TRIA-Net
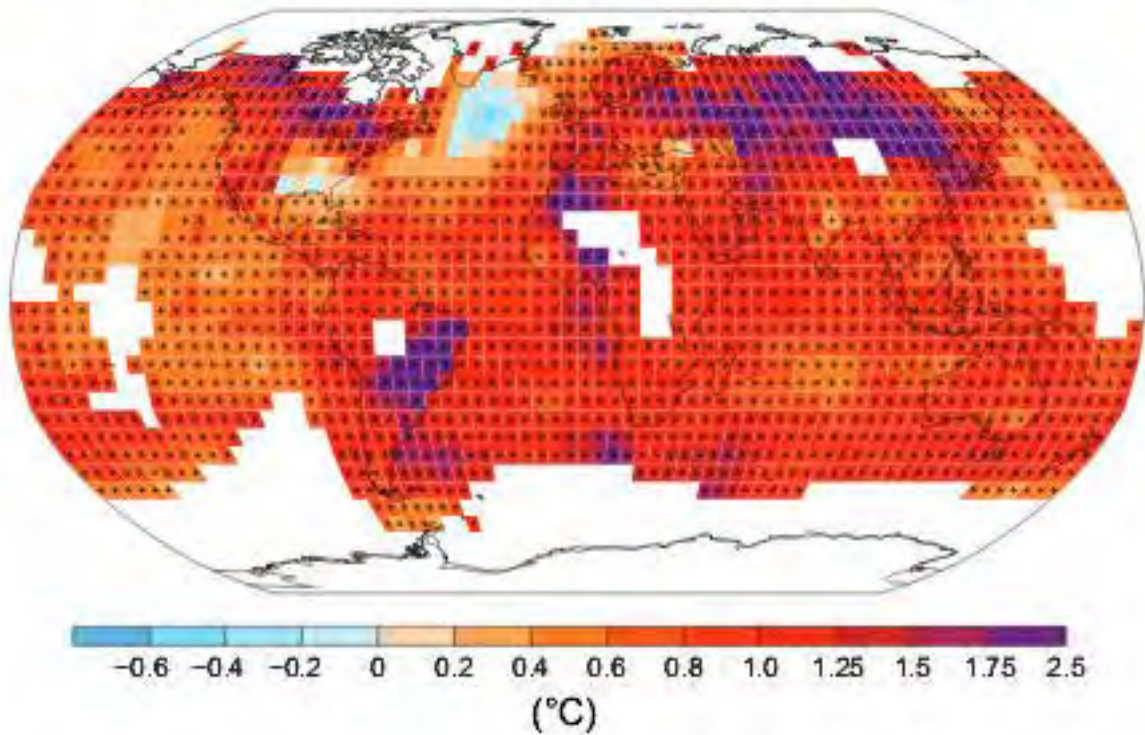Turning Risk Into Action for the Mountain Pine Beetle Epidemic

Modelling the development of spatial genetic structure during range expansion: the case of the mountain pine beetle (*Dendroctonus ponderosae*)

PAUL MAYRAND – ÉLISE FILOTAS – JULIAN WITTISCHE – PATRICK M. A. JAMES

Université de Montréal

NSERC CRSNG

Modélisation de la Complexité de la Forêt

cef
Centre d'étude de la forêt

CSBQ QCBS

Range expansion – Main drivers

Observed change in surface temperature 1901–2012

(°C)

IPCC 2013

Tiffany Turner

Why do we care?

Important to understand spatial genetic variation during range expansion:

o To study the evolutionary consequences of range expansions

o To understand the patterns favoring biological invasions

o To predict the future distribution and viability of expanding populations

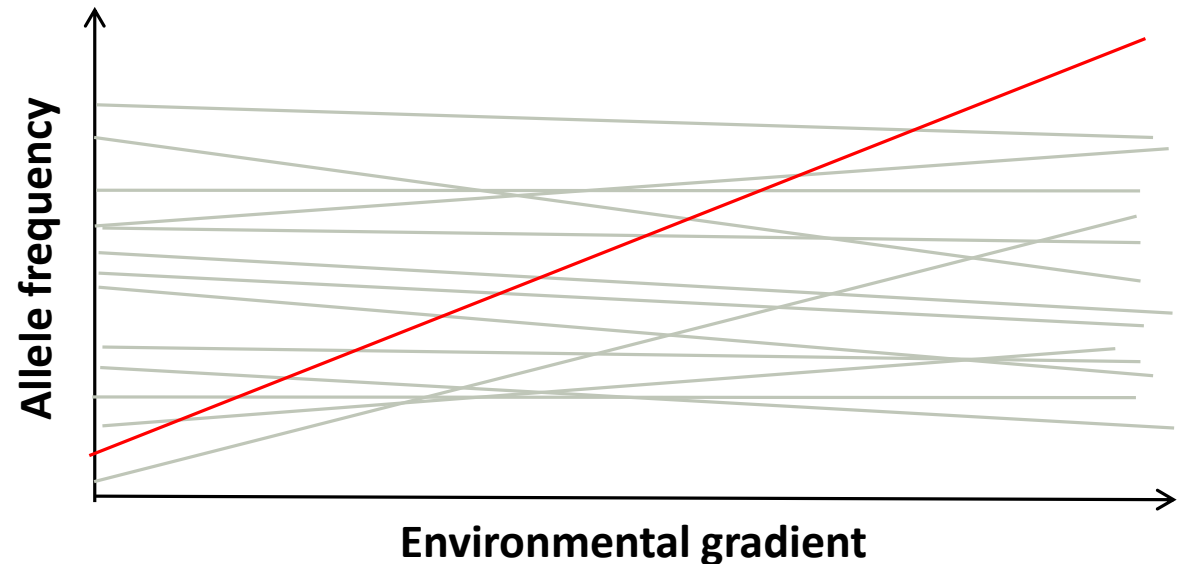Identify in non model species genes which matter (i.e. adaptive loci).

