Landscape-level Genetic Diversity

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ITAC Extension Meeting

Project Members & Collaborators

Genome BritishColumbia

British Columbia | Ministry of Forests

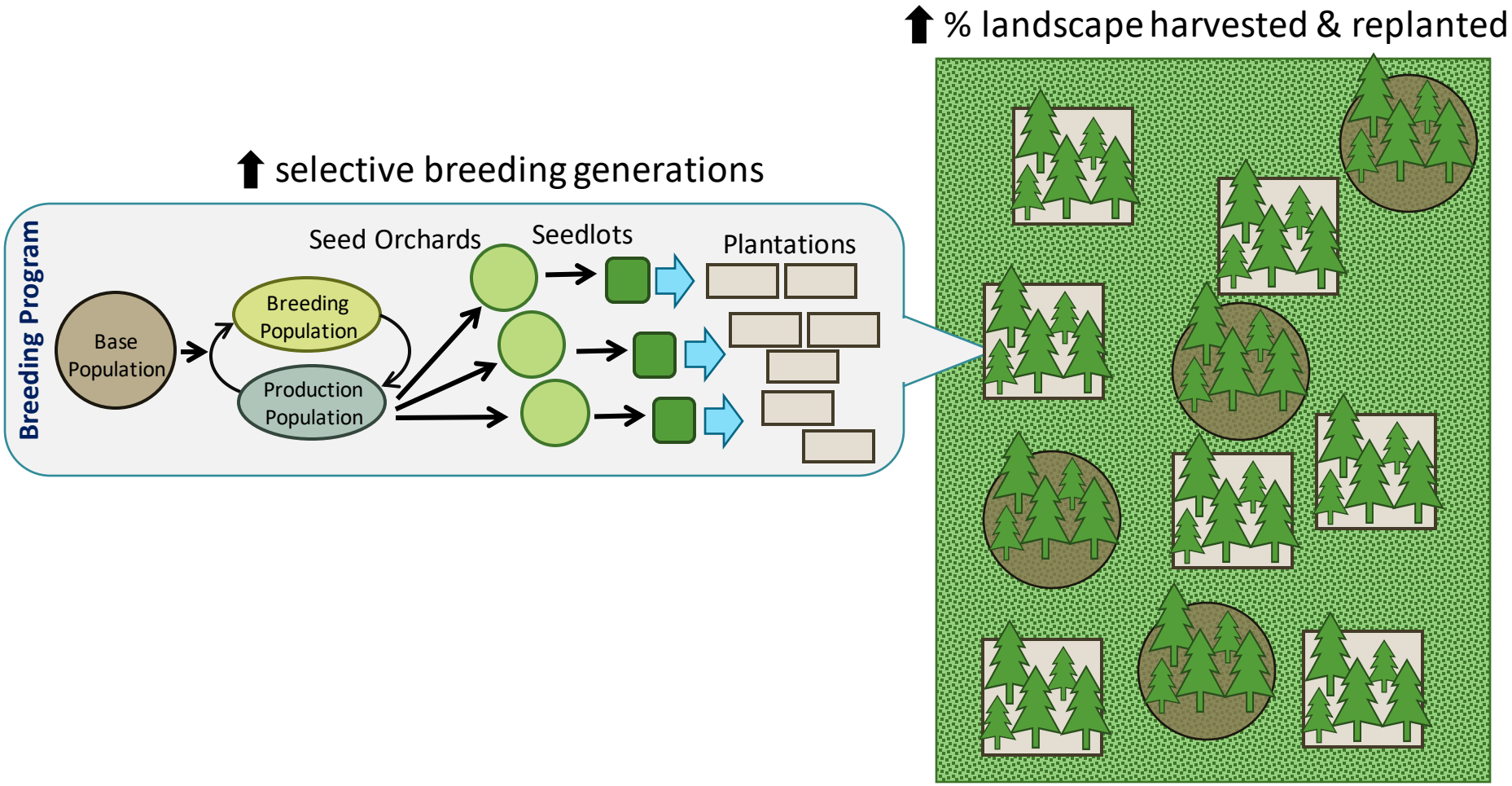
FGC Forest Genetics Council of British Columbia

