The peripatric coalescent

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Abstract

We consider a dynamic metapopulation involving one large population of size $N$ surrounded by colonies of size $\varepsilon_N N$, usually called peripheral isolates in ecology, where $N \to \infty$ and $\varepsilon_N \to 0$ in such a way that $\varepsilon_N N \to \infty$. The main population periodically sends propagules to found new colonies (emigration), and each colony eventually merges with the main population (fusion). Our aim is to study the genealogical history of a finite number of lineages sampled at stationarity in such a metapopulation.

We make assumptions on model parameters ensuring that the total outer population has size of the order of $N$ and that each colony has a lifetime of the same order. We prove that under these assumptions, the scaling limit of the genealogical process of a finite sample is a censored coalescent where each lineage can be in one of two states: an inner lineage (belonging to the main population) or an outer lineage (belonging to some peripheral isolate). Lineages change state at constant rate and inner lineages (only) coalesce at constant rate per pair.

This two-state censored coalescent is also shown to converge weakly, as the landscape dynamics accelerate, to a time-changed Kingman coalescent.

Running head. The peripatric coalescent.

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1 Introduction

Many plant and animal populations in nature are highly fragmented, and this fragmentation plays a prominent role in the context of adaptation and speciation. Indeed, the emergence of new species is usually thought to be driven by geographical processes \[5\]. First, \textit{allopatric speciation} occurs
when various subpopulations belonging to the same initial species are separated by a geographical barrier that prevents hybridization between them (gene flow) and allows them to diverge (genetical differentiation) by local adaptation. Second, *parapatric speciation* is a version of allopatric speciation where local adaptation is mediated by the existence of an environmental gradient (resource availability, environmental conditions). Third, when a species is present in one large, panmictic population surrounded by small colonies, usually called peripheral isolates, it is believed that the combination of founder events and of local adaptation to borderline environmental conditions leads to the formation of new species within the isolates. This phenomenon is called *peripatric speciation*. We aim to study the genealogy of populations embedded in such a spatial context. The present study should then serve as a building brick for future work in the field of speciation modeling.

Population dynamic models specifying explicitly the spatial context are called *metapopulation models* (Hanski and Gilpin [8]). Typical such models include: island model, isolation by distance, stepping stone models, extinction-recolonization models. From the point of view of speciation, all these models suffer from the same defect: they assume a given, constant number of subpopulations in the metapopulation, with fixed migration rates between them. As one of the authors of the present paper suggested (Lambert [13]), an alternative method would consist in considering species as “spread out on a randomly evolving number of locations, allowing for repeated fragmentations of colonies, colonizations of new locations, as well as secondary contacts between subpopulations”. This author and others have designed such dynamic landscape models [11, 2, 3], but usually in detailed ecological contexts whose study is only possible through numerical simulations (to the exception of [1]).

Here we propose a mathematical study of a dynamic landscape of the peripatric type. More specifically, we consider a dynamic population subdivision which involves one large main population surrounded by a random number of small peripheral isolates, that we will call colonies for simplicity. The size of the main population is constant equal to $N$, the size of each colony is constant equal to $\varepsilon N$, and the genealogy in each population is given by the Moran model. The number of colonies at time $t$ is denoted by $\xi_N(t)$. The landscape dynamics is as follows (see Figure 1):

- At constant rate $\theta N$, each individual sends independently $\varepsilon N$ offspring to found a new colony;
- Each colony independently merges again with the main population at rate $\gamma N \xi_N^{\alpha-1}$, where $\alpha \geq 1$; at such so-called fusion time, $\varepsilon N$ individuals among the new $(1+\varepsilon N) N$ individuals of the main population are chosen uniformly and simultaneously killed to keep its size constant.

Note that $(\xi_N(t); t \geq 0)$ is a pure-death process with immigration. The parameter $\alpha$ is meant to model the competition for space, since the fusion rate per colony grows with the number of colonies. This density-dependence disappears if $\alpha$ is chosen equal to 1.

The main purpose of this paper is to investigate the genealogy of a finite sample of lineages in the above peripatric metapopulation model. We will show that the history of such a sample, viewed backward in time, can be approximated, as $N \to \infty$ under certain assumptions, by a two-state censored coalescent, where the state of a lineage can be inner (lying in the main population) or outer (lying in a colony). Lineages change state at a constant rate per lineage, but only inner lineages can coalesce, at a constant rate per pair of lineages, as in Kingman coalescent [12].

A two-state censored coalescent can be viewed as a new type of structured coalescent. The structured coalescent (see Takahata [16], Notohara [15] and Herbots [9]) describes the ancestral genealogical process of a sample of lineages in a subdivided population connected by migration. The coalescent on two subpopulations was considered by [16]; for a finite number of subpopulations by [15], and placed in a rigorous framework by [9]. To date, there have been a number of works dealing with the structured coalescent arising in various special types of metapopulations; see
Nordborg and Krone [14], Eldon [6] and the references therein. Our results show that new types of structured coalescents can arise in some specific dynamic metapopulations.

We now give the heuristics giving rise to the result. We assume that $N \to \infty$ and $\varepsilon_N \to 0$ in such a way that $\varepsilon_N N \to \infty$, so that the size of colonies is large but neglectable compared to the main population (Assumption A). It is known that in a Moran model, inner lineages coalesce at constant rate per pair when time is rescaled by $N$ (Kingman coalescent [12]). We make assumptions on the parameters ensuring that all events changing the configuration of ancestral lineages occur on this time scale. This can only be done to the exception of coalescences in colonies, which happen instantaneously in the new time scale, leading to outer lineages which always all lie in different colonies. Also, in order to have a total outer population size of the order of $N$, we need to have a number of colonies of the order of $\varepsilon_N^{-1}$. This can be achieved by the following choice of parameters (Assumption B). The per capita emigration rate $\theta_N$ is taken equal to

$$\theta_N = \frac{\theta}{\varepsilon_N N^2},$$

and the fusion rate $\gamma_N$ is taken equal to

$$\gamma_N = \gamma \varepsilon_N^{\alpha-1} N.$$

Under these assumptions, the number of colonies is asymptotically deterministic, equal to $\varepsilon_N^{-1} (\theta/\gamma)^{1/\alpha}$.

Now the rate at which a single inner lineage changes state is the rate at which a single lineage is taken in a fusion event (backward in time), which happens at rate

$$\frac{\varepsilon_N}{1 + \varepsilon_N} \gamma_N \xi_N^\alpha \approx \frac{\varepsilon_N}{1 + \varepsilon_N} \gamma_N \varepsilon_N^{-\alpha} \frac{\theta}{\gamma},$$

which is equivalent to $\theta/N$ as $N \to \infty$. As a consequence, in the new time scale, inner lineages become outer lineages at constant rate $\theta$.

Also note that the probability that two lineages are taken in the same fusion vanishes, so that no two lineages can lie within the same colony. As a consequence, outer lineages are not allowed to coalesce.

Now the lifetime of a colony is approximately exponential with parameter

$$\gamma_N \xi_N^{\alpha-1} \approx \gamma_N \varepsilon_N^{1-\alpha} \left(\frac{\theta}{\gamma}\right)^{1-1/\alpha},$$

which is equivalent to $(\theta/N) (\gamma/\theta)^{1/\alpha}$. As a consequence, in the new time scale, outer lineages become inner lineages at constant rate $\theta (\gamma/\theta)^{1/\alpha}$. By making these heuristics rigorous we get the results stated in Theorem 3.1. Namely, the genealogical history of a finite sample of lineages, seen as a process backward in time, converges weakly (except at time 0, where instantaneous coalescences within colonies makes the limiting process not right-continuous) to the following two-state censored coalescent. Inner lineages coalesce at constant rate 1 per pair, and lineages change type at constant rate per lineage: inner lineages become outer lineages at rate $\theta$ and outer lineages become inner lineages at rate $\theta (\gamma/\theta)^{1/\alpha}$.

