requires attention to seed selection and sourcing [2].

Atlantic Rain Forest
12% remaining

Hotspot for global biodiversity

Several examples of successful ecological restoration projects [2]

Cetrolobium tomentosum

Tree widely used in restoration projects in the Atlantic Rain Forest, because is a typical gap species, with relatively fast growth and has symbiotic associations with nitrogen fixation microorganisms.
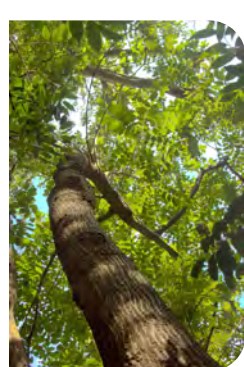
Fabaceae
Melittophily
Anemochory

Question

What is the effect of the following factors on genetic diversity and long-term population viability in restoration zones?
1. Initial genetic composition (allele and genotipic frequencies)
2. Forest patch size
3. Forest patch shape

Model

Individual based model

The model accounts for:
- population demography
- reproductive patterns (pollen flow and seed dispersal)
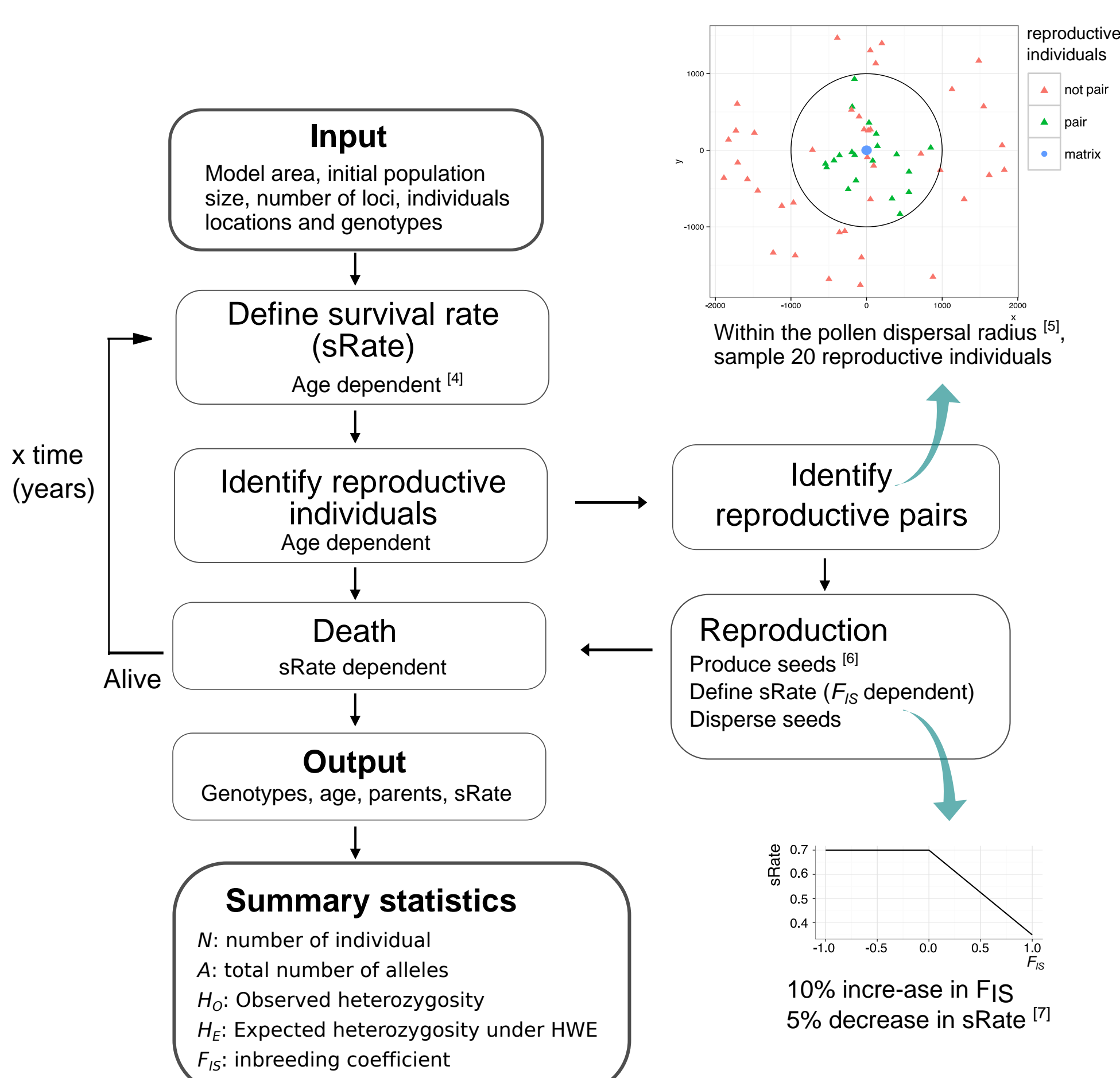- germination probability based on inbreeding

