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The Confounding Effect of Population Structure on Bayesian Skyline Plot Inferences of Demographic History

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Abstract

Many coalescent-based methods aiming to infer the demographic history of populations assume a single, isolated and panmictic population (i.e. a Wright-Fisher model). While this assumption may be reasonable under many conditions, several recent studies have shown that the results can be misleading when it is violated. Among the most widely applied demographic inference methods are Bayesian skyline plots (BSPs), which are used across a range of biological fields. Violations of the panmixia assumption are to be expected in many biological systems, but the consequences for skyline plot inferences have so far not been addressed and quantified. We simulated DNA sequence data under a variety of scenarios involving structured populations with variable levels of gene flow and analysed them using BSPs as implemented in the software package BEAST. Results revealed that BSPs can show false signals of population decline under biologically plausible combinations of population structure and sampling strategy, suggesting that the interpretation of several previous studies may need to be re-evaluated. We found that a balanced sampling strategy whereby samples are distributed on several populations provides the best scheme for inferring demographic change over a typical time scale. Analyses of data from a structured African buffalo population demonstrate how BSP results can be strengthened by simulations. We recommend that sample selection should be carefully considered in relation to population structure previous to BSP analyses, and that alternative scenarios should be evaluated when interpreting signals of population size change.

Introduction

Coalescent-based methods can be used to infer demographic change (used here in the narrow sense of population size change) from genetic data [1,2]. The coalescent framework has contributed important information about the demographic history of humans [3–5] and other species [6–8]. This has improved our understanding of the factors that have affected past ecosystems, whether climatic or anthropogenic, recent or ancient. Demographic inference methods based on the coalescent usually assume panmixia, i.e. the absence of population structure, although this is not a realistic assumption in many biological situations. A number of recent studies have investigated the effect of violating the panmixia assumption for inferring population size changes [9–11]. These studies suggest that population structure can lead to erroneous conclusions about demographic changes in a population that in fact has remained stationary through time.

Bayesian skyline plots (BSPs [2]), or derivatives thereof such as the extended Bayesian skyline plot (EBSP [12]), have become increasingly popular for inferring demographic changes using sequence data. A search on the exact term (conducted December 2012) returned 1310 hits in Google Scholar, covering the spectrum of organisms from viruses to large mammals. Skyline plots assume a single panmictic population and use inferred patterns of coalescence to fit a demographic model to a set of sequence data. Although a recent review highlights the danger of violating the panmixia assumption in BSP inference [13], the structure effect on BSPs has not been quantified. Importantly, the confounding structure effect is not a fault of the skyline methods per se, but rather a case of fitting a wrong model (panmixia) to the data. As shown by several authors [11,14–16] it is fundamentally due to the fact that genes sampled within one population (or deme) within a set of inter-connected demes (or a structured population) exhibit genealogies that resemble those of panmictic populations that have declined in size. Structured populations have genealogies that differ from panmictic ones in some crucial aspects. In a seminal paper, Wakeley [14] identified two distinct phases when the genealogy of a structured population is considered backwards in time: the recent scattering phase, which lasts until all sampled lineages have coalesced or migrated so that each remaining lineage is in a separate deme. At this point the genealogy enters the collecting phase, where two or more lineages have to migrate to the same deme before coalescence can occur. Pannell [17] showed how the presence of these distinct genealogical phases will cause an apparent decline in estimates of effective population size going from the ancient (collecting phase) to the recent (scattering phase) part of the genealogy. BSPs derive population sizes from inferred genealogies and will consequently be prone to confound the effect of structure with declines in population size. We define this confounding of structure and demographic change as the
‘structure effect’. The structure effect remains under-appreciated in BSP analyses, and consequently there is a danger of deriving erroneous demographic conclusions from BSP analyses of structured populations. Some BSP-based studies do consider and discuss the possible confounding effect of structure (e.g. [7,21]), but an evaluation of the magnitude of the structure effect and the conditions that are especially prone to it is lacking. The present study is intended to serve this purpose.

