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Integrating Multiple Lines of Evidence into Historical Biogeography Hypothesis Testing: A Bison bison Case Study

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Integrating multiple lines of evidence into historical biogeography hypothesis testing: a *Bison bison* case study

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One of the grand goals of historical biogeography is to understand how and why species' population sizes and distributions change over time. Multiple types of data drawn from disparate fields, combined into a single modelling framework, are necessary to document changes in a species's demography and distribution, and to determine the drivers responsible for change. Yet truly integrated approaches are challenging and rarely performed. Here, we discuss a modelling framework that integrates spatio-temporal fossil data, ancient DNA, palaeoclimatological reconstructions, bioclimatic envelope modelling and coalescence models in order to statistically test alternative hypotheses of demographic and potential distributional changes for the iconic American bison (*Bison bison*). Using different assumptions about the evolution of the bioclimatic niche, we generate hypothetical distributional and demographic histories of the species. We then test these demographic models by comparing the genetic signature predicted by serial coalescence against sequence data derived from subfossils and modern populations. Our results supported demographic models that include both climate and human-associated drivers of population declines. This synthetic approach, integrating palaeoclimatology, bioclimatic envelopes, serial coalescence, spatio-temporal fossil data and heterochronous DNA sequences, improves understanding of species' historical biogeography by allowing consideration of both abiotic and biotic interactions at the population level.

1. Introduction

A main goal of historical bioegeography is to determine drivers of species distributions and demography through time. Doing so, however, is challenging, as multiple types of biotic and abiotic processes affect population dynamics, and, ideally, all these processes should be considered when making inferences about a species's past distribution and demography. Carstens & Richards [1] combined advances in bioclimatic envelope models (BEMs), statistical phylogeography and coalescence in an attempt to integrate disparate processes into a common modelling framework. Their workflow began by developing hypotheses in the form of demographic models that characterize potential past

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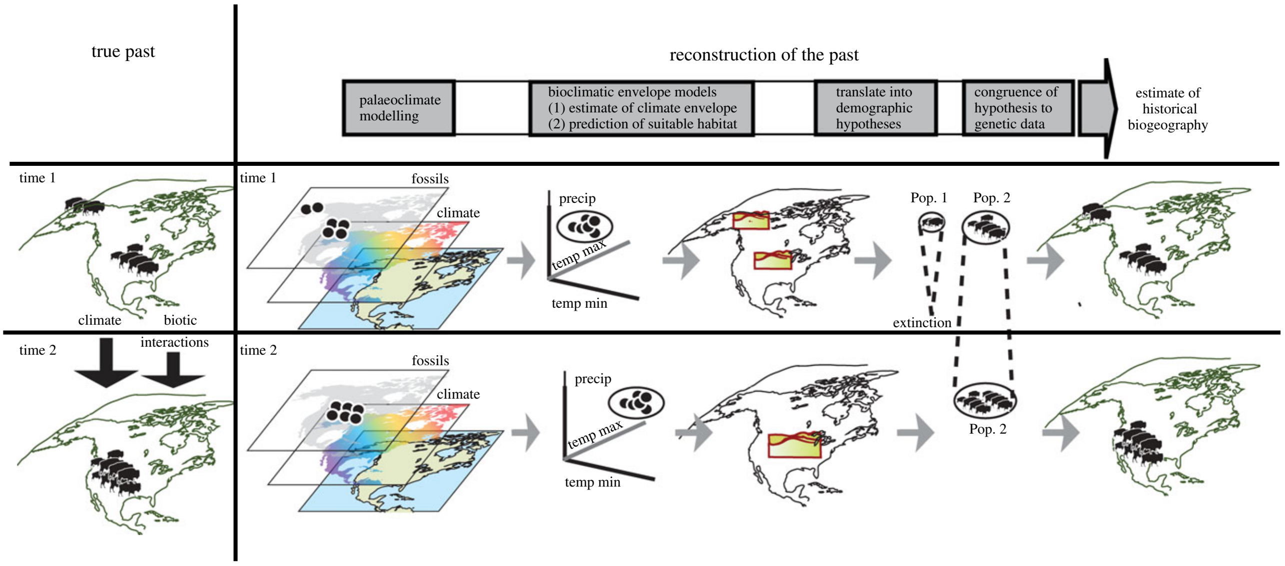

Figure 1. A workflow for reconstructing a species's historical biogeography by integrating multiple data types. We show how fossils, palaeoclimate data along with radiocarbon dating and BEM techniques can be used to develop a hypothesis testing framework to be assessed with ancient and modern DNA datasets. The goal of combining several data types over multiple time frames is to improve estimates of historical biogeography so that they are closer to the species's true history. (Online version in colour.)

distributions of species using BEMs as a guide, and then testing those alternatives using coalescent methods [1]. Despite opportunities for integration of multiple lines of evidence, the vast majority of the many subsequent studies are still limited along multiple dimensions. These limitations include: using only modern genetic data and modern occurrence data to train and test demographic models about the past (e.g. [1]); using only a single approach or method to build BEMs (e.g. [2]); considering only climate as a potential driver of species' distribution and demography (e.g. [3]); using ancient DNA but only modern occurrence data (e.g. [4]), and quantifying only coarse parameters of overall range extent when population-level scales are likely to be very important (e.g. [5]). We argue that demographic modelling approaches should also incorporate characterizations of species niches with differing degrees of data completeness, including both abiotic and biotic drivers, and use spatially explicit, mathematically rigorous and temporally precise model sets.

Late Pleistocene and Holocene subfossil deposits, characterized by dramatic biotic and climatic changes, and rich in heterogeneous, high-quality data, provide an ideal temporal window for developing synthetic, model-based approaches (e.g. [5]). Such datasets are becoming further enriched by advances in data generation from fossil material, including increased accuracy and precision of radiocarbon dating and the recovery of ancient DNA. Such advances, coupled with growing population-genetic modelling toolkits, have provided Quaternary scientists with unprecedented views of genetic diversity over space and time, showing, for example, that Late Pleistocene extinctions account for only part of the major loss of diversity during this period [6–8]. At the same time, BEMs have vastly enhanced our understanding of past species' distributions [9–12], which can then be further used as inputs into biogeographic hypotheses. By combining rich data on fossil localities and radiocarbon datasets, it is possible to use BEMs to estimate the realized climatic envelope, an n-dimensional space of climatic variables where populations have been maintained or have thrived, over multiple time periods [13,14].

Herein, we develop a multi-step, methodological workflow, which rigorously tests drivers of distributional and demographic changes, utilizing the American bison (*Bison bison*) as a focal case study group. Bison populations were once extremely large, probably spanning most of western North America [7]. It remains unclear to what extent the changing climate and interactions with humans may have contributed to their decline [5,7,15]. For example, bison were almost hunted to extinction in the nineteenth century, leaving populations today founded from as few as 30 to 50 individuals [16]. We explore in particular the following key questions. Are BEM-predicted changes in bison population structure and size supported by genetic data? Does incorporating biotic interactions between bison and humans improve demographic model support?

Bison have one of the largest datasets of accelerator mass spectrometry-dated fossils and ancient DNA available for any Late Pleistocene species. Given these abundant data, bison are ideal for seeking a consensus among multiple lines of spatial ecological, palaeontological, demographic and distributional evidence. Figure 1 illustrates how time-calibrated and georeferenced fossils, ancient DNA and palaeoclimate reconstructions can be used to best determine whether changes in species bioclimatic envelopes are associated, temporally, with changes in effective population size and population structure.

2. Material and methods

(a) Step 1: estimating the bioclimatic envelope of bison through time

Estimating a species's bioclimatic envelope is an important first step for reconstructing and understanding its past distribution [13,17]. We included climate data from multiple time periods, which allowed us to compare estimates of bison BEMs calculated independently 'within' each time period against 'pooled' estimates obtained using the full fossil record. The 'within period' analysis refers to climatic niches calibrated using only data from within each time period. The 'pooled period' used all the data to create a conglomerate of the climatic niche conditions experienced by the species throughout the Late Quaternary, which was then projected to each time slice. The advantage of this approach is that it limits possible spatial and environmental bias, but it requires accepting that niches are conserved over time (but see [18]).

Two palaeoclimatic simulations were performed to represent the climatic conditions during the Marine Isotope Stage 3 (MIS 3): the warmer middle part, around 42 thousand years ago (ka) and the colder later part, around 30 ka. We also used one simulation for the Last Glacial Maximum (LGM; approx. 21 ka) and one for the Mid-Holocene (approx. 6 ka). Carbon dioxide levels were specified at 200 ppm for the MIS 3 and LGM simulations [19], and 280 ppm for the Mid-Holocene simulation [20]. The 0 ka simulation is pre-industrial and built using the same general circulation model, to ensure temporal and spatial comparability of our climatic surfaces and BEM outputs. Sea surface temperatures (SSTs) for the MIS 3 and LGM simulations were taken primarily from CLIMAP [21], with modifications from GLAMAP-2000 and other sources [22]. SSTs for the Mid-Holocene simulation were prescribed at present-day values [23]. In all cases, insolation was calculated using orbital parameters [24,25]. All simulations were spun up to equilibrium; results are 10-year averages. Areas known to be under ice sheets given palaeoclimate models were masked as unsuitable habitat. Although palaeoclimatic simulations based on different AOGCMs might differ, previous studies comparing the effect of AOGCM (GENESIS v. 2 versus HadCM3) on modelled ranges show that trends in range size are highly correlated for six different megafauna species, including the bison [5]. Together, these climate data provided five time periods (42, 30, 21, 6 and 0 ka) for estimating BEMs.

A comprehensive set of fossil and historic bison localities was assembled from multiple sources [7,26]. Fossils were calibrated using the IntCal09 calibration curve [27], available through OxCal online (http://c14.arch.ox.ac.uk/). Georeferencing was accomplished using Google Earth and according to best practices as defined in Chapman & Wieczorek [28] (see the electronic supplementary material, table S1).

Fossils were considered contemporaneous with a climate layer if the calibrated estimate of the radiocarbon-dated fossil was within ± 3000 years, following Nogues-Bravo *et al.* [9]. We note that the bin of ± 3000 years may not be appropriate for all climate layers and should not be considered as a hard and fast rule of our suggested framework. Three climate predictors were used: average minimum temperature of the coldest month ($t_{\min}$), average maximum temperature of the warmest month ($t_{\max}$) and mean annual precipitation sum (pre). Following ensemble forecasting methodologies [29], we fitted models with a fully factorial combination of predictor variables allowing an exploration of the resulting range of uncertainties [30].

All models were fitted with BIOENSEMBLES, a platform for computer-intensive ensemble forecasting of bioclimatic models (e.g. [30]). Models included three presence-only methods (BIOCLIM, DOMAIN and Mahalanobis [31]), two presence-background methods (MaxEnt [32] and GARP [33]) and four presence–absence methods (GLM, GAM, MARS and GBM). As we do not have true absences in our data, we generated randomly selected pseudo-absences across the cells in the region of interest without records of bison while keeping prevalence constant at 0.13 (the value found in the pooled dataset).

We randomly split the fossil and contemporaneous distributions data into 75% for calibration and 25% for evaluation, repeating the procedure 10 times. Every model run yielded a projection; 'True Skill Statistics' (TSS) measured the matching between predictions and observations in the 25% evaluation data. TSS-weights, indicating model performance, were obtained for every model run and eventually used to weight the different models for their ability to predict the data. For each dataset (five periods and one 'pooled' set), bison data were modelled using nine model types × seven variable combinations × 10 cross-validated samples for a total of 630 model runs per dataset (i.e. 3780 model runs in total).

To generate a consensus across all individual model projections, first we removed all poorly performing projections (i.e. with $\text{TSS} < 0.4$ in the evaluation data) [34]. Then, we overlaid the remaining projections and considered a site suitable if models agreed at least 40% of the time. This is an arbitrary measure of agreement among models that is less conservative than the 50% consensus threshold used in several forecasting studies (e.g. [30,35]), and which provided reasonable results in tests using artificial data (F. G. Guilhaumon & M. B. Araújo 2012, unpublished data; see also [36]). With presence–absence methods and MaxEnt, we used the 0.13 prevalence value as the cut-off to convert probabilities or continuous suitability scores (from 0 to 1) into estimates of presence and absence [37,38]. With the distance-based presence-only methods, we used thresholds usually fixed in the literature at 0.95 for BIOCLIM and DOMAIN, and 0.75 for Mahalanobis, while for GARP we used default options to set the threshold internally. Specific details on the parametrization of each model are provided (see the electronic supplementary material, table S2). We used the binary thresholded results (figure 2) from both the 'within' and pooled' probability of occurrences to help calibrate coalescence models.

(b) Step 2: demographic model set-up for bison

The first step to create demographic models from the BEMs involved examining the number of separate populations at each time slice and the relative geographic extents of those populations through time. Criteria for defining a population were: (i) a continuous set of cells separated from other such continuous groups by modelled unsuitable habitats; (ii) clear evidence that bison had existed at locations at some point in the past; and (iii) that enough fossil evidence and ancient DNA were available to generate population parameters usable for demographic model testing.

The approach so far only considers climate drivers in the creation of demographic models. However, biotic interactions (e.g. predation) can dramatically impact demography, and this is especially true with regard to bison. Archaeological evidence supports increased human occupation [39], decreased numbers of bison fossils [39] and bison hunting from Alaska to New Mexico [40–42] starting around 10 ka. Most evidence of large-scale bison hunting, including communal bison hunting with use of corrals and jumps, occurred in the Mid-Holocene, beginning at approximately 5–6 ka (reviewed by Bamforth [43]). For example, the oldest corral site is in Scoggin, Wyoming and dates to approximately 5.2 ka [43]. Furthermore, jump sites, which date back to a similar time period, became increasing frequent after approximately 3.2 ka [43]. Together, evidence of bison hunting suggests that most large-scale hunting occurred after approximately 5 ka and into the Late Holocene. The arrival of European settlers on bison populations during historic times is perhaps an even greater impact on Bison demography. The introduction of firearms and the European horse in approximately AD 1700 resulted in large-scale slaughter for private and commercial interests, which ultimately almost drove the species to extinction by the end of the nineteenth century [43,44]. We used all the information above to create alternative demographic models that represent either 'within' or 'pooled' BEM results, along with different biotic interactions. The models are described in more detail in the Results section, as well as in figure 3 and table 1.