The paper is organized as follows. In Section 2, we give a detailed description of our dynamic metapopulation model in forward and backward time. The main result, Theorem 3.1, is stated in Section 3. In addition, we also prove that under fast landscape dynamics, the censored coalescent converges weakly to a time-changed version of the Kingman coalescent [12]. Finally, a section is dedicated to the formal proofs of the above results.
2 Metapopulation model

2.1 Forward dynamics

Let \( N \in \mathbb{N} \) with \( \mathbb{N} := \{0, 1, 2, \cdots \} \) and let \( \varepsilon_N \) be any positive number such that \( \varepsilon_N N \in \mathbb{N} \). Let \( \theta_N, \gamma_N \) and \( \alpha \) be positive constants. Consider a dynamic metapopulation model involving one large population of size \( N \), called main population, and a random number of small populations, called colonies, of size \( \varepsilon_N N \). The main population periodically sends propagules (or emigrants) that found new colonies and ultimately each colony merges again with the main population. A further assumption is as follows. See Figure 1 for an illustration.

(1) The number of colonies, denoted by \( \{\xi_N(t) : t \geq 0\} \), evolves as a pure death density-dependent process with immigration and the transition rates are given by

\[
\begin{align*}
  j \to j + 1 & \quad \text{at rate } N\theta_N, \\
  j \to j - 1 & \quad \text{at rate } \gamma_N j^{\alpha}.
\end{align*}
\]

(2.1)

When \( \alpha = 1 \), the process \( \{\xi_N(t)\} \) is reduced to a pure death branching process with immigration. It follows from Kelly [10] that \( \{\xi_N(t)\} \) with any initial value has the stationary distribution \( \pi_N \) given by

\[
\pi_N(0) = \left(1 + \sum_{j=1}^{\infty} \frac{(N\theta_N/\gamma_N)^j}{(j!)^\alpha}\right)^{-1} \quad \text{and} \quad \pi_N(k) = \frac{(N\theta_N/\gamma_N)^k}{(k!)^\alpha} \left(1 + \sum_{j=1}^{\infty} \frac{(N\theta_N/\gamma_N)^j}{(j!)^\alpha}\right)^{-1}
\]

(2.2)

for \( k \geq 1 \). We assume that \( \xi_N(0) \) is distributed as \( \pi_N \). Then \( \{\xi_N(t)\} \) is a stationary Markov chain. Let \( (P_t^N)_{t \geq 0} \) be its semigroup. For any finite set \( \{t_1 < t_2 < \cdots < t_n\} \subset \mathbb{R} \) define the probability measure on \( \mathbb{N} \) by

\[
\eta_{t_1, t_2, \cdots, t_n}^N(j_1, j_2, \cdots, j_n) = \pi_N(j_1) P_{t_2-t_1}^N(j_1, j_2) \cdots P_{t_n-t_{n-1}}^N(j_{n-1}, j_n).
\]

(2.3)

Then \( \{\eta_{t_1, t_2, \cdots, t_n}^N : t_1 < t_2 < \cdots < t_n \in \mathbb{R}\} \) is a consistent family. By Kolmogorov’s theorem, there is a stochastic process \( \{\xi_N(t) : t \in \mathbb{R}\} \) with finite-dimensional distributions given by (2.3). Clearly, \( \{\xi_N(t) : t \in \mathbb{R}\} \) is a stationary Markov chain with one-dimensional marginal distribution \( \pi_N \) and transition semigroup \( (P_t^N)_{t \geq 0} \).

(2) At the jump times of \( \xi_N(t) \) from \( j \) to \( j + 1 \), one individual, chosen uniformly at random from the large population, gives birth to \( \varepsilon_N N \) emigrant offspring individuals which found a new colony. We refer to such an event as “emigration” (of new colonies) or “fission”.

(3) At the jump times of \( \xi_N(t) \) from \( j \) to \( j - 1 \), one colony is chosen at random from the \( j \) current colonies and all the \( \varepsilon_N N \) individuals within this colony immediately migrate back into the main population. We refer to such an event as a “fusion” (of colonies with the main population). Instead of keeping all those \( (1 + \varepsilon_N)N \) individuals in the main population alive, only \( N \) of them survive this fusion event, which are chosen uniformly at random among the \( (1 + \varepsilon_N)N \) previously existing individuals.

(4) Between the jump times of \( \xi_N(t) \), the large population and the colonies independently evolve as Moran models, that is, at rate 1 each individual independently gives birth to a single offspring, and simultaneously a uniformly chosen individual is killed.
2.2 Backward dynamics

Now we start with a sample of \( n \) lineages at time 0 and proceed backward in time. Let \( X_N(t) = (X^0_N(t), X^1_N(t), \ldots, X^n_N(t)) \) be the ancestral process of this sample defined for \( t \geq 0 \) by

\[
X^0_N(t) = \text{the number of lineages in the main population at time } -t,
\]
\[
X^i_N(t) = \text{the number of colonies containing } i \text{ lineages at time } -t \ (1 \leq i \leq n).
\]

We set \( X_N(0) = x \), where \( x = (x_0, x_1, \ldots, x_n) \in \mathbb{N}^{n+1} \) with \( x_0 + \sum_{j=1}^n jx_j = n \). The process \( \{X_N(t) : t \geq 0\} \) has state-space

\[
E := \{(x_0, x_1, \ldots, x_n) \in \mathbb{N}^{n+1} : 1 \leq x_0 + \sum_{j=1}^n jx_j \leq n\}.
\]

Define the subspace \( \Pi \) of \( E \) by

\[
\Pi := \{(x_0, x_1, 0, \ldots, 0) \in \mathbb{N}^{n+1} : 1 \leq x_0 + x_1 \leq n\}.
\]

Consider the projection \( \Gamma : (x_0, x_1, 0, \ldots, 0) \mapsto (x_0, x_1) \) from \( \Pi \) to \( \mathbb{N}^2 \).

\[
\Gamma(\Pi) = \{(x_0, x_1) \in \mathbb{N}^2 : 1 \leq x_0 + x_1 \leq n\}.
\]

By the action of the homeomorphism \( \Gamma \), \( \Gamma(\Pi) \) can be regarded as a subspace of \( E \), and we thus still denote it by \( \Pi \) for simplicity. For \( x \in E \), let

\[
\bar{x} := \left(x_0, \sum_{j=1}^n x_j\right).
\]

We will use this notation for the following reason. Because in the new time scale lineages lying in the same colony immediately coalesce, the configuration \( x \) immediately turns into \((x_0, \sum_{j=1}^n x_j, 0, \ldots, 0)\) where all outer lineages are now alone in their respective colonies. Note that \( x \mapsto \bar{x} \) is an injection.
from $E$ to $\Pi$. We also write $e_j = (0, \ldots, 0, 1, 0, \ldots, 0) \in \mathbb{N}^{n+1}$ whose $(j+1)$-th component is 1 for $j = 0, \ldots, n$.

Let $\eta_N(t) = \xi_N(-t)$ for $t \geq 0$. It follows from [10] Lemma 1.5, P.9 that $\{\eta_N(t) : t \geq 0\}$ is still a stationary Markov process with the same transition rates as (2.1). Thus, the fission events (fusions seen backward) happen at rate $\theta_N N$ and, conditioned on $\eta_N(t)$, the fusion events (fissions seen backward) happen at rate $\gamma_N N \eta_N(t)$). At any fission time, every lineage independently exits from the main population with probability $\varepsilon_N/(1 + \varepsilon_N)$. At any fusion time, one colony is chosen at random from the existing colonies and the (say) $i$ lineages in this colony enter the main population, and simultaneously coalesce together (if $i \geq 2$), and coalesce with their ancestor in the main population (if it is also in the sample; but asymptotically, with high probability $i = 1$ and the ancestor is not in the sample). Between fission and fusion times, coalescences within the main population or within colonies may happen. We again refer to Figure 1 for an illustration.