This study expands on previous studies evaluating the structure effect. Stadler et al. [9] examined the effect of structure on Tajima’s \( D \) and Fu and Li’s \( D \) statistics in growing or constant values are more directly comparable across marker types and |

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The most simple simulation scenario was an island model with 40 demes of 500 mtDNA copies (corresponding to 500 females) connected by equal migrants per generation, since we are concerned with maternally inherited mtDNA sequences throughout. These rates represent the extremes and an intermediary level of gene flow found in structured populations [9,10]. The corresponding equilibrium \( F_{ST} \) values (for an mtDNA marker in an infinite island model [24]) are 0.30, 0.28 and 0.04, respectively. We use the number of migrants \( (N_m) \) to denote the level of gene flow, although we point out that \( F_{ST} \) values are more directly comparable across marker types and inheritance scalars. In keeping with Stadler et al. [9] and Chikhi et al. [10], we supplemented the island model with simulations under a stepping-stone model (see Supporting Information S1) using similar parameter values. We also considered a structured population identical to the 40-deme island model, but with only ten demes \( (N_d = 2000) \) in each to evaluate the structure effect under these conditions that match more closely a typical population genetic study (although the limited number of sampled demes is probably often indicative of logistic or resource limitations rather than the actual number of demes in structured populations).

The analyses were divided in two parts: first, we simulated data under an idealised model with a simplified migration pattern connecting the demes. This was done to illustrate the structure effect on BSPs under standardized conditions. We also considered more complex models that—in addition to the idealised structure—involved changes in either population size or structure. Second, we used data from a set of 755 African buffalo D-loop sequences distributed on 34 distinct populations in sub-Saharan Africa to test the structure effect under a data-informed migration matrix and on real sequence data.

### Simulated Scenarios

**Simulation settings.** We used the program Bayesian Serial SimCoal (BSSC [22]) to simulate DNA sequence data under different structural and demographic models. We simulated a 600bp fragment of the mitochondrial D-loop, commonly used in BSP studies due to its high nucleotide diversity. The sequences were set to evolve according to a HKY model with kappa = 50, gamma distributed rate heterogeneity (shape parameter 0.5) and a rate of 32% per million years per bp [6] (note that this rate is subject to estimation uncertainty, but here it serves to provide a conversion between genetic distance and real time), equivalent to 0.001344 mutations per sequence per generation (using the estimated buffalo generation time of 7 years [20]). We emulated the actual marker used in the buffalo case study in the simulations to facilitate comparisons, and because BSPs are almost always used in the context of dated genealogies with time measured in years. For all scenarios, we carried out 100 replicate simulations to incorporate coalescent stochasticity [23] and identify general patterns across stochastic replicates of the same demographic history. Essentially, this corresponds to simulating 100 non-linked genetic markers with the high information content of the D-loop.

We were thus able to assess the performance of multi-locus inference and ensure that our conclusions were not limited by the use of a single locus. This makes our results more comparable to multi-locus data that are likely to become common in the genomic era. Two example input files for BSSC are supplied to show the details of our simulations (File S1 and File S2).

**Sampling strategy.** The influence of the sampling scheme was investigated by drawing 40 samples in three different ways: 1) all 40 samples from a single deme, 2) 4 samples from each of 10 demes and 3) one sample from each of the 40 demes in the structured population. These correspond respectively to the local, pooled and scattered (not to be confused with the term ‘scattering phase’, which refers to aspects of the underlying genealogy) sampling regimes described in Stadler et al. [9] and Chikhi et al. [10], and we retain that terminology (always in italics) throughout this study. Unless otherwise stated, these three sampling strategies were explored for all simulated scenarios.