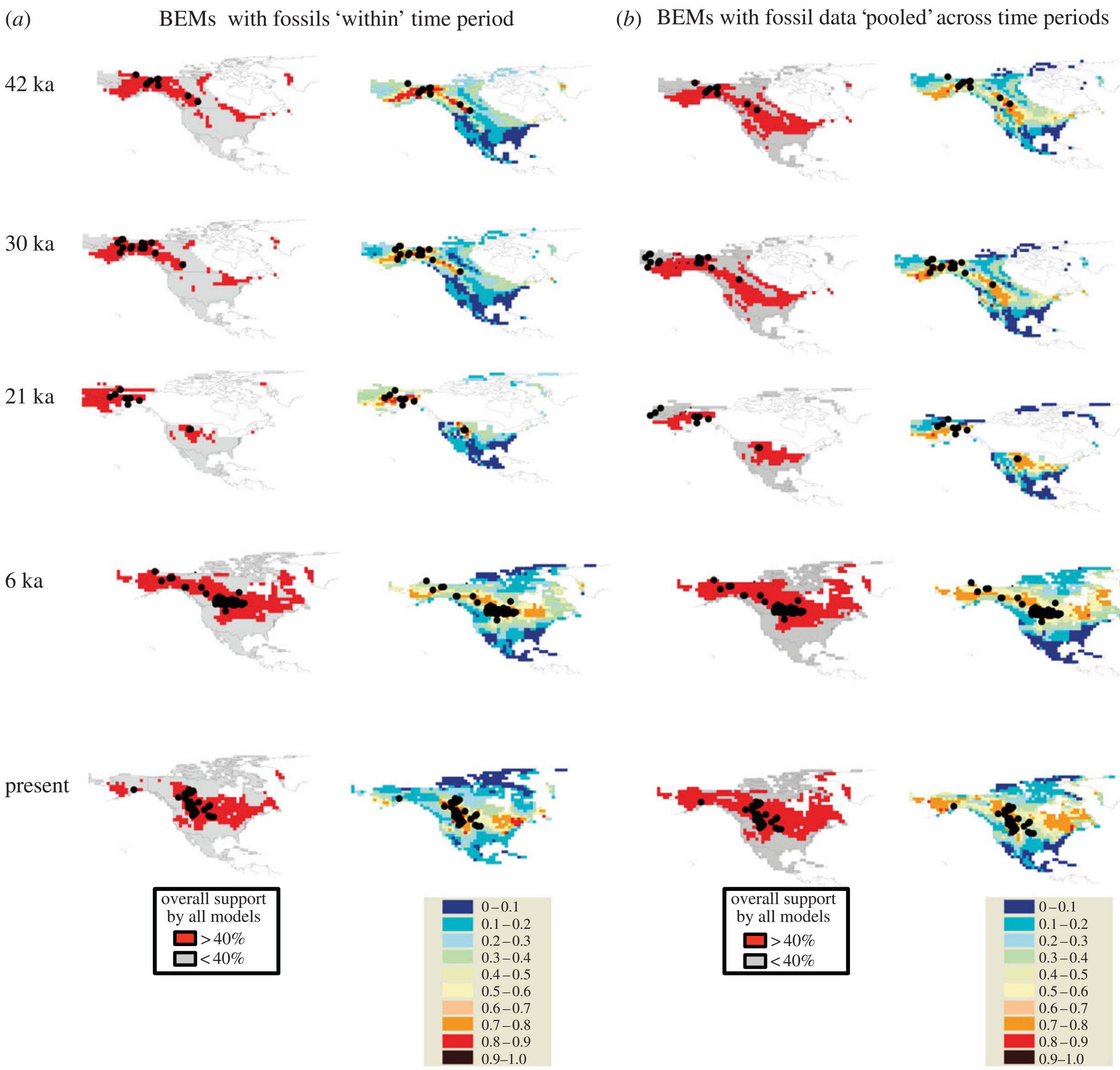

Figure 2. BEMs predicting suitable habitat for *B. bison* over five time periods: 42, 30, 21, 6 and 0 ka. The areas for which over 40% of models resulted in suitable habitat are shown in dark shading on the left side of each panel and the overall probability of an area containing suitable bison habitat is shown on the right of each panel. (*a*) The 'within period' refers to climatic envelopes calibrated and projected within each period of time. (*b*) The 'pooled period' uses all the data for each period to create a summary environmental niche space that is projected to each time slice. Fossil localities are shown as black dots. (Online version in colour.)

(c) Step 3: genetic data and analysis

Ancient DNA sequence data for bison were originally published and analysed by Shapiro *et al.* [7] and Drummond *et al.* [15]. To estimate the probability of each of the three demographic models, we used 615 bp of control region mitochondrial DNA sequence data for 159 North American, contemporary, historic and radiocarbon-dated bison samples spanning 60 000 years [7].

We used the software program Bayesian Serial Simcoal (BayeSSC) [45] to simulate 500 000 iterations of the different demographic scenarios (see the electronic supplementary material, input files for prior distributions) and the 'abc' R package [46] to estimate demographic parameters and determine the best-supported demographic model. We chose an approximate Bayesian computational (ABC) setting [47] to determine which demographic model was best supported. In general, estimates obtained with full likelihood-based approaches should be more reliable than ABC estimates because they use information from the complete data rather than summarized statistics. However, ABC is more flexible, can compute multi-population demographic models in a reasonable amount of time and computational power, and can be used for direct model selection [47,48]. To model demographic scenarios using BayeSSC, populations were grouped in different statistics groups using age ranges (in generations) that reflected the BEM time frames described in step 1 (i.e. 42, 30, 21, 6, 0 ka ±3000 years) and the time frames between BEMs (before 45 ka, 33–39 ka and 9–18 ka). For time periods with two populations, fossils were either assigned to the northern or southern population depending on their location (see the electronic supplementary material, tables S1 and S3, and input files).

We chose segregating sites, nucleotide diversity and pairwise Fst as summary statistics for the analysis. This adds up to a total of 28 summary statistics. In general, more information can be added by increasing the number of summary statistics; however, too many summary statistics add stochastic noise to the analysis, and thus increase the error estimating the distance between empirical to simulated data during the regression step [47,49]. We thus used an algorithm introduced by Blum & Francois [50], which is based on nonlinear regression and uses neural networks to optimize the dimensionality. The choice of the tolerance level used in the analysis can have a strong impact on the demographic model results, and thus we used different levels in our analysis. We used tolerance levels of 0.002, 0.004 and 0.008, thereby accepting the 1000, 2000 and 4000 closest values, respectively, for the ABC parameter estimations. Expected deviance according to the deviance information criterion (DIC) [51],

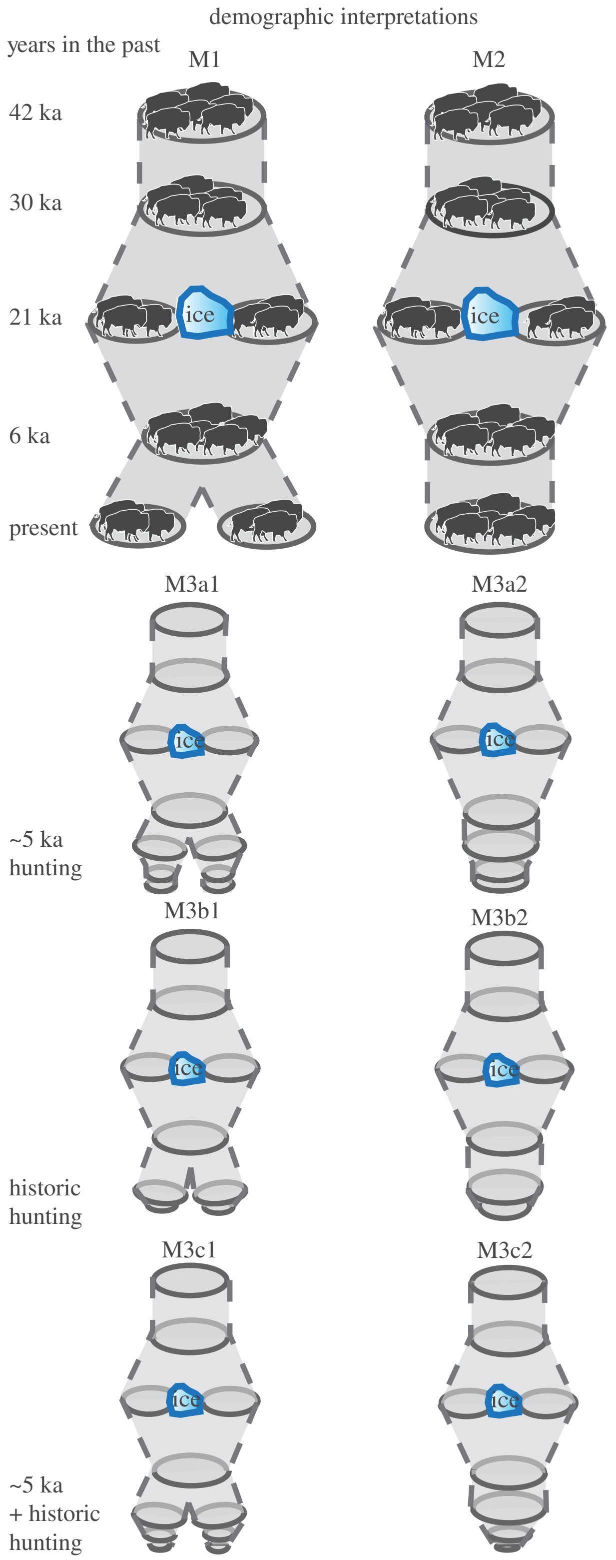

Figure 3. Demographic models based on BEMs (M1 and M2) and a combination of BEMs and additional data (M3 variants). Each model illustrates the number of populations (number of discs) and relative size (width of disc) through time. Model 3 includes six variants that include large-scale bison hunting by Native Americans starting around 5 ka (M3a), large-scale bison hunting by European settlers (M3b) and a combination of both hunting events (M3c). Each hunting scenario is included in a model based on M1 (e.g. M3a1, M3b1 and M3c1) or M2 (e.g. M3a2, M3b2 and M3c2). (Online version in colour.)

implemented in the R package 'abc', was applied to infer the best-supported demographic model. We simulated the respective demographic models with 1000 iterations using the parameters of each iteration separately (sampled from the posterior distribution) as fixed model parameters. The summary statistics were then used to calculate DIC values.

To determine meaningful upper limits for the modern population size, we first performed initial runs using broad uniform priors ranging up to 30 000 000. Excessively broad priors can destabilize ABC parameter estimation. We simulated 1000 datasets and performed an ABC analysis, which showed that the higher values resulted in unreasonably high estimates of genetic diversity and that the ABC analysis clearly favoured smaller modern population size values. Thus, the upper limit for the modern population size was refined to 100 000, which resulted in a much higher effective number of simulations. This estimate was used in the full 500 000-iteration simulations.

3. Results

(a) Step 1: estimating the bioclimatic envelope of bison through time

Both 'within period' and 'pooled period' BEMs showed similar trends but with some key differences (figure 2). Overall, bison appear to have relatively continuous ranges across temperate and boreal North America from 42 ka to present, with habitat expanding after the LGM at 21 ka, when the Laurentide ice sheet began to retreat. The most notable difference between the two sets of suitable habitat predictions was the separation of northern and southern populations between 6 ka and the present day in the 'within period' BEMs (M1), while the 'pooled period' BEMs suggested panmixia during this time period.

(b) Step 2: demographic model parameterizations

We generated three main demographic model sets: (i) those based solely on climatic drivers from the 'within time-period BEMs'; (ii) those based solely on climatic drivers from the 'pooled BEMs'; and (iii) those that deviate from the BEMs (both 'within' and 'pooled') at certain time periods given the evidence of human impacts, including presumed impacts of Native American 'jump' and 'corral' hunting from approximately 5 to 0.9 ka and the massive impact of European settlement and hunting from approximately 0.3 ka to present. The first two models, M1 and M2, are consistent with the BEM results, and show single populations at 42 and 30 ka, and split at the LGM owing to the ice sheet covering large portions of North America. Populations re-merge in the Holocene for both M1 and M2. The models differ in that in M1 populations split again between 6 ka and the present, while in M2 there is no split. The models M3a1 (based on M1) and M3a2 (based on M2) include a bison population bottleneck resulting from human hunting between 5 and 0.9 ka (figure 3 and table 1). Models M3b1 and M3b2 include a bottleneck during historic times, reflecting intesive, large-scale hunting by European settlers from 300 years ago to the present. Finally, models M3c1 and M3c2 include both potential hunting-caused bottlenecks.

(c) Step 3: genetic data and analysis

The DIC analyses inferred the best support for the M3b2 model (using a tolerance level of 0.008; see table 2; electronic supplementary material, table S4). This model includes the historic bottleneck and is based on M2, thus including only one panmictic modern population. The second-best-supported model is M2 (tolerance: 0.002), followed by M3a2 (tolerance: 0.002).

Table 1. Description of demographic models tested with modern and ancient genetic data. Model 1 is based on BEMs calculated independently 'within' each time period, whereas model 2 is based on a conglomerate of 'pooled' climatic niche conditions experienced by the species throughout the Quaternary. Model 3 variants are based on models 1 and 2, but include potential bison population declines owing to hunting by humans.

	model 1	model 2
BEMs demographic model	single population between 42 and 30 ka; population splits between 30 and 21 ka; population merge between 11 and 8 ka, and split between approximately 5 and 1 ka	single population between 42 and 30 ka; population splits between 30 and 21 ka; population merge between 11 and 8 ka
BEM + end Pleistocene/Mid–Late Holocene decline (M3a)	BEM Model 1 + population decline between approximately 5 and 0.9 ka (M3a1)	BEM Model 2 + population decline between approximately 5 and 0.9 ka (M3a2)
BEM + historic decline (M3b)	BEM Model 1 + population decline between the approximately 0.3 ka and the present (M3b1)	BEM Model 2 + population decline between approximately 0.3 ka and the present (M3b2)
BEM + end Pleistocene/Mid–Late Holocene decline + historic decline (M3c)	BEM Model 1 + population decline between approximately 5 and 0.9 ka + decline between the approximately 0.3 ka and the present (M3c1)	BEM Model 2 + population decline between approximately 5 and 0.9 ka + decline between approximately 0.3 ka and the present (M3c2)

4. Discussion

(a) Best-supported model

In our case study, we integrated multiple lines of evidence to determine the patterns, and perhaps some of the processes, that have led to bison demographic and distribution shifts through time. Our demographic models included population subdivisions and reconnection over time rather than simply considering range-wide estimates of area, such as did Lorenzen *et al.* [5]. Of the demographic models we generated, the best-supported model was based on a combination of climate and potential influences of bison hunting by humans during historic (later than 0.3 ka) times (M3b2). The decrease in population size of bison in historic times can be reasonably attributed to decimation of bison populations by European settlers, a well-documented event [52,53]. It is notable that despite variation in importance of human impacts, the three best models were based on the 'pooled' BEM outputs, supporting the view of negligible climate niche evolution during the Late Quaternary (e.g. [54]) and the advantage of characterizing species climatic niches with as much fossil data as possible [9].

Overall, these results highlight the complexity of integrating multiple data types and attempting to invoke causation from various drivers. Additionally, integration of these data types is particularly challenging given that each step has assumptions and data limitations that may compromise the ability to make proper inferences. We think it is essential to detail those challenges for each step as our main goal is to critically assess and advance methods for rigorous hypothesis testing and falsification frameworks.

(b) Challenges in constructing bioclimatic envelope models over time (step 1)

We observed differences in BEM results across methods in our study, and also highlight that our results are different compared with those of Lorenzen *et al.* [5]. Overall, there was less suitable habitat predicted using the 'within period' approach, which was to be expected because the bioclimatic 'envelope' characterized was a subset of the envelope characterized with all data. A more substantial difference in projected suitable habitat was observed by Lorenzen *et al.* [5]. Lorenzen and colleagues predicted a decrease in suitable habitat for bison at 6 ka, while our results showed a clear increase in suitable bison habitat for this time period, a result also found by Martinez-Meyer *et al.* [10]. These differences may be driven by our use of additional fossil locality data for Holocene North American bison from Harington [26], illustrating the pitfalls of incomplete sampling that is nearly ubiquitous for fossil datasets [11,55]. Additionally, in our study, we masked ice sheets during the LGM as unsuitable habitat to further improve the accuracy of our BEMs.

Another consideration when constructing BEMs is that the palaeoclimate data are modelled based on incomplete pollen and isotope records interpolated across very coarse geographic scales (in our case, the grain of the climate data layers was approx. 48 000 km^2). Further, bioclimatic modelling choices may add additional sources of uncertainty [56,57]. Here, we have used an ensemble modelling approach to account for differences generated from modelling approaches, and thresholds based on current best practices. We recognize, as has been shown in the literature, that such choices impact model results [38], and future efforts can better quantify uncertainties based on differences in those choices.

