

# On the ancestral process of long-range seedbank models

Jochen Blath, Adrián González Casanova, Noemi Kurt, Dario Spanò

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## Abstract

We present a new model for seed banks, where individuals may obtain their type from ancestors which have lived in the near as well as the very far past. We discern three parameter regimes of the seed bank age distribution, which lead to substantially different behaviour in terms of genetic variability, in particular with respect to fixation of types and time to the most recent common ancestor. The classical Wright-Fisher model, as well as a seed bank model with bounded age distribution considered by Kaj, Krone and Lascoux (2001) are boundary cases of our model. The mathematical methods are based on renewal theory as well as on a Gibbsian approach introduced by Hammond and Sheffield (2011) in a different context.

## 1 Introduction

In this paper we construct a mathematical model for the description of the genetic variability of neutral haploid populations of fixed size under the influence of a general *seedbank* effect. In contrast to previous models, such as the Kaj, Krone and Lascoux model [8], we are particularly interested in situations where ancestors of individuals of the present generation may have lived in the rather remote past.

Seedbanks are of significant evolutionary importance, and come in various guises. Typical situations range from plant seeds which fall dormant for several generations during unfavourable ecological circumstances, see e.g. [12], to bacteria which may turn into endospores if the concentration of nutrients in the environment falls below a certain threshold. Such spores may in principle persist for an unlimited amount of time before they become active again (see, e.g. [2]).

Seedbank related effects can be viewed as sources of genetic novelty [9] and are generally believed to increase observed genetic variability. In [8], a mathematical model for a (moderate) seedbank effect is being investigated, with the number of generations backwards in time that may influence the current population being bounded by a constant  $m$  and being small when compared to the total population size (resp. during passage to a scaling limit). Under such circumstances, it is shown that the ancestral process of the population can be approximately described by a time-changed Kingman coalescent, where the (constant) time-change leads to a linear increase of the coalescence rates of ancestral lineages depending on the square of the expected seedbank age distribution. Overall, genetic variability is thus increased (in particular if mutation is taken into account), but the qualitative features of the ancestral history of the population remain unchanged.

In the present paper, we consider a neutral seedbank model with haploid Wright-Fisher-type dynamics, assuming constant population size  $N$ . However, the generation of the potential ancestors will not necessarily be bounded, but sampled according to some age distribution  $\mu$  on  $\mathbb{N}$ . For  $\mu = \delta_1$ , we are back in the classical Wright-Fisher, and classical scaling yields a Kingman coalescent. For  $\mu$  with bounded support, say with a maximum value  $m$ , we are in the setup of

[8], and obtain a timechange of Kinman's coalescent appearing in the limit (again after classical scaling).

Yet, some species suggest (i.e. bacteria transforming into endospores) that  $\mu$  should in principle be unbounded, and sampling generations backwards might potentially be on the order of magnitude as the total population size. This leads to an entirely different regime.

In this situation, mathematical modelling problems arise. In particular, to obtain a new generation of such a population *in equilibrium*, one requires information about the whole history, i.e. needs to start sampling at  $-\infty$ . For fixed population size  $N$ , it turns out that this can be done in an elegant way with the help of a Gibbs measure formalism recently developed by Hammond and Sheffield [6] in a different context. To us, it appears that this is the first time that Gibbs measure methods from statistical physics are used for population genetic modeling. This will be carried out in the next section.

A particularly interesting situation is reached if one considers age-distributions  $\mu$  with a power-law decay, that is

$$\mu(n, \dots, \infty) = n^{-\alpha} L(n)$$

for some  $\alpha > 0$  and some slowly varying function  $L$ . Depending on the choice of  $\alpha$ , we investigate the time to the most recent common ancestor of two individuals, if it exists. It turns out that (Theorem 2.1) for  $\alpha > 1/2$ , there is always a common ancestor, but the expected time is finite if and only if  $\alpha > 1$ . If  $\alpha < 1/2$ , with positive probability two ancestral lineages never meet. In this case, we compute the correlations between the relative frequencies of one allele at different times.

In the following section, we present the two constructions of our model and present the main results. In section 3 we prove Theorem 2.1 and Theorem 2.6. The appendix is devoted to proving the Gibbs measure characterisation, following [6].