**Idealised structured population.** The most simple simulation scenario was an island model with 40 demes of 500 mtDNA copies (corresponding to 500 females) connected by equal migration and with a stationary population size throughout. Three levels of migration rates were simulated: \( N_e m = 0.125, N_e m = 1.25 \) and \( N_e m = 12.5 \) (where \( N_e m \) is the number of female migrants per generation, since we are concerned with maternally inherited mtDNA sequences throughout). These rates represent the extremes and an intermediary level of gene flow found in structured populations [9,10]. The corresponding equilibrium \( F_{ST} \) values (for an mtDNA marker in an infinite island model [24]) are 0.30, 0.28 and 0.04, respectively. We use the number of migrants \( (N_m) \) to denote the level of gene flow, although we point out that \( F_{ST} \) values are more directly comparable across marker types and inheritance scalars. In keeping with Stadler et al. [9] and Chikhi et al. [10], we supplemented the island model with simulations under a stepping-stone model (see Supporting Information S1) using similar parameter values. We also considered a structured population identical to the 40-deme island model, but with only ten demes \( (N_d = 2000) \) in each to evaluate the structure effect under these conditions that match more closely a typical population genetic study (although the limited number of sampled demes is probably often indicative of logistic or resource limitations rather than the actual number of demes in structured populations).

In addition to the constant-size idealised scenarios, we considered scenarios where population sizes varied, maintaining structure as above. The population size changes we explored were 1) a single transition from a constant to a ten-fold exponentially declining/expanding population at either a Holocene or Pleistocene time point (see Supporting Information S1 regarding the...
selected time points); 2) a boom-bust (combining the above Pleistocene growth and Holocene decline) demographic history as recently inferred for the African buffalo [21]. In this way, we wanted to test how different demographic changes might be mimicked or concealed by concomitant population structure under different sampling regimes. For all non-constant demographic scenarios, we explored only the intermediate $\Lambda_{\text{r,m}} = 1.25$ gene flow level to reduce computation time and because we already demonstrated the effect of varying gene flow. Finally, we simulated date under an ‘IM-like’ model where structure was not permanent (Supporting Information S1).

**Data-informed structured population.** To assess the structure effect under more complex conditions than the idealised, equal-migration scenarios mentioned above, we carried out simulations that mimicked the structure in a data set consisting of 755 D-loop sequences from the African buffalo collected in 34 locations (treated as demes hereafter) across sub-Saharan Africa. First, we assumed an island model of connectivity between the demes and used the population pairwise $F_{ST}$ matrix to estimate female migration rates through the formula $F_{ST} = \frac{2Nm^2}{N_o + 2Nm}$ [24]. This was intended as an approximation only, as the equation only holds under certain assumptions—notably migration-drift equilibrium in Wright’s infinite island model—which are probably not met here [25]. However, it does allow us to explore the structure effect in a more complex and realistic scenario represented by unequal migration rates among demes. Simulations were carried out with the data-informed migration matrix and assuming a deme size of 500 females. We simulated data under a constant and a boom-bust demographic history. Replication in the data-informed simulations was slightly different from the idealised simulations because we now had to take into account that under a non-uniform migration matrix, it matters which populations are represented in the sample. Under local sampling we analysed ten replicates of each deme (340 data sets in total); under pooled sampling we analysed four samples from each of ten randomly selected demes, replicated 100 times. Under scattered sampling, we simply performed 100 replicates of the scenarios and analysed a single individual from each deme. Because of these differences in replication, the variance as evident from the different individual lines in the EBSPs is not directly comparable among the two parts of the analyses, as we discuss below.

**Skyline Plot Analyses**

**Simulated data analyses.** All data sets were analysed with the extended Bayesian Skyline Plot (EBSP) coalescent prior in BEAST [2]. This model allows the data to guide the selection of the most probable piece-wise linear demographic function, hence in principle allows it to take any shape, although this is affected by prior settings. The number of change-points in the demographic function is influenced by the parameter ‘demographic.popSizeChange’ (PSC in the following), which was given a Poisson prior with a mean of ln(2). This corresponds to a prior assumption that zero and all non-zero PSCs have equal probability. For consistency and due to the low number of change points in the simple demographic scenarios explored here, we did not vary the PSC prior, but simulations have shown that it does influence the ability of EBSPs to pick up complex demographic patterns [12]. For each simulated scenario, we plotted the median inferred population size from each EBSP analysis (100 data sets per scenario) and the prior and posterior of the PSC parameter. The BEAST priors on substitution model parameters were chosen to conform to the values from the simulated data, and we fixed the substitution rate to that used in the simulations. BEAST analyses were run for $10^7$ steps drawing samples every $10^3$ step, which was found to be sufficient to reach convergence in trial runs.