(c) Challenges in constructing demographic models (step 2)

The translation of distribution predictions into demographic models requires several major assumptions about suitable habitat, population size and gene flow. First, it is assumed that suitable habitat predictions reflect *actual distributions* rather than *potential distributions*. However, BEMs represent potential distributions, but actual distributions are most likely to link to demographic estimates generated from

Table 2. DIC values for the ABC model selection. Models are ranked according to their support. Model description can be found in table 1. The no. of accepted values indicates the number of values accepted in the nonlinear regression step.

model	no. of accepted values	DIC
M3b2	4000	8.978
M2	1000	9.093
M3a2	1000	9.324
M3c1	1000	9.366
M1	1000	9.366
M3a1	1000	9.531
M3c1	2000	9.565
M3c2	4000	9.631
M2	2000	9.645
M3c1	4000	9.650
M3a2	4000	9.679
M3b2	1000	9.742
M2	4000	9.793
M3b1	4000	9.798
M1	4000	9.878
M3a1	4000	9.951
M3b1	1000	10.171
M1	2000	10.207
M3a1	2000	10.713
M3b1	2000	10.839
M3c2	2000	11.273
M3c2	1000	199.855
M3a2	2000	199.855
M3b2	2000	199.855

genetic data. Second, changes in effective population size (N_e—as estimated by genetics data) may lag or not reflect changes in census size (N_c—as counted on the landscape) [58]. Third, when a population subdivides at some point in the past, but reunites in the future, the two previously distinct populations may not interchange genetic information after contact, as presumed in our demographic models. A challenge for the future is to investigate how past potential distributions relate to demographic events and evolutionary processes such as introgression or reinforcement likely to be recorded in the genetic signal.

Another major issue is whether the five time periods covered by the BEMs were the most important for driving demographic changes in bison. Of particular concern is the lack of a climate reconstruction for the tumultuous climatic time period at the Pleistocene/Holocene transition. The transition between the Late Pleistocene Younger Dryas cold period (approx. 12.9–11.7 ka) and the onset of Holocene warming was rapid [59–62], and associated with the extinction of iconic North American Late Pleistocene megafauna [39,63]. During that climatically chaotic time period, human populations were expanding across North America after their initial arrival around 15 ka [64]. This time period would have been important for a robust model of bison historical demography.

Finally, the time periods covered by the BEMs left large temporal gaps and included large bins (±3000 years) around each time period. Future research should explore the breadth of time bins for different palaeoclimate periods because ±3000 years may not be appropriate in some cases. Recent advances in climate modelling allow for climate reconstructions for tighter and sequential time periods, which will be likely to improve our ability to iteratively test results and better correlate suitable habitat and genetic demographic signals.

(d) Challenges testing the demographic models with genetic data (step 3)

The use of ABC methods to estimate parameter values such as population size and timing of bottlenecks helps us to get around some of the limitations of hypothesis testing in that it is possible to explore a broad range of priors for each demographic model (i.e. hypothesis) without being limited to a strict interpretation of population-genetic parameters. However, even with the use of ABC approaches, it is still necessary to select a set of informative summary statistics useful for comparing the simulated and empirical datasets in order to assess the fit of the model to the data (see [46,65–67]).

A final challenge with genetic data is a lack of power. In our case study, we estimate values for population-genetic parameters using a single-gene ancient DNA dataset. Population-genetic estimates based on a single gene with small sample sizes (approx. $n = 10–15$) covering many time periods will carry a large amount of uncertainty and, in the case of mitochondrial DNA, only represent the biogeographic history of the maternal lineage. In general, we found a lack of power given our genetic data during important climatic time frames (e.g. LGM and Mid-Holocene), which is partly limited by opportunistic sampling of the fossil record. Temporal genetic data from multiple genes will provide much better power in discriminating among alternative demographic models. Genomic ancient DNA datasets will allow evolutionary biologists to refine estimates of effective population size and migration rates through time.

5. Overall conclusion

Combining datasets from multiple sources (e.g. climate, fossil and DNA), while powerful and needed, can also lead to compounding uncertainty with progress through the workflow (see electronic supplementary material, figure S1). While it is tempting to believe that more data will help untangle the thorny problems of inferring past events, it is possible that what is required is not more data, but the right kind of data with limited biases and uncertainties. For example, the addition of large archaeological datasets documenting human presence, such as in Nogues-Bravo *et al.* [9] and Lorenzen *et al.* [5], is another important data type to include in studies of species biogeography. These data may be helpful for understanding time periods when species' demographies may become strongly decoupled from their previous distributions owing to biotic interactions (e.g. high kill rates by humans).

The approach championed here is to consider multiple datasets over multiple time periods with direct translation of suitable habitat predictions into demographic models that can be contrasted with demographic models that diverge from climate at particular time points where evidence of other biotic or abiotic drivers exist. We believe that despite the challenges, full utilization of multiple data types (e.g. DNA, fossils and palaeoclimate) considered over multiple time periods is essential for taking the next steps towards more realistic models and tests of species' historical biogeography.

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Legend for Supplementary Figure

Supplemental Figure 1. A summary of data inputs and subsequent analysis for the workflow presented here, with an outline of assumptions at each step. Analysis results that become the input for another step in the workflow are highlighted with a red arrow. This figure illustrates the possible compounding of uncertainty that may be integrated into a workflow and affect the final estimate of a species' historical biogeography.

Supplementary Tables

Table S1. Sample information. Samples included in this study. Samples with reference names beginning with "BS" were originally published in Shapiro *et al.* [7] and those labeled "Harrington" were published in Harrington [21], and those labeled "Guthrie" were published in [42]. We list museum, accession number, fossil locality information, associated latitude and longitude data, radiocarbon data and reference, age (radiocarbon) of fossils, calibrated age of fossils (Cal) and standard error (SE), whether the sample was included in BEMs, time frame of fossil relevant for BEM and BayeSSC models, whether the samples was included in Bayesian Serial Simcoal analyses (SSC) and if it was in the north or south region (N/S), the genbank number for genetic data, and the age of the fossil in number of generations (for BayeSSC simulations). Generation time was based on a generation time of 4years.

Sample	Museum	Accn. No.	Location	latitude	longitude	Radiocarbon Accn. No.	Age	Cal	SE	in BEMs	BEM bin (kya)	in SSC	N/S	Genbank #	# gens
BS162	UAF	NA	Anchorage, AK	61.220	-149.900	Beta 136732	170±30	178	87	yes	0	yes	n	AY748509	44.5
BS123	ADFG	RS-9201	Black R.. Yukon Flats, AK	66.654	-143.722	NA	1730±60	1644	76	yes	0	yes	n	AY748489	411
BS289	ADFG	RS-0105	Black R.. Yukon Flats, AK	66.654	-143.722	OxA-11248	2172±37	2205	74	yes	0	yes	n	AY748581	551.25
BS490	ADFG	RS-0201	Birch Cr., Yukon Flats, AK	66.256	-145.850	OxA-11990	2415±25	2430	90	yes	0	yes	n	AY748717	607.5
BS517	ADFG	RS-0202	Birch Cr., Yukon Flats, AK	66.256	-145.850	OxA-11989	2526±26	2614	76	yes	0	yes	n	AY748734	653.5
BS503	ADFG	RS-0001	Black R.. Yukon Flats, AK	66.654	-143.722	OxA-11631	2776±36	2872	48	yes	0	yes	n	AY748728	718
BS102	CMN	CMN 10405	Murdoch Cr., Wood Bison NP, AB	58.700	-113.530		collected 1928	22	-	yes	0	yes	s	AY748478	5.5
BS099	CMN	CMN 8755	Salt R., Salt Prarie, AB	55.661	-115.830		collected 1924	26	-	yes	0	yes	s	NA	6.5
BS100	CMN	CMN 4538	Fort Smith, AB	60.017	-111.967		collected 1921	29	-	yes	0	yes	s	AY748477	7.25
BS469	PMA	1912R1A1-8	Banff National Park, AB	51.600	-116.100	BGS-2054,	50±75,	119	82, 44	yes	0	yes	s	AY748705	29.75

						OxA-11988	305±24								
BS456	PMA	P68.2.1052	Boss Hill Arch site, Stettler, AB	52.311	-112.622	OxA-11580	125±30	123	80	yes	0	yes	s	AY748695	30.75
BS200	SFU	6584	Fort D'Epinette, Peace R., BC	56.233	-120.750	OxA-10579	145±37	146	84	yes	0	yes	s	AY748530	36.5
BS175	KU	KU 23002	Ice Cave, MT	45.160	-108.400	OxA-11195	186±30	179	90	yes	0	yes	s	AY748519	44.75
BS424	PMA	P02.1.1	Fort Vermilion, AB	58.400	-116.020	OxA-11625	202±32	179	94	yes	0	yes	s	AY748675	44.75
BS454	PMA	1797R1A1-1	Panther R., Banff NP, AB	*51.400*	*-116.200*	OxA-11587	287±29	382	55	yes	0	yes	s	AY748693	95.5
BS445	PMA	1326R100A1-1	Banff NP, AB	51.600	-116.100	OxA-11593	378±30	445	59	yes	0	yes	s	AY748690	111.25
BS444	PMA	P85.13.1	Edmonton, AB	53.340	-113.310	OxA-11582	636±29	598	34	yes	0	yes	s	AY748689	149.5
BS437	PMA	P68.2.1077	Boss Hill Arch site, Stettler, AB	52.311	-112.622	OxA-11578	693±33	658	41	yes	0	yes	s	NA	164.5
BS434	PMA	P68.2.1039	Boss Hill Arch site, Stettler, AB	52.311	-112.622	OxA-11623	809±32	718	28	yes	0	yes	s	AY748682	179.5
BS422	PMA	P00.1.12	Byrtus Site, Athabasca, AB	54.716	-113.300		908±31	838	49	yes	0	yes	s	AY748673	209.5
BS417	PMA	572R30E6-2	Waterton Lakes NP, AB	49.100	-113.900	OxA-11590	909±29	842	48	yes	0	yes	s	AY748669	210.5
BS441	PMA	572R30G-2	Waterton Lakes NP, AB	49.100	-113.900	OxA-11591	1273±32	1221	42	yes	0	yes	s	AY748687	305.25
BS198	YDFW	YG	Braeburn, YT	61.250	-135.750	Beta 137731	2460±40	2539	103	yes	0	yes	s	AY748528	634.75
BS560	MW	#30, MW07	Hitching Post Ranch, Calgary, AB	51.080	-114.080	OxA-12123	2807±28	2908	37	yes	0	yes	s	AY748739	727
H1	NA	NA	Ward et al. 1999	NA	NA	NA	modern	NA	NA	no	0	yes	s	AF083357	~0
H2	NA	NA	Ward et al. 1999	NA	NA	NA	modern	NA	NA	no	0	yes	s	AF083358	~0
H3	NA	NA	Ward et al. 1999	NA	NA	NA	modern	NA	NA	no	0	yes	s	AF083359	~0
H4	NA	NA	Ward et al. 1999	NA	NA	NA	modern	NA	NA	no	0	yes	s	AF083360	~0
H5	NA	NA	Ward et al. 1999	NA	NA	NA	modern	NA	NA	no	0	yes	s	AF083361	~0
H6	NA	NA	Ward et al. 1999	NA	NA	NA	modern	NA	NA	no	0	yes	s	AF083362	~0
H7	NA	NA	Ward et al. 1999	NA	NA	NA	modern	NA	NA	no	0	yes	s	AF083363	~0
H8	NA	NA	Ward et al. 1999	NA	NA	NA	modern	NA	NA	no	0	yes	s	AF083364	~0
u12935	NA	NA	Beech	NA	NA	NA	modern	NA	NA	no	0	yes	s	u12935	~0
u12936	NA	NA	Beech	NA	NA	NA	modern	NA	NA	no	0	yes	s	u12936	~0
u12941	NA	NA	Beech	NA	NA	NA	modern	NA	NA	no	0	yes	s	u12941	~0
u12943	NA	NA	Beech	NA	NA	NA	modern	NA	NA	no	0	yes	s	u12943	~0

u12944	NA	NA	Beech	NA	NA	NA	modern	NA	NA	no	0	yes	s	u12944	~0
u12945	NA	NA	Beech	NA	NA	NA	modern	NA	NA	no	0	yes	s	u12945	~0
u12946	NA	NA	Beech	NA	NA	NA	modern	NA	NA	no	0	yes	s	u12946	~0
u12947	NA	NA	Beech	NA	NA	NA	modern	NA	NA	no	0	yes	s	u12947	~0
u12948	NA	NA	Beech	NA	NA	NA	modern	NA	NA	no	0	yes	s	u12948	~0
u12955	NA	NA	Beech	NA	NA	NA	modern	NA	NA	no	0	yes	s	u12955	~0
u12956	NA	NA	Beech	NA	NA	NA	modern	NA	NA	no	0	yes	s	u12956	~0
u12957	NA	NA	Beech	NA	NA	NA	modern	NA	NA	no	0	yes	s	u12957	~0
u12958	NA	NA	Beech	NA	NA	NA	modern	NA	NA	no	0	yes	s	u12958	~0
u12959	NA	NA	Beech	NA	NA	NA	modern	NA	NA	no	0	yes	s	u12959	~0
Harington	NA	NA	Oldman River Dam Area	-114.000	49.580	AECV-1242C	190±100	195	128	yes	0	no	NA	NA	NA
Harington	NA	NA	Old Woman's Buffalo Jump, S of Calgary, AB, CAN	-113.883	50.467	AECV-1899C	180±70	174	105	yes	0	no	NA	NA	NA
Harington	NA	NA	Pine Coulee Reservoir, AB, CAN	-113.767	50.217	AECV-1917C	170±70	168	101	yes	0	no	NA	NA	NA
Harington	NA	NA	Miller Site, AB, CAN	-113.367	52.250	AECV-293C	210±60	191	114	yes	0	no	NA	NA	NA
Harington	NA	NA	St. Mary R., AB, CAN	-113.200	49.117	S-844	130±85	148	98	yes	0	no	NA	NA	NA
Harington	NA	NA	Fryberger Coulee: Dinosaur Provincial Pk, Red Deer, AB, CAN	-111.550	50.770	AECV-1270C	180±90	182	119	yes	0	no	NA	NA	NA
Harington	NA	NA	Forty Mile Coulee, AB, CAN	-111.417	49.583	Beta-19801	230±90	245	135	yes	0	no	NA	NA	NA
Harington	NA	NA	See-everywhere, Suffield Military Reserve, S Saskatchewan drainage, AB, CAN	-110.900	50.360	S-1014	160±60	159	91	yes	0	no	NA	NA	NA
Harington	NA	NA	Wanuskewin Heritage Pk., S Saskatchewan R, SK, CAN	-106.500	52.170	S-2805	<100	~0		yes	0	no	NA	NA	NA
Harington	NA	NA	Lovstrom, S of Brandon, 373.5m asl, MB, CAN	-99.942	49.500	S-2823	230±90	245	135	yes	0	no	NA	NA	NA
Harington	NA	NA	Tiger Hills, N of Ninette, Pembina drainage, AB, CAN	-99.617	49.500	S-3500	140±140	188	131	yes	0	no	NA	NA	NA
BS173	KU	KU 42887	Natural Trap Cave, WY	44.500	-108.200	OxA-11271	3220±45	3,438	51	yes	6	yes	s	AY748518	859.5
BS177	KU	KU 44361	Natural Trap Cave, WY	44.500	-108.200	OxA-11169	3155±36	3,383	39	yes	6	yes	s	AY748521	845.75