## 2 Construction of the model and main results

We work in discrete time (measured in units of non-overlapping generations) and with fixed finite population size  $N$ . Time in generations is indexed by  $\mathbb{Z}$ . At each time  $i \in \mathbb{Z}$  we have  $N$  individuals with type  $X_{i,k} \in \{a, A\}$ ,  $1 \leq k \leq N$ . The dynamics of the population forwards in time is given in the following way: Each individual of generation  $i$  chooses the generation of its father according to a law  $\mu$  on  $\mathbb{N}$ , where we assume that the age distribution  $\mu$  is of the form

$$\mu(n, \dots, \infty) = n^{-\alpha} L(n)$$

for some  $\alpha \in (0, \infty)$  and some slowly varying function  $L$ . We denote by  $\Gamma_\alpha$  the set of all such measures  $\mu$ . To avoid degeneracies, we will always assume  $\mu(\{1\}) > 0$ . After having chosen the generation, the individual gets the type of a uniformly chosen ancestor among the  $N$  possible ancestors from that generation. One quantity we consider is the frequency process

$$Y_N(i) := \frac{1}{N} \sum_{k=1}^N 1_{\{X_{i,k}=a\}},$$

which describes the proportion of  $a$ -alleles in the population at time  $i$ . We are interested in the question of whether or not one type eventually fixates in the whole population, and if this happens in finite time almost surely. In the backward picture, this is related to asking if a finite set of individuals has a most recent common ancestor.

In the construction we give, it turns out that the ancestral lines can be described by a renewal process with interarrival law  $\mu$ . The question of fixation and time to the most recent

common ancestor can therefore be investigated via classical results of Lindvall [10] on coupling times of discrete renewal processes, which are controlled in the power law case via applications of Karamata's Tauberian Theorem for power series, see e.g. [1]. In addition to these nice features, the model allows a Gibbs measure construction, which is inspired by a paper of Hammond and Sheffield [6], where the case  $N = 1$  is considered in order to construct a discrete process with long-range correlations that converges to fractional Brownian motion. Note that one of the strengths of this Gibbs measures approach is the fact that it leads an a.s. embedding of the (backwards) genealogical process into a (forwards) Wright-Fisher type model with long correlations, in particular allowing the definition of a frequency process at any time  $n \in \mathbb{Z}$ . The forward process is easy to describe intuitively in the way we just did. The key observation is then that there exists a one-parameter family of extremal Gibbs measures on  $\{a, A\}^{\mathbb{Z} \times N}$  such that the conditional distribution given the past is given by this process (here and throughout the paper we abbreviate the set  $\mathbb{Z} \times \{1, \dots, N\}$  by  $\mathbb{Z} \times N$ ). This Gibbs measure in a sense encodes the whole genealogy of the population until the infinite past and future, hence a population in equilibrium. Once we have constructed the Gibbs measure, we can go forward in time and obtain a process of relative frequencies, or backward in time following the ancestral lines.

## 2.1 Renewal construction of ancestral lineages and time to the most-recent common ancestor

We start with a description of the ancestral lineages of samples in our model in terms of renewal theory. Fix  $N \in \mathbb{N}$  and a probability measure  $\mu \in \Gamma_\alpha$  as before. Let  $v \in V_N := \mathbb{Z} \times N$  denote an individual of our population (the fact that we use  $\mathbb{Z}$  to index time is not relevant in the renewal process construction, but will become important in the tree-construction we will give later). For  $v \in V_N$  we write  $v = (i_v, k_v)$  with  $i_v \in \mathbb{Z}$ , and  $1 \leq k_v \leq N$ , hence  $i_v$  indicating the generation of the individual in  $\mathbb{Z}$ , and  $k_v$  the label among the  $N$  individuals alive in this generation.

The ancestral process  $A(v) = \{v_0 = v, v_1, v_2, \dots\}$  of our individual  $v$  is a set of sites in  $V_N$ , where  $i_{v_0}, i_{v_1}, \dots \downarrow -\infty$  is a strictly decreasing sequence of generations, with decrements  $i_{v_l} - i_{v_{l-1}} =: \eta_l$  being i.i.d. random variables with distribution  $\mu \in \Gamma_\alpha$ , and where the  $k_{v_0}, k_{v_1}, \dots$  are i.i.d. Laplace random variables with values in  $\{1, \dots, N\}$ , independent of the  $\{\eta_l\}$ . Letting

$$S_n := \sum_{l=0}^n \eta_l,$$

where we assume  $S_0 = \eta_0 = 0$ , we obtain a discrete renewal process with interarrival law  $\mu$ . In the language of [11], we say that a renewal takes place at each of the times  $S_n, n \geq 0$ , and we write