reproductive individuals
not pair
pair
matrix

Within the pollen dispersal radius [5], sample 20 reproductive individuals

Input
Model area, initial population size, number of loci, individuals locations and genotypes

Define survival rate (sRate)
Age dependent [4]

Identify reproductive individuals
Age dependent

Identify reproductive pairs

Death
sRate dependent

Reproduction
Produce seeds [6]
Define sRate (F_{IS} dependent)
Disperse seeds

x time (years)

Alive

Output
Genotypes, age, parents, sRate

Summary statistics
N: number of individual
A: total number of alleles
H_O: Observed heterozygosity
H_E: Expected heterozygosity under HWE
F_{IS}: inbreeding coefficient

10% incre-ase in F_{IS}
5% decrease in sRate [7]

Figure 1. Schematic represenation of simulation model structure and order of operations.

References

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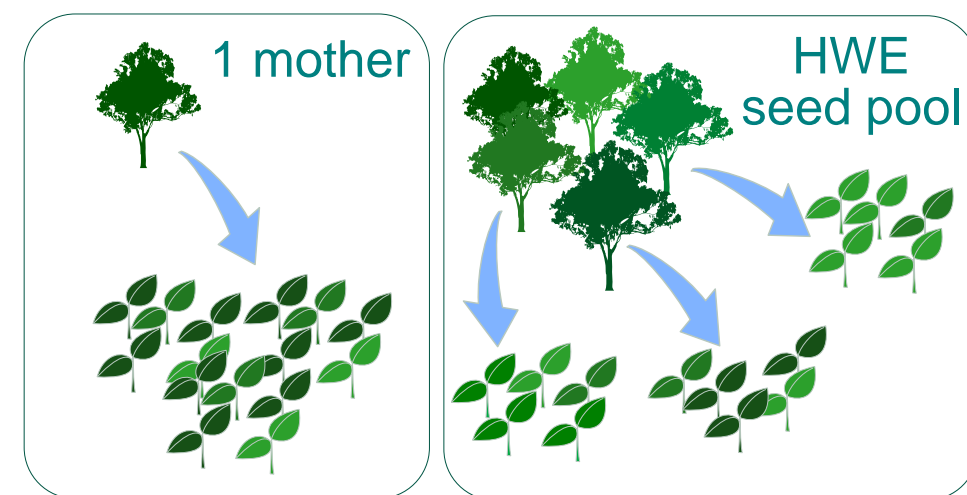
Simulations

We simulated an isolated population of *C. tomentosum* in a restoration area with three experimental treatments:

1. Population initial genetic composition

Initial population in the restoration area was composed by:
a. seeds colected from one mother tree
b. pool of seeds with genotypes in HWE, colected from many mother trees

1 mother   HWE seed pool

2. Size of restoration area

For each initial genetic composition, we simulated large, medium and small areas.