Based on the above description, it is not hard to see that $\{(X_N(t), \eta_N(t)) : t \geq 0\}$ is a time-homogeneous Markov chain taking values in $E \times \mathbb{R}_+$. The corresponding generator is given by

$$\tilde{A}_N g(x, k) = \tilde{\psi}_N g(x, k) + \tilde{\phi}_N g(x, k) + \tilde{\Gamma}_N g(x, k)$$

for any bounded function $g$ on $E \times \mathbb{N}$. Here

$$\tilde{\psi}_N g(x, k) = \sum_{j=2}^{N} x_j \binom{j}{2} \frac{2}{\varepsilon_N N - 1} \left( g(x - e_j + e_{j-1}, k) - g(x, k) \right),$$

which corresponds to coalescences within colonies. Note that $\psi_N g(x, u) \equiv 0$ if $x \in \Pi$. Then

$$\tilde{\phi}_N g(x, k) = \left( \frac{x_0}{2} \right) \frac{2}{N-1} \left( g(x - e_1, k) - g(x, k) \right)$$

$$+ N \theta_N \sum_{r=1}^{x_0} \left( \frac{x_0}{r} \right) \left( \frac{\varepsilon_N}{1 + \varepsilon_N} \right)^r \left( \frac{1}{1 + \varepsilon_N} \right)^{x_0-r} \left( g(x - re_0 + e_r, k+1) - g(x, k) \right)$$

$$+ \gamma_N k^\alpha (x_1/k)(1 - (x_0/N)) \left( g(x - e_1 + e_0, k-1) - g(x, k) \right) 1_{\{k>0\}}$$

$$+ \gamma_N k^\alpha \sum_{j=2}^{N} (x_j/k)(1 - (x_0/N)) \left( g(x - e_j + e_0, k-1) - g(x, k) \right) 1_{\{k>0\}}$$

$$+ \gamma_N k^\alpha \sum_{j=1}^{N} (x_j/k)(x_0/N) \left( g(x - e_j, k-1) - g(x, k) \right) 1_{\{k>0\}}.$$

In $\tilde{\phi}_N$, the first term corresponds to coalescences within the main population, the second term corresponds to exit from the main population, the third term corresponds to entrance into the main population, the last two terms correspond to simultaneous entrance into the main population and coalescence. The fourth term is identically equal to 0 if $x \in \Pi$. Last,

$$\tilde{\Gamma}_N g(x, k) = N \theta_N \left( \frac{1}{1 + \varepsilon_N} \right)^{x_0} \left( g(x, k+1) - g(x, k) \right)$$

$$+ \gamma_N k^\alpha \left(1 - \sum_{j=1}^{N} (x_j/k) \right) \left( g(x, k-1) - g(x, k) \right) 1_{\{k>0\}},$$

which corresponds to the event that the number of colonies increases or decreases but the ancestral process does not change.
3 Convergence to the two-state censored coalescent

3.1 Main results

Let $D([0,\infty),S)$ be the space of all càdlàg functions $x : [0,\infty) \to S$ endowed with the Skorokhod topology for any separable and complete metric space $S$; see Ethier and Kurtz [11, p.116] for details. For $N \in \mathbb{N}$, we consider the sequence of processes $\{\langle X_N(\cdot), \eta_N(\cdot) \rangle\}$. Define

$$Y_N(t) = X_N(Nt) \quad \text{and} \quad \tilde{\eta}_N(t) = \varepsilon_N \eta_N(Nt).$$

Let $\theta > 0$ and $\gamma > 0$ be constants. We further assume the following conditions:

(A) $\varepsilon = \varepsilon_N$ satisfying $\varepsilon_N \to 0$ and $\varepsilon_N N \to \infty$ as $N \to \infty$;

(B) $\theta_N = \theta/(\varepsilon_N N^2)$ and $\gamma_N = \gamma \varepsilon_N^{-1}/N$.

Recall that $y \in E$ and the corresponding $\tilde{y} \in \Pi$. The main result of the paper follows.

Theorem 3.1 Let $x \in E$. Under conditions (A) and (B), the finite-dimensional distributions of the ancestral process $\{Y_N(t), t \geq 0\}$ starting at $y$ converges to those of a $\Pi$-valued continuous time Markov chain $\{Y(t), t \geq 0\}$ starting at $\tilde{y}$, except at time 0. The corresponding infinitesimal generator $Q = (q_{r,r'}) r, r' \in \Pi$ is given by

$$q_{r,r'} = \begin{cases}
-(\theta r_0 + \theta \gamma/\theta)^{1/\alpha} r_1 + r_0 (r_0 - 1), & \text{if } r' = r, \\
\theta r_0, & \text{if } r_0 \neq 0 \text{ and } r' = r + (-1,1), \\
\theta (\gamma/\theta)^{1/\alpha} r_1, & \text{if } r_1 \neq 0 \text{ and } r' = r + (1,-1), \\
r_0 (r_0 - 1), & \text{if } r' = r + (-1,0), \\
0, & \text{otherwise}.
\end{cases} \quad (3.1)$$

where $r = (r_0, r_1) \in \Pi$. Furthermore, if the initial value $y \in \Pi$, weak convergence on $D([0,\infty),\Pi)$ to $\{Y(t)\}$ holds.

The previous statement describes the asymptotic genealogical history of a finite sample of lineages, seen as a process backward in time. Except at time 0, where instantaneous coalescences within colonies makes the limiting process not right-continuous, this process converges weakly to a two-state censored coalescent, where type 0 corresponds to inner lineages (lying in the main population) and type 1 to outer lineages (lying in pairwise distinct colonies). Inner lineages coalesce at constant rate 1 per (ordered) pair, and lineages change type at constant rate per lineage: inner lineages become outer lineages at rate $\theta$ and outer lineages become inner lineages at rate $\theta (\gamma/\theta)^{1/\alpha}$.

Now consider a sequence of censored coalescent processes $\{Y_k(t)\}$ defined by (3.1) with parameters $\theta$ and $\gamma$ replaced by $\theta_k$ and $\gamma_k$, and the initial value $Y_k(0) = y \in \Pi$ with $y_0 + y_1 = n$. Let $Y_k(t) = Y_k^0(t) + Y_k^1(t)$ and let $I_n = \{0,1,2,\ldots,n\}$. We assume that

(C) As $k \to \infty$, $\theta_k \to \infty$, $\gamma_k \to \infty$ and $\theta_k/\gamma_k \to p$ for some constant $p > 0$.

The above condition corresponds to the acceleration of the landscape dynamics (emigration and fusion). The following theorem states that such an acceleration gives rise to a single state coalescent process, where coalescence rates are obtained by averaging over the probability of presence in the main population.
**Theorem 3.2** Under condition (C), the process \( \{Y_k(t), t \geq 0\} \) starting at \( n \) converges weakly to the time-changed \( n \)-Kingman coalescent process \( \{K(t), t \geq 0\} \) on \( D([0, \infty), I_n) \). When \( K = l \), the coalescence rate is given by

\[
c_l = \sum_{j=1}^{l} j(j-1) \left( \frac{l}{j} \right) \left( \frac{p^{1/\alpha}}{1 + p^{1/\alpha}} \right)^{j} \left( \frac{1}{1 + p^{1/\alpha}} \right)^{l-j}.
\]

**Remark 3.3** It is easy to see that if \( p = 0 \) which corresponds to predominant emigrations, \( \{Y_k(t), t \geq 0\} \) converges weakly to the constant process \( \{K(t) \equiv n, t \geq 0\} \); if \( p = \infty \) which corresponds to predominant fusions, \( \{Y_k(t), t \geq 0\} \) converges weakly to the standard Kingman coalescent \( \{K(t), t \geq 0\} \) (i.e., \( c_l = l(l-1) \)).

