arXiv:q-bio.PE/0609046 v1 26 Sep 2006

September 26, 2006

# A MUTATION-SELECTION MODEL FOR GENERAL GENOTYPES WITH RECOMBINATION

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ABSTRACT. A probability model is presented for the dynamics of mutation-selection balance in a infinite-population infinite-sites setting sufficiently general to cover mutation-driven changes in full age-specific demographic schedules. An earlier work by the same authors presented a haploid model — without genetic recombination — of similar scope. This work complements that model, adding genetic recombination, based on a well-known general discrete-population genetic model of N. Barton and M. Turelli. The model with recombination is a flow on Poisson intensities, substantially different from the haploid model. It is shown that the new model arises from the haploid model when recombination is added, in the limit as generations per unit time go to infinity, and selection strength and mutation per generation go to 0.

## 1. INTRODUCTION

Mathematical models of persistent selection and recurring deleterious mutation are staples of evolutionary theory [1]. Applications to the evolution of senescence pose the extra challenge of associating mutant alleles with demographic structures, typically with age-specific effects on vital rates [2]. Pletcher and Curtsinger [3] point out that early progress has relied on simplifying assumptions — additive effects of mutations on age-specific survival, equal impacts from all mutations, and the existence of mutations with impacts confined to late ages — which are severely limiting and unfounded. This list could also include the assumption of additive selective costs for survival decrements. With costs measured on a logarithmic scale, additive costs correspond to multiplicative effects on fitness. This assumption is both unrealistic and inconsistent with additive impacts on survival.

In a previous paper [4] we proposed a model which allowed for flexible and general non-additive representations of demographic structures, within a common but necessarily stylized framework for the underlying genetic processes, as we shall shortly describe. The model leads to computable solutions for mutation-selection equilibria and the demographic hazard functions which they imply, along with time paths for distributions of numbers of mutant alleles.

Non-additivity in selective costs drives solutions away from the Poisson distributions prevailing under additive assumptions. The model in [4], however, only applies when effects of genetic recombination can be neglected.

In this paper we define and analyze a parallel model emphasizing recombination, in which mutation and selection operate slowly in comparison to the timescale on which recombination shuffles the distributions of alleles. We establish conditions in which a process with discrete generations converges to a continuous time limit with strictly Poisson solutions. Demographic predictions from this "free recombination" limit process can be compared to predictions based on [4] with no recombination. Realistic predictions may plausibly interpolate between them.

We adopt a general picture of the genome and selection similar to that of [5, 6]. We follow the assumption that selection and mutation act more slowly than recombination. Whereas the Quasi-linkage Equilibrium (QLE) approach then goes on to treat the effects of alleles at different loci as nearly independent, we offer a full asymptotic treatment in a standard scaling regime. In our version, as the intensity of selection and mutation per generation goes to zero, the genotype evolution process converges to the complete linkage equilibrium represented by a Poisson point process. Of course, it is not enough simply to show that the distributions at a fixed time converge to a Poisson distribution. We must keep track of the accumulated errors over time, demonstrating the convergence of the entire time evolution of the genotype distribution to a dynamical system of Poisson distributions.

Our models provide a basis for addressing a number of questions in the biodemography of longevity [7]. They allow full analysis of the proposals of Charlesworth [8] for explanations of Gompertz hazards and mortality plateaus through mutation accumulation, along with hyperexponential hazards as discussed by Horiuchi [9], mutation specification effects as discussed by Baudisch [10], and so-called "Walls of Death". A sample of the kinds of insights which may be gleaned from our model for the evolution of senescence is offered in section 4.1.

Broad references to the literature on mutation-selection balance are given in [4]. Here we focus on the incorporation of non-additive demographic effects. Mutation accumulation, as it figures in the study of aging, involves large numbers of small effects and hence a multi-locus perspective. Several algebraic formalisms have been proposed for multilocus selection, including the completely general formalism of [6], which is designed to be able to represent any conceivable regime of selection, mating, linkage, mutation, and phenotypic effects. These systems have not been exploited for studies of aging, in part because so much detail is counterproductive when what concerns us is not the fate of any individual allele but the mass of overlapping phenotypic effects. By making the locus the basic unit of analysis, they generate a computational explosion when applied to vast numbers of loci, many remaining of wild type.

A more serviceable approach is the Kimura-Maruyama rare-allele approximation [11, 1]. K. Dawson [12] has presented a variant amenable to computation, with applications to senescence, but without provision for fully articulated demographic structures.

Our earlier model [4] combines features of the Kimura-Maruyama setup with flexible descriptions of genotypes and phenotypes similar to the algebraic frameworks. We are able to derive formal and computable solutions, both for finite time and in the asymptotic limit. The model is an infinite population model with weak selection in continuous time. Like many models for mutation-selection balance in the literature, however, it is narrowly specified in terms of its representation of the genome. It is, in effect, a haploid model with asexual reproduction and no allowance for genetic recombination.

The model defined and analysed in the present paper augments the model from [4] with provisions for recombination. It is a natural extension that goes as far toward a diploid formulation as demands of tractability appear to allow. In the model, a recombination operator acts on an abstract space of linked loci, at each of which is found either a wild-type or a single mutant allele. The dynamics are predicated on a diploid system of inheritance with random mating within an infinite population, but no detailed two-sex structure at an individual level is involved. Selection operates on haplotypes. Basic assumptions are as follows:

(1) Homozygotes for mutant alleles are negligible;
(2) Selection is slow relative to recombination;
(3) Recombination can ultimately split all parts of the genome.

Assumptions 1 and 2 are essentially the hypotheses that underly the quasi-linkage equilibrium (QLE) approximation [5, 6]. Assumption 2 provides that many cycles of recombination can reshuffle the distribution of alleles before sizable effects from selection restructure the population. We call this setting "free recombination" or "FR". A principal result, Theorem 3.2, is a proof that our continuous-time free-recombination model is the limit of a discrete-time quasi-linkage equilibrium model, like the model in [5], as the strength of selection per generation goes to zero relative to recombination and the length of a generation decreases proportionately. At any point in time, the genotype distribution for the FR process turns out to be Poisson, with an intensity function that satisfies an easy and intuitive dynamic equation. We define the model and establish the existence of solutions to this dynamic equation in Section 2 before establishing the convergence results for our process in Section 3.

The limit theorem requires the additional assumption that the selective cost is bounded. This seems restrictive, but it should be noted that when mutation effects are defined by their influence on mortality schedules, this will automatically be satisfied if mortality increments begin only at some age after the onset of reproduction.

## 2. The model: Existence

2.1. **Definitions.** We consider an infinite population subject to mutation and selection. There is a complete, separable metric space $\mathcal{M}$ of potential

mutations, on which is defined a finite Borel measure $\nu$. We call $\nu$ the "mutation measure", as it describes the rate at which mutants appear. Points in $\mathcal{M}$ might, for example, represent age-specific effects of mutations given by functions of age or sample paths of a stochastic process to be added onto the demographic hazard function, along with coordinates which represent position in the genome with respect to the operation of recombination.

The space of "genotypes" $\mathcal{G}$ is identified with the integer–valued finite Borel measures on $\mathcal{M}$, with a topology to be described shortly. An element of $\mathcal{G}$ has the form $\sum \delta_{m_i}$, where the $m_i \in \mathcal{M}$ are not necessarily distinct and the number of $m_i$ in any bounded subset of $\mathcal{M}$ is finite. The notation $\delta_x$ stands in general for a unit mass at the point $x$ in the space to which $x$ belongs. Each genotype represents a set of mutant alleles that an individual may carry. The "null genotype" has wild-type alleles at every locus and carries none of these mutant alleles.

There is a selective cost $S : \mathcal{G} \to \mathbb{R}^+$, such that $S(0) = 0$, $S(g) \leq S(g+h)$ for all $g, h \in \mathcal{G}$ (that is, adding extra mutant alleles to a genotype increases the selective cost), and a Lipschitz condition (1), which is defined in section 2.2.

The state of the population at time $t$ is denoted $P_t$, which is a Borel probability measure on the space of measures $\mathcal{G}$. For any Borel set $A \subset \mathcal{G}$, $P_t(A)$ is the proportion of the population at time $t$ whose genotype is in the set $A$. In the absence of recombination, a dynamic equation for $P_t$ can be specified and solved using Feynman-Kac methods, as shown in our earlier paper [4]. The solution is an unfamiliar but computable random measure. In contrast, in the presence of sufficiently extensive recombination, completely mixing the mutations in genotypes, we expect $P_t$ to be the distribution of a Poisson random measure for all times $t > 0$. This Poisson characterization is borne out by section 3.

For the sake of continuity, we assume that the initial state $P_0$ is also Poisson. Then $P_t$, a measure on $\mathcal{G}$, being Poisson, is entirely determined by its intensity measure $\rho_t$, which is a finite measure on the simpler metric space $\mathcal{M}$. We adopt the following notation for spaces which include intensity measures:

**Notation 2.1.**
- *$\mathcal{H}$ is the space of finite signed measures on $\mathcal{M}$;*
- *$\mathcal{H}^+$ (the space of intensities for Poisson random genotypes) is the subset of $\mathcal{H}$ consisting of nonnegative measures;*
- *for $\pi \in \mathcal{H}$, write $\pi^+, \pi^- \in \mathcal{H}^+$ for the positive and negative parts of $\mathcal{H}$ appearing in the Hahn-Jordan decomposition. Thus $\pi = \pi^+ - \pi^-$.*

2.2. **The Wasserstein metric.** The basic objects of our analysis are measures, and measures on spaces of measures. In fact, there are three different kinds of measures under consideration:

- Genotypes (elements of $\mathcal{G}$), which are integer-valued measures on the space of potential mutations $\mathcal{M}$;
- Probability distributions on $\mathcal{G}$;

- Poisson intensities, elements of $\mathcal{H}^+$ (as defined in section 2.1).

We have a unified definition of distances and sizes for all these different measures, using the metric of Wasserstein, (also transliterated as Vasershtein, or otherwise).

**Notation 2.2.** *For $\pi$ a measure on some space and $f$ a real-valued function on the same space, we adopt the notation*

$$\pi[f] := \int f d\pi.$$

**Notation 2.3.** *For each space of measures, we start with a metric space $(X, d)$ and let Lip be the space of functions $f : X \to \mathbb{R}$ such that*

$$\|f\|_{\text{Lip}} := \sup_x |f(x)| + \sup_{x \neq y} \frac{|f(x) - f(y)|}{d(x, y)} < \infty,$$

*We define a norm $\|\cdot\|_{\text{Was}}$ on the space of finite signed measures on $(X, d)$ by*

$$\|\pi\|_{\text{Was}} := \sup \{|\pi[f]| : \|f\|_{\text{Lip}} \leq 1\}.$$

This metric metrizes the topology of weak convergence on compacta. An extensive account may be found in [13], while the properties used here are described in Problem 3.11.2 of [14]. The construction allows us to build Wasserstein metrics on top of Wasserstein metrics. We start by taking $\mathcal{M}$ for the metric space $X$. Then $\mathcal{G}$, as a space of measures on $\mathcal{M}$, has a Wasserstein metric. Next we take $\mathcal{G}$ with its Wasserstein metric for the metric space $X$, and obtain a Wasserstein metric on the finite signed measures on $\mathcal{G}$, including the measures $P_t$. With $\mathcal{M}$ for $X$, we also obtain a Wasserstein metric on $\mathcal{H}$.

We note that the designation "Wasserstein metric" is often applied to the analogous definition where the constraining Lipschitz norm $\|\cdot\|_{\text{Lip}}$ does not include the $\|f\|_\infty$ term. It should be noted that this distance, which is always greater than or equal to the Wasserstein metric as we are defining it, metrizes the weak topology. It is equivalent to the Kantorovich-Rubinstein distance, which is a member of the class of Monge-Kantorovich distances, a class defined by a single parameter $p$; the Kantorovich-Rubinstein distance is the element of this class corresponding to $p = 1$. Details may be found in [15, Section 7.1] or [16, Section 7.1].

Having defined the metric on $\mathcal{G}$, we are in a position to define the essential Lipschitz condition on the selective costs:

**Notation 2.4.** *We assume there is a constant $K$ such that*

$$\big|S(g) - S(h)\big| \leq K \big\|g - h\big\|_{\text{Was}} \text{ for all } g, h \in \mathcal{G}. \tag{1}$$

2.3. **The existence theorem.** The change in the genotype distribution $P_t$ over time is entirely determined by the change in its intensity function $\rho_t$ in $\mathcal{H}$. We expect the change to have two components: an increase proportional to $\nu$ resulting from new mutations and a decrease proportional to the average selective cost imposed by each present mutant allele. Since the cost

of a mutant allele depends on its context, the selective change will depend on $\rho_t$, while the mutation change (proportional to $\nu$) is independent of $\rho_t$. Recombination, as we shall see, restores the Poisson character of $P_t$ but does not alter its intensity measure $\rho_t$.

A dynamic equation for $\rho_t$ was proposed in [4] and will be derived in Section 3. In this section, we state the equation and prove that it has a unique solution which therefore determines a well-defined process for the genotype distribution $P_t$.

We first introduce notation for intensities and Poisson variables.

**Notation 2.5.** *Given a distribution $P$ on $\mathcal{G}$, we define $\mu P$ to be the first-moment measure of $P$. That is, for $A$ a Borel subset of $\mathcal{M}$,*

$$\mu P(A) = \int_{\mathcal{G}} g(A) dP(g). \tag{2}$$

*Conversely, if $q \in \mathcal{H}^+$, we define $\Pi_q$ to be the Poisson random measure with intensity $q$. Thus, a Poisson random measure $P$ satisfies $P = \Pi_{\mu P}$. Let $X^\pi$ denote a Poisson random variable with intensity $\pi$.*

The change in $\rho_t$ is expressed in terms of expectation values for the underlying Poisson measures in terms of a function $F$ and operator $D$.

**Definition 2.6.** *Define $F : \mathcal{M} \times \mathcal{H}^+ \to \mathbb{R}^+$ by*

$$F_\pi(x) := \mathbb{E}\big[S(X^\pi + \delta_x) - S(X^\pi)\big] \text{ for } x \in \mathcal{M} \text{ and } \pi \in \mathcal{H}^+. \tag{3}$$

**Definition 2.7.** *Define the operator $D : \mathcal{H}^+ \to \mathcal{H}^+$ by*

$$\frac{d(D\pi)}{d\pi}(x) := F_\pi(x). \tag{4}$$

*That is, for any bounded $f : \mathcal{M} \to \mathbb{R}$,*

$$\int_{\mathcal{M}} f(x) d(D\pi)(x) = \int_{\mathcal{M}} f(x) F_\pi(x) d\pi(x). \tag{5}$$

**Theorem 2.1.** *Fix $\nu \in \mathcal{H}^+$. For any $\rho_0 \in \mathcal{H}^+$ there exists a continuous $\mathcal{H}^+$-valued function $t \mapsto \rho_t$, such that for $t \geq 0$,*

$$\rho_t = \rho_0 + t\nu - \int_0^t D\rho_s ds. \tag{6}$$

*This solution is unique.*

Equation (6) depends on integration of a measure-valued function, which can have a number of different meanings. We require only fairly weak assumptions: If $\mu_s$ is a function taking values in $\mathcal{H}$ and $t \geq 0$, the integral $\mathcal{I}_t = \int_0^t \mu_s ds$ is the element of $\mathcal{H}$ satisfying

$$\mathcal{I}_t(A) = \int_0^t \mu_s(A) ds \text{ for every Borel } A \subset \mathcal{M}. \tag{7}$$

For more information about weak integration on Banach spaces, see chapter 2 of [17].