20 ha
N = 400

10 ha
N = 200

5 ha
N = 100
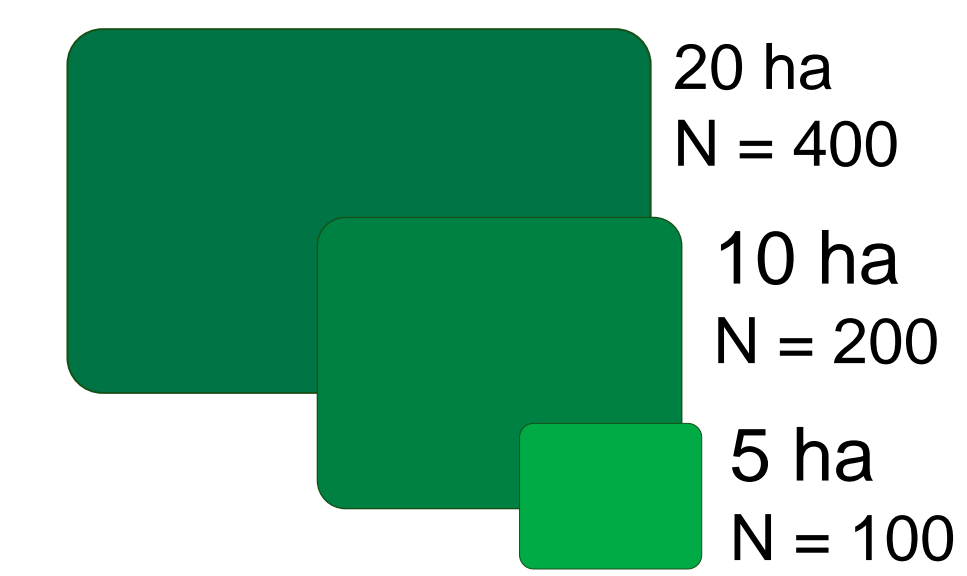
3. Shape of restoration area

The areas could have a long and narrow rectangle shape, as riparian forests, or more square like shape, with length similar to width.

Square like   Long and narrow

Matrix
Restoration area
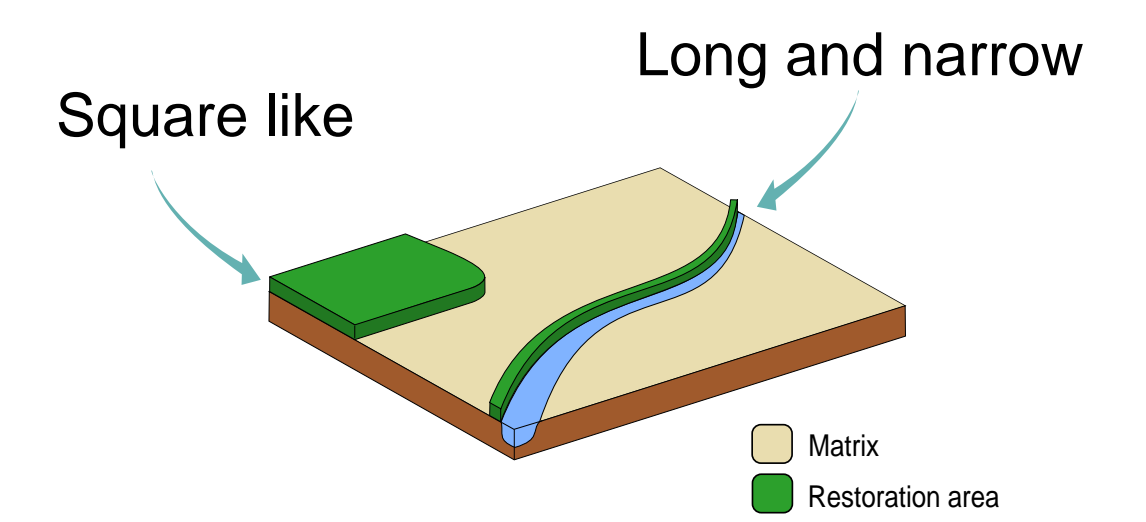
Repetions and time span

Each initial condition was simulated at least 200 times.
Populations from long and narrow areas were simulated for 500 years.
Populations from more square like areas were simulated for 250 years, for limitation of computational power.

