

Bison results

152 bison mtDNA sequences sampled from the present to 55,182 years BP (602bp).

Louis du Plessis

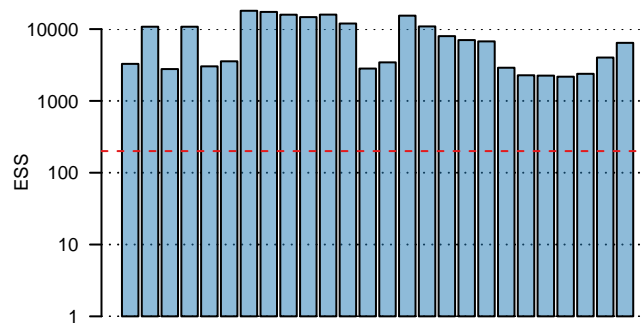
Last modified: 22 Nov 2019

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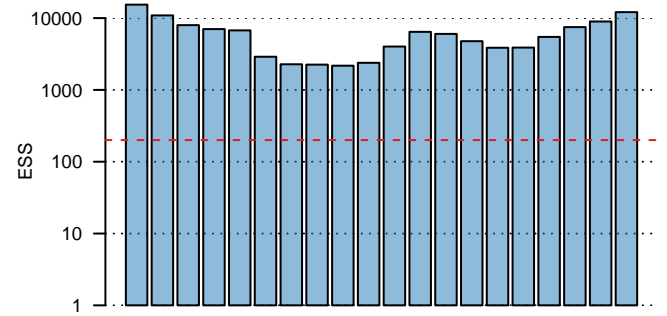
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1 Combine chains and check convergence