We denote the resulting flow by $\phi_t$. That is, $\phi_t(\rho) = \rho_t$, where the initial condition is $\rho_0 = \rho$. For mnemonic purposes, it is convenient to write out the formal expression

$$\rho_t = \rho_0 + t\nu - \int_0^t \mathbb{E}\big[S(X^{\rho_s} + \delta_x) - S(X^{\rho_s})\big]\,\rho_s ds. \tag{8}$$

whose precise meaning is given by (6).

2.4. **Proof of Theorem 2.1.** Fix any positive $T$. Let $c > 0$ be a constant that will be chosen later. Let $C([0,T], \mathcal{H})$ be the Banach space of continuous $\mathcal{H}$-valued functions on $[0,T]$, equipped with the norm

$$\|\alpha\|_c = \sup_{0\le t\le T} e^{-ct}\|\alpha_t\|_{\mathrm{Was}}.$$

Write $\Gamma$ for the closed subset of $C([0,T], \mathcal{H})$ consisting of functions $\alpha$ with $\alpha_0 = \rho_0$ and

$$\alpha_t^+(\mathcal{M}) \le \rho_0(\mathcal{M}) + t\nu(\mathcal{M})$$

for $0 \le t \le T$. Define a map $\mathcal{D} : C([0,T], \mathcal{H}) \to C([0,T], \mathcal{H})$ by

$$(\mathcal{D}\alpha)_t = \rho_0 - \int_0^t D\alpha_s^+ ds + t\nu.$$

Note that $\mathcal{D}$ maps $\Gamma$ into itself. Moreover, for $\alpha, \beta \in \Gamma$,

$$\begin{aligned}
\|\mathcal{D}\alpha - \mathcal{D}\beta\|_c &\le \sup_{0\le t\le T} e^{-ct}\int_0^t \big\|D\alpha_s^+ - D\beta_s^+\big\|_{\mathrm{Was}} ds \\
&\le \sup_{0\le t\le T} e^{-ct}\int_0^t K\big(2 + 6\{\alpha_s^+(\mathcal{M}) \wedge \beta_s^+(\mathcal{M})\}\big)\big\|\alpha_s - \beta_s\big\|_{\mathrm{Was}} ds \\
&\qquad \text{by Lemma 2.5 below} \\
&\le \sup_{0\le t\le T} e^{-ct}\int_0^t K\big(2 + 6\{\rho_0(\mathcal{M}) + s\nu(\mathcal{M})\}\big)e^{cs}\big\|\alpha - \beta\big\|_c ds \\
&\le \sup_{0\le t\le T} e^{-ct}\Big[K(2 + 6\rho_0(\mathcal{M}))\frac{e^{ct}-1}{c} + 6K\nu(\mathcal{M})\frac{(ct-1)e^{ct}+1}{c^2}\Big]\|\alpha - \beta\|_c.
\end{aligned}$$

Thus $\mathcal{D} : \Gamma \to \Gamma$ is a contraction, provided $c$ is chosen sufficiently large. It follows from the Contraction Mapping Theorem that the equation

$$\rho_t = \mathcal{D}\rho_t = \rho_0 - \int_0^t D\rho_s^+ ds + t\nu \tag{9}$$

has a unique solution in $\Gamma$. Furthermore, any function in $C([0,T], \mathcal{H})$ which is a solution to (9) must automatically be in $\Gamma$. Therefore, the solution is unique.

This solution is a function taking values in $\mathcal{H}$, and it remains to show that the solution is actually $\mathcal{H}^+$-valued. For any Borel set $A \subset \mathcal{M}$,

$$\rho_t(A) = \rho_0(A) - \int_0^t \int_A F_{\rho_s^+}(x) d\rho_s^+(x) ds + t\nu(A).$$

In particular, $t \mapsto \rho_t(A)$ is continuous. For any Borel set $A \subset \mathcal{M}$ we have

$$\rho_t^+(A) \leq \rho_0(A) + t\nu(A).$$

Since $F_\pi(x) \leq K$ for all $x$,

$$\begin{aligned}\rho_t(A) &\geq \rho_0(A) - K\int_0^t \big(\rho_0(A) + s\nu(A)\big)ds + t\nu(A) \\ &= (1-Kt)\rho_0(A) + t\left(1 - \frac{Kt}{2}\right)\nu(A).\end{aligned}$$

Hence $\rho_t(A) \geq 0$ for $0 \leq t \leq 1/K$. Because this is true for all $A$, we have $\rho_t \in \mathcal{H}^+$ for $0 \leq t \leq 1/K$. Iterating this argument, with time 0 replaced successively by times $1/K, 2/K, \ldots$ gives the result.

### 2.5. **Technical lemmas.**

**Lemma 2.2.** *For each $\pi \in \mathcal{H}^+$ the function $F_\pi$ is in* Lip *and*

$$\sup_{\pi \in \mathcal{H}^+} \|F_\pi(\cdot)\|_{\mathrm{Lip}} \leq 2K.$$

*Proof.* By definition,

$$\begin{aligned}\|F(\cdot,\pi)\|_{\mathrm{Lip}} &= \sup_x |\mathbb{E}[S(X^\pi + \delta_x) - S(X^\pi)]| \\ &\quad + \sup_{x \neq y} |\mathbb{E}[S(X^\pi + \delta_x) - S(X^\pi)] - \mathbb{E}[S(X^\pi + \delta_y) - S(X^\pi)]|/d(x,y) \\ &\leq \sup_x K\|\delta_x\|_{\mathrm{Was}} + \sup_{x \neq y} K\|\delta_x - \delta_y\|_{\mathrm{Was}}/d(x,y) \\ &\leq 2K.\end{aligned}$$

□

**Lemma 2.3.** *For $\pi', \pi'' \in \mathcal{H}^+$ we have*

$$\big\|\Pi_{\pi'} - \Pi_{\pi''}\big\|_{\mathrm{Was}} \leq 4\big\|\pi' - \pi''\big\|_{\mathrm{Was}}. \tag{10}$$

*Proof.* Let $f : \mathcal{G} \to \mathrm{Lip}$ have $\|f\|_{\mathrm{Lip}} \leq 1$. Fix $\pi', \pi'' \in \mathcal{H}^+$. If $\pi' = \pi'' = 0$ there is nothing to prove. Therefore suppose without loss of generality that $\pi' \neq 0$ and $\pi'(\mathcal{M}) \geq \pi''(\mathcal{M})$. Set $\pi^* = (\pi''(\mathcal{M})/\pi'(\mathcal{M}))\pi' \in \mathcal{H}^+$. We have

$$\big|\Pi_{\pi'}[f] - \Pi_{\pi''}[f]\big| \leq \big|\Pi_{\pi'}[f] - \Pi_{\pi^*}[f]\big| + \big|\Pi_{\pi^*}[f] - \Pi_{\pi''}[f]\big|$$

Note that

$$\begin{aligned}\big|\Pi_{\pi'}[f]-\Pi_{\pi^*}[f]\big| &\le 2\mathbb{P}\big\{X_{\pi'}(\mathcal{M})\neq X_{\pi^*}(\mathcal{M})\big\}\\ &\le 2\sum_{k=0}^{\infty}\frac{1}{k!}\left|e^{-\pi'(\mathcal{M})}\pi'(\mathcal{M})^k-e^{-\pi'(\mathcal{M})}\pi''(\mathcal{M})^k\right|\\ &\le 2e^{-\pi'(\mathcal{M})\vee\pi''(\mathcal{M})}\sum_{k=0}^{\infty}\frac{1}{k!}\left|\pi'(\mathcal{M})^k-\pi''(\mathcal{M})^k\right|\\ &\le 2\big|\pi'(\mathcal{M})-\pi''(\mathcal{M})\big|\\ &\le 2\big\|\pi'(\mathcal{M})-\pi''(\mathcal{M})\big\|_{\mathrm{Was}}\end{aligned}$$

Setting $r=\pi^*(\mathcal{M})=\pi''(\mathcal{M})$, we have

$$\begin{aligned}&\big|\Pi_{\pi^*}[f]-\Pi_{\pi''}[f]\big|\\ &\quad\le\sum_{n=0}^{\infty}\frac{e^{-r}}{n!}\left|\int\cdots\int f\left(\sum_{k=1}^{n}\delta_{y_k}\right)\pi^*(dy_1)\ldots\pi^*(dy_n)\right.\\ &\qquad\left.-\int\cdots\int f\left(\sum_{k=1}^{n}\delta_{y_k}\right)\pi''(dy_1)\ldots\pi''(dy_n)\right|\end{aligned}$$

$$\begin{aligned}&\le\sum_{n=0}^{\infty}\frac{e^{-r}}{n!}\sum_{\ell=0}^{n-1}\left|\int\cdots\int f\left(\sum_{k=1}^{n}\delta_{y_k}\right)\pi^*(dy_1)\ldots\pi^*(dy_\ell)\pi''(dy_{\ell+1})\ldots\pi''(dy_n)\right.\\ &\qquad\left.-\int\cdots\int f\left(\sum_{k=1}^{n}\delta_{y_k}\right)\pi^*(dy_1)\ldots\pi^*(dy_{\ell+1})\pi''(dy_{\ell+2})\ldots\pi''(dy_n)\right|\\ &\le\sum_{n=0}^{\infty}\frac{e^{-r}}{n!}r^{n-1}n\sup_g\left|\int f(g+\delta_z)\pi^*(dz)-\int f(g+\delta_z)\pi''(dz)\right|\\ &\le\|\pi^*-\pi''\|_{\mathrm{Was}}\\ &\le\|\pi'-\pi''\|_{\mathrm{Was}}+\big|\pi'(\mathcal{M})-\pi''(\mathcal{M})\big|.\end{aligned}$$

Putting these bounds together yields

$$\big|\Pi_{\pi'}[f]-\Pi_{\pi''}[f]\big|\le 4\|\pi'-\pi''\|_{\mathrm{Was}}.$$

□

**Lemma 2.4.** *For $\pi',\pi''\in\mathcal{H}^+$ we have*

$$\sup_{x\in\mathcal{M}}|F_{\pi'}(x)-F_{\pi''}(x)|\le 8K\|\pi'-\pi''\|_{\mathrm{Was}}.$$

*Proof.* Define $G(X):=(S(X+\delta_x)-S(X))/2K$. Then $\|G\|_{\mathrm{Lip}}\le 1$ and $F_\pi(x)=2K\Pi_\pi[G]$. By definition,

$$|F_{\pi'}(x)-F_{\pi''}(x)|=2K\big|\Pi_{\pi'}[G]-\Pi_{\pi''}[G]\big|\le 2K\big\|\Pi_{\pi'}[G]-\Pi_{\pi''}[G]\big\|_{\mathrm{Was}}$$

This lemma follows then from Lemma 2.3. □

**Lemma 2.5.** *For $\sigma, \tau \in \mathcal{H}$,*

$$\|D\sigma^+ - D\tau^+\|_{\mathrm{Was}} \leq K(2 + 8\{\sigma^+(\mathcal{M}) \wedge \tau^+(\mathcal{M})\}) \, \|\sigma - \tau\|_{\mathrm{Was}}.$$

*Proof.* Suppose without loss of generality that $\sigma^+(\mathcal{M}) \leq \tau^+(\mathcal{M})$. By Lemmas 2.2 and 2.4,

$$\begin{aligned}
&\left| \int f(x) D\sigma^+(dx) - \int f(x) D\tau^+(dx) \right| \\
&\qquad \leq \left| \int F(x, \sigma^+) f(x) \sigma^+(dx) - \int F(x, \tau^+) f(x) \sigma^+(dx) \right| \\
&\qquad\qquad + \left| \int F(x, \tau^+) f(x) \sigma^+(dx) - \int F(x, \tau^+) f(x) \tau^+(dx) \right| \\
&\qquad \leq 8K \|\sigma^+ - \tau^+\|_{\mathrm{Was}} \|f\|_\infty \sigma^+(\mathcal{M}) + 2K \|f\|_{\mathrm{Lip}} \|\sigma^+ - \tau^+\|_{\mathrm{Was}} \\
&\qquad \leq (2K + 8K\sigma^+(\mathcal{M})) \|f\|_{\mathrm{Lip}} \|\sigma - \tau\|_{\mathrm{Was}},
\end{aligned}$$

where we have used the fact that $\|f' f''\|_{\mathrm{Lip}} \leq \|f'\|_{\mathrm{Lip}} \|f''\|_{\mathrm{Lip}}$ for $f', f'' \in \mathrm{Lip}$. □

## 3. Convergence to limit

Our models may be seen as limits of standard mutation-selection-recombination model, such as that of Barton-Turelli-Johnson (once it has been suitably extended), in the standard asymptotic regime of weak selection and mutation, both scaling at the same infinitesimal rate. The outline of this section is as follows:

- Section 3.1 defines the discrete-time model whose convergence is at issue. A plausibility argument is given for the model of [4] to be the limit when there is no recombination.
- Section 3.2 defines recombination, and states our main convergence result, Theorem 3.1.
- Sections 3.3 and 3.4 prove Theorem 3.1. Section 3.3 proves that the discrete-generation Poisson intensity that results from complete Poissonization in every generation does shadow the continuous-time process. Section 3.4 rounds out the proof by linking the completely Poissonized process to the process that is only partially Poissonized by recombination.
- Section 3.5 justifies the initial Poisson distribution that Theorem 3.1 requires, by showing that a general class of alternative starting distributions on $\mathcal{G}$ would be rapidly shuffled into Poisson by successive rounds of recombination.
- Finally, Section 3.6 collects some technical lemmas that are used in the earlier sections.

3.1. **Framework of the asymptotic theory.** Consider first the haploid model without recombination. Our model has similarities to that of [5], except that our genotypes are defined by arbitrary collections of mutations, rather than by the genetic contents of a fixed set of loci. For a population of size $n$ we write the fitness of a genotype $g$ as $e^{-S(g)/n}$. There is a mutation measure $\nu/n$ on the mutation space, such that each new birth gets a random choice $X_{\nu/n}$ from the Poisson random measure with intensity $\nu/n$.

We define mutation and selection operators $\mathfrak{M}_n$ and $\mathfrak{S}_n$, acting on the space of probabilities on $\mathcal{G}$.

**Notation 3.1.** *Let $f : \mathcal{M} \to \mathbb{R}^+$ be bounded, and define $F : \mathcal{G} \to \mathbb{R}$ as $F(g) := e^{-g(f)}$. Then define*

$$\mathfrak{M}_n P[F] = P\left[F \cdot e^{\nu(e^{-f}-1)/n}\right]; \tag{11}$$

$$\mathfrak{S}_n P[F] = \frac{\int e^{-S(g)/n} F(g) dP(g)}{\int e^{-S(g)/n} dP(g)}. \tag{12}$$

*We will generally drop the subscript $n$ from $\mathfrak{M}_n$ and $\mathfrak{S}_n$, except where the dependence on $n$ needs to be emphasized.*

The operator $\mathfrak{M}_n$ describes the transformation in genotype distribution by one round of mutation, while $\mathfrak{S}_n$ describes the transformation by one round of selection. We note that for any distribution $P$ on $\mathcal{G}$ such that $P[S]$ is finite,

$$\lim_{n\to\infty} n\big(\mathfrak{M}_n P[F] - P[F]\big) = \nu\big[e^{-f} - 1\big]P[F],$$

and

$$\lim_{n\to\infty} n\big(\mathfrak{S}_n P[F] - P[F]\big) = P[SF] - P[S]P[F].$$

For some purposes, we will want to maintain the temporal order of mutations. We denote by $\mathcal{G}^*$ the space of finite sequences of genotypes. That is,

$$\mathcal{G}^* := \emptyset \coprod \mathcal{G} \coprod \mathcal{G}^2 \coprod \cdots, \tag{13}$$

where $\coprod$ denotes disjoint union. There is a natural projection $\Sigma$ of $\mathcal{G}^*$ onto $\mathcal{G}$ by summing the components. Probability measures $Q$ on $\mathcal{G}^*$ may be described as sequences of measures $(Q^{(i)})$, where $Q^{(i)}$ is the portion of the probability concentrated on $i$-tuples. (Thus $\sum_{i=0}^{\infty} Q^{(i)}(\mathcal{G}^i) = 1$.) The operator $\mathfrak{M}^*$ is the mutation operator, adding a new mutation onto the existing distribution on $i$-tuples. It will act on distributions on $i$-tuples, turning them into $(i+1)$-tuples by tacking on an extra component, independent of the first $i$ components, which is the distribution of a Poisson random measure with intensity $\nu/n$. Similarly, $\mathfrak{S}^*$ will reweight tuples of mutations according to the selection cost of the total collection of mutations in the tuple.