Landscape genomics

Tools to identify loci under selection.

Looks for correlations between allele frequencies and environmental variables.
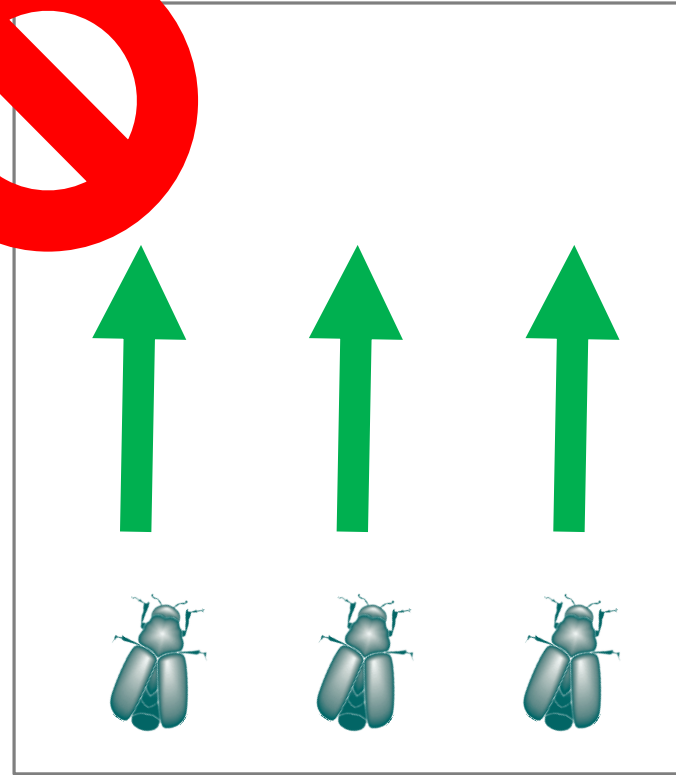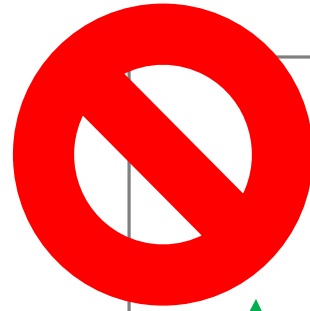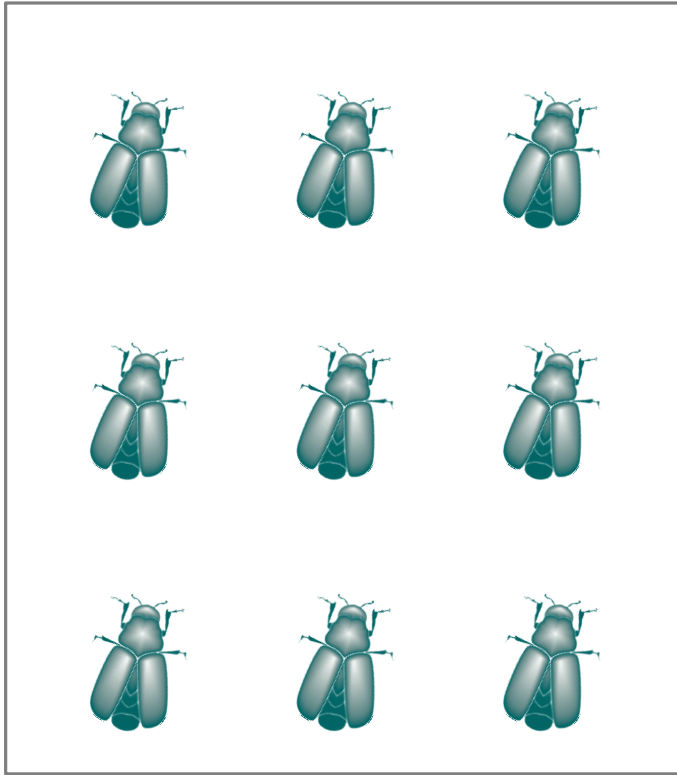
Many different approaches and methods already exist :

◦ E.g., Joost et al. 2007, Coop et al. 2010, Frichot et al. 2013, Guillot et al. 2014.