To quantify the difference between simulated (i.e. the sum of all deme sizes) and inferred population sizes and supplement the visual observations of the EBSPs themselves, we calculated the following measures across all 100 simulation replicates for all constant-size simulations: Coverage, or the proportion of time points from the inferred EBSP demographic function where the 95% highest posterior density interval included the simulated population size, and the mean (over all time points as above) relative departure (MRD) of the median inferred population size from the simulated one. These measures are related to those applied in Heled & Drummond [12].

**Real data analyses.** Finally, we applied the three different sampling strategies to the real D-loop data: local (all samples from each of the buffalo populations ranging from three to 85 individuals per population), pooled (four samples picked randomly from ten of the 34 populations, replicated 100 times) and scattered (one sample picked randomly from each population, replicated 100 times). It should be noted that this resampling is not equivalent to the replication of simulations to display coalescent stochasticity, since the case data represents just one realization of the coalescent process. It was done to ensure that results were not biased by sampling effects.

**Results**

**Idealised Structured Population**

Our first series of simulations with no demographic change demonstrates that population structure can mimic population size changes in the absence of any such change (Fig. 1). The probability of such a misinterpretation depends on the interplay between the sampling strategy and the level of gene flow. Locally sampled scenarios under all levels of migration as well as pooled samples from the lowest migration class showed a clear trend towards declining EBSPs. The posterior distribution of the population size change (PSC) parameter confirmed this qualitative observation, as the above scenarios showed a strong tendency towards overestimating PSC (Fig. 1 insert panels). The measures of coverage and mean relative departure (MRD) corroborated the visual inspection of EBSPs and the PSC distributions, showing that the inferred population size at the present was notoriously lower than the simulated one under local sampling (Table 1). Other notable observations include a consistently higher inferred population size than the simulated one in the older parts of the EBSPs under scattered and pooled sampling for the two lowest migration classes (though less pronounced for the pooled strategy). This discrepancy between effective and actual (i.e total number of individuals) population size at low migration rates under scattered sampling is in fact expected as shown in Wakeley’s Eq. (6.18) [26]. The MRD of the inferred from the simulated population sizes is close to the expected magnitude of this effect (expected MRD from Wakeley’s Eq. (6.18): 4.00, 0.40 and 0.04 at $N_o = 0.125, 1.25$ and 12.5, respectively, to be compared with our calculated values of 4.33, 0.54 and 0.08; Table 1), showing the ability of EBSPs to correctly infer the structured effective population size in the collecting phase.

When a single population change point was introduced (either a Holocene decline or a Pleistocene expansion) in the simulated demography we observed an interesting phenomenon. The expansion was unobservable in scenarios under local sampling (Fig. 2A), whereas it was the decline that was unobservable under scattered sampling (Fig. 2F). The pooled sampling strategy captured both phases more reliably (Fig. 2B,E). This pattern was also
evident in the more complex boom-bust demographic simulations where both change points were included (Fig. 2G–I), although not all replicates of the pooled boom-bust scenario revealed the expansion phase (Fig. 2H).

The 10-deme scenarios showed the same overall trend as the 40-deme scenarios, but the severity of the structure effect was reduced relative to the comparable 40-deme scenarios (Fig. S1). Results for the stepping-stone simulations showed the same qualitative patterns as the island model simulations, but they were generally more extreme (Fig. S2). This is not surprising, as the stepping-stone model makes the effect of migration even more dominant over demographic changes because the average waiting time for lineages to find the same deme is longer. Results from the ‘IM-like’ models were similar to the permanent structure models (Table S1; Fig. S3).