**Notation 3.2.**

$$(\mathfrak{M}^*Q)^{(i)} \text{ is the distribution of } (X^{\nu/n}, X_{i-1}, \ldots, X_1),$$
$$\text{where } (X_{i-1}, \ldots, X_1) \text{ has distribution } Q^{(i-1)};$$
$$(\mathfrak{S}^*Q)^{(i)}[F] = \frac{\int_{\mathcal{G}^i} \exp\{-S(\Sigma(g))/n\} F(g) dQ^{(i)}(g)}{\int_{\mathcal{G}^*} \exp\{-S(\Sigma(g))/n\} dQ(g)} \text{ for } F : \mathcal{G}^* \to \mathbb{R}.$$

These operators commute with the pullback by $\Sigma$. That is,

$$\Sigma(\mathfrak{M}^*Q) = \mathfrak{M}\Sigma(Q) \text{ and } \Sigma(\mathfrak{S}^*Q) = \mathfrak{S}\Sigma(Q).$$

We will also identify the Wasserstein distance between probability measures on $\mathcal{G}$ and those on $\mathcal{G}^*$ (or between two probabilities on $\mathcal{G}^*$) with the distance between their pullbacks. (Of course, this is only a semimetric.)

If we start with the genotype distribution $P$, then the genotype distribution after one generation of mutation and selection in the standard model is $\mathfrak{M}_n\mathfrak{S}_nP$ (assuming that selection precedes mutation). A trajectory of this process is defined by iteration: Given a starting distribution $P$, the distribution after $m$ generations is $\big(\mathfrak{M}_n\mathfrak{S}_n\big)^m P$.

We rescale time with the mutation and selection, so that $n$ generations in our model pass in 1 unit of time. If the trajectory has a continuously differentiable limit $P_t$, this should satisfy the equation

$$\begin{aligned}\lim_{\epsilon\downarrow 0} \epsilon^{-1}\big(P_{t+\epsilon}[F] - P_t[F]\big) &= \lim_{n\to\infty} n\big(\mathfrak{M}_n\mathfrak{S}_nP[F] - P[F]\big)\\ &= \lim_{n\to\infty} n\big(\mathfrak{S}_nP[F] - P[F]\big) + \lim_{n\to\infty} n\big(\mathfrak{M}_n\mathfrak{S}_nP[F] - \mathfrak{S}_nP[F]\big)\\ &= P[SF] - P[S]P[F] + \nu\big(e^{-f} - 1\big)P[F]\end{aligned}$$

For this special choice of test function, this is precisely the dynamical equation defining the recombination-free process, that we introduced in [4]. In fact, these test functions are enough to consider, since they determine the distribution. Formally, a proof that the discrete-time process converges to this continuous-time process would require that we prove the existence of the continuously differentiable limit, which we assumed above.

3.2. **Defining recombination.** We now introduce recombination. Imitating [5], we define the "segregating set" $R$ in a recombination event as the subset of $\mathcal{M}$ of mutation sites that segregate together. (The complement of $R$ could, of course, equally well be called the segregating set.) Following the Davidson-Kendall recipe [18], we define a $\sigma$-algebra on sets of Borel subsets of $\mathcal{M}$, under which all incidence functions with Borel subsets are measurable. This means that if $\Xi$ is a random Borel set, and $\kappa$ a finite measure, then $\kappa(\Xi)$ is a real-valued random variable. In this context we suppose we are given a probability distribution $\mathfrak{R}$, which defines the random set of mutation sites that segregate together. We may assume, without loss of generality, that $\mathfrak{R}$ is symmetric; that is,

$$\mathcal{R}(A) = \mathcal{R}\big(\{R^c : R \in A\}\big).$$

(Of course, from a biological point of view, the recombination process would more legitimately be defined on loci, as in [5]. Substituting abstract mutations for loci is perhaps a weakness, but also a useful simplification, of our approach.)

**Notation 3.3.** *For any measure $g$ on $\mathcal{M}$, we use the notation $g|_R$, or $g_R$, to represent the restriction of $g$ to the subset $R$. That is,*

$$g\big|_R(A) = g_R(A) = g(A \cap R)$$

*for Borel $A \subset \mathfrak{M}$. For probability measures $Q$ on $\mathcal{G}$, the pullback under this restriction map will be $Q_R$; that is, $Q_R$ is the probability on genotypes concentrated on $R$, defined for $A \subset \mathcal{G}$ by $Q_R(A) = Q\{g : g_R \in A\}$.*

**Notation 3.4.** *Given a distribution $P$ on $\mathcal{G}$, and a function $f : \mathcal{G} \to \mathbb{R}$, set*

$$\mathfrak{R}P[f] = \int\int\int f(g_1 \,\big|_R + g_2 \,\big|_{R^c}) dP(g_1) dP(g_2) d\mathcal{R}(R). \tag{14}$$

*We also define the annealed recombination operator $\mathfrak{R}_{\mathcal{A}}Q$ to act on functions $F : \mathcal{G} \to \mathbb{R}$ by*

$$\mathfrak{R}_{\mathcal{A}}Q[F] = \int \cdots \int F\left(X^{(1)}\big|_{A_1} + \cdots + X^{(K)}\big|_{A_K}\right) dQ(X^{(1)}) \cdots dQ(X^{(K)}).$$

*We define the probability $\mathcal{R}_n$ on partitions of $\mathcal{M}$ to be the distribution of partitions generated by $n$ independent rounds of intersection with $R$ and $R^c$ chosen from $\mathcal{R}$.*

Note that the number of sets in a partition chosen from $\mathcal{R}_n$ is at most $2^n$, but may be smaller, since some of the intersections may be empty. We may also consider $\mathcal{R}_n$ to define a probability on sequences of partitions $\mathcal{A}_1, \ldots, \mathcal{A}_n$, where $\mathcal{A}_{i+1}$ is the refinement of $\mathcal{A}_i$, determined by intersecting with an independent pair $A_{i+1}, A_{i+1}^c$.

Trivially,

$$\mathfrak{R}^k = \int \mathfrak{R}_{\mathcal{A}} d\mathcal{R}_k(\mathcal{A}). \tag{15}$$

Furthermore, if $\mathcal{A}$ and $\mathcal{A}'$ are partitions, then $\mathfrak{R}_{\mathcal{A}}\mathfrak{R}_{\mathcal{A}'} = \mathfrak{R}_{\mathcal{A}\wedge\mathcal{A}'}$, where $\mathcal{A}\wedge\mathcal{A}'$ is the partition comprised of intersections of sets from $\mathcal{A}$ and sets from $\mathcal{A}'$.

The annealed recombination operator acts componentwise on $\mathcal{G}^*$, and $\mathfrak{R}^{*k}$ is defined on $\mathcal{G}^*$ by $\mathfrak{R}^{*k} = \int \mathfrak{R}^*_{\mathcal{A}} d\mathcal{R}(\mathcal{A})$.

**Notation 3.5.** *The complete Poissonization operator $\mathfrak{P}$ acts on probabilities $P$ on $\mathcal{G}$ by $\mathfrak{P}P = \Pi_{\mu P}$. Similarly, $\mathfrak{P}^*$ acts on probabilities concentrated on $k$-tuples in $\mathcal{G}^*$ by acting separately on the components.*

**Definition 3.6.** *Given a recombination measure $\mathfrak{R}$ and a finite measure $\lambda$ on $\mathcal{M}$, we define the pair $(\mathfrak{R}, \lambda)$ to be* shattering *if there is a positive constant $\alpha$ such that for any Borel set $A$,*

$$\lambda(A)^3 \leq \alpha \left[\lambda(A)^2 - 2\int \lambda(A \cap R)^2 d\mathcal{R}(R)\right] \tag{16}$$

**Notation 3.7.** *If $\pi = (M_1, \ldots, M_k)$ is a partition of $\mathcal{M}$, and $\lambda$ a measure on $\mathcal{M}$, we define for each positive $r$,*

$$|\pi|_r^{(\lambda)}(t) = \sum_{i=1}^{k} \lambda(M_i)^r.$$

Note that, by the symmetry of $\mathfrak{R}$ the right-hand side of (16) is always nonnegative, since it may be rewritten as

$$2\alpha \int \lambda(A \cap R)\lambda(A \cap R^c) d\mathfrak{R}(R).$$

For example, consider the following model of chromosomal recombination: Suppose $\mathcal{M} = [0,1]$ and $\lambda$ is Lebesgue measure. The recombination measure $\mathfrak{R}$ is realized by picking a point $r$ uniformly on $[0,1]$, and then with probability $1/2$ selecting $R = [0,r]$ or its complement. Let $A$ be a Borel subset of $[0,1]$, and let $f(r) = \lambda(A \cap [0,r])$. Then

$$\begin{aligned}
\lambda(A)^2 - 2\int \lambda(A \cap R)^2 d\mathfrak{R}(R) &= 2\int_0^1 f(r)\,(\lambda(A) - f(r))\,dr \\
&\geq 2\int_0^{\lambda(A)} u(\lambda(A) - u) du \\
&\qquad \text{because } f \text{ has Lipschitz constant} \leq 1 \\
&\geq \frac{1}{3}\lambda(A)^3,
\end{aligned}$$

so the pair is shattering with constant $\alpha = 3$.

**Notation 3.8.** *Our starting condition $P_0$ is the distribution of a Poisson random measure. Fix any Borel partition $\mathcal{A}$. Suppose $\mathcal{A}$ is generated by sets $(A_1, \ldots, A_\ell)$; that is, $\mathcal{A}$ is the coarsest partition on $\mathcal{M}$ such that each $A_i$ is a union of sets from $\mathcal{A}$.*

*For positive integers $k \leq \ell$, put*

$$\begin{aligned}
Q_k^* &= \left\{ \prod_{i=\ell-k+1}^{\ell} \mathfrak{R}_{A_i}^* \mathfrak{M}_n^* \mathfrak{S}_n^* \right\} P_0, \\
P_k^* &= (\mathfrak{M}_n^*)^k P_0.
\end{aligned} \tag{17}$$

*Note that $P_k^*$ and $Q_k^*$ are probability measures on $\mathcal{G}^*$, both concentrated on $(k+1)$-tuples. These are the pullbacks under $\Sigma$ of*

$$Q_k := (\mathfrak{R}\mathfrak{M}_n\mathfrak{S}_n)^k P_0 \text{ and } P_k := (\mathfrak{M}_n)^k P_0.$$

*We similarly define $Q_\ell'^*$ by applying the full Poissonization:*

$$Q_k'^* = (\mathfrak{P}^*\mathfrak{S}^*\mathfrak{M}^*)^k P_0,$$

*and*

$$Q_k' = (\mathfrak{P}\mathfrak{S}_n\mathfrak{M}_n)^k P_0.$$

Note that $P_k^*$ consists of $k$-tuples of independent Poisson random measures, each with intensity $\nu/n$, with a final independent coordinate with distribution $P_0$. The projection $P_k$ is a Poisson random measure with intensity $\frac{k}{n}\nu + \rho_0$.

If $Q$ is a probability measure on $\mathcal{G}$, and $A$ a Borel subset of $\mathcal{M}$, we may define a regular conditional distribution on $\mathcal{G}_{\mathcal{M}\setminus A}$, the space of genotypes concentrated on $M \setminus A$, determined by $g_A$ on $A$. We write this as $Q[\cdot \,|\, X_A = g_A]$. That is, if $F : \mathcal{G} \to \mathbb{R}$,

$$Q[F \,|\, X_A = g_A] = \int_{\mathcal{G}_{\mathcal{M}\setminus A}} F(X + g_A) dQ_{g_A}^{(A)}(X).$$

**Notation 3.9.** *Fix a partition $\mathcal{A} = (A_1, \ldots, A_K)$ of $\mathcal{M}$ into Borel subsets. Given $Q$ any probability distribution on $\mathcal{G}$, define*

$$\hat{S}_{Q,\mathcal{A}}(g) = \\ - n \sum_{i=1}^{K} \left( \log Q \left[ e^{-S(X)/n} \,\middle|\, X_{A_i} = g_{A_i} \right] - \log Q \left[ e^{-S(X)/n} \right] \right). \tag{18}$$

**Notation 3.10.** *For complete Poissonization, the object corresponding to $\hat{S}$ is*

$$\hat{S}'_Q(g) := g[s_Q] - n \frac{\int X(\mathcal{M}) e^{-S(X)/n} dQ(X)}{\int e^{-S(X)/n} dQ(X)} + n \int X(\mathcal{M}) dQ(X), \tag{19}$$

*where for each $x \in \mathcal{M}$,*

$$s_Q(x) := -n \log \int e^{-S(X)/n} d\mathcal{P}_Q^{(x)}(X) + n \log \int e^{-S(X)/n} dQ(X), \tag{20}$$

*and $\mathcal{P}_Q^{(x)}$ is the Palm distribution. (The Palm distribution $\mathcal{P}_Q^{(x)}$ may be thought of as the distribution of a random measure $X$ with distribution $Q$, conditioned on $X(\{x\}) \geq 1$. A thorough account may be found in* [19] *or* [20].*)*

Note that $\hat{S}_{Q,\mathcal{A}}$ is uniquely defined only up to arbitary modification on $Q$-null sets. For other $g$, we define $\hat{S}_{Q,\mathcal{A}}$ to be 0. We define $\hat{\mathfrak{S}}_{Q,\mathcal{A}}$ to be the selection operator with $\hat{S}_{Q,\mathcal{A}}$ in place of $S$. We show in Lemma 3.9 that $\hat{S}_{Q,\mathcal{A}}$ determines the Radon-Nikodym derivative of $dQ_k^*/dP_k^*$.

We can now state our main result:

**Theorem 3.1.** *Suppose the recombination measure and mutation intensity $(\mathcal{R}, \nu)$ are shattering, the initial measure $P_0$ is Poisson (with intensity $\rho_0$), and the fitness cost $S$ is bounded. (We write $\sigma := \sup_{\mathcal{G}} S$.) Then for any positive $T$,*

$$\lim_{n\to\infty} \sup_{t \leq T} \left\| \Pi_{\rho t} - Q_{\lfloor tn \rfloor} \right\|_{\text{Was}} = 0. \tag{21}$$

This result is proved in sections 3.3 and 3.4.

3.3. **Convergence with complete Poissonization.** We show that the process defined in section 2 is the limit of successive selection and mutation operators, interspersed with bouts of complete Poissonization. This is essentially a shadowing result, but none of the standard shadowing theorems, such as those in [21], can be technically applied to this setting. In any case, the direct proof is not difficult.

