REVIEW

On the importance of skewed offspring distributions and background selection in virus population genetics

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Many features of virus populations make them excellent candidates for population genetic study, including a very high rate of mutation, high levels of nucleotide diversity, exceptionally large census population sizes, and frequent positive selection. However, these attributes also mean that special care must be taken in population genetic inference. For example, highly skewed offspring distributions, frequent and severe population bottleneck events associated with infection and compartmentalization, and strong purifying selection all affect the distribution of genetic variation but are often not taken into account. Here, we draw particular attention to multiple-merger coalescent events and background selection, discuss potential misinference associated with these processes, and highlight potential avenues for better incorporating them into future population genetic analyses.
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INTRODUCTION

Viruses appear to be excellent candidates for studying evolution in real time; they have short generation times, high levels of diversity often driven by very large mutation rates and population sizes (both census and effective), and they experience frequent positive selection in response to host immunity or antiviral treatment. However, despite these desired attributes, standard population genetic models must be used with caution when making evolutionary inference.

First, population genetic inference is usually based on a coalescence model of the Kingman type, under the assumption of Poisson-shaped offspring distributions where the variance equals the mean and is always small relative to the population size; consequently, only two lineages may coalesce at a time. In contrast, viruses have highly variable reproductive rates, taken as rates of replication; these may vary based on cell or tissue type, level of cellular differentiation or stage in the lytic/lysogenic cycle (Knipe and Howley, 2007), resulting in highly skewed offspring distributions. This model violation is further intensified by the strong bottlenecks associated with infection and by strong positive selection (Neher and Hallatschek, 2013). Therefore, virus genealogies may be best characterized by *multiple-merger* coalescent (MMC) models (see, for example, Donnelly and Kurtz, 1999; Pitman, 1999; Sagitov, 1999; Schweinsberg, 2000; Möhle and Sagitov, 2001; Eldon and Wakeley, 2008), instead of the Kingman coalescent.

Second, the mutation rates of many viruses, particularly RNA viruses, are among the highest observed across taxa (Lauring *et al.*, 2013; Cuevas *et al.*, 2015). Although these high rates of mutation are what enables new beneficial mutations to arise, potentially allowing for rapid resistance to host immunity or antiviral drugs, they also render high mutational loads (Sanjuán, 2010; Lauring *et al.*, 2013). Specifically, the distribution of fitness effects has now been described across

taxa—demonstrating that the input of deleterious mutations far outnumbers the input of beneficial mutations (Acevedo *et al.*, 2014; Bank *et al.*, 2014; Bernet and Elena, 2015; Jiang *et al.*, 2016). The purging of these deleterious mutants through purifying selection can affect other areas in the genome through a process known as background selection (BGS) (Charlesworth *et al.*, 1993). Accounting for these effects is important for accurate evolutionary inference in general (Ewing and Jensen, 2016), but essential for the study of viruses because of their particularly high rates of mutation and compact genomes (Renzette *et al.*, 2016).

Given these distinctive features of virus populations and the increasing use of population genetic inference in this area (see, for example, Renzette *et al.*, 2013; Foll *et al.*, 2014; Pennings *et al.*, 2014; Renzette *et al.*, 2016), it is crucial to account for these processes that are shaping the amount and distribution of variation across their genomes. We aim here to draw particular attention to MMC events and background selection, and the repercussions of ignoring them in population genetic inference, highlighting particular applications to viruses. We conclude with general recommendations for how best to address these topics in the future.

SKEWED OFFSPRING DISTRIBUTIONS AND THE MMC

Inferring evolutionary history using the Wright–Fisher model: benefits and shortcomings

Many population genetic statistics and subsequent inference are based on the Kingman coalescent and the Wright–Fisher (WF) model (Wright, 1931; Kingman, 1982). With increasing computational power, the WF model has also been implemented in forward-time methods, allowing the modeling of more complex evolutionary scenarios versus backward-time methods. This also allows for the

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is the number of lineages coalescing simultaneously), a probability distribution for k-merger events determines coalescence.

