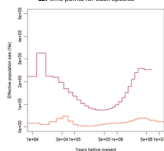


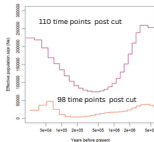
## Plotted raw output

The PSMC analyses (-N25 -t15 -r5 -p "4\*25\*2+4\*6")  
4\*25+4\*6=39 bins fitted  
4 \* 25\*2 = 4 \* 6 = 64 Total atomic intervals  
127 time points for each species



## Step one Overlapping data

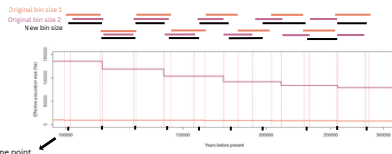
Cut to overlap between trends after disregarding the first 12 time points



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



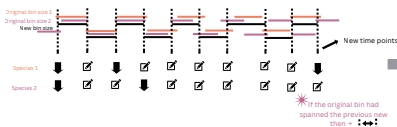
## Step two Common grid alignment



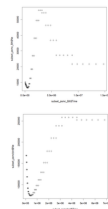
## Step three Weighted interpolation of Ne in the common time series grid

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:

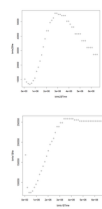
- Inside bin → use Ne
- Between bins → interpolate Ne (rarely happens)
- Spans bins → average Ne



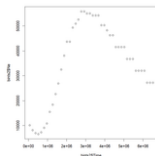
## Plotted raw output



## Resulting interpolation



## Step four Correlation of Ne trajectories



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