Figure 1. The structure effect in a 40-deme constant-size island model. For each scenario, 100 replicate data sets were generated and analysed with EBSPs. Light blue lines represent the median inferred female effective population size through time from each replicate. Time is measured in kya or thousands of years ago and is based on a molecular clock for buffalo D-loop sequences. Bold black lines represent the simulated size of the structured population (500 females * 40 demes = 20,000 females). Insert into each panel is a histogram of PSC values (on x-axis; see main text) across replicates. Dashed lines show the prior distribution for PSC. The y-axis in the insert histograms marks the frequency of occurrence in each PSC bin out of 100 replicates.

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Table 1. Comparison of EBSP and simulated population sizes under different structural scenarios.

<table>
<thead>
<tr>
<th>Scenario</th>
<th>Nm</th>
<th>EBSP</th>
<th>Sampling</th>
<th>coverage</th>
<th>MRD</th>
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<tbody>
<tr>
<td>constant</td>
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<td>Fig. 1A</td>
<td>local</td>
<td>0.72</td>
<td>−0.77</td>
</tr>
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<td>island model</td>
<td>0.125</td>
<td>Fig. 1B</td>
<td>pooled</td>
<td>0.86</td>
<td>0.90</td>
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<tr>
<td>0.125 (Fig. 1C) scattered</td>
<td>0.61</td>
<td>4.33</td>
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<tr>
<td>1.25 (Fig. 1D) local</td>
<td>0.78</td>
<td>−0.76</td>
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<tr>
<td>1.25 (Fig. 1E) pooled</td>
<td>0.98</td>
<td>0.13</td>
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<tr>
<td>1.25 (Fig. 1F) scattered</td>
<td>0.90</td>
<td>0.54</td>
<td></td>
<td></td>
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</tr>
<tr>
<td>12.5 (Fig. 1G) local</td>
<td>0.83</td>
<td>−0.50</td>
<td></td>
<td></td>
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</tr>
<tr>
<td>12.5 (Fig. 1H) pooled</td>
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<td>0.06</td>
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<tr>
<td>12.5 (Fig. 1I) scattered</td>
<td>0.99</td>
<td>0.08</td>
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<td>10 demes</td>
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<td>Fig. 1A</td>
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<td>0.69</td>
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<tr>
<td>1.25 (Fig. 1B) local</td>
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<td>−0.66</td>
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<tr>
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<tr>
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<td>0.07</td>
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<tr>
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<tr>
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<td>−0.50</td>
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<tr>
<td>12.5 (Fig. 2H) pooled</td>
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<td>−0.28</td>
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<td>0.99</td>
<td>0.14</td>
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</table>

Coverage is the proportion of time points at which the simulated population size lies within the inferred EBSP 95% highest probability density interval. MRD (mean relative departure) is the average relative deviation of the median inferred population size from the simulated size (e.g., 4.33 means that on average the inferred median population size is 4.33 times larger than the simulated one). For the 10 demes scenario, only local and pooled sampling was applied as scattered sampling would have resulted in low sample size (10 samples).

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Data-informed Structured Population

Our simulations mimicking the inferred gene flow connecting 34 African buffalo populations revealed that under this structural configuration, the risk of a false signal of population size change was relatively low (Fig. 3) and resembled those of the high-migration scenarios under the idealised island model (Fig. 1G–I). Interestingly, the local sampling—when analysed dey dey–revealed that there was a high correlation between the deme connectedness (measured as the mean of all pairwise FST values involving a given deme) and PSC (Fig. S4). This shows that within a structured population with unequal deme connectedness, the risk of false positives of population decline depends on which demes are sampled. We expanded on this observation by simulating local sampling in a structured population with a wide range of gene flow among demes (Nm 0.12–79.86, corresponding to an equilibrium FST of 0.007–0.827; see Supporting Information S1 for details). This revealed a clear separation between two phases in the relation between FST and PSC (which quantifies the risk of a structure effect): when Nm < 2 (FST < 0.2), there was a strong positive correlation between the two and when Nm > 2, the correlation was negative (Fig. S4). The latter was initially surprising, but then we considered that in very isolated demes, there is a high probability that all lineages coalesce in the scattering phase (i.e. in the sampled deme) so that there will be no collecting phase (see the Discussion). We show EBSPs and PSC histograms for the two most extreme demes in terms of connectedness (Fig. S5) to illustrate the importance of deme connectedness.