$$R_n := 1_{\{n \text{ is a renewal time}\}}.$$

The renewal sequence of this process is thus given by

$$q_n := P_\mu(R_n = 1).$$

It is now straightforward to give a formal construction of the full ancestral process starting from  $N$  individuals at time 0 in terms of a family of  $N$  independent renewal processes with interarrival law  $\mu$  and a sequence of independent uniform random variables  $U^r(i), i \in -\mathbb{N}, r \in \{1, \dots, N\}$ , with values in  $\{1, \dots, N\}$  (independent also of the renewal processes). Indeed, let the ancestral processes pick previous generations according to their respective renewal times, and then among the generations labels according to their respective uniform random variables. As soon as at least two ancestral lineages hit a joint common ancestor, their renewal processes

couple, i.e. follow the same realization of one of their driving renewal processes (chosen arbitrarily, and discarding those remaining parts of the renewal processes and renewal times which aren't needed anymore). We leave the details to the reader.

Denote by  $P_N^\mu$  the law of the thus well-defined ancestral process. For  $v \in V_N$  with  $i_v = 0$ , we have

$$q_n = P_N^\mu \left( A(v) \cap (\{-n\} \times \{1, \dots, N\}) \neq \emptyset \right),$$

and the probability that  $w \in V_N$  is an ancestor of  $v$  is given by

$$P_N^\mu(w \in A(v)) = \frac{1}{N} q_{i_v - i_w}.$$

For notational convenience, let us extend  $q_n$  to  $n \in \mathbb{Z}$  by setting  $q_n = 0$  if  $n < 0$ . Note that  $q_0 = 1$ . Two individuals  $v, w \in V_N$  have a common ancestor if and only if  $A(v) \cap A(w) \neq \emptyset$ . If this is the case, and if  $v$  and  $w$  belong to the same generation, we denote by  $\tau$  the time to the most recent common ancestor,

$$\tau := \inf\{n \geq 0 : A(v) \cap A(w) \cap (\{-n\} \times \{1, \dots, N\}) \neq \emptyset\}.$$

Clearly,  $\tau$  is the same for all  $v, w$  with  $i_v = i_w$ . Our first main result distinguishes three regimes:

**Theorem 2.1** (Existence of the (expected) time to the most recent common ancestor). *Let  $\mu \in \Gamma_\alpha$ . Let  $N$  be fixed and let  $v, w \in V_N$ .*

- (a) *If  $\alpha > 1$ , then  $P_N^\mu(A(v) \cap A(w) \neq \emptyset) = 1$  and  $E_N^\mu[\tau] = c_\alpha \cdot N$ , where  $0 < c_\alpha < \infty$  does not depend on  $N$ .*
- (b) *If  $\alpha \in (1/2, 1)$ , then  $P_N^\mu(A(v) \cap A(w) \neq \emptyset) = 1$  and  $E_N^\mu[\tau] = \infty$ ,*
- (c) *If  $\alpha \in (0, 1/2)$ , then  $P_N^\mu(A(v) \cap A(w) \neq \emptyset) < 1$ .*

In other words, for  $\alpha > 1/2$  two individuals almost surely share a common ancestor, but the expected time to the most recent common ancestor is finite for  $\alpha > 1$  and infinite if  $\alpha \in (1/2, 1)$ . Hence in real-world populations observed over realistic time-scales, for  $\alpha \in (1/2, 1)$ , the assumption that a population is in equilibrium has to be treated with care.

*Remark 2.2.* In the boundary case  $\alpha = 1$ , the choice of the slowly varying function  $L$  becomes relevant. If we choose  $L = \text{const.}$ , then it is easy to see from the proof that  $E_N^\mu[\tau] = \infty$ . The case  $\alpha = 1/2$  requires further investigation.

*Remark 2.3.* Note that so-far, we have only constructed the ancestral process of our population. The Gibbs measure approach presented in the next section will be a both elegant and powerful tool to characterize the whole population process and its frequency process in equilibrium.