BS466	PMA	P79.26.1	Llyodminster, AB	53.283	-110.000	OxA-11618	3298±37	3,524	47	yes	6	yes	s	AY748702	881
BS569	MW	EiPo-51, MW03	Hitching Post Ranch, Calgary, AB	51.080	-114.080	Beta-1627	3600±70	3,910	102	yes	6	yes	s	AY748747	977.5
BS423	PMA	Unit14 Level V	Stampede Site, Cypress Hills, AB	49.630	-110.210	OxA-11579	4660±38	5,402	59	yes	6	yes	s	AY748674	1350.5
BS464	PMA	P96.10.34	Edmonton, AB	53.340	-113.310	OxA-11610	5205±45	5,965	68	yes	6	yes	s	AY748700	1491.25
BS222	CMN	CMN 12087	Baillie Island, NWT	70.517	-128.350	OxA-11165	6110±45	6,991	83	yes	6	yes	s	AY748545	1747.75
BS439	PMA	P80.42.1	Horse Hills Pit, Edmonton, AB	51.080	-114.080	OxA-11624	5845±45	6,661	61	yes	6	yes	s	AY748685	1665.25
BS429	PMA	17 R 9	Tuscany Site, Calgary, AB	51.080	-114.080	OxA-11585	6775±40	7,626	29	yes	6	yes	s	AY748678	1906.5
BS419	PMA	47 T 10	Tuscany Site, Calgary, AB	51.080	-114.080	OxA-11622	7475±45	8,295	55	yes	6	yes	s	AY748671	2073.75
BS426	PMA	12 Q 62	Stampede Site, Cypress Hills, AB	49.630	-110.210	OxA-11589	7060±45	7,891	46	yes	6	yes	s	AY748676	1972.75
BS428	PMA	30 O 1	Stampede Site, Cypress Hills, AB	49.630	-110.210	OxA-11581	7105±45	7,938	45	yes	6	yes	s	AY748677	1984.5
BS432	PMA	41 Q 1	Tuscany Site, Calgary, AB	51.080	-114.080	OxA-11583	7310±45	8,108	55	yes	6	yes	s	AY748680	2027
BS465	PMA	Unit9 Level A	Stampede Site, Cypress Hills, AB	49.630	-110.210	OxA-11614	7115±50	7,945	49	yes	6	yes	s	AY748701	1986.25
BS425	PMA	P69.17.19	Duffield Site, AB	53.340	-114.200	OxA-11586	6400±400	7263	411	yes	6	no	NA	NA	NA
BS414	ADFG	RS-9202	Black R.. Yukon Flats, AK	66.654	-143.722	Beta 65662	4495±60	5,149	107	yes	6	no	NA	NA	NA
BS171	UAF	A-191	Chalkyitsik, AK	66.650	-143.720	Beta 136731	4390±70	4992	125	yes	6	no	NA	NA	NA
Harrington	NA	NA	Finn Bog, SE of Strehlow Pond, 517m asl. 8.5 km N of Dundurn, SK, CAN	-106.330	51.830	NA	2925 or 3005±110			yes	6	no	NA	NA	NA
Harrington	NA	NA	Bellis, N Saskatchewan R, AB, CAN	-112.230	54.050	NA	2980±130			yes	6	no	NA	NA	NA
Harrington	NA	NA	Aldon Plant, S. Saskatchewan drainage, AB, CAN	-110.720	50.030	NA	3000±80			yes	6	no	NA	NA	NA
Harrington	NA	NA	N shore of Whitemouth R., 259 m asl, MB, CAN	-96.035	50.122	NA	3125 or 3205±135			yes	6	no	NA	NA	NA
Harrington	NA	NA	N bank of Souris R, 542 m asl, SK, CAN	-103.500	49.330	NA	3250 or 3330±95			yes	6	no	NA	NA	NA
Harrington	NA	NA	Whitemud Ck, N. Saskatchewan R valley, near Edmonton, AB, CAN	-113.670	53.500	NA	3255±90			yes	6	no	NA	NA	NA
Harrington	NA	NA	Mitigation, AB, CAN	-112.220	51.970	NA	3420±100			yes	6	no	NA	NA	NA

Harrington	NA	NA	Kame Hills, NW corner of Southern Indian L., 259 m asl, MB, CAN	-98.550	57.500	NA	3510 or 3590±90	yes	6	no	NA	NA	NA
Harrington	NA	NA	S. Saskatchewan River, 500m asl, AB, Can	-107.091	51.438	NA	3530 or 3610±115	yes	6	no	NA	NA	NA
Harrington	NA	NA	Red River, MB, CAN	-97.038	50.025	NA	3560 or 3640±100	yes	6	no	NA	NA	NA
Harrington	NA	NA	Okotoks, AB, CAN	-113.920	50.750	NA	3660 or 3740±150	yes	6	no	NA	NA	NA
Harrington	NA	NA	Conglomerate valley: on a bench near the confluence with Frenchman R, 950 m asl, SK, CAN	-109.050	49.500	NA	3970 or 4050±80	yes	6	no	NA	NA	NA
Harrington	NA	NA	Kirriemuir Bison: Sounding Ck.drainage, aB, CAN	-110.320	51.820	NA	3970±110	yes	6	no	NA	NA	NA
Harrington	NA	NA	Fort Saskatchewan Urban Park, AB, CAN	-113.230	53.700	NA	4100±90	yes	6	no	NA	NA	NA
Harrington	NA	NA	Belly River, AB, CAN	-113.583	49.583	NA	4150 or 4230±105	yes	6	no	NA	NA	NA
Harrington	NA	NA	Charlie L. Cave, NW of Fort St. John, BC, CAN	-120.930	56.275	NA	4270 or 4350±160	yes	6	no	NA	NA	NA
Harrington	NA	NA	10.5 km upstream from the Francois-Finlay Dam, SK, CAN	-104.000	53.170	NA	4295 or 4375±85	yes	6	no	NA	NA	NA
Harrington	NA	NA	Harder site near Sakatoon, SK, CAN	-107.050	52.220	NA	4410 or 4515±120	yes	6	no	NA	NA	NA
Harrington	NA	NA	Riddell site, 4.8 km N of Sutherland, S Saskatchewan R, SK, CAN	-106.600	52.150	NA	4560 or 4640±115	yes	6	no	NA	NA	NA
Harrington	NA	NA	Pine Coulee Reseervoir	-113.767	50.217	NA	4610±90	yes	6	no	NA	NA	NA
Harrington	NA	NA	Fisherman L., Liard drainage , NT, CAN	-123.870	60.370	NA	4720 or 4800±160	yes	6	no	NA	NA	NA
Harrington	NA	NA	Whitemouth Falls, S of Lac du Bonnet, 267 m asl, MB, CAN	-96.017	50.117	NA	4860 or 4940±150	yes	6	no	NA	NA	NA
Harrington	NA	NA	Beaver Ck., S. Sasakatchewan R, SK, CAN	-106.750	51.917	NA	4940±155	yes	6	no	NA	NA	NA
Harring	NA	NA	Wanuskewin Heritage Park, S. Saskatchewan R, SK,CAN	-106.330	52.170	NA	5010 or	yes	6	no	NA	NA	NA

ton							5090±90						
Harrington	NA	NA	Elbow River, AB, CAN	-114.750	50.917	NA	5070 or 5150±160	yes	6	no	NA	NA	NA
Harrington	NA	NA	Harrow Bay, Cape Bathurst, Pen, NT, CAN	-127.999	70.533	NA	5230±200	yes	6	no	NA	NA	NA
Harrington	NA	NA	7 km S of Morris, 68 km S of Winnipeg, 228 m asl, in the Red River Valley, MB, CAN	-97.355	49.321	NA	5280 or 5380±120	yes	6	no	NA	NA	NA
Harrington	NA	NA	Bowsman R 6.4 km Wof Bowsman, MB, CAN	-101.310	52.238	NA	5350 or 5430±120	yes	6	no	NA	NA	NA
Harrington	NA	NA	Ste. Agathe, MB, CAN	-97.183	49.567	NA	5430±70	yes	6	no	NA	NA	NA
Harrington	NA	NA	McIntyre CK., Whitehorse, YT, CAN	-135.140	60.743	NA	5800 or 5840±70	yes	6	no	NA	NA	NA
Harrington	NA	NA	Strawberry Ck, N Saskatchewan R. valley, near Edmonton, AB, CAN	-113.830	53.500	NA	5865±135	yes	6	no	NA	NA	NA
Harrington	NA	NA	Pakan, N Saskatchewan R, AB, CAN	-112.330	54.030	NA	5900 or 6040±140	yes	6	no	NA	NA	NA
Harrington	NA	NA	Chin Coulee, 50 km SSE of Tabor, AB, CAN	-111.817	49.600	NA	5960 or 6020±230	yes	6	no	NA	NA	NA
Harrington	NA	NA	Waggle Springs, Assiniboine R, MB, CAN	-99.720	49.780	NA	6300 or 6380±100	yes	6	no	NA	NA	NA
Harrington	NA	NA	Castle R, near Pincher Creek, AB, CAN	-114.060	49.480	NA	6340 or 6420±140	yes	6	no	NA	NA	NA
Harrington	NA	NA	Ikpikpuk R., North Slope, AK	-154.410	70.810	NA	6400±50	yes	6	no	NA	NA	NA
Harrington	NA	NA	Battle Valley, on terrace in the Battle Ck valley, 1080 m asl, near Ft Walsh, SK, CAN	-109.520	49.520	NA	6570 or 6650±95	yes	6	no	NA	NA	NA
Harrington	NA	NA	Bow River, Calgary, AB, CAN	-114.080	51.030	NA	6580 or 6825±205	yes	6	no	NA	NA	NA
Harrington	NA	NA	village of bellvue, crownnest pass, ab, CAN	-114.691	49.635	NA	6610 or 6690±160	yes	6	no	NA	NA	NA
Harrington	NA	NA	bow corridor, AB, CAN	-115.133	51.067	NA	6630±100	yes	6	no	NA	NA	NA

Harrington	NA	NA	Lec des arc, bow valley, AB, CAN	-115.200	51.050	NA	6720±80			yes	6	no	NA	NA	NA
Harrington	NA	NA	Sullivan Pit, Sullivan Ck,tofty area, AK, USA	-150.865	65.098	NA	6730±260			yes	6	no	NA	NA	NA
Harrington	NA	NA	oxbow Dam, Scouris R., SK, CAN	-102.167	49.217	NA	6810±90			yes	6	no	NA	NA	NA
Harrington	NA	NA	Swan River, 2.5 Km SW of Harlington, MB, CAN	-101.470	52.000	NA	6960 or 7040±100			yes	6	no	NA	NA	NA
Harrington	NA	NA	Head-smashed in buff jump, AB, CAN	-113.650	49.717	NA	7065±175			yes	6	no	NA	NA	NA
Harrington	NA	NA	S. Saskatchewan Valley, AB, Can	-111.670	50.670	NA	7150±150			yes	6	no	NA	NA	NA
Harrington	NA	NA	Notukeu CK, Wood R drainage, SK, Can	-107.400	49.720	NA	7165±320			yes	6	no	NA	NA	NA
Harrington	NA	NA	Crowsnest Pass, AB, Can	-114.600	49.630	NA	7200±230			yes	6	no	NA	NA	NA
BS449	PMA	L EE31 No. 21068	Stampede Site, Cypress Hills, AB	49.630	-110.210	OxA-11621	6195±45			yes	6	no	NA	AY748691	NA
BS130	UAF	UA-79-123-59	Porcupine R. Cave, AK	66.500	-145.300	Beta 18552	9000±250	10113	342	yes	9-18	yes	n	AY748496	2528.25
BS321	UAF	XMH-246	Gerstle R., near Fairbanks, AK	64.060	-145.140	OxA-11962	9506±38	10785	134	yes	9-18	yes	n	AY748604	2696.25
BS150	BLM	IK-98-343	Ikpikpuk R., North Slope, AK	70.810	-154.410	CAMS 53767	10510±50	12473	91	yes	9-18	yes	n	AY748506	3118.25
BS342	SFU	2294	Charlie Lake Cave, Peace R., BC	56.140	-120.440	OxA-12084	10340±40	12190	107	yes	9-18	yes	n	AY748617	3047.5
BS348	SFU	16422	Charlie Lake Cave, Peace R., BC	56.140	-120.440	OxA-12085	10505±45	12474	85	yes	9-18	yes	n	AY748620	3118.5
BS297	BLM	IK-98-1114	Ikpikpuk R., North Slope, AK	70.810	-154.410	CAMS 53891	10990±50	12854	103	yes	9-18	yes	n	AY748587	3213.5
BS124	ADFG	RS-9200	Black R.. Yukon Flats, AK	66.654	-143.722		11900±70	13754	100	yes	9-18	yes	n	AY748490	3438.5
BS146	BLM	IK-98-027	Ikpikpuk R., North Slope, AK	70.810	-154.410	CAMS 53756	11810±50	13663	91	yes	9-18	yes	n	AY748502	3415.75
BS145	BLM	IK-98-528	Ikpikpuk R., North Slope, AK	70.810	-154.410	CAMS 53774	12270±50	14148	208	yes	9-18	yes	n	AY748501	3537
BS176	UAF	V-54-365	Lost Chicken Cr., Chicken, AK	64.060	-141.890	OxA-11226	12380±60	14427	236	yes	9-18	yes	n	AY748520	3606.75
BS248	CMN	CMN 33039	Old Crow, YT	67.570	-139.080	OxA-10546	12350±70	14389	244	yes	9-18	yes	n	AY748558	3597.25
BS172	UAF	V-54-1105	Lost Chicken Cr., Chicken, AK	64.060	-141.890	OxA-10541	12525±70	14693	246	yes	9-18	yes	n	AY748517	3673.25

BS253	UAF	V-54-677	Lost Chicken Cr., Chicken, AK	64.060	-141.890	OxA-10855	12665±65	14988	206	yes	9-18	yes	n	AY748562	3747
BS311	ADFG	RS-9901	Black R.. Yukon Flats, AK	66.654	-143.722	OxA-12067	12425±45	14493	231	yes	9-18	yes	n	AY748598	3623.25
BS318	BLM	IK-98-142	Ikpikpuk R., North Slope, AK	70.810	-154.410	CAMS 53760	12410±50	14468	232	yes	9-18	yes	n	AY748602	3617
IB179	UAF	V-54-320	Lost Chicken Cr., Chicken, AK	64.060	-141.890	OxA-111	12465±75	14580	250	yes	9-18	yes	n	AY748474	3645
BS163	UAF	V-54-1157	Lost Chicken Cr., Chicken, AK	64.060	-141.890	OxA-10543	13240±75	16190	337	yes	9-18	yes	n	AY748510	4047.5
BS170	CMN	CMN 46699	Bison Cave, Fishing Branch, YT	66.450	-138.530	OxA-10681	13040±70	15738	341	yes	9-18	yes	n	AY748515	3934.5
BS201	CMN	CMN 46695	Dawson City, YT	64.800	-139.530	OxA-11197	12960±60	15525	308	yes	9-18	yes	n	AY748531	3881.25
BS224	AMNH	A-93-8430	Chatanika, AK	65.110	-147.470	OxA-11277	13125±75	15929	347	yes	9-18	yes	n	AY748547	3982.25
BS261	CMN	CMN 25856	Lost Chicken Cr., Chicken, AK	64.060	-141.890	OxA-10544	12915±70	15446	295	yes	9-18	yes	n	AY748570	3861.5
BS284	CMN	CMN 46696	Bison Cave, Fishing Branch, YT	66.450	-138.530	OxA-11166	13135±65	15954	339	yes	9-18	yes	n	AY748576	3988.5
BS472	AMNH	A-556-4160	Fairbanks Cr., Fairbanks, AK	65.040	-147.110	OxA-11617	13235±65	16187	329	yes	9-18	yes	n	AY748707	4046.75
BS202	UVic	#1 Williston L.	Fort D'Epinette, Peace R., BC	56.233	-120.750	OxA-11272	10460±65	12382	131	yes	9-18	yes	s	AY748532	3095.5
BS254	SFU	20043	Charlie Lake Cave, Peace R., BC	56.140	-120.440	OxA-10580	10230±55	11961	116	yes	9-18	yes	s	AY748563	2990.25
BS433	PMA	P00.1.4	Byrtus Site, Athabasca, AB	54.716	-113.300	OxA-11584	10450±55	12362	126	yes	9-18	yes	s	AY748681	3090.5
BS460	PMA	P00.1.11	Byrtus Site, Athabasca, AB	54.716	-113.300	OxA-11592	10425±50	12305	118	yes	9-18	yes	s	AY748699	3076.25
BS237	UVic	#2, E. Pine gp	Chetwynd, BC	55.683	-121.630	OxA-11274	11240±70	13146	97	yes	9-18	yes	s	AY748551	3286.5
BS570	MW	MW01	Gallelli Pit, Calgary, AB	51.080	-114.080	RL-757	11300±290	13175	295	yes	9-18	yes	s	AY748748	3293.75
BS246	UAF	V-54-1088	Lost Chicken Cr., Chicken, AK	64.060	-141.890	OxA-10540	13160±70	16010	341	yes	9-18	no	NA	NA	NA
BS259	UAF	V-54-226	Lost Chicken Cr., Chicken, AK	64.060	-141.890	OxA-10538	12960±70	15537	317	yes	9-18	no	NA	NA	NA
BS315	UAF	VA-2000-54-77	Gerstle R., near Fairbanks, AK	64.060	-145.140		8960±70			yes	9-18	no	NA	NA	NA
BS288	UAF	VA-97-061-229	Gerstle R., near Fairbanks, AK	64.060	-145.140	OxA-11246	9400±55			yes	9-18	no	NA	NA	NA
BS421	PMA	Unit27 Level T	Stampede Site, Cypress Hills, AB	49.630	-110.210	OxA-11577	8145±45	9085	69	yes	9-18	no	NA	NA	NA

