

Modelling climate impacts on genetic diversity in metapopulations



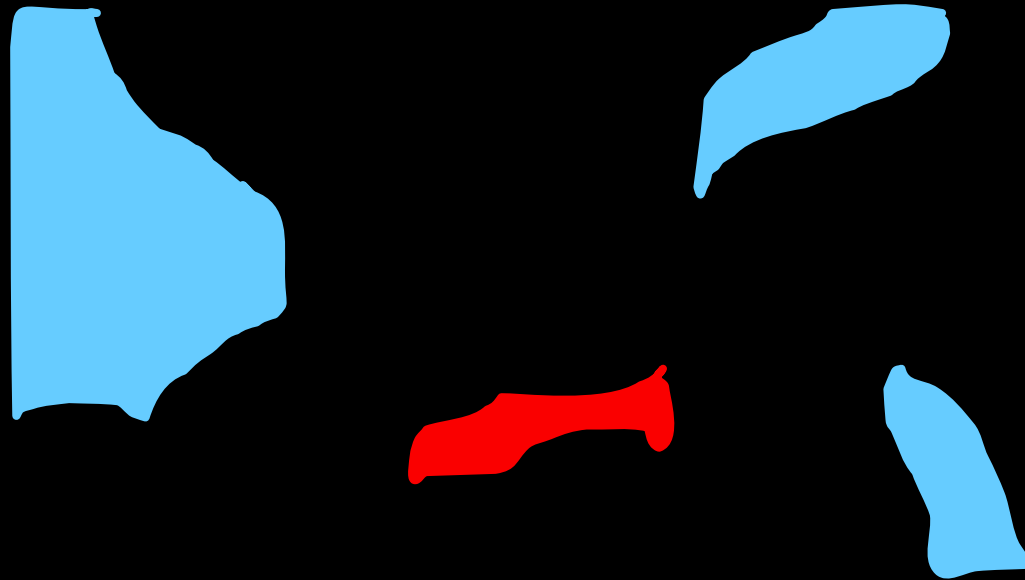
Metapopulations

in fragmented landscapes species are often confined to metapopulations



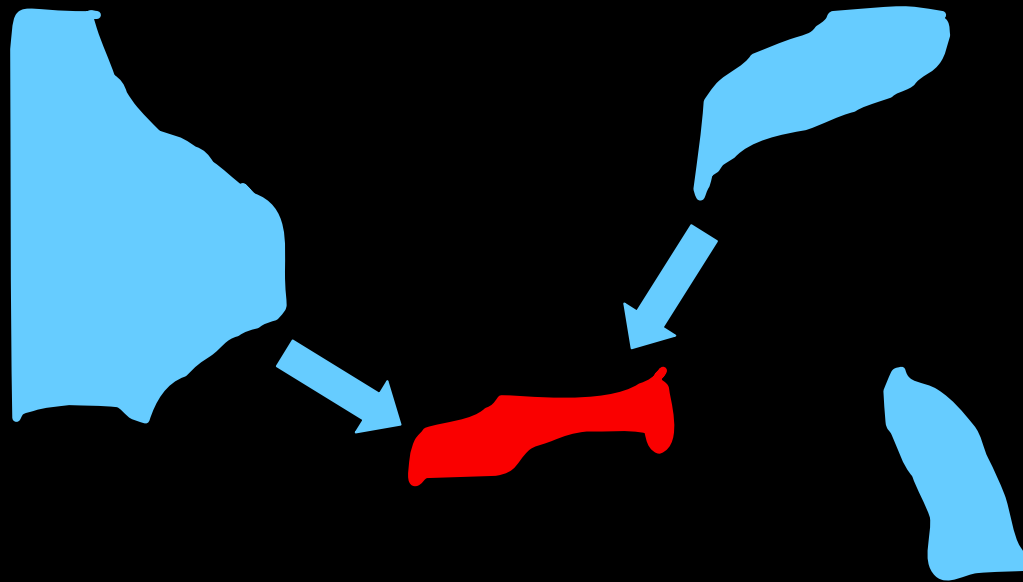
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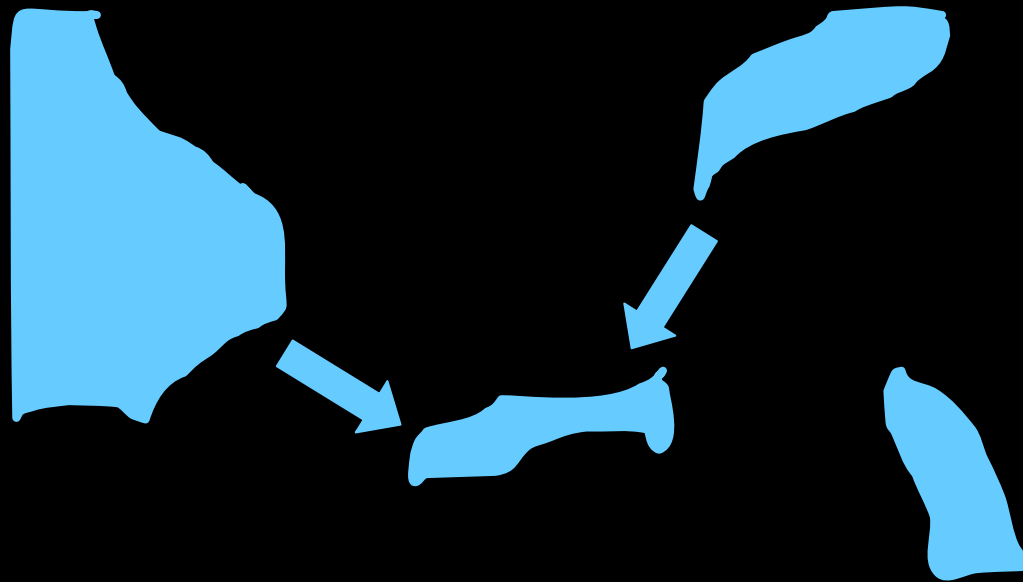
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Climate change

- Overall increased temperature
 - Hadley Centre:
 - 1 °C warming by 2100
 - 2 °C warming by 2100
 - 4 °C warming by 2100
- Increased weather variability: more weather extremes

Research question

How will the level of genetic diversity be affected by current climate changes?

3 temperature increase scenarios and 2 levels of weather variability + controls of zero

numbers of alleles per locus and effective numbers of alleles per locus

Simulation study

- METAPHOR: simulates metapopulation demography
- + shaking windows: simulates temperature isocline shift and weather variability
- + genetics: each individual has its own genome
100 genes, diploid

WHAT DOES IT LOOK LIKE?