**Notation 3.11.** *We define*

$$\pi_m := \mu(Q'_m) = \mu(\mathfrak{P}\mathfrak{M}_n\mathfrak{S}_n)^m P_0.$$

*That is, $\pi_m$ is the intensity of the Poisson measure resulting from $m$ iterations of mutation and selection of intensity $1/n$, with complete Poissonization after every round.*

Note that we assume throughout, for notational convenience, a particular order of operations: In each generation there is first selection, then mutation, then recombination. This order has no special significance, and it is easy to see that the proofs would hold equally well for another order, or if the same total amounts of mutation and selection were split up into multiple bouts within a generation, whether before or after recombination.

**Proposition 3.2.** *There are constants $A, B, C$, depending on $K$, $\nu(\mathcal{M})$, and $\rho_0(\mathcal{M})$, such that for every $T > 0$*

$$\sup_{0\le t\le T} \|\pi_{\lfloor tn\rfloor} - \rho_t\|_{\mathrm{Was}} \le e^{AT}(BT + C)n^{-1}. \tag{22}$$

*Proof.* For any $0 \le s \le t$,

$$\big\|\rho_t - \rho_s\big\|_{\mathrm{Was}} \le \|(t-s)\nu\|_{\mathrm{Was}} + \left\|\int_s^t F_{\rho_u}\rho_u du\right\|_{\mathrm{Was}}.$$

The first term on the right is simply $(t-s)\|\nu\|_{\mathrm{Was}} = (t-s)\nu(\mathcal{M})$. For the second term we use Lemma 2.2 and the triangle inequality, together with the universal bound $\|\rho_u\|_{\mathrm{Was}} \le \|\rho_0\|_{\mathrm{Was}} + u\|\nu\|_{\mathrm{Was}}$, to obtain the bound

$$2K\int_s^t \|\rho_u\|_{\mathrm{Was}}\, du \le 2K(t-s)\big(\rho_0(\mathcal{M}) + t\nu(\mathcal{M})\big).$$

Putting these together,

$$\big\|\rho_t - \rho_s\big\|_{\mathrm{Was}} \le (t-s)\nu(\mathcal{M}) + 2K(t-s)\big(\rho_0(\mathcal{M}) + t\nu(\mathcal{M})\big). \tag{23}$$

Note that

$$\frac{d(\pi_{m+1} - \nu/n)}{d\pi_m}(x) = \frac{\mathbb{E}[e^{-S(X^{\pi_m}+\delta_x)/n}]}{\mathbb{E}[e^{-S(X^{\pi_m})/n}]}, \tag{24}$$

so that

$$\begin{aligned}\left\|\pi_{m+1} - \frac{\nu}{n} - \pi_m\left(1 - \frac{1}{n}F_{\pi_m}(\cdot)\right)\right\|_{\mathrm{Was}} \\ \le n^{-2}\cdot 2e^{2K/n}(\mathbb{E}[S(X^{\pi_m})^2] + K^2)\exp\{\mathbb{E}[S(X^{\pi_m})/n]\}.\end{aligned} \tag{25}$$

Next,

$$\begin{aligned}\left\|\pi_m\left(1-\frac{1}{n}F(\cdot,\pi_m)\right)-\pi_m\left(1-\frac{1}{n}F(\cdot,\rho_{m/n})\right)\right\|_{\text{Was}}&\\ \le \frac{1}{n}\sup_{x\in\mathfrak{M}}\left|F_{\pi_m}(x)-F_{\rho_{m/n}}(x)\right|&\\ \le \frac{8K}{n}\|\pi_m-\rho_{m/n}\|_{\text{Was}}&\end{aligned}\tag{26}$$

by Lemma 2.4 and

$$\left\|\pi_m\left(1-\frac{1}{n}F_{\rho_{m/n}}\right)-\rho_{m/n}\left(1-\frac{1}{n}F_{\rho_{m/n}}\right)\right\|_{\text{Was}}\le\|\pi_m-\rho_{m/n}\|_{\text{Was}}\tag{27}$$

since $F_\rho(x)$ is always nonnegative. Finally,

$$\begin{aligned}&\|\rho_{(m+1)/n}-\frac{\nu}{n}-\rho_{m/n}\left(1-\frac{1}{n}F(\cdot,\rho_{m/n})\right)\|_{\text{Was}}\\ &\quad\le\left\|\int_0^{1/n}F(\cdot,\rho_{m/n})\rho_{m/n}-\int_0^{1/n}F(\cdot,\rho_{s+m/n})\rho_{s+m/n}ds\right\|\\ &\quad\le\int_0^{1/n}\sup_{x\in\mathcal{M}}\left|F_{\rho_{m/n}}(x)-F_{\rho_{s+m/n}}(x)\right|\left\|\rho_{m/n+s}\right\|_{\text{Was}}ds\\ &\qquad+\sup_{x\in\mathcal{M}}F_{\rho_{m/n}}(x)\int_0^{1/n}\left\|\rho_{m/n}-\rho_{s+m/n}\right\|_{\text{Was}}ds\\ &\quad\le\int_0^{1/n}8Ks\left(\frac{m+1}{n}\nu(\mathcal{M})+\rho_0(\mathcal{M})\right)ds\\ &\qquad+K\int_0^{1/n}\left\|s\nu-\int_0^s D\rho_{u+m/n}du\right\|\\ &\quad\le Kn^{-2}\left(4+\frac{1}{2}\right)\frac{m+1}{n}\left(\nu(\mathcal{M})+\rho_0(\mathcal{M})\right)+K\nu(\mathcal{M})n^{-2}.\end{aligned}\tag{28}$$

Putting these together, we see that there are constants $a$ and $b$, such that

$$\|\pi_{m+1}-\rho_{(m+1)/n}\|_{\text{Was}}\le\frac{a}{n}\|\pi_m-\rho_{m/n}\|_{\text{Was}}+\frac{bT+c}{n^2}.$$

Thus,

$$\|\pi_m-\rho_{m/n}\|_{\text{Was}}\le n^{-1}e^{aT}\frac{bT+c}{a}.$$

Combining this with (23), the proposition follows immediately. □

3.4. **Convergence of the partially Poissonized process.** Recalling the notation of Notation 3.8, we split up

$$\begin{aligned}\|Q_k-Q'_k\|_{\text{Was}}&\le\|Q_k-\mathfrak{P}Q_k\|_{\text{Was}}+\|\mathfrak{P}Q_k-Q'_k\|_{\text{Was}}\\ &\le\|Q_k-\mathfrak{P}Q_k\|_{\text{Was}}+4\|\mu Q_k-\mu Q'_k\|_{\text{Was}}\\ &\qquad\text{(by Lemma 2.3).}\end{aligned}\tag{29}$$

Define $a_k = \left\|Q_k - \mathfrak{P}Q_k\right\|_{\mathrm{Was}}$ and $b_k = \left\|\mu Q_k - \mu Q'_k\right\|_{\mathrm{Was}}$ (*cf.* Notations 2.5 and 3.5). Let $f : \mathfrak{M} \to [-1,1]$ and $F(X) := X[f]$. Then

$$Q_{k+1}[F] = \mu Q_{k+1}[f] = \frac{\nu[f]}{n} + \mathfrak{S}_n Q_k[f].$$

Thus,

$$\begin{aligned} b_{k+1} &\le \sup\left\{\left|\mathfrak{S}_n Q_k[f] - \mathfrak{S}_n Q'_k[f]\right| : \|f\|_{\mathrm{Lip}} \le 1\right\} \\ &\le e^{\sigma/n}\left|Q_k\left[fe^{-S/n}\right] - Q'_k\left[fe^{-S/n}\right]\right| \\ &\le e^{\sigma/n}\left(\left|Q_k[f] - Q'_k[f]\right| + \frac{1}{n}\left|Q_k\left[S\cdot f\right] - Q'_k\left[S\cdot f\right]\right| + \frac{2\sigma^2}{n^2}\right) \\ &\le e^{\sigma/n}\left(b_k + \frac{2\sigma}{n}a_k + \frac{2\sigma^2}{n^2}\right). \end{aligned} \tag{30}$$

Now we need to bound $a_k$. By (54) and repeated application of Corollary 3.13,

$$\frac{d\mathfrak{P}Q^*_k}{dP^*_k}(g_0,\dots,g_k) = \exp\left\{-\frac{1}{n}\sum_{i=0}^{k-1}\hat{S}'_{Q_i}(g_0+\cdots+g_i)\right\}.$$

By Lemma 3.14,

$$\begin{aligned} &\left\|Q_k - \mathfrak{P}Q_k\right\|_{\mathrm{Was}} \\ &\quad\le \int d\mathcal{R}_k(\mathcal{A}) \int\left|\exp\left\{-\frac{1}{n}\sum_{i=0}^{k-1}\hat{S}'_{Q^*_i}(g_0+\cdots+g_i)\right\}\right. \\ &\qquad\left. - \exp\left\{-\frac{1}{n}\sum_{i=0}^{k-1}\hat{S}_{Q^*_i,\mathcal{A}_{k-i}}(g_0+\cdots+g_i)\right\}\right| dP^*_k(g_0,\dots,g_k) \end{aligned} \tag{31}$$

By Lemma 3.12 and (31), we can bound $d\mathfrak{P}Q_k/dP_k(g)$ from below by

$$\frac{d\mathfrak{P}Q_k}{dP_k} \ge \exp\left\{-kg(\mathcal{M})\left(2\frac{\sigma}{n} + \frac{\sigma^2}{2n}\right)\right\} \ge \exp\left\{-3kg(\mathcal{M})\frac{\sigma}{n}\right\}.$$

Combining this with Lemma 3.10, we get

$$\begin{aligned} &\left\|Q_k - \mathfrak{P}Q_k\right\|_{\mathrm{Was}} \\ &\quad\le \frac{1}{n}\sum_{i=0}^{k-1}\int d\mathcal{R}_k(\mathcal{A}) \int\left|\hat{S}'_{Q_i}(g) - \hat{S}_{Q^*_i,\mathcal{A}_{k-i}}(g)\right| \exp\left\{\kappa + \frac{3\sigma i}{n}g(\mathcal{M})\right\} dP_i(g), \end{aligned}$$

where

$$\kappa := \kappa_k := (e^{\sigma k/n} - 1)\left(\rho_0 + \frac{k}{n}\nu\right)(\mathcal{M}).$$

From (67) of Lemma 3.15,

$$\begin{aligned}
&\int_{\mathcal{G}}\left|\hat{S}'_{Q_i^*}(g)-\hat{S}_{Q_i^*,\mathcal{A}_{k-i}}(g)\right|\exp\left\{\frac{3\sigma i}{n}g(\mathcal{M})\right\}dP_i(g)\\
&\quad\le\int e^{3\sigma iX(\mathcal{M})/n}dP_i(X)\left(\frac{5\sigma^2}{n}+5\sigma\sum_{A\in\mathcal{A}}Q_i\{X(A)>0\}^2\right)\\
&\quad\quad+\frac{4\sigma^2}{n}\int e^{3\sigma iX(\mathcal{M})/n}X(\mathcal{M})dP_i(X)\\
&\quad\quad+\int_{\mathcal{G}}\int_{\mathcal{M}}e^{\sigma 3ig(\mathcal{M})/n}\Big(4\sigma Q_i\{X:X(A(x))>0\}\\
&\quad\quad\quad\quad+\sigma\mathcal{P}_{Q_i}^{(x)}\{X:X(A(x))\ge 2\}\Big)dg(x)dP_i^*(g).
\end{aligned}\tag{32}$$

We recall here the notation $\mathcal{P}_Q^{(x)}$ for the Palm distribution, defined in Notation 3.10.

Now, for any bounded $f,h:\mathcal{M}\to\mathbb{R}$,

$$\int e^{X[f]}dP_i(X)=\exp\left\{\mu P_i\left[e^f-1\right]\right\},\tag{33}$$

$$\int X[h]e^{X[f]}dP_i(X)=\mu P_i\left[he^f\right]\exp\left\{\mu P_i\left[e^f-1\right]\right\}.\tag{34}$$

Taking $f=3i\sigma/n$, and $h=\mathbf{1}_A$ for some Borel $A\subset\mathcal{M}$, we get

$$\begin{aligned}
\int_{\mathcal{G}}e^{3i\sigma X(\mathcal{M})/n}dP_i(X)&=\exp\left\{\mu P_i(\mathcal{M})\left(e^{3i\sigma/n}-1\right)\right\}\le e^{\kappa_{3k}},\\
\int_{\mathcal{G}}X(A)e^{3i\sigma X(\mathcal{M})/n}dP_i(X)&=\mu P_i(A)\exp\left\{\frac{3i\sigma}{n}+\left(e^{3i\sigma/n}-1\right)\mu P_i(\mathcal{M})\right\}\\
&\le\left(\rho_0+\frac{k}{n}\nu\right)(\mathcal{M})e^{\kappa_{3k}+3i\sigma/n}.
\end{aligned}$$

According to Lemma 3.10,

$$\begin{aligned}
Q_i\{X(A)>0\}&\le\int_{\mathcal{G}}X(A)e^{\frac{i\sigma}{n}X(\mathcal{M})+\kappa}dP_i(X)\\
&\le\mu P_i(A)e^{i\sigma/n+2\kappa}.
\end{aligned}$$

Thus

$$\begin{aligned}
&\int_{\mathcal{G}}\int_{\mathcal{M}} e^{3\sigma i g(\mathcal{M})/n} Q_i\{X : X(A(x)) > 0\} dg(x) dP_i(g) \\
&\qquad = \sum_{A\in\mathcal{A}} \int_{\mathcal{G}}\int_{\mathcal{M}} e^{\sigma 3 i g(\mathcal{M})/n} Q_i\{X : X(A) > 0\} \mathbf{1}_{\{x\in A\}} dg(x) dP_i(g) \\
&\qquad \le e^{2\kappa} \sum_{A\in\mathcal{A}} \mu P_i(A) \int_{\mathcal{G}}\int_{\mathcal{M}} e^{\sigma 4 i g(\mathcal{M})/n} 4\sigma X(A) dg(x) dP_i(g) \\
&\qquad \le e^{3\kappa + 4i\sigma/n} \sum_{A\in\mathcal{A}} \mu P_i(A)^2,
\end{aligned}$$

and, by Corollary 3.11

$$\begin{aligned}
&\int_{\mathcal{G}}\int_{\mathcal{M}} e^{\sigma 3 i g(\mathcal{M})/n} \mathcal{P}_{Q_i}^{(x)}\big\{X : X(A(x)) \ge 2\big\} dg(x) dP_i^*(g) \\
&\qquad \le e^{2\kappa + 4i\sigma/n} \int_{\mathcal{G}}\int_{\mathcal{M}} e^{\sigma 3 i g(\mathcal{M})/n} P_i\big\{X : X(A(x)) \ge 1\big\} dg(x) dP_i(g) \\
&\qquad \le e^{3\kappa + 7i\sigma/n} \sum_{A\in\mathcal{A}} \mu P_i(A)^2.
\end{aligned}$$

Applying this to (32), integrating $\mathcal{A}_{k-i}$ with respect to $\mathcal{R}_k$ (from Notation 3.4), and making use of Corollary 3.5, we arrive at the bound

$$\begin{aligned}
&\big\|Q_k - \mathfrak{P}Q_k\big\|_{\mathrm{Was}} \\
&\quad \le \frac{e^\kappa}{n} \sum_{i=0}^{k-1} \Bigg( \frac{5\sigma^2}{n} e^{\kappa_{3k}} + \frac{4\sigma^2}{n} \left(\rho_0 + \frac{k}{n}\nu\right)(\mathcal{M}) e^{\kappa_{3k} + 3k\sigma/n} \\
&\qquad + \left(5\sigma e^{7\kappa + 6k\sigma/n} + 4\sigma e^{3\kappa + 7k\sigma/n} + \sigma e^{3\kappa + 10k\sigma/n}\right) \\
&\qquad\qquad \times \int \left(\sum_{A\in\mathcal{A}} \mu P_i(A)^2\right) d\mathcal{R}_{k-i}(\mathcal{A}) \Bigg).
\end{aligned} \tag{35}$$

By the assumption that $\mathcal{R}$ is shattering, we have a constant $\alpha^*$ such that

$$\int \left(\sum_{A\in\mathcal{A}} \mu P_i(A)^2\right) d\mathcal{R}_{k-i}(\mathcal{A}) \le \frac{\alpha^*}{k-i+1}.$$

Since the other constants depend only on $k/n$, we may find a constant $C_T$ such that for $k \le Tn$,

$$\big\|Q_k - \mathfrak{P}Q_k\big\|_{\mathrm{Was}} \le C_T \frac{\log n}{n}. \tag{36}$$

Returning to (30), we have for $k \le Tn$,

$$b_{k+1} \le e^{\sigma/n} \left(b_k + 3\sigma C_T \frac{\log n}{n^2}\right).$$

Thus

$$b_k \le 3\sigma C_T \frac{\log n}{n^2} \frac{e^{k\sigma/n}-1}{e^{\sigma/n}-1} \le 3C_T e^{\sigma T} \frac{\log n}{n}.$$

Thus, the result holds with $C_T^* = C_T(1+3e^{\sigma T})$.