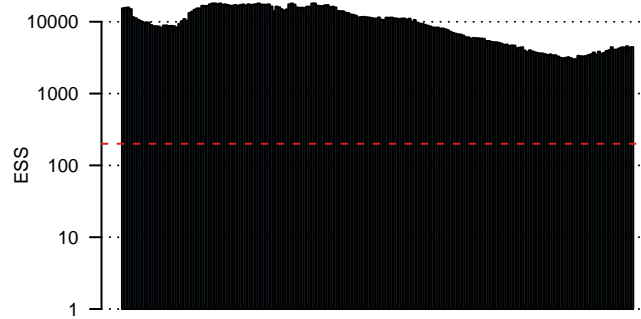
1.1 BSP 20



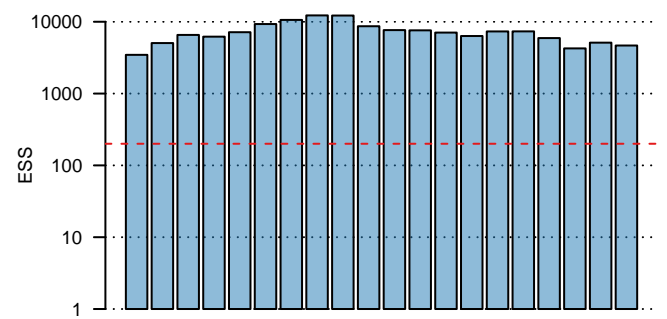
General parameters



PopSize parameters

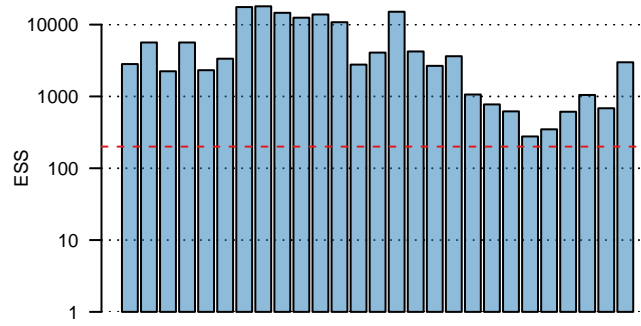


Gridded PopSize parameters

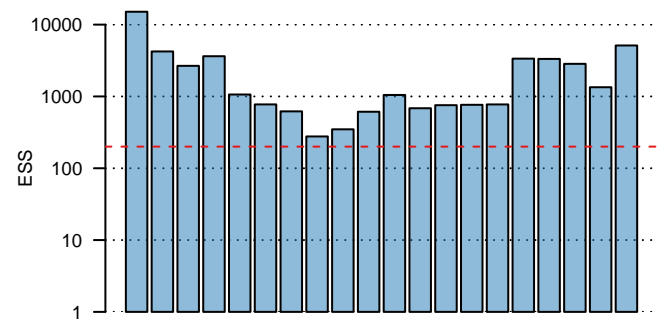


GroupSize parameters

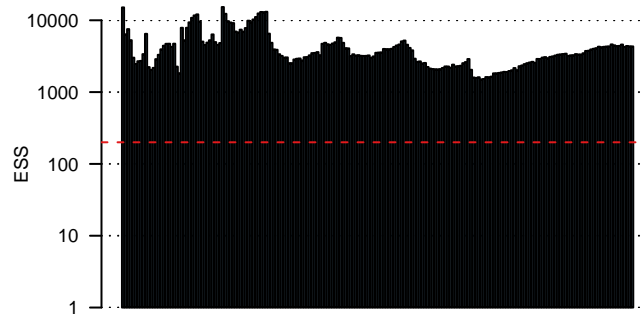
1.2 BESP 20/1



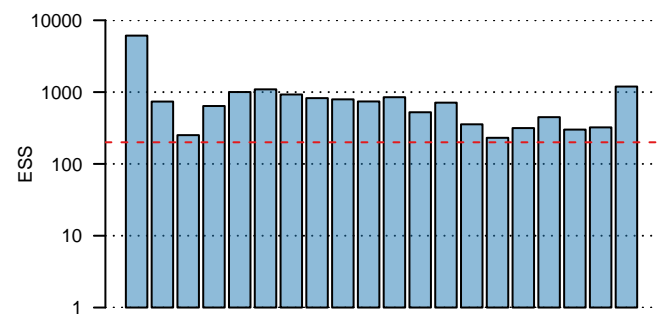
General parameters



PopSize parameters

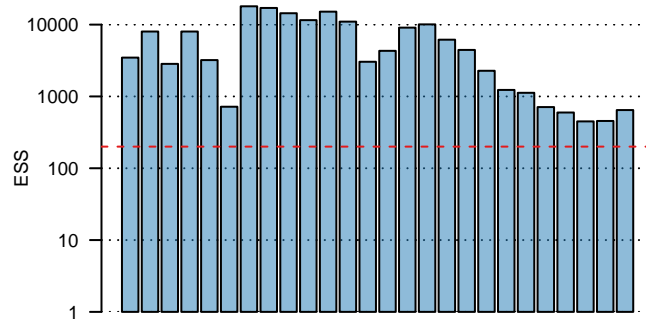


Gridded PopSize parameters

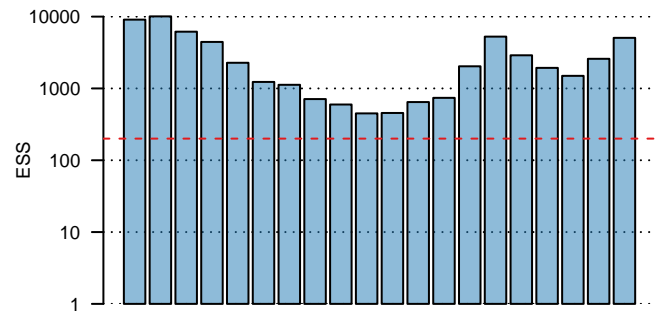


GroupSize parameters

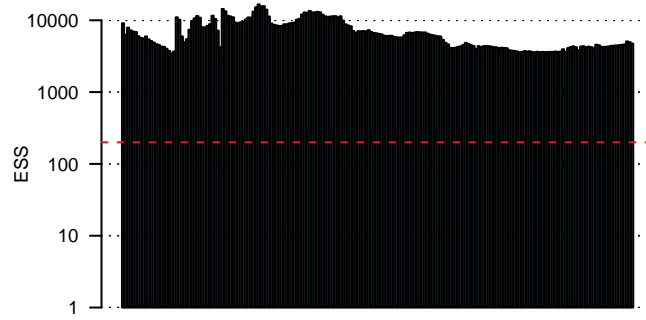
1.3 BESP 20/12



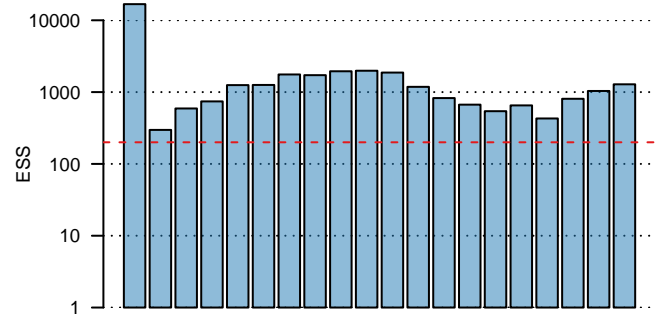
General parameters



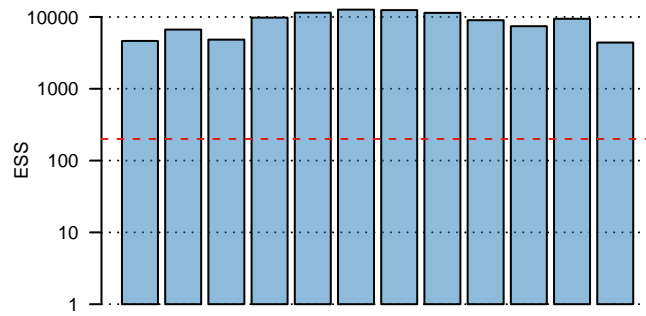
PopSize parameters



Gridded PopSize parameters



GroupSize parameters



Sampling intensity parameters

1.4 Convergence summary

Table 1: Number of nonstationary parameters for different models and subsets of parameters.

	BSP 20	BESP 20/1	BESP 20/12
PopSize	0	0	0
Gridded PopSize	0	0	0
Other parameters	0	0	0

Table 2: Lowest ESS values for different models and subsets of parameters.

	BSP 20	BESP 20/1	BESP 20/12
PopSize	-	-	-
Gridded PopSize	-	-	-
Other parameters	-	-	-

For checking convergence and combining chains a burn-in of 10% was used, and chains are thinned by a factor of 3, effectively sampling from the MCMC chains every 3×10^4 states and resulting in chains with 18003 posterior samples.

For convergence only the general parameters and the gridded population size parameters are important. The logged population size and group size parameters are not always expected to mix well.

