

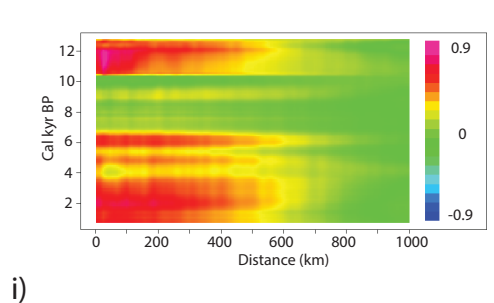
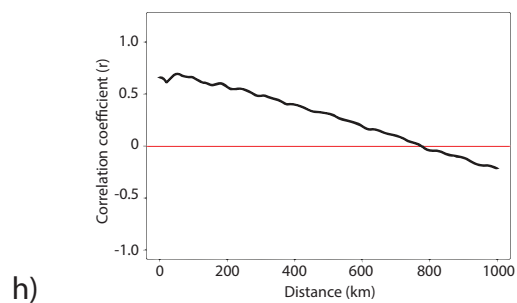
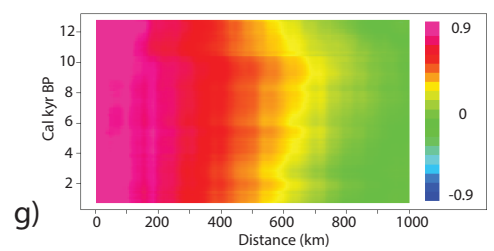
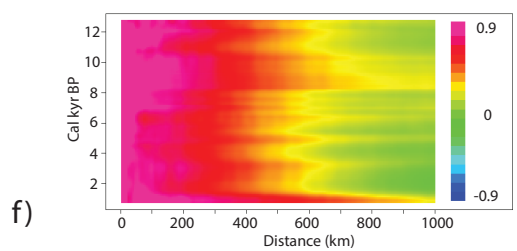
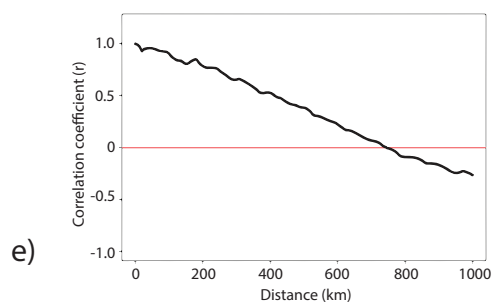
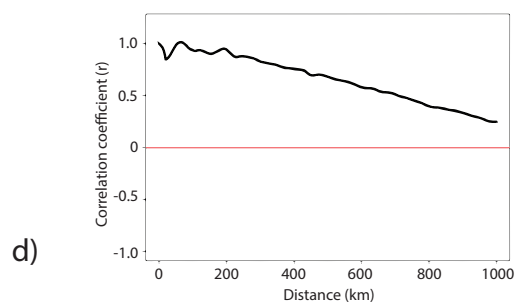
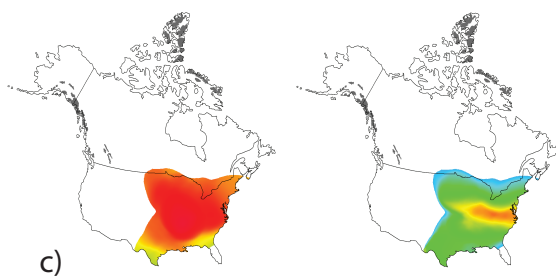
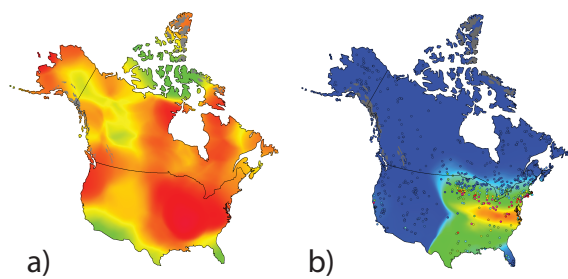
Appendix S1. Detailed description of methodology used in this paper.

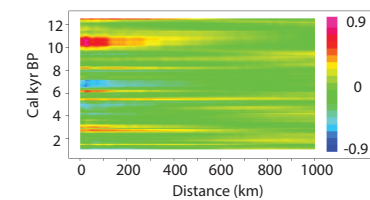
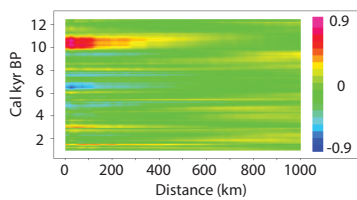
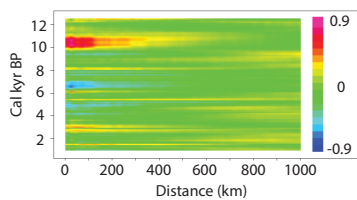
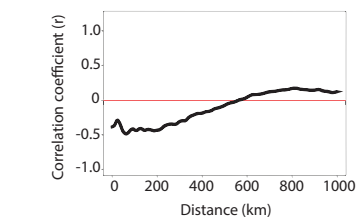
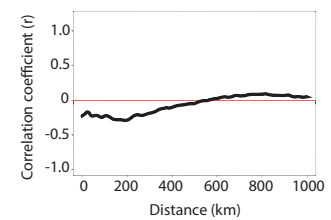
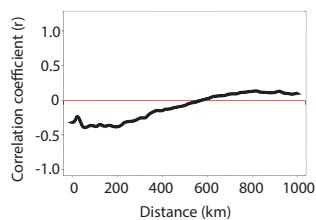
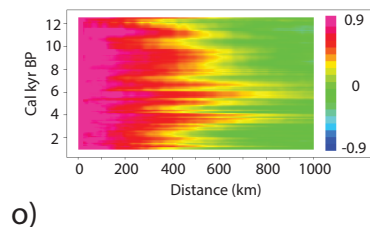
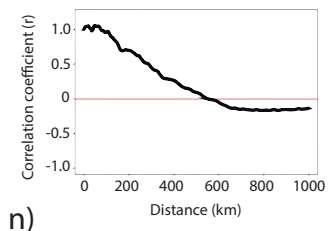
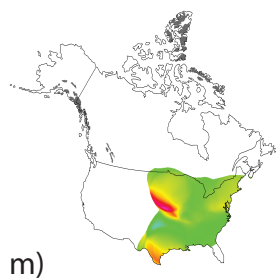
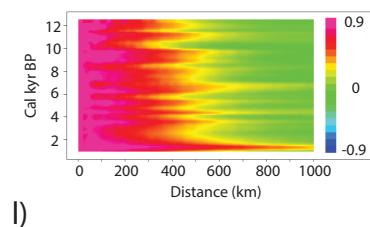
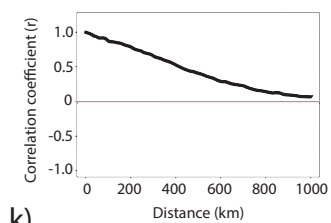
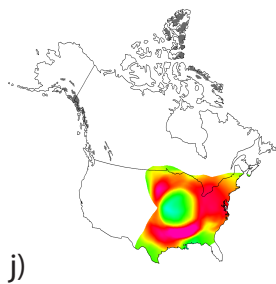
To illustrate the series of steps involved in the methodology, we include an example that shows how population is compared to one tree taxon (*Quercus*) for one time period (0.75ka). In total, figures were produced for 121 time periods and 10 taxa: boreal and widespread taxa (*Picea*, *Pinus*), major genera of the eastern deciduous forests (*Quercus*, *Castanea*), important food sources (*Carya*, *Juglans*), important trees of closed forests of the eastern deciduous forests (*Acer*, *Fagus*), and disturbance indicators (*Populus*, Poaceae). The results were obtained as follows:

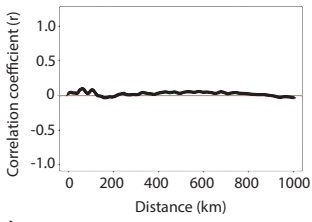
- a) Chaput et al. (2015) produced a series of maps showing the spatial distribution of human population density of North America through time. Each map was based on data from a 500-year window (Fig. S1a), and subsequent maps were produced at overlapping intervals of 100 years: 0.5-1.0 ka, 0.6-1.1 ka, ..., 12.5-13.0 ka. Smooth population maps were prepared from the point clouds (radiocarbon dates from archaeological sites; a subset of Figure 1b using data from the appropriate interval) using a kernel density estimator, which appropriately accounts for biases from inhomogeneous sampling strategies, taphonomic loss, and boundary effects. The present study is based on the period 0.75 ka - 12.75 ka, where the central age of the 500-yr period is used as the age index. This resulted in a total of 121 maps.
- b) A series of comparable maps showing the pollen percentage distributions was prepared for each of the 10 taxa. First, pollen percentages were temporally smoothed to the target ages for each site individually. Then, an estimator from kernel regression (Kriesche et al., unpubl.) was used to determine the spatial distribution of pollen percentages at the central age of each 500-year time period (Fig. S1b), resulting in a comparable set of 121 maps per taxon. To enable comparability, the same configurations of the estimators that were used in step (a) were used for the population maps, except that the population was illustrated on a logarithmic scale and the pollen percentages on a linear scale.
- c) Since it would be illogical to compare population and pollen values from outside the taxon range (where pollen percentages are practically zero), only the values of population (Fig. S1c, left map) within the range of the taxon (Fig. S1c right map) were studied. The range of a plant taxon at a given year was determined as the region where estimated pollen percentages have a value of at least 0.2 times the maximum of pollen percentages in that time-slice (Kriesche et al., unpubl.). The threshold of 0.2 was determined by visual comparison of the taxon ranges for most recent maps (computed with several different thresholds) with the modern range of the taxon. In the remainder of the study, only estimates of vegetation abundance and population within this range were used for correlation and cross-correlation analysis. A series of the maps, at 2000 year intervals are shown in S2. These estimated values were used in the following for correlation analyses.
- d) Spatial correlation functions of both population and pollen percentage maps (separately) were estimated for each time period; an example is shown of *Quercus* and population for the time period centred on 0.75 ka (Figs. S1d, S1e). Note that positive correlations are caused in part by the smoothing parameter of the kernel methods, but the strength of the functions also reflect the degree of spatial homogeneity in the underlying archaeological and paleoecological data.
- e) Step (d) produced 121 graphs for each taxon and for population. To facilitate interpretation and discussion of these results, all of the correlation functions for each taxon within the range and for population were summarized in one graph. These “heat maps” (Figs. S1f, S1g) show the spatial autocorrelation of the taxon or population through time.
- f) Spatial cross-correlation functions were estimated that describe statistical relationships between estimates of population density and pollen abundance of each taxon (both being

restricted to the estimated taxon range). There are 121 graphs for each taxon-population pair (Fig. S1h is an example for 0.75 ka), and the series of each taxon were summarized in one plot (Fig. S1i) which consists of 121 cross-correlation functions, which identify times of strong spatial correlation between population and taxa.

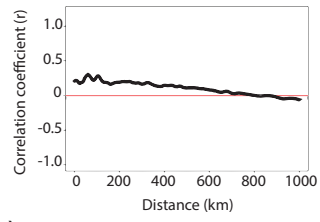
- g) To determine if *changes* in population density (Fig. S1j) and taxon abundance (Fig. S1m) were correlated, difference maps were produced subtracting maps with a temporal distance of 500 years to provide 116 maps of 500-year changes in population and taxon abundance (in 100-year steps). The series of these at 2000-yr intervals are shown in S2. These map pairs compare population and pollen changes that correspond to the same 500-year change interval and also to intervals that are shifted by the temporal lags +100, +200, ..., +1000 years, and -100, -200, ..., -1000 years since it seems plausible that vegetation does not respond to population change immediately but some hundred years later or vice versa. A positive lag means that vegetation change corresponds to a more recent 500-year change interval than change in population and a negative lag means the opposite.
- h) Similarly to the actual maps, spatial correlation functions were estimated for the difference maps of vegetation abundance (Fig. S1k) and population (Fig. S1n) for each 500-year change interval, and the series of correlation functions were summarized as heat maps (Figs. S1l, S1o). Cross-correlations between the difference maps for vegetation abundance and population were also prepared for lags of -1000, -900, ..., -100, 0, 100, ..., 900, 1000 years; selected examples are shown (Figs. S1p (lag 0), S1q (+100), S1r (-100), S1v (+300), S1w (+500), S1x (+1000), S1ab (-300), S1ac (-500), S1ad (-1000)) and the comparable summaries for all time periods are shown as heat maps below the individual example cross-correlation graphs. Inspection of these figures shows that in general we obtained similar cross-correlation results for similar lags, which arise in part from the temporal smoothing parameters, but also due to the association between the fields. For more distinct lags, however, larger differences in cross-correlation functions are observed.
- i) Finally, the mean cross-correlations between differences in taxon abundance and population density at small distances (between 30 and 200 km) are summarized in a matrix plot. These are the most expressive results summarizing all estimated statistical cross-correlations between changes in the considered taxon and population (for all temporal lags) in one graph to enable a meaningful interpretation (Fig. 2).
- j) Appendix S3 presents a taxon-by-taxon summary of the major results. A one-page set of heat maps is provided for each of the ten taxa which includes a summary of the cross-correlations between difference maps (a), correlation functions of the maps of taxon abundance (b), cross-correlations of maps of taxon abundance and population surfaces (c), correlation functions of differences in taxon abundance and cross-correlation of these maps with population (d) at zero lag (e), lag of +100 years (f), lag of -100 years (g), lag of +300 years (h), lag of -300 years (i), lag of +500 years (j), lag of -500 years (k), lag of +1000 years (l), lag of -1000 years (m).
- k) Nonparametric resampling methods were used to assess the significance of obtained correlation results (Kriesche et al., unpubl.). For each taxon a minimal correlation coefficient has been determined such that all estimated (cross-) correlations with higher absolute values are considered to indicate a real signal. These minimal values are ca. 0.15 (*Picea*, *Pinus*), 0.2 (*Acer*, *Carya*, *Juglans*), 0.25 (*Fagus*), 0.3 (*Castanea*, *Poaceae*, *Quercus*) and 0.4 (*Populus*).