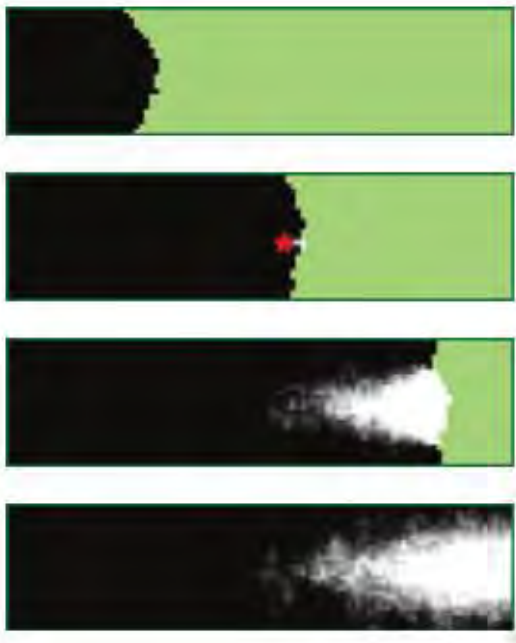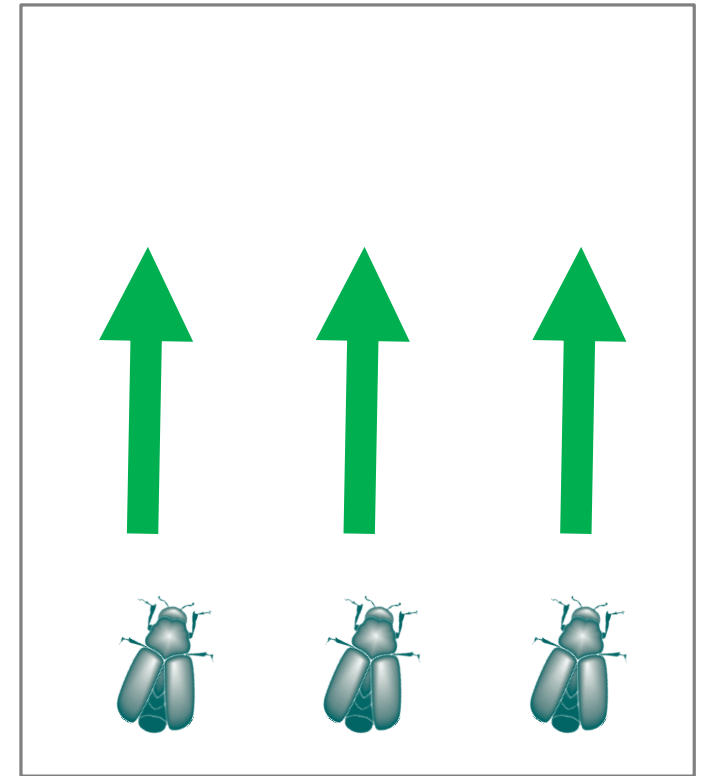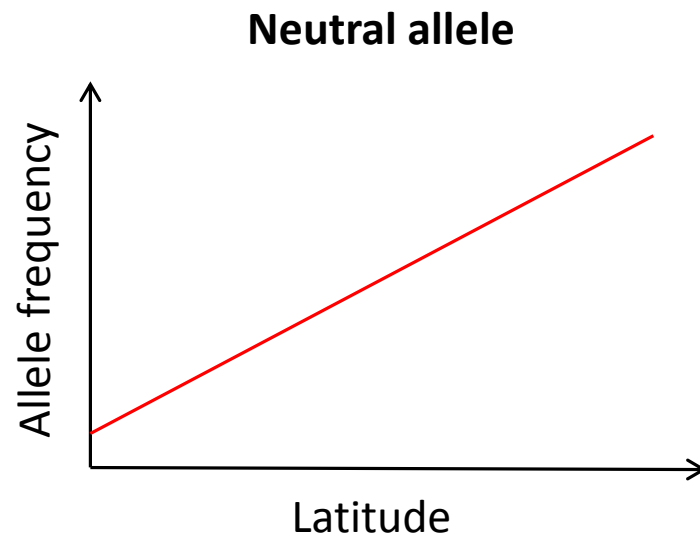# The trouble with the expansions …

BUT…

Genetic consequences of range expansion

o Multiple founder effects at the expansion's front

o Allele surfing

Excoffier et al. 2009

Neutral allele

Allele frequency

Latitude

Research questions

1. How does **dispersal** and **timing** of sampling affect the development of spatial genetic variation during range expansion?