The parameters inferred under the MMC differ from those inferred under the Kingman coalescent in several notable respects. In the Kingman coalescent, effective size N_e scales linearly with census size N, whereas for the MMC it does not (Huillet and Möhle, 2011). Thus genetic diversity is a nonlinear function of population size. Coalescent trees under the MMC also have more pronounced star-like genealogies with longer branches (Figure 1), and their site frequency spectra (SFSs) are skewed toward an excess of low-frequency and high-frequency variants because of these branch lengths (Eldon and Wakeley, 2006; Blath et al., 2016), generating a more negative Tajima's D (Birkner et al., 2013). With similar migration and population size, alleles fix at a higher rate per population in the MMC than under the Kingman coalescent, and thus higher F_{ST} is expected between subpopulations (Eldon and Wakeley, 2009). Furthermore, the efficacy of selection increases, as selection acts almost deterministically between multiple-merger events; in the WF model, genetic drift counteracts selection fairly strongly (Der et al., 2011), but in generalized models where offspring distributions are wide, beneficial mutations may be more likely to escape stochastic loss and thus continue to fixation. Furthermore, the fixation probability of a new mutant with a positive selection coefficient approaches 1 as the population size increases, in stark contrast with traditional expectations under the standard WF model (Der et al., 2011).

Not accounting for skewed offspring distributions can lead to misinference. For instance, Eldon and Wakeley (2006) showed that for Pacific oysters, which have been argued to undergo sweepstake-like reproductive events (Hedgecock, 1994a), the estimated population-wide mutation rate θ inferred under the Kingman coalescent is two orders of magnitude larger than that obtained from the Ψ-coalescent
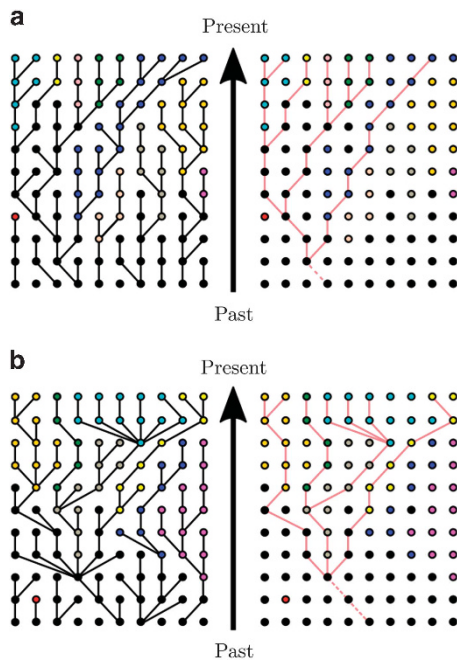

Figure 1 Multiple-merger and Kingman coalescent realizations. Example of genealogies and samples from (**a**) the Kingman coalescent and (**b**) a multiple-merger coalescent. Panels on the left show the evolutionary process of the whole population, whereas those on the right show a possible sampling and its resulting genealogy. Colors correspond to different (neutral) derived allelic states, where black denotes the wild type.

(see below)—9 vs 0.0308, respectively—and, indeed, provides a poor fit to the data.

The Ψ-coalescent
Introduced by Eldon and Wakeley (2006), the Ψ-coalescent (also called the 'Dirac-coalescent') differentiates two possible reproductive events in the underlying forward process (Figure 2). Either a standard Moran model reproduction event occurs (with probability $1 - \varepsilon$), where a single individual is randomly chosen to reproduce and the (single) offspring replaces one randomly chosen nonparental individual; all other individuals, including the parent, persist. Alternatively, a 'sweepstake' reproductive event occurs (with probability ε) (Hedgecock, 1994b), where a single parent replaces Ψ^*N individuals. If these sweepstake events happen frequently enough, the rate of Ψ^*N-reproduction events will be much greater than that of two-reproduction events, and the underlying coalescent process will consequently be characterized by MM events; if two or more parents were to replace Ψ^*N individuals, simultaneous MM events may occur in a single generation resulting in a Ξ-coalescent. However, in contrast to other MMC models (for example, Ξ-coalescent or other Λ-coalescents), the parameter Ψ has a clear biological interpretation as the fraction of the population that is replaced in each sweepstake reproductive event. Though the assumption of a fixed Ψ (as in the normal Ψ-coalescent) seems biologically unrealistic, it can be avoided by treating Ψ as a Poisson parameter. Finally, despite its appealing connection to biologically relevant measures, the appropriateness of making inferences based on the Ψ-coalescent still depends on the biology of the specific virus being studied. Thus, model choice is still essential, and the best-fit coalescent should be assessed on a case-by-case basis.