Results

Among simulated restoration areas that were long and narrow in shape, we found that the larger areas resulted in smaller effects of genetic drift, measured here as loss of total number of alleles.
Our square 5 ha restoration areas were as affected by genetic drift as the 10 ha long and narrow areas (Figure 2).
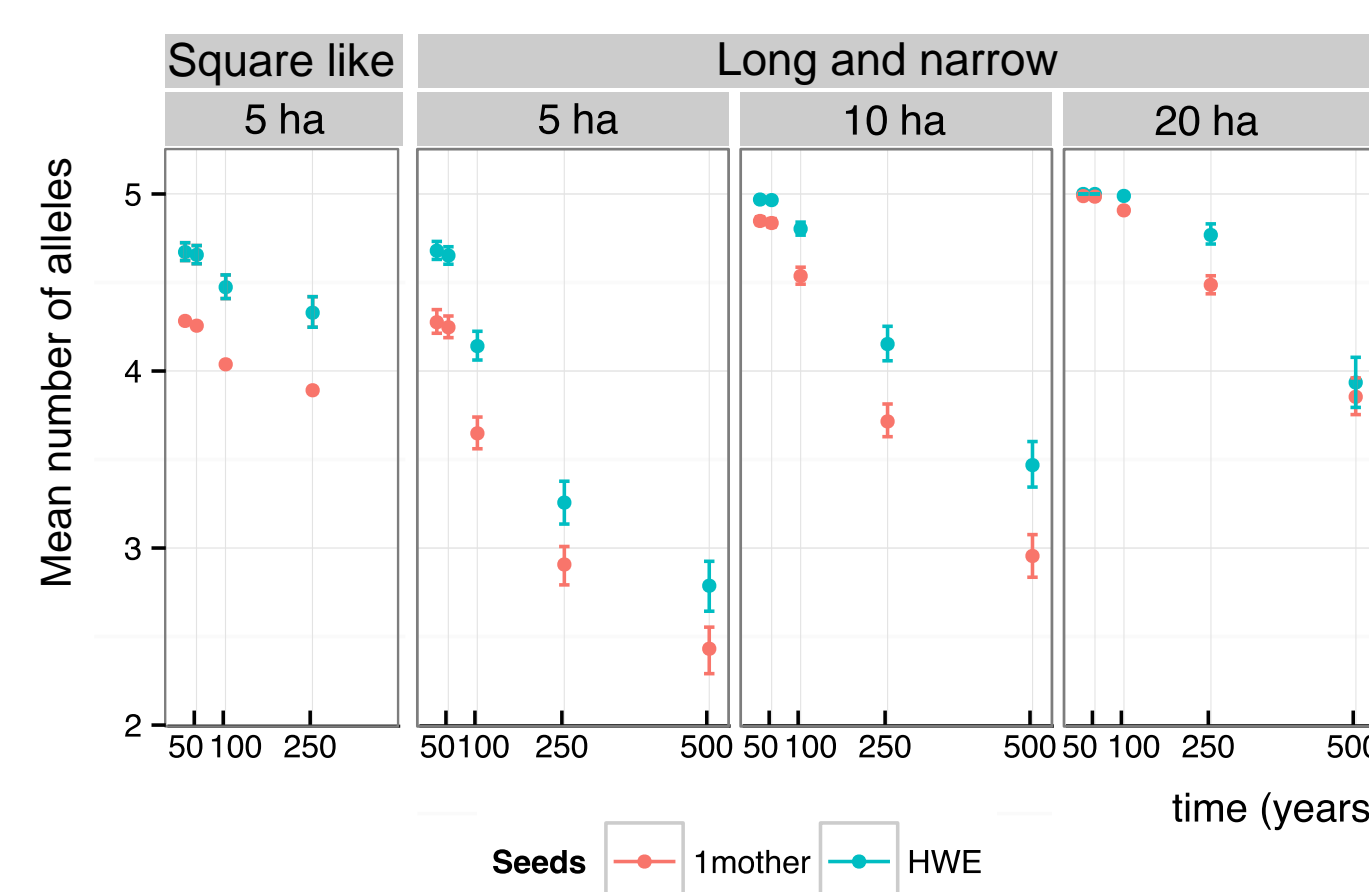

Figure 2. Mean number of alleles observed in each population after different time spans for each treatment.