### 3.2 Proofs

To prove Theorem 3.1, we start by proving the following lemmas.

**Lemma 3.4** Under conditions (A) and (B), as \( N \to \infty \),

\[
\tilde{\pi}_N(\cdot) \xrightarrow{P} (\theta/\gamma)^{1/\alpha}
\]

in \( D([0, \infty), \mathbb{R}_+) \).

**Proof.** Recall that the number \( \xi_N(Nt) \) of colonies of size \( \varepsilon_N N \) is a pure death density-dependent process with immigration with transition rates given by

- \( j \to j + 1 \) at rate \( \theta/\varepsilon_N \),
- \( j \to j - 1 \) at rate \( \gamma_{\varepsilon_N}^{\alpha} j^{-\alpha} \).

By (2.2), it has the stationary distribution \( \pi_N \) given by

\[
\pi_N(0) = \left( 1 + \sum_{j=1}^{\infty} \frac{(\theta/(\gamma_{\varepsilon_N})^{\alpha})^j}{(j!)^\alpha} \right)^{-1} \quad \text{and} \quad \pi_N(k) = \frac{(\theta/(\gamma_{\varepsilon_N})^{\alpha})^k}{(k!)^\alpha} \left( 1 + \sum_{j=1}^{\infty} \frac{(\theta/(\gamma_{\varepsilon_N})^{\alpha})^j}{(j!)^\alpha} \right)^{-1}.
\]

Recall that \( \xi_N(0) \) is distributed as \( \pi_N \). Let \( M_N = [(\theta/\gamma)^{2/\alpha}]/\varepsilon_N \). For \( k > M_N \),

\[
\pi_N(k) = \frac{(\theta/(\gamma_{\varepsilon_N})^{\alpha})^{M_N} (\theta/(\gamma_{\varepsilon_N})^{\alpha})^{k-M_N}}{(M_N! \prod_{j=M_N+1}^{k} j^{\alpha}) \left( 1 + \sum_{j=1}^{M_N} + \sum_{j=M_N+1}^{\infty} \frac{(\theta/(\gamma_{\varepsilon_N})^{\alpha})^j}{(j!)^\alpha} \right)^{-1}} \left( 1 + \sum_{j=M_N+1}^{\infty} \sum_{i=M_N+1}^{\infty} \frac{(\theta/(\gamma_{\varepsilon_N})^{\alpha})^j}{(j!)^\alpha} \right)^{-1}.
\]

Note that if \( j > M_N, j^{\alpha} > \theta/(\gamma_{\varepsilon_N})^{\alpha} \) and if \( j > 3M_N, \frac{\theta/(\gamma_{\varepsilon_N})^{\alpha}}{j^{\alpha}} \leq \frac{\theta/(\gamma_{\varepsilon_N})^{\alpha}}{(3M_N)^{\alpha}} < \frac{1}{2^a} \) for sufficiently large \( N \). Then \( \prod_{j=M_N+1}^{4M_N} \frac{\theta/(\gamma_{\varepsilon_N})^{\alpha}}{j^{\alpha}} \leq 2^{-aM_N} \) and

\[
\sum_{k=4M_N+1}^{\infty} \prod_{j=M_N+1}^{k} \frac{\theta/(\gamma_{\varepsilon_N})^{\alpha}}{j^{\alpha}} \leq \prod_{j=M_N+1}^{4M_N} \frac{\theta/(\gamma_{\varepsilon_N})^{\alpha}}{j^{\alpha}} \sum_{k=1}^{\infty} 2^{-ak} \leq O(2^{-aM_N}).
\]


If follows that \( \pi_N([4M_N, \infty)) \leq O(2^{-\alpha M_N}) \). Thus the sequence \( \{\varepsilon_N \xi_N(0)\} \) is tight. On the other hand, \( \{i\varepsilon_N : i \in \mathbb{N}\} \) and its generator is given by
\[
L_N f(z) = \gamma \varepsilon_N^{-1}(z/\varepsilon_N) \alpha(f(z - \varepsilon_N) - f(z)) + (\theta/\varepsilon_N)(f(z + \varepsilon_N) - f(z)),
\]
for any continuous bounded function \( f \) on \( \mathbb{R}_+ \). Let \( C^2_c(\mathbb{R}_+) \) be the set of twice differentiable functions with compact support on \( \mathbb{R}_+ \). It is not hard to see that as \( N \to \infty \), for \( f \in C^2_c(\mathbb{R}_+) \),
\[
\|L_N f - Lf\| \to 0 \quad \text{and} \quad Lf(z) = (\theta - \gamma z^\alpha)f'(z),
\]
where \( \|f\| = \sup_{x \in \mathbb{R}_+} |f(x)| \). The Markov process \( \xi \) with generator \( L \) is actually deterministic and satisfies the ODE:
\[
\xi'(t) = \theta - \gamma \xi^\alpha(t),
\]
which has the unique equilibrium point \((\theta/\gamma)^{1/\alpha}\). It follows from [8,2], [7] Theorem 6.1, P.28] and [7, Theorem 9.10, P.241] that \( \varepsilon_N \xi_N(0) \xrightarrow{w} (\theta/\gamma)^{1/\alpha} \) as \( N \to \infty \). Again by [8,2], [7, Corollary 8.7, p.231] shows that \( \{\xi_N(t) : t \geq 0\} \) converges weakly to the constant function \( \{\xi(t) \equiv (\theta/\gamma)^{1/\alpha}, t \geq 0\} \) on \( D([0, \infty), \mathbb{R}_+) \). Since \( \xi_N(\cdot) \) is stationary and time-reversible, the same weak convergence holds for \( \tilde{\eta}_N(\cdot) \). Then this lemma is proved. 

As in Section 2 it is easy to see that \((Y_N(\cdot), \tilde{\eta}_N(\cdot))\) is a continuous time Markov chain taking values in \( E \times \mathbb{R}_+ \). Based on [2,4] and Conditions (A) and (B), a simple calculation shows that the corresponding generator is given by
\[
A_N g(y, u) = \psi_N g(y, u) + \phi_N g(y, u) + \Gamma_N g(y, u) \quad (3.3)
\]
for any bounded function \( g \) on \( \mathbb{R}_+ \times E \). Here
\[
\psi_N g(y, u) = 2 \sum_{j=2}^n j \xi_N \left( \frac{1}{2} \frac{1}{\varepsilon_N} 1 + \frac{1}{\varepsilon_N N - 1} \right) \left( g(y - e_j + e_{j-1}, u) - g(y, u) \right).
\]
Note that \( 1/(\varepsilon_N N - 1) \to 0 \) as \( N \to \infty \) by Condition (A). We also have
\[
\phi_N g(y, u) = 2 \left( \frac{y}{2} \right) \left( g(y - e_0, u) - g(y, u) \right) + \theta y_0 \left( g(y - e_0 + e_1, u + \varepsilon_N) - g(y, u) \right) + \gamma u^{\alpha-1} y_1 \left( g(y - e_1 + e_0, u - \varepsilon_N) - g(y, u) \right) 1_{\{u > 0\}} + \gamma u^{\alpha-1} \sum_{j=2}^N y_j \left( g(y - e_j + e_0, u - \varepsilon_N) - g(y, u) \right) 1_{\{u > 0\}} + \left( \varepsilon_N R_{1,N} g(y, u) + \frac{1}{N} u^{\alpha-1} 1_{\{u > 0\}} R_{2,N} g(y, u) \right).
\]
Here the fourth term is identically equal to 0 if \( y \in \Pi \). In the last term, \( R_{1,N} \) and \( R_{2,N} \) are bounded linear operators satisfying \( \|R_{i,N}\| \leq C \) for some constant \( C \). This last term includes the simultaneous entrance into the main population and coalescence and it vanishes if \( c_1 \leq u \leq c_2 \) for positive numbers \( c_1 \) and \( c_2 \). Last, we have
\[
\Gamma_N g(y, u) = \theta \varepsilon_N^{-1} (1 - y_0 \varepsilon_N) \left( g(y, u + \varepsilon_N) - g(y, u) \right) + \gamma u^{\alpha-1} \left( 1 - \varepsilon_N u^{-1} \sum_{j=1}^N y_j \right) \left( g(y, u - \varepsilon_N) - g(y, u) \right) 1_{\{u > 0\}}.
\]
Let us write \( c_N^\psi(y) \) (resp. \( c_N^\phi(y,u), c_N^\Gamma(y,u) \)) the total rate of the events generated by \( \psi_N \) (resp. \( \phi_N, \Gamma_N \)) when \( A_N g \) is applied to \((y,u)\). Then