UBC The University of British Columbia Faculty of Forestry

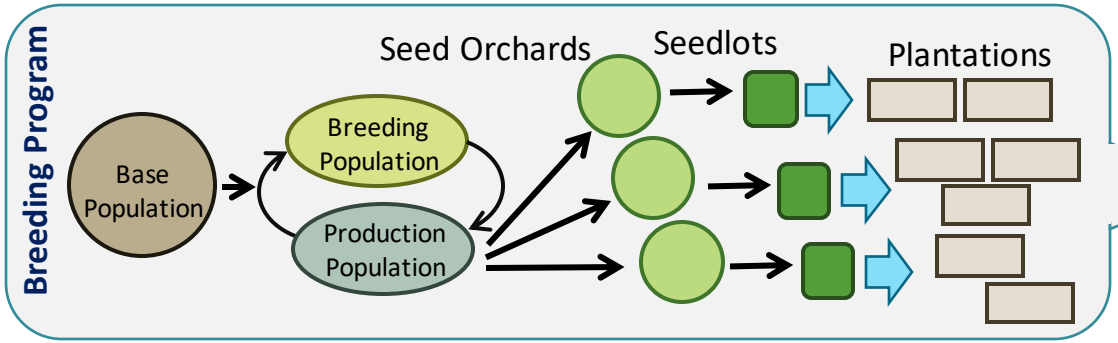
MOSAIC FOREST MANAGEMENT

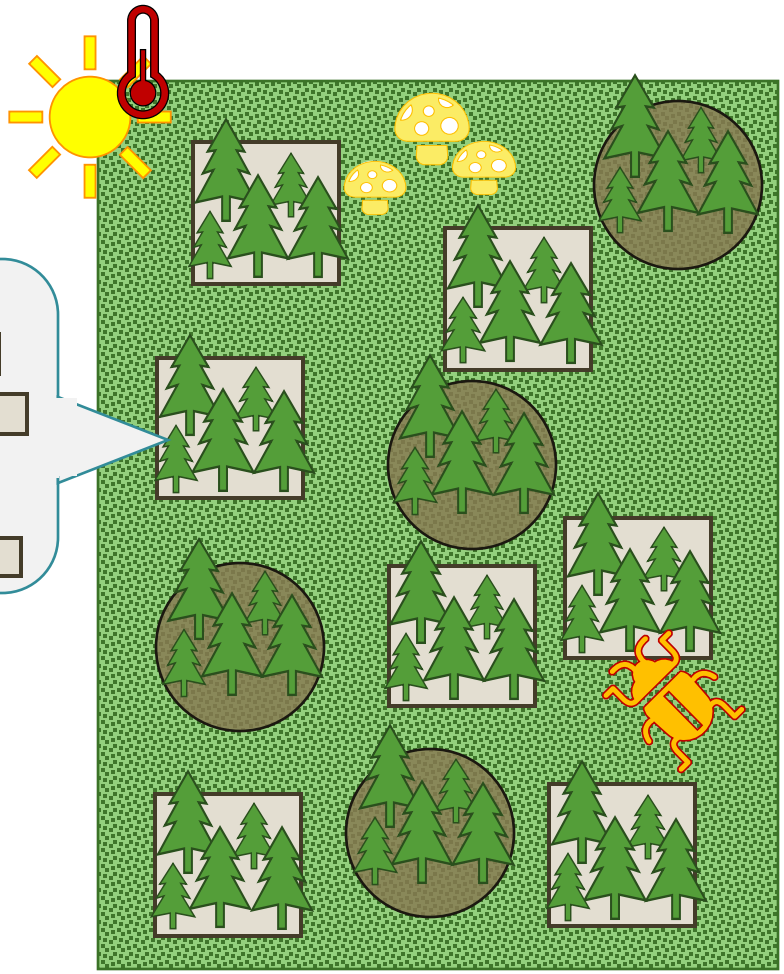
WFP Western Forest Products DEFINING A HIGHER STANDARD®

University of Montana

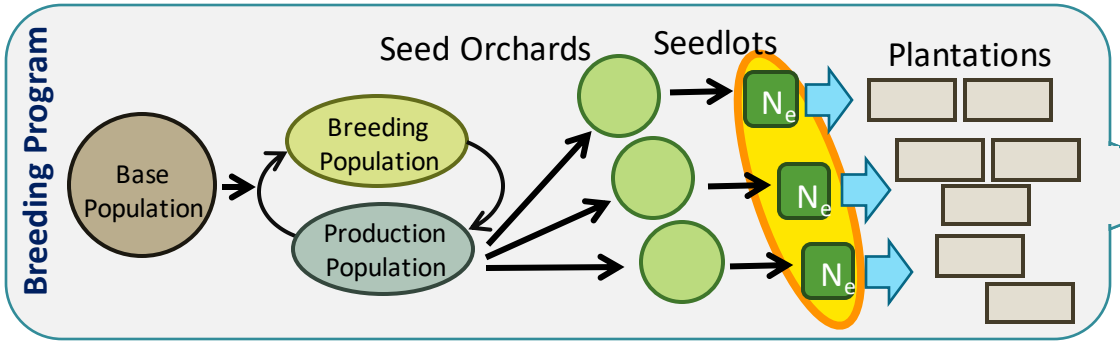

% landscape harvested & replanted
selective breeding generations
Breeding Program
Base Population
Breeding Population
Production Population
Seed Orchards
Seedlots
Plantations

What are the consequences for landscape level genetic diversity?

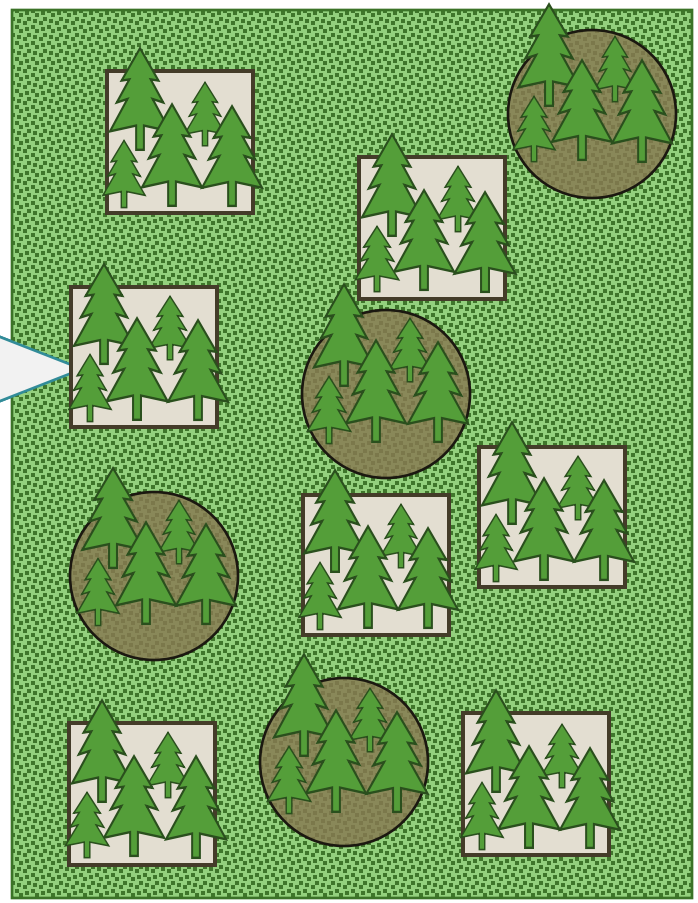




Activity 1:
Assess current metrics for genetic diversity in the breeding program using genomics



Effective population size (N_e) = number of individuals in an idealized population experiencing the same rate of genetic drift