3.5. **Initial convergence to Poisson.** Our main result, Theorem 3.1, states that the mutation-selection process, when started in a Poisson distribution, stays close to the Poisson distribution described in section 2, for large $n$. One would like to know, as well, that the recombination process would shuffle a non-Poisson starting measure rapidly into a Poisson state when $n$ is large.

**Definition 3.12.** *A distribution $P$ on $\mathcal{G}$ is* dispersive *if there is a constant $\beta$ such that for any Borel $A \subset \mathcal{M}$,*

$$\int g(A)\mathbf{1}_{\{g(A)\ge 2\}} dP(g) \le \beta \mu P(A)^2.$$

Of course, the distribution of a Poisson random measure is always dispersive.

**Proposition 3.3.** *For all $n$ and $k$, $\mu\mathfrak{R}^k P = \mu P$. If the recombination measure is shattering with respect to $\mu P$, and $P$ is dispersive, then $\mathfrak{R}^k P$ converges to $\mathfrak{P}P$, as $k \to \infty$, with*

$$\|\mathfrak{R}^k P - \mathfrak{P}P\|_{\text{Was}} \le (3\beta+2)\left(\nu(\mathcal{M})^2 \vee 2\alpha\nu(\mathcal{M})\right)(k+1)^{-1}. \tag{37}$$

*Proof.* We note first that

$$\mu\mathfrak{R}^{k+1}P(B) = \int\int_{\mathcal{G}}\int_{\mathcal{G}} (g_1\big|_R + g_2\big|_{R^c})(B)\, d\mu\mathfrak{R}^k P(g_1)\, d\mu\mathfrak{R}^k P(g_2)\, d\mathfrak{R}(R) = \mu_n(B).$$

Let $\mathcal{A} = (A_1, \ldots, A_N)$ be a partition of $\mathcal{M}$. Then $\mathfrak{R}_{\mathcal{A}}P$ defines a random genotype which has independent components on each $A_i$, with distribution $P\big|_{A_i}$. The distance between two probabilities on genotypes is the sum of the distances between the restrictions to a partition of $\mathcal{M}$. Thus

$$\begin{aligned} \left\|\mathfrak{R}^k_{\mathcal{A}}P - \Pi_{\mu P}\right\|_{\text{Was}} &= \sum_{i=1}^N \left\|\mathfrak{R}^k_{\mathcal{A}}P\big|_{A_i} - \Pi_{\mu P}\big|_{A_i}\right\|_{\text{Was}} \\ &\le \sum_{i=1}^N \left\|P\big|_{A_i} - \Pi_{\mu P}\big|_{A_i}\right\|_{\text{Was}}. \end{aligned} \tag{38}$$

Pick any Borel subset $A$ of $\mathcal{X}$. Define $\mu_A$ to be the measure on $A$ defined for Borel subsets $B \subset A$ by

$$\mu_A(B) = \int_{\mathcal{G}} g(B)\mathbf{1}_{\{g(A)=1\}} dP(g).$$

Clearly $\mu_A \leq \mu P$. Also define the subprobability measure $P_A$ on genotypes restricted to $A$ by

$$P_A[f] = \int_{\mathcal{G}} f(g\big|_A)\mathbf{1}_{\{g(A)\leq 1\}} dP(g).$$

Then $\mu_A$ is the first-moment measure of $P_A$. Note also that

$$\mu P(A) = \mu_A(A) + \int_{\mathcal{G}} g(A)\mathbf{1}_{\{g(A)\geq 2\}}. \tag{39}$$

We have

$$\begin{aligned} &d_{\mathrm{Was}}(P\big|_A, \Pi_{\mu P}\big|_A) \\ &\quad \leq d_{\mathrm{Was}}(P\big|_A, P_A) + d_{\mathrm{Was}}(P_A, \Pi_{\mu_A}) + d_{\mathrm{Was}}(\Pi_{\mu_A}), \Pi_{\mu P}\big|_A). \end{aligned} \tag{40}$$

We bound first

$$\big\|P\big|_A - P_A\big\|_{\mathrm{Was}} \leq P\big\{g : g(A) \geq 2\big\} \leq \beta \mu P(A)^2. \tag{41}$$

Next, for any $f : \mathcal{G} \to \mathbb{R}$ with $\|f\|_{\mathrm{Lip}} \leq 1$,

$$\begin{aligned} \big|P_A f - \Pi_{\mu_A} f\big| &\leq \big|P\big\{g : g(A) = 0\big\} - \Pi_{\mu_A}\big\{g : g(A) = 0\big\}\big| \\ &\quad + \big|P_A f \mathbf{1}_{\{g:g(A)=1\}} - \Pi_{\mu_A} f \mathbf{1}_{\{g:g(A)=1\}}\big| + \Pi_{\mu_A}\big\{g : g(A) \geq 2\big\} \\ &\leq \Big|1 - \mu_A(A) + P\big\{g : g(A) \geq 2\big\} - e^{-\mu_A(A)}\Big| \\ &\quad + \Big|\mu_A(f)\left(1 - e^{-\mu_A(A)}\right)\Big| + \frac{\mu_A(A)^2}{2} \\ &\leq P\big\{g : g(A) \geq 2\big\} + \frac{\mu P(A)^2}{2} + \mu P(A)^2 + \frac{\mu P(A)^2}{2}. \end{aligned}$$

Thus,

$$\big\|P_A - \Pi_{\mu_A}\big\|_{\mathrm{Was}} \leq (\beta + 2)\mu P(A)^2. \tag{42}$$

Finally, by Lemma 2.3,

$$d_{\mathrm{Was}}(\Pi_{\mu_A}), \Pi_{\mu P}\big|_A) \leq d_{\mathrm{Was}}(\mu_A, \mu P\big|_A) + \big|\mu_A(A) - \mu P(A)\big| + \frac{1}{2}\big(\mu_A(A)^2 + \mu P(A)^2\big)$$

For any $f : A \to \mathbb{R}$ with $\|f\|_{\mathrm{Lip}} \leq 1$, since $\mu_A$ is the first-moment measure of $P_A$, we have by Campbell's Theorem [19, (6.4.11)],

$$\begin{aligned} \big|\mu_A f - \mu P f\big| &= \left|\int_{\mathcal{G}} g(f) dP_A(g) - \int_{\mathcal{G}} g(f) dP(g)\right| \\ &= \int_{\mathcal{G}} g(f)\mathbf{1}_{\{g(A)\geq 2\}} dP(g). \end{aligned}$$

Thus,

$$\big\|\Pi_{\mu_A} - \Pi_{\mu P}\big|_A\big\|_{\mathrm{Was}} \leq \beta \mu P(A)^2. \tag{43}$$

Putting (41), (42) and (43) into (40), we get

$$\big\|P\big|_A - \Pi_{\mu P}\big|_A\big\|_{\mathrm{Was}} \leq (3\beta + 2)\mu P(A)^2 \tag{44}$$

By (38), then,

$$\left\|\mathfrak{R}^k P - \Pi_{\mu P}\right\|_{\mathrm{Was}} \le (3\beta+2)\mathbb{E}|\pi|_2, \tag{45}$$

where the expectation is taken with respect to partitions $\pi$ chosen from the distribution $\mathfrak{R}^k$. Applying Lemma 3.4 completes the proof of (37). □

Note that Proposition 3.3 is essentially a point-process version of Le Cam's Theorem from [22].

3.6. **Technical lemmas.** The first lemma proves that recombination, as we have defined it, does sufficiently shuffle genotypes to allow them to shadow a Poisson random measure, for large $n$.

**Lemma 3.4.** *Recall Definition 3.6 and Notation 3.7. If $(\mathfrak{R},\lambda)$ is shattering, then for all $k \ge 1$,*

$$\int |\pi|_2^{(\lambda)} d\mathfrak{R}_k(\pi) \le \frac{\alpha^*}{k+1}, \tag{46}$$

*where*

$$\alpha^* = \lambda(\mathcal{M})^2 \vee 2\alpha\lambda(\mathcal{M}). \tag{47}$$

*Proof.* Define a sequence of random partitions $\pi_0, \pi_1, \ldots$ by successively applying $\mathfrak{R}$; that is, $\pi_0$ is the trivial partition, and $\pi_{k+1}$ is formed by intersecting the subsets of $\pi_k$ with $R$ and $R^c$ chosen from the distribution $\mathfrak{R}$. (The novelty is that we have coupled the distributions $\mathfrak{R}_k$ into a process.) Let $X_k = |\pi_k|_2$. Then

$$\int |\pi|_2^{(\lambda)} d\mathfrak{R}_k(\pi) = \mathbb{E}X_k.$$

By symmetry of $\mathfrak{R}$,

$$\begin{aligned}
\mathbb{E}\big[X_{k+1} \,\big|\, \pi_1,\ldots,\pi_k\big] &= \int \left( \sum_{A\in\pi_k} \lambda(A\cap R)^2 + \lambda(A\cap R^c)^2 \right) d\mathfrak{R}(R) \\
&= \sum_{A\in\pi_k} 2\int \lambda(A\cap R)^2 d\mathfrak{R}(R) \\
&\le \sum_{A\in\pi_k} \lambda(A)^2(1-\alpha\lambda(A)) \\
&= |\pi_k|_2^{(\lambda)} - \alpha|\pi_k|_3^{(\lambda)}.
\end{aligned}$$

We note, now, that it must always be the case for any partition $\pi$ of $\mathcal{M}$ that

$$|\pi|_3^{(\lambda)} \ge \big(|\pi|_1^{(\lambda)}\big)^{-1}\big(|\pi|_2^{(\lambda)}\big)^2 = \lambda(\mathcal{M})^{-1}\big(|\pi|_2^{(\lambda)}\big)^2.$$

Thus, setting $c = 2/\alpha\lambda(\mathcal{M})$,

$$\mathbb{E}\big[X_{k+1} \,\big|\, \pi_1,\ldots,\pi_k\big] \le X_k(1-cX_k).$$

Applying Jensen's inequality to the concave function $x(1-cx)$, we see that

$$\mathbb{E}X_{k+1} \le \mathbb{E}\big[X_k(1-cX_k)\big] \le (\mathbb{E}X_k)\big(1-c\mathbb{E}X_k\big). \tag{48}$$

We complete the proof by induction. We have $X_0 = \lambda(\mathcal{M})^2$. Suppose that $\mathbb{E}X_k \leq \alpha^*/(k+1)$. Since $\alpha^* \geq 1/c$,

$$\begin{aligned}\mathbb{E}X_{k+1} &\leq \frac{\alpha^*}{k+1}\left(1 - \frac{c\alpha^*}{k+1}\right) \\ &\leq \frac{\alpha^*}{k+1} \cdot \frac{k}{k+1} \\ &\leq \frac{\alpha^*}{k+2}.\end{aligned}$$

□

The following is a straightforward consequence:

**Corollary 3.5.** *Suppose $\mathfrak{R}$ is shattering for $\mu P_0$ and for $\nu$ with constant $\alpha$. Let $\nu_t = t\nu + \mu P_0$. Then for all $k \geq 1$,*

$$\mathfrak{R}_k|\pi|_2^{(\nu_t)} \leq \frac{\alpha^*}{k+1}, \tag{49}$$

*where*

$$\alpha^* := (2\nu_t(\mathcal{M})^2) \vee (4\alpha\nu_t(\mathcal{M})). \tag{50}$$

**Lemma 3.6.** *Let $X$ be a nonnegative random variable with finite second moment. Then*

$$-\mathbb{E}[X] + \frac{1}{2}\operatorname{Var}(X)e^{\mathbb{E}[X]} \geq \log \mathbb{E}\left[e^{-X}\right] \geq -\mathbb{E}X. \tag{51}$$

*Proof.* The second inequality holds directly from Jensen's inequality, by the convexity of $x \mapsto e^{-x}$.