METAPHOR

individuals of the species

2 sexes

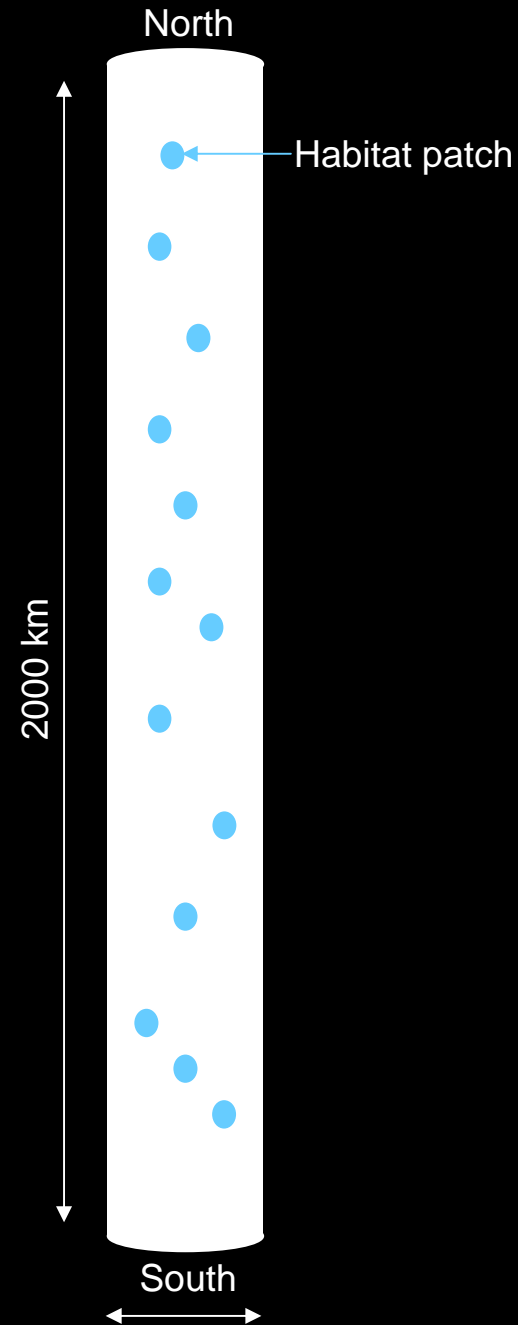
2 lifestages

chance to survive

chance to breed

chance to disperse

max 3 x 15 km / year



METAPHOR

individuals of the species

2 sexes

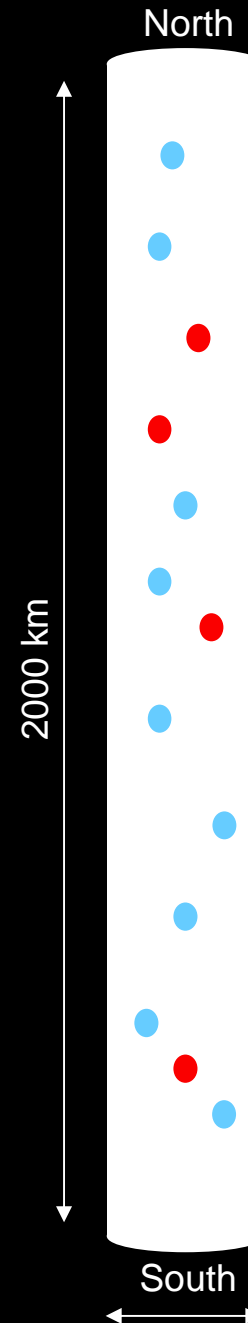
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METAPHOR

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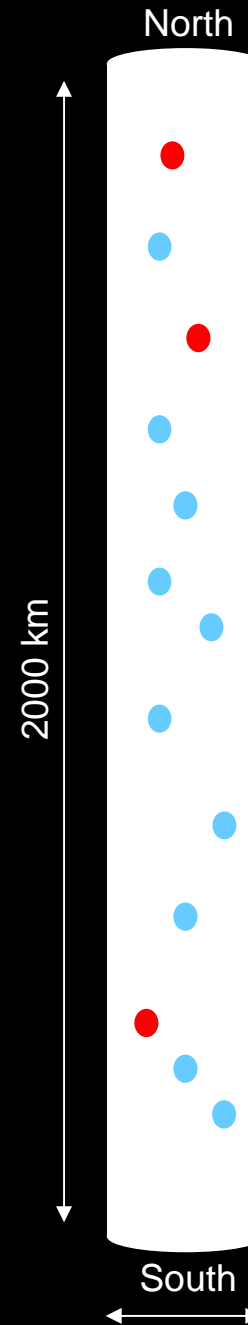
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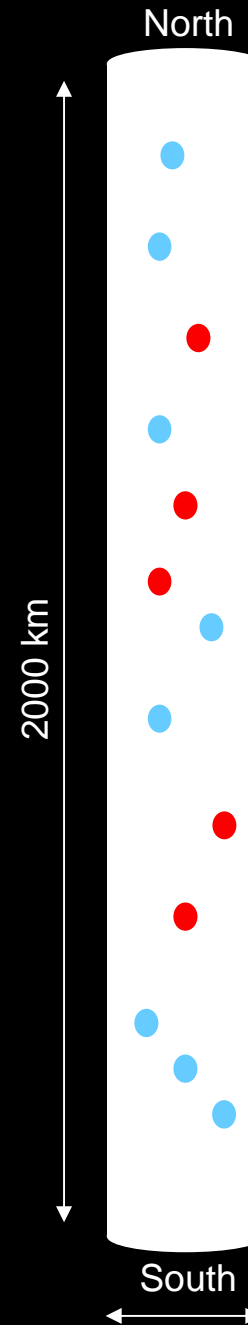
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+ shaking windows

climate translates to habitat quality

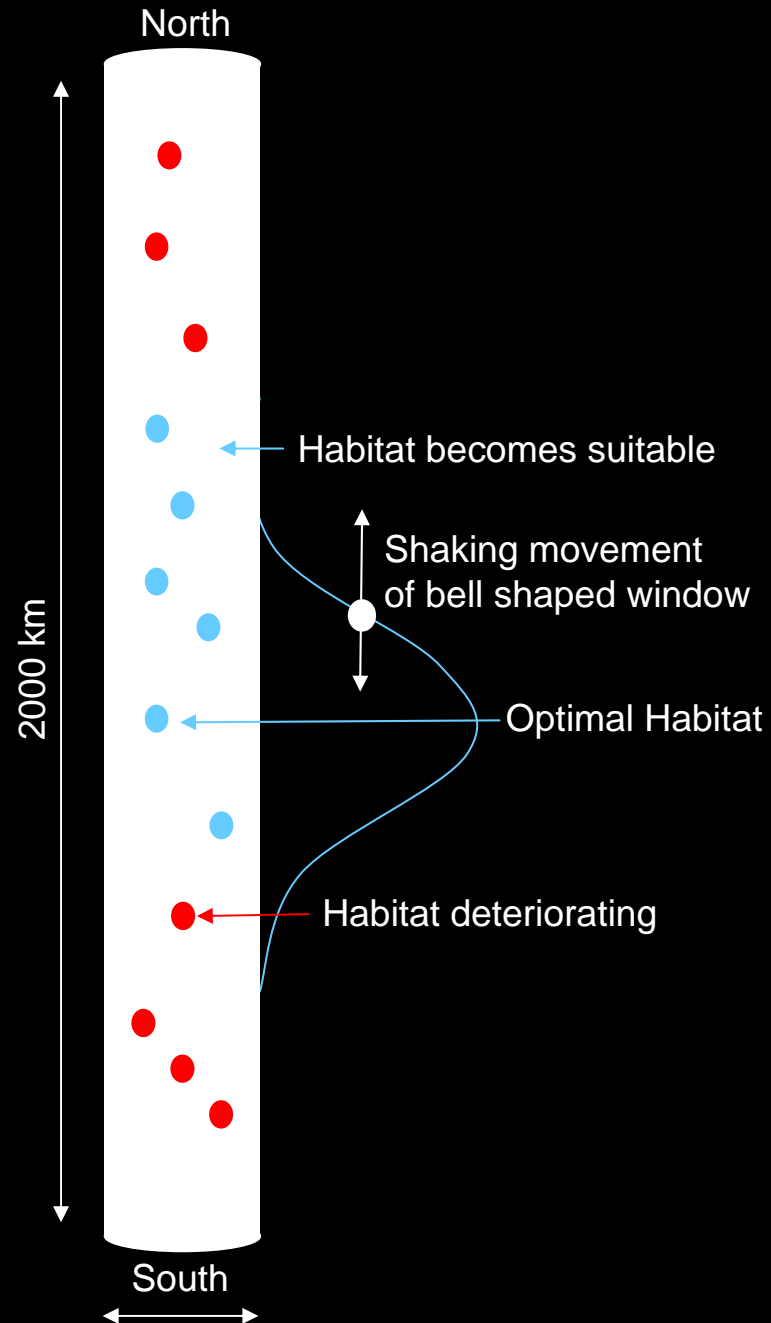
each year varies randomly around the optimum