2 Figures

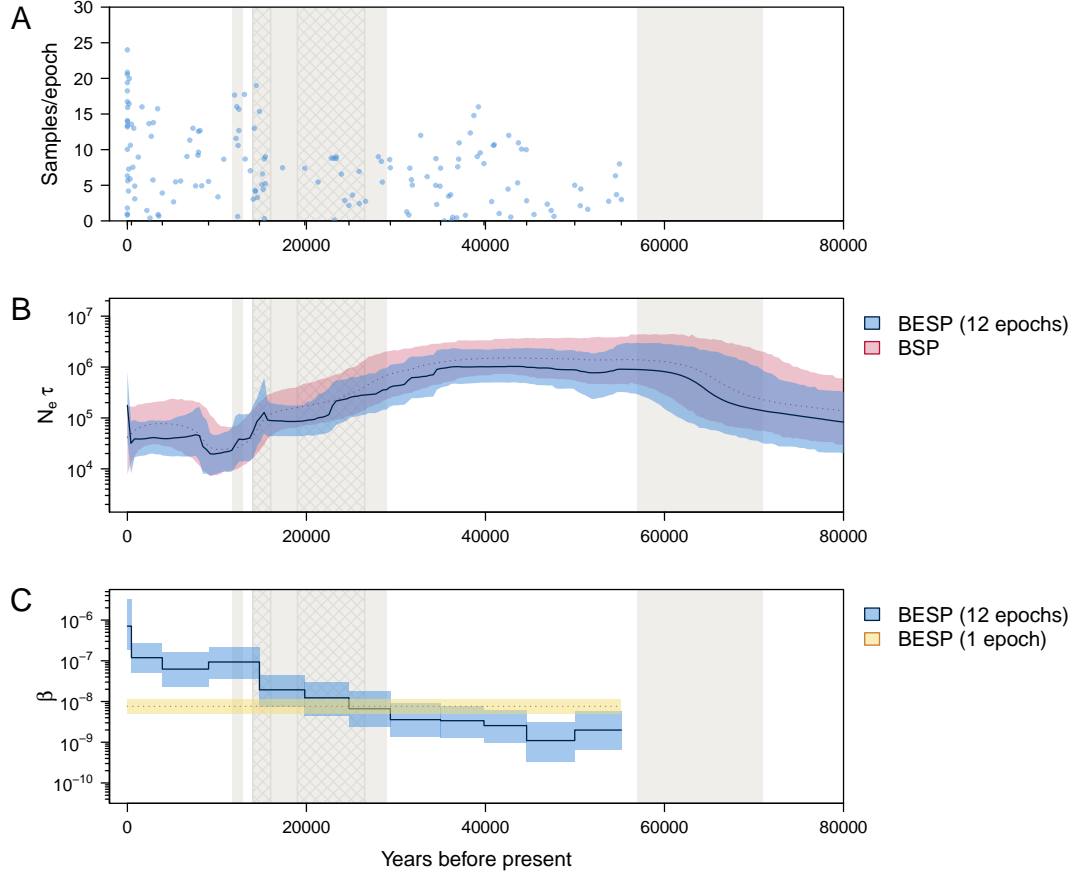


Figure 1: (A) Density of sequence sampling dates through time for the alignment of 152 bison mtDNA sequences that we used. Blue dots indicate stripcharts of individual samples for each sampling epoch. The height of the stripcharts are equal to the number of samples in each epoch. Small tick marks on the x-axis represent epoch times. Grey shading indicates cool periods in the Earth's climate (from the present: Younger Dryas, Marine Isotope Stages (MIS) 2, MIS 4). The two cross hatched areas delimit the time of the last glacial maximum (~26.5-19 ka BP) and approximate time of substantial human settlement of the Americas (~16-14 ka BP). (B) Median (solid/dotted line) and 95% highest posterior density (HPD) intervals (shaded areas) for the genetic diversity estimates ($N_e \tau$) through time. The BESP estimate is shown in blue and the BSP estimate in red. (C) Median (solid line/dotted line) and 95% HPD intervals (shaded areas) of the estimated sampling intensities (beta) for each sampling epoch. The 12-epoch BESP estimates are in blue and a single-epoch (density-defined) estimate is in yellow.