The function $x \mapsto e^{-x} - \frac{x^2}{2}$ is concave for $x \geq 0$, so that by Jensen's inequality,

$$\mathbb{E}\left[e^{-X} - \frac{X^2}{2}\right] \leq e^{-\mathbb{E}[X]} - \frac{\mathbb{E}[X]^2}{2}.$$

Consequently,

$$\mathbb{E}\left[e^{-X}\right] \leq e^{-\mathbb{E}[X]} + \frac{1}{2}\operatorname{Var}(X) = e^{-\mathbb{E}[X]}\left(1 + \frac{1}{2}\operatorname{Var}(X)e^{\mathbb{E}[X]}\right).$$

Taking logarithms of both sides, and using the bound $\log(1+x) \leq x$ completes the proof. □

**Lemma 3.7.** *For any $Q$ and $\mathcal{A}$, and $g, g' \in \mathcal{G}$,*

$$\hat{S}_{Q,\mathcal{A}}(g) - \hat{S}_{Q,\mathcal{A}}(g') \leq \sigma(g(\mathcal{M}) + g'(\mathcal{M})), \tag{52}$$

*where $\sigma = \sup_{g\in\mathcal{G}} S(g)$ and $\hat{S}$ is defined in Notation 3.9.*

*Proof.* We may write

$$\hat{S}_{Q,\mathcal{A}}(g) = -n \sum_{A\in\mathcal{A}} \left( \log Q \left[ e^{-S(X)/n} \,\middle|\, X_A = g_A \right] - \log Q \left[ e^{-S(X)/n} \,\middle|\, X_A = 0 \right] \right) - n \sum_{A\in\mathcal{A}} \left( \log Q \left[ e^{-S(X)/n} \,\middle|\, X_A = g_A \right] - \log Q \left[ e^{-S(X)/n} \right] \right).$$

If $A$ is any set for which $g_A = 0$, the summand is 0; if $A$ is a set for which $g_A \neq 0$, the summand is bounded in absolute value by $\sigma/n$. Thus, the first term is bounded by $\sigma g(\mathcal{M})$. The second term is independent of $g$, so vanishes from the difference $\hat{S}_{Q,\mathcal{A}}(g) - \hat{S}_{Q,\mathcal{A}}(g')$ in (52). □

**Lemma 3.8.** *For any partition $\mathcal{A}$, following Notations 3.1 and 3.4,*

$$\frac{d\mathfrak{R}_{\mathcal{A}}\mathfrak{S}_n Q}{d\mathfrak{R}_{\mathcal{A}} Q}(g) = e^{-\hat{S}_{Q,\mathcal{A}}/n}. \tag{53}$$

*Proof.* By definition, for any measurable $F : \mathcal{G} \to [0,1]$,

$$\begin{aligned}
\mathfrak{R}_{\mathcal{A}}\mathfrak{S}_n Q F &= \int\cdots\int F\left( X^{(1)}\big|_{A_1} + \cdots + X^{(K)}\big|_{A_K} \right) d\mathfrak{S}_n Q(X^{(1)}) \cdots d\mathfrak{S}_n Q(X^{(K)}) \\
&= Q\left[e^{-S/n}\right]^{-K} \int\cdots\int F\left( \sum_{i=1}^K X^{(i)}\big|_{A_i} \right) \exp\left\{ -\sum_{i=1}^K S(X^{(i)})/n \right\} dQ(X^{(1)}) \cdots dQ(X^{(K)}) \\
&= Q\left[e^{-S/n}\right]^{-K} \int\cdots\int F(g) \left( \prod_{i=1}^K \int_{\mathcal{G}} e^{-S(X)/n} dQ(X \,\big|\, X\big|_{A_i} = g\big|_{A_i}) \right) d\mathfrak{R}_{\mathcal{A}} Q(g) \\
&= \mathfrak{R}_{\mathcal{A}} Q e^{-\hat{S}_{Q,\mathcal{A}}/n} F.
\end{aligned}$$

□

**Lemma 3.9.** *For any integer $k$, and any $g \in \mathcal{G}$,*

$$\frac{dQ_k^*}{dP_k^*}(g_0,\ldots,g_k) = \int \exp\left\{ -\frac{1}{n} \sum_{\ell=0}^{k-1} \hat{S}_{Q_\ell,\mathcal{A}_{\ell-k}}(g_0 + \cdots + g_\ell) \right\} d\mathfrak{R}(A_1)\cdots d\mathfrak{R}(A_k). \tag{54}$$

*Here, the partition $\mathcal{A}_i$ is understood to be generated by the sets $A_1,\ldots,A_i$, so that $\mathcal{A} = \mathcal{A}_k$.*

*Proof.* This follows by inductive application of Lemma 3.8, and the fact that $\mathfrak{R}^*$ commutes with $\mathfrak{M}_n^*$. □

**Lemma 3.10.** *For every $g$*

$$\begin{aligned}
\exp\left\{ -\frac{\sigma k}{n} g(\mathcal{M}) - \left(e^{\sigma k/n} - 1\right) \left( \rho_0(\mathcal{M}) + \frac{k}{n}\nu(\mathcal{M}) \right) \right\} &\leq \frac{dQ_k}{dP_k}(g) \\
&\leq \exp\left\{ \frac{\sigma k}{n} \left( g(\mathcal{M}) + \rho_0(\mathcal{M}) + \frac{k}{n}\nu(\mathcal{M}) \right) \right\}.
\end{aligned} \tag{55}$$

*Proof.* By Lemmas 3.7 and 3.9, for any $g \in \mathcal{G}$,

$$\begin{aligned}\left|\log \frac{dQ_k/dP_k(g)}{dQ_k/dP_k(0)}\right| &\le \frac{k}{n} \sup_{(g_0,\ldots,g_k):g_0+\cdots+g_k=g} \sup_{\mathcal{A}} \sup_{0\le i\le k} \left|\hat{S}_{Q_i,\mathcal{A}}(g_0+\cdots+g_i)\right| \\ &\le \frac{\sigma k g(\mathcal{M})}{n}.\end{aligned}$$

Thus

$$\begin{aligned}\frac{dQ_k}{dP_k}(g) &= \frac{\frac{dQ_k/dP_k(g)}{dQ_k/dP_k(0)}}{\int_{\mathcal{G}} \frac{dQ_k/dP_k(X)}{dQ_k/dP_k(0)} dP_k(X)} \\ &\le \frac{e^{\sigma k g(\mathcal{M})/n}}{\int_{\mathcal{G}} e^{-\sigma k X(\mathcal{M})/n} dP_k(X)} \\ &\le \exp\left\{\sigma \frac{k}{n}(g(\mathcal{M}) + \int_{\mathcal{G}} X(\mathcal{M}) dP_k(X)\right\} \\ &\le \exp\left\{\sigma \frac{k}{n}(g(\mathcal{M}) + \mu P_0(\mathcal{M})) + \sigma \left(\frac{k}{n}\right)^2 \nu(\mathcal{M})\right\}\end{aligned}$$

by Jensen's inequality.

The lower bound is essentially the same, except that Jensen's inequality points in the wrong direction. However, since $P_k$ is a Poisson random measure, we have

$$\int_{\mathcal{G}} e^{\sigma k X(\mathcal{M})/n} dP_k(X) = \exp\left\{\left(e^{\sigma k/n} - 1\right) \mu P_k(\mathcal{M})\right\}.$$

□

**Corollary 3.11.** *For $\nu$-almost every $x \in \mathcal{M}$, any bounded nonnegative test function $F : \mathcal{G} \to \mathbb{R}^+$, and postive integer $k$,*

$$\mathcal{P}^{(x)}_{Q_k}[F] \le e^{4\kappa + 2\sigma k/n} \int F(X + \delta_x) dP_k(X). \tag{56}$$

*Proof.* Following [20, (1.7)], the Palm distribution may be defined for measures $Q$ with finite first-moment measure $\mu Q$ as the Radon-Nikodym derivative

$$\mathcal{P}^{(x)}_Q(A) = \frac{d\mu_A Q}{d\mu Q}(x),$$

where $\mu_A Q$ is the measure on $\mathcal{M}$ defined by

$$\mu_A Q[f] = \int_A X[f] dQ(X).$$

For the particular choice $Q = Q_k$, we can decompose this into

$$\mathcal{P}^{(x)}_{Q_k}(A) = \frac{d\mu_A Q_k}{d\mu_A P_k}(x) \frac{d\mu_A P_k}{d\mu P_k}(x) \frac{d\mu P_k}{d\mu Q_k}(x). \tag{57}$$

If $h : \mathcal{M} \to \mathbb{R}^+$ is a bounded test function, by Lemma 3.10

$$\begin{aligned}\mu Q_k[h] &= \int_{\mathcal{G}} X[h] dQ_k(X) \\ &\geq \int_{\mathcal{G}} X[h] e^{-\frac{\sigma k}{n} X(\mathcal{M}) - \kappa} \\ &= e^{-2\kappa - \sigma k/n} \mu P_k[h].\end{aligned}$$

Thus

$$\frac{d\mu P_k}{d\mu Q_k}(x) \leq e^{2\kappa + \sigma k/n}$$

for $(\nu + \rho_0)$-almost every $x$. The same bound holds for $d\mu_A P_k / d\mu_A Q_k(x)$. Combining these with (57) yields the almost-everywhere bound

$$\mathcal{P}^{(x)}_{Q_k}(A) \leq e^{4\kappa + 2\sigma k/n} \mathcal{P}^{(x)}_{P_k}(A). \tag{58}$$

The result then follows from the characterization of the Palm distribution for Poisson random measures in [19, Example 12.1(b)]. □

**Lemma 3.12.** *Recall Definition 2.6 and Notation 3.10. If $Q$ is Poisson with intensity $\pi$, then*

$$s_Q(x) = -n \log \int \left( e^{-S(X+\delta_x)/n} dQ(X) + n \log \int e^{-S(X)/n} \right) dQ(X), \tag{59}$$

*and*

$$\left| s_Q(x) - F_\pi(x) \right| \leq e^{\sigma/n} \frac{\sigma^2}{n}. \tag{60}$$

*In addition,*

$$\frac{d\mathfrak{P}\mathfrak{S}Q}{dQ}(g) = e^{-\hat{S}'_Q(g)/n} \tag{61}$$

*We may restate* (61) *as*

$$\frac{d\mu(\mathfrak{P}\mathfrak{S}Q)}{d\pi}(x) = e^{-s_Q(x)/n}. \tag{62}$$

*(Recall that $\mu Q$, defined by* (2)*, is the first-moment measure.)*

*Finally,*

$$\frac{dQ'^*_\ell}{d\mathfrak{M}^\ell P_0^*}(g_0, \ldots, g_\ell) = \exp\left\{ -\sum_{i=0}^{\ell-1} \hat{S}'_{Q'^*_i}(g_0 + \cdots + g_i) \right\}. \tag{63}$$

*Proof.* Statement (59) is a direct consequence of the characterization of the Palm distribution for Poisson random measures in [19, Example 12.1(b)]. Applying Lemma 3.6 and the universal bound $S \leq \sigma$ then proves (60).

Consider now a bounded function $f : \mathcal{M} \to \mathbb{R}$, and let $F(g) = g[f]$. Then

$$\begin{aligned}\mathfrak{P}\mathfrak{S}Q[F] &= \mathfrak{S}Q[F] \\ &= \frac{Q[e^{-S/n}F]}{Q[e^{-S/n}]} \\ &= \int \frac{\mathcal{P}_Q^{(x)}[e^{-S/n}]}{Q[e^{-S/n}]} f(x) d\pi(x) \\ &= \int e^{-s_Q(x)/n} f(x) d\pi(x)\end{aligned}$$

by Campbell's Theorem [19, (6.4.11)], proving (62). Thus

$$\frac{d\mathfrak{P}\mathfrak{S}Q}{dQ}(g) = \frac{e^{-g[s_Q/n]}}{\int e^{-g'[s_Q/n]} dQ(g')}.$$

We have

$$\int e^{-g'[s_Q/n]} dQ(g') = \exp\left\{ - \int \left( e^{-s_Q(x)/n} - 1 \right) d\pi(x) \right\}.$$

By another application of Campbell's Theorem,

$$\begin{aligned}\int \left( e^{-s_Q(x)/n} - 1 \right) d\pi(x) &= \left( \int \frac{\mathcal{P}_Q^{(x)}[e^{-S/n}]}{Q[e^{-S/n}]} d\pi(x) \right) e^{-\pi(\mathcal{M})} \\ &= \frac{\int e^{-S(X)/n} X(\mathcal{M}) dQ(X)}{\int e^{-S(X)/n} dQ(X)} e^{-\int X(\mathcal{M}) dQ(X)}.\end{aligned}$$

Putting these equations together proves (61). Iterating this relation proves (63). □

**Corollary 3.13.** *Let $\mathcal{A}$ be any partition of $\mathfrak{M}$, and $Q$ a probability on $\mathcal{G}$ under which the masses of sets of $\mathcal{A}$ are independent. Let $\widetilde{Q}$ be defined to have $d\widetilde{Q}/dQ = \exp\{-\hat{S}_{Q,\mathcal{A}}/n\}$. Then*

$$\frac{d\mathfrak{P}\widetilde{Q}}{d\mathfrak{P}Q} = e^{-\hat{S}'_{\widetilde{Q}}/n}. \tag{64}$$

*Proof.* By assumption, $Q = \mathfrak{R}_{\mathcal{A}} Q$. By Lemma 3.8 we may write

$$\widetilde{Q} = \mathfrak{R}_{\mathcal{A}} \mathfrak{S} Q$$

Thus

$$\frac{d\mathfrak{P}\widetilde{Q}}{d\mathfrak{P}Q} = \frac{d\mathfrak{P}\mathfrak{S}Q}{d\mathfrak{P}Q} = e^{-\hat{S}'_{\widetilde{Q}}/n}$$

by Lemma 3.12. □

**Lemma 3.14.** *Let $P, Q, R$ be equivalent probability measures on a measurable space $\mathcal{X}$. Let $dP/dR = e^{-p}$ and $dQ/dR = e^{-q}$ for $p, q : \mathcal{X} \to \mathbb{R}$. Then*

$$\big\|P - Q\big\|_{\mathrm{Was}} \le \int_{\mathcal{X}} \big|p(x) - q(x)\big| e^{-\min\{p(x), q(x)\}} dR(x). \tag{65}$$

*Proof.* By definition,

$$\begin{aligned}
\big\|P - Q\big\|_{\mathrm{Was}} &= \sup_f \left| \int_{\mathcal{X}} f(x) dP(x) - \int_{\mathcal{X}} f(x) dQ(x) \right| \\
&= \sup_f \left| \int_{\mathcal{X}} f(x) \frac{dP}{dR}(x) dR(x) - \int_{\mathcal{X}} f(x) \frac{dQ}{dR}(x) dR(x) \right| \\
&\le \sup_f \left| \int_{\mathcal{X}} f(x) \frac{dP}{dR}(x) dR(x) - \int_{\mathcal{X}} f(x) \frac{dQ}{dR}(x) dR(x) \right| \\
&\le \int_{\mathcal{X}} \left| e^{-p(x)} - e^{-q(x)} \right| dR(x),
\end{aligned}$$

where the supremum is over test functions $f$ with $\|f\|_{\mathrm{Lip}} \le 1$, and we use the observation

$$\begin{aligned}
e^{-a} - e^{-b} &= \left(1 - e^{-(b-a)}\right) e^{-a} \\
&\le (b - a) e^{-a}
\end{aligned}$$

for $a \le b$. □

**Lemma 3.15.** *For any probability $Q$, partition $\mathcal{A}$, and $g \in \mathcal{G}$, and $n > 5\sigma$,*

$$\begin{aligned}
&\left| \hat{S}_{Q,\mathcal{A}}(g) - \sum_{A \in \mathcal{A}} \big( Q\big[S \,\big|\, X_A = g_A\big] - Q\big[S \,\big|\, X_A = 0\big] \big) + \mathrm{Cov}_Q(S, |\cdot|) \right| \\
&\qquad \le \frac{\sigma^2}{2n} g(\mathcal{M}) + 4\frac{\sigma^2}{n} \int X(\mathcal{M}) dQ(X) \\
&\qquad\qquad + 4\sigma \sum_{A \in \mathcal{A}} Q\big\{X : X(A) > 0\big\}^2
\end{aligned} \tag{66}$$

*where* $\mathrm{Cov}_Q(S, |\cdot|)$ *is shorthand for*

$$\mathrm{Cov}_Q(S, |\cdot|) := \int_{\mathcal{G}} S(X) X(\mathcal{M}) dQ(X) - \left( \int_{\mathcal{G}} X(\mathcal{M}) dQ(X) \right) \left( \int_{\mathcal{G}} S(X) dQ(X) \right).$$

*We also have*

$$
\begin{aligned}
&\left|\hat{S}_{Q,\mathcal{A}}(g) - \hat{S}'_Q(g)\right| \\
&\qquad \le \frac{\sigma^2}{2n}\big(g(\mathcal{M}) + 10\big) + 4\frac{\sigma^2}{n}\int X(\mathcal{M})\,dQ(X) \\
&\qquad\qquad + 5\sigma \sum_{A\in\mathcal{A}} Q\{X : X(A) > 0\}^2 \\
&\qquad\qquad + \frac{4\sigma^2}{n}\cdot\int \#\{A\in\mathcal{A} : X(A) \ge 2\}\,dQ(X) \\
&\qquad\qquad + \int\Big(4\sigma Q\{X : X(A(x)) > 0\} \\
&\qquad\qquad\qquad \sigma\mathcal{P}_Q^{(x)}\{X(A(x)) \ge 2\}\Big)\,dg(x),
\end{aligned}
\tag{67}
$$

*where $A(x)$ is the unique element $A$ of the partition $\mathcal{A}$ containing $x$.*

*Proof.* By the definition (18),

$$
\begin{aligned}
\hat{S}_{Q,\mathcal{A}}(g) = &-n\sum_{A\in\mathcal{A}}\left(\log Q\left[e^{-S(X)/n}\,\middle|\,X_A = g_A\right] - \log Q\left[e^{-S(X)/n}\,\middle|\,X(A) = 0\right]\right) \\
&- n\sum_{A\in\mathcal{A}}\left(\log Q\left[e^{-S(X)/n}\,\middle|\,X(A) = 0\right] - \log Q\left[e^{-S(X)/n}\right]\right).
\end{aligned}
$$

In the first sum, the summand can only be nonzero when $g(A) > 0$. By Lemma 3.6, the first sum is approximately

$$
\sum_{A\in\mathcal{A}\text{ s.t. }g(A)>0}\left(Q\big[S(X)\,\big|\,X_A = g_A\big] - Q\big[S(X)\,\big|\,X(A) = 0\big]\right),
$$

with an error bounded by $g(\mathcal{M})\sigma^2/2n$.