BS430	PMA	UA No. 600	Cloverbar Pit, Edmonton, AB	53.340	-113.100	OxA-11588	9270±50	10449	83	yes	9-18	no	NA	NA	NA
BS442	PMA	PMA, AA63/62	Old Womens Buffalo Jump	50.600	-113.000	OxA-11612	9510±55	10829	140	yes	9-18	no	NA	NA	NA
BS559	MW	MW02	Vancouver Island, BC				11750±110	13597	122	yes	9-18	no	NA	NA	NA
BS256	UAF	V-54-17	Lost Chicken Cr., Chicken, AK	64.060	-141.890	OxA-10679	12340±65	14368	241	yes	9-18	no	NA	NA	NA
BS233	UAF	V-16-28	Elephant Point, AK	66.260	-161.350	OxA-11223	16685±80	19,822	177	yes	LGM 21	yes	n	AY748548	4955.5
BS389	BLM	IK-98-661	Ikpikpuk R., North Slope, AK	70.810	-154.410	CAMS 53777	17160±80	20,362	200	yes	LGM 21	yes	n	AY748644	5090.5
BS178	UAF	V-54-1137	Lost Chicken Cr., Chicken, AK	64.060	-141.890	OxA-10542	17960±90	21,426	149	yes	LGM 21	yes	n	AY748522	5356.5
BS126	AMNH	A-112-3346	Upper Cleary Cr., Fairbanks, AK	65.460	-147.380	NA	19150±280	22,876	361	yes	LGM 21	yes	n	AY748492	5719
BS121	AMNH	A-112-6450	Ester Cr., Fairbanks, AK	64.840	-147.960	NA	19360±280	23,072	382	yes	LGM 21	yes	n	AY748488	5768
BS196	BLM	IK-98-504	Ikpikpuk R., North Slope, AK	70.810	-154.410	CAMS 53772	19420±100	23,136	253	yes	LGM 21	yes	n	AY748526	5784
BS236	AMNH	FAM 32761	Seward Pininsula, Alder Cr., AK	60.810	-149.430	OxA-11247	19420±100	23,136	253	yes	LGM 21	yes	n	AY748550	5784
BS164	UAF	V-54-1099	Lost Chicken Cr., Chicken, AK	64.060	-141.890	OxA-11139	19540±120	23,361	266	yes	LGM 21	yes	n	AY748511	5840.25
BS107	AMNH	A-100-7749	Ester Cr., Fairbanks, AK	64.840	-147.960	NA	19570±290	23,367	420	yes	LGM 21	yes	n	AY748480	5841.75
BS109	AMNH	A-237-7970	Lower Gold Stream, Fairbanks, AK	65.570	-148.380		20730±350	24763	463	yes	LGM 21	yes	n	AY748482	6190.75
BS108	AMNH	A-169-3115	Lower Eldorado Cr., Fairbanks, AK	65.570	-148.380		21020±360	25141	492	yes	LGM 21	yes	n	AY748481	6285.25
BS161	BLM	IK-98-1090	Ikpikpuk R., North Slope, AK	70.810	-154.410	CAMS 53890	21040±120	25106	230	yes	LGM 21	yes	n	AY748508	6276.5
BS151	BLM	IK-98-401	Ikpikpuk R., North Slope, AK	70.810	-154.410	CAMS 53770	21530±130	25766	253	yes	LGM 21	yes	n	AY748507	6441.5
BS111	AMNH	A-105-6641	Ester Cr., Fairbanks, AK	64.840	-147.960		21580±370	25852	559	yes	LGM 21	yes	n	AY748483	6463
BS258	UAF	Ak-316-V-11	Fairbanks Cr., Fairbanks, AK	65.040	-147.110	OxA-10581	22120±130	26540	286	yes	LGM 21	yes	n	AY748567	6635
BS359	KU	KU 26057	Natural Trap Cave, WY	44.500	-108.200	OxA-12068	20020±150	23,925	230	yes	LGM 21	yes	s	AY748626	5981.25
BS605	KU	KU 51275	Natural Trap Cave, WY	44.500	-108.200	OxA-12124	20380±90	24314	175	yes	LGM 21	yes	s	AY748759	6078.5
BS252	CMN	CMN 34726	Gold Run Cr., Dawson City, YT	63.600	-138.500	OxA-10547	21500±130	25725	252	yes	LGM 21	yes		AY748561	6431.25

Guthrie 2006bison	NA		Fbks. Area	64.836	-147.645	SI-454	17210±500	20558	622	yes	LGM 21	no	NA	NA	NA
Guthrie 2006bison	NA		Fbks. Cr.	65.040	-147.113	SI-453	15380±300	18604	348	yes	LGM 21	no	NA	NA	NA
Guthrie 2006bison	NA		Manley	65.356	-150.985	SI-841	18000±200	21513	327	yes	LGM 21	no	NA	NA	NA
BS105	AMNH	A-144-9359	Ester Cr., Fairbanks, AK	64.840	-147.960	NA	23380±460	28,209	574	yes	30	yes	n	AY748479	7052.25
BS396	BLM	IK-98-1254	Ikpikpuk R., North Slope, AK	70.810	-154.410	CAMS 53901	23680±170	28,427	254	yes	30	yes	n	AY748651	7106.75
BS340	BLM	IK-98-302	Ikpikpuk R., North Slope, AK	70.810	-154.410	CAMS 53764	24500±180	29,335	277	yes	30	yes	n	AY748616	7333.75
BS498	BLM	IK-98-1184	Ikpikpuk R., North Slope, AK	70.810	-154.410	CAMS 53899	25980±230	30,745	201	yes	30	yes	n	AY748723	7686.25
BS244	UAF	V-54-29	Lost Chicken Cr., Chicken, AK	64.060	-141.890	OxA-11227	26210±170	30,918	161	yes	30	yes	n	AY748554	7729.5
BS192	BLM	P-013	Palisaides, AK	65.120	-153.340	Beta 110938	26300±300	30,937	217	yes	30	yes	n	AY748523	7734.25
BS165	UAF	V-54-60	Lost Chicken Cr., Chicken, AK	64.060	-141.890	OxA-11131	26460±160	31,075	112	yes	30	yes	n	AY748512	7768.75
BS398	BLM	IK-98-095	Ikpikpuk R., North Slope, AK	70.810	-154.410	CAMS 53758	27400±260	31,556	286	yes	30	yes	n	AY748653	7889
BS125	AMNH	A-160-6681	Ester Cr., Fairbanks, AK	64.840	-147.960		27440±790	32,035	849	yes	30	yes	n	AY748491	8008.75
BS388	BLM	IK-98-374	Ikpikpuk R., North Slope, AK	70.810	-154.410	CAMS 53768	27590±280	31,760	360	yes	30	yes	n	AY748643	7940
BS147	BLM	IK-98-1115	Ikpikpuk R., North Slope, AK	70.810	-154.410	CAMS 53892	28120±290	32,357	436	yes	30	yes	n	AY748503	8089.25
BS329	CMN	CMN 49692	Hester Cr., Dawson City, YT	63.890	-139.030	OxA-11193	27060±190	31,331	120	yes	30	yes	n	AY748611	7832.75
BS385	CMN	CMN 35891	Hunker Cr., Dawson City, YT	64.030	-139.200	OxA-12087	26760±120	31202	83	yes	30	no	NA	NA	NA
BS296	UAF	V-54-55	Lost Chicken Cr., Chicken, AK	64.060	-141.890	OxA-10537	24950±170			yes	30	no	NA	NA	NA
BS138	AMNH	A-148-9294	Ester Cr., Fairbanks, AK	64.840	-147.960		25310±580			yes	30	no	NA	NA	NA
Harrington	NA	NA	E of Edmonton along N Saskatchewan R, AB, CAN	53.536	-113.545	AECV-1201C	25210±760	30017	691	yes	30	no	NA	NA	NA
Harrington	NA	NA	Ketza River, Locality, Ross River area, YT, CAN	61.548	-132.250	TO-393	26350±280	30977	203	yes	30	no	NA	NA	NA

Harrington	NA	NA	Lime Hills, Cave 1, 527 m asl., AK, USA	61.750	-155.500	Beta-67670	27950±560	32323	684	yes	30	no	NA	NA	NA
Harrington	NA	NA	Cripple CK, AK, USA	64.820	-148.020	SI-842	29295±2440	34778	3339	yes	30	no	NA	NA	NA
Harrington	NA	NA	Fairbanks CK, AK, USA	65.067	-147.167	SI-445	24140±2200	29347	3246	yes	30	no	NA	NA	NA
Harrington	NA	NA	Porcupine, River Loc 100, YT, Can	67.480	-139.920	QU-781	26640±2800			yes	30	no	NA	NA	NA
Harrington	NA	NA	Old Crow River (Loc. 11A)	67.850	-139.970	SI-2825-A	28050±500			yes	30	no	NA	NA	NA
BS195	BLM	IK-98-616	Ikpikpuk R., North Slope, AK	70.810	-154.410	CAMS 53775	29040±340	33711	494	yes	33-39	yes	n	AY748525	8427.75
BS262	CMN	CMN 35365	Hunker Cr., Dawson City, YT	64.030	-139.200	OxA-10680	29150±500	33767	614	yes	33-39	yes	n	AY748571	8441.75
BS495	BLM	IK-98-1164	Ikpikpuk R., North Slope, AK	70.810	-154.410	CAMS 53897	29570±340	34177	407	yes	33-39	yes	n	AY748720	8544.25
BS497	BLM	IK-98-430	Ikpikpuk R., North Slope, AK	70.810	-154.410	CAMS 53771	30000±540	34638	657	yes	33-39	yes	n	AY748722	8659.5
BS412	YHR	3.124	Finning, Whitehorse, YT	60.729	-135.083	OxA-11280	30500±250	34978	348	yes	33-39	yes	n	AY748665	8744.5
BS260	CMN	CMN 49583	Quartz Cr., Dawson City, YT	63.750	-139.120	OxA-10574	30750±290	35277	454	yes	33-39	yes	n	AY748569	8819.25
BS415	CMN	CMN 46320	Nugget Gulch, Dawson City, YT	63.870	-139.280	Beta 33192	30810±975	35585	1097	yes	33-39	yes	n	AY748668	8896.25
BS499	BLM	IK-98-256	Ikpikpuk R., North Slope, AK	70.810	-154.410	CAMS 53763	31412±420	35845	461	yes	33-39	yes	n	AY748724	8961.25
BS327	CMN	CMN 49764	Eldorado Cr., Dawson City, YT	*63.920*	*-139.300*	OxA-11137	31530±230	35878	381	yes	33-39	yes	n	AY748609	8969.5
BS390	BLM	IK-98-096	Ikpikpuk R., North Slope, AK	70.810	-154.410	CAMS 53759	31630±440	36002	527	yes	33-39	yes	n	AY748645	9000.5
BS387	BLM	IK-98-1323	Ikpikpuk R., North Slope, AK	70.810	-154.410	CAMS 53903	33320±540	38023	703	yes	33-39	yes	n	AY748642	9505.75
BS397	BLM	IK-98-1035	Ikpikpuk R., North Slope, AK	70.810	-154.410	CAMS 53885	32370±470	37030	650	yes	33-39	yes	n	AY748652	9257.5
BS377	CMN	CMN 47551	Last Chance Cr., Dawson City, YT	64.000	-139.100	OxA-11626	28850±220	33412	437	yes	33-39	no	NA	NA	NA
BS137	AMNH	A-179-2052	Cripple Cr., Fairbanks, AK	*65.000*	*-147.200*	NA	33300±1600	NA	NA	yes	33-39	no	NA	NA	NA
BS133	AMNH	A-174-3123	Lower Eldorado Cr., Fairbanks, AK	65.570	-148.380	NA	33880±1900	39,065	2,118	yes	42	yes	n	AY748497	9766.25
BS478	ABC	110.19	Evergreen Cr., Dawson City, YT	64.050	-139.530	OxA-11991	34470±200	39,424	387	yes	42	yes	n	AY748711	9856

BS500	BLM	IK-98-1211	Ikpikpuk R., North Slope, AK	70.810	-154.410	CAMS 53894	35580±550	40,733	617	yes	42	yes	n	AY748725	10183.25
BS292	BLM	IK-98-916	Ikpikpuk R., North Slope, AK	70.810	-154.410	CAMS 53782	35710±730	40,808	747	yes	42	yes	n	AY748583	10202
BS392	BLM	IK-98-1222	Ikpikpuk R., North Slope, AK	70.810	-154.410	CAMS 53900	36320±780	41,375	697	yes	42	yes	n	AY748647	10343.75
BS394	BLM	IK-98-1120	Ikpikpuk R., North Slope, AK	70.810	-154.410	CAMS 53893	37460±890	42,248	680	yes	42	yes	n	AY748649	10562
BS243	AMNH	FAM 14344	Seward Pininsula, Alder Cr., AK	60.810	-149.430	OxA-11196	37550±400	42,244	303	yes	42	yes	n	AY748553	10561
BS350	BLM	IK-98-377	Ikpikpuk R., North Slope, AK	70.810	-154.410	CAMS 53769	38700±1000	43,150	761	yes	42	yes	n	AY748621	10787.5
BS364	BLM	IK-98-889	Ikpikpuk R., North Slope, AK	70.810	-154.410	CAMS 53779	38800±1100	43,245	839	yes	42	yes	n	AY748628	10811.25
BS249	AMNH	A-606-1082	Fairbanks Cr., Fairbanks, AK	65.040	-147.110	OxA-10683	39200±550	43,433	456	yes	42	yes	n	AY748559	10858.25
BS345	BLM	IK-98-915	Ikpikpuk R., North Slope, AK	70.810	-154.410	CAMS 53781	39800±1200	43,942	964	yes	42	yes	n	AY748619	10985.5
BS393	BLM	IK-98-174	Ikpikpuk R., North Slope, AK	70.810	-154.410	CAMS 53761	39850±1200	43,976	968	yes	42	yes	n	AY748648	10994
BS395	BLM	IK-98-1122	Ikpikpuk R., North Slope, AK	70.810	-154.410	CAMS 53895	40700±1300			yes	42	yes	n	AY748650	11000
BS281	ADFG	RS-0104	Black R.. Yukon Flats, AK	66.654	-143.722	OxA-11275	40800±600	44,607	468	yes	42	yes	n	AY748573	11151.75
BS443	PMA	P94.1.932	Cons. Pit 48, Edmonton, AB	53.500	-113.100	OxA-11613	34050±450	39,044	668	yes	42	no	NA	NA	9761
BS496	BLM	IK-98-863	Ikpikpuk R., North Slope, AK	70.810	-154.410	CAMS 53914	36520±800			yes	42	no	NA	NA	NA
BS463	PMA	P89.13.255	Cons. Pit 48, Edmonton, AB	53.500	-113.100	AECV:1664c	40000±3070			yes	42	no	NA	NA	NA
Harrington	NA	NA	Pearl CK, AK, USA	-147.309	64.993	QC-891	36425 +2575 -1974			yes	42	no	NA	NA	NA
Harrington	NA	NA	Old Crow River (Loc. 11), YT, Can	-139.970	67.850	SI-2816-A	36650±1300			yes	42	no	NA	NA	NA
Harrington	NA	NA	Old Crow River, YT, Can	-139.750	67.916	RIDDL-730	39500±900			yes	42	no	NA	NA	NA
Harrington	NA	NA	Old Crow River (Loc. 20), YT, Can	-139.500	68.083	RIDDL - 196	37000±950			yes	42	no	NA	NA	NA
Harrington	NA	NA	Ostero Gravel Pitt, NW side of Peace River, near Taylor	-120.083	57.127	AECV-1559C	38750±3850			yes	42	no	NA	NA	NA
BS149	BLM	IK-98-032	Ikpikpuk R., North Slope, AK	70.810	-154.410	CAMS	46100±2	48337	1163	yes	>45	yes	n	AY748505	12084.