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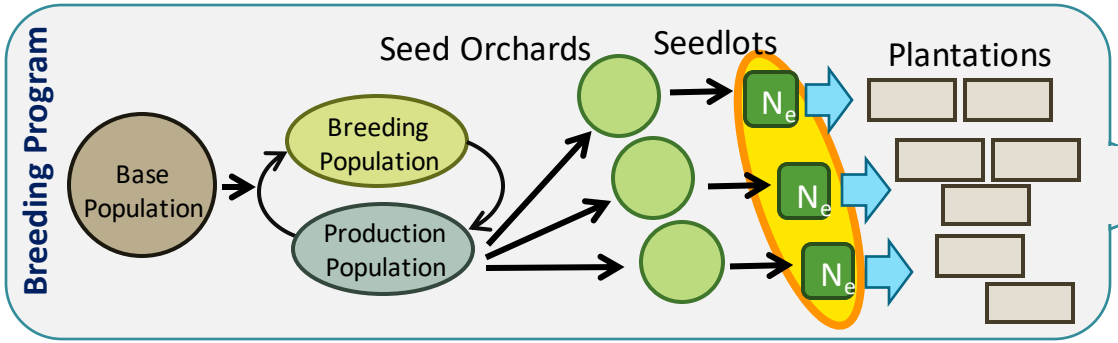
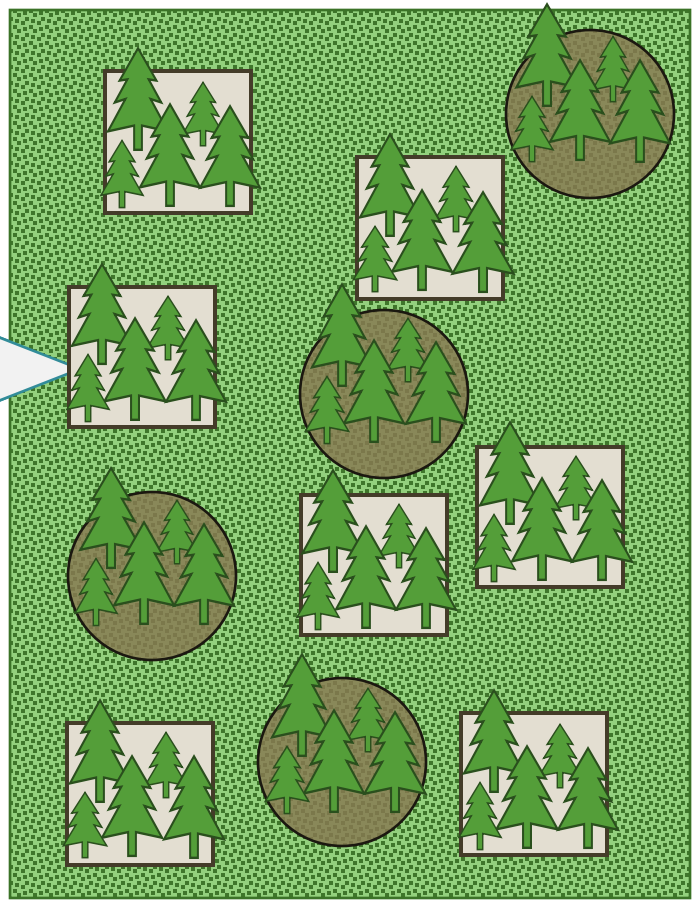
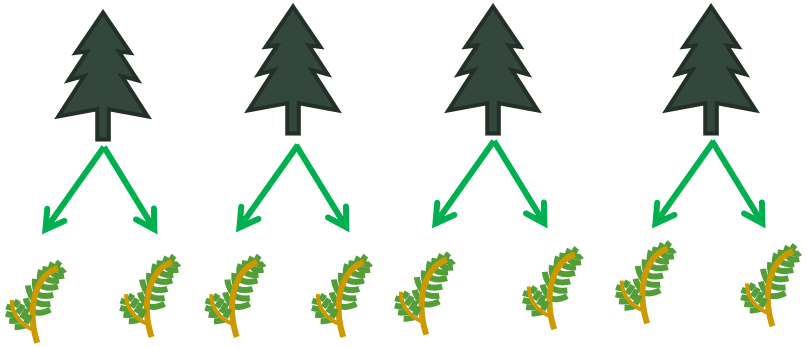