Application to viruses
There are several reasons why a modified Moran model may better capture virus evolution than models converging to the Kingman coalescent, even though it does not account for fitness differences between individuals. First, virus evolution is driven by strong bottlenecks during host transmission and intrahost selection processes that likely result in skewed offspring distributions (Figure 3) (Gutiérrez et al., 2012; Tellier and Lemaire, 2014). Furthermore, viruses display the MMC-typical low N_e/N ratio (Pennings et al., 2014; Tellier and Lemaire, 2014), can adapt rapidly (Neher and Hallatschek, 2013), and may have sweepstake-like reproductive events in which a single virion can propagate a large fraction of the entire population (Grenfell et al., 2004; Pybus and Rambaut, 2009). For example, the influenza virus hemagglutinin segment appears to be under strong directional selection imposed by host immunity (and sometimes drug treatment), resulting in a ladder-like genealogy (as depicted in Figure 3a), suggesting that only a few viruses seed the entire next generation (Grenfell et al., 2004). That being said, some challenges remain (see Box 1), such
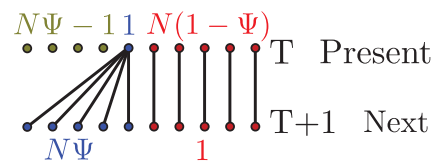
Figure 2 Depiction of the modified Moran model underlying the Ψ-coalescent. Lineages between the present and the next generation, where N is the population size, ε is the probability of a sweepstake event and Ψ is the fraction of the population that is replaced in each such event. Labels in the top row give the number of parental individuals reproducing in a given manner (represented by color), whereas labels in the bottom row give the number of corresponding offspring per parent.
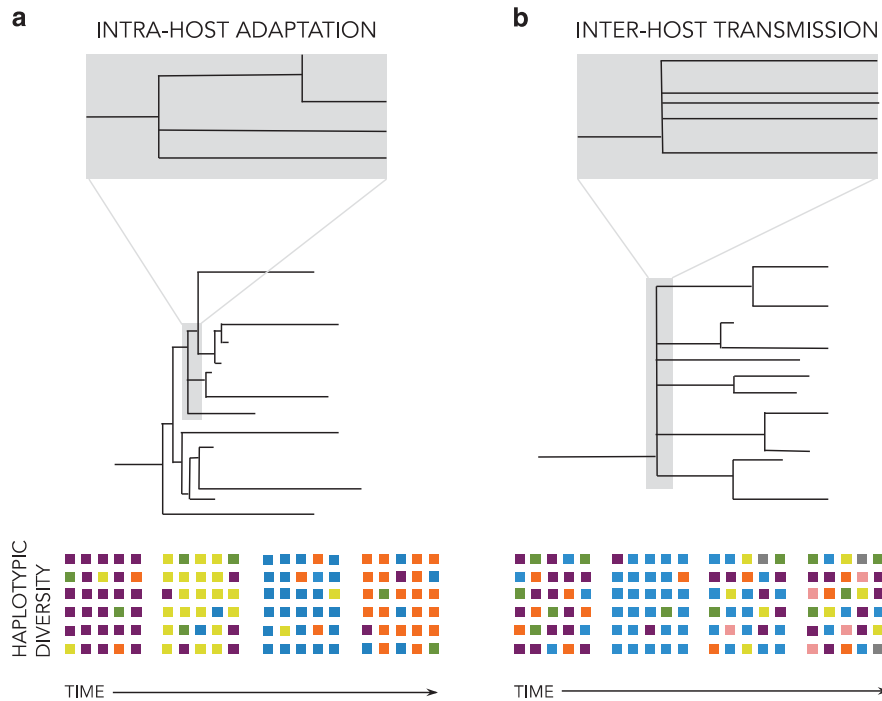
Figure 3 Example of processes spurring MM events in virus populations. Examples include (**a**) intrahost adaptation (a selective process) and (**b**) interhost transmission (a demographic process). The tree in (**a**) characterizes, for example, neuraminidase (NA) or hemagglutinin (HA) evolution in the influenza A virus, driven by positive selection; selection by host immunity is ongoing, whereas that from drug treatment may be intermittent. The tree in (**b**) represents interhost transmission and its associated bottleneck; for viruses that compartmentalize (such as human cytomegalovirus and HIV), similar patterns follow transmission to new compartments. The colored squares below the trees roughly indicate the diversity of the population through time. Intrahost adaptation may temporally decrease diversity owing to genetic hitchhiking, though single snapshots may not reflect varying temporal levels of diversity. During interhost transmission, diversity decreases owing to the associated bottleneck but then may quickly recover in the new host.

as rigorously defining the term 'generation' for virus populations, and subsequently confirming that the per-generation mutation rate is on the order of the coalescent timescale c_N, a prerequisite for the use of any coalescent approach. Finally, viruses with little or no recombination may be prone to clonal interference, and this should be explicitly accounted for in population models and resulting coalescents (see, for example, Strelkowa and Lässig, 2012).