The second sum requires more care, because the sum extends over all (the potentially very large number of) sets of the partition $\mathcal{A}$. Fix one of these sets $A$. Then

$$
\log Q\left[e^{-S(X)/n}\,\middle|\,X(A) = 0\right] - \log Q\left[e^{-S(X)/n}\right] = \log\frac{Q\left[e^{-S(X)/n}\mathbf{1}_{\{X(A)=0\}}\right]}{Q\left[e^{-S(X)/n}\right]Q\{X : X(A) = 0\}}.
$$

We apply the approximation $\log(y) \approx y - 1$, with error bounded by $(y-1)^2/2y$. The first-order term is

$$
\begin{aligned}
\frac{Q\left[e^{-S(X)/n}\mathbf{1}_{\{X(A)=0\}}\right]}{Q\left[e^{-S(X)/n}\right]Q\{X : X(A) = 0\}} - 1 &= \frac{\operatorname{Cov}_Q(e^{-S/n}, \mathbf{1}_{\{X(A)=0\}})}{Q\left[e^{-S(X)/n}\right]Q\{X : X(A) = 0\}} \\
&\approx -\frac{1}{n}\operatorname{Cov}_Q(S, \mathbf{1}_{\{X(A)>0\}}).
\end{aligned}
$$

The difference between the left-hand and right-hand sides is bounded by

$$\begin{aligned}(68)\qquad &\frac{\sigma^2 Q\{X : X(A) > 0\}}{2n^2} \\ &+ \mathrm{Cov}_Q(S, \mathbf{1}_{\{X(A)>0\}}) \left( \frac{1}{Q[e^{-S/n}]Q\{X : X_A = 0\}} - 1 \right) \\ &\qquad \le \frac{\sigma}{n} Q\big\{X(A) > 0\big\} \left( \frac{\sigma}{n} + Q\big\{X(A) > 0\big\} \right).\end{aligned}$$

The main error term $(y-1)^2/y$ is bounded by

$$(69)\quad \frac{1}{2} \left( \frac{\mathrm{Cov}_Q(e^{-S/n}, \mathbf{1}_{\{X(A)=0\}})}{Q[e^{-S/n}]Q\{X(A)=0\}} \right)^2 \le e^{3\sigma/n} \frac{\sigma^2}{2n^2} \left( \frac{Q\{X(A)>0\}^2}{Q\{X(A)=0\}^2} \wedge 1 \right).$$

Putting these bounds together, we see that

$$\begin{aligned}(70)\qquad &\log Q\Big[e^{-S(X)/n} \,\Big|\, X(A) = 0\Big] \\ &\qquad - \log Q\left[e^{-S(X)/n}\right] \approx -\frac{1}{n} \mathrm{Cov}_Q(S, \mathbf{1}_{\{X(A)>0\}}),\end{aligned}$$

with error bounded by

$$\begin{aligned}(71)\qquad &\frac{3}{2}\frac{\sigma^2}{n^2} Q\big\{X : X(A) > 0\big\} + \frac{\sigma}{n} Q\big\{X : X(A) > 0\big\}^2 \\ &\qquad + \frac{20\sigma^2}{n^2} Q\{X(A) > 0\}^2.\end{aligned}$$

Here we have used the fact that

$$\mathbf{1}\Big\{Q\{X(A) > 0\} > \frac{1}{2}\Big\} \le 4Q\{X(A) > 0\}^2.$$

Summing (70) and (71) over $A \in \mathcal{A}$, we see that

$$-n \sum_{A \in \mathcal{A}} \left( \log Q\left[e^{-S(X)/n} \,\Big|\, X(A) = 0\right] - \log Q\left[e^{-S(X)/n}\right] \right) \approx \mathrm{Cov}_Q(S, |\cdot|),$$

with error bounded by

$$(72)\qquad 8\frac{\sigma^2}{n} \int X(\mathcal{M}) dQ(X) + 5\sigma \sum_{A \in \mathcal{A}} Q\big\{X : X(A) > 0\big\}^2$$

We now compare the approximation in (66) to the definition of $\hat{S}'_Q$. Let $\mathcal{E}$ be the left-hand side of (66). Then

$$\begin{aligned}
\left|\hat{S}_{Q,\mathcal{A}}(g) - \hat{S}'_Q(g)\right| \leq \\
\mathcal{E} + \Bigg| g(s_Q) - n\frac{\int X(\mathcal{M}) e^{-S(X)/n} dQ(X)}{\int e^{-S(X)/n} dQ(X)} + n\int X(\mathcal{M}) dQ(X) \\
- \left( \sum_{A\in\mathcal{A}} \left( Q\big[S \,\big|\, X_A = g_A\big] - Q\big[S \,\big|\, X_A = 0\big]\right) + \mathrm{Cov}_Q(S(X), |X|)\right)\Bigg| \\
\leq \mathcal{E} + \sum_{A\in\mathcal{A}: g(A)=1} \left| s_Q(g_A) - \left( Q\big[S \,\big|\, X_A = g_A\big] - Q\big[S \,\big|\, X_A = 0\big]\right)\right| \\
+ \sum_{A\in\mathcal{A}: g(A)>1} \left| \int s_Q(x) dg_A(x) - \left( Q\big[S \,\big|\, X_A = g_A\big] - Q\big[S \,\big|\, X_A = 0\big]\right)\right| \\
+ \left| \mathrm{Cov}_Q(S, |\cdot|) + n\frac{\int X(\mathcal{M}) e^{-S(X)/n} dQ(X)}{\int e^{-S(X)/n} dQ(X)} - n\int X(\mathcal{M}) dQ(X)\right|.
\end{aligned}$$

We bound first

$$\begin{aligned}
\left| n\log \int e^{-S(X)/n} dQ(X) + Q\big[S \,\big|\, X(A) = 0\big]\right| \\
&\leq \left| QS - \frac{QS\mathbf{1}_{\{X(A)=0\}}}{Q\{X(A)=0\}}\right| + \frac{\sigma^2}{2n} \\
&\leq \sigma \frac{Q\{X(A)>0\}}{Q\{X(A)=0\}} + \frac{\sigma^2}{2n} \\
&\leq 2\sigma Q\{X(A)>0\} + \frac{\sigma^2}{2n}
\end{aligned} \tag{73}$$

if $Q\{X : X(A) > 0\} \leq \frac{1}{2}$, and it is bounded by $\sigma$ otherwise. Also,

$$\begin{aligned}
\left| n\log \int e^{-S(X)/n} d\mathcal{P}_Q^{(x)}(X) + Q\big[S \,\big|\, X_A = \delta_x\big]\right| \\
&\leq \sigma \mathcal{P}_Q^{(x)}\{X : X(A) \geq 2\}.
\end{aligned} \tag{74}$$

Integrating against $g$ yields then

$$\begin{aligned}
\int \left| s_Q(x) - \left( Q\big[S \,\big|\, X_A = g_A\big] - Q\big[S \,\big|\, X_A = 0\big]\right)\right| dg(x) \\
\leq \int \Big( 2\sigma Q\{X(A)>0\} + \sigma \mathbf{1}\big\{Q\{X(A)>0\} > \frac{1}{2}\big\} + \frac{\sigma^2}{n} \\
+ \sigma \mathcal{P}_Q^{(x)}\{X(A(x)) \geq 2\}\Big) dg(x).
\end{aligned}$$

A much simpler calculation shows that,

$$\left|\mathrm{Cov}_Q(S,|\cdot|) - n\frac{\int X(\mathcal{M})e^{-S(X)/n}dQ(X)}{\int e^{-S(X)/n}dQ(X)} + n\int X(\mathcal{M})dQ(X)\right| \leq \frac{2\sigma^2}{n}.$$

□

## 4. Some special cases

4.1. **A demographic example.** For a concrete example of our model in action, we describe a demographic application motivated by a proposal of Brian Charlesworth [8]. We identify the mutation space $\mathcal{M}$ with continuous non-negative functions on $[b,\infty)$ vanishing at infinity, a complete separable space under the supremum norm. The constant $b$ is a minimum age of reproduction. Each mutation $m$ represents an additive increment to the age-specific hazard function at adult ages above $b$. By definition, the hazard function at age $x$ is minus the slope of the logarithm of the probability of surviving to age $x$.

In our example, the age-specific profile $m(x)$ for the action of a mutation $m$ is generated by a stochastic process. We take a realization of a Brownian excursion with an infinitesimal variance $\sigma^2$, starting point uniformly chosen in the interval $[b,c]$ for some fixed $c$, and with a maximum height conditioned to equal unity, subsequently rescaled by a small factor $\eta$, here set at 0.01. The construction gives us a translation-invariant family of profiles with a variety of irregular shapes such as one might expect, in the current absence of specific information, for weak deleterious mutations. An example is shown in Figure 1.

The mutation measure $\nu$ is the product measure of the uniform distribution on $[b,c]$ with the law of the conditioned Brownian excursion, rescaled to have a given overall finite mass $\nu(\mathcal{M})$ specifying the total mutation rate per generation.

Each element $g$ of the genotype space $\mathcal{G}$ is some finite sample of the excursion profiles. We sum up the profiles, and, in our example, we add them to a constant exogenous background hazard function $\lambda$ independent of age $x$. The probability of survival $l_x$ to age $x$ for genotype $g$ is given by

$$l_x(g) = \exp\left(-\lambda x - \sum_{m\in g}\int_0^x m(a)da\right)$$

The selective cost $S(g)$ is set equal to the decrement in the Net Reproduction Ratio induced by the mutations in $g$. In simple versions focused on modeling survival, fertility is taken to be independent of genotype and of age above age $b$, and scaled to a level $f$ which produces zero population

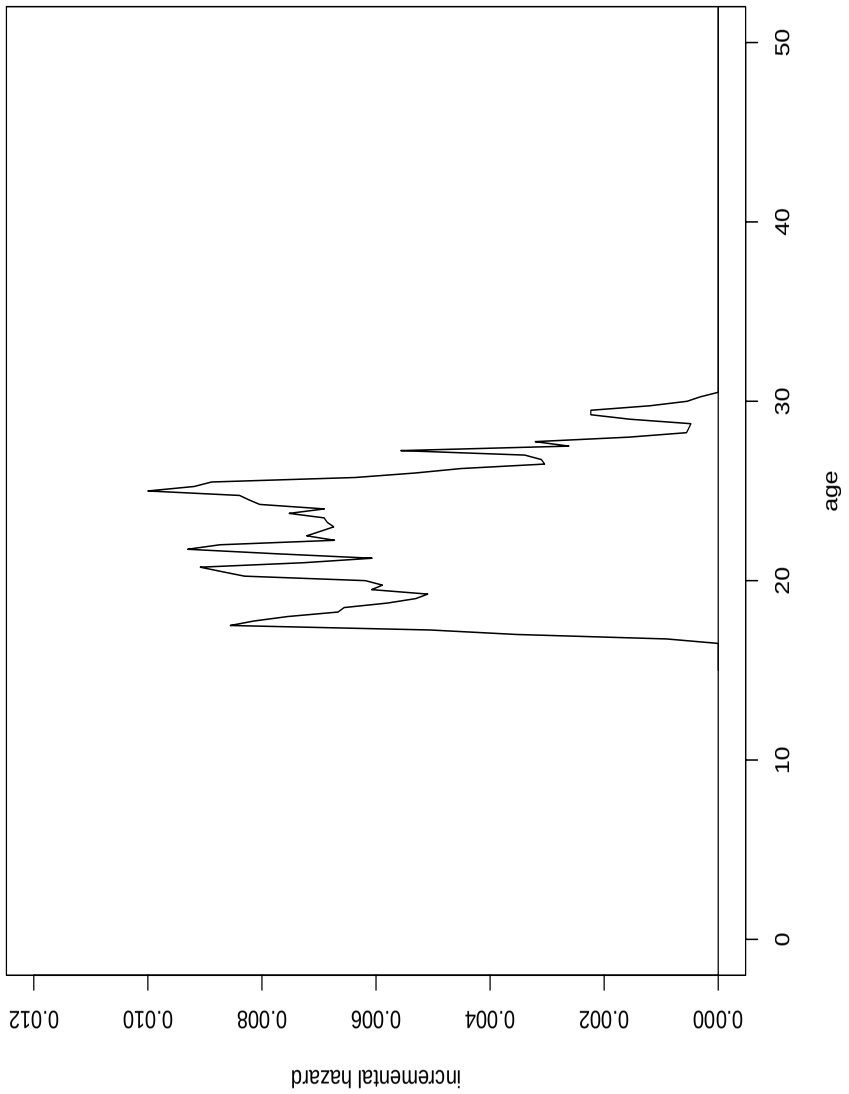


FIGURE 1. An example of a mutation profile generated from a conditioned Brownian excursion process with a randomized starting age. Such a function $m(x)$ would be added onto the age-specific hazard function for genotypes including $m$ in their support.

growth at equilibrium.

$$S(g) = 1 - \int_b^\infty f l_x(g) dx$$

The expected difference in cost from adding $m$ to the genotype, the quantity which drives mutation accumulation according to Equation (6), turns out to depend on $g$ only through the expectation value of $l_x(g)$:

$$\int \left(1 - e^{-m(x)}\right) f\, \mathbb{E}l_x(g)\, dx \tag{75}$$

For the purposes of this example, the choice of recombination measure does not matter, as long as it is shattering for $\nu$. One choice would be to let the random set $R$ for the recombination measure be, with probability one-half, a union of balls in $\mathcal{M}$, and, with probability one-half, the complement of the union. The number of balls could be some fixed number, the centers could be drawn at random according to the measure $\nu$, and the radii could be random unit-exponential variates. Any other measure which reflects ignorance about the distribution of linkage disequilibrium prior to Poissonization would do as well.

The question of demographic interest for models like this one is the extent to which they generate aggregate population hazard rates which are close at equilibrium to the widely observed Gompertzian exponential form. More precisely, one asks whether the increment in predicted hazards over and above the constant background mortality tends to an exponential form after an initial stretch of ages during which mutational effects on adult mortality are commencing.

The idea, due to Charlesworth [8], is that a constant background hazard rate $\lambda$ acting on its own would produce an exponentially decreasing survival curve $\exp(-\lambda x)$. If the effects of mutations were small enough for the expected survival curve to remain close to this background survival curve, then an upward shift in age of onset for a mutation $m$ would align $m(x)$ with exponentially smaller values of $l_x$ in the integral in Equation (75). As the selective cost difference falls, the equilibrium representation of a mutation rises and so does the increment to the hazard function beyond the age of onset. In this way, a translation-invariant law for the distribution of $m$ could tend to imprint an exponential form on hazard function increments.