Estimate the **effective population size (N_e)** =



# of parents, relatedness of parents, evenness of parental contributions

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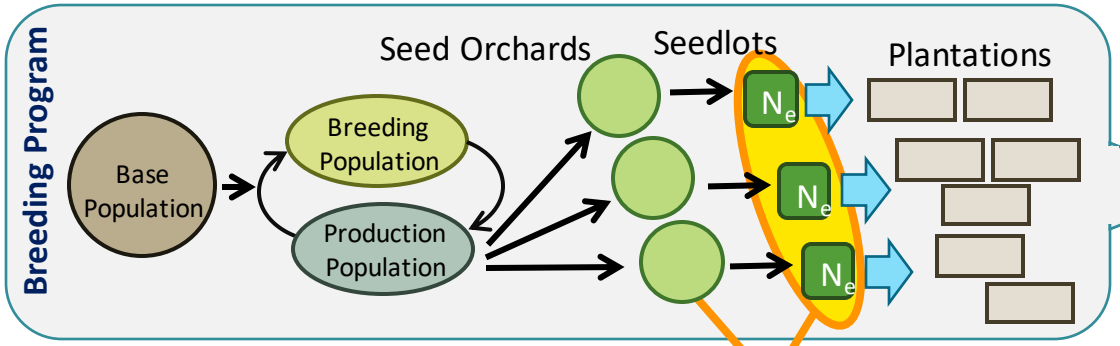
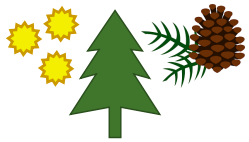
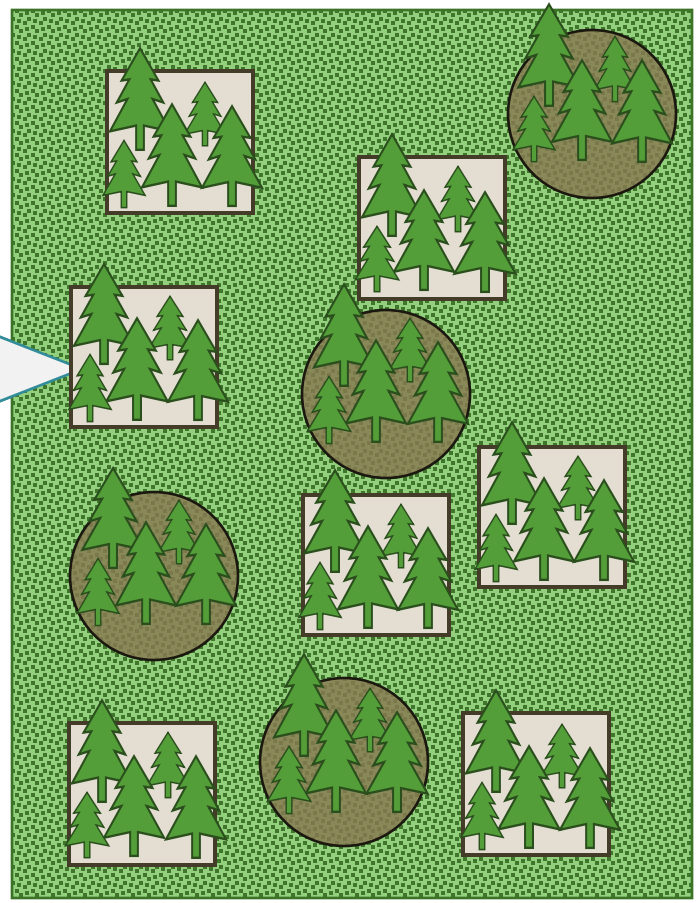
Assess current metrics for genetic diversity in the breeding program using genomics



How do these estimates compare to genomic estimates?



Parent tree gametic contributions



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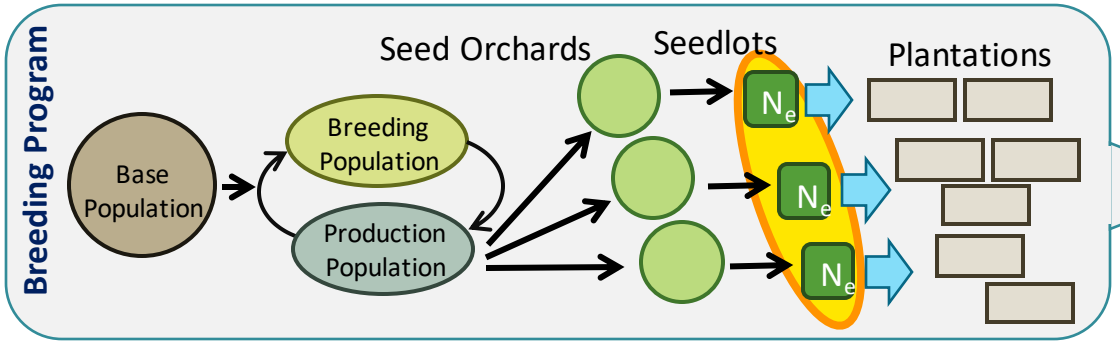
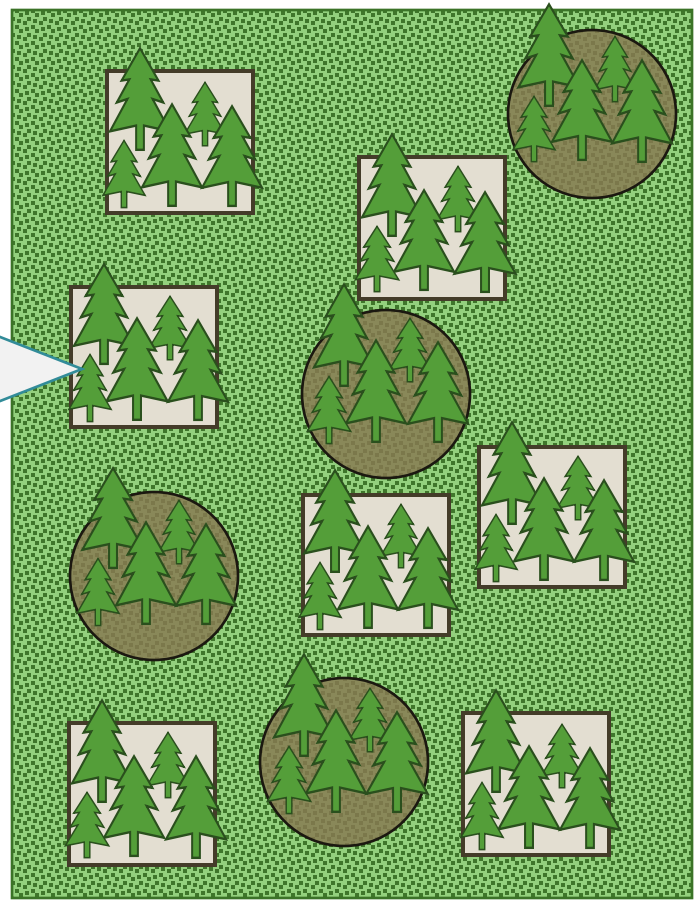
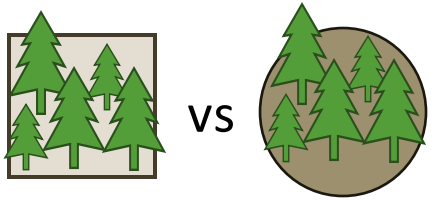