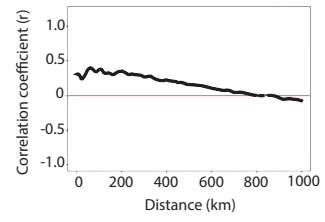




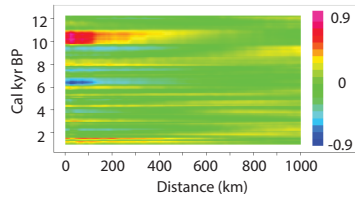
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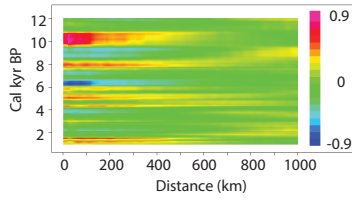
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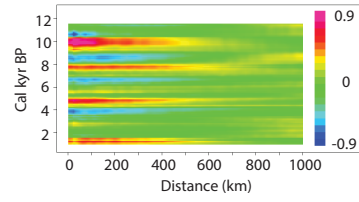
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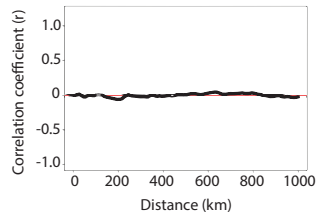
y)



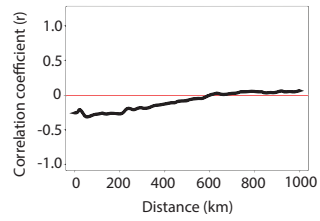
z)



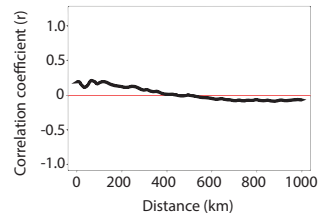
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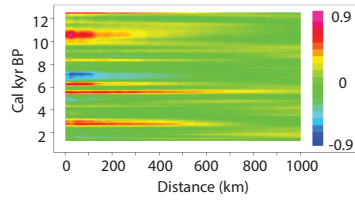
ab)



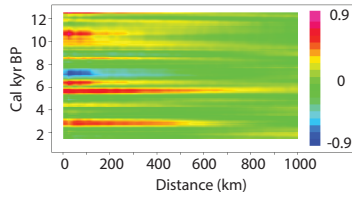
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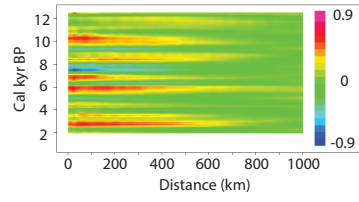
ad)



ae)



af)



ag)

Appendix S2. Series of 10 pages, one page per taxon, showing maps at 2000 year intervals, illustrating taxon range and population density within that range, and change in taxon and change in population within the range. The taxa included are, in order: *Picea*, *Pinus*, *Quercus*, *Castanea*, *Juglans*, *Carya*, *Acer*, *Fagus*, *Populus*, *Poaceae*.

- a) Smoothed pollen abundances within the taxon range (with the range determined by a pollen threshold of 0.2 of the maximum for that taxon).
- b) Population density within the range of the taxon.
- c) Change maps of the pollen taxon, derived by subtracting one abundance map from the one 500 years earlier.
- d) Corresponding change maps for population.

Maps in columns a and b represent 2050, 4050, 6050, 8050, 10050, and 12050 cal yr BP from top to bottom. Maps in columns c and d represent 2050-2550, 4050-4550, 6050-6550, 8050-8550, 10050-10550, and 12050-12550 cal yr BP from top to bottom.

Picea Range

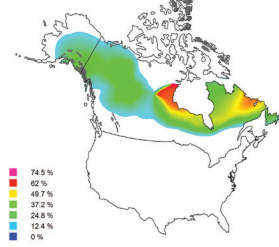
Population Density

Picea Change

Population Change

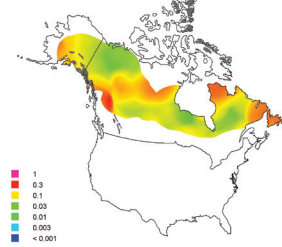
a)

Picea: taxon range threshold = 0.2 2050 BP



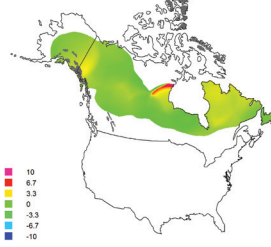
b)

Population in taxon range threshold = 0.2 2050 BP



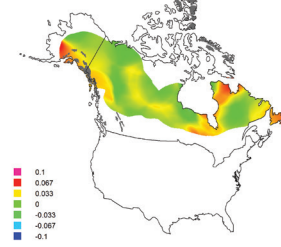
c)

change in Picea 2050-2550 BP



d)

change in Population 2050-2550 BP

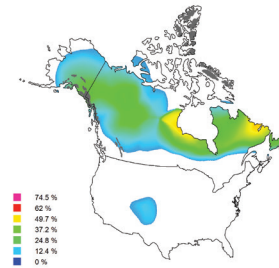


2050 BP

2050-2550 BP

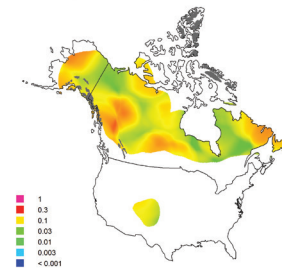
a)

Picea: taxon range threshold = 0.2 4050 BP



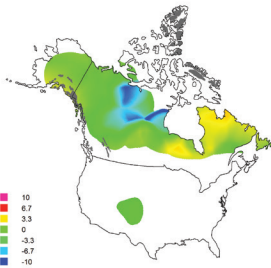
b)

Population in taxon range threshold = 0.2 4050 BP



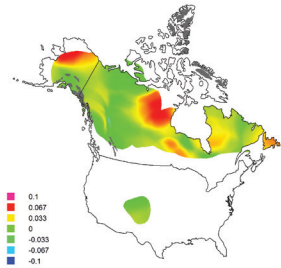
c)

change in Picea 4050-4550 BP



d)

change in Population 4050-4550 BP

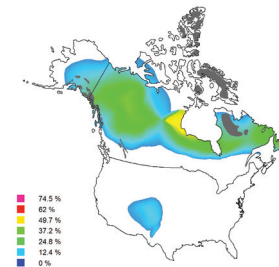


4050 BP

4050-4550 BP

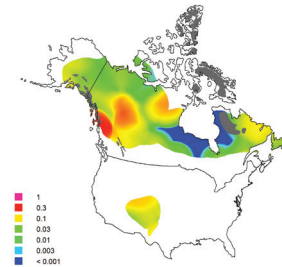
a)

Picea: taxon range threshold = 0.2 6050 BP



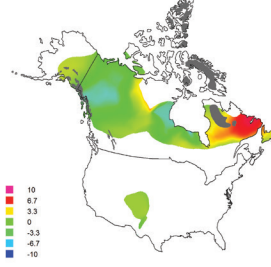
b)

Population in taxon range threshold = 0.2 6050 BP



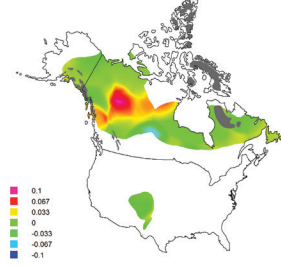
c)

change in Picea 6050-6550 BP



d)

change in Population 6050-6550 BP

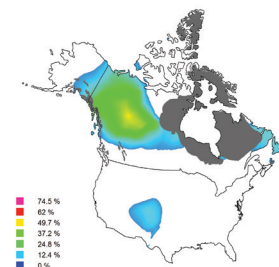


6050 BP

6050-6550 BP

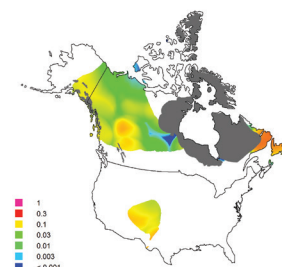
a)

Picea: taxon range threshold = 0.2 8050 BP



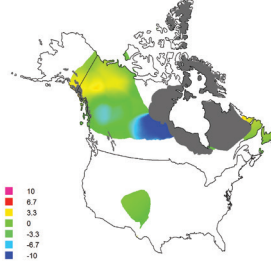
b)

Population in taxon range threshold = 0.2 8050 BP



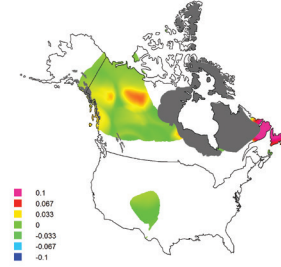
c)

change in Picea 8050-8550 BP



d)

change in Population 8050-8550 BP

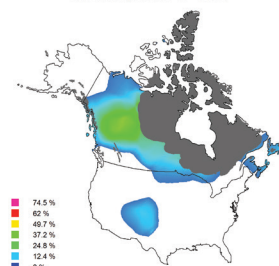


8050 BP

8050-8550 BP

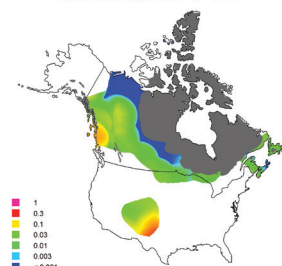
a)

Picea: taxon range threshold = 0.2 10050 BP



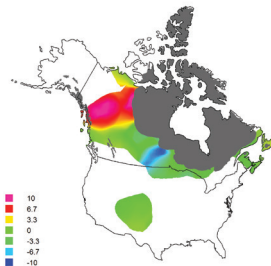
b)

Population in taxon range threshold = 0.2 10050 BP



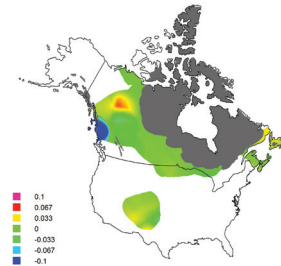
c)

change in Picea 10050-10550 BP



d)

change in Population 10050-10550 BP

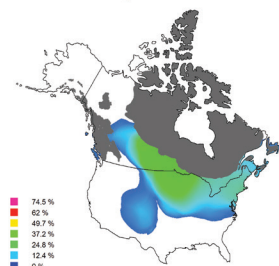


10050 BP

10050-10550 BP

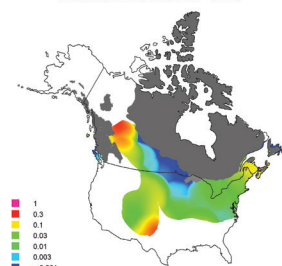
a)

Picea: taxon range threshold = 0.2 12050 BP



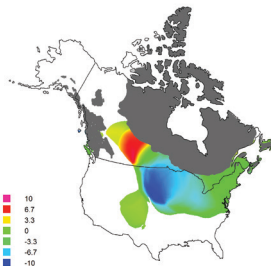
b)

Population in taxon range threshold = 0.2 12050 BP



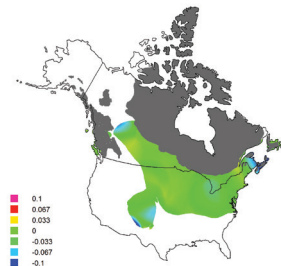
c)

change in Picea 12050-12550 BP



d)

change in Population 12050-12550 BP



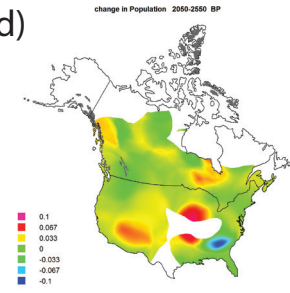
12050 BP

12050-12550 BP

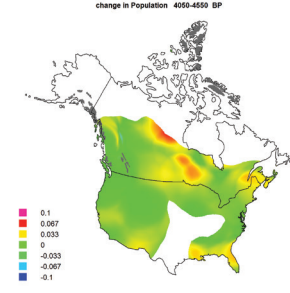
Population Change

d)

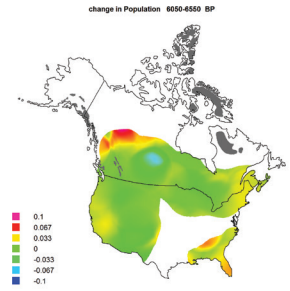
2050-2550 BP



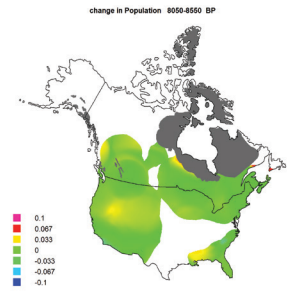
4050-4550 BP



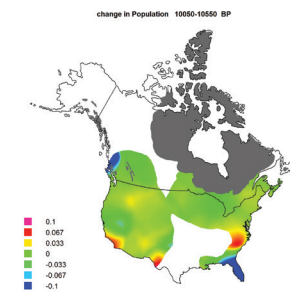
6050-6550 BP



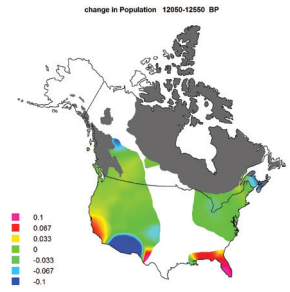
8050-8550 BP



10050-10550 BP



12050-12550 BP



Quercus Range

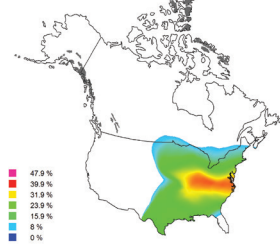
Population Density

Quercus Change

Population Change

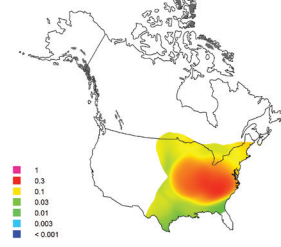
a)

Quercus: taxon range threshold = 0.2 2050 BP



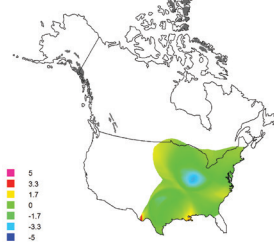
b)

Population in taxon range threshold = 0.2 2050 BP



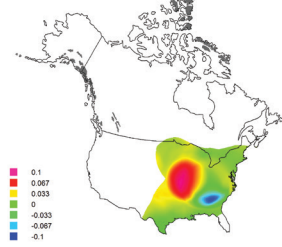
c)

change in Quercus 2050-2550 BP



d)

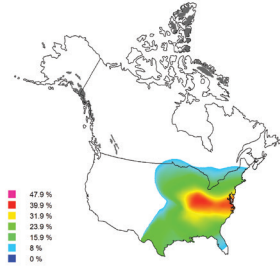
change in Population 2050-2550 BP



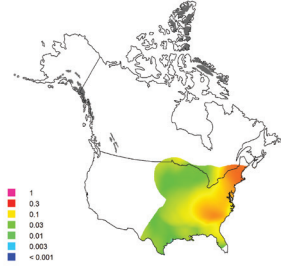
2050 BP

2050-2550 BP

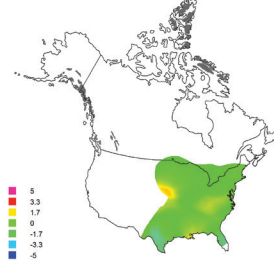
Quercus: taxon range threshold = 0.2 4050 BP