2. How do these factors affect our ability to identify **loci under selection**?
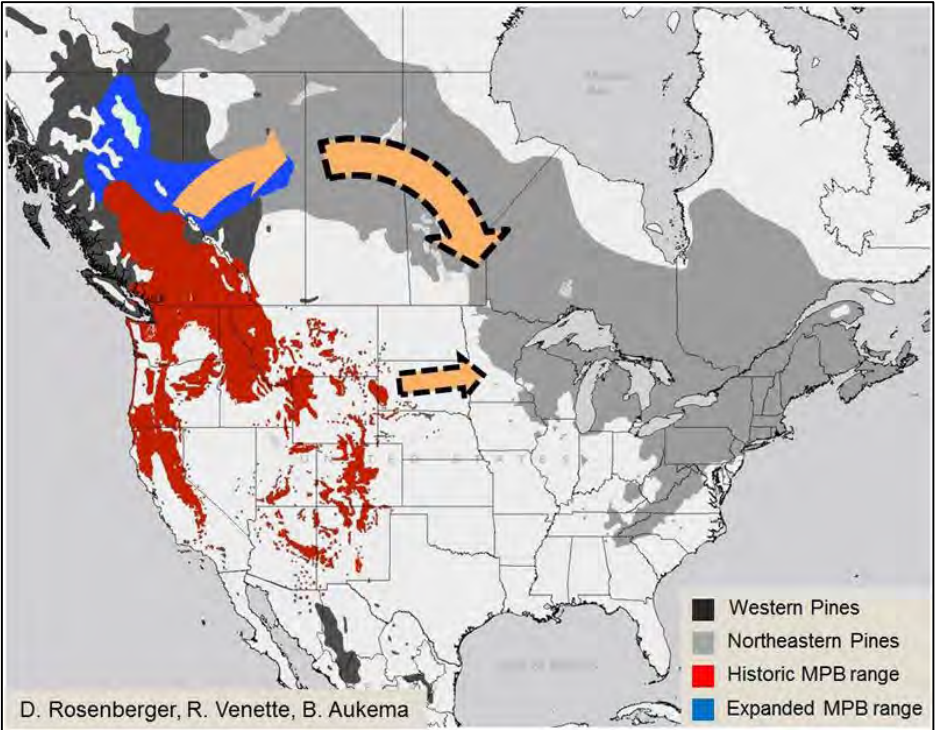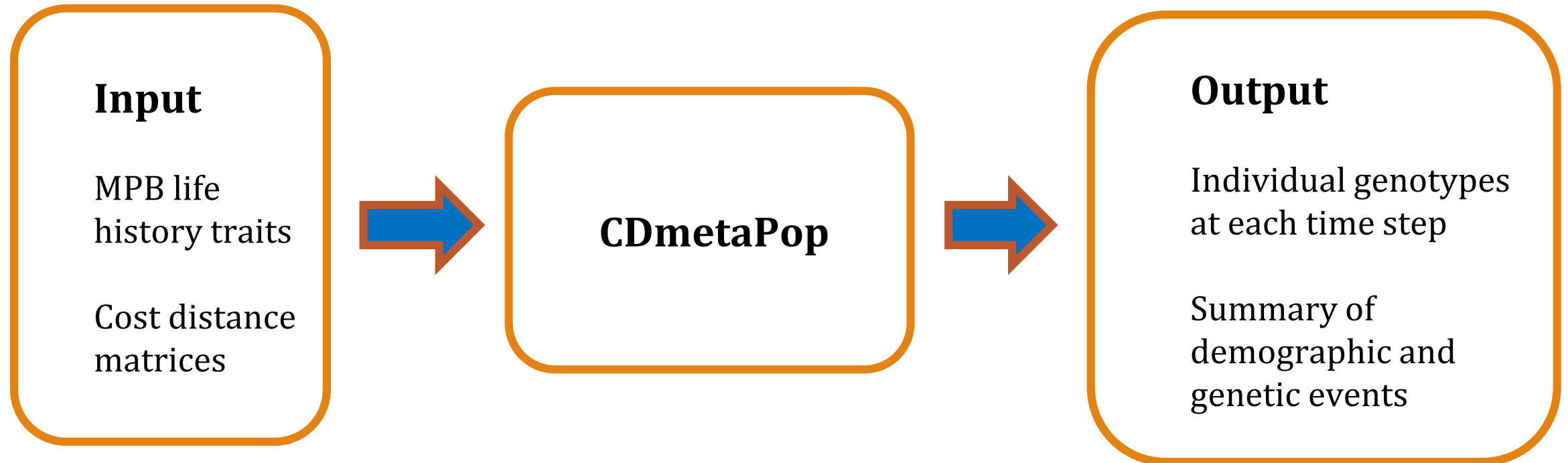
Mountain pine beetle outbreak system
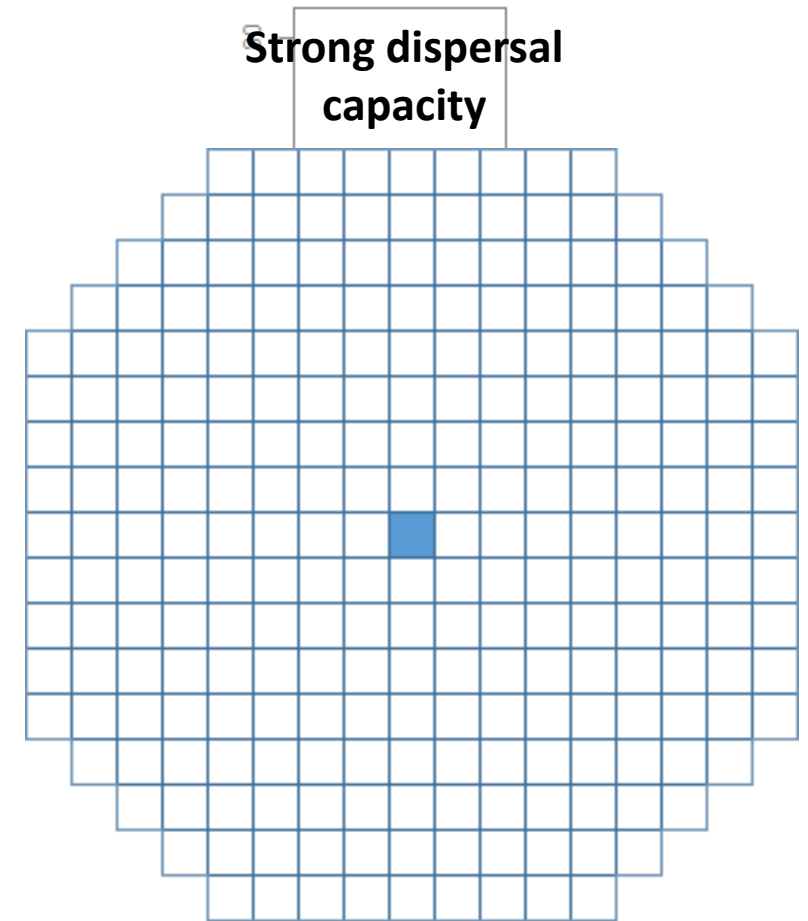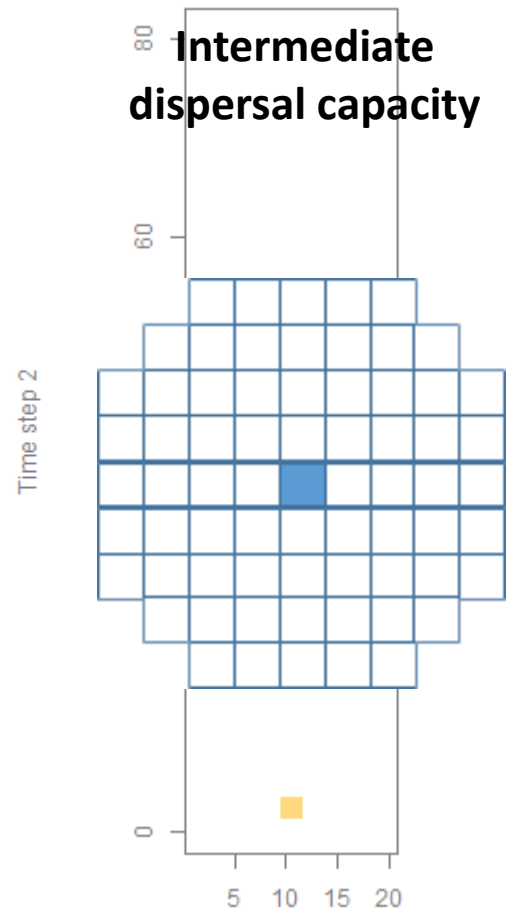