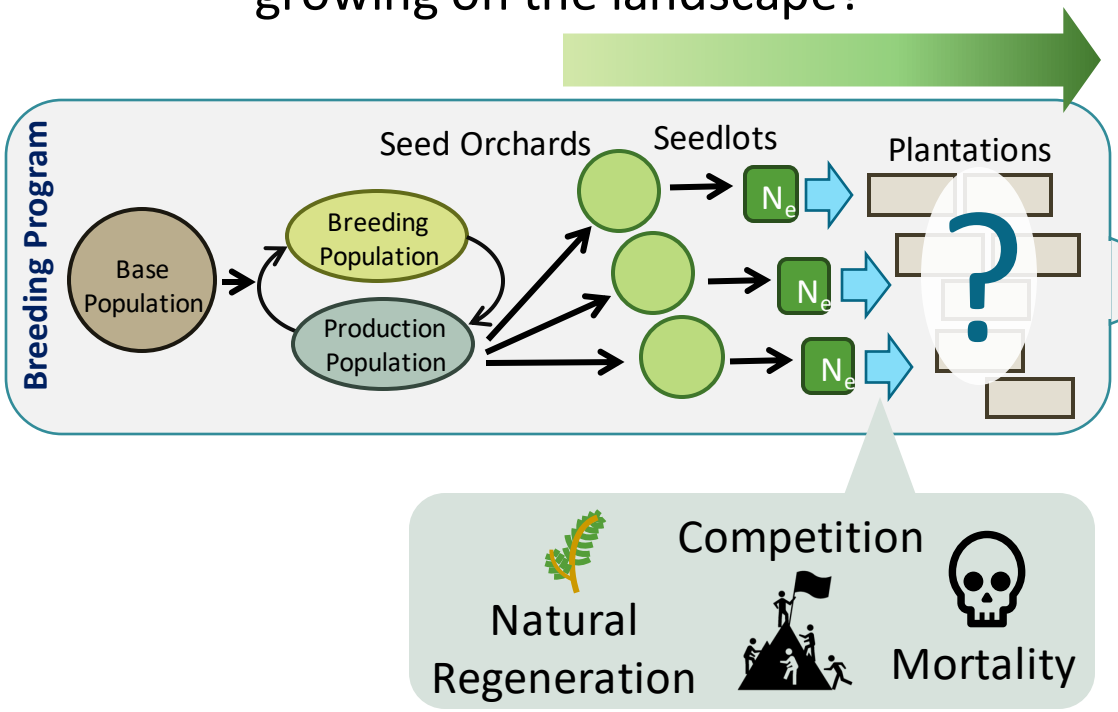


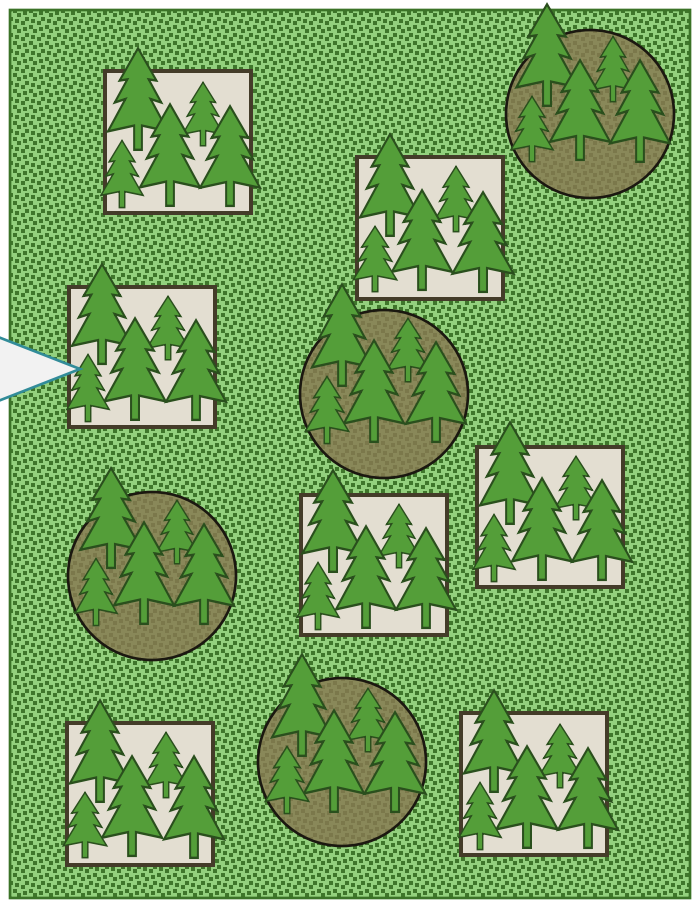
How do orchard seedlots compare to natural seed?



Activity 2:

How does this genetic diversity and composition shift across stages to what is growing on the landscape?