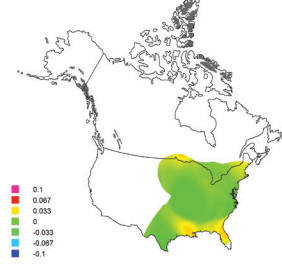
Population in taxon range threshold = 0.2 4050 BP



change in Quercus 4050-4550 BP



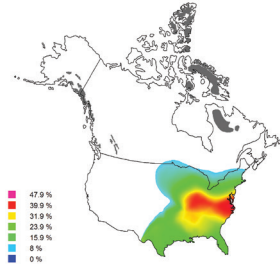
change in Population 4050-4550 BP



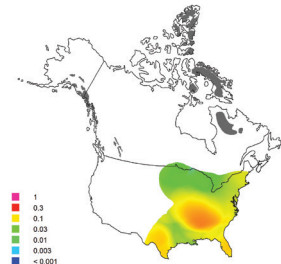
4050 BP

4050-4550 BP

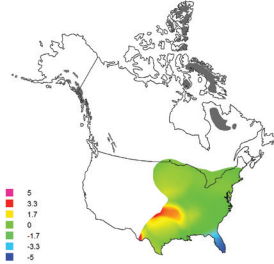
Quercus: taxon range threshold = 0.2 6050 BP



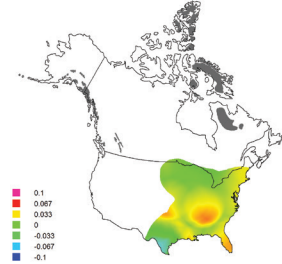
Population in taxon range threshold = 0.2 6050 BP



change in Quercus 6050-6550 BP



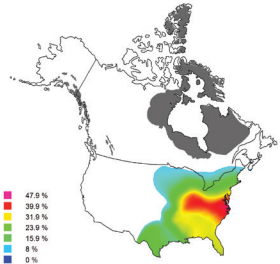
change in Population 6050-6550 BP



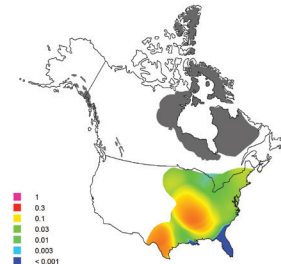
6050 BP

6050-6550 BP

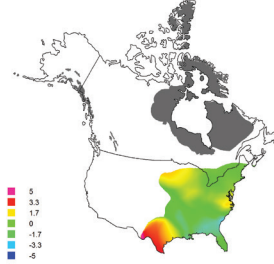
Quercus: taxon range threshold = 0.2 8050 BP



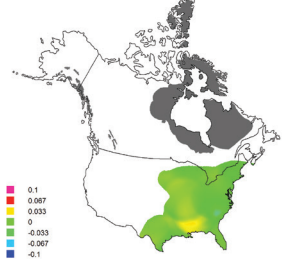
Population in taxon range threshold = 0.2 8050 BP



change in Quercus 8050-8550 BP



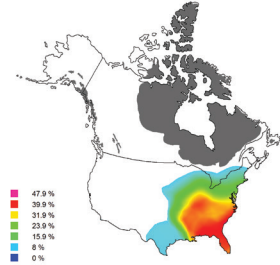
change in Population 8050-8550 BP



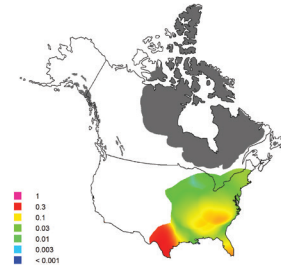
8050 BP

8050-8550 BP

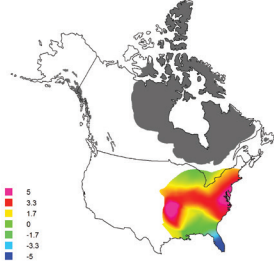
Quercus: taxon range threshold = 0.2 10050 BP



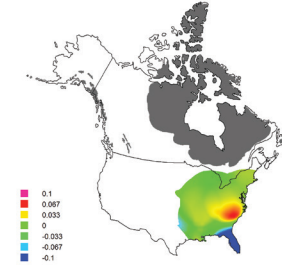
Population in taxon range threshold = 0.2 10050 BP



change in Quercus 10050-10550 BP



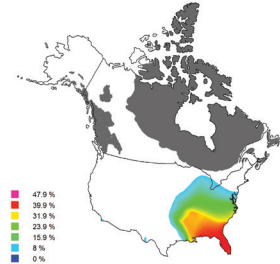
change in Population 10050-10550 BP



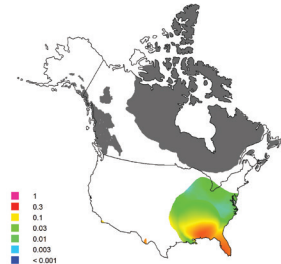
10050 BP

10050-10550 BP

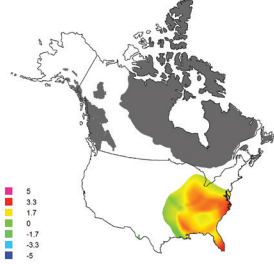
Quercus: taxon range threshold = 0.2 12050 BP



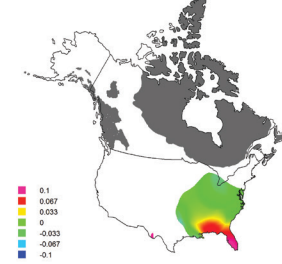
Population in taxon range threshold = 0.2 12050 BP



change in Quercus 12050-12550 BP



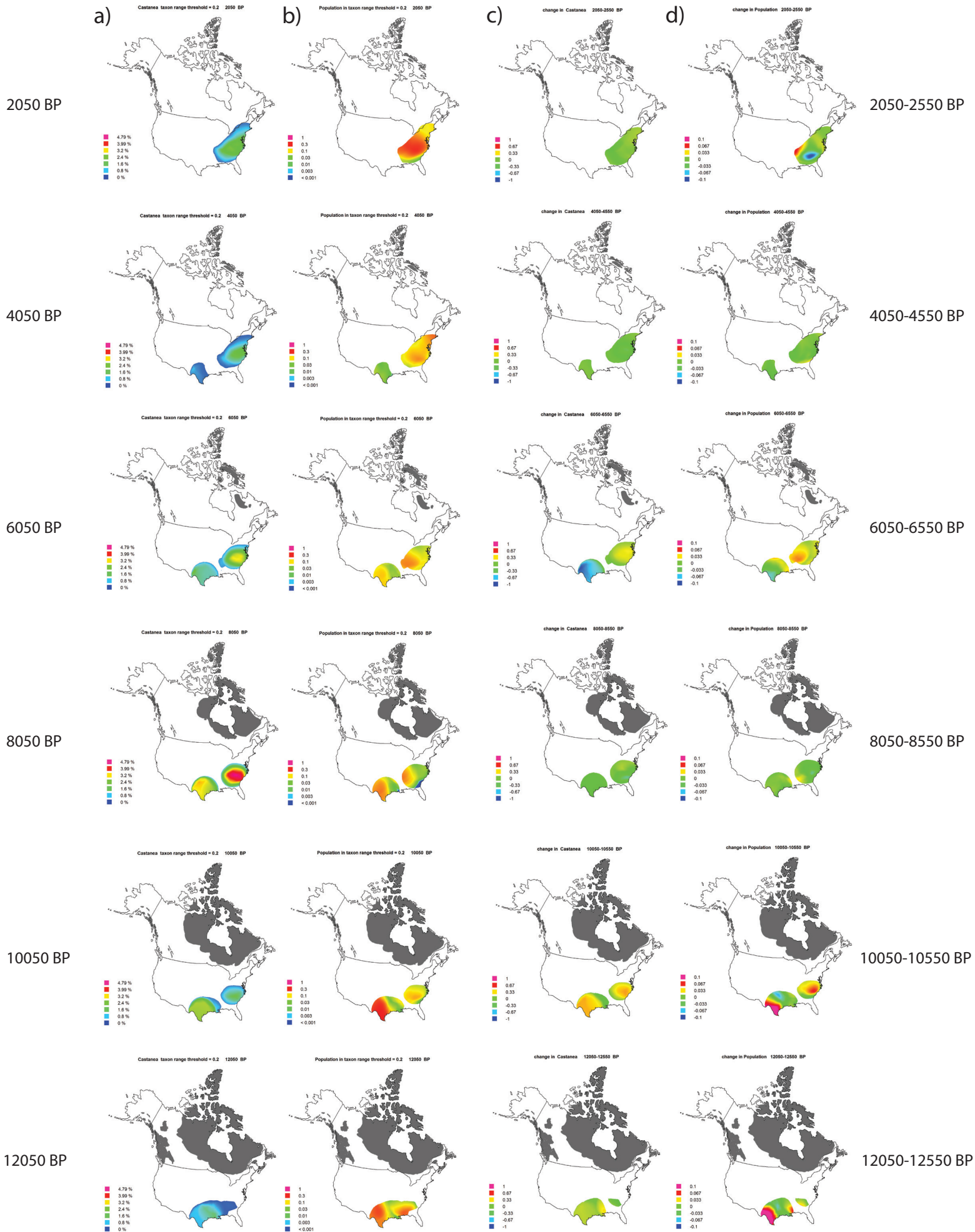
change in Population 12050-12550 BP



12050 BP

12050-12550 BP

Castanea Range Population Density *Castanea* Change Population Change



Juglans Range

Population Density

Juglans Change

Population Change

a)

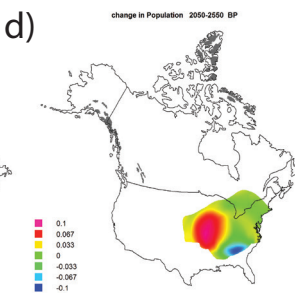
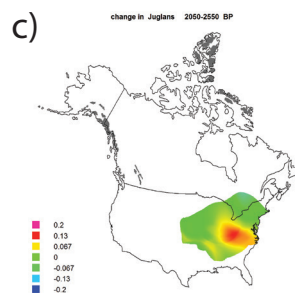
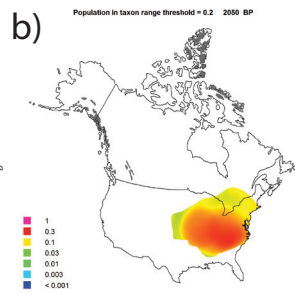
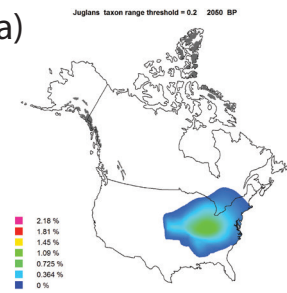
b)

c)

d)

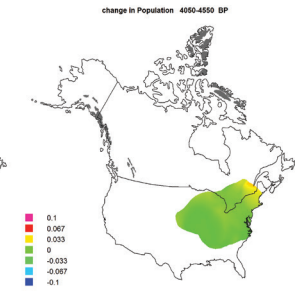
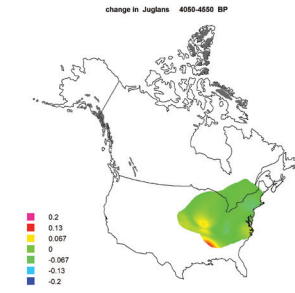
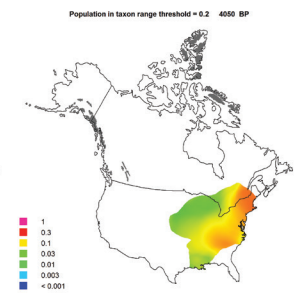
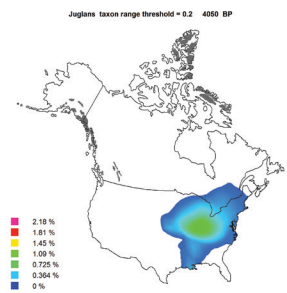
2050 BP

2050-2550 BP



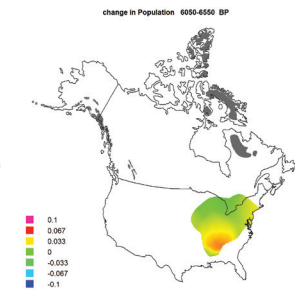
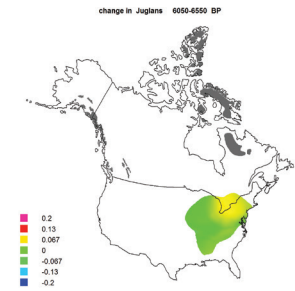
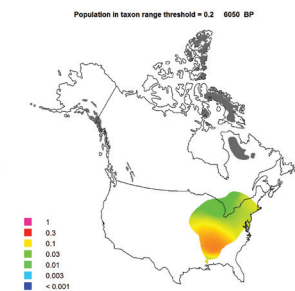
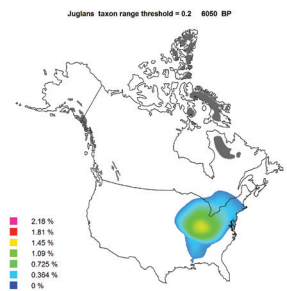
4050 BP

4050-4550 BP



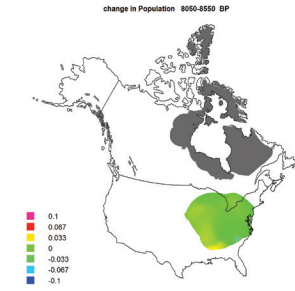
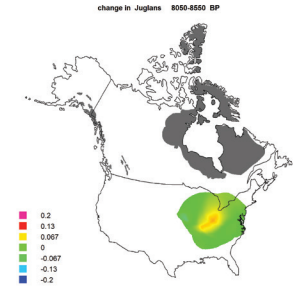
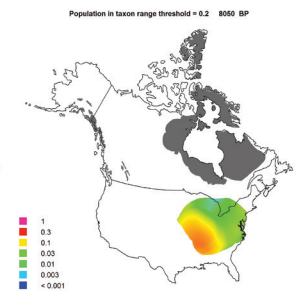
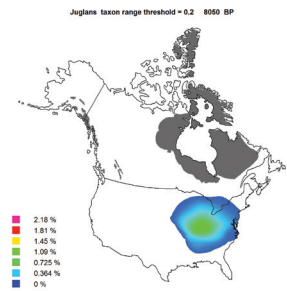
6050 BP

6050-6550 BP



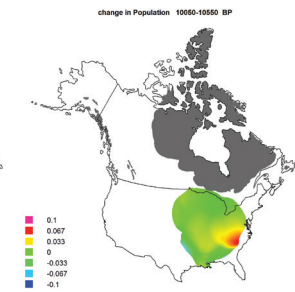
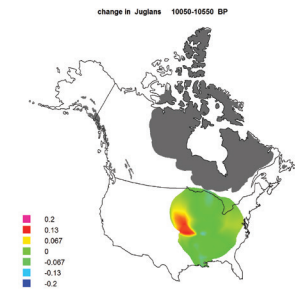
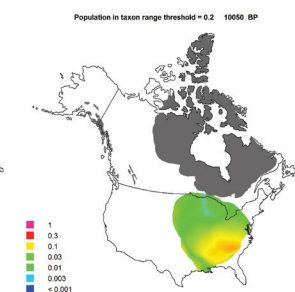
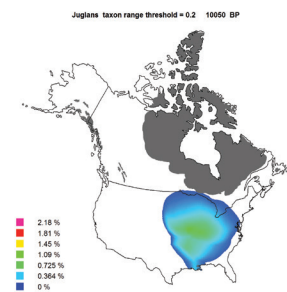
8050 BP