\[
c_N^\psi(y) = 2 \sum_{j=2}^n y_j \left( \frac{j-1}{2} \right) \frac{1}{\varepsilon_N} \left( 1 + \frac{1}{\varepsilon_N N - 1} \right),
\]

\[
c_N^\phi(y,u) = 2 \left( \frac{y_0}{2} \right) + \theta y_0 + \gamma u^{\alpha-1} \mathbb{1}_{\{u > 0\}} \sum_{j=1}^N y_j + \varepsilon_N (1 + u^{\alpha-1} \mathbb{1}_{\{u > 0\}})
\]

and

\[
c_N^\Gamma(y,u) = \theta \varepsilon_N^{-1} (1 - y_1 \varepsilon_N) + \gamma u^{\alpha} \varepsilon_N^{-1} \left( 1 - \varepsilon_N u^{-1} \sum_{j=1}^N y_j \right) \mathbb{1}_{\{u > 0\}}.
\]

Let us introduce the following notation,

\[
\sigma_0^N = \inf \{ t \geq 0 : Y_N(t) \in \Pi \}
\]

and

\[
\sigma_1^N = \inf \{ t \geq 0 : \phi_N\text{-event occurs at } t \}.
\]

**Lemma 3.5** \( \sigma_0^N \xrightarrow{p} 0 \) as \( N \to \infty \).

**Proof.** By Lemma 1.3, we have for any \( T \) and \( 0 < \delta < (\theta/\gamma)^{1/\alpha} \), as \( N \to \infty \),

\[
P\left( \sup_{0 \leq t \leq T} |\tilde{\eta}_N(t) - (\theta/\gamma)^{1/\alpha}| > \delta \right) \to 0. \tag{3.4}
\]

Fix above \( \delta \). Let \( c_1 = (\theta/\gamma)^{1/\alpha} - \delta \) and \( c_2 = (\theta/\gamma)^{1/\alpha} + \delta \). Conditioned on \( (Y_N(t), \tilde{\eta}_N(t)) = (y,u) \) with \( (y,u) \in (E \setminus \Pi) \times [c_1,c_2] \) at the current time \( t \),

\[
P(\text{the next event is a } \phi_N\text{-event}) = \frac{c_N^\phi(y,u)}{c_N^\psi(y) + c_N^\phi(y,u) + c_N^\Gamma(y,u)} \leq C \varepsilon_N,
\]

for some positive constant \( C \);

\[
P(\text{the next event is a } \psi_N\text{-event}) = \frac{c_N^\psi(y)}{c_N^\psi(y) + c_N^\phi(y,u) + c_N^\Gamma(y,u)} \leq \frac{2n^3}{2n^3 + \theta + \gamma c_1^2},
\]

for sufficiently large \( N \);

\[
P(\text{the next event is a } \Gamma_N\text{-event}) = \frac{c_N^\Gamma(y,u)}{c_N^\psi(y) + c_N^\phi(y,u) + c_N^\Gamma(y,u)} \leq \frac{\theta + \gamma c_2^2}{2 + \theta + \gamma c_2^2},
\]

for sufficiently large \( N \). Inspired by Taylor and Véber [17, Lemma 3.1], we fix some \( s > 0 \) and consider

\[
P(\sigma_0^N > s) = P(D) + o(1),
\]

where

\[
D = \{ \sigma_0^N > s, \sup_{0 \leq t \leq s} |\tilde{\eta}_N(t) - (\theta/\gamma)^{1/\alpha}| \leq \delta \}. 
\]
Then
\[
\mathbf{P}(D) = \mathbf{P}(\{\text{at most } n \, \psi^N\text{-events occur in }[0, s]\} \cap D)
\]
\[
= \mathbf{P}(\{\text{at most } n \, \psi^N\text{- and at least } j \, \phi^N\text{-events occur in }[0, s]\} \cap D)
+ \mathbf{P}(\{\text{at most } n \, \psi^N\text{- and no } \phi^N\text{-events occur in }[0, s]\} \cap D)
=: I_1 + I_2.
\]

Note that we have \(Y^N(t) \in E \setminus \Pi\) for \(t \in [0, s]\) if \(\sigma_0^N > s\). Let \(p = \frac{2n^3}{2n^3 + \theta + \gamma c_1^N} \vee \frac{\theta + \gamma c_2^N}{2n^3 + \theta + \gamma c_2^N}\). Then
\[
I_1 \leq \sum_{k=0}^{n} \sum_{l=0}^{\infty} \mathbf{P}(\{\text{at least } k \, \psi^N\text{-events before a } \phi^N\text{-event occur in }[0, s]\} \cap D)
\]
\[
= \sum_{k=0}^{n} \sum_{l=0}^{\infty} \mathbf{P}(\{\text{at least } k \, \psi^N\text{- and } l \, \Gamma^N\text{-events before a } \phi^N\text{-event occur in }[0, s]\} \cap D)
\]
\[
\leq \sum_{k=0}^{n} \sum_{l=0}^{\infty} \binom{k + l}{k} p^{k+l} (C\varepsilon_N),
\]
(3.5)

Since \(0 < p < 1\), \(\sum_{k=0}^{n} \sum_{l=0}^{\infty} \binom{k + l}{k} p^{k+l} < \infty\). Then \(I_1 \to 0\) as \(N \to \infty\). Let \(U_j^N\) be the arrival time of the \(j\)'th event occurring to \((Y_N, \tilde{\eta}_N)\). For \(I_2\),
\[
I_2 = \sum_{k=0}^{n} \sum_{l=0}^{\infty} \mathbf{P}(\{\text{at least } k \, \psi^N\text{-events, } l \, \Gamma^N\text{-events and no } \phi^N\text{-events occur in }[0, s]\} \cap D)
\]
\[
\leq \sum_{k=0}^{n} \sum_{l=0}^{\infty} \binom{k + l}{k} p^{k+l} \mathbf{P}(\{U_{k+l}^N < s, U_{k+l+1}^N > s\} \cap D).
\]

Conditioned on \((Y_N(t), \tilde{\eta}_N(t)) = (y, u)\) with \(y \in (E \setminus \Pi)\), the rate for the event occurring to \((Y_N, \tilde{\eta}_N)\) at time \(t\) is \(c_\psi^N(y) + c_\phi^N(y, u) + c_\Gamma^N(y, u)\) and \(c_\psi^N(y) \geq 2/\varepsilon_N\). Then \(U_{k+l+1}^N\) is stochastically bounded by the sum of \(k+l+1\) i.i.d. exponential variables with parameter \(2/\varepsilon_N\), whose distribution becomes concentrated close to 0 as \(N \to \infty\). Thus as \(N \to \infty\), \(\mathbf{P}(\{U_{k+l+1}^N < s, U_{k+l+1}^N > s\} \cap D) \to 0\) and by the dominated convergence theorem, \(I_2 \to 0\).