USDA

Lorraine Maclauchlan

D. Rosenberger, R. Venette, B. Aukema

Western Pines
Northeastern Pines
Historic MPB range
Expanded MPB range

Simulating range expansions

Simulation approach using CDmetaPop (Landguth et al.)

Input

MPB life
history traits

Cost distance
matrices

CDmetaPop

Output

Individual genotypes
at each time step

Summary of
demographic and
genetic events

Modelling framework and experimental design
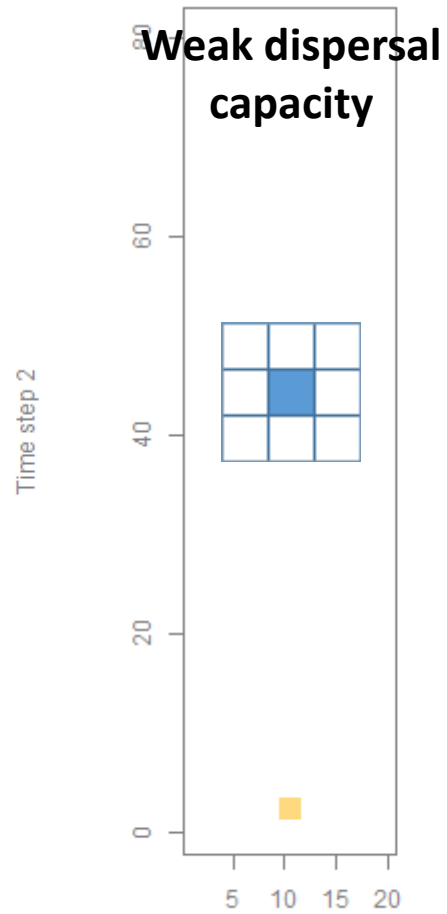
Modelling framework and experimental design
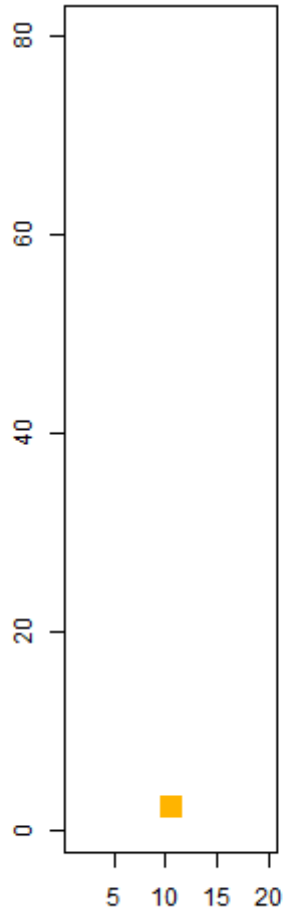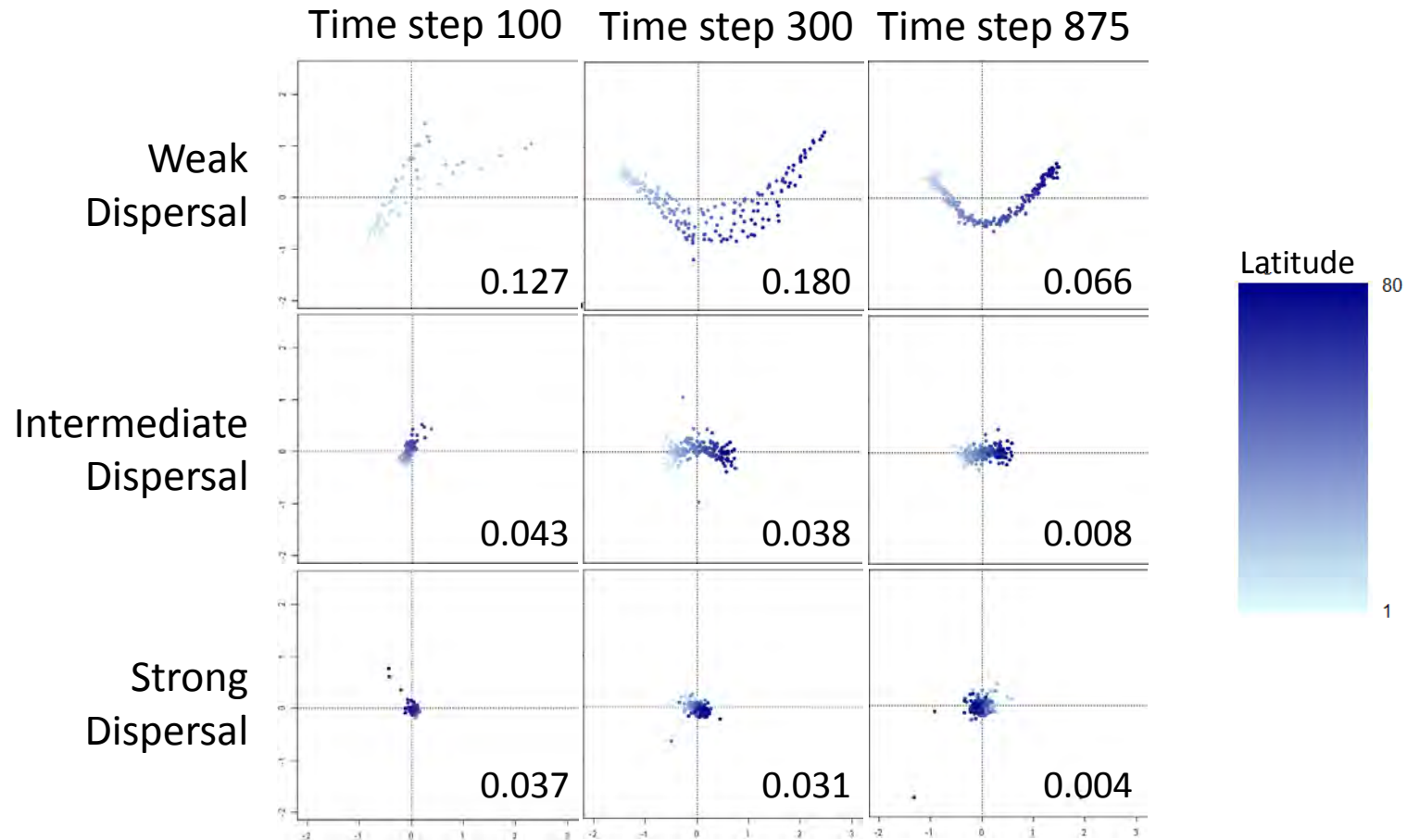