8050-8550 BP



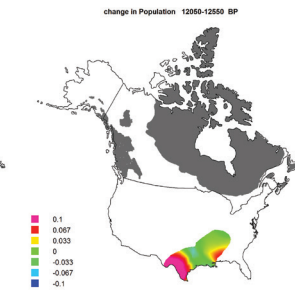
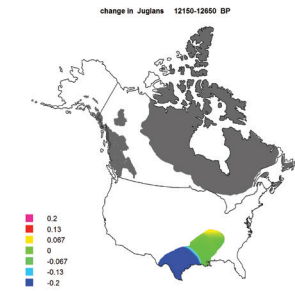
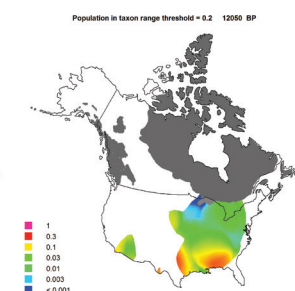
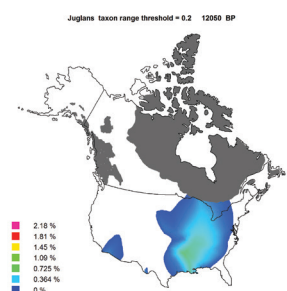
10050 BP

10050-10550 BP



12050 BP

12050-12550 BP



Carya Range

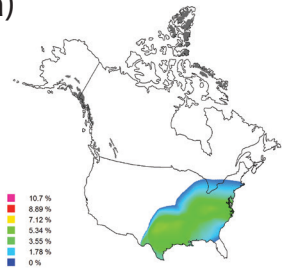
Population Density

Carya Change

Population Change

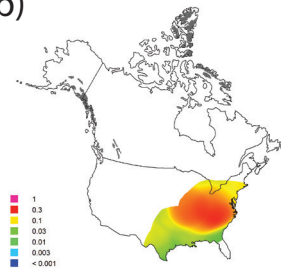
a)

Carya taxon range threshold = 0.2 2050 BP



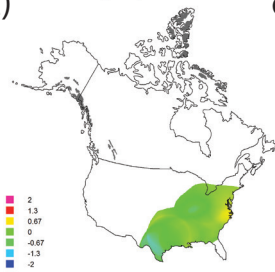
b)

Population in taxon range threshold = 0.2 2050 BP



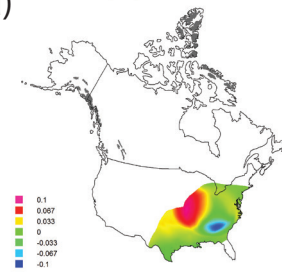
c)

change in Carya 2050-2550 BP



d)

change in Population 2050-2550 BP



2050 BP

2050-2550 BP

4050 BP

4050-4550 BP

6050 BP

6050-6550 BP

8050 BP

8050-8550 BP

10050 BP

10050-10550 BP

12050 BP

12050-12550 BP

Acer Range

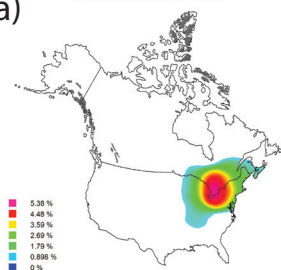
Population Density

Acer Change

Population Change

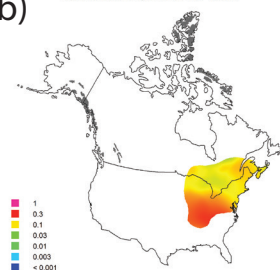
a)

Acer taxon range threshold = 0.2 2050 BP



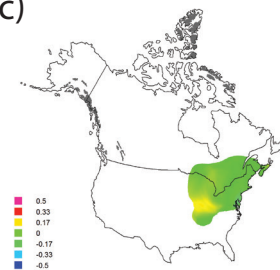
b)

Population in taxon range threshold = 0.2 2050 BP



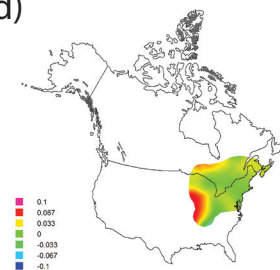
c)

change in Acer 2050-2550 BP



d)

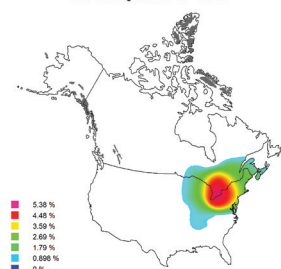
change in Population 2050-2550 BP



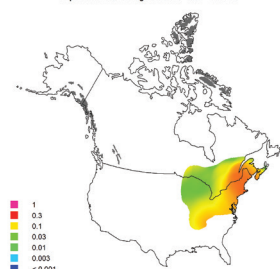
2050 BP

2050-2550 BP

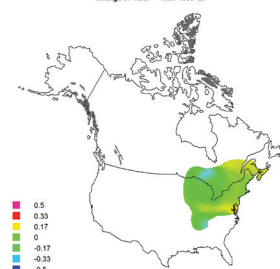
Acer taxon range threshold = 0.2 4050 BP



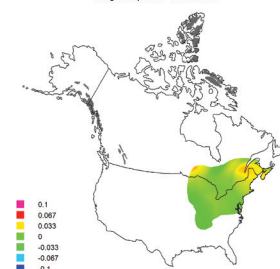
Population in taxon range threshold = 0.2 4050 BP



change in Acer 4050-4550 BP



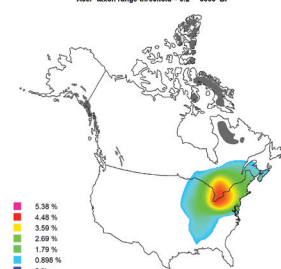
change in Population 4050-4550 BP



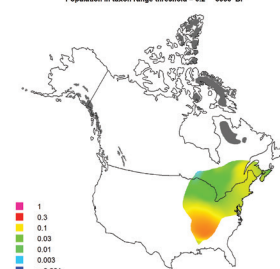
4050 BP

4050-4550 BP

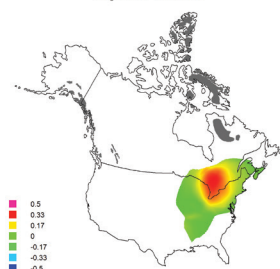
Acer taxon range threshold = 0.2 6050 BP



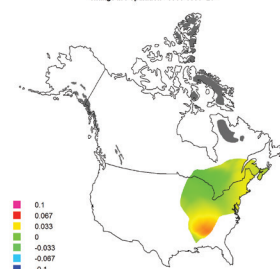
Population in taxon range threshold = 0.2 6050 BP



change in Acer 6050-6550 BP



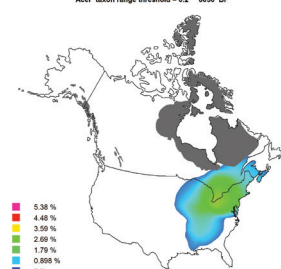
change in Population 6050-6550 BP



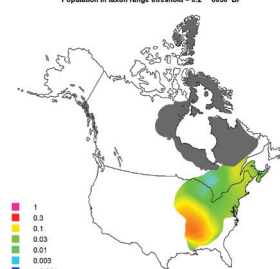
6050 BP

6050-6550 BP

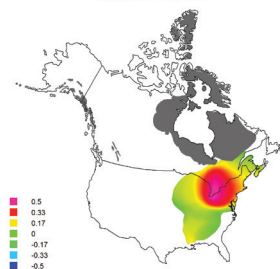
Acer taxon range threshold = 0.2 8050 BP



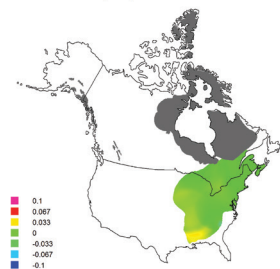
Population in taxon range threshold = 0.2 8050 BP



change in Acer 8050-8550 BP



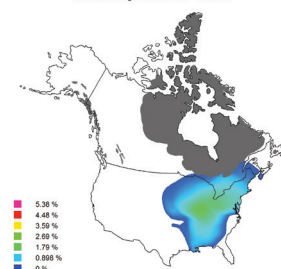
change in Population 8050-8550 BP



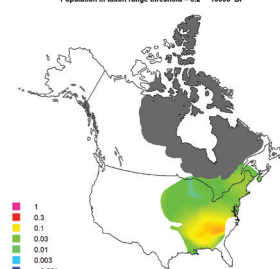
8050 BP

8050-8550 BP

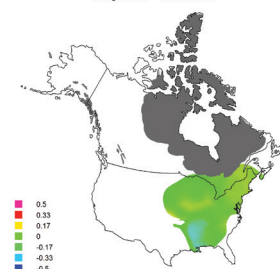
Acer taxon range threshold = 0.2 10050 BP



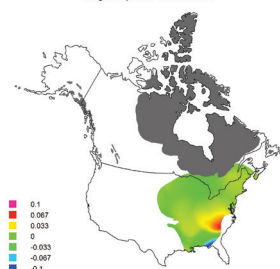
Population in taxon range threshold = 0.2 10050 BP



change in Acer 10050-10550 BP



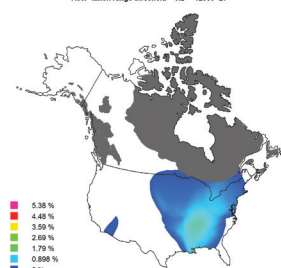
change in Population 10050-10550 BP



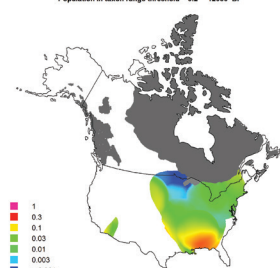
10050 BP

10050-10550 BP

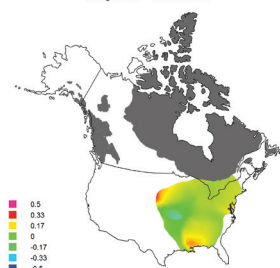
Acer taxon range threshold = 0.2 12050 BP



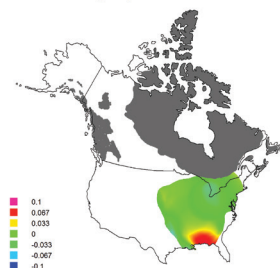
Population in taxon range threshold = 0.2 12050 BP



change in Acer 12050-12550 BP



change in Population 12050-12550 BP



12050 BP

12050-12550 BP

Fagus Range

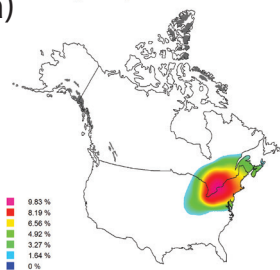
Population Density

Fagus Change

Population Change

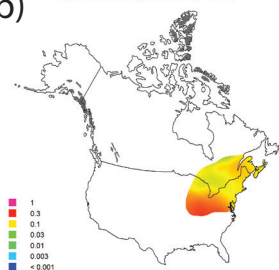
a)

Fagus taxon range threshold = 0.2 2050 BP



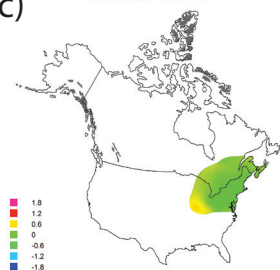
b)

Population in taxon range threshold = 0.2 2050 BP



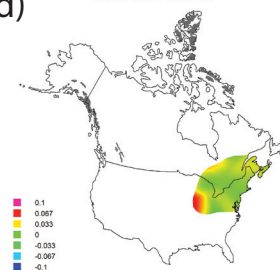
c)

change in Fagus 2050-2550 BP



d)

change in Population 2050-2550 BP

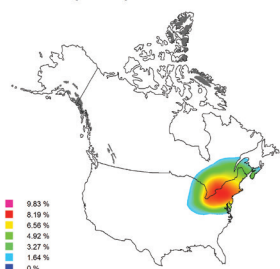


2050 BP

2050-2550 BP

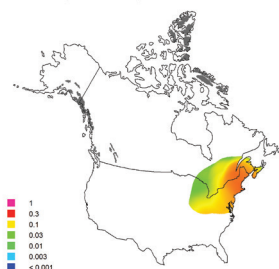
a)

Fagus taxon range threshold = 0.2 4050 BP



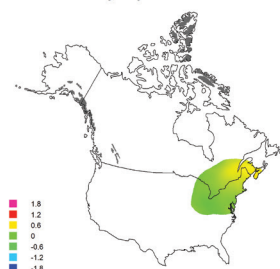
b)

Population in taxon range threshold = 0.2 4050 BP



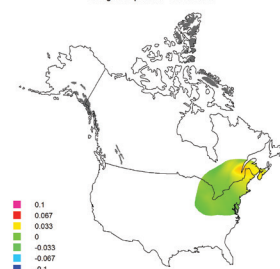
c)

change in Fagus 4050-4550 BP



d)

change in Population 4050-4550 BP

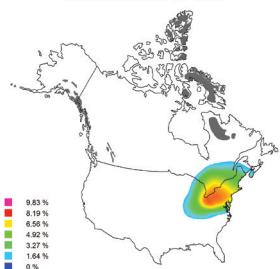


4050 BP

4050-4550 BP

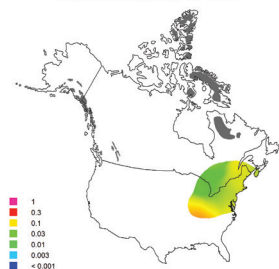
a)

Fagus taxon range threshold = 0.2 6050 BP



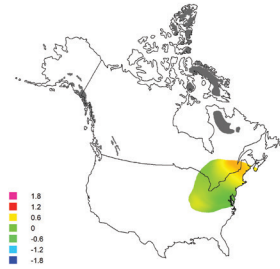
b)

Population in taxon range threshold = 0.2 6050 BP



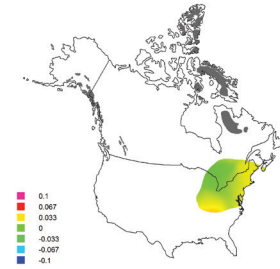
c)

change in Fagus 6050-6550 BP



d)

change in Population 6050-6550 BP

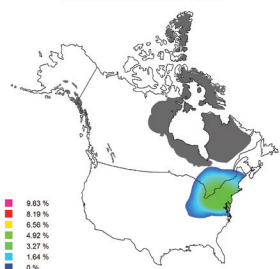


6050 BP

6050-6550 BP

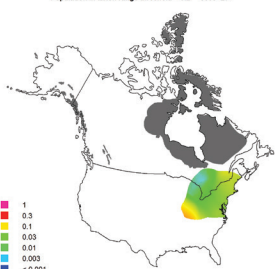
a)