**Lemma 3.6** There exist positive constants \(M\) and \(K_1\) such that for any \(s > 0\),
\[
\lim_{N \to \infty} \sup_{s} \mathbf{P}(\sigma_1^N \leq s) \leq M(1 - e^{-K_1 s}).
\]

**Proof.** By the proof of (3.5), \(\mathbf{P}(\text{at least one } \phi^N\text{-event occurs before } \sigma_0^N ) \to 0\) as \(N \to \infty\). Then by (3.3), we have
\[
\mathbf{P}(\sigma_1^N \leq s) = \mathbf{P}(G) + o(1),
\]
where
\[
G = \{\text{only } \psi^N\text{- or } \Gamma^N\text{- events before } \sigma_0^N, \sup_{0 \leq t \leq s} |\tilde{\eta}_N(t) - (\theta/\gamma)^{1/\gamma}| \leq \delta \text{ and } \sigma_1^N \leq s\}.
\]

Recall that \(Y_N(0) = y\). If only \(\psi^N\text{- or } \Gamma^N\text{- events occur before } \sigma_0^N, \sigma_0^N < \sigma_1^N\) and \(Y_N(t) = \tilde{y}\) for \(t \in [\sigma_0^N, \sigma_1^N]\). Furthermore \(Y_N(t) \in \Pi\) and \(c_\psi^N \equiv 0\) for \(t \geq \sigma_0^N\). Conditioned on \((Y_N(t), \tilde{\eta}_N(t)) = (y, u)\) with \((y, u) \in \Pi \times [c_1, c_2]\),
\[
K_1 \leq c_\psi^N (y, u) \leq K_2, \quad \varepsilon_N^{-1}(\theta + \gamma c_1^N)/2 \leq c_\Gamma^N (y, u) \leq \varepsilon_N^{-1}(\theta + \gamma c_2^N),
\]

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for sufficiently large $N$, where $K_1 = [\gamma (c_1^{\theta - 1} \land c_2^{\theta - 1})] \land \theta$ and $K_2 = n^2 + n\theta + \gamma n(c_1^{\theta - 1} \lor c_2^{\theta - 1})$. Then

$$\frac{c_N^0(y, u) - c_N^0(y, u)}{c_N^0(y, u) + c_N^0(y, u)} \leq \frac{2K_2 \varepsilon_N}{2K_2 \varepsilon_N + \theta + \gamma c_1^\theta}, \quad \frac{c_N^0(y, u) - c_N^0(y, u)}{c_N^0(y, u) + c_N^0(y, u)} \leq \frac{\theta + \gamma c_2^\theta}{K_1 \varepsilon_N + \theta + \gamma c_2^\theta}.$$  

For $(Y_N(\cdot), \tilde{\eta}_N(\cdot))$ with initial value $(y, u) \in \Pi \times [c_1, c_2]$, recall that $U_j^N$ denotes the arrival time of the $j$'th event occurring to $(Y_N, \tilde{\eta}_N)$ and $U_0^N = 0$. It is not hard to see that $U_j^N$ is stochastically larger than the sum of $j$ i.i.d. exponential variables with parameter $\varepsilon_N^{-1}(\theta + \gamma c_2^\theta) + K_2$. We have

$$P(G) = \sum_{k=0}^{\infty} P\left(\{\text{exactly } k \text{ } \Gamma_N \text{-events occur in } [\sigma_0^N, \sigma_1^N]\} \cap G\right)$$

$$\leq \sum_{k=0}^{\infty} \left(\frac{\theta + \gamma c_2^\theta}{K_1 \varepsilon_N + \theta + \gamma c_2^\theta}\right)^k \frac{2K_2 \varepsilon_N}{2K_2 \varepsilon_N + \theta + \gamma c_1^\theta} P\left(\sigma_0^N + U_k^N \leq s\right)$$

$$\leq \sum_{k=0}^{\infty} \left(\frac{\theta + \gamma c_2^\theta}{K_1 \varepsilon_N + \theta + \gamma c_2^\theta}\right)^k \frac{2K_2 \varepsilon_N}{2K_2 \varepsilon_N + \theta + \gamma c_1^\theta} P\left(\sigma_0^N + \sum_{j=1}^{K} \tilde{V}_j^N \leq s\right)$$

$$\leq MP\left(\sigma_0^N + \sum_{j=1}^{T_N} \tilde{V}_j^N \leq s\right),$$

for some positive constant $M$ and sufficiently large $N$, where $\{\tilde{V}_j^N\}$ are i.i.d. exponential variables with parameter $\varepsilon_N^{-1}(\theta + \gamma c_2^\theta) + K_2$, and $T_N$ is a geometric variable with parameter $\frac{K_1 \varepsilon_N}{K_1 \varepsilon_N + \theta + \gamma c_2^\theta}$ independent of $\{\tilde{V}_j^N\}$. Since $\sigma_0^N \overset{P}{\to} 0$, a simple calculation shows that $\sigma_0^N + \sum_{j=1}^{T_N} \tilde{V}_j^N$ converges weakly to an exponential variable with parameter $K_1$. The lemma is proved.

**Lemma 3.7** Under conditions (A) and (B), the ancestral process $\{Y_N(t), t \geq 0\}$ starting at $y$ with $y \in \Pi$ converges weakly on $D([0, \infty), \Pi)$ to $\{Y(t), t \geq 0\}$ given by (3.3) starting at $y$.

**Proof.** If the process $Y_N(t)$ stays in the space of $\Pi$, $\psi_N$ and the fourth term in $\phi_N$ vanishes. Then for any bounded function $g$ on $E \times R_+$ define $B_N g = \tilde{\phi}_N g + \Gamma_N g$, where $\Gamma_N$ is given in (3.3) and

$$\tilde{\phi}_N g(y, u) = 2 \left(\frac{y_0}{2}\right) \left(g(y - e_0, u) - g(y, u)\right) + \theta y_0 \left(g(y - e_0, e_1, u + \varepsilon_N) - g(y, u)\right) + \gamma y^{n-1} y_1 \left(g(y - e_1, e_0, u - \varepsilon_N) - g(y, u)\right) 1_{\{u > 0\}} + \left(\varepsilon_N R_1, N g(y, u) + \frac{1}{N} u^{a-1} 1_{\{u > 0\}} R_2, N g(y, u)\right).$$

Let $F^N_t = \{\{Y_N(s), \tilde{\eta}_N(s)\} : 0 \leq s \leq t\}$. Because of the Markov property of $(Y_N(\cdot), \tilde{\eta}_N(\cdot))$,

$$g(Y_N(t), \tilde{\eta}_N(t)) - g(y, \tilde{\eta}_N(0)) - \int_0^t (B_N g)(Y_N(s), \tilde{\eta}_N(s)) ds$$

is a local $(F^N_t)$-martingale. Let

$$\tau_N = \inf\{t \geq 0, |\tilde{\eta}_N(t-) - (\theta/\gamma)^{\alpha} | \geq \delta \text{ or } |\tilde{\eta}_N(t) - (\theta/\gamma)^{\alpha} | \geq \delta\},$$