						53757	200								25
BS193	BLM	IK-98-928	Ikpikpuk R., North Slope, AK	70.810	-154.410	CAMS 53783	49600±4000	52926	7172	yes	>45	yes	n	AY748524	13231.5
BS216	BLM	IK-98-671	Ikpikpuk R., North Slope, AK	70.810	-154.410	CAMS 53778	47000±2900	48432	4376	yes	>45	yes	n	AY748542	12108
BS235	UAF	No # (BSX2)	Yukon R., AK	66.660	-144.730	OxA-11163	43400±900	46701	1026	yes	>45	yes	n	AY748549	11675.25
BS242	AMNH	FAM 14332	Eschscholtz Bay, AK	65.120	-147.530	OxA-11273	53800±2900	55232	4376	yes	>45	yes	n	AY748552	13808
BS287	ADFG	RS-0102	Black R.. Yukon Flats, AK	66.654	-143.722	OxA 11164	49100±1700	49501	1970	yes	>45	yes	n	AY748579	12375.25
BS291	UAF	IK-01-216	Ikpikpuk R., North Slope, AK	70.810	-154.410	OxA-11136	49700±1400	49962	1541	yes	>45	yes	n	AY748582	12490.5
BS294	ADFG	RS-0103	Black R.. Yukon Flats, AK	66.654	-143.722	OxA-11276	58200±3900	61310	6915	yes	>45	yes	n	AY748585	15327.5
BS351	ADFG	RS/BSX1	Black R.. Yukon Flats, AK	66.654	-143.722	OxA-11138	57700±3200	59546	5118	yes	>45	yes	n	AY748622	14886.5
BS400	BLM	IK-98-305	Ikpikpuk R., North Slope, AK	70.810	-154.410	CAMS 53766	46100±2600	48191	1241	yes	>45	yes	n	AY748655	12047.75
BS493	BLM	IK-98-527	Ikpikpuk R., North Slope, AK	70.810	-154.410	CAMS 53773	50000±4200	53784	7681	yes	>45	yes	n	AY748718	13446
BS494	BLM	IK-98-1042	Ikpikpuk R., North Slope, AK	70.810	-154.410	CAMS 53887	44800±2200	47782	1335	yes	>45	yes	n	AY748719	11945.5
BS407	CMN	CMN 21096	Eskimo Lakes, NWT	69.250	-132.283	OxA-11630	55500±3100	57200	4867	yes	>45	yes	s	AY748661	14300
BS473	PMA	P95.12.2	Twin Bridges Gravel Pit, AB	53.300	-113.200	OxA-11615	56300±3100	58000	4867	yes	>45	yes	s	AY748708	14500
BS438	PMA	P94.1.201	Cons. Pit 48, Edmonton, AB	53.500	-113.100	OxA-11620	53800±2200	54525	2838	yes	>45	yes	s	AY748684	13631.25
BS440	PMA	P89.13.692	Cons. Pit 48, Edmonton, AB	53.500	-113.100	OxA-12086	60400±2900	61832	4376	yes	>45	no	NA	NA	NA

Table S2. Parameters used for each BEM method.

	BioClim	GowerDist	MahalanobisDist	GLM	GARP	GAM	MARS	GBM	MaxEnt
Probability CutOff	0.95	0.95	0.75	0.13	-	Automatic Search using ROC	0.13	0.13	0.13
Variable Selection	Yes, 1.00	Yes, 1.00	Yes, 1.00	Yes, 1.00	Yes, 1.00	Yes, 1.00	Yes, 1.00	Yes, 1.00	Yes, 1.00

Permutation	Cross-Validation	Cross-Validation	Cross-Validation	Cross-Validation	Cross-Validation	Cross-Validation	Cross-Validation	Cross-Validation	Cross-Validation
PermutReplicates	10	10	10	10	10	10	10	10	10
PercentReplicateTraining	0.75	0.75	0.75	0.75	0.75	0.75	0.75	0.75	0.75
					Max Generation Number: 100 Convergence: 0.01 Population Size: 50 Number of Samples: 1000	n Spline Degrees: 3		Learning Rate: 0.005 Bagging Fraction: 0.5	Regularization applied to linear, quadratic and product features: -1 Regularization applied to hinge features: -1 Regularization applied to threshold features: -1 (Negative regularization values enable automatic setting)

Table S3 – Summary Statistics used in the ABC analysis. We list the time fame and corresponding statistic groups, number of generations, and region (population) of the samples used for the BayeSSC simulation (see input files and main text for more information). We include the three summary statistics used to assess the relative support of our demographic models – segregating sites (SegSites), nucleotide diversity (NucltdDiv), and Fst.

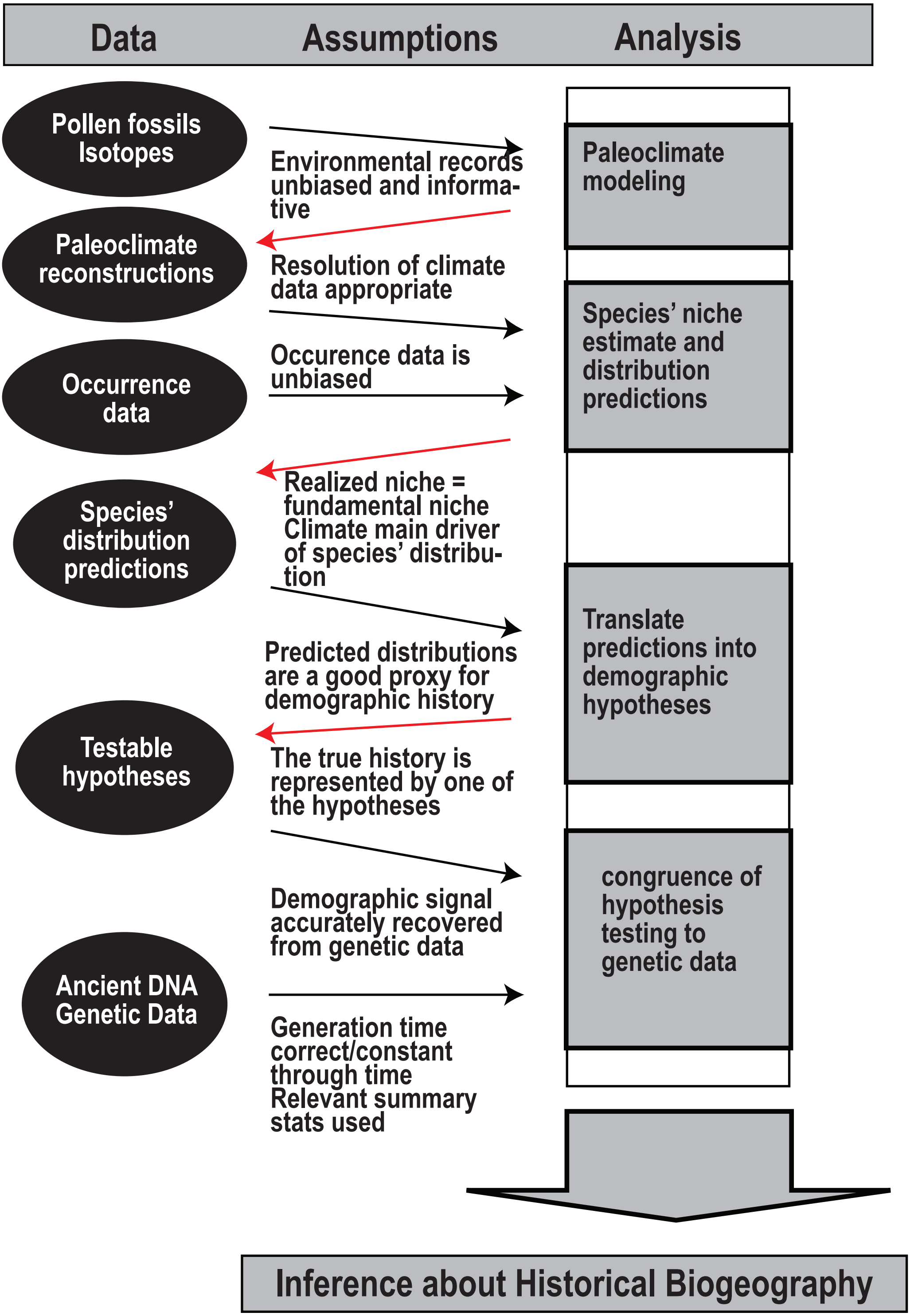
Timeframe (kya)	Statistic Group	#gens	Pop	SegSites	NucltdDiv	Fst
0-3	0	0-750	N	24	0.0193	0.6401
0-3	1	0-750	S	42	0.0116	
3-9	2	750-2250	S	22	0.0081	
9-18	3	2250-4500	N	54	0.0354	0.2079
9-18	4	2250-4500	S	19	0.0241	
18-27	5	4500-6750	N	51	0.0317	-0.0909
18-27	6	4500-6750	S	15	0.0366	
27-33	7	6750-8250	N	41	0.0272	
33-39	8	8250-9750	N	43	0.02	

39-45	9	9750-11250	N	48	0.0292	
>45	10	>11250	N	42	0.0242	0.0006
>45	11	>11250	S	26	0.0346	

Table S4: Estimated ABC parameters for the best supported model (M3c2). Timings are estimated in generations (we assumed 4 years / generation). Mutation rate is given as per site per million years.

	Fem. Effect. Pop. Size (North)	**Bottleneck Timing**	**Bottleneck Intensity (factor)**	**Population Merge Timing**	**Event Migrants**
1st Qu.:	27,640	20	0.071	2,198	0.066
Mode:	41,105	22	0.064	2,450	0.094
Median :	50,876	42	0.119	2,372	0.093
Mean :	51,378	42	0.351	2,369	0.095
3rd Qu.:	75,584	63	0.255	2,534	0.123

	Fem. Effect. Pop Size (South)	**Pop. Size Change Timing (North)**	**Pop. Size Change (factor)**	**Split Timing**	**Ancestral Pop. size factor**	**Mutation Rate**
1st Qu.:	976	2,194	1.356	5,842	0.337	0.0005168
Mode:	1,111	2,450	2.144	6,483	0.314	0.0007083
Median :	2,070	2,373	2.421	6,388	0.593	0.0006501
Mean :	2,346	2,369	3.502	6,389	0.888	0.0006571
3rd Qu.:	3,324	2,538	4.362	6,910	1.089	0.0007778


Data
Assumptions
Analysis
Pollen fossils Isotopes
Paleoclimate reconstructions
Occurrence data
Species' distribution predictions
Testable hypotheses
Ancient DNA Genetic Data
Environmental records unbiased and informative
Resolution of climate data appropriate
Occurence data is unbiased
Realized niche = fundamental niche
Climate main driver of species' distribution
Predicted distributions are a good proxy for demographic history
The true history is represented by one of the hypotheses
Demographic signal accurately recovered from genetic data
Generation time correct/constant through time
Relevant summary stats used
Paleoclimate modeling
Species' niche estimate and distribution predictions
Translate predictions into demographic hypotheses
congruence of hypothesis testing to genetic data
Inference about Historical Biogeography

M1

```
//Parameters for the coalescence simulation program : simcoal.exe
2 populations with ancient DNA
//Population effective sizes (number of genes)
{U:1000,100000}
1
//samples
133 sample groups
1 45 0 0
1 411 0 0
1 551 0 0
1 607 0 0
1 654 0 0
1 635 0 0
1 31 0 1
1 37 0 1
1 45 0 1
1 45 0 1
1 96 0 1
1 30 0 1
1 112 0 1
1 150 0 1
1 165 0 1
1 180 0 1
2 210 0 1
1 305 0 1
1 718 0 1
1 727 0 1
25 20 0 1
1 860 0 2
1 846 0 2
1 881 0 2
1 978 0 2
1 1351 0 2
1 1491 0 2
1 1748 0 2
1 1665 0 2
1 1907 0 2
5 2074 0 2
1 1973 0 2
1 1985 0 2
1 2027 0 2
1 1987 0 2
1 2529 0 3
1 2696 0 3
```

2	3119	0	3
1	3048	0	3
1	3213	0	3
2	3439	0	3
2	3416	0	3
1	3537	0	3
1	3607	0	3
1	3597	0	3
1	3673	0	3
1	3747	0	3
1	3623	0	3
1	3617	0	3
1	3645	0	3
1	4048	0	3
1	3935	0	3
1	3881	0	3
1	3982	0	3
1	3861	0	3
1	3989	0	3
1	4047	0	3
1	3096	1	4
1	2990	1	4
1	3091	1	4
1	3076	1	4
1	3286	1	4
1	3294	1	4
1	4956	0	5
1	5091	0	5
1	5357	0	5
1	5719	0	5
1	5768	0	5
2	5784	0	5
1	5840	0	5
1	5842	0	5
1	6191	0	5
1	6285	0	5
1	6276	0	5
1	6442	0	5
1	6463	0	5
1	6635	0	5
1	5981	0	6
1	6079	0	6
1	7052	0	7
1	7107	0	7
1	7334	0	7
1	7686	0	7

```
1 7730 0 7
1 7734 0 7
1 7769 0 7
1 7832 0 7
1 7889 0 7
1 8009 0 7
1 7940 0 7
1 8089 0 7
1 8428 0 8
1 8441 0 8
1 8544 0 8
1 8660 0 8
1 8745 0 8
1 8819 0 8
1 8896 0 8
1 8861 0 8
1 8970 0 8
1 9001 0 8
1 9256 0 8
1 9506 0 8
1 9766 0 9
1 9856 0 9
1 10183 0 9
1 10202 0 9
1 10344 0 9
1 10561 0 9
1 10562 0 9
1 10788 0 9
1 10811 0 9
1 10858 0 9
1 10986 0 9
1 10994 0 9
1 11000 0 9
1 11152 0 9
1 9761 0 9
1 12084 0 10
1 13232 0 10
1 12108 0 10
1 11675 0 10
1 13808 0 10
1 12375 0 10
1 12491 0 10
1 15328 0 10
1 14887 0 10
1 12048 0 10
1 13446 0 10
```

```
1 11946 0 10
1 14300 0 11
1 13631 0 11
1 14500 0 11
//Growth rates          : negative growth implies population expansion
0
0
//Number of migration matrices
0
//historical event: time, source, sink, migrants, new deme size, new growth rate,
migration matrix index
4
{U:1,80} 0 0 0 {[12]/[1]} 0 0
{U:2000,2750} 0 1 {[14]/([14]+[13])} {[14]} 0 0
{[4]+1} 0 0 0 {[13]/[12]} 0 0
{U:5250,7500} 1 0 1 {[15]/[13]} 0 0
//Mutation rate per generation for the whole sequence
{N:0.00102443,0.00025}
//Number of loci
615
//data type either DNA, RFLP, or MICROSAT : If DNA, we need a second term for the
transition bias
DNA 0.792
//Gamma parameter (if 0: even mutation rates, if >0 :shape parameter of the
Gamma distribution
0
{U:1000,30000000} //prehist [12]
{U:1000,30000000} //Ice N0 [13]
{U:1000,30000000} //Ice N1 [14]
{U:1000,30000000} //Ancient [15]
```