Fagus taxon range threshold = 0.2 8050 BP



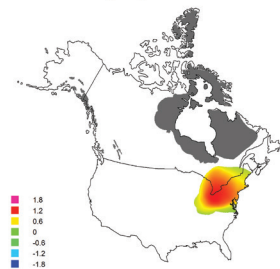
b)

Population in taxon range threshold = 0.2 8050 BP



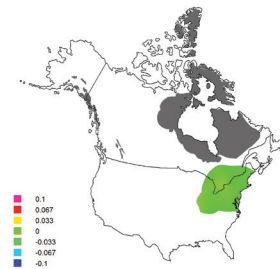
c)

change in Fagus 8050-8550 BP



d)

change in Population 8050-8550 BP

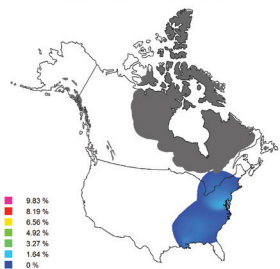


8050 BP

8050-8550 BP

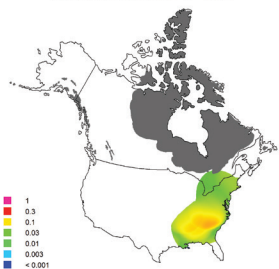
a)

Fagus taxon range threshold = 0.2 10050 BP



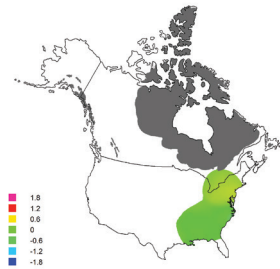
b)

Population in taxon range threshold = 0.2 10050 BP



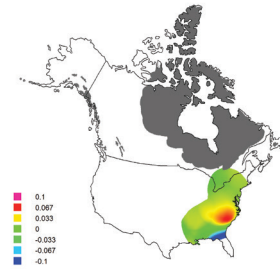
c)

change in Fagus 10050-10550 BP



d)

change in Population 10050-10550 BP

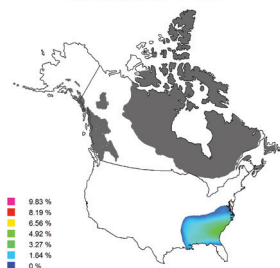


10050 BP

10050-10550 BP

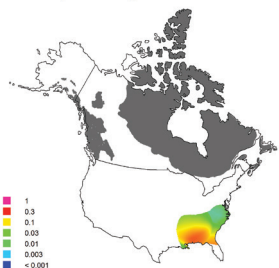
a)

Fagus taxon range threshold = 0.2 12050 BP



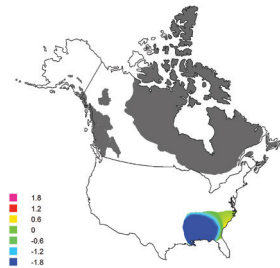
b)

Population in taxon range threshold = 0.2 12050 BP



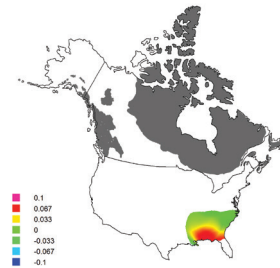
c)

change in Fagus 12050-12550 BP



d)

change in Population 12050-12550 BP



12050 BP

12050-12550 BP

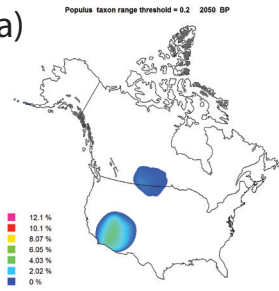
Populus Range

Population Density

Populus Change

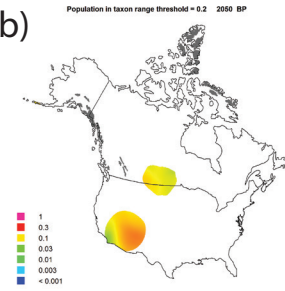
Population Change

a)

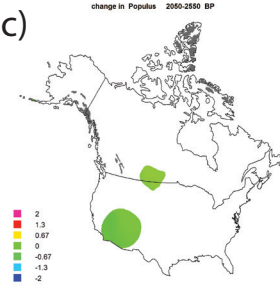


2050 BP

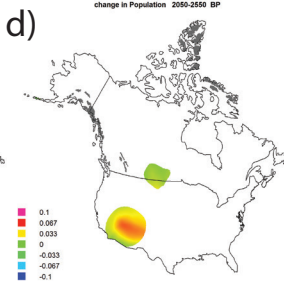
b)



c)

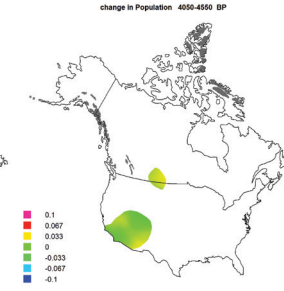
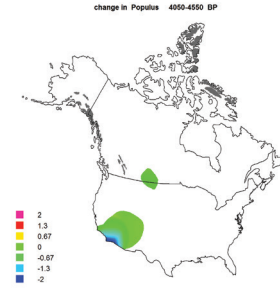
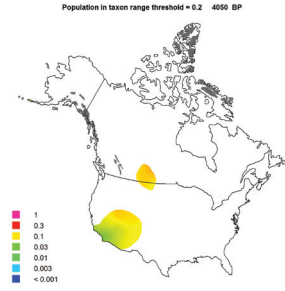
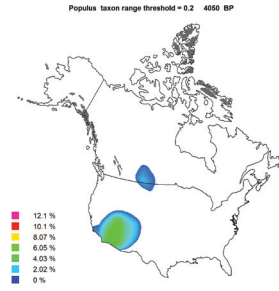


d)



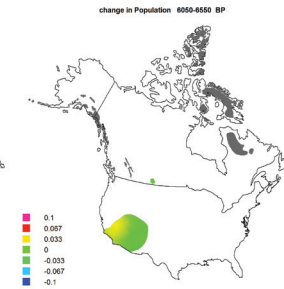
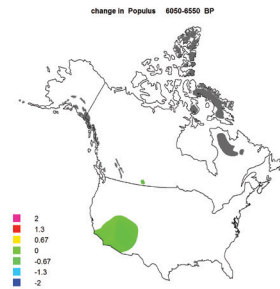
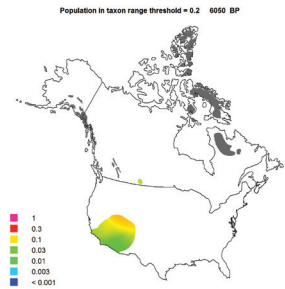
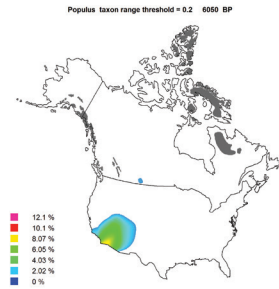
2050-2550 BP

4050 BP



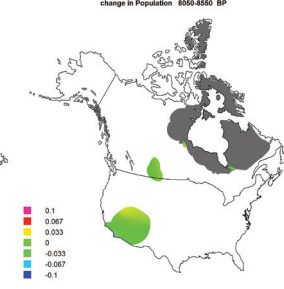
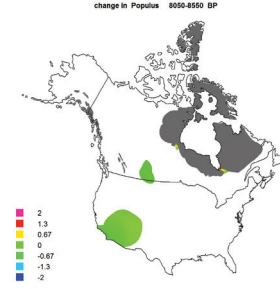
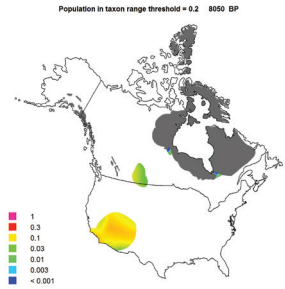
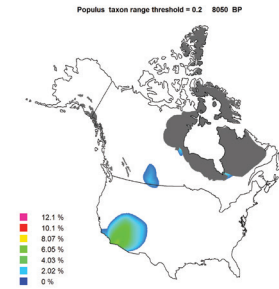
4050-4550 BP

6050 BP



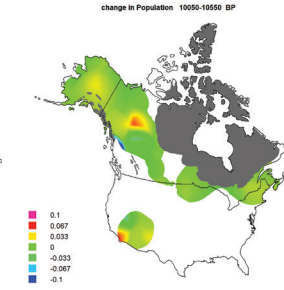
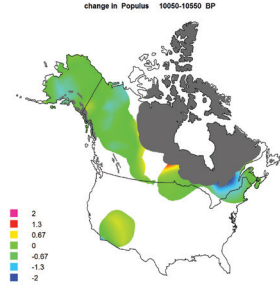
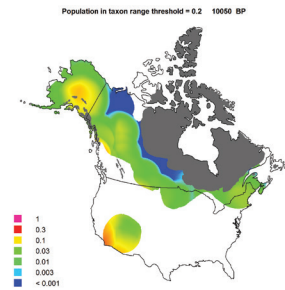
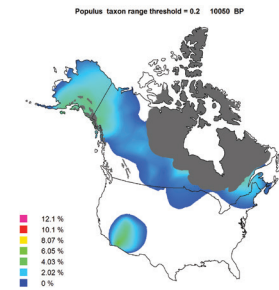
6050-6550 BP

8050 BP



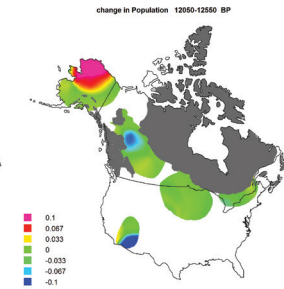
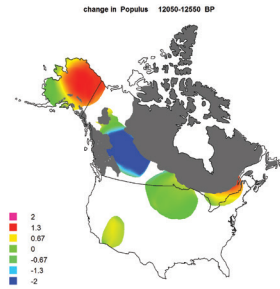
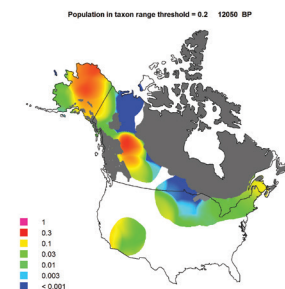
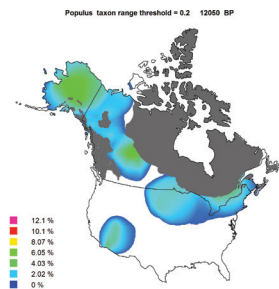
8050-8550 BP

10050 BP



10050-10550 BP

12050 BP



12050-12550 BP

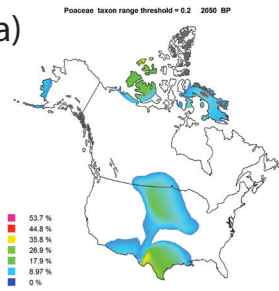
Poaceae Range

Population Density

Poaceae Change

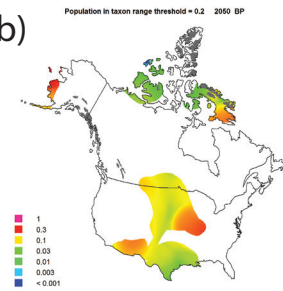
Population Change

a)

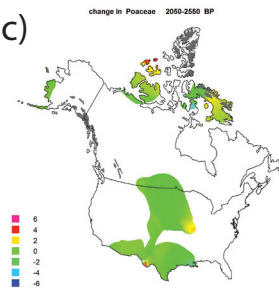


2050 BP

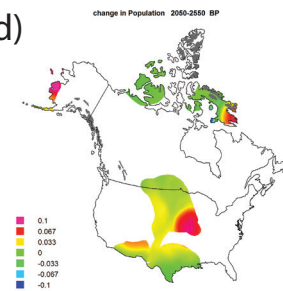
b)



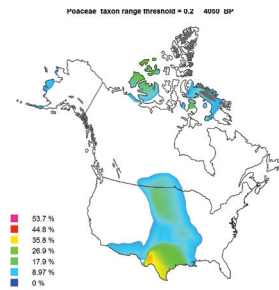
c)



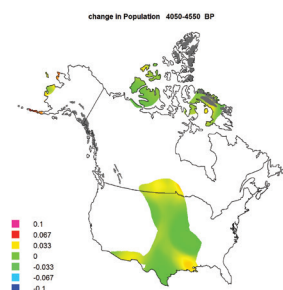
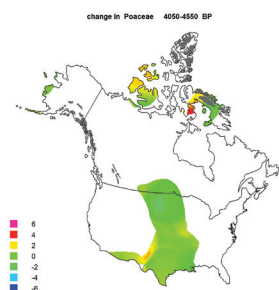
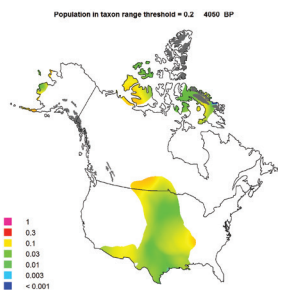
d)



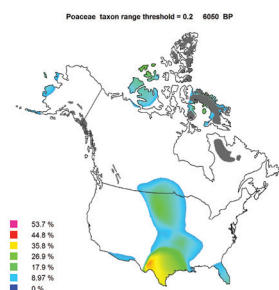
2050-2550 BP



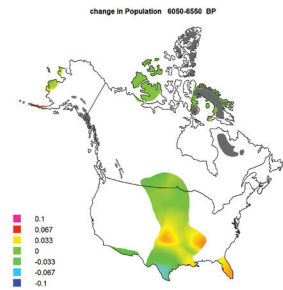
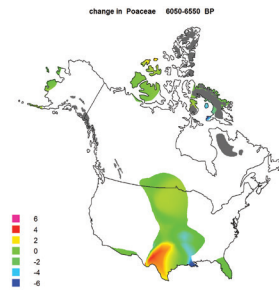
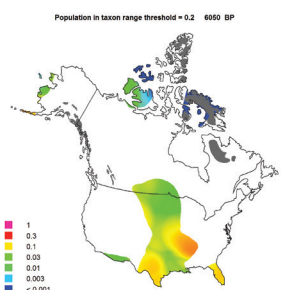
4050 BP



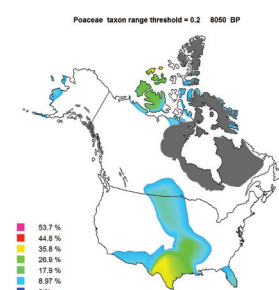
4050-4550 BP



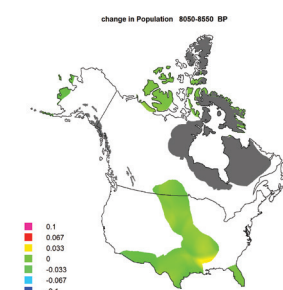
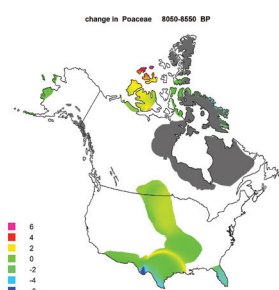
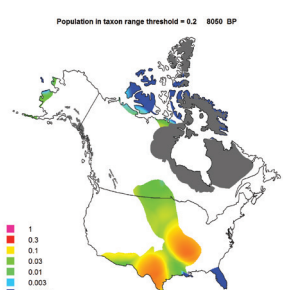
6050 BP