Model Parameters	
Landscape size	20 x 80 cells
Individuals	Maximum 30 individuals per cell (max . total = 48000)
SNP loci	1000
Replicates	15 / experiment
Simulation time horizon	875 time steps; annual

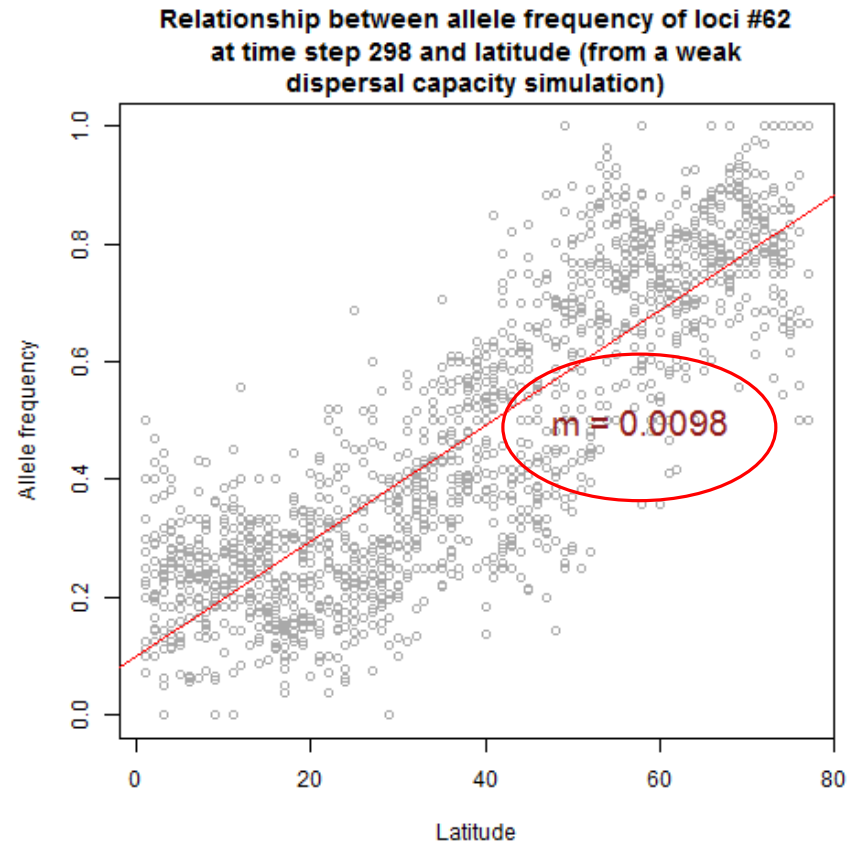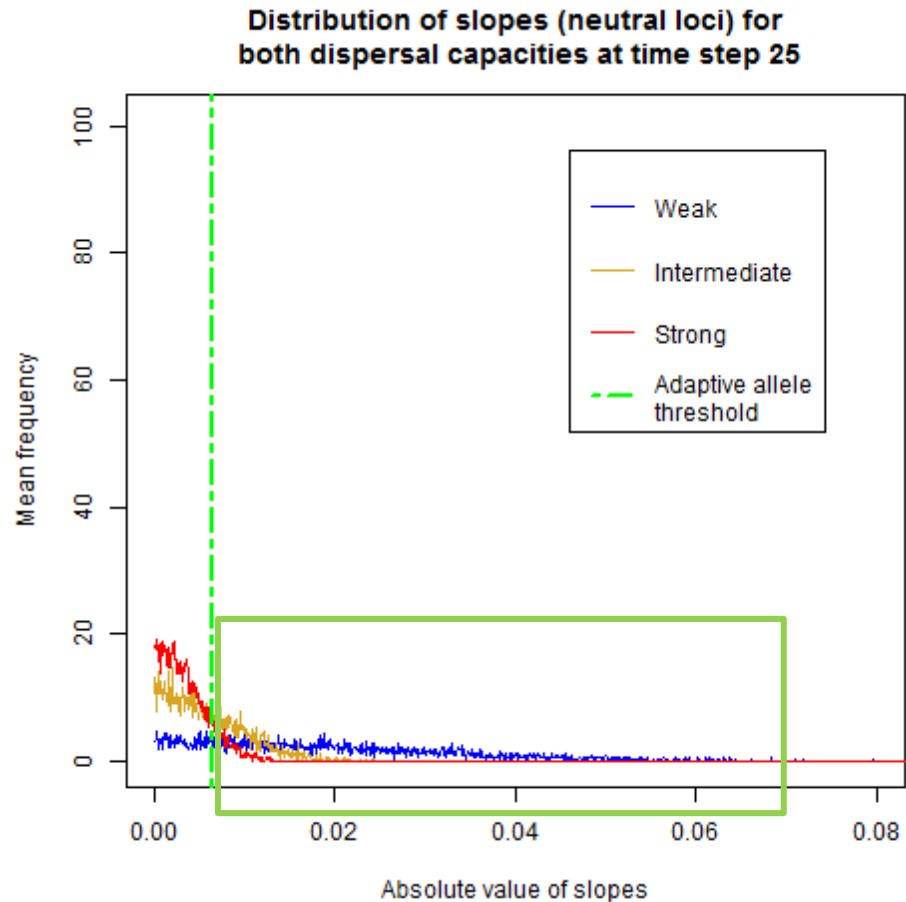# Results – Genetic structure (IBD)
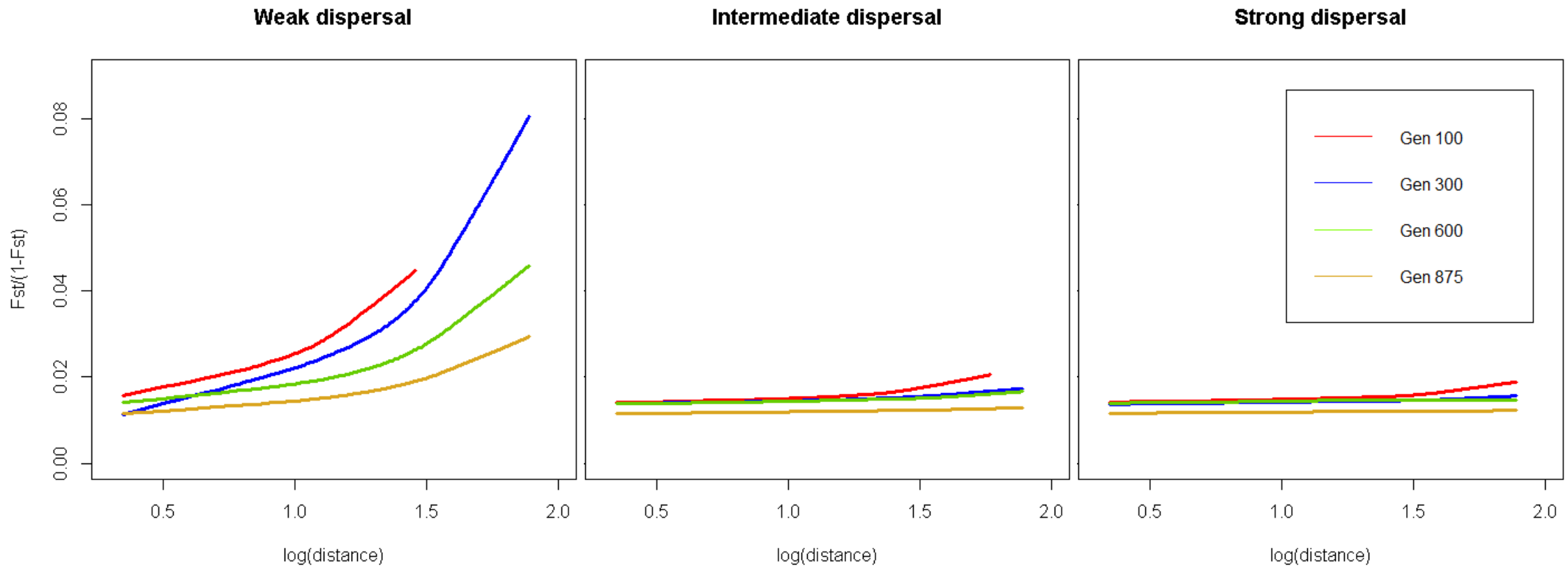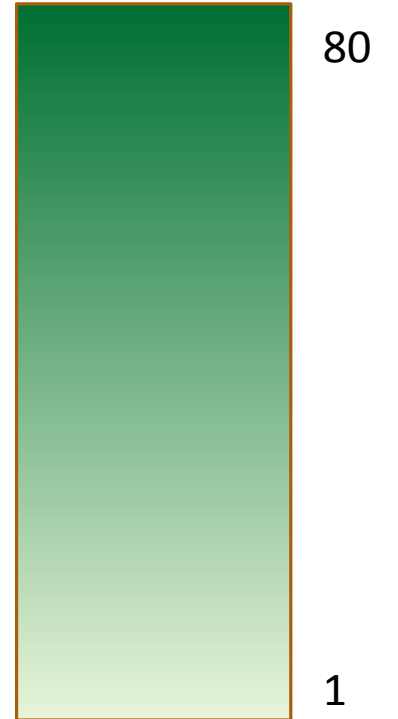
Results – Genetic structure (PCA)

Results – Slope of a neutral allele

Relationship between allele frequency of loci #62 at time step 298 and latitude (from a weak dispersal capacity simulation)

m = 0.0098

Results – Distribution of slopes and adaptive model

Distribution of slopes (neutral loci) for both dispersal capacities at time step 25