This argument, however, assumes mutational effects small enough to be neglected, whereas the aim is to model mutational effects large enough to be important. The presence of significant numbers of mutations in a genotype reduces survival probabilities and reduces the marginal impact on net reproduction of each further mutation, bringing to the fore the non-additivity in $S(g)$. How much of an exponential pattern persists in the face of non-additive costs, under the assumption of free recombination? . Theorem 2.1 provides the computational tools for answering this question.

Competing effects are under scrutiny. Non-additivity could be expected to make aggregate hazard rates increase more rapidly than exponentially, leading to so-called "hyperexponential hazards". On the other hand, the heterogeneity implicit in the Poisson distribution of genotypes implies culling, or demographic selection, by age. Individuals whose genotypes carry a heavier

mutational load die at younger ages, leaving genetically robust individuals surviving to older ages and tending to make aggregate hazard rates increase less rapidly than exponentially. Furthermore, the lower cutoff on ages of onset in our model would be expected to produce a "commencement effect" with more rapid increases at young ages as mutational accumulation first comes into play. Our model lets us determine what effect wins out, under what parameter values.

Full analysis must be reserved for another paper, but illustrative results are shown in Figure 2. The figure shows the logarithm of the difference of the predicted aggregate hazard function from the constant background hazard $\lambda$ for three parameter choices. On such a plot, Gompertzian outcomes would correspond to straight lines. The three pairs of curves correspond to three choices for the total mutation rate per generation $\nu(\mathcal{M})$, namely (from left to right) 0.150, 0.100, and 0.010. One curve in each pair shows the aggregate hazard and the other curve the mean hazard for each population. Differences between the aggregate hazard and the mean hazard would reveal effects of culling. In all case the differences turn out to be miniscule, indicating that culling is not driving hazard function shape.

The curves for small and intermediate mutation rates both, however, bend downward not only initially but over much of their range. This effect, which could easily be mistaken for a sign of culling, appears to be a prolonged commencement effect. Only in the curve for the high mutation rate does the figure show pronounced upward bending. Hyperexponential hazards appear as a prelude to ages where the power of mutation accumulation drives hazards toward infinity.

These results are computed by iterating Equation (6) from a starting state with no mutations. Brownian excursions have been simulated via the Williams decomposition from three-dimensional Bessel processes, with $\eta = 0.01$ and $\sigma = 0.10$. The background mortality $\lambda$ is 0.05 per year, the age of maturity $b$ is 15 years, and the maximum i age of onset is $c = 50$ years. The measure $\nu$ is approximated by the empirical measure for a sample of size 100 and Poisson expectations are calculated by summing over samples of sizes of 5000. The example is offered as an illustration of the amenability of the model to applied calculations. Needless to say, full demographic analysis would require extended consideration of details and alternatives not covered here.

4.2. **Quadratic cost functions.** The obvious next simplest case after linear cost functions (for which the solution was completely described in [4]) is a cost function in which epistatic interactions are confined to pairs of genes. This allows us to model basic cases of modifier mutations, and also, if we treat the mutation space as being composed of two separate parental contributions, to model something like genuine diploidy with general dominance relations.

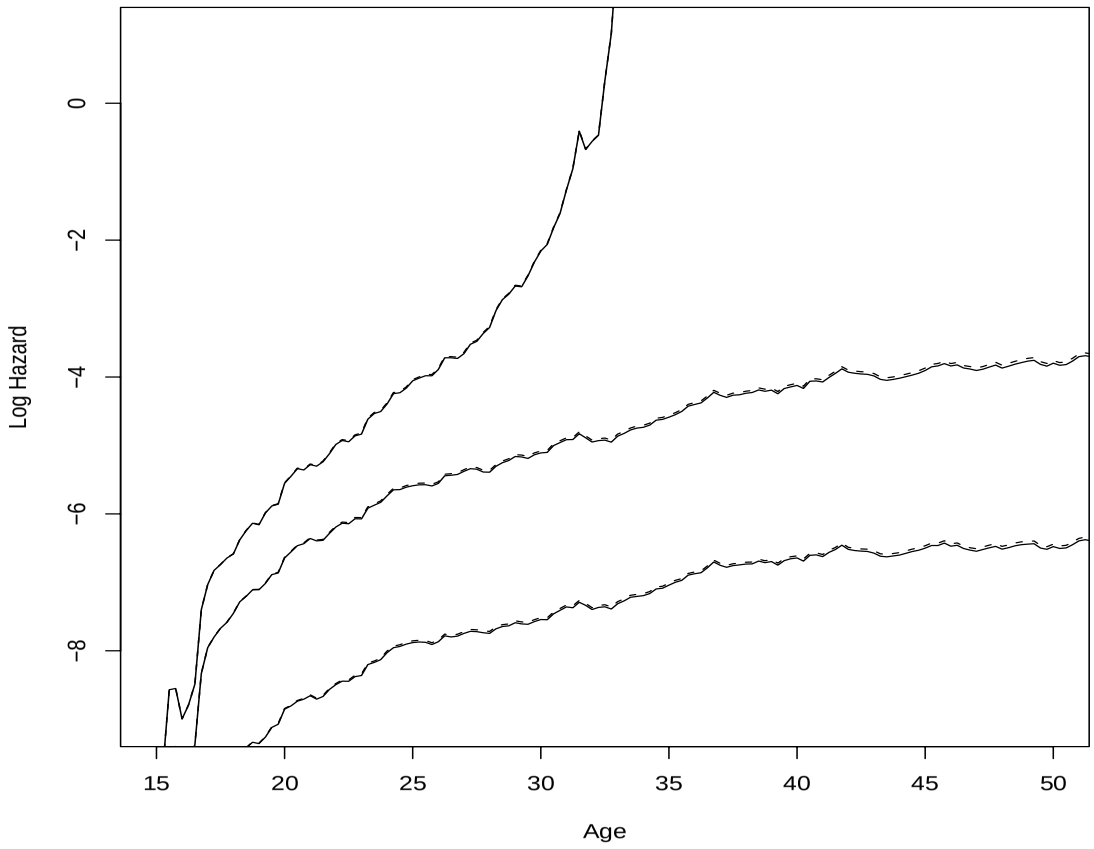


FIGURE 2. The logarithm of the increment to the hazard function due to mutation accumulation as a function of age for three values of the total mutation rate $\nu(\mathcal{M})$.

The basic mathematical representation is

$$S(g) = \int_{\mathcal{M}\times\mathcal{M}} K(m', m'')\, dg^{\otimes 2}(m', m''). \tag{76}$$

for some function $K : \mathcal{M} \times \mathcal{M} \to \mathbb{R}^+$. We may suppose, without loss of generality that the kernel $K$ is symmetric.

Suppose the system defined by (6) has an equilibrium $\bar{\rho}$. Then $\bar{\rho}$ must be absolutely continuous with respect to $\nu$; that is, there is a density $\phi : \mathcal{M} \to \mathbb{R}^+$ such that

$$\bar{\rho}(dm) = \phi(m)\nu(dm).$$

Stating that $\bar{\rho}$ is an equilibrium means that

$$\mathbb{E}\big[S(X^{\bar{\rho}} + \delta_m) - S(X^{\bar{\rho}})\big]\phi(m) = 1. \tag{77}$$

This yields

$$\phi(m) = \frac{1}{K(m,m) + 2\int_{\mathcal{M}} K(m,m')\phi(m')d\nu(m')}. \tag{78}$$

In other words, if we define $\psi : \mathcal{M} \to \mathcal{M}$ by

$$\psi(m) = \int_{\mathcal{M}} K(m,m')\phi(m')d\nu(m'),$$

we have $\phi(m) = 1/(K(m,m) + 2\psi(m))$, where $\psi$ is a fixed point of the map $T : L^1(\nu)^+ \to L^1(\nu)^+$ (the nonnegative functions integrable against $\nu$) defined by

$$T\eta(m) := \int_{\mathcal{M}} \frac{K(m,m')}{K(m,m') + 2\eta(m')} d\nu(m').$$

We have

$$\begin{aligned} \|T(\eta^*) - T(\eta^{**})\|_1 &\leq \int_{\mathcal{M}\times\mathcal{M}} \frac{2K(m',m'')\left|\eta^*(m') - \eta^{**}(m'')\right|}{K(m'',m'')^2} d\nu^{\otimes 2}(m',m'') \\ &\leq \left[2\int_{\mathcal{M}} \operatorname*{ess\,sup}_{m''} \frac{K(m',m'')}{K(m'',m'')^2} d\nu(m'')\right] \left\|\eta^* - \eta^{**}\right\|_1. \end{aligned}$$

By the Contraction Mapping Theorem, we then have

**Proposition 4.1.** *The dynamical equation* (6) *has a unique equilibrium if*

$$\int_{\mathcal{M}} \operatorname*{ess\,sup}_{m''} \frac{K(m',m'')}{K(m'',m'')^2} d\nu(m'') < \frac{1}{2}. \tag{79}$$

4.3. **Multiplicative fitnesses.** Another special case of interest is a fitness cost of the form

$$S(g) = 1 - \exp\left(-\int_{\mathcal{M}} \sigma(m)\, g(dm)\right) \tag{80}$$

or

$$S(g) := \exp\left(\int_{\mathcal{M}} \sigma(m)\, g(dm)\right) - 1, \tag{81}$$

where $\sigma : \mathcal{M} \to \mathbb{R}^+$. The former describes a broad class of subadditive fitness costs, the latter describes superadditive fitness costs.

Substituting into equation (77), we can compute immediately:

**Proposition 4.2.** *(1) If the fitness cost has the form* (80)*, then the dynamical equation* (6) *has an equilibrium if and only if* $\nu(\mathcal{M}) \leq 1/e$*. In this case,*

If we take the equation

$$\frac{d\rho_t(dm)}{dt} = \nu(dm) - \mathbb{E}[S(X^{\rho_t} + \delta_m) - S(X^{\rho_t})]\, \rho_t(dm).$$

and take $\rho_0$ absolutely continuous with respect to $\nu$, then $\rho_t$ will have a density $\phi_t$ again $\nu$ for all $t \geq 0$. These densities will solve the equation

$$\frac{d\phi_t(m)}{dt} = 1 - \mathbb{E}[S(X^{\rho_t} + \delta_m) - S(X^{\rho_t})]\,\phi_t(m).$$

Let us once again take the fitness cost

$$S(g) := 1 - \exp(-\int_{\mathcal{M}} \sigma(m)\, g(dm))$$

Put $b_k(t) := \int \exp(-k\sigma(m))\phi_t(m)\,\nu(dm)$ for $k \in \mathbb{N}$, then

$$\frac{d\phi_t(m)}{dt} = 1 - (1 - \exp(-\sigma(m)))\exp(b_1(t) - b_0(t))\,\phi_t(m). \tag{82}$$

This is an ODE that has solution

$$\phi_t(m) = \exp\left(-\int_0^t (1 - \exp(-\sigma(m)))\exp(b_1(s) - b_0(s))\,ds\right)$$
$$\times \left[\phi_0(m) + \int_0^t \exp\left(-\int_0^s (1 - \exp(-\sigma(m)))\exp(b_1(r) - b_0(r))\,dr\right) ds\right]$$

Of course, we need to compute $b_0$ and $b_1$. To this end, set $a_k := \int \exp(-k\sigma(m))\,\nu(dm)$ for $k \in \mathbb{N}$. Then from (82) we have

$$\frac{db_k(t)}{dt} = a_k + \exp(b_1(t) - b_0(t))(b_{k+1}(t) - b_k(t)). \tag{83}$$

Introduce the generating functions

$$A(z) := \sum_{k=0}^{\infty} a_k \frac{z^k}{k!}$$

and

$$B(z,t) := \sum_{k=0}^{\infty} b_k(t) \frac{z^k}{k!}.$$

The system of ODEs (83) then becomes the linear PDE

$$\frac{\partial B(z,t)}{\partial t} = A(z) + \exp(b_1(t) - b_0(t))\left[\frac{\partial B(z,t)}{\partial z} - B(z,t)\right].$$

We need to find the general solution of this PDE via the method of characteristic curves. Once we get the general solution (which will involve the unknown functions $b_0$ and $b_1$), we have to impose the conditions

$$B(0,t) = b_0(t)$$

and

$$\frac{\partial B(0,t)}{\partial z} = b_1(t)$$

to get the solution we are after.

Using *Mathematica*, the PDE has the solution

$$B(z,t) = \int_0^t \exp\left(-\int_u^t \exp(b_1(s)-b_0(s))\,ds\right) A\left(z+\int_u^t \exp(b_1(s)-b_0(s))\,ds\right) du + \exp\left(-\int_0^t \exp(b_1(s)-b_0(s))\,ds\right) B\left(z+\int_0^t \exp(b_1(s)-b_0(s))\,ds\right)$$

where $B(z) := \sum_{k=0}^{\infty} b_k(0)\frac{z^k}{k!}$.

Therefore, the functions $b_0$ and $b_1$ solve the system of equations

$$b_0(t) = \int_0^t \exp\left(-\int_u^t \exp(b_1(s)-b_0(s))\,ds\right) A\left(\int_u^t \exp(b_1(s)-b_0(s))\,ds\right) du + \exp\left(-\int_0^t \exp(b_1(s)-b_0(s))\,ds\right) B\left(\int_0^t \exp(b_1(s)-b_0(s))\,ds\right)$$

and

$$b_1(t) = \int_0^t \exp\left(-\int_u^t \exp(b_1(s)-b_0(s))\,ds\right) A'\left(\int_u^t \exp(b_1(s)-b_0(s))\,ds\right) du + \exp\left(-\int_0^t \exp(b_1(s)-b_0(s))\,ds\right) B'\left(\int_0^t \exp(b_1(s)-b_0(s))\,ds\right).$$

4.4. **Finite mutation space.** When the mutation space consists of $k$ discrete points, the Poisson intensity follows a $k$-dimensional dynamical system on $(\mathbb{R}^+)^k$. We denote the available mutations by $\{1,\dots,k\}$. A genotype may be expressed as a $k$-tuple of natural numbers, indicating the number of mutations of each type that are present.

We write

$$\widetilde{S}_i(n_1,\dots,n_k) := n_i\big(S(n_1,\dots,n_i,\dots,n_k) - S(n_1,\dots,n_i-1,\dots,\dots,n_k)\big).$$

Then the state $\rho_t = (\rho_t^1,\dots,\rho_t^k)$ satisfies

(84)

$$\begin{aligned}\frac{\rho_t^i}{dt} &= \nu^i - e^{-\rho_t^1-\cdots-\rho_t^k}\rho_t^i \\ &\quad\times \sum_{n_1=0}^{\infty}\cdots\sum_{n_k=0}^{\infty}\frac{(\rho_t^1)^{n_1}}{n_1!}\cdots\frac{(\rho_t^k)^{n_i+1}}{(n_i+1)!}\cdots\frac{(\rho_t^k)^{n_k}}{n_k!}\widetilde{S}_i(n_1,\dots,n_i+1,\dots,n_k) \\ &= \nu_i - \mathbb{E}\widetilde{S}_i(X_\rho)\end{aligned}$$

An easy case is the quadratic fitness costs of section 4.2. In this case $\widetilde{S}_i$ is always increasing, and goes to infinity in all directions.

## Acknowledgements

D.S. was supported by Grant K12-AG00981 from the National Institute on Aging and a Discovery Grant from the National Science and Engineering Research Council, S.N.E. was supported in part by Grant DMS-04-05778 from the National Science Foundation and by the Miller Foundation, and

K.W.W. was supported by Grant P01-008454 from the National Institute on Aging.

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