but on average moves northwards:

1 °C : 2 km/year

2 °C : 4 km/year

4 °C : 8 km/year



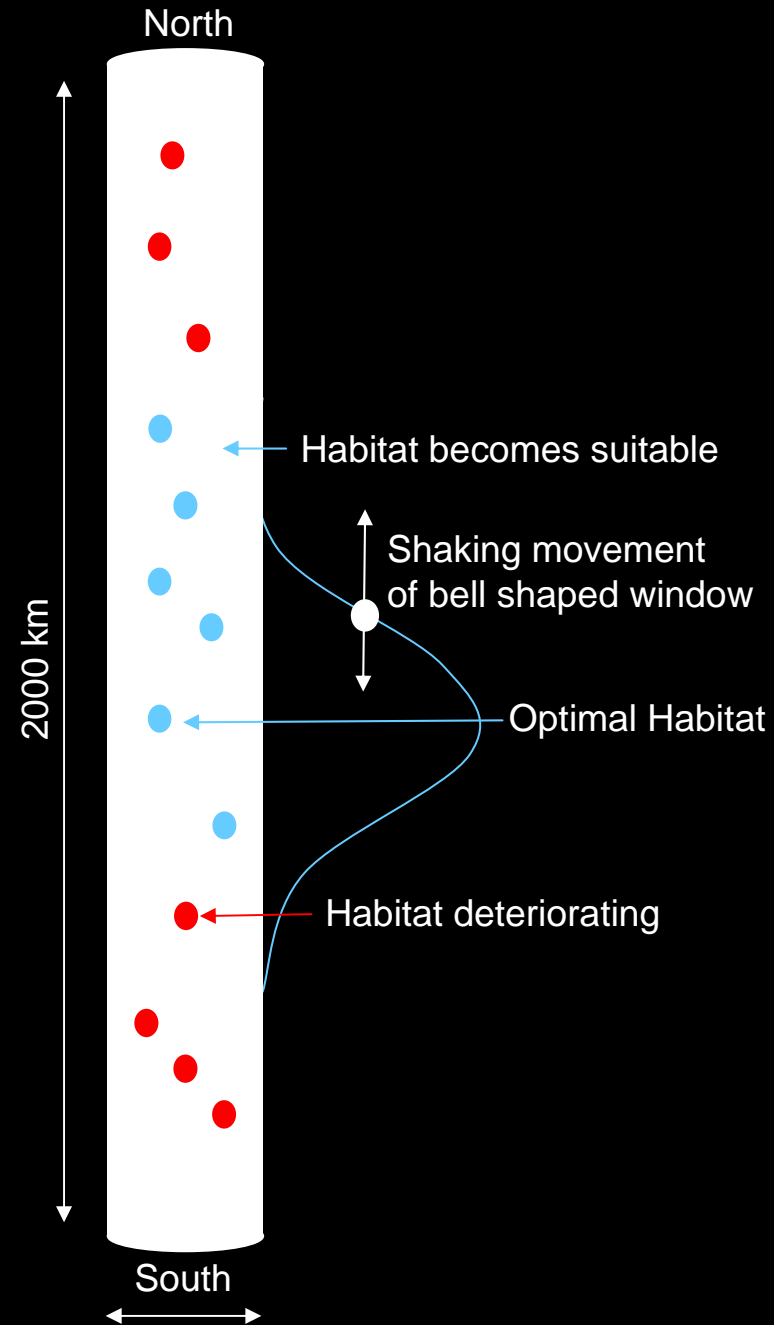
+ shaking windows

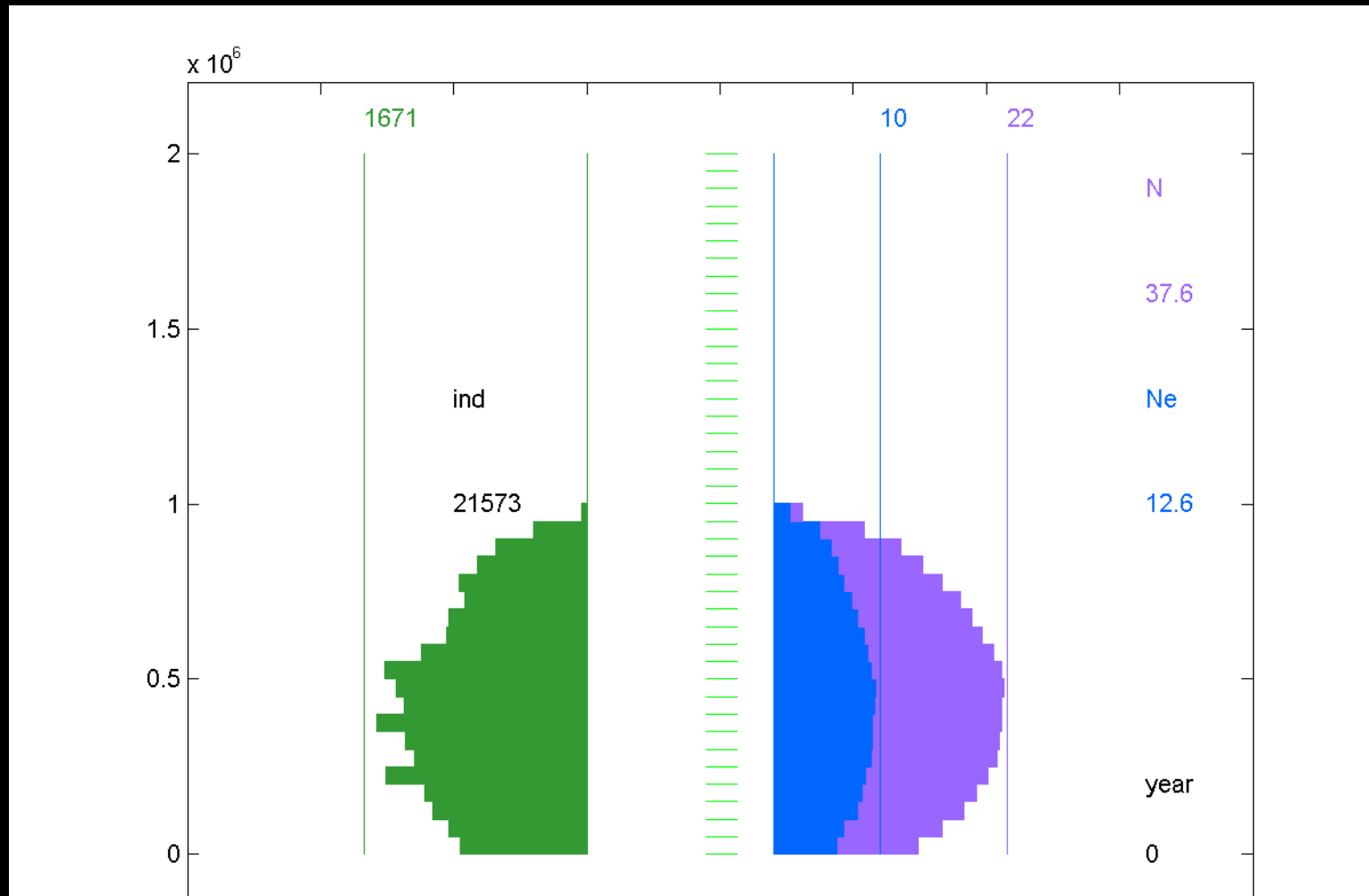
habitat quality affects:

chance to survive

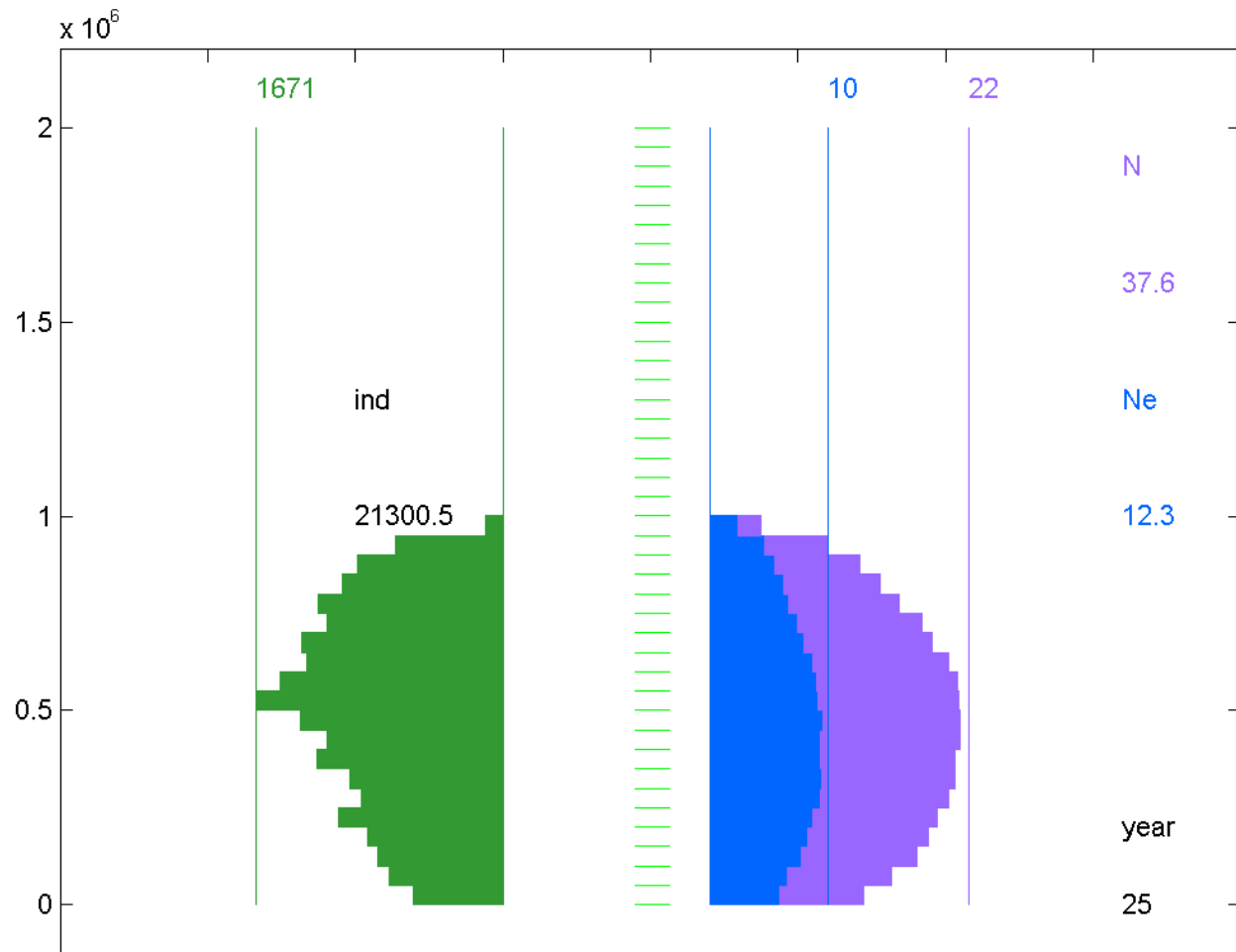
chance to breed

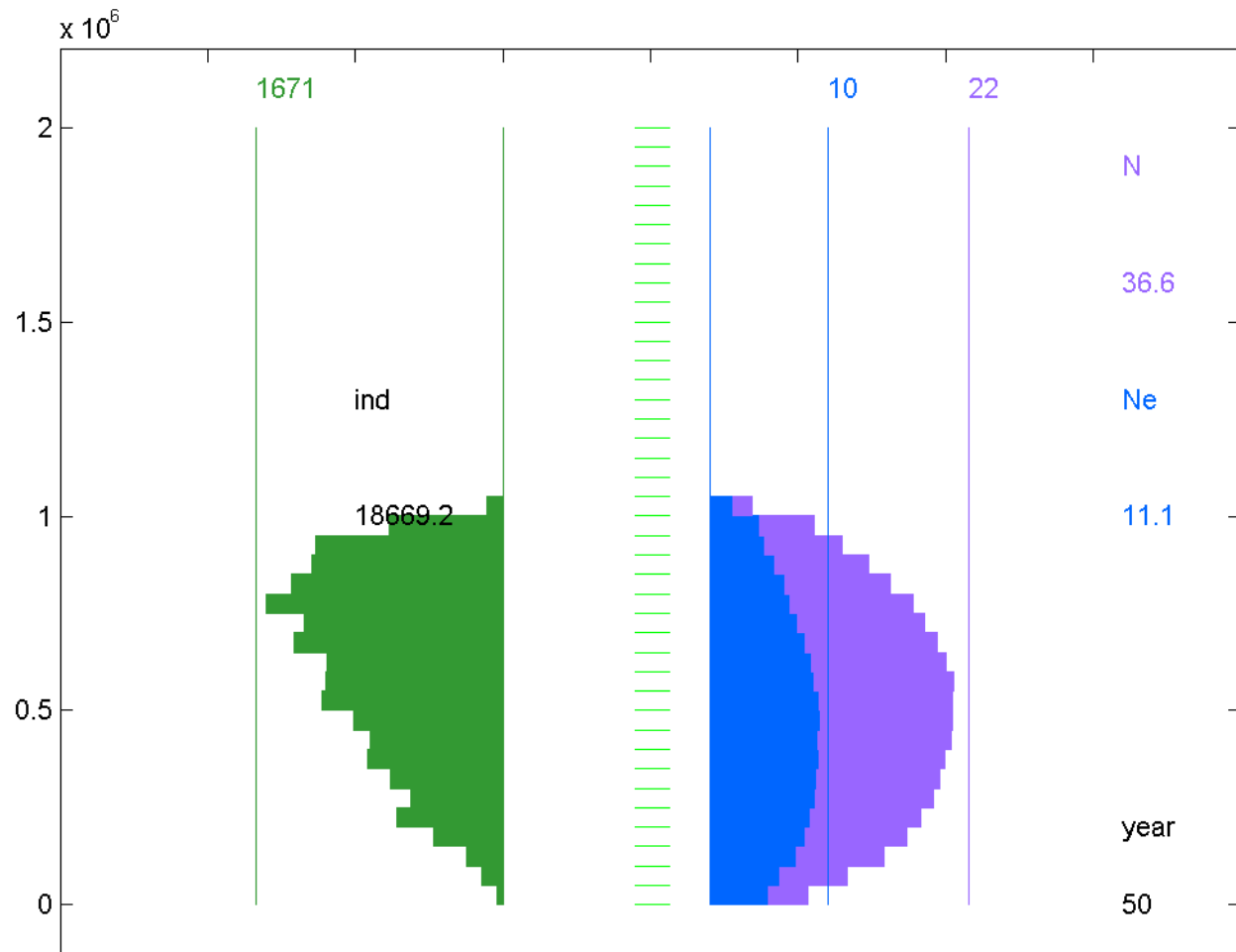