Legend:
— Weak
— Intermediate
— Strong
-·- Adaptive allele threshold

Mean frequency (y-axis), Absolute value of slopes (x-axis)

Hypothesized relationship between adaptive allele and latitude

m = 0.00633

Allele frequency (y-axis), Latitude (x-axis)

80

1
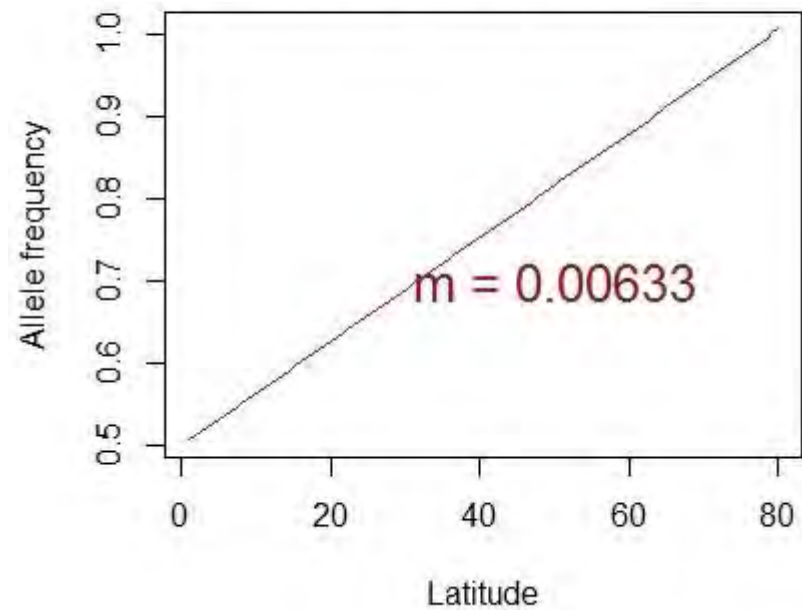
Results – Distribution of outlier slopes through time

Number of slope values exceeding the adaptive slope thresholds at each time step and for the three dispersal capacities
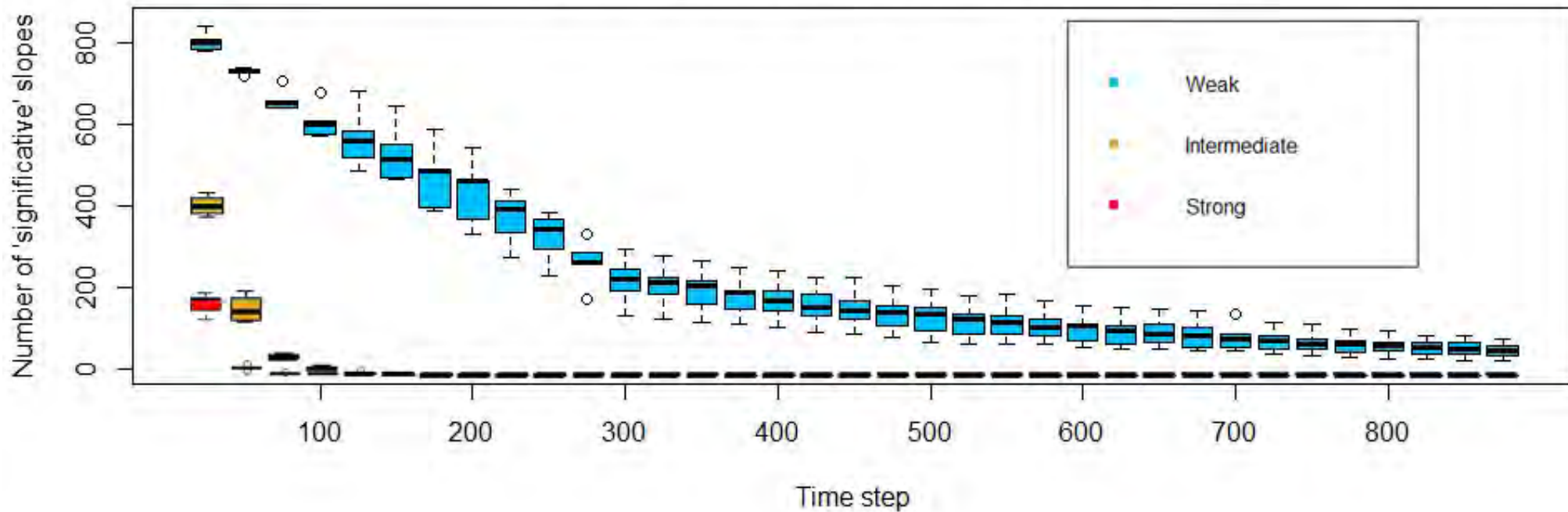
Interpretations...

Using a simulation approach, we found that during range expansion :

◦ **Weaker dispersal** produces stronger population genetic structure

  ◦ A greater number of neutral alleles exhibit patterns in allele frequencies similar to what one might expect due to selection.

  ◦ As the expansion progresses, the number of outlier neutral slopes decreases.

◦ **Stronger dispersal** results in weak population genetic structure

  ◦ Reduces the probability of a neutral alleles from mimicking an adaptive allele.

Next Steps

1. Improvement of adaptive model: explicit simulation of adaptive loci in CDmetaPop

2. Comparison of these simulated slopes using theoretical models (e.g., Haldane's rule)

3. Application of existing landscape genomics tools (e.g. LFMM, BayEnv) to compare their performances in response to variation in demographic context.

Thank you!

jameslab.ca

D.J. Huber