The African buffalo data yielded different results depending on the sampling strategy (Fig. 4). Under the pooled sampling we observed a conspicuous boom-bust signal that resembled the signal in the data-informed simulated data closely (Fig. 3F) and was very distinct from any of the false signals observed in Fig. 1. Under the scattered sampling the EBSP approached Fig. 2F and Fig. 3D, where the decline phase towards the present was almost absent. The qualitative differences between Fig. 4B and 4C were confirmed by the corresponding PSC values, with lower PSC values for the scattered sampling strategy (Fig. 4 insert panels). Finally, the locally sampled buffalo data showed variable skyline plots including boom-bust-like dynamics, pure expansions, pure declines and nearly constant population sizes (Fig. 4A). Note that low sample sizes for some of the demes (the three smallest samples consisted of three, four and ten individuals respectively) could lead to unreliable EBSPs.

Discussion

The Genealogical Background for the Structure Effect

Our results clearly demonstrate the dangers of using skyline plot methods for inferring demographic history without considering violations of the panmixia assumption. Overall, our results show that an apparent BSP population decline towards the present should always be regarded with caution, as it may be an artefact of structure. Such a confounding structure effect is not surprising, as it has been predicted in earlier theoretical studies [11,14,15,17,27] and identified in practical studies using various analysis methods [9,10]. However, the effect has not been quantified under Bayesian skyline plot methods, which have become very popular in recent years. The intuitive, visual appeal coupled with a real risk of erroneous demographic inferences make BSPs vulnerable to misinterpretations. It should be underlined, however, that this is not a shortcoming of the methods themselves, but rather an under-appreciation of the dynamics of coalescent intervals in structured genealogies. As we show, the EBSPs actually do a fairly good job of inferring the theoretical effective size in the individual demes and the structured population (corresponding to the start of the scattering and the collecting phase, respectively). The problem is that these two are expected to differ (being smaller and larger than the sum of individuals across demes, respectively), even when the total population size remains constant over time. This phenomenon manifests itself as a declining population trajectory in BSPs. It should be noted that the structure effect in addition to the false positive of a population decline can also lead to the false negative of failing to detect a true population expansion towards the present, so the absence of a decline signal in a BSP is not necessarily evidence of the absence of a structure effect.

Using Simulations to Assess the Risk of the Structure Effect

We show here that a critical approach is required before accepting the demographic history inferred from skyline plots. The inclusion of a case of real data allowed us to expand the scope of the analyses to include more complex connectivity among populations, to incorporate realistic historical events and to compare the idealised simulation results to analyses of real data,
which we believe is a sound approach to validate BSP results in empirical studies [21]. Collectively, our simulations (not all of which we were able to report here) show that the magnitude of the structure effect depends on all of the following: the number of demes, the population size of the demes, the migration rate, the migration pattern (i.e. island or stepping-stone model, whether or not gene flow is equal among demes), the sampling scheme and the interaction between all of these. This makes it hard to predict the structure effect in a given biological system and a priori evaluate how it will affect demographic inferences. Hence, it is important to use simulations emulating biologically reasonable scenarios to evaluate whether an observed skyline plot is robust [7,21]. When using the pairwise $F_{ST}$ matrix of the D-loop data set to inform the migration matrix, we found evidence that pooled sampling should be able to distinguish between constant and fluctuating populations under this particular structural architecture, an important insight that was not evident from the idealised simulations. This part of the analyses also allowed us to make an important observation: the risk of a structure effect depends almost linearly on the ‘connectedness’ of the sampled demes up to a certain point.