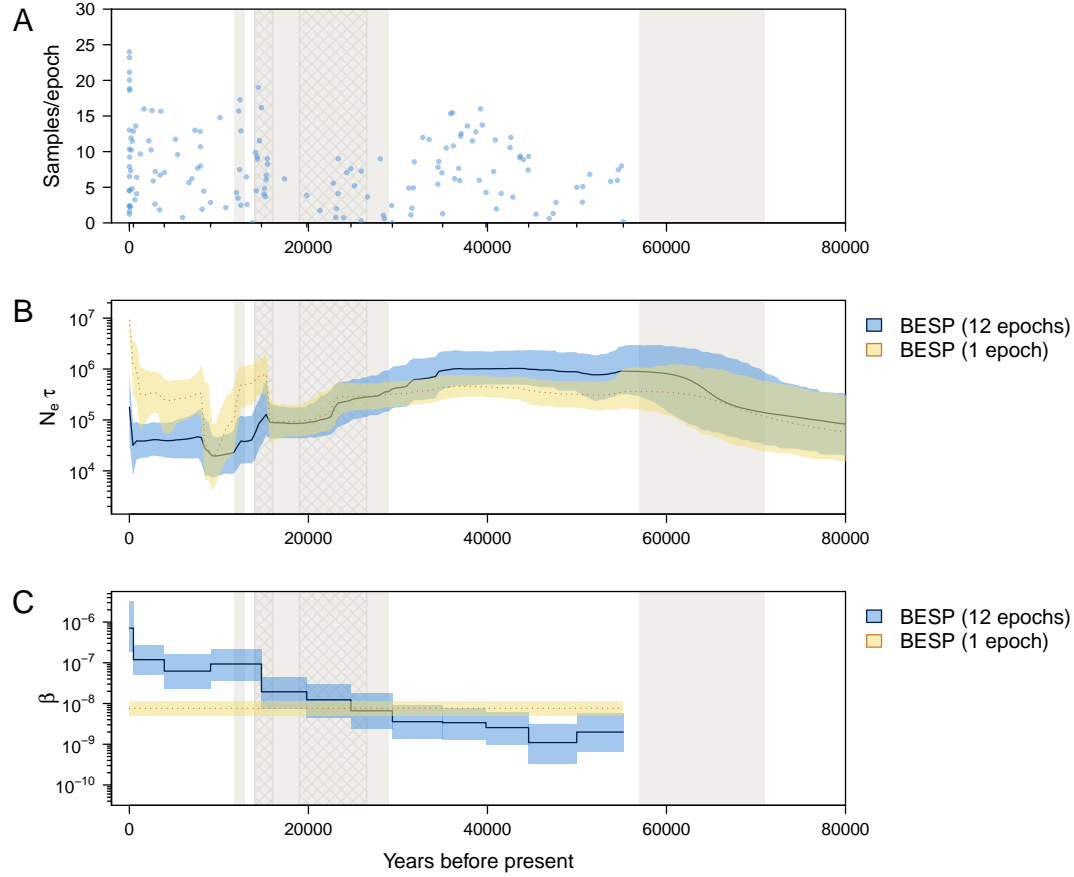


Figure 2: (A) Density of sequence sampling dates through time for the alignment of 152 bison mtDNA sequences that we used. Blue dots indicate stripcharts of individual samples for each sampling epoch. The height of the stripcharts are equal to the number of samples in each epoch. Small tick marks on the x-axis represent epoch times. Grey shading indicates cool periods in the Earth's climate (from the present: Younger Dryas, Marine Isotope Stages (MIS) 2, MIS 4). The two cross hatched areas delimit the time of the last glacial maximum (~26.5-19 ka BP) and approximate time of substantial human settlement of the Americas (~16-14 ka BP). (B) Median (solid/dotted line) and 95% highest posterior density (HPD) intervals (shaded areas) for the genetic diversity estimates ($N_e \tau$) through time. The 12-epoch BESP estimate is shown in blue and the single-epoch BESP estimate in yellow. (C) Median (solid line/dotted line) and 95% HPD intervals (shaded areas) of the estimated sampling intensities (beta) for each sampling epoch. The 12-epoch BESP estimates are in blue and a single-epoch (density-defined) estimate is in yellow.