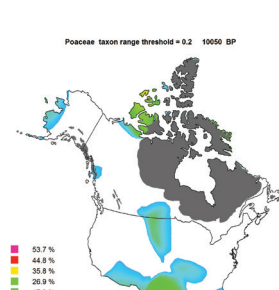
6050-6550 BP



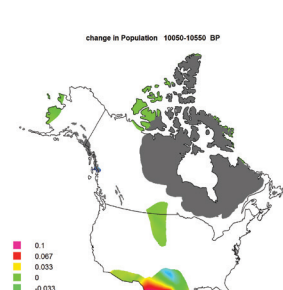
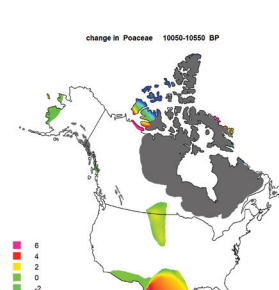
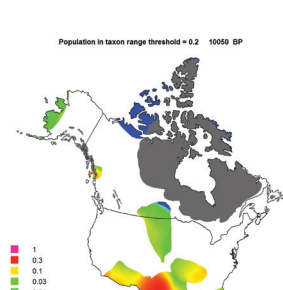
8050 BP



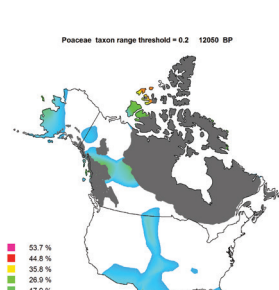
8050-8550 BP



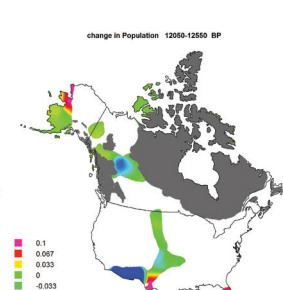
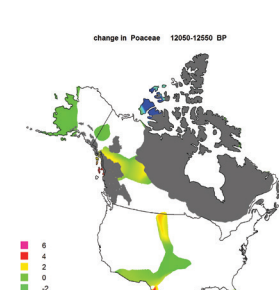
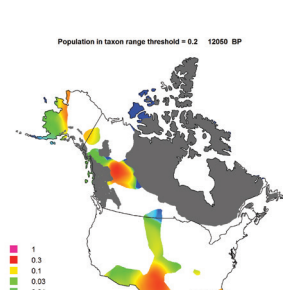
10050 BP



10050-10550 BP



12050 BP



12050-12550 BP

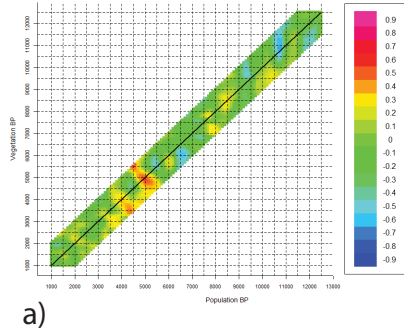
Appendix S3. Series of ten pages, one per taxon, showing heat maps summarizing spatial correlations of maps of 10 taxa and their cross-correlation with population.

Each page is dedicated to one taxon, and each graph is the stacked summary of 121 spatial correlation or cross-correlation functions. The taxa included are, in order: *Picea*, *Pinus*, *Quercus*, *Castanea*, *Juglans*, *Carya*, *Acer*, *Fagus*, *Populus*, Poaceae.

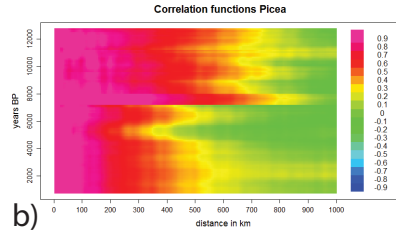
- a) Summary of cross-correlations between difference maps; as in Figure 2.
- b) Correlation functions of the maps of taxon abundance.
- c) Cross-correlations of maps of taxon abundance and population estimates.
- d) Correlation functions of 500-year differences in taxon abundance and cross-correlation of these maps with population at:
 - e) zero lag,
 - f) lag of +100 years and g) lag of -100 years,
 - h) lag of +300 years and i) lag of -300 years,
 - j) lag of +500 years and k) lag of -500 years,
 - l) lag of +1000 years and m) lag of -1000 years.

A positive lag means that vegetation change corresponds to a more recent 500-year change interval than change in population and a negative lag means the opposite.

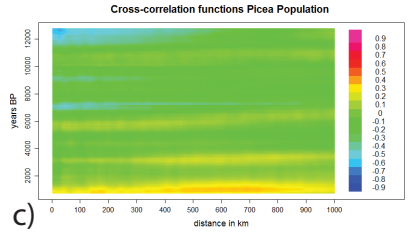
Picea



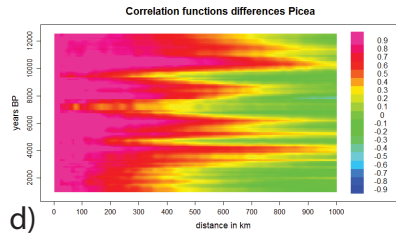
a)



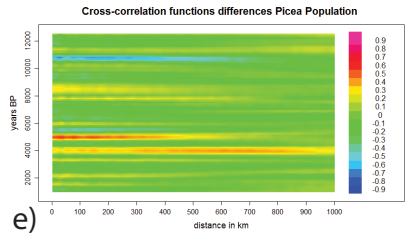
b)



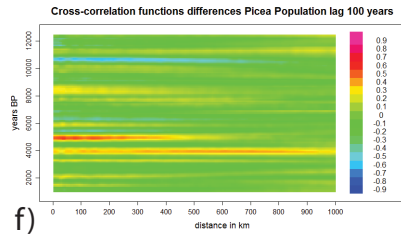
c)



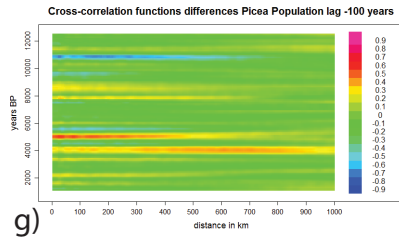
d)



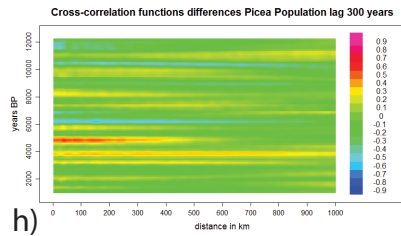
e)



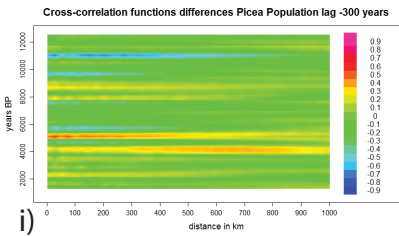
f)



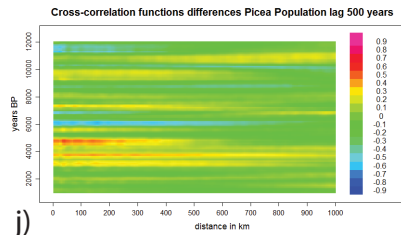
g)



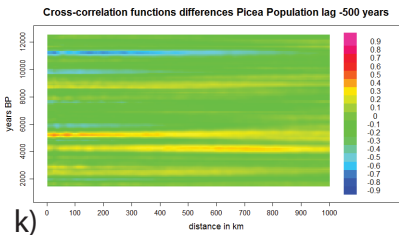
h)



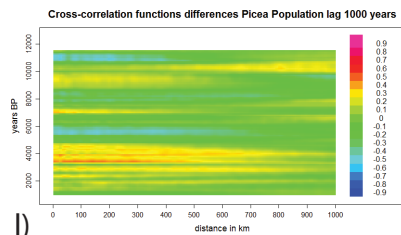
i)



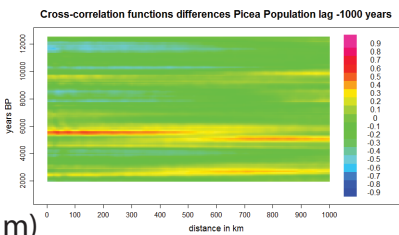
j)



k)

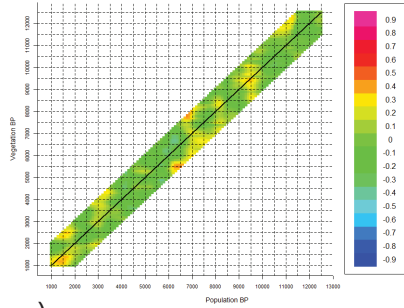


l)

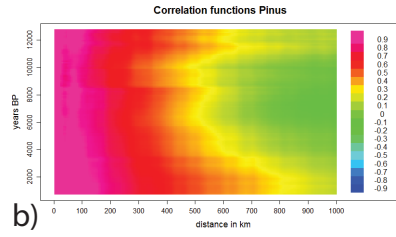


m)

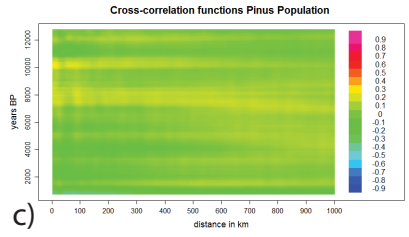
Pinus



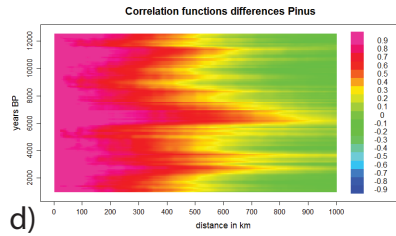
a)



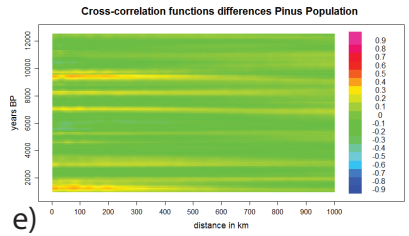
b)



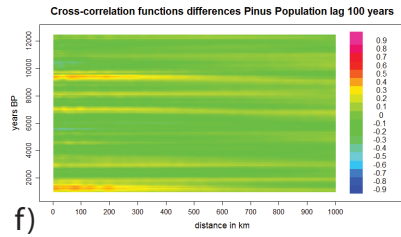
c)



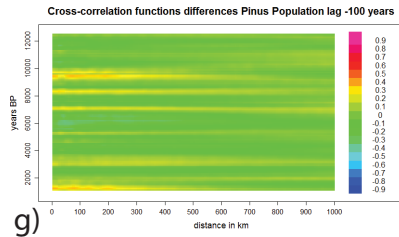
d)



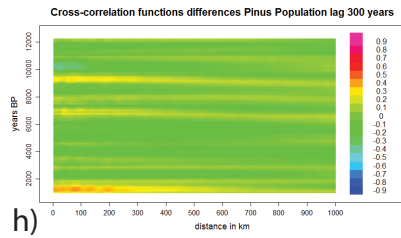
e)



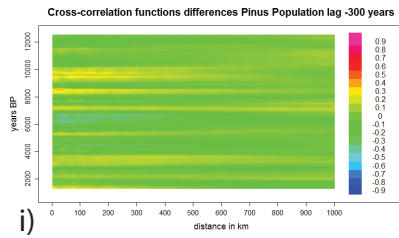
f)



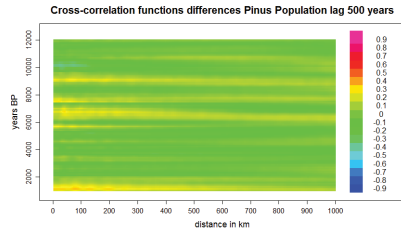
g)



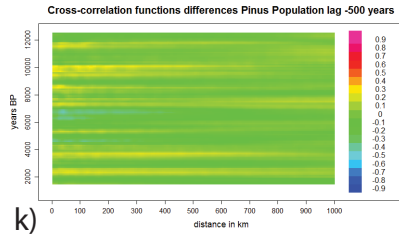
h)



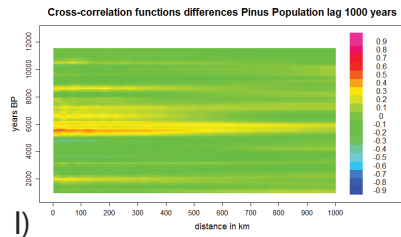
i)



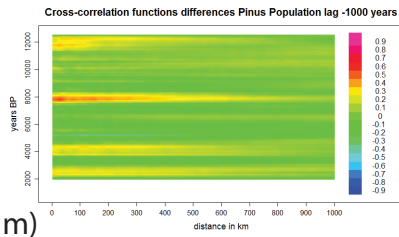
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k)