chance to disperse

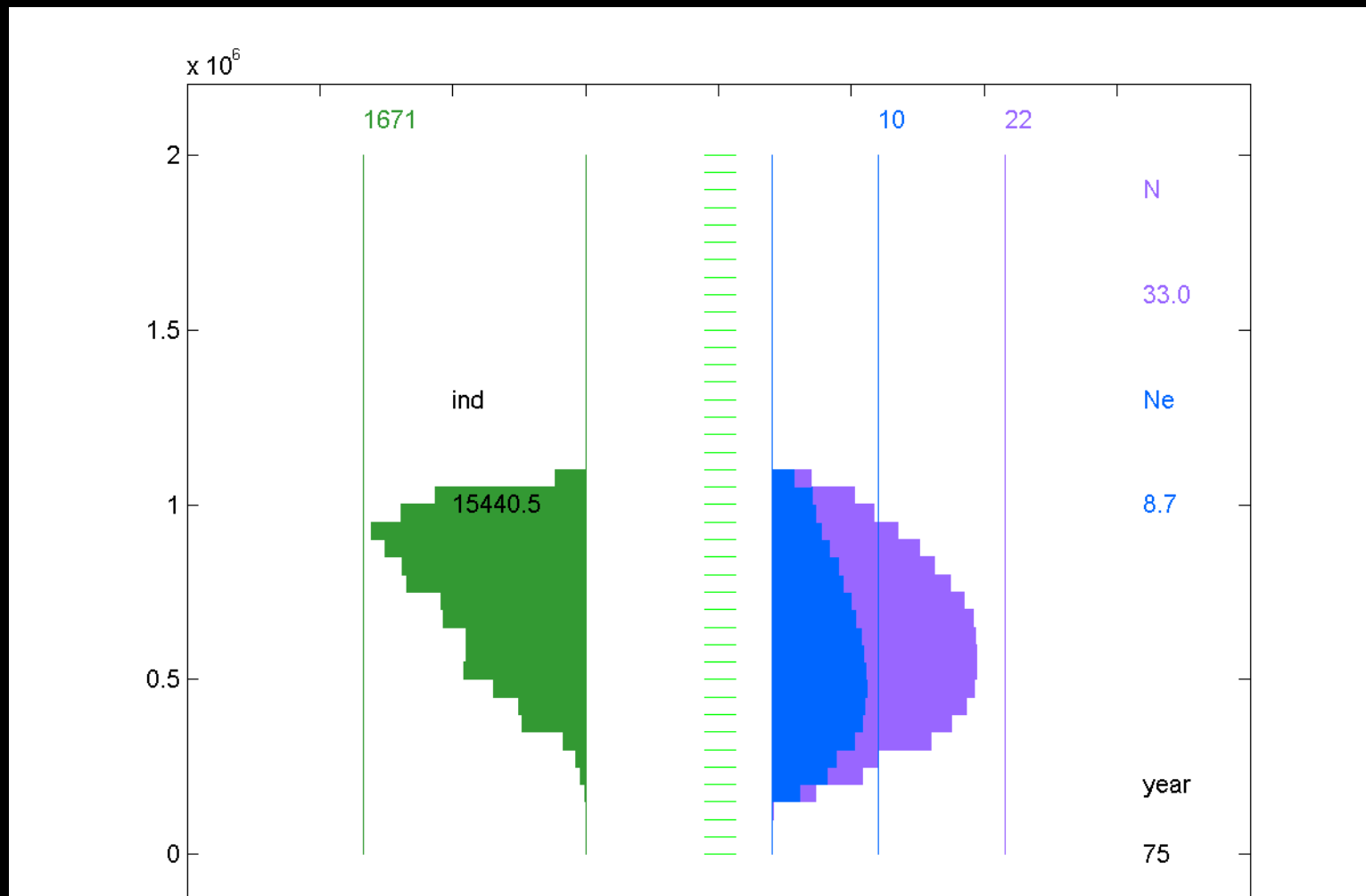


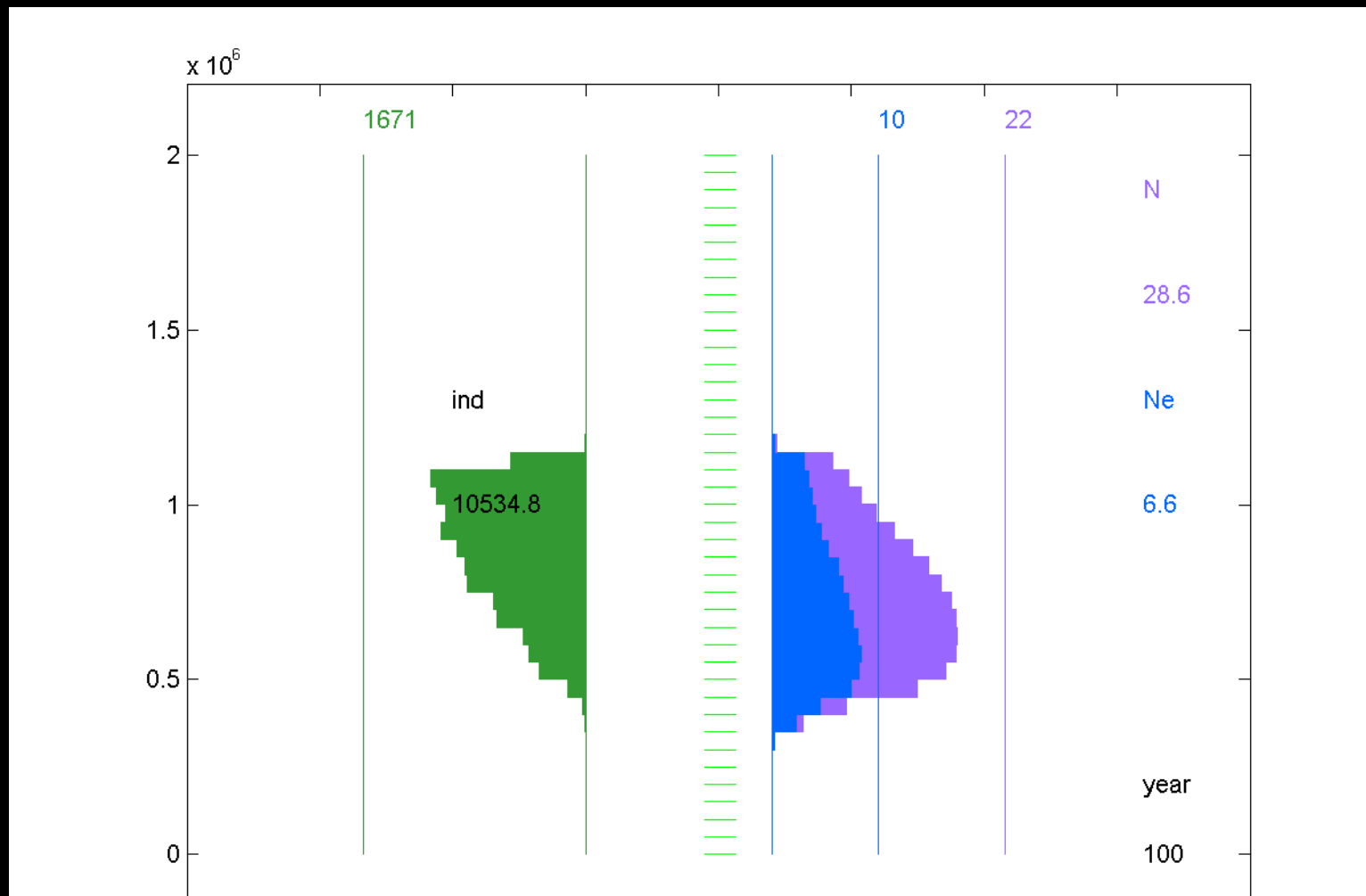