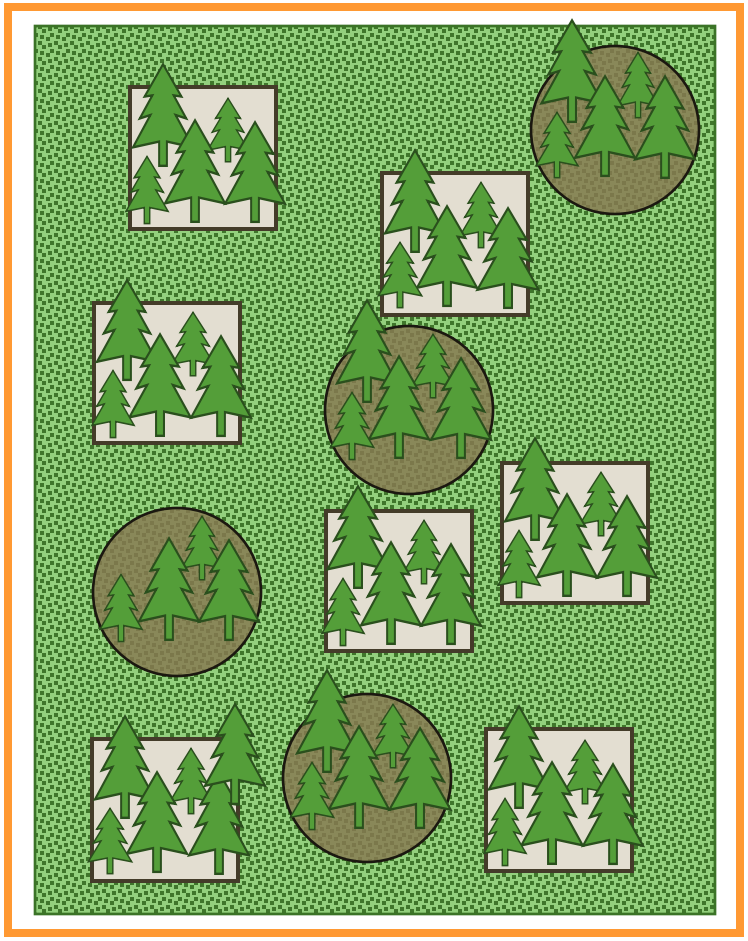


Ryman-Laikre Effect

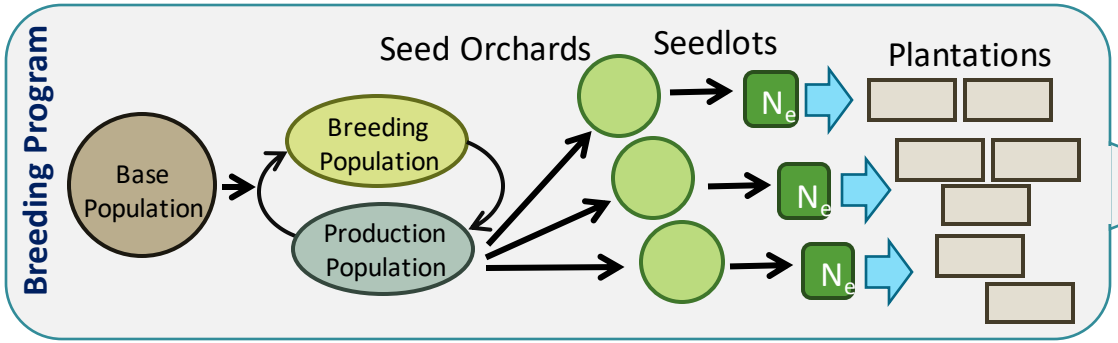
an increase in inbreeding and a reduction in total effective population size (N_{eT}) in a combined captive–wild system, which arises when a few captive parents produce large numbers of offspring

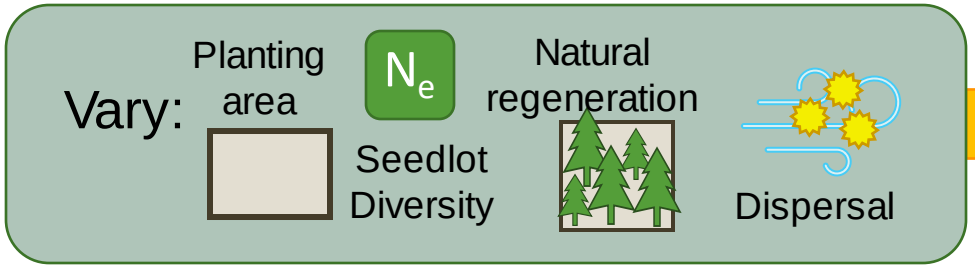
- Waples et al. 2016

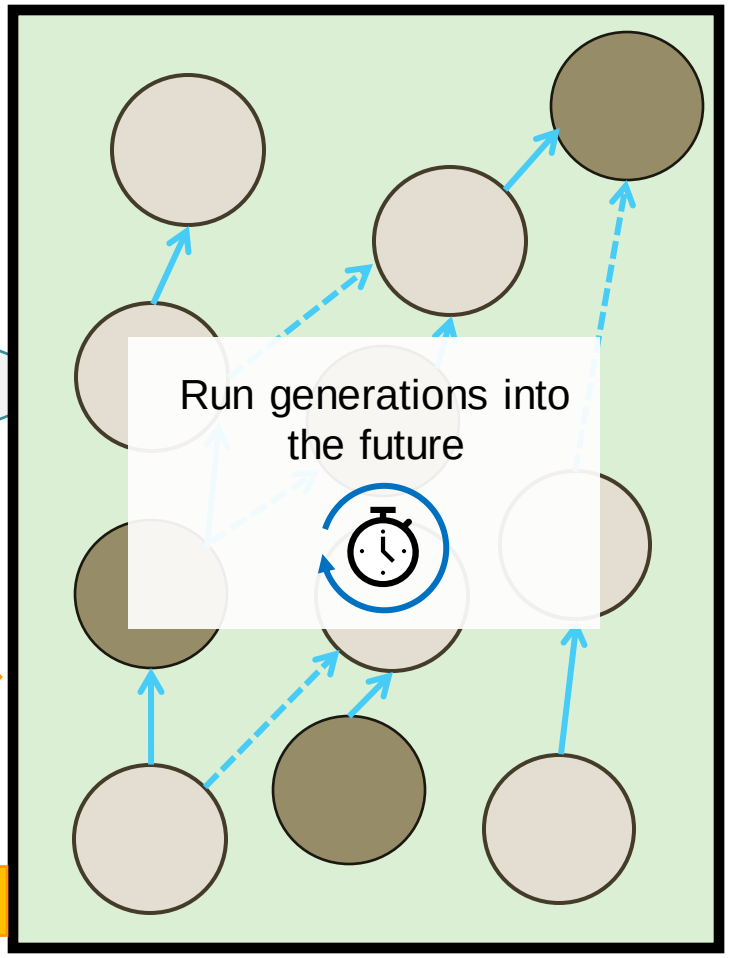
Could something similar be happening in selectively-bred – natural forest systems when we look at N_e at the landscape scale?



Activity 3:
How might forest management influence landscape-level genetic diversity?