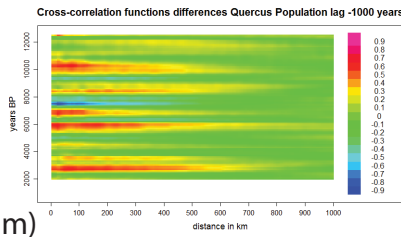
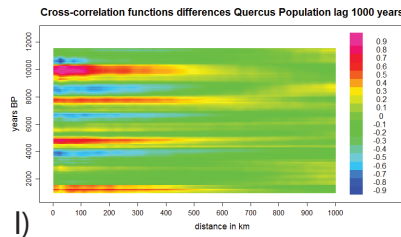
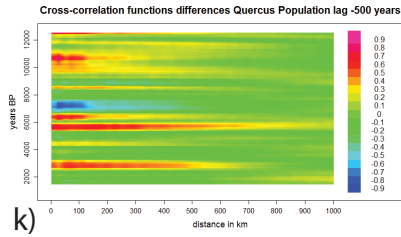
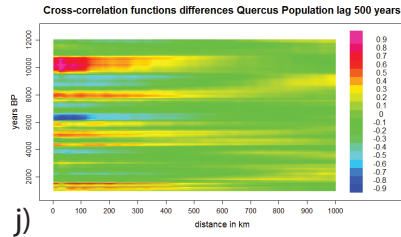
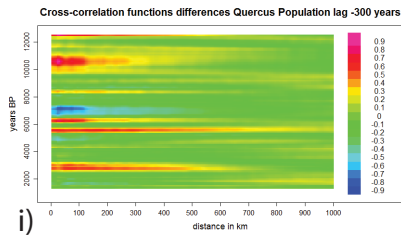
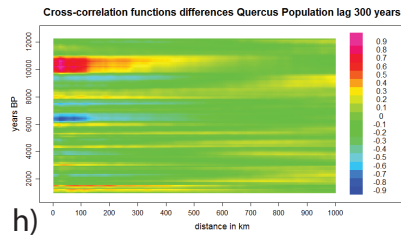
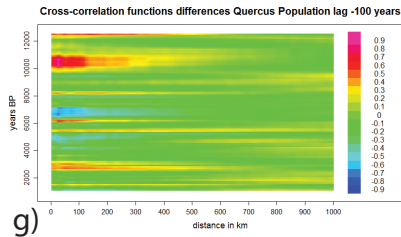
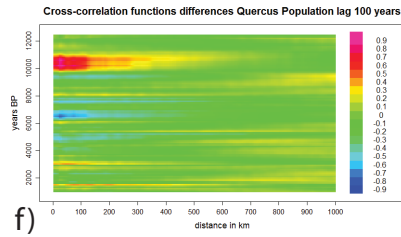
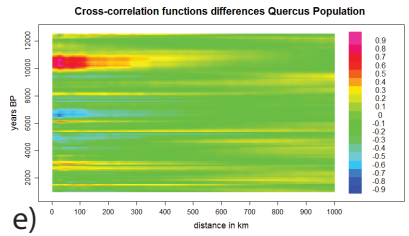
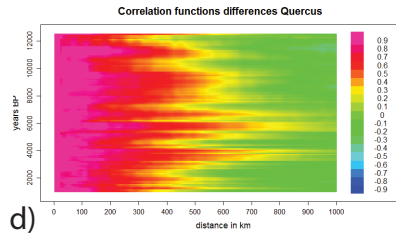
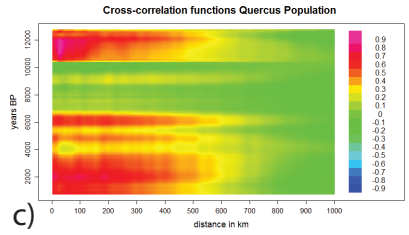
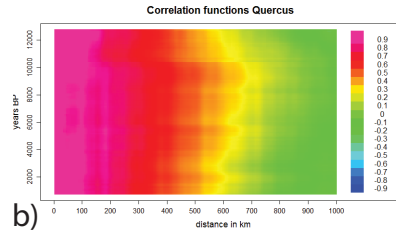
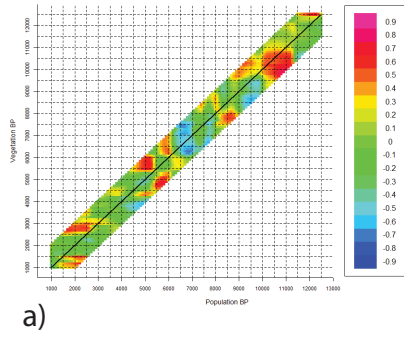


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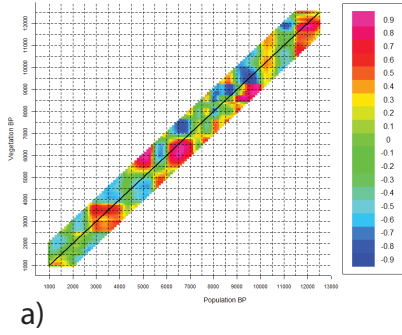


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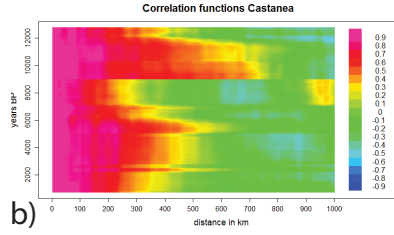
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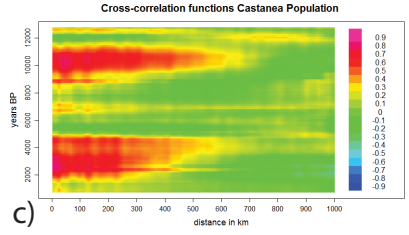
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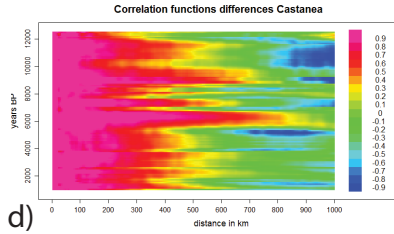
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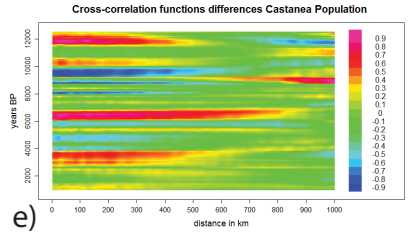
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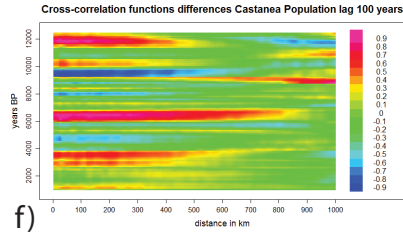
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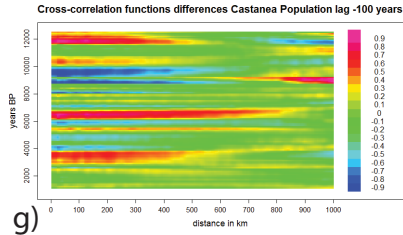
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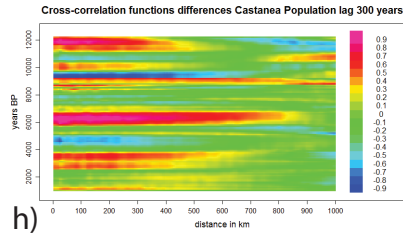
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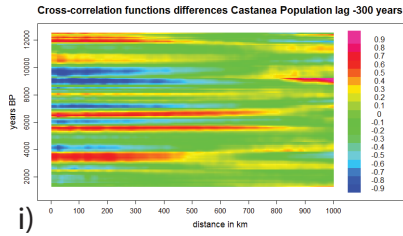
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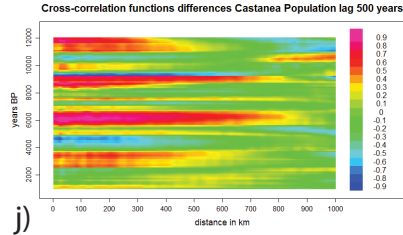
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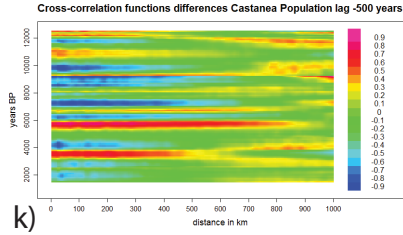
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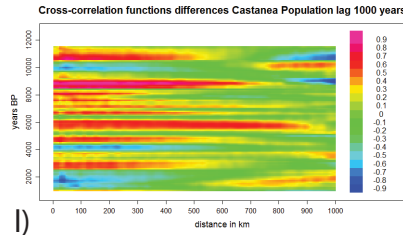
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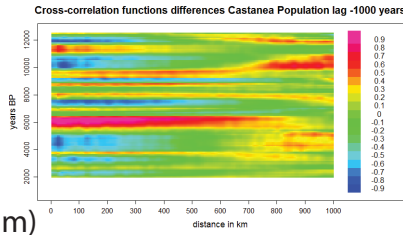
j)



k)

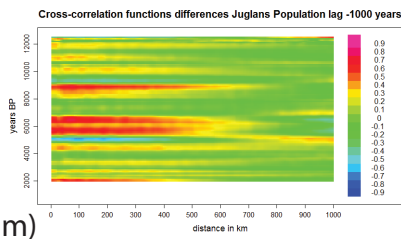
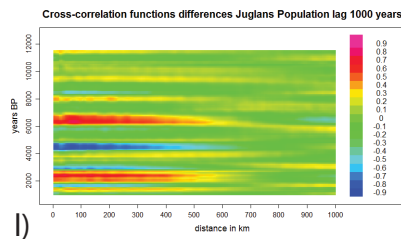
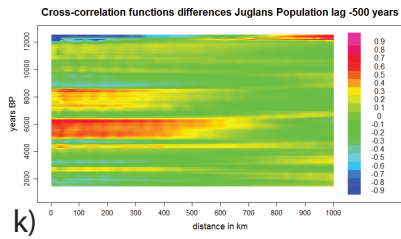
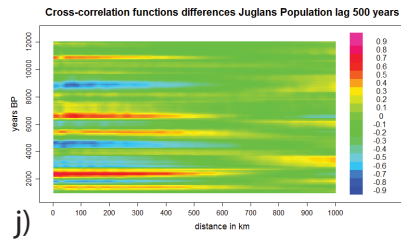
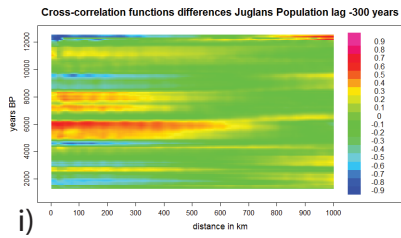
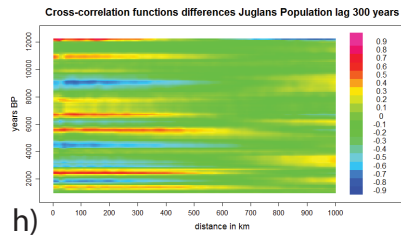
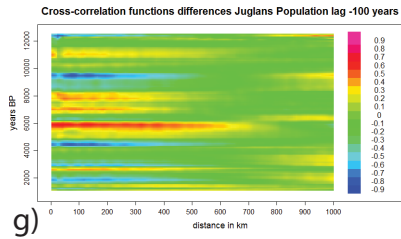
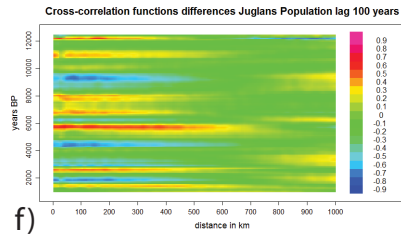
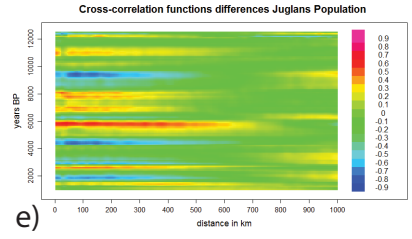
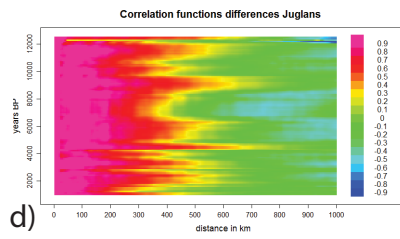
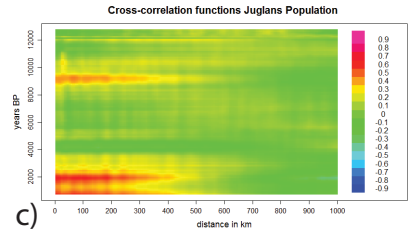
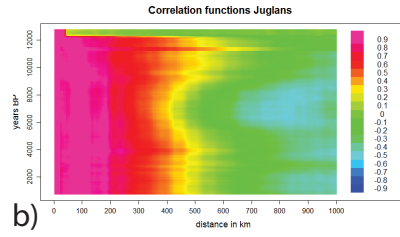
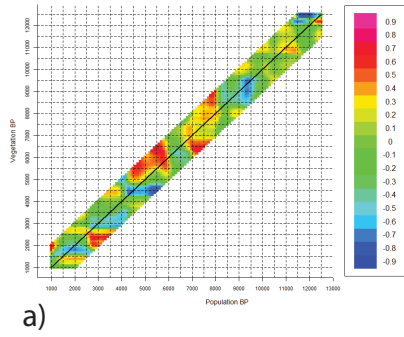


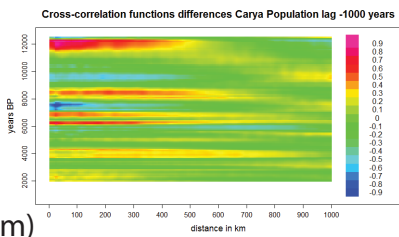
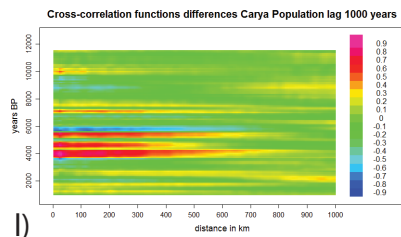
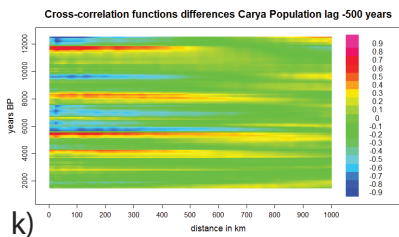
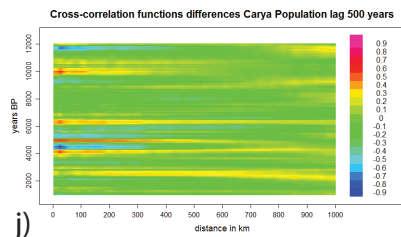
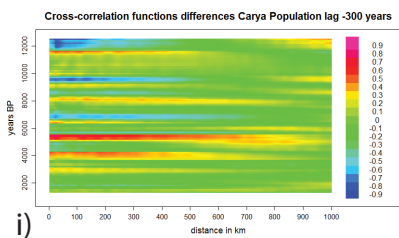
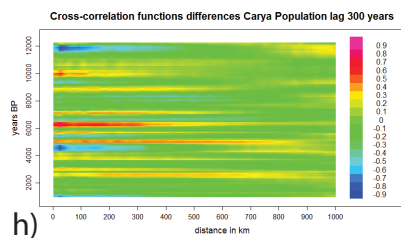
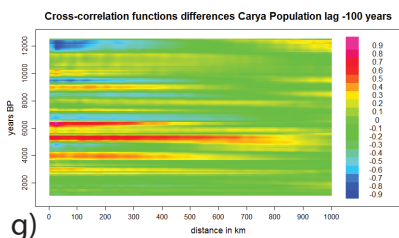
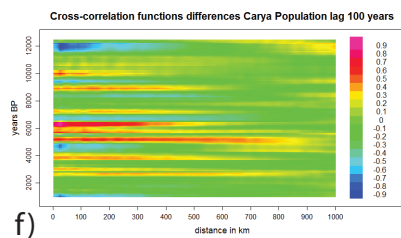
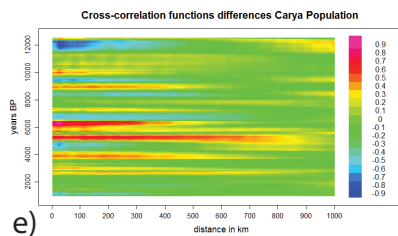
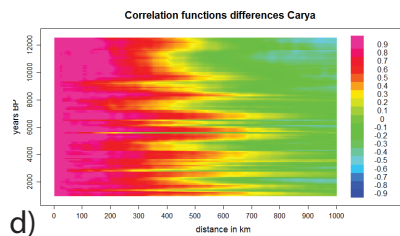
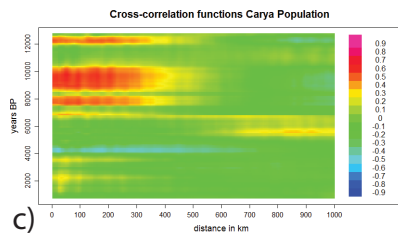
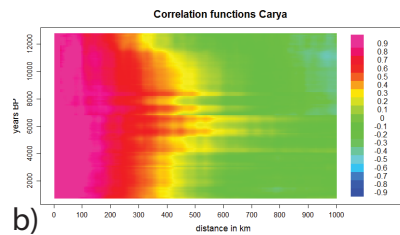
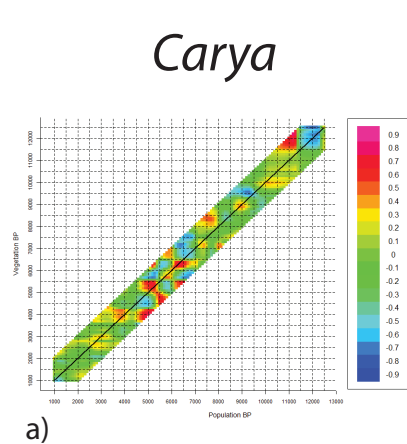
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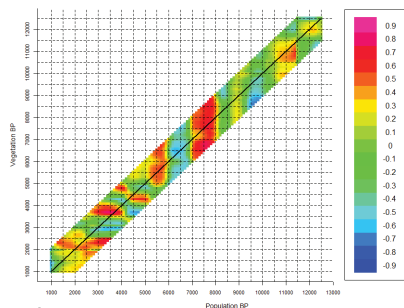
m)