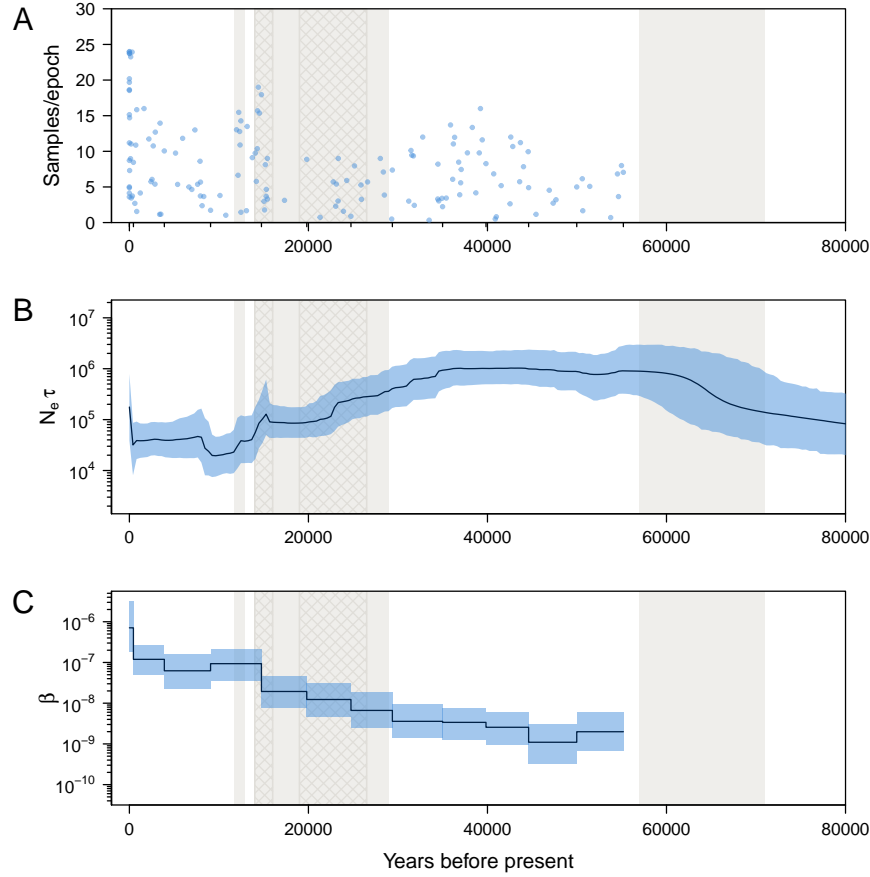


Figure 3: (A) Density of sequence sampling dates through time for the alignment of 152 bison mtDNA sequences that we used. Blue dots indicate stripcharts of individual samples for each sampling epoch. The height of the stripcharts are equal to the number of samples in each epoch. Small tick marks on the x-axis represent epoch times. Grey shading indicates cool periods in the Earth's climate (from the present: Younger Dryas, Marine Isotope Stages (MIS) 2, MIS 4). The two cross hatched areas delimit the time of the last glacial maximum (~26.5-19 ka BP) and approximate time of substantial human settlement of the Americas (~16-14 ka BP). (B) Median (solid line) and 95% highest posterior density (HPD) intervals (shaded areas) for the genetic diversity estimates ($N_e \tau$) through time of the 12-epoch BESP. (C) Median (solid line) and 95% HPD intervals (shaded areas) of the estimated sampling intensities (beta) for each sampling epoch of the 12-epoch BESP.

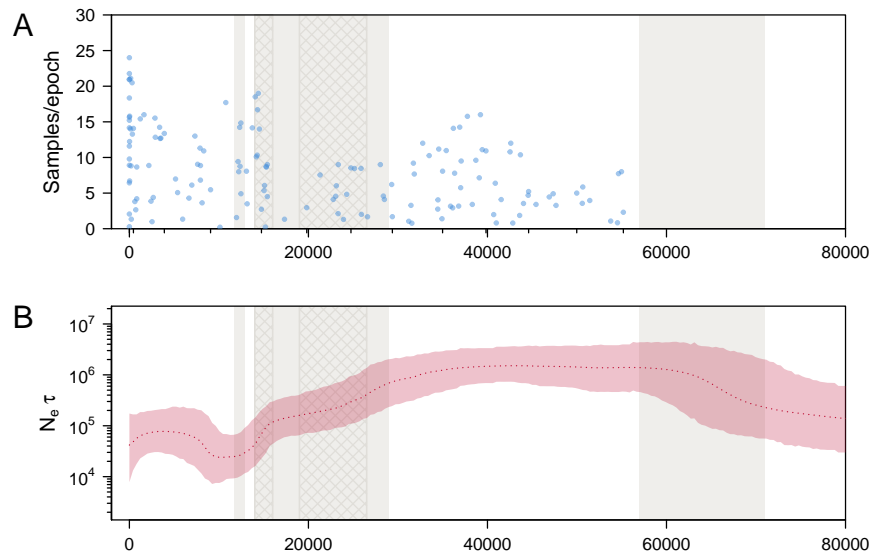


Figure 4: (A) Density of sequence sampling dates through time for the alignment of 152 bison mtDNA sequences that we used. Blue dots indicate stripcharts of individual samples for each sampling epoch. The height of the stripcharts are equal to the number of samples in each epoch. Small tick marks on the x-axis represent epoch times. Grey shading indicates cool periods in the Earth's climate (from the present: Younger Dryas, Marine Isotope Stages (MIS) 2, MIS 4). The two cross hatched areas delimit the time of the last glacial maximum (~26.5-19 ka BP) and approximate time of substantial human settlement of the Americas (~16-14 ka BP). (B) Median (dotted line) and 95% highest posterior density (HPD) intervals (shaded areas) for the genetic diversity estimates ($N_e \tau$) through time of the BSP.