The number of individuals increased over time, achieving approximately 20 individuals/ha after 500 years, except for the square restoration area in which the population size increased at a higher rate. In the narrow areas, a large proportion trees are at the borders of the forest and more seeds fall out of the forest area, and are not able to germinate (Figure 3).
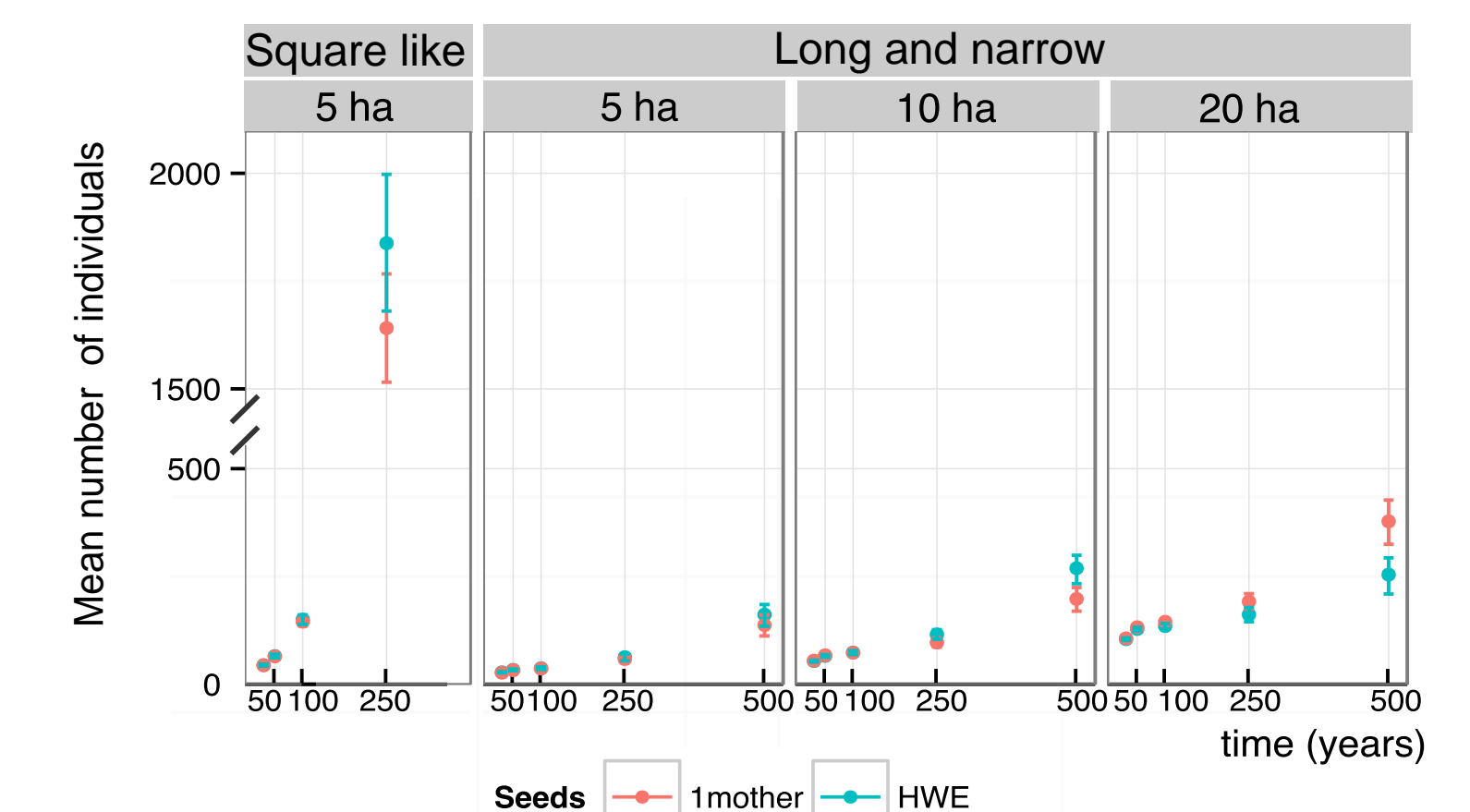

Figure 3. Mean number of individual observed in each population after different time spans for each treatment.