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where \( \delta \) is a positive constant satisfying \( 0 < \delta < (\theta/\gamma)^{1/\alpha} \). For sufficiently large \( N \), there exist \( c_1 > 0 \) and \( c_2 > 0 \) such that \( c_1 \leq \bar{\eta}_N(t \wedge \tau_N) \leq c_2 \) for any \( t \geq 0 \). Then for any function \( f \) on \( E \),

\[
\zeta_N(t) = f(Y_N(t \wedge \tau_N)) - f(y) - \int_0^{\tau_N} (B_N f)(Y_N(s \wedge \tau_N), \bar{\eta}_N(s \wedge \tau_N)) ds
\]

is a bounded martingale. Indeed, for sufficiently large \( N \), \(|(B_N f)(Y_N(s \wedge \tau_N), \bar{\eta}_N(s \wedge \tau_N))| \leq 2(n^2 + n\theta + n\gamma(c_1^{\alpha - 1} \vee c_2^{\alpha - 1}))\|f\| \) for any \( s \geq 0 \). Note that \( E \) is a finite set, so the discrete topology on \( E \) makes it a complete and compact metric space and any real valued function \( f \) on \( E \) is bounded and continuous. By Ethier and Kurtz [7, Theorem 9.1 and 9.4, p.142], the process \( \{Y_N(t \wedge \tau_N)\} \) is relatively compact. On the other hand, for any \( t \geq 0 \),

\[
P(\tau_N < t) \leq P \left( \sup_{0 \leq s \leq t} |\bar{\eta}_N(s) - (\theta/\gamma)^{1/\alpha}| \geq \delta \right) \rightarrow 0,
\]

which shows that \( \tau_N \xrightarrow{\mathbb{P}} \infty \). Let \( \{Y(t)\} \) be any limit point of \( \{Y_N(t \wedge \tau_N)\} \). By Skorokhod’s representation theorem we may assume that on some Skorokhod space \((\tau_N, Y_N(t \wedge \tau_N), \bar{\eta}_N(t \wedge \tau_N), (\tau_N, Y(t), (\theta/\gamma)^{1/\alpha}) \) in the topology of \( \mathbb{R}_+ \times D([0, \infty), E \times \mathbb{R}_+) \). Thus \( \zeta_N(t) \xrightarrow{\mathbb{P}} \zeta(t) \) and \( \zeta(t) \) is given by

\[
\zeta(t) = f(Y(t)) - f(x) - \int_0^t (B f)(Y(s)) ds,
\]

where

\[
B f(u, y) = 2 \left( \sum_{i=1}^k f(y_i) - f(y) \right) + \theta_0 \left( f(y_i) - f(y) \right) + \theta (\gamma/\theta)^{1/\alpha} y_1 \left( f(y_i) - f(y) \right).
\]

Since \( \sup_N |\zeta_N(t)| < \infty \), \( \zeta_N(t) \xrightarrow{\mathbb{P}} \zeta(t) \) for any \( t \geq 0 \). Thus \( \zeta(t) \) is a martingale. Since \( \{Y(t)\} \) given by (3.1) is the unique solution to the martingale problem (3.3). We have that \( \{Y_N(t \wedge \tau_N)\} \) converges weakly to \( \{Y(t)\} \) given by (3.1) in \( D([0, \infty), E) \). Furthermore, for any \( \epsilon > 0 \) and any \( t \geq 0 \),

\[
P \left( \sup_{0 \leq s \leq t} |Y_N(s \wedge \tau_N) - Y_N(s)| > \epsilon \right) \leq P(\tau_N < t) \rightarrow 0,
\]

as \( N \rightarrow \infty \). The lemma follows from the above limit. \( \square \)

**Proof of Theorem 3.1** Let \( \mathbf{P}_Y(\cdot) \) be the distribution of \((Y_N(\cdot), \bar{\eta}_N(\cdot)) \) with initial value \((y, \bar{\eta}_N(0)) \), where \( \bar{\eta}_N(\cdot) \) is distributed as \( \pi_N \) given in Section 2. Let \( f_1, \ldots, f_k \) be real-valued functions on \( E \). Choose \( 0 < s < t_1 < \cdots < t_k \). Let \( Q_N = \{\sigma_0^N < s < \sigma_1^N \} \). Then

\[
E_Y \left[ \prod_{i=1}^k f_i(Y_N(t_i)) 1_{Q_N} \right]
= E_Y \left[ 1_{Q_N} E \left[ \prod_{i=1}^k f_i(Y_N(t_i)) | \mathcal{F}_s^N \right] \right]
= E_Y \left[ 1_{Q_N} E_{(y, \bar{\eta}_N(s))} \left[ \prod_{i=1}^k f_i(Y_N(t_i - s)) \right] \right]
= E_Y \left[ E_{(y, \bar{\eta}_N(s))} \left[ \prod_{i=1}^k f_i(Y_N(t_i - s)) \right] \right] - E_Y \left[ 1_{Q_N} E_{(y, \bar{\eta}_N(s))} \left[ \prod_{i=1}^k f_i(Y_N(t_i - s)) \right] \right]
= E_Y \left[ \prod_{i=1}^k f_i(Y_N(t_i - s)) \right] - E_Y \left[ 1_{Q_N} E_{(y, \bar{\eta}_N(s))} \left[ \prod_{i=1}^k f_i(Y_N(t_i - s)) \right] \right].
\]
where $\bar{Q}_N$ is the complement of the set $Q_N$. The last equality follows from the fact that $\bar{n}_N(\cdot)$ is stationary. Then by Lemmas 3.5, 3.6 and 3.7,

$$\limsup_{N \to \infty} \left| \mathbb{E}_Y \left[ \Pi_{i=1}^k f_i(Y_N(t_i)) \right] - \mathbb{E}_Y \left[ \Pi_{i=1}^k f_i(Y(t_i-s)) \right] \right|$$

$$\leq 2 \max_i \|f_i\| \limsup_{N \to \infty} \mathbb{P}(\bar{Q}_N) + \limsup_{N \to \infty} \left| \mathbb{E}_Y \left[ \Pi_{i=1}^k f_i(Y_N(t_i-s)) \right] - \mathbb{E}_Y \left[ \Pi_{i=1}^k f_i(Y(t_i-s)) \right] \right|$$

$$\leq 2M \max_i \|f_i\|(1-e^{-K_1s}),$$

which goes to 0 as $s \to 0$. Note that $Y(t)$ is stochastically continuous. $\mathbb{E}_Y \left[ \Pi_{i=1}^k f_i(Y(t_i-s)) \right]$ converges to $\mathbb{E}_Y \left[ \Pi_{i=1}^k f_i(Y(t_i)) \right]$ as $s \to 0$. Then we have that $\lim_{N \to \infty} \mathbb{E}_Y \left[ \Pi_{i=1}^k f_i(Y_N(t_i)) \right] = \mathbb{E}_Y \left[ \Pi_{i=1}^k f_i(Y(t_i)) \right]$. □

**Proof of Theorem 5.2**

Step 1: recall the notation in Section 2.2. Under the homeomorphism, the subspace $\Pi$ can be regarded as $\Gamma(\Pi)$ for simplicity. It follows from (3.6) that for any function $f$ on $\Pi$,

$$f(Y_k(t)) - f(y) - \int_0^t (B_kf)(Y_k(s))ds$$

is a martingale, where

$$B_kf(y) = 2 \begin{pmatrix} y_0 \\ 2 \end{pmatrix} \left( f(y + (-1,0)) - f(y) \right) + \theta_k y_0 \left( f(y + (-1,1)) - f(y) \right)$$

$$+ \theta_k (\gamma_k/\theta_k)^{1/\alpha} y_1 \left( f(y + (1,-1)) - f(y) \right).$$

Recall that $Y_k(t) = (Y_k^0(t), Y_k^1(t))$ and $Y_k(t) = Y_k^0(t) + Y_k^1(t)$. For any function $g$ on $I_n$, let $f(y) = g(y_0 + y_1)$ for $y \in \Pi$. Then

$$g(Y_k(t)) - g(n) - \int_0^t (\bar{B}_kg)(Y_k^0(s), Y_k^1(s))ds$$

is also a martingale, where $\bar{B}_kg(y) = 2 \begin{pmatrix} y_0 \\ 2 \end{pmatrix} (g(y-1) - g(y))$. Note that $I_n$ is a finite set, so the discrete topology on $I_n$ makes it a complete and compact metric space. Any real valued function $g$ on $I_n$ is bounded and continuous. Then $Y_k(\cdot)$ satisfies the compact containment condition. For each $T > 0$, $\sup_k \int_0^T |\bar{B}_kg(Y_k^0(s), Y_k^1(s))|ds \leq 2n^2T\|g\|$, where $\|g\| = \sup_{y \in I_n} |g(y)|$. By Ethier and Kurtz [4] Theorem 9.1 and 9.4, p.142, $Y_k(\cdot)$ is relatively compact in $D([0, \infty), I_n)$.

