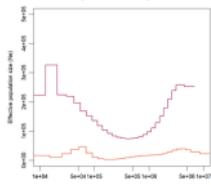


Plotted raw output

The PSMC analyses i=125 - b15 = 5 - p = "4<25*2+4*B"

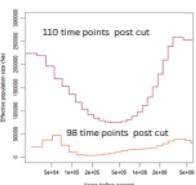
$$4+25*2+4+6=64$$

Total atomic intervals
127 time points for each species



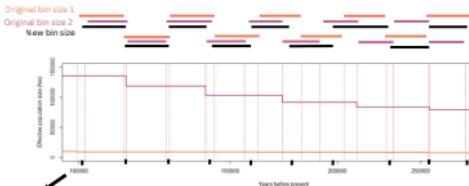
Step one Overlapping data

Cut to overlap between trends after disregarding the first 12 time points



This means that the new time grid should have 98 new time points.

Step two Common grid alignment

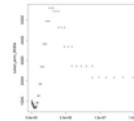


Step three Weighted interpolation of Ne in a comparable time series grid

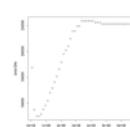
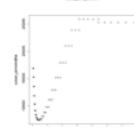
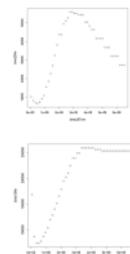
A Ne value is to be assigned for each trend at each new time point.
The Ne value is interpolated based on how the original bins span each new bin under the following rules:

- Inside bin → use Ne
 - Between bins → interpolate Ne (rarely happens)
 - Spans bins → average Ne
- Species 1**
- Species 2**
- New time points
- If the original bin had spanned the previous new then →

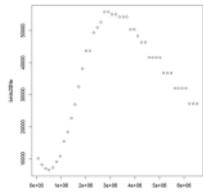
Plotted raw output



Resulting interpolation



Step four Correlation of Ne trajectories



Utilizing the BINCOR-package
(v 0.2.0): Estimate the correlation between two regular time series
<https://www.documentation.org/packages/BINCOR/>