Initial genetic composition had a stronger effect on the inbreeding coefficient in populations from the small and narrow restoration areas. Selection against overall homozygosity at the germination phase kept the inbreeding coefficient small or moderated, even with fixation of alleles at some loci (Figure 4).
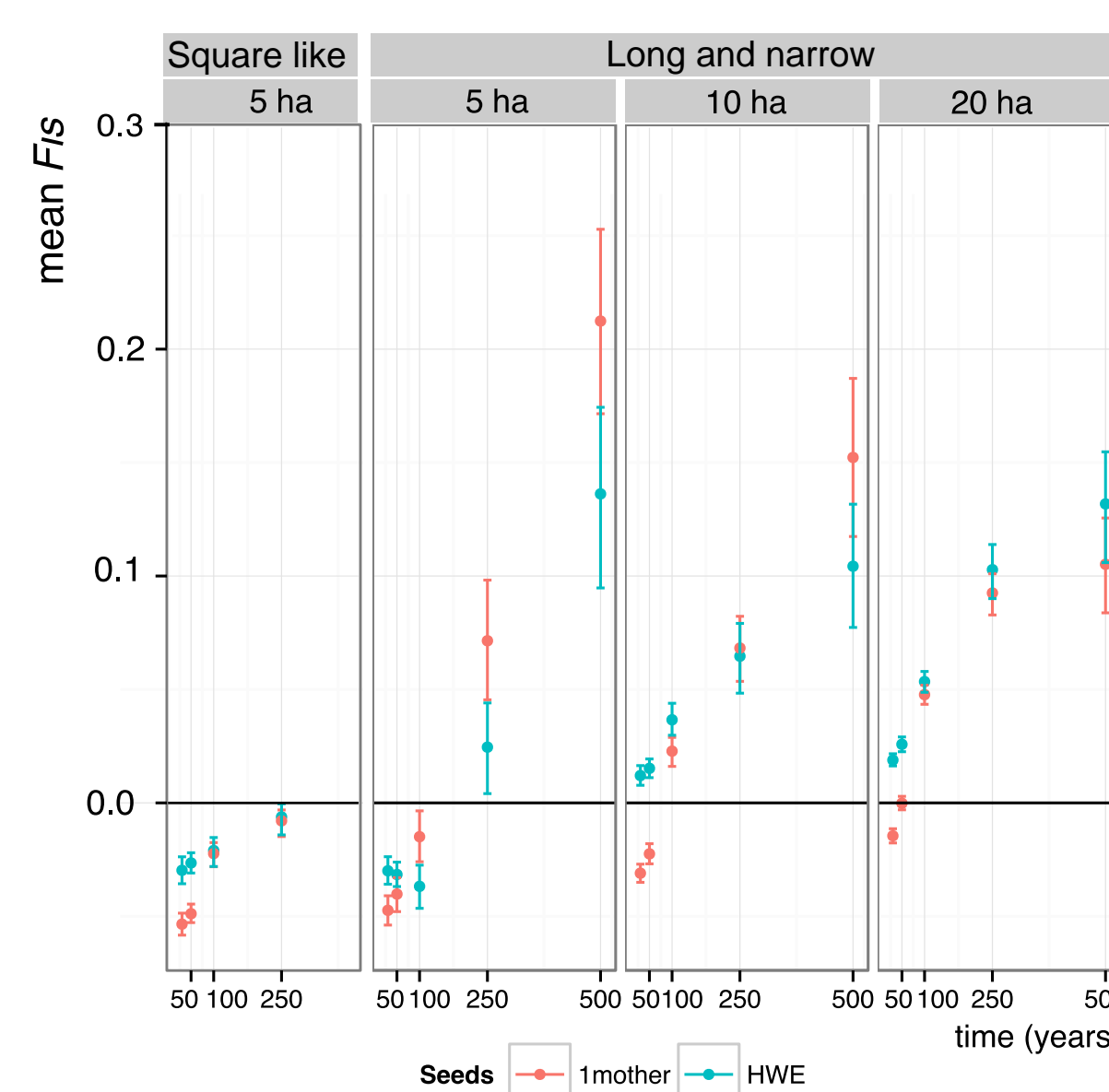

Figure 4. Mean inbreeding coefficient (F_{IS}) observed in each population after different time spans for each treatment.