Figure 2. The structure effect in a 40-deme island model with demographic change. As Fig. 1, but the bold black line shows the simulated demographic change scenarios (see main text) with one or two changes in population size. Only the intermediary level of gene flow ($N_m = 1.25$) is shown. doi:10.1371/journal.pone.0062992.g002
(\(F_{ST} \sim 0.2\)) beyond which it actually decreases slowly (Fig. S4), but at the cost of EBSPs no longer reflecting the size of the whole structured population, but rather that of the sampled deme only. These results are important for devising sampling strategies when the level of differentiation is approximately known.

The EBSPs from the real data closely resembled those from simulations including actual boom-bust dynamics, suggesting that we can explain the signal from the case data by invoking structure and demographic change according to the parameters of the data-informed simulations, but not by invoking structure alone. Although this does not prove that our case is entirely collapsible to the data-informed model with two demographic change points, it makes us more confident that such a model represents the demographic history of the buffalo reasonably well.

Sampling Strategy and Practical Considerations
Locally collected samples always showed a false signal of population decline towards the present. Even at the high migration

Figure 3. Two demographic scenarios under a real data informed island model. As Figs. 1 and 2, but the island model was modified to conform to the migration matrix estimated for a real biological system, the African buffalo. Only pooled and scattered sampling is shown. Bold lines mark the appropriate simulated population size. Replication was slightly different from Fig. 1 and 2 because it now matters which demes were included in the sample, see main text. Note also that the number of demes was 34, so the sum of the deme size differs from Fig. 1 and 2 (17,000 as opposed to 20,000 females).
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rate $N/m = 12.5$ (corresponding to an equilibrium $F_{ST}$ of 0.04), local sampling resulted in a 97% false positive rate of mean PSC > 1 in constant-size simulations (Fig. 1G). This is a very important observation underlining that local samples should not be used to draw conclusions about demographic history in the presence of even limited population structure. The reason for the false signals of population decline is conceptually simple. Looking backwards in time, the first part of the structured genealogy will be the scattering phase [14,17] where the effective population size is estimated to something intermediary between that of the local deme and the structured population. The balance between these two is governed by the migration process, if all lineages coalesce within demes before any migration occurs, the inferred population size will correspond to the deme size, as was shown in the comparison of deme connectedness and PSC (Fig. S4). The structure effect is only present when there is a separation of the genealogy into a scattering and a collecting phase, so in very isolated demes the BSP will be more reflective of just the local deme population size (see also the low population size estimates and lower PSC in Fig. 1A and Fig. S2A). When the population enters the collecting phase, it starts behaving entirely like a structured population with an effective population size $(1+1/Nm)$ times that of the census size (from equation 6.18 in [26]).

Although the scattered sampling approach does not suffer from the tendency to show false declines, this sampling strategy is apparently not optimal for inferring changes in the recent past (Fig. 2F). The reason for this is that under scattered sampling there is no scattering phase, so lineage migration has to take place before any coalescent events can occur. Unless the migration rate is very high (or the number of demes is very low) this leads to a low rate of coalescence in the recent part of the genealogy, hence reducing the inferential power in this period. This observation challenges the recommendation in [10] of using scattered sampling when inferring the recent demographic history of structured populations. We confirmed the robustness assertion, but found that power decreased concomitantly. In that study however, the object was explicitly to identify false positives of population size change (maximize robustness), and we confirm that this risk is lowest under scattered sampling.

On balance, the pooled strategy was the most appropriate sampling scheme under both the idealised and the data-informed structural architecture. This strategy was most capable of capturing both the expansion and the decline phase of the simulated population size change. It is of course important to emphasize that the pooled strategy can be varied continuously between the two extremes of local and scattered sampling and is hence less clearly defined than the two extremes. Consequently, the results presented here are strictly only valid for the somewhat arbitrarily chosen strategy of four samples from each of ten demes, which can be considered closer to the scattered than to the local extreme (any number $d$ in the interval 2–20 samples could be sampled from any number between 2–20 demes to make reasonably balanced pooled sampling). As expected, changing $d$ from 4 to 10 under the boom-bust scenario yielded a signal closer to that under local sampling (Fig. 2A), with the expansion phase becoming less detectable (results not shown). A pooled sampling strategy can thus be varied among the two extremes of local and scattered sampling according to the trade-off between the power to detect recent changes and the risk of getting a false positive from a structure effect.