## 2.2 A Gibbs measure characterization and covariances of the frequency process

In the case  $\alpha < 1/2$ , Theorem 2.1 tells us that both types may persist for all time. In this case, a Gibbs measure approach, generalizing the method of [6], turns out to be useful. We introduce this concept now. We consider graphs – in fact at trees – with vertex-set  $V_N = \mathbb{Z} \times N$  and a set of bonds  $E_N$  which will be a (random) subset of  $B_N := \{(v, w) : v, w \in V_N\}$  where we consider *directed* edges. For  $v \in V_N$  we write as before  $v = (i_v, k_v)$  with  $i_v \in \mathbb{Z}$ , and  $1 \leq k_v \leq N$ . We consider the set of directed spanning trees of  $V_N$ , which we can write down as follows: Let

$$\mathcal{T}_N := \{G = (V_N, E_N) : E_N \subset B_N \text{ s.th. } \forall v \in V_N, \exists! w \in V_N, i_w < i_v, \text{ with } e = (w, v) \in E_N\}.$$

This means, we consider trees where each vertex  $v$  has exactly one outgoing (to the past) edge, which we denote by  $e_v$ . This unique outgoing vertex, or equivalently, the unique ancestor of  $v$  is determined as follows. Let  $\{\eta_v\}_{v \in V_N}$  be a countable family of independent  $\mu$ -distributed random variables, and let  $\{U_v\}_{v \in V_N}$  denote independent uniform random variables with values in  $\{1, \dots, N\}$  independent of the  $\eta_v$ . This infinite product measure induces a law on  $\mathcal{T}_N$  if we define

$$e_v := ((i_v - \eta_v, U_v), v).$$

We denote this probability measure by  $\hat{P}_N^\mu$ . In words, the ancestor of  $v$  is found by sampling the generation according to  $\mu$ , and then choosing the individual uniformly. We see that

$$\hat{P}_N^\mu(e_v = (w, v) \in E_N) = \frac{1}{N} \mu(i_v - i_w). \quad (1)$$

Comparing this to our previous construction of the ancestral process, we realise that  $P_N^\mu$  can be considered as being the restriction of  $\hat{P}_N^\mu$  to situations regarding the ancestry of a sample, and hence, with slight abuse of notation, we will identify the two measures, dropping the notation  $\hat{P}_N^\mu$ . A tree  $G \in \mathcal{T}_N$  is interpreted as the ancestral tree of the whole bi-infinite population.

In order to construct the Gibbs measure, we start with prescribing the distribution of types conditional on the (infinite) past. Let  $S_N := \{a, A\}^N$  denote the finite dimensional state space. Let  $X_v = X_{(i_v, k_v)} \in \{a, A\}$  denote the type of individual  $v$  that is the  $k$ th individual of generation  $i$ . We denote by  $\mathcal{C}$  the sigma-algebra of cylinder events, and write  $\sigma_n$  for the  $\sigma$ -algebra generated by cylinder sets contained in  $\{1, \dots, n\}$ . For  $i \in \mathbb{Z}$ , we define the probability kernel  $\lambda_{N,i}(\cdot | \cdot)$  from  $(S_N^\mathbb{Z}, \sigma_i)$  to  $(S_N^\mathbb{Z}, \mathcal{C})$  by saying that for any finite set  $B \subset \{i+1, \dots, \}$ , and  $x_B \in \{a, A\}^B$ , and for  $\xi \in S_N^\mathbb{Z}$  the conditional probability

$$\lambda_{N,i}^\xi(X|_B = x_B) := \lambda_{N,i}(\{X|_B = x_B\} | \xi)$$

is obtained by first sampling  $G \in \mathcal{T}_N$ , tracing back the ancestral line of every  $v \in B$  until it first hits  $\{\dots, i\}$ , and then assigning the type  $\xi$  of this ancestor to  $v$ . This is well defined because under  $P_N^\mu$  the tree until it first hits  $\{\dots, i\}$  is independent of  $\sigma_i$ . These kernels  $\lambda_{N,i}^\xi, i \in \mathbb{Z}$  are now used to construct the Gibbs measures. Due to the construction via product measures it is clear that they are consistent: If  $i < j$ , then for  $B \subset \{j+1, \dots\} \times \{1, \dots, N\}$ ,

$$\lambda_{N,i}^{\xi^1}(X_v = x_v, v \in B | X_w = \xi_w^2, i+1 \leq i_w \leq j) = \lambda_{N,j}^{\xi^1 \vee \xi^2}(X_v = x_v, v \in B).$$

Here,  $\xi^1 \vee \xi^2$  denotes the configuration which is equal to  $\xi^1$  on  $\{\dots, i\}$  and equal to  $\xi^2$  on  $\{i+1, \dots, j\}$ . So we can now define the Gibbs measures for our model:

**Definition 2.4.** A probability measure  $\lambda_N$  on  $(\{a, A\}^N)^\mathbb{Z}$  is called a  $\mu$ -Gibbs measure if for all  $i \in \mathbb{Z}$ , for all finite subsets  $B \subset \{i+1, \dots, \} \times \{1, \dots, N\}$ , and for all  $x_B \in \{a, A\}^B$  the mapping  $\xi \mapsto \lambda_{N,i}^\xi(x_B)$  is a version of the conditional probability

$$\lambda_N(X|_B = x_B | \sigma_i).$$

In other words, to sample from the Gibbs measure conditional on the past up to generation  $i$ , we first sample a  $G \in \mathcal{T}_N$  according to  $P_N^\mu$ , and assigning each  $X_v, i_v \geq i+1, 1 \leq k_v \leq N$ , its type according to the ancestors. It is clear that such measures exist: In fact, we can construct one by sampling a  $G \in \mathcal{T}_N$  according to  $P_N^\mu$ , and then assigning each of the connected components of  $G$  the value  $a$  or  $A$  independently with probability  $p \in [0, 1]$ . We call this particular measure  $\lambda_N^p$ . For a finite subset  $B \subset V_N$  its conditional distribution given  $\xi_w, w \in B^c$  is

$$\begin{aligned}
& \lambda_N^p(X_v = x_v, v \in B) \\
&= \sum_{\{C_i\} \text{ partition of } v_N} P_N^\mu(G = \cup_i C_i) \prod_{i: C_i \cap B \neq \emptyset} (p 1_{\{(x \vee \xi)_v = a \forall v \in C_i\}} + (1-p) 1_{\{(x \vee \xi)_v = A \forall v \in C_i\}}).
\end{aligned} \tag{2}$$

It is clear that  $\lambda_N^p$ , for  $p \in \{0, 1\}$ , is a  $\mu$ -Gibbs measure, hence the set of  $\mu$ -Gibbs measures is non-empty. If  $G \in \mathcal{T}_N$  has infinitely many components almost surely, then for all  $p \in [0, 1]$ , the measures  $\lambda_N^p$  are  $\mu$ -Gibbs measures. According to Theorem 2.1 this is the case if  $0 < \alpha < 1/2$ . In fact, in a sense that we will see later, the measures of the form  $\lambda_N^p$  are the only relevant  $\mu$ -Gibbs measures, which is a nice feature of this model, since it simplifies many calculations, and is important for the mathematical modelling.

Let us for a second come back to the biological interpretation. Any  $\mu$ -Gibbs measure  $\lambda_N$  describes the type distribution in a population in the whole bi-infinite time, that is including the whole past and future. As in statistical physics, it can only describe a population in equilibrium. For population models where fixation of one type occurs, the Gibbs measure will therefore be concentrated on populations of all  $a$ 's or all  $A$ 's. We have seen that for our model this is the case if  $\alpha$  is bigger than  $1/2$ . The Gibbs measure approach looks therefore particularly promising for the case  $\alpha \in (0, 1/2)$ , where no fixation occurs. However, our construction also works for  $\alpha \in (1/2, \infty]$ .

A particularly useful feature of our model is that the only relevant Gibbs measures are of the form  $\lambda_N^p$  described above. Note that the  $\mu$ -Gibbs measures form a convex set, as can be seen easily, and we can characterise the extremal points of this set generalizing Proposition 1 of [6].

**Proposition 2.5.** (a) *Let  $\alpha \in (0, 1/2)$ . For each fixed  $N$ , for each  $p \in [0, 1]$ , there is precisely one extremal  $\mu$ -Gibbs measure  $\lambda_N$  on  $\{a, A\}^{\mathbb{Z} \times N}$  such that  $\lambda_N(X_{i,k} = a) = p$  for all  $i \in \mathbb{Z}, 1 \leq k \leq N$ .*

(b) *Let  $\alpha \in (1/2, \infty]$ . The only extremal Gibbs measures are  $\lambda_N^0$  and  $\lambda_N^1$ . For  $p \in (0, 1)$ , the measures  $\lambda_N^p$  are given by  $\lambda_N^p = p\lambda_N^0 + (1-p)\lambda_N^1$ .*

This allows us to easily compute some correlations for the frequency process of the seed bank model. Recall  $q_n = P_N^\mu(A(0) \cap (\{-n\} \times \{1, \dots, N\}) \neq \emptyset)$ .