M2

```
//Parameters for the coalescence simulation program : simcoal.exe
2 populations with ancient DNA
//Population effective sizes (number of genes)
{U:1000,100000}
1
//samples
133 sample groups
1 45 0 0
1 411 0 0
1 551 0 0
1 607 0 0
1 654 0 0
```

```
1 635 0 0
1 31 0 1
1 37 0 1
1 45 0 1
1 45 0 1
1 96 0 1
1 30 0 1
1 112 0 1
1 150 0 1
1 165 0 1
1 180 0 1
2 210 0 1
1 305 0 1
1 718 0 1
1 727 0 1
25 20 0 1
1 860 0 2
1 846 0 2
1 881 0 2
1 978 0 2
1 1351 0 2
1 1491 0 2
1 1748 0 2
1 1665 0 2
1 1907 0 2
5 2074 0 2
1 1973 0 2
1 1985 0 2
1 2027 0 2
1 1987 0 2
1 2529 0 3
1 2696 0 3
2 3119 0 3
1 3048 0 3
1 3213 0 3
2 3439 0 3
2 3416 0 3
1 3537 0 3
1 3607 0 3
1 3597 0 3
1 3673 0 3
1 3747 0 3
1 3623 0 3
1 3617 0 3
1 3645 0 3
1 4048 0 3
```

```
1 3935 0 3
1 3881 0 3
1 3982 0 3
1 3861 0 3
1 3989 0 3
1 4047 0 3
1 3096 1 4
1 2990 1 4
1 3091 1 4
1 3076 1 4
1 3286 1 4
1 3294 1 4
1 4956 0 5
1 5091 0 5
1 5357 0 5
1 5719 0 5
1 5768 0 5
2 5784 0 5
1 5840 0 5
1 5842 0 5
1 6191 0 5
1 6285 0 5
1 6276 0 5
1 6442 0 5
1 6463 0 5
1 6635 0 5
1 5981 0 6
1 6079 0 6
1 7052 0 7
1 7107 0 7
1 7334 0 7
1 7686 0 7
1 7730 0 7
1 7734 0 7
1 7769 0 7
1 7832 0 7
1 7889 0 7
1 8009 0 7
1 7940 0 7
1 8089 0 7
1 8428 0 8
1 8441 0 8
1 8544 0 8
1 8660 0 8
1 8745 0 8
1 8819 0 8
```

```
1 8896 0 8
1 8861 0 8
1 8970 0 8
1 9001 0 8
1 9256 0 8
1 9506 0 8
1 9766 0 9
1 9856 0 9
1 10183 0 9
1 10202 0 9
1 10344 0 9
1 10561 0 9
1 10562 0 9
1 10788 0 9
1 10811 0 9
1 10858 0 9
1 10986 0 9
1 10994 0 9
1 11000 0 9
1 11152 0 9
1 9761 0 9
1 12084 0 10
1 13232 0 10
1 12108 0 10
1 11675 0 10
1 13808 0 10
1 12375 0 10
1 12491 0 10
1 15328 0 10
1 14887 0 10
1 12048 0 10
1 13446 0 10
1 11946 0 10
1 14300 0 11
1 13631 0 11
1 14500 0 11
//Growth rates         : negative growth implies population expansion
0
0
//Number of migration matrices
0
//historical event: time, source, sink, migrants, new deme size, new growth rate, migration matrix index
3
{U:2000,2750} 0 1 {[11]/([11]+[10])} {[11]} 0 0
{[2]+1} 0 0 0 {[10]/[1]} 0 0
```

```
{U:5250,7500} 1 0 1 {[12]/[10]} 0 0
//Mutation rate per generation for the whole sequence
{N:0.00102443,0.00025}
//Number of loci
615
//data type either DNA, RFLP, or MICROSAT : If DNA, we need a second term for the transition bias
DNA 0.792
//Gamma parameter (if 0: even mutation rates, if >0 :shape parameter of the Gamma distribution
0
{U:1000,30000000} //Ice D0 10
{U:1000,30000000} //Ice D1 11
{U:1000,30000000} //ancient 12
```

M3a1

```
//Parameters for the coalescence simulation program : simcoal.exe
2 populations with ancient DNA
//Population effective sizes (number of genes)
{U:1000,100000}
{U:1000,100000}
//samples
133 sample groups
1 45 0 0
1 411 0 0
1 551 0 0
1 607 0 0
1 654 0 0
1 635 0 0
1 31 1 1
1 37 1 1
1 45 1 1
1 45 1 1
1 96 1 1
1 30 1 1
1 112 1 1
1 150 1 1
1 165 1 1
1 180 1 1
2 210 1 1
1 305 1 1
25 20 1 1
1 718 0 2
1 727 0 2
1 860 0 2
```

```
1 846 0 2
1 881 0 2
1 978 0 2
1 1351 0 2
1 1491 0 2
1 1748 0 2
1 1665 0 2
1 1907 0 2
5 2074 0 2
1 1973 0 2
1 1985 0 2
1 2027 0 2
1 1987 0 2
1 2529 0 3
1 2696 0 3
2 3119 0 3
1 3048 0 3
1 3213 0 3
2 3439 0 3
2 3416 0 3
1 3537 0 3
1 3607 0 3
1 3597 0 3
1 3673 0 3
1 3747 0 3
1 3623 0 3
1 3617 0 3
1 3645 0 3
1 4048 0 3
1 3935 0 3
1 3881 0 3
1 3982 0 3
1 3861 0 3
1 3989 0 3
1 4047 0 3
1 3096 1 4
1 2990 1 4
1 3091 1 4
1 3076 1 4
1 3286 1 4
1 3294 1 4
1 4956 0 5
1 5091 0 5
1 5357 0 5
1 5719 0 5
1 5768 0 5
```

2 5784 0 5
1 5840 0 5
1 5842 0 5
1 6191 0 5
1 6285 0 5
1 6276 0 5
1 6442 0 5
1 6463 0 5
1 6635 0 5
1 5981 0 6
1 6079 0 6
1 7052 0 7
1 7107 0 7
1 7334 0 7
1 7686 0 7
1 7730 0 7
1 7734 0 7
1 7769 0 7
1 7832 0 7
1 7889 0 7
1 8009 0 7
1 7940 0 7
1 8089 0 7
1 8428 0 8
1 8441 0 8
1 8544 0 8
1 8660 0 8
1 8745 0 8
1 8819 0 8
1 8896 0 8
1 8861 0 8
1 8970 0 8
1 9001 0 8
1 9256 0 8
1 9506 0 8
1 9766 0 9
1 9856 0 9
1 10183 0 9
1 10202 0 9
1 10344 0 9
1 10561 0 9
1 10562 0 9
1 10788 0 9
1 10811 0 9
1 10858 0 9
1 10986 0 9

```
1 10994 0 9
1 11000 0 9
1 11152 0 9
1 9761 0 9
1 12084 0 10
1 13232 0 10
1 12108 0 10
1 11675 0 10
1 13808 0 10
1 12375 0 10
1 12491 0 10
1 15328 0 10
1 14887 0 10
1 12048 0 10
1 13446 0 10
1 11946 0 10
1 14300 0 11
1 13631 0 11
1 14500 0 11
//Growth rates         : negative growth implies population expansion
0
0
//Number of migration matrices
0
//historical event: time, source, sink, migrants, new deme size, new growth rate,
migration matrix index
6
{([7]-130)*[19]+130} 0 0 0 {[17]/[1]} 0 0
{([7]-130)*[20]+130} 1 1 0 {[18]/[2]} 0 0
{U:350,1200} 1 0 1 {[21]/[17]} 0 0
{U:2000,2750} 0 1 {[23]/([23]+[22])} {[23]/[18]} 0 0
{[9]+1} 0 0 0 {[22]/[21]} 0 0
{U:5250,7500} 1 0 1 {[24]/[22]} 0 0
//Mutation rate per generation for the whole sequence
{N:0.00102443,0.00025}
//Number of loci
615
//data type either DNA, RFLP, or MICROSAT : If DNA, we need a second term for the
transition bias
DNA 0.792
//Gamma parameter (if 0: even mutation rates, if >0 :shape parameter of the
Gamma distribution
0
{U:1000,30000000} //prehist N0; [17]
{U:1000,30000000} //prehist N1; [18]
{U:0,1} //time of size decrease, deme 0 [19]
```

```
{U:0,1} //time of size decrease, deme 1 [20]
{U:1000,30000000} //Merged [21]
{U:1000,30000000} //Ice N0 [22]
{U:1000,30000000} //Ice N1 [23]
{U:1000,30000000} //Ancient [24]
```

M3a2

```
//Parameters for the coalescence simulation program : simcoal.exe
2 populations with ancient DNA
//Population effective sizes (number of genes)
{U:1000,100000}
1
//samples
133 sample groups
1 45 0 0
1 411 0 0
1 551 0 0
1 607 0 0
1 654 0 0
1 635 0 0
1 31 0 1
1 37 0 1
1 45 0 1
1 45 0 1
1 96 0 1
1 30 0 1
1 112 0 1
1 150 0 1
1 165 0 1
1 180 0 1
2 210 0 1
1 305 0 1
1 718 0 1
1 727 0 1
25 20 0 1
1 860 0 2
1 846 0 2
1 881 0 2
1 978 0 2
1 1351 0 2
1 1491 0 2
1 1748 0 2
1 1665 0 2
1 1907 0 2
5 2074 0 2
```

1	1973	0	2
1	1985	0	2
1	2027	0	2
1	1987	0	2
1	2529	0	3
1	2696	0	3
2	3119	0	3
1	3048	0	3
1	3213	0	3
2	3439	0	3
2	3416	0	3
1	3537	0	3
1	3607	0	3
1	3597	0	3
1	3673	0	3
1	3747	0	3
1	3623	0	3
1	3617	0	3
1	3645	0	3
1	4048	0	3
1	3935	0	3
1	3881	0	3
1	3982	0	3
1	3861	0	3
1	3989	0	3
1	4047	0	3
1	3096	1	4
1	2990	1	4
1	3091	1	4
1	3076	1	4
1	3286	1	4
1	3294	1	4
1	4956	0	5
1	5091	0	5
1	5357	0	5
1	5719	0	5
1	5768	0	5
2	5784	0	5
1	5840	0	5
1	5842	0	5
1	6191	0	5
1	6285	0	5
1	6276	0	5
1	6442	0	5
1	6463	0	5
1	6635	0	5

```
1 5981 0 6
1 6079 0 6
1 7052 0 7
1 7107 0 7
1 7334 0 7
1 7686 0 7
1 7730 0 7
1 7734 0 7
1 7769 0 7
1 7832 0 7
1 7889 0 7
1 8009 0 7
1 7940 0 7
1 8089 0 7
1 8428 0 8
1 8441 0 8
1 8544 0 8
1 8660 0 8
1 8745 0 8
1 8819 0 8
1 8896 0 8
1 8861 0 8
1 8970 0 8
1 9001 0 8
1 9256 0 8
1 9506 0 8
1 9766 0 9
1 9856 0 9
1 10183 0 9
1 10202 0 9
1 10344 0 9
1 10561 0 9
1 10562 0 9
1 10788 0 9
1 10811 0 9
1 10858 0 9
1 10986 0 9
1 10994 0 9
1 11000 0 9
1 11152 0 9
1 9761 0 9
1 12084 0 10
1 13232 0 10
1 12108 0 10
1 11675 0 10
1 13808 0 10
```

```
1 12375 0 10
1 12491 0 10
1 15328 0 10
1 14887 0 10
1 12048 0 10
1 13446 0 10
1 11946 0 10
1 14300 0 11
1 13631 0 11
1 14500 0 11
//Growth rates: negative growth implies population expansion
0
0
//Number of migration matrices
0
//historical event: time, source, sink, migrants, new deme size, new growth rate, migration matrix index
4
{130+([4]-130)*[13]} 0 0 0 {[12]/[1]} 0 0
{U:2000,2750} 0 1 {[15]/([14]+[15])} {[15]} 0 0
{[4]+1} 0 0 0 {[14]/[12]} 0 0
{U:5250,7500} 1 0 1 {[16]/[14]} 0 0
//Mutation rate per generation for the whole sequence
{N:0.00102443,0.00025}
//Number of loci
615
//data type either DNA, RFLP, or MICROSAT : If DNA, we need a second term for the transition bias
DNA 0.792
//Gamma parameter (if 0: even mutation rates, if >0 :shape parameter of the Gamma distribution
0
{U:1000,30000000} //prehist N0; [12]
{U:0,1} //time of size decrease, deme 0 [13]
{U:1000,30000000} //Ice N0 [14]
{U:1000,30000000} //Ice N1 [15]
{U:1000,30000000} //Ancient [16]
```

M3b1

```
//Parameters for the coalescence simulation program : simcoal.exe
2 populations with ancient DNA
//Population effective sizes (number of genes)
{U:1000,100000}
{U:1000,100000}
//samples
```

```
133 sample groups
1 45 0 0
1 411 0 0
1 551 0 0
1 607 0 0
1 654 0 0
1 635 0 0
1 31 1 1
1 37 1 1
1 45 1 1
1 45 1 1
1 96 1 1
1 30 1 1
1 112 1 1
1 150 1 1
1 165 1 1
1 180 1 1
2 210 1 1
1 305 1 1
25 20 1 1
1 718 0 2
1 727 0 2
1 860 0 2
1 846 0 2
1 881 0 2
1 978 0 2
1 1351 0 2
1 1491 0 2
1 1748 0 2
1 1665 0 2
1 1907 0 2
5 2074 0 2
1 1973 0 2
1 1985 0 2
1 2027 0 2
1 1987 0 2
1 2529 0 3
1 2696 0 3
2 3119 0 3
1 3048 0 3
1 3213 0 3
2 3439 0 3
2 3416 0 3
1 3537 0 3
1 3607 0 3
1 3597 0 3
```