Step 2: suppose that $\{\xi_{ij}(\cdot)\}_{j=1}^n$ is the sequence of i.i.d. Markov chains taking values in $\{0,1\}$ and whose transition rate matrix is given by

$$\begin{pmatrix} -1 & 1 \\ \frac{1}{\theta_k} & -\frac{1}{\theta_k} \end{pmatrix}.$$ 

Let $P_{ij}^k(t) = P(\xi_{ij}^k(t) = j|\xi_{ij}^k(0) = i)$. A simple calculation shows that

$$P_{00}^k(t) = 1 - P_{01}^k(t) = \frac{(\theta_k/\gamma_k)^{1/\alpha}}{1 + (\theta_k/\gamma_k)^{1/\alpha}} + \frac{1}{1 + (\theta_k/\gamma_k)^{1/\alpha}} e^{-(1+(\theta_k/\gamma_k)^{1/\alpha})t},$$

$$P_{10}^k(t) = 1 - P_{11}^k(t) = \frac{(\theta_k/\gamma_k)^{1/\alpha}}{1 + (\theta_k/\gamma_k)^{1/\alpha}} - \frac{(\theta_k/\gamma_k)^{1/\alpha}}{1 + (\theta_k/\gamma_k)^{1/\alpha}} e^{-(1+(\theta_k/\gamma_k)^{1/\alpha})t}.$$
Let $\zeta_n^k(t) = \sum_{j=1}^{n} 1_{\{z_j^k(t) = 0\}}$. Since $\{z_j^k(t)\}_{j=1}^{n}$ are independent of each other, it is not hard to see that for any $g$ on $I_n$,

$$\sup_{x,y \in I_n} \left| E_x[g(\zeta_n^k(t))] - E_y[g(\zeta_n^k(t))] \right| \leq 2n\|g\|e^{-(1+\gamma)\gamma \alpha}t, \ t \geq 0.$$  

This implies $\zeta_n^k(t)$ satisfies the $\phi$-mixing condition (see [4, P.111]). By (1.13) of [4, p.109],

$$\sup_{y \in I_n} \left| E_y[g(\zeta_n^k(t_2))g(\zeta_n^k(t_1))] - E_y[g(\zeta_n^k(t_2))]E_y[g(\zeta_n^k(t_1))] \right| \leq 2\sqrt{2n\|g\|^2}e^{-(1+\gamma)\alpha/(2\gamma)}(t_2-t_1)^2/2$$

for any $t_2 \geq t_1 \geq 0$. Then

$$E_y \left[ \left( \int_0^t \left( g(\zeta_n^k(\theta_k s)) - E_y[g(\zeta_n^k(\theta_k s))] \right) ds \right)^2 \right]$$

$$= E_y \left[ \int_0^t \int_0^t ds \left( g(\zeta_n^k(\theta_k s)) - E_y[g(\zeta_n^k(\theta_k s))] \right) \left( g(\zeta_n^k(\theta_k s_1)) - E_y[g(\zeta_n^k(\theta_k s_1))] \right) ds \right]$$

$$= \int_0^t \int_0^t ds \left( E_y[g(\zeta_n^k(\theta_k s_2))g(\zeta_n^k(\theta_k s_1))] - E_y[g(\zeta_n^k(\theta_k s_2))]E_y[g(\zeta_n^k(\theta_k s_1))] \right)$$

$$\leq C(n)\|g\|^2 \int_0^t \int_0^t e^{-\gamma \alpha (1+\gamma)\alpha/(2\gamma)}(s_2-s_1)^2 ds$$

$$\leq C(n)\|g\|^2 t/(\gamma \alpha), \ (3.7)$$

where $C(n)$ is a constant only depending on $n$. Since $P_{00}(\theta_k t) \to \frac{p^{1/\alpha}}{1+p^{1/\alpha}}$ and $P_{01}(\theta_k t) \to \frac{1}{1+p^{1/\alpha}}$ as $k \to \infty$, it is easy to see for any $t \geq 0$, $\zeta_n^k(\theta_k t) \to \zeta_n$ as $k \to \infty$, where $\zeta_n$ follows the Binomial distribution, i.e., $\zeta_n \sim B(n, \frac{p^{1/\alpha}}{1+p^{1/\alpha}})$. Note that $I_n$ is finite. The dominated convergence theorem shows that

$$\sup_{y \in I_n} \int_0^t \left| E_y[g(\zeta_n(\theta_k s))] - E[g(\zeta_n)] \right| ds \to 0,$$

as $k \to \infty$. Combined with (3.7), we have as $k \to \infty$,

$$\sup_{y \in I_n} E_y \left[ \left( \int_0^t \left( g(\zeta_n(\theta_k s)) - E[g(\zeta_n)] \right) ds \right)^2 \right] \to 0. \ (3.8)$$

Step 3: $(Y_0^k(t), Y_k(t))$ is a Markov process as in Step 1. Let $F_t^k = \sigma\{(Y_s^k(s), Y_k(s)) : 0 \leq s \leq t\}$. Define $T_j^k = \inf\{t \geq 0 : Y_k(t) = n - j\}$ with $T_0^k = 0$ and $T_1^k = T_j^k - T_{j-1}^k$. Set $h(y) = y(y-1)$ for $y \in I_n$. By (3.8), we have

$$P(T_{j+1}^k > t) = E\left[ P(T_{j+1}^k > t | F_t^k) \right]$$

$$= E\left[ P(Y_k(T_{j+1}^k), n-j | T_{j+1}^k > t) \right]$$

$$= E\left[ E_{Y_k(T_{j+1}^k)} \left( \exp \left\{ - \int_0^T h(Y_k(s)) ds \right\} \right) \right]$$

$$\rightarrow e^{-E[h(Y_{n-j})]t},$$

as $k \to \infty$. Similarly

$$P(T_1^k > t, T_2^k > s) = E\left[ 1_{\{T_1^k > t\}} E_{Y_k(T_{1}^k)} \left( \exp \left\{ - \int_0^T h(Y_k(s)) ds \right\} \right) \right].$$
Then
\[ |P(\tau_1^k > s, \tau_2^k > t) - e^{-E[h(\zeta_n)]|s-E[h(\zeta_{n-1})]|t}| \]
\[ \leq |P(\tau_1^k > s) - e^{-E[h(\zeta_n)]|s} + \sup_{y \in I_n} E_y \left[ \left| \int_0^t \left( h(\zeta_{n-1}^k(\theta_k s)) - E[h(\zeta_{n-1})] \right) ds \right| \right]. \]

By (3.8) and (3.9) we have that the second term in the right-hand side of the above inequality goes to 0 as \( k \to \infty \). By induction, \((\tau_1^k, \cdots, \tau_{n-1}^k) \xrightarrow{d} (\tau_1, \cdots, \tau_{n-1})\), where \( \{\tau_j\}_{j=1}^{n-1} \) is independent of each other and \( \tau_j \) follows the exponential distribution with parameter \( c_{n-j+1} \). It follows that \( \{Y_k(t), t \geq 0\} \) converges in the sense of finite-dimensional distributions to the \( n \)-Kingman coalescent process \( \{K(t), t \geq 0\} \). Since \( \{Y_k(t)\} \) is relatively compact, the theorem is proved. \( \square \)

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