The processes that make viruses ideal candidates for MMCs can differ by scale (see Figure 3); for example, following transmission events, there are severe founder effects and potentially high recombination within the host (for example, HIV and human cytomegalovirus). Subsequent compartmentalization may introduce intrahost population structure through bottlenecks, colonization events, and extinction events (Renzette *et al.*, 2013). To date, it remains unclear how often MMCs fit the patterns of variation observed in intrahost versus interhost virus populations—but such comparisons are increasingly feasible (Box 1). Finally, periods of latency—temporary virus inactivation with cessation of reproduction—should be incorporated in such modeling, potentially as recurring mass extinction events (Taylor and Véber, 2009). Thus, multiple MMC models are a necessary but not final step toward addressing the various patterns observed at different scales of virus evolution (Table 1).

The large data sets often generated from viruses may also prove impractical for the likelihood-based methods commonly employed for MMCs. This limitation has partially been overcome by Eldon *et al.* (2015), who proposed an approximate likelihood method along with an approximate Bayesian computation approach based on the SFS to distinguish between the MMC and exponential population growth. Although both effects are expected to result in very similar SFSs,

characterized by an excess of singletons as compared with the Kingman coalescent, the bulk and tail of the SFS (that is, the higher-order frequency classes) typically differ, which can be assessed by approximate likelihood-ratio tests and approximate Bayes factors (Eldon *et al.*, 2015; see Box 1).

PURIFYING SELECTION AND LINKAGE IN VIRUS POPULATIONS

Modeling background selection

The joint modeling of the effects of genetic drift and positive selection, including in experimental evolution studies of virus populations, has improved our ability to distinguish adaptive from neutral mutations by minimizing the chance that the rapid fixation of a neutral allele is incorrectly interpreted as strong positive selection (Li *et al.*, 2012; Foll *et al.*, 2014; see Box 2). However, there is another process that must be incorporated if we are to fully understand mutation trajectories in virus populations: background selection.

BGS was originally proposed to explain patterns of reduced diversity in regions of low recombination—patterns that were previously suggested to be the signature of genetic hitchhiking around strongly beneficial mutations (see Begun and Aquadro, 1992 and Charlesworth *et al.*, 1993). It was argued that only neutral mutations present on the 'least-loaded' chromosomes—that is, those with the fewest deleterious mutations—have appreciable probabilities of reaching high frequencies or fixation. Kimura and Maruyama (1966) showed that the proportion of chromosomes belonging to the least-loaded class is

$$f_0 = \exp\left(-\frac{U}{2hs}\right), \tag{1}$$

where U is the rate of mutation to a deleterious state, s is the selection coefficient against homozygous mutations and h is the dominance coefficient. For simplicity of modeling, h is usually set to 1 for viruses that carry a single copy of their genome in each virion, although polyploid effects could arise in the case of multiple virions infecting the same cell.

The least-loaded class, and thus genetic diversity in the presence of BGS, is dependent on the balance between the influx of deleterious mutations (occurring at rate U) and their removal by natural selection (according to the product hs). Assuming that offspring exclusively originate from the least-loaded class of individuals, Charlesworth *et al.* (1993) expressed the expected neutral diversity due to background selection as

$$\pi = 4 f_o N_e \mu, \qquad (2)$$

where N_e is the effective population size and μ is the mutation rate. As BGS reduces the number of reproducing individuals, genetic drift increases, thus reducing genetic diversity and increasing stochasticity in allele trajectories. Furthermore, as only the genetic diversity segregating in the least-loaded class can be observed, population size inferred from measures of genetic diversity may be underestimated if BGS is not properly taken into account (Ewing and Jensen, 2016).

In the BGS model described above, strongly deleterious mutations are maintained in mutation-selection balance such that no skew in the SFS is expected, as rare variants are rapidly purged. Thus, a simple rescaling of N_e is often used as a proxy for the effects of BGS (see, for example, Hudson and Kaplan, 1995; Zeng and Charlesworth, 2011; Prüfer *et al.*, 2012; Zeng, 2013). However, recent work has demonstrated that although this rescaling is appropriate for strongly deleterious mutations, it is largely inappropriate for weakly deleterious mutations that may segregate in the population. Figure 4 shows the skew in estimates of population size obtained using an approximate Bayesian computation approach when BGS is prevalent for two populations A and B that have split at time $\tau = 2N_e$ generations (reproduced from Ewing and Jensen, 2016). Furthermore, experimental work on the shape of the distribution of fitness effects in many organisms indicates that weakly deleterious mutations represent an important class (see, for example, Eyre-Walker and Keightley, 2007; Bank *et al.*, 2014). These mutations may act to skew the SFS toward rare alleles as they decrease the expected frequency of linked neutral mutations relative to neutral expectations. As subsequent demographic inference is based on the shape of this SFS, this effect should be properly accounted for by directly simulating weakly deleterious mutations rather than implementing a simple rescaling, as is common practice (Box 2). Though important analytical progress has been made in this area (see, for example, McVean and Charlesworth, 2000), simulations remain the best option for the nonequilibrium demographic models and alternative coalescents recommended here for inference in virus populations.