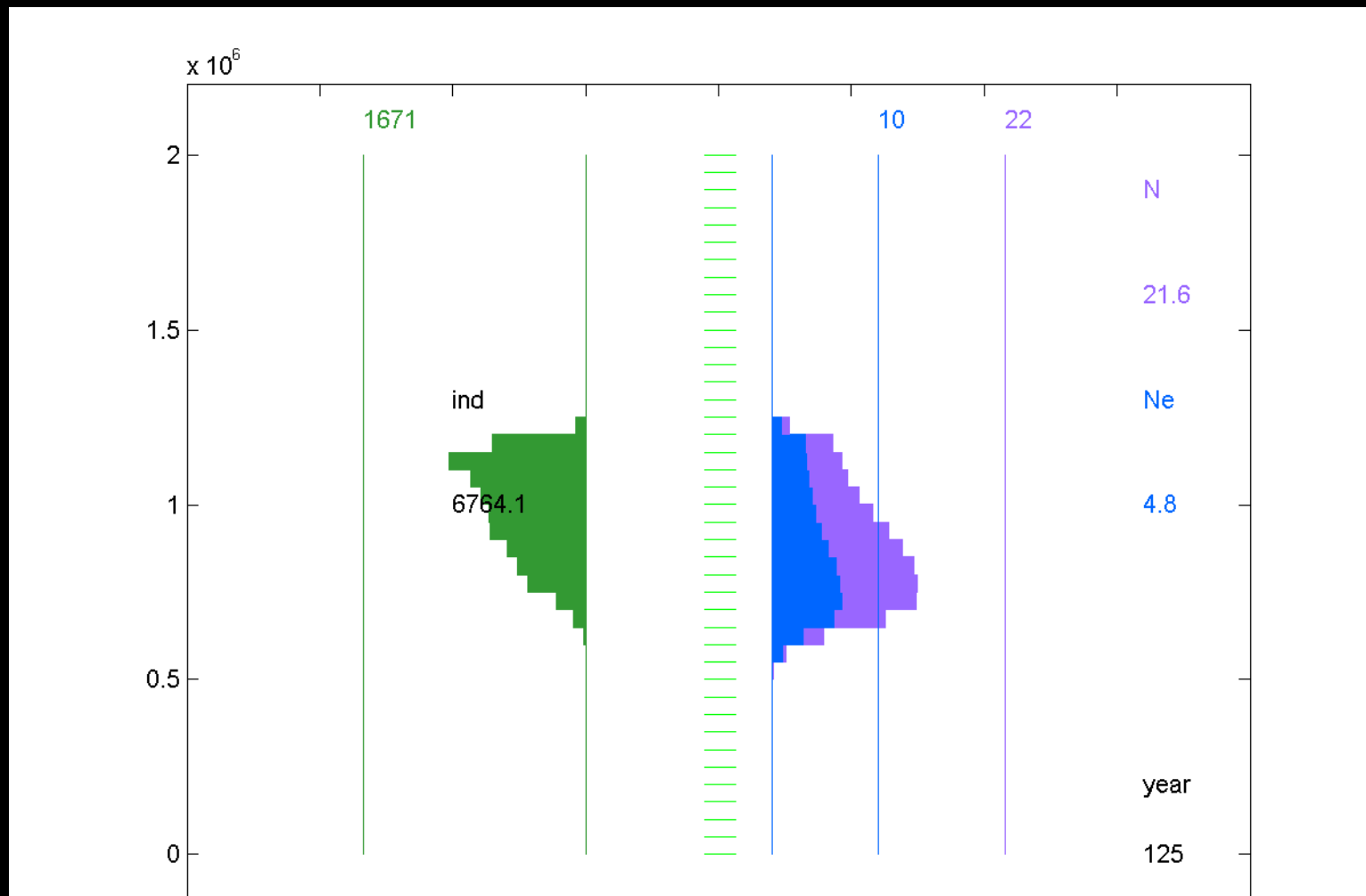
climate optimum: 400 km
 temperature speed: 4 °C so 8 km/year
 weather variability: 140 km