Juglans

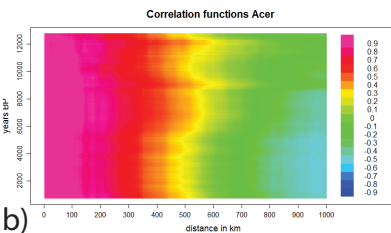




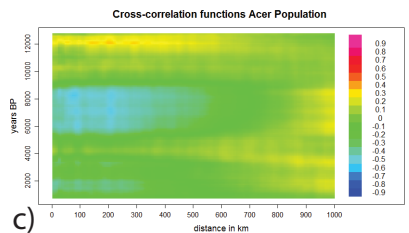
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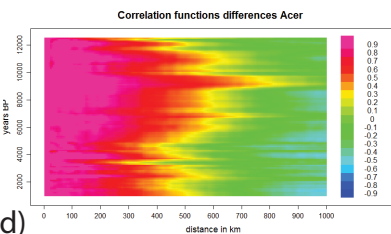
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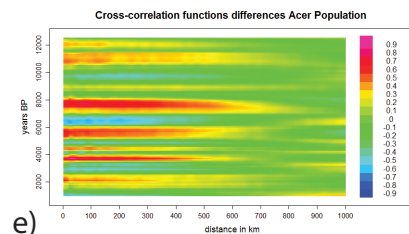
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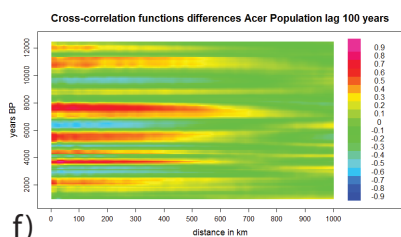
c)



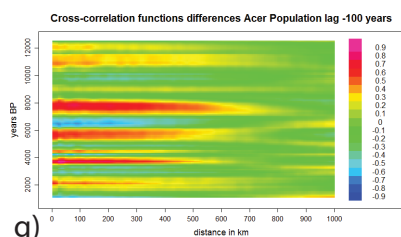
d)



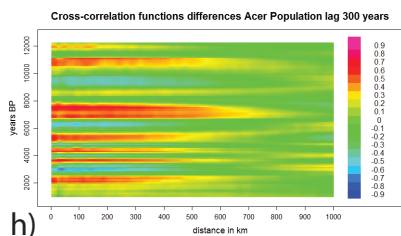
e)



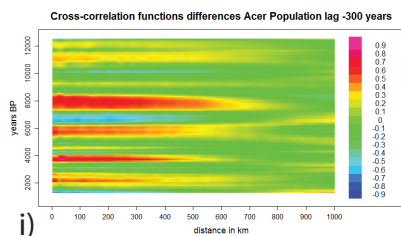
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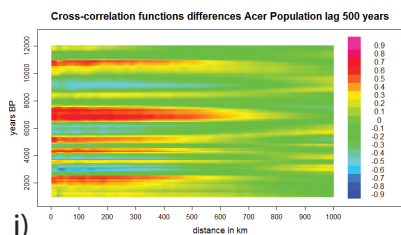
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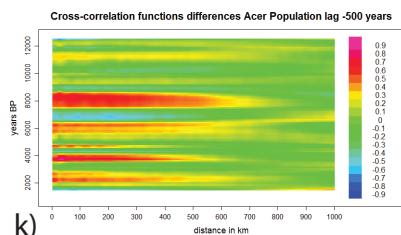
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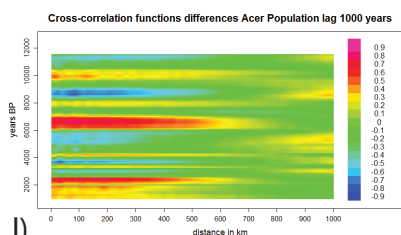
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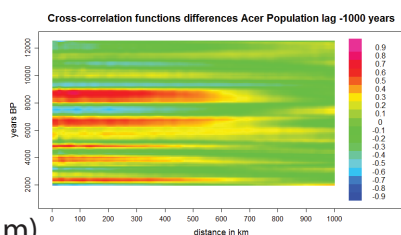
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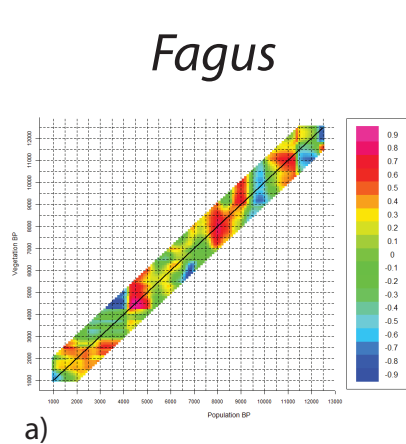
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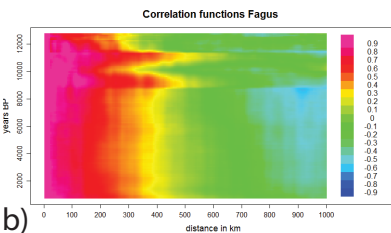
l)



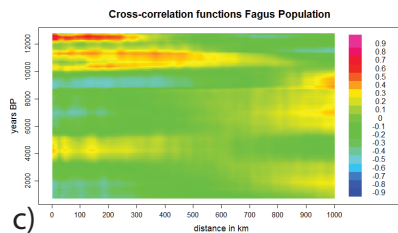
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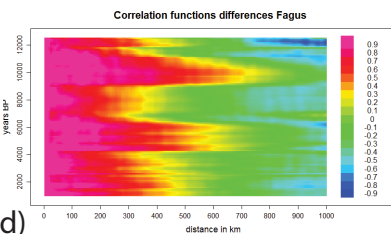
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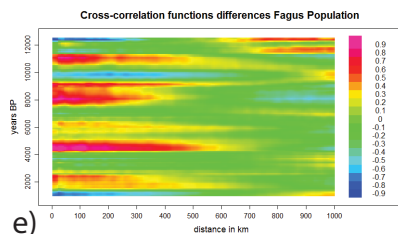
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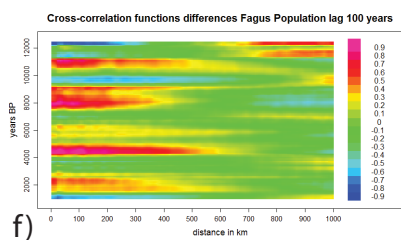
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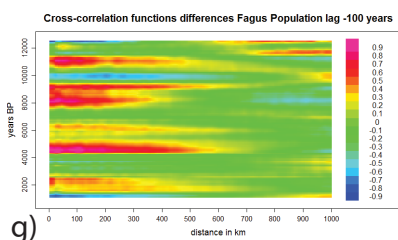
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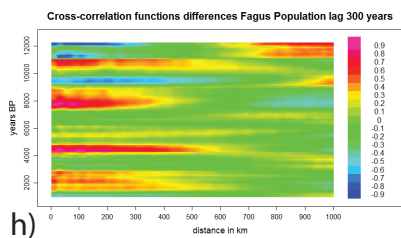
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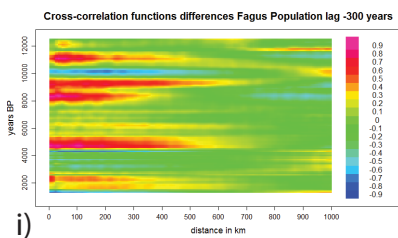
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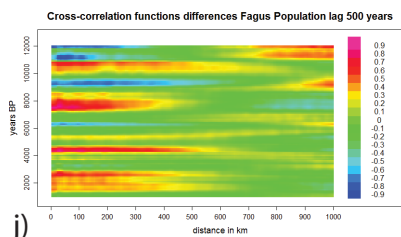
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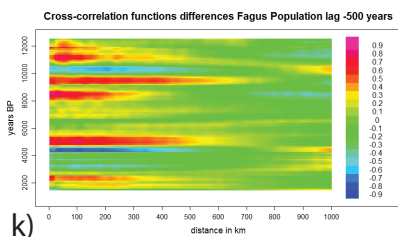
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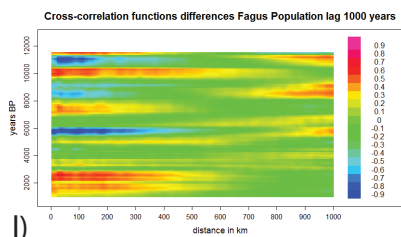
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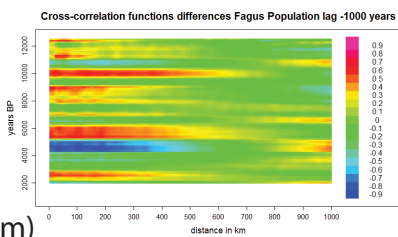
j)



k)

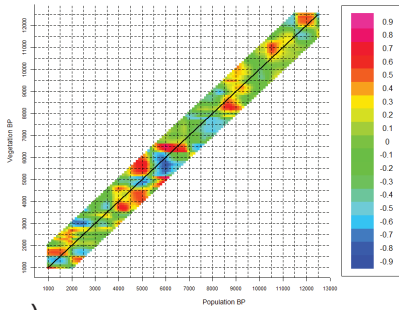


l)

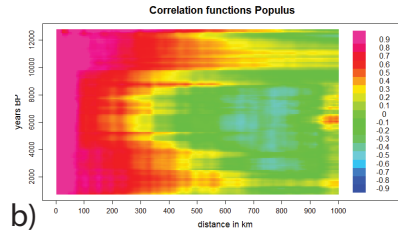


m)

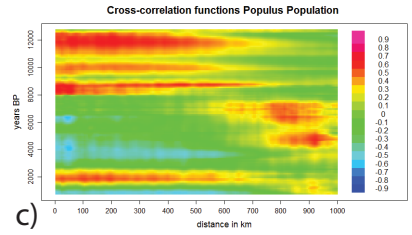
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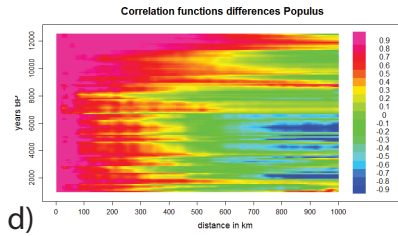
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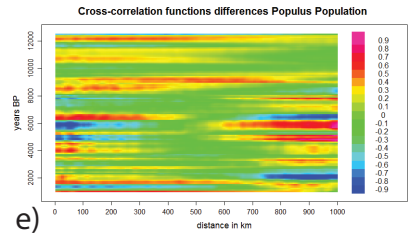
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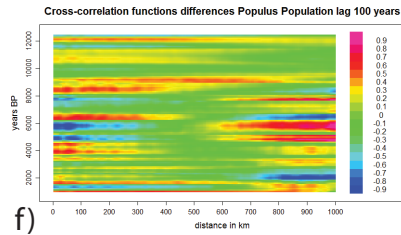
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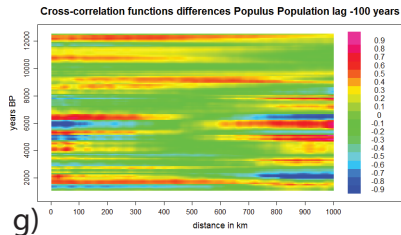
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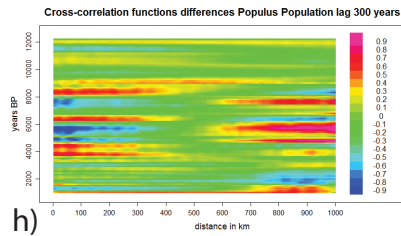
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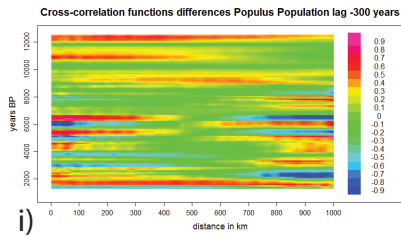
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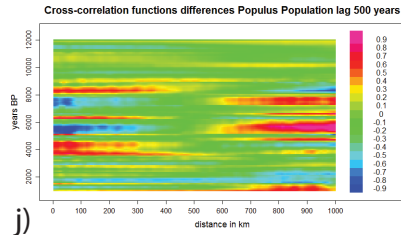
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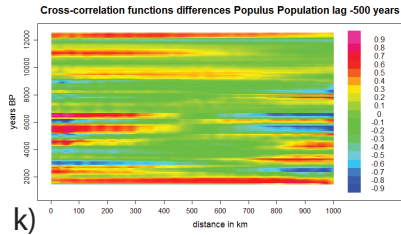
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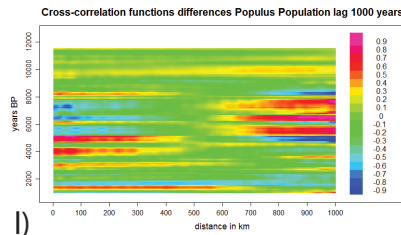
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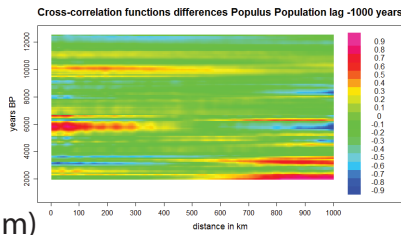
j)



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