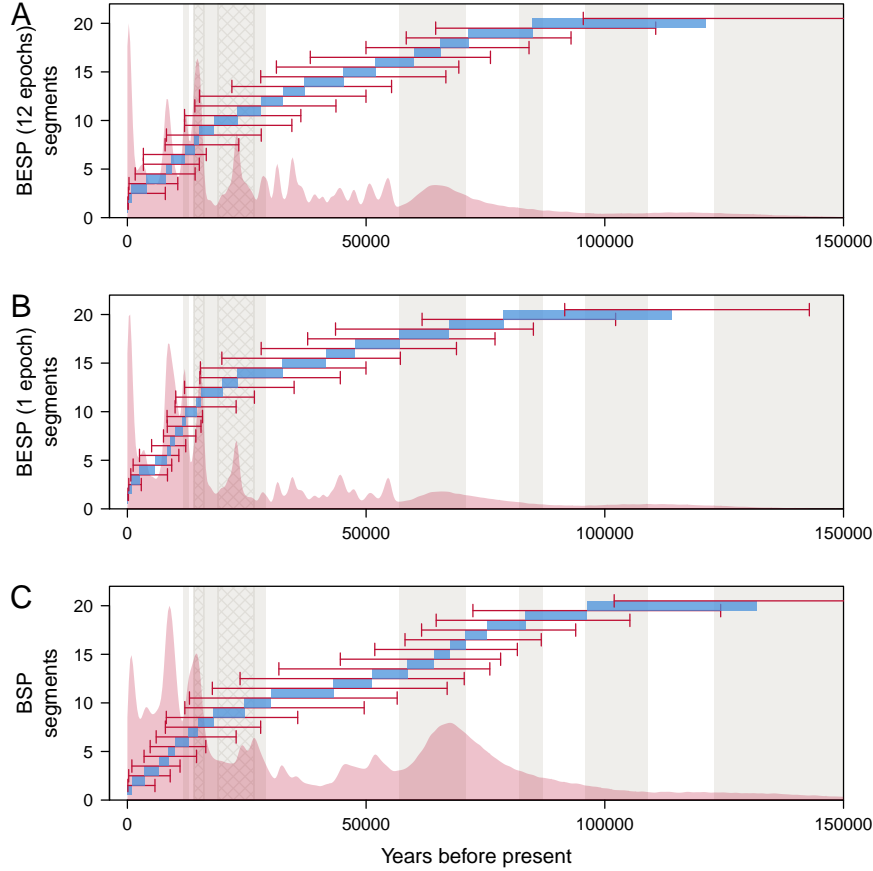


Figure 5: Population size segments for the alignment of 152 bison mtDNA sequences, as estimated under the 12-epoch BESP (A), single-epoch BESP (B) and BSP (C), with $p = 20$. Median posterior estimates of segments ($t_{j-1}-t_j$) are shown in blue. HPD intervals for the segment end-times are indicated by red arrows. Red shading shows the kernel density estimate of the posterior segment times (t_j). Grey shading indicates cool periods in the Earth's climate (from the present: Younger Dryas, Marine Isotope Stages (MIS) 2, MIS 4). The two cross hatched areas delimit the time of the last glacial maximum (~26.5-19 ka BP) and approximate time of substantial human settlement of the Americas (~16-14 ka BP).



Figure 6: MCC tree of the alignment of 152 bison mtDNA sequences estimated under the 12-epoch BEBP. Grey shading indicates cool periods in the Earth's climate (from the present: Younger Dryas, Marine Isotope Stages (MIS) 2, MIS 4). The two cross hatched areas delimit the time of the last glacial maximum (~26.5-19 ka BP) and approximate time of substantial human settlement of the Americas (~16-14 ka BP).