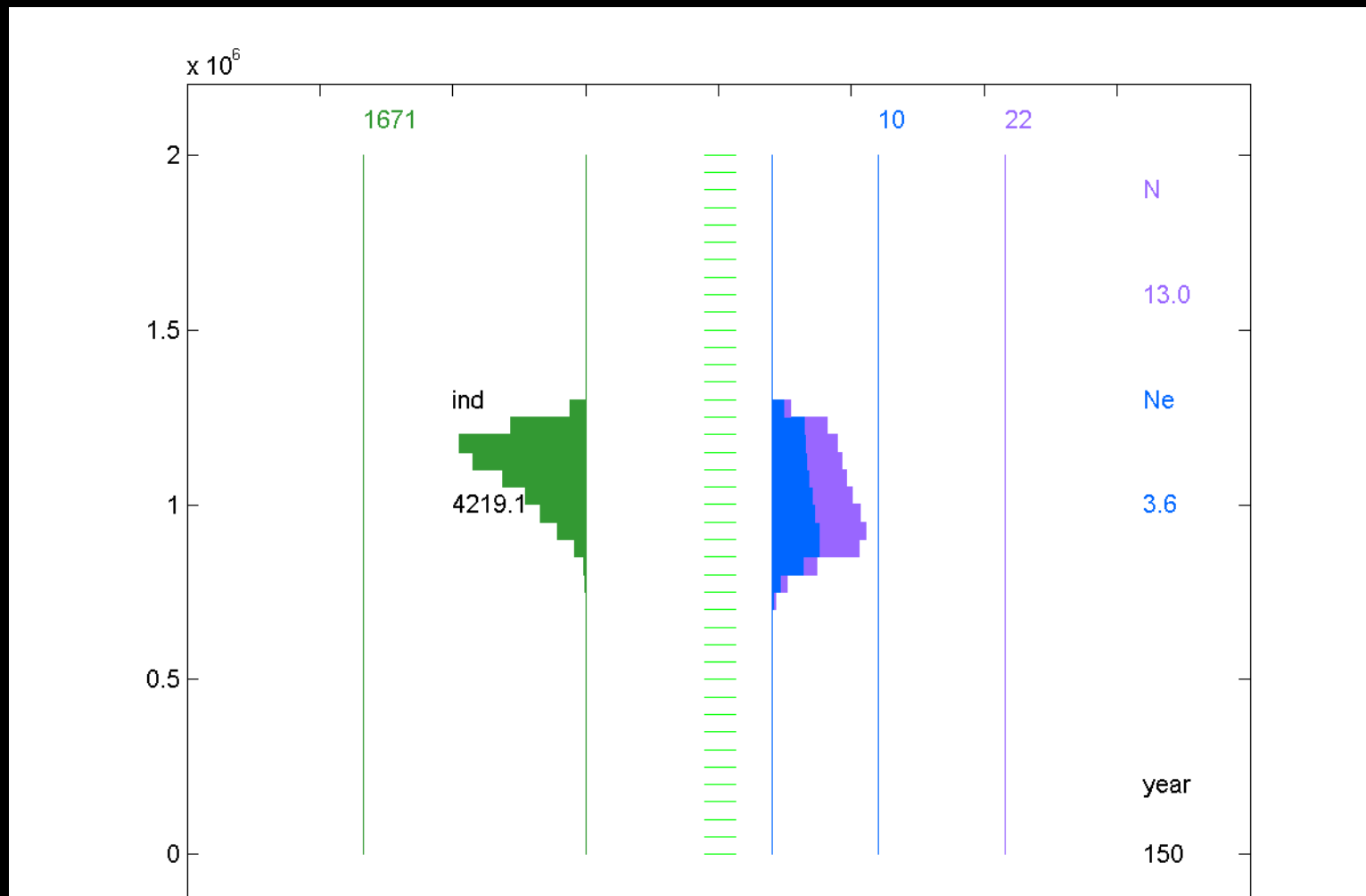


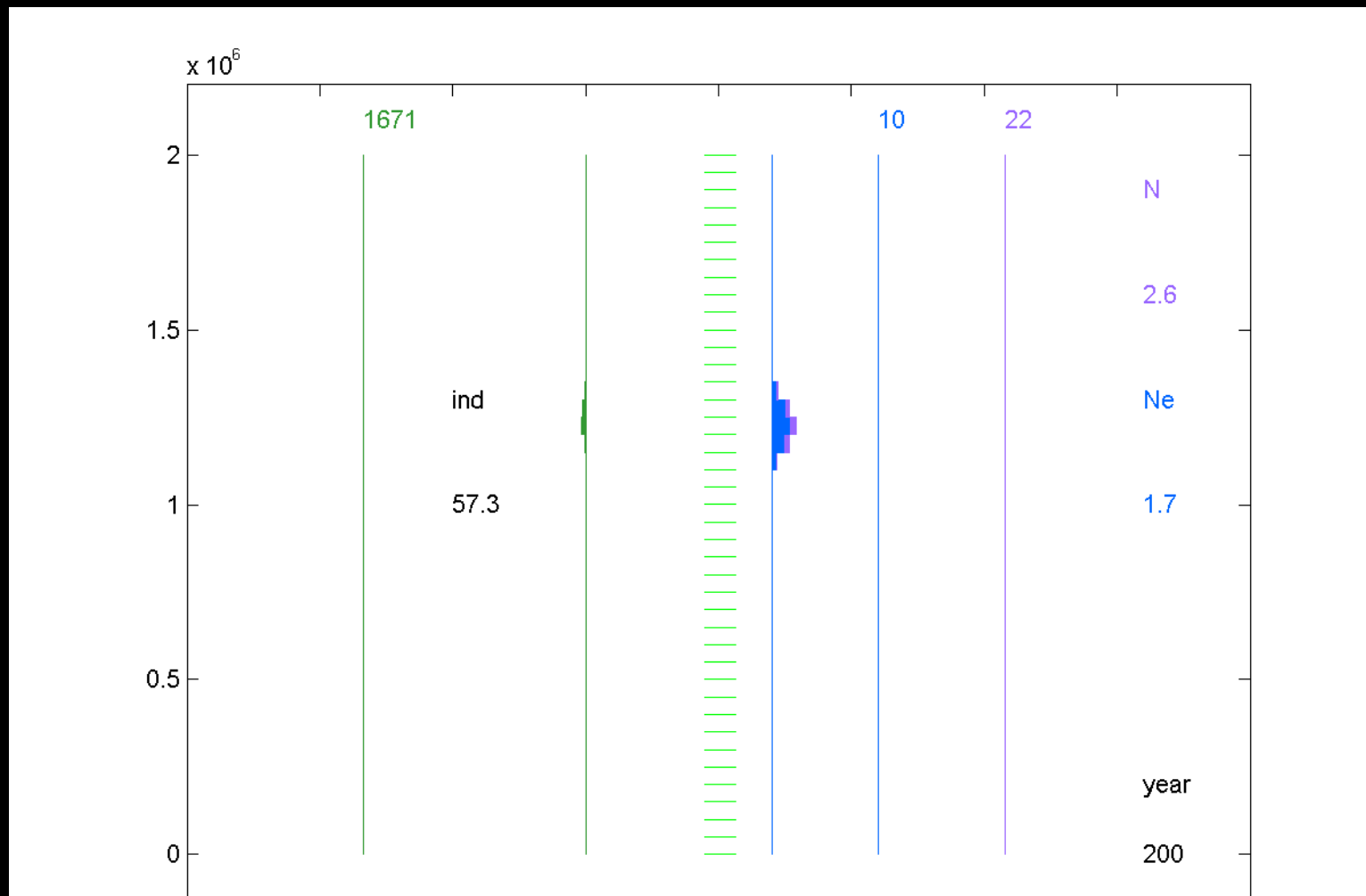


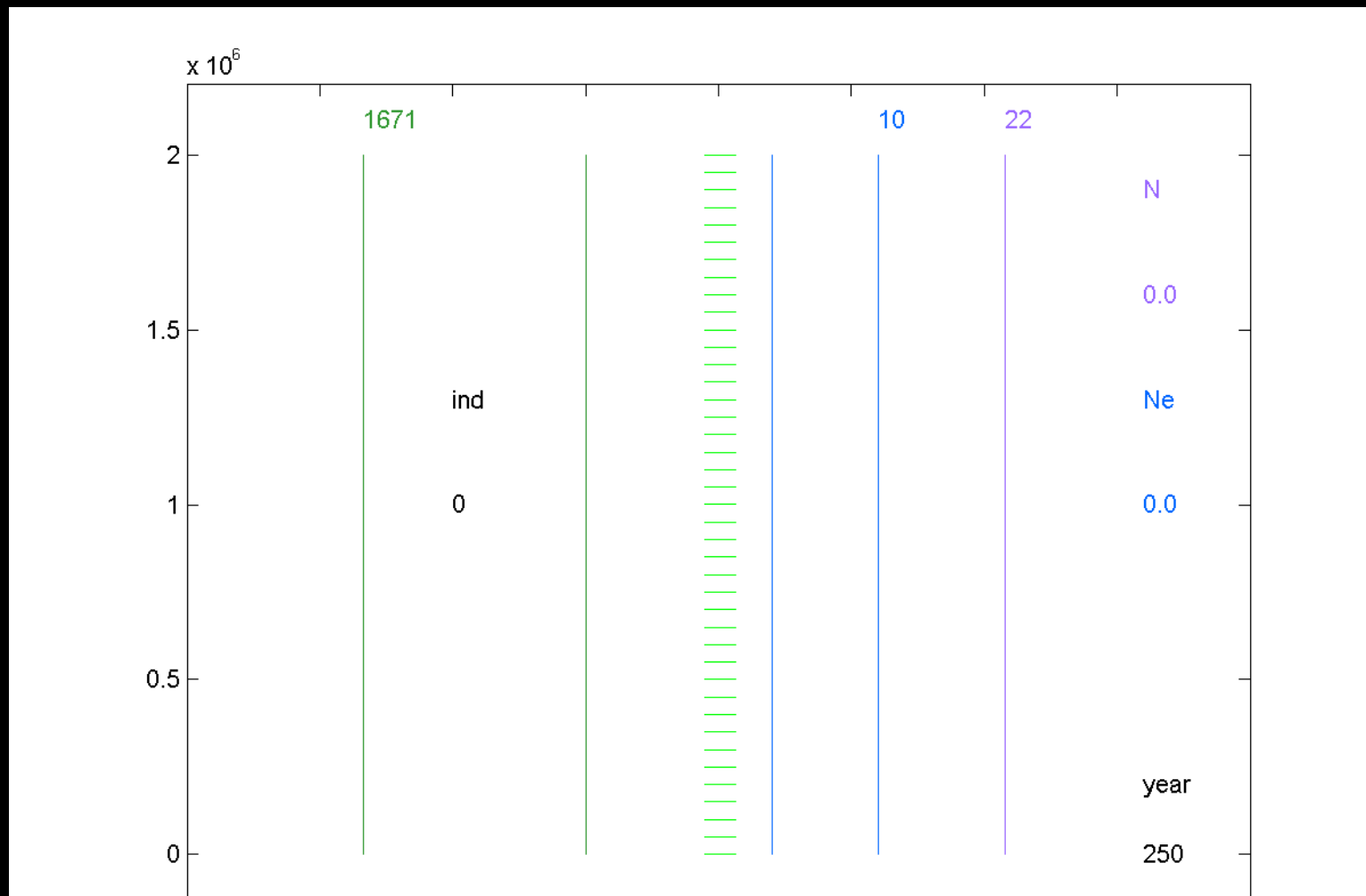




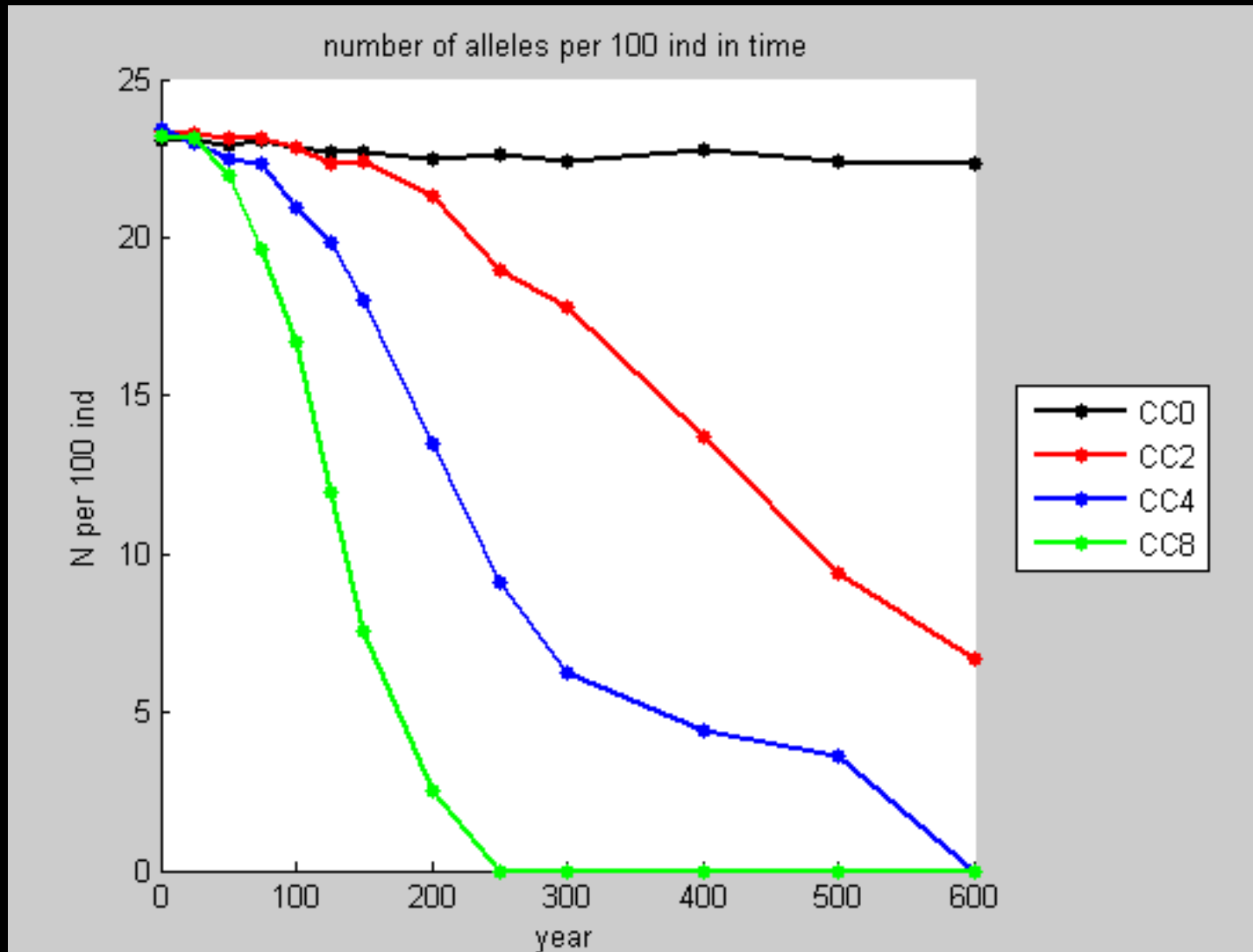








Corrected for number of individuals



Concluding

- This kind of models shows that even species with relatively high dispersal capacities may not be able to track suitable climate space
- All temperature increase scenarios show loss of standing genetic diversity as a combination of 'allele surfing' at the leading edge and 'allele wipe-out' at the trailing edge

Thank you

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