Populations in the smaller areas that were founded by seeds from only one mother tree had a greater probability of extinction. However, the shape of the restoration area, and consequently the initial population size, had a stronger effect on probability of extinction than the initial genetic composition (Figure 5)
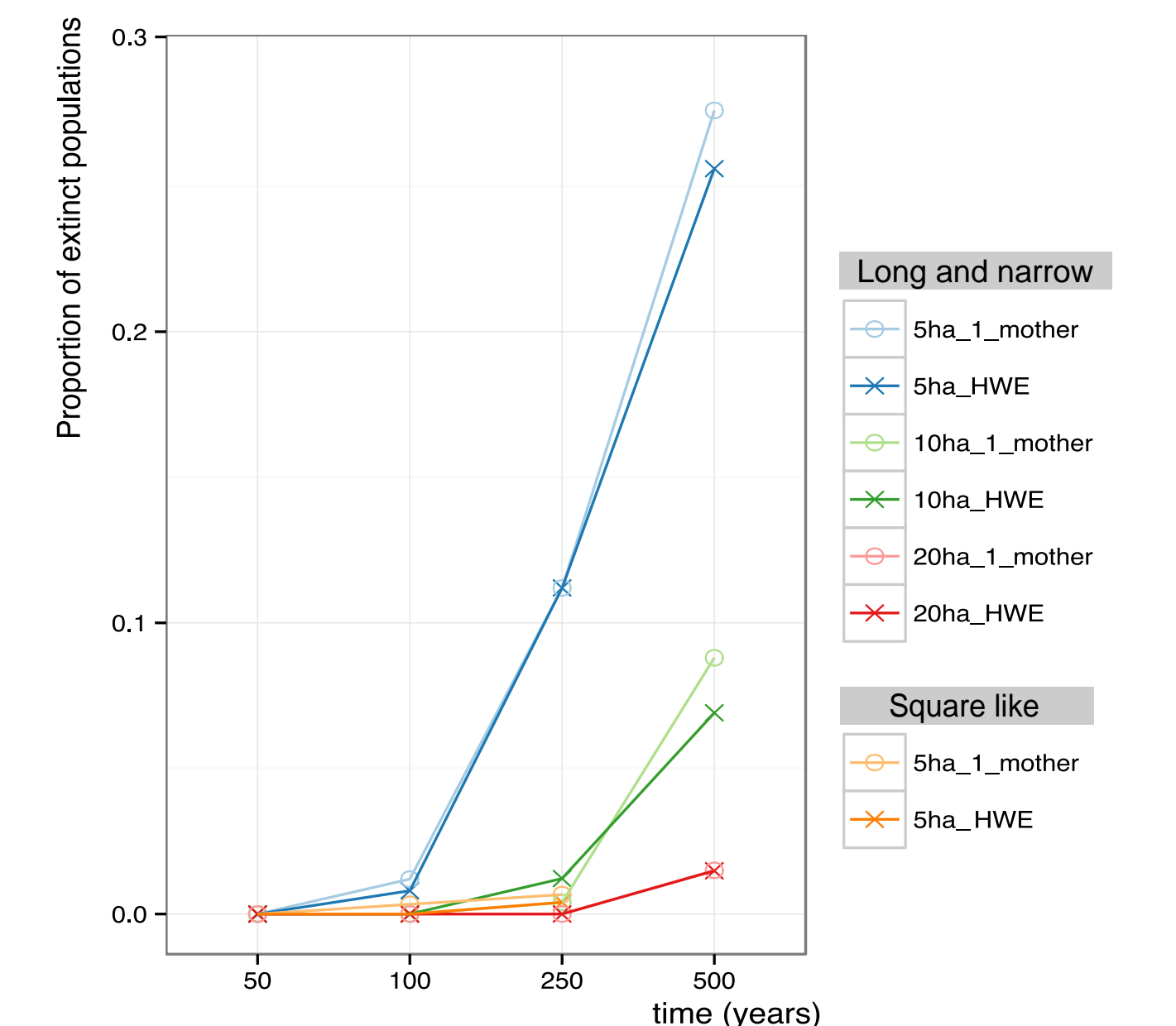

Figure 5. Proportion of populations that became extinct after each time span for each treatment.

Conclusion and perspectives

If the restoration area is long and narrow, as in riparian forests, its length and the initial population size are important characteristics to consider to reduce the risk of strong genetic bottlenecks. The shape of the area has large effect on mid-term genetic diversity loss and population viability due to the weaker border effect. So, the smaller and narrower the area, the greater should be the concern with the genetic composition of seed pool to maintain high genetic diversity and increase the long-term viability.
The next simulations will test:
- different initial genetic diversity (number of alleles and heterozigosity)
- initial saplings distribution over the restoration area

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