The effects of background selection on inference in virus populations

Efforts to estimate the impact of BGS in nonviral organisms have been well reported. One of the most notable examples is that of Comeron (2014), who estimated levels of BGS in *Drosophila melanogaster* based on the results of Hudson and Kaplan (1995) and Nordborg *et al.* (1996) using a high-definition recombination map, with results indicating strong effects across the genome. For viruses, similar efforts are in their infancy (Box 2), with the first attempt at such estimation in a virus reported recently by Renzette *et al.* (2016), utilizing the theoretical predictions of Innan and Stephan (2003). Interestingly, the full spectrum of recombination frequencies is available in viruses—from non-recombining (for example, most negative-sense RNA viruses), to re-assorting (for example, influenza viruses), to rarely recombining (for example, hepatitis C and West Nile viruses), to frequently recombining (for example, HIV) — offering a highly promising framework for comparative analyses investigating the pervasiveness of BGS effects (Chare *et al.*, 2003; Simon-Loriere and Holmes, 2011). Furthermore, given the high mutation rates and compact genomes of many viruses, evolutionary theory suggests effects at least equal to those seen in *Drosophila*.

In order to accomplish such inference, improved recombination maps for virus genomes will be important. With such maps in hand, and given the amenability of viruses to experimental perturbation, it may indeed be feasible to understand and account for BGS in models of virus evolution.

FUTURE DIRECTIONS

Given that skewed offspring distributions and pervasive linked selection are likely important factors influencing the inference of virus population parameters, it is important to note that multiple backward and forward simulation programs have recently been developed that make the modeling of these processes feasible (Hernandez, 2008; Messer, 2013; Thornton, 2014; Eldon *et al.*, 2015; Zhu *et al.*, 2015). This will allow researchers to directly simulate from parameter ranges relevant for their population of interest, developing a better intuition for the importance of these processes in shaping the observed genomic diversity. More concretely, the ability to now
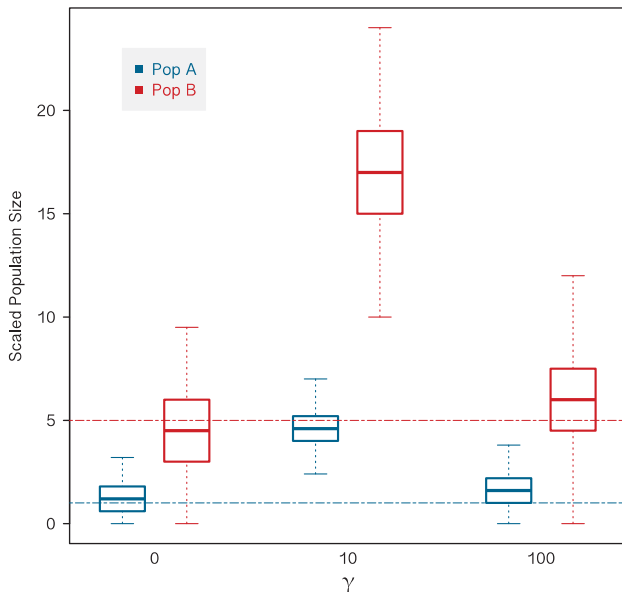
Figure 4 Bias in parameter inference at intermediate levels of BGS. Bias in parameter inference for different levels of BGS, redrawn from Ewing and Jensen (2016). Posterior densities from approximate Bayesian computation (ABC) inference for population size are shown. The strength of purifying selection is given as γ, where $\gamma = 2N_es$. Population A (Pop A) has a true scaled size of 1 (blue line), and population B (Pop B) a true scaled size of 5 (red line). Both population sizes are scaled relative to the size of the ancestral population. As shown, the greatest misinference occurs in the presence of weakly deleterious mutations and subsequent strong BGS effects.

simulate in a computationally efficient framework opens the possibility of directly implementing approximate Bayesian computation inference approaches under these models. Thus, by drawing mutations from a biologically realistic distribution of fitness effects and allowing offspring distributions to appropriately vary, it is now possible to reimplement common demographic estimation or genome scan approaches; these modified approaches would be based on more appropriate null expectations of the shape of the SFS, the extent of linkage disequilibrium, and the degree of population divergence.

DATA ARCHIVING
As a review article, no new data were processed, analyzed, or used directly.

CONFLICT OF INTEREST
The authors declare no conflict of interest.

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