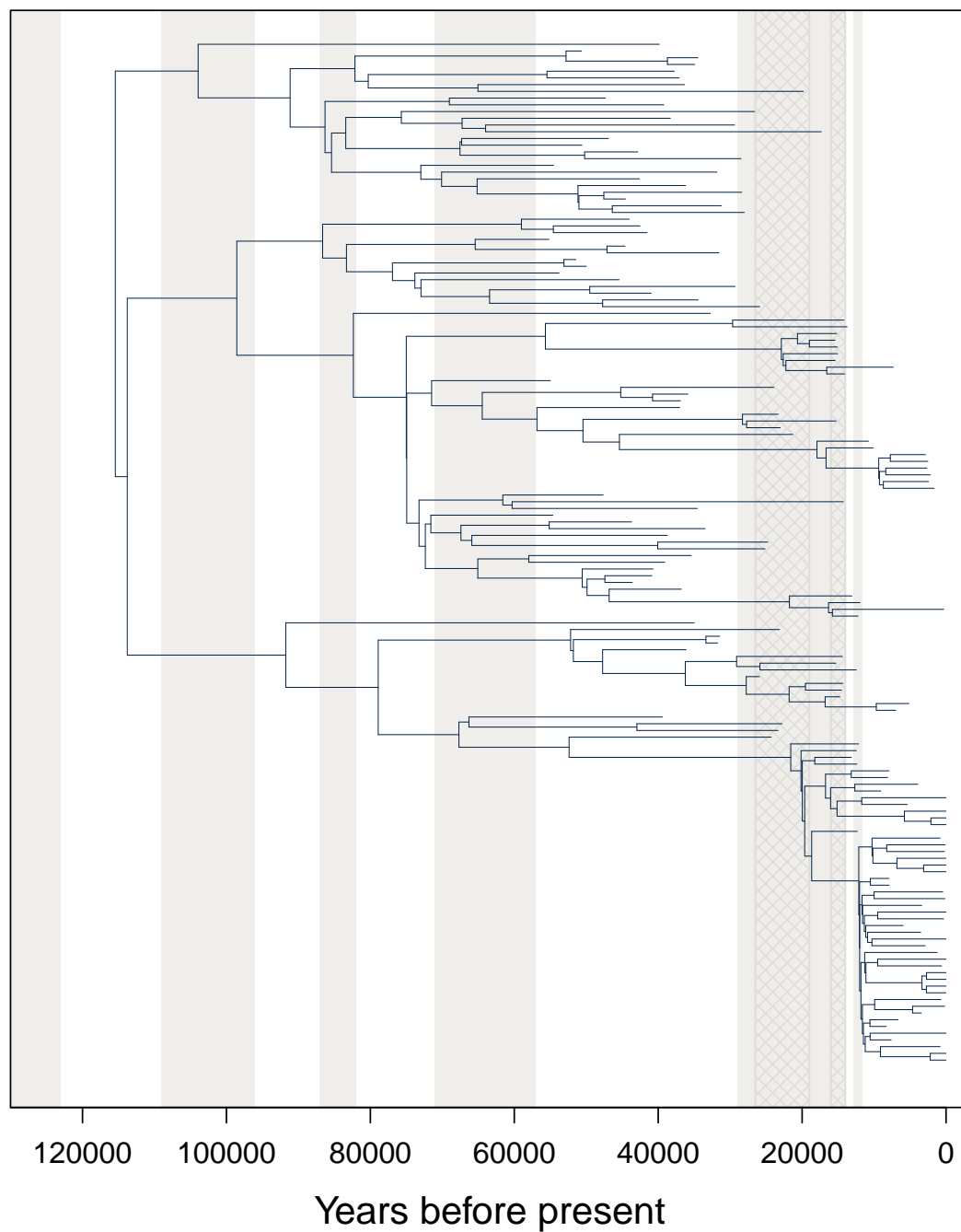


Figure 7: MCC tree of the alignment of 152 bison mtDNA sequences estimated under the single-epoch BESP. Grey shading indicates cool periods in the Earth's climate (from the present: Younger Dryas, Marine Isotope Stages (MIS) 2, MIS 4). The two cross hatched areas delimit the time of the last glacial maximum (~26.5-19 ka BP) and approximate time of substantial human settlement of the Americas (~16-14 ka BP).



Figure 8: MCC tree of the alignment of 152 bison mtDNA sequences estimated under the BSP. Grey shading indicates cool periods in the Earth's climate (from the present: Younger Dryas, Marine Isotope Stages (MIS) 2, MIS 4). The two cross hatched areas delimit the time of the last glacial maximum (~26.5-19 ka BP) and approximate time of substantial human settlement of the Americas (~16-14 ka BP).

3 Session info

```
## R version 3.5.1 (2018-07-02)
## Platform: x86_64-apple-darwin15.6.0 (64-bit)
## Running under: macOS Sierra 10.12.6
##
## Matrix products: default
## BLAS: /Library/Frameworks/R.framework/Versions/3.5/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/3.5/Resources/lib/libRlapack.dylib
##
## locale:
## [1] en_GB.UTF-8/en_GB.UTF-8/en_GB.UTF-8/C/en_GB.UTF-8/en_GB.UTF-8
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods    base
##
## other attached packages:
## [1] rskylinetools_0.2.1 coda_0.19-3      beastio_0.2.5
## [4] ape_5.3
##
## loaded via a namespace (and not attached):
## [1] Rcpp_1.0.2      knitr_1.25      magrittr_1.5
## [4] lattice_0.20-38 rlang_0.4.0     highr_0.8
## [7] stringr_1.4.0   caTools_1.17.1.2 tools_3.5.1
## [10] parallel_3.5.1  grid_3.5.1     nlme_3.1-141
## [13] xfun_0.10       KernSmooth_2.23-16 htmltools_0.4.0
## [16] gtools_3.8.1    yaml_2.2.0      digest_0.6.21
## [19] RColorBrewer_1.1-2 codetools_0.2-16 bitops_1.0-6
## [22] evaluate_0.14   rmarkdown_1.16  gdata_2.18.0
## [25] stringi_1.4.3   compiler_3.5.1  gplots_3.0.1.1
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