1 3673 0 3
1 3747 0 3
1 3623 0 3
1 3617 0 3
1 3645 0 3
1 4048 0 3
1 3935 0 3
1 3881 0 3
1 3982 0 3
1 3861 0 3
1 3989 0 3
1 4047 0 3
1 3096 1 4
1 2990 1 4
1 3091 1 4
1 3076 1 4
1 3286 1 4
1 3294 1 4
1 4956 0 5
1 5091 0 5
1 5357 0 5
1 5719 0 5
1 5768 0 5
2 5784 0 5
1 5840 0 5
1 5842 0 5
1 6191 0 5
1 6285 0 5
1 6276 0 5
1 6442 0 5
1 6463 0 5
1 6635 0 5
1 5981 0 6
1 6079 0 6
1 7052 0 7
1 7107 0 7
1 7334 0 7
1 7686 0 7
1 7730 0 7
1 7734 0 7
1 7769 0 7
1 7832 0 7
1 7889 0 7
1 8009 0 7
1 7940 0 7
1 8089 0 7

```
1 8428 0 8
1 8441 0 8
1 8544 0 8
1 8660 0 8
1 8745 0 8
1 8819 0 8
1 8896 0 8
1 8861 0 8
1 8970 0 8
1 9001 0 8
1 9256 0 8
1 9506 0 8
1 9766 0 9
1 9856 0 9
1 10183 0 9
1 10202 0 9
1 10344 0 9
1 10561 0 9
1 10562 0 9
1 10788 0 9
1 10811 0 9
1 10858 0 9
1 10986 0 9
1 10994 0 9
1 11000 0 9
1 11152 0 9
1 9761 0 9
1 12084 0 10
1 13232 0 10
1 12108 0 10
1 11675 0 10
1 13808 0 10
1 12375 0 10
1 12491 0 10
1 15328 0 10
1 14887 0 10
1 12048 0 10
1 13446 0 10
1 11946 0 10
1 14300 0 11
1 13631 0 11
1 14500 0 11
//Growth rates          : negative growth implies population expansion
0
0
//Number of migration matrices
```

```
0
//historical event: time, source, sink, migrants, new deme size, new growth rate, migration matrix index
8
{U:1,80} 0 0 0 {[21]/[1]} 0 0
{U:1,80} 1 1 0 {[22]/[2]} 0 0
{([11]-[3])*[25]+[3]} 0 0 0 {[23]/[21]} 0 0
{([11]-[5])*[26]+[5]} 1 1 0 {[24]/[22]} 0 0
{U:350,1200} 1 0 1 {[27]/[23]} 0 0
{U:2000,2750} 0 1 {[29]/([28]+[29])} {[29]/[24]} 0 0
{[13]+1} 0 0 0 {[28]/[27]} 0 0
{U:5250,7500} 1 0 1 {[30]/[28]} 0 0
//Mutation rate per generation for the whole sequence
{N:0.00102443,0.00025}
//Number of loci
615
//data type either DNA, RFLP, or MICROSAT : If DNA, we need a second term for the transition bias
DNA 0.792
//Gamma parameter (if 0: even mutation rates, if >0 :shape parameter of the Gamma distribution
0
{U:1000,30000000} //prehist1 N0; [21]
{U:1000,30000000} //prehist1 N1; [22]
{U:1000,30000000} //prehist2 N0; [23]
{U:1000,30000000} //prehist2 N1; [24]
{U:0,1} //time of size decrease 2, deme 0 [25]
{U:0,1} //time of size decrease 2, deme 1 [26]
{U:1000,30000000} //Merged [27]
{U:1000,30000000} //Ice N0 [28]
{U:1000,30000000} //Ice N1 [29]
{U:1000,30000000} //Ancient [30]
```

M3b2

```
//Parameters for the coalescence simulation program : simcoal.exe
2 populations with ancient DNA
//Population effective sizes (number of genes)
{U:1000,100000}
1
//samples
133 sample groups
1 45 0 0
1 411 0 0
1 551 0 0
1 607 0 0
```

1 654 0 0
1 635 0 0
1 31 0 1
1 37 0 1
1 45 0 1
1 45 0 1
1 96 0 1
1 30 0 1
1 112 0 1
1 150 0 1
1 165 0 1
1 180 0 1
2 210 0 1
1 305 0 1
1 718 0 1
1 727 0 1
25 20 0 1
1 860 0 2
1 846 0 2
1 881 0 2
1 978 0 2
1 1351 0 2
1 1491 0 2
1 1748 0 2
1 1665 0 2
1 1907 0 2
5 2074 0 2
1 1973 0 2
1 1985 0 2
1 2027 0 2
1 1987 0 2
1 2529 0 3
1 2696 0 3
2 3119 0 3
1 3048 0 3
1 3213 0 3
2 3439 0 3
2 3416 0 3
1 3537 0 3
1 3607 0 3
1 3597 0 3
1 3673 0 3
1 3747 0 3
1 3623 0 3
1 3617 0 3
1 3645 0 3

```
1 4048 0 3
1 3935 0 3
1 3881 0 3
1 3982 0 3
1 3861 0 3
1 3989 0 3
1 4047 0 3
1 3096 1 4
1 2990 1 4
1 3091 1 4
1 3076 1 4
1 3286 1 4
1 3294 1 4
1 4956 0 5
1 5091 0 5
1 5357 0 5
1 5719 0 5
1 5768 0 5
2 5784 0 5
1 5840 0 5
1 5842 0 5
1 6191 0 5
1 6285 0 5
1 6276 0 5
1 6442 0 5
1 6463 0 5
1 6635 0 5
1 5981 0 6
1 6079 0 6
1 7052 0 7
1 7107 0 7
1 7334 0 7
1 7686 0 7
1 7730 0 7
1 7734 0 7
1 7769 0 7
1 7832 0 7
1 7889 0 7
1 8009 0 7
1 7940 0 7
1 8089 0 7
1 8428 0 8
1 8441 0 8
1 8544 0 8
1 8660 0 8
1 8745 0 8
```

```
1 8819 0 8
1 8896 0 8
1 8861 0 8
1 8970 0 8
1 9001 0 8
1 9256 0 8
1 9506 0 8
1 9766 0 9
1 9856 0 9
1 10183 0 9
1 10202 0 9
1 10344 0 9
1 10561 0 9
1 10562 0 9
1 10788 0 9
1 10811 0 9
1 10858 0 9
1 10986 0 9
1 10994 0 9
1 11000 0 9
1 11152 0 9
1 9761 0 9
1 12084 0 10
1 13232 0 10
1 12108 0 10
1 11675 0 10
1 13808 0 10
1 12375 0 10
1 12491 0 10
1 15328 0 10
1 14887 0 10
1 12048 0 10
1 13446 0 10
1 11946 0 10
1 14300 0 11
1 13631 0 11
1 14500 0 11
//Growth rates	: negative growth implies population expansion
0
0
//Number of migration matrices
0
//historical event: time, source, sink, migrants, new deme size, new growth rate, migration matrix index
5
{U:1,80} 0 0 0 {[14]/[1]} 0 0
```

```
{([6]-[2])*[16]+[2]} 0 0 0 {[15]/[14]} 0 0
{U:2000,2750} 0 1 {[19]/([18]+[19])} {[19]} 0 0
{[6]+1} 0 0 0 {[18]/[17]} 0 0
{U:5250,7500} 1 0 1 {[20]/[18]} 0 0
//Mutation rate per generation for the whole sequence
{N:0.00102443,0.00025}
//Number of loci
615
//data type either DNA, RFLP, or MICROSAT : If DNA, we need a second term for the
transition bias
DNA 0.792
//Gamma parameter (if 0: even mutation rates, if >0 :shape parameter of the
Gamma distribution
0
{U:1000,30000000} //prehist1; [14]
{U:1000,30000000} //prehist2; [15]
{U:0,1} //time of size decrease 2 [16]
{U:1000,30000000} //Merged [17]
{U:1000,30000000} //Ice N0 [18]
{U:1000,30000000} //Ice N1 [19]
{U:1000,30000000} //Ancient [20]
```

M3c1

```
//Parameters for the coalescence simulation program : simcoal.exe
2 populations with ancient DNA
//Population effective sizes (number of genes)
{U:1000,100000}
{U:1000,100000}
//samples
133 sample groups
1 45 0 0
1 411 0 0
1 551 0 0
1 607 0 0
1 654 0 0
1 635 0 0
1 31 1 1
1 37 1 1
1 45 1 1
1 45 1 1
1 96 1 1
1 30 1 1
1 112 1 1
1 150 1 1
1 165 1 1
```

```
1 180 1 1
2 210 1 1
1 305 1 1
25 20 1 1
1 718 0 2
1 727 0 2
1 860 0 2
1 846 0 2
1 881 0 2
1 978 0 2
1 1351 0 2
1 1491 0 2
1 1748 0 2
1 1665 0 2
1 1907 0 2
5 2074 0 2
1 1973 0 2
1 1985 0 2
1 2027 0 2
1 1987 0 2
1 2529 0 3
1 2696 0 3
2 3119 0 3
1 3048 0 3
1 3213 0 3
2 3439 0 3
2 3416 0 3
1 3537 0 3
1 3607 0 3
1 3597 0 3
1 3673 0 3
1 3747 0 3
1 3623 0 3
1 3617 0 3
1 3645 0 3
1 4048 0 3
1 3935 0 3
1 3881 0 3
1 3982 0 3
1 3861 0 3
1 3989 0 3
1 4047 0 3
1 3096 1 4
1 2990 1 4
1 3091 1 4
1 3076 1 4
```

1 3286 1 4
1 3294 1 4
1 4956 0 5
1 5091 0 5
1 5357 0 5
1 5719 0 5
1 5768 0 5
2 5784 0 5
1 5840 0 5
1 5842 0 5
1 6191 0 5
1 6285 0 5
1 6276 0 5
1 6442 0 5
1 6463 0 5
1 6635 0 5
1 5981 0 6
1 6079 0 6
1 7052 0 7
1 7107 0 7
1 7334 0 7
1 7686 0 7
1 7730 0 7
1 7734 0 7
1 7769 0 7
1 7832 0 7
1 7889 0 7
1 8009 0 7
1 7940 0 7
1 8089 0 7
1 8428 0 8
1 8441 0 8
1 8544 0 8
1 8660 0 8
1 8745 0 8
1 8819 0 8
1 8896 0 8
1 8861 0 8
1 8970 0 8
1 9001 0 8
1 9256 0 8
1 9506 0 8
1 9766 0 9
1 9856 0 9
1 10183 0 9
1 10202 0 9

```
1 10344 0 9
1 10561 0 9
1 10562 0 9
1 10788 0 9
1 10811 0 9
1 10858 0 9
1 10986 0 9
1 10994 0 9
1 11000 0 9
1 11152 0 9
1 9761 0 9
1 12084 0 10
1 13232 0 10
1 12108 0 10
1 11675 0 10
1 13808 0 10
1 12375 0 10
1 12491 0 10
1 15328 0 10
1 14887 0 10
1 12048 0 10
1 13446 0 10
1 11946 0 10
1 14300 0 11
1 13631 0 11
1 14500 0 11
//Growth rates: negative growth implies population expansion
0
0
//Number of migration matrices
0
//historical event: time, source, sink, migrants, new deme size, new growth rate, migration matrix index
6
{U:1,80} 0 0 0 {[17]/[1]} 0 0
{U:1,80} 1 1 0 {[18]/[2]} 0 0
{U:350,1200} 1 0 1 {[19]/[17]} 0 0
{U:2000,2750} 0 1 {[21]/([20]+[21])} {[21]/[18]} 0 0
{[9]+1} 0 0 0 {[20]/[19]} 0 0
{U:5250,7500} 1 0 1 {[22]/[20]} 0 0
//Mutation rate per generation for the whole sequence
{N:0.00102443,0.00025}
//Number of loci
615
//data type either DNA, RFLP, or MICROSAT : If DNA, we need a second term for the transition bias
```

```
DNA 0.792
//Gamma parameter (if 0: even mutation rates, if >0 :shape parameter of the Gamma distribution
0
{U:1000,30000000} //prehist1 N0; [17]
{U:1000,30000000} //prehist1 N1; [18]
{U:1000,30000000} //Merged [19]
{U:1000,30000000} //Ice N0 [20]
{U:1000,30000000} //Ice N1 [21]
{U:1000,30000000} //Ancient [22]
```

M3c2

```
//Parameters for the coalescence simulation program : simcoal.exe
2 populations with ancient DNA
//Population effective sizes (number of genes)
{U:1000,100000}
1
//samples
133 sample groups
1 45 0 0
1 411 0 0
1 551 0 0
1 607 0 0
1 654 0 0
1 635 0 0
1 31 0 1
1 37 0 1
1 45 0 1
1 45 0 1
1 96 0 1
1 30 0 1
1 112 0 1
1 150 0 1
1 165 0 1
1 180 0 1
2 210 0 1
1 305 0 1
1 718 0 1
1 727 0 1
25 20 0 1
1 860 0 2
1 846 0 2
1 881 0 2
1 978 0 2
1 1351 0 2
```

1	1491	0	2
1	1748	0	2
1	1665	0	2
1	1907	0	2
5	2074	0	2
1	1973	0	2
1	1985	0	2
1	2027	0	2
1	1987	0	2
1	2529	0	3
1	2696	0	3
2	3119	0	3
1	3048	0	3
1	3213	0	3
2	3439	0	3
2	3416	0	3
1	3537	0	3
1	3607	0	3
1	3597	0	3
1	3673	0	3
1	3747	0	3
1	3623	0	3
1	3617	0	3
1	3645	0	3
1	4048	0	3
1	3935	0	3
1	3881	0	3
1	3982	0	3
1	3861	0	3
1	3989	0	3
1	4047	0	3
1	3096	1	4
1	2990	1	4
1	3091	1	4
1	3076	1	4
1	3286	1	4
1	3294	1	4
1	4956	0	5
1	5091	0	5
1	5357	0	5
1	5719	0	5
1	5768	0	5
2	5784	0	5
1	5840	0	5
1	5842	0	5
1	6191	0	5

1 6285 0 5
1 6276 0 5
1 6442 0 5
1 6463 0 5
1 6635 0 5
1 5981 0 6
1 6079 0 6
1 7052 0 7
1 7107 0 7
1 7334 0 7
1 7686 0 7
1 7730 0 7
1 7734 0 7
1 7769 0 7
1 7832 0 7
1 7889 0 7
1 8009 0 7
1 7940 0 7
1 8089 0 7
1 8428 0 8
1 8441 0 8
1 8544 0 8
1 8660 0 8
1 8745 0 8
1 8819 0 8
1 8896 0 8
1 8861 0 8
1 8970 0 8
1 9001 0 8
1 9256 0 8
1 9506 0 8
1 9766 0 9
1 9856 0 9
1 10183 0 9
1 10202 0 9
1 10344 0 9
1 10561 0 9
1 10562 0 9
1 10788 0 9
1 10811 0 9
1 10858 0 9
1 10986 0 9
1 10994 0 9
1 11000 0 9
1 11152 0 9
1 9761 0 9

```
1 12084 0 10
1 13232 0 10
1 12108 0 10
1 11675 0 10
1 13808 0 10
1 12375 0 10
1 12491 0 10
1 15328 0 10
1 14887 0 10
1 12048 0 10
1 13446 0 10
1 11946 0 10
1 14300 0 11
1 13631 0 11
1 14500 0 11
//Growth rates          : negative growth implies population expansion
0
0
//Number of migration matrices
0
//historical event: time, source, sink, migrants, new deme size, new growth rate,
migration matrix index
4
{U:1,80} 0 0 0 {[12]/[1]} 0 0
{U:2000,2750} 0 1 {[14]/([14]+[13])} {[14]} 0 0
{[4]+1} 0 0 0 {[13]/[12]} 0 0
{U:5250,7500} 1 0 1 {[15]/[13]} 0 0
//Mutation rate per generation for the whole sequence
{N:0.00102443,0.00025}
//Number of loci
615
//data type either DNA, RFLP, or MICROSAT : If DNA, we need a second term for the
transition bias
DNA 0.792
//Gamma parameter (if 0: even mutation rates, if >0 :shape parameter of the
Gamma distribution
0
{U:1000,30000000} //prehist [12]
{U:1000,30000000} //Ice N0 [13]
{U:1000,30000000} //Ice N1 [14]
{U:1000,30000000} //Ancient [15]
```