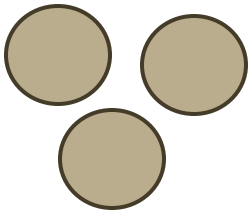
Output:
Survival and genetic data

Activity 1: Genetic diversity in seedlots

Use existing genomic datasets from AdapTree and CoAdapTree to quantify and compare genetic diversity in orchard and natural seedlots, and compare measures from genomic data to indirect estimates used to rate seedlots

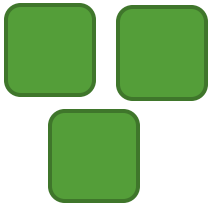
Lodgepole Pine

Natural Seedlots



vs

Orchard Seedlots

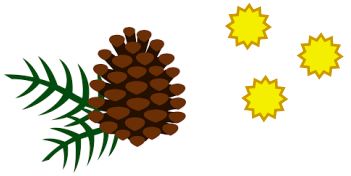


Interior Spruce

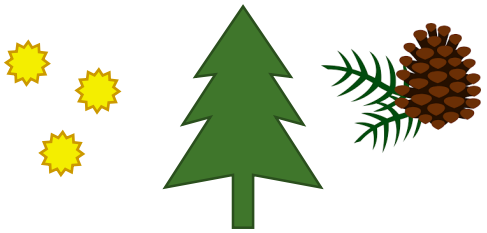
Genomic Estimates

vs

Indirect Estimates

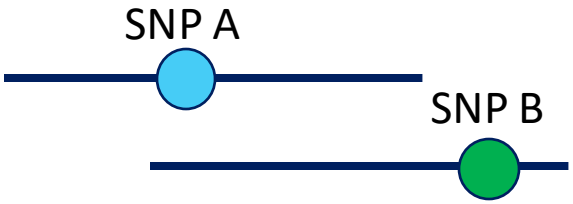


Activity 1: Effective Population Size



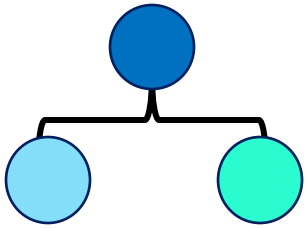
Gamete Production

Male (pollen) and female (seed) contributions used to calculate parental contribution and overall N_e



Linkage Disequilibrium

Alleles at different unlinked loci will become more correlated as genetic drift increases

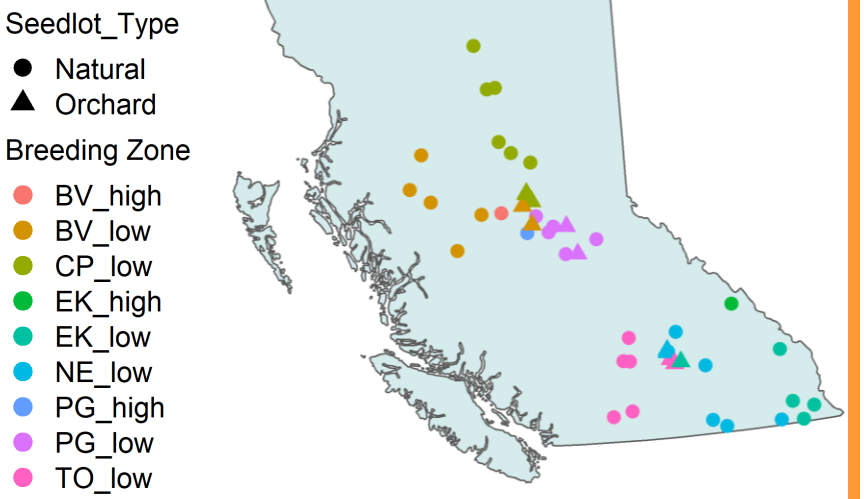


Sibship Frequency

Relatedness among samples will increase as N_e decreases

Available Data

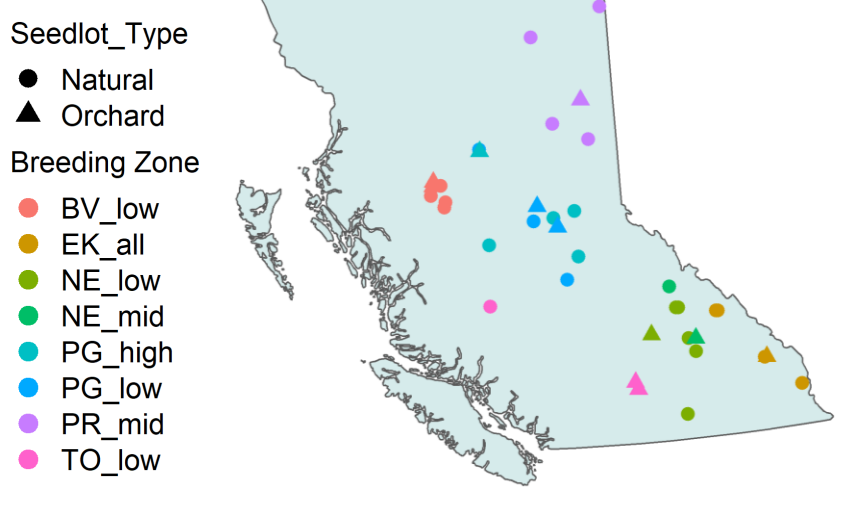
Lodgepole Pine



6 Breeding Zones

- 12 orchard seedlots
- 34 natural seedlots
- 50,298 SNP array
  - 7,467 control SNPs