Results from the three different sampling strategies applied to the real data confirmed that sampling can heavily influence the demographic signal in the presence of population structure. Therefore, we recommend that BSP-users at least explore different sampling schemes along the continuum between local and scattered sampling for their data sets, because it may reveal whether the structure effect is confounding the demographic inference. We recommend that whenever possible one considers the underlying population structure before planning sampling, yet in many cases some variety of pooled sampling will be desirable for inferring population dynamics if structure is present.

**Methodological Considerations**

The coalescent effective population size is only defined for the collecting phase of a structured genealogy [14,28,29], therefore it was impossible to compare the inferred values with the expected ones throughout EBSPs. Consequently, our EBSP plots (Figs. 1, 2, 3, 4) and the measures calculated in Table 1 should not be regarded as an evaluation of the accuracy of EBSPs; rather they show the discrepancy between the sum of the deme sizes and the effective size in a structured population. However, the shape of the EBSPs and the PSC histograms demonstrate that even if EBSPs are accurate in inferring the theoretical (structured) effective population size at any given time, the change in effective size caused by the transition from a scattering to a collecting phase can be misleading if not interpreted in the proper context.

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**Figure 4. Three different sampling strategies for real data from the buffalo.** Local, pooled and scattered sampling of real D-loop data from 34 African buffalo populations. The replication of each sampling strategy involved random drawing of the appropriate number of samples from demes as explained in the main text.

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The replication of each scenario enabled us to assess the coalescent stochasticity [23] under any demographic scenario. As the plots show, individual EBSPs vary among repetitions—more so when the demographic history departs from simple, constant-sized populations (Fig. 2 and 3)—and only converge on the “true” simulated demographic history when viewed across many repetitions (i.e., many independent loci). This demonstrates the importance of multi-locus data when inferring demographic history. The type of simulated marker (600 bp of mtDNA) appeared suitable to shed light on the problem at hand, as the simulated demographies were always consistently detected in the EBSPs under at least one of the sampling strategies.

We stress that we were only able to address the structure effect on RBSPs under a limited set of conditions. It is not possible to evaluate all the factors that influence the structure effect in a single study. Here we identify some general aspects of the problem, and we hope this will serve as a starting point for further studies on the factors that influence the structure effect in coalescent-based methods. As we show with the buffalo data, the structure effect will not always lead to serious misinterpretations, especially when a balanced (pooled) sampling strategy is followed.

The structure effect is not restricted to certain coalescent methods, but is rather a general problem that affects all methods that do not explicitly take subdivision into account. Hence, all methods that assume panmictic populations will suffer from confounding effects qualitatively similar to those reported here. One ad hoc approach to evaluate the structure effect in BSP analyses is to inspect the inferred genealogy and assess whether coalescent rates are obviously correlated with the structural conformation, i.e., if any substantial increase in coalescence rate towards the present predominantly occurs within demes. Ultimately, the best way of circumventing the confounding structure effect involves incorporating explicitly the spatial or structural information into the genealogical reconstruction. The LAMARC [30] and IM [31] software packages do this to some extent by allowing specification of population structure and hence co-estimation of migration and population size parameters, but currently they only handle simple demographic trajectories without any demographic change points [19,20]. BSP methods could benefit from integration with such approaches. This should facilitate distinguishing between the transition from a scattering to a collecting phase and a true change in the census size of a structured population.

Supporting Information

Figure S1  The structure effect in a 10-deme population.
As Fig. 1, but simulating a 10-deme instead of a 40-deme population. Only local and pooled sampling was applied, as scattered sampling would have yielded unreasonably low sample sizes (10 samples).

References