Interior Spruce

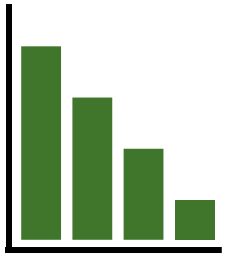


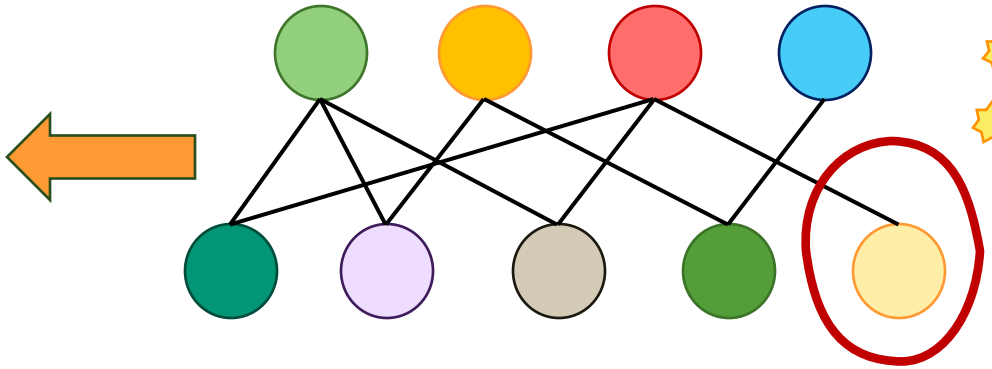
8 Breeding Zones

- 11 orchard seedlots
- 26 natural seedlots
- 51,029 SNP array
  - 4,493 control SNPs

Adding Lodgepole Pine Parent Samples

Parental Contributions





Pollen Contamination

Method Validation

Activity 2: Genetic diversity in stands

Genotype orchard parents, seedlots, and established planted stands that reflect multiple selection pressures to examine shifts in genetic diversity and composition across stages and scales.

Douglas-fir

x = Natural Regeneration

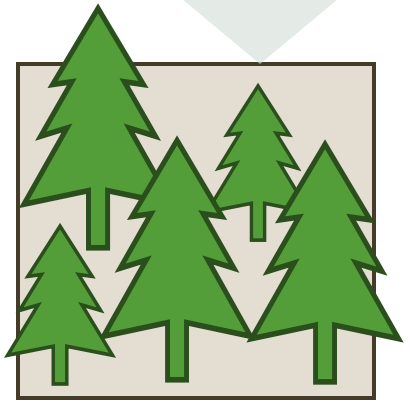
Competition

Mortality

Seed Orchard

Seedlot

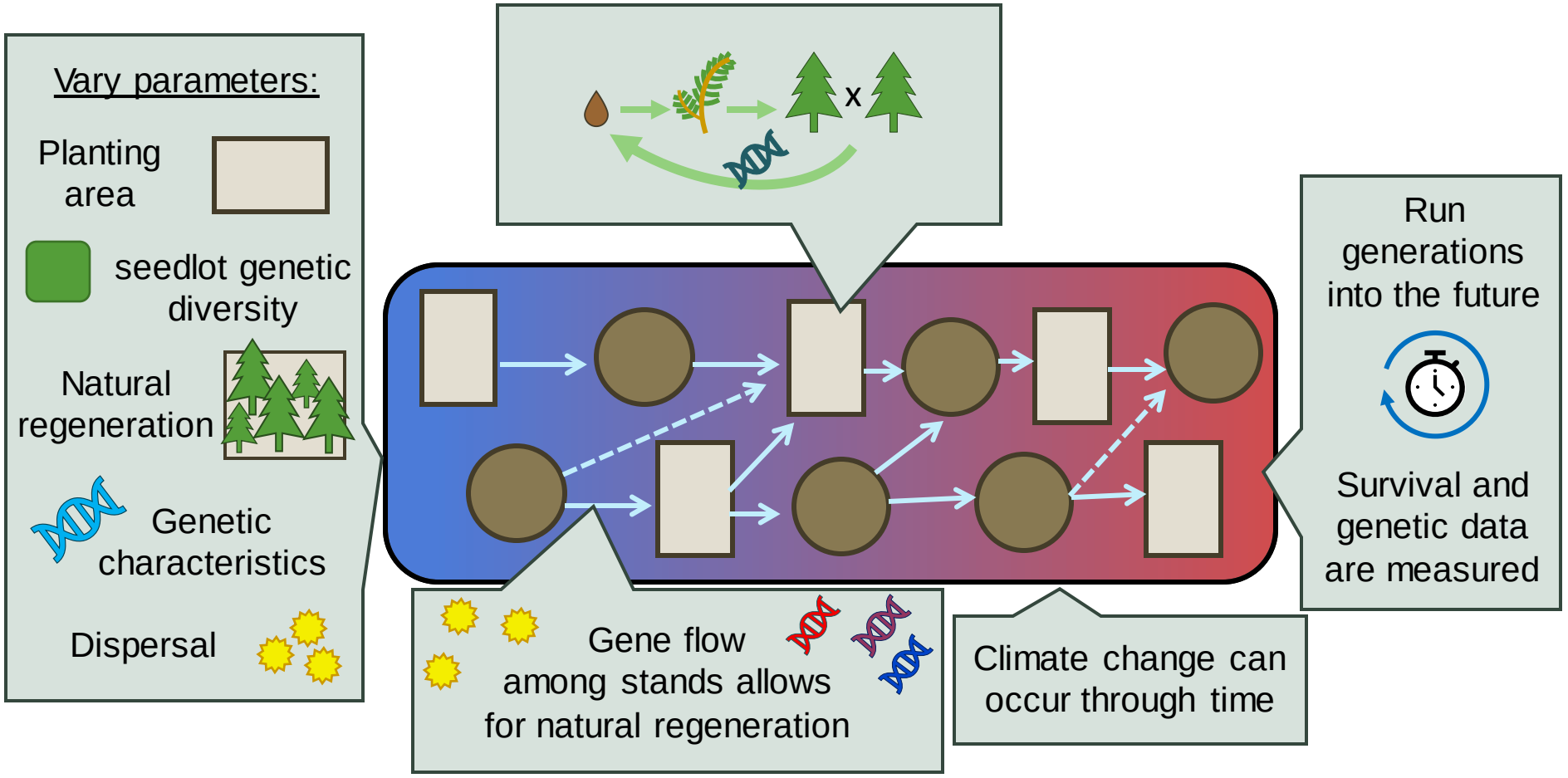
N_e



Genetic Diversity & Genetic Composition

Activity 3: Landscape diversity

Use a population genetic simulation model to predict genetic diversity and survival across several generations into the future, testing multiple management scenarios.



Thank you!

- Sally Aitken
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Questions?