**Theorem 2.6.** *Let  $\alpha \in (0, 1/2)$  and let  $\lambda = \lambda_N^p$ . Then  $\sum_{n=0}^\infty q_n^2 < \infty$ , and*

(a) *For  $i \in \mathbb{Z}$ ,*

$$E_\lambda[Y_N(i)] = p,$$

(b) *For any  $i \in \mathbb{Z}$ ,*

$$\lim_{N \rightarrow \infty} \text{var}_\lambda(Y_N(i)) = p(1-p) \left( 1 - \frac{1}{\sum_{n=0}^\infty q_n^2} \right),$$

(c) *As  $i \rightarrow \infty$ , for some constant  $c$  and some slowly varying function  $L$ , independent of  $N$ ,*

$$\text{cov}_\lambda(Y_N(0), Y_N(i)) \sim \frac{(1-\alpha)^2 \cdot p(1-p)}{\Gamma(2-\alpha)^2 \Gamma(2\alpha) \sum_{n=0}^\infty q_n^2} \cdot i^{2\alpha-1} L(i),$$

*where  $\sim$  means that the ratio of the two sides tends to 1.*

*Remark 2.7.* If  $\alpha > 1/2$ , we have that  $\sum_{n=0}^{\infty} q_n^2 = \infty$ , hence in the limit it follows in that case  $\text{var}_{\lambda}(Y_N(i)) = p(1-p)$  and  $\text{cov}(Y_N(0), Y_N(i)) = p(1-p)$ . Note that this is what one would expect, since  $\lambda_N^p$  describes the population in equilibrium, that is, with probability  $p$  all individuals have type  $a$  and with probability  $(1-p)$  all individuals have type  $A$ . In this case,  $E_{\lambda}(Y_N(i)) = p$ ,  $\text{var}_{\lambda}(Y_N(i)) = p(1-p)$  and  $\text{corr}_{\lambda}((Y_N(0), Y_N(i))) = 1$ .

In the next section, we prove Theorem 2.1 and Theorem 2.6. The proof of Proposition 2.5 follows very closely the proof of [6]. For the sake of completeness and to indicate the necessary adaptations we need to make, we give the full proof as well as some general facts about the  $\mu$ -Gibbs measures in the Appendix. Note that strictly speaking, our Definition 2.4 does not define a Gibbs-measure, since we condition only on the past. In the notation of [4], these are  $g$ -measures, which need not necessarily be Gibbsian. However, the  $\lambda_N^p$ -measures clearly are Gibbsian, so Proposition 2.5 implies that indeed our  $\mu$ -Gibbs measures are Gibbs measures. Since we are not applying any Gibbs measure theory that can not be verified directly in this particular case, this discussion is purely notational.

### 3 Proof of the main results

In this section we prove Theorem 2.1 and Theorem 2.6 using a renewal process approach. The crucial observation is that the time to the most recent common ancestor is related to the coupling time of two versions of the renewal process. We will need some bounds on the  $q_n$  that can be obtained via Tauberian theorems.

**Lemma 3.1.** *Let  $\mu \in \Gamma(\alpha)$ .*

(a) *Let  $\alpha \in (0, 1)$ . Then*

$$\sum_{n=0}^i q_n \sim \frac{1-\alpha}{\Gamma(2-\alpha)\Gamma(1+\alpha)} \cdot i^{\alpha} L(i)^{-1} \text{ as } i \rightarrow \infty,$$

(b) *The sum*

$$\sum_{n=0}^{\infty} q_n^2$$

*is finite if  $\alpha \in (0, 1/2)$  and infinite if  $\alpha > 1/2$ .*

(c) *Let  $\alpha \in (0, 1/2)$ . Then*

$$\sum_{n=0}^{\infty} q_n q_{n-i} \sim \frac{(1-\alpha)^2}{\Gamma(2-\alpha)^2 \Gamma(2\alpha)} \cdot i^{2\alpha-1} L(i) \text{ as } i \rightarrow \infty.$$

**Proof.** Part (a) can also be found in [6], but we sketch the proof here. Let  $\mu_n := \mu(\{n\})$ . Recall that the Laplace transform of a sequence  $(a_n)_{n \in \mathbb{N}}$  is given by  $\hat{a}(t) := \sum_{n=0}^{\infty} a_n e^{-nt}$ . By conditioning on the value of  $\eta_n$ , we realise that

$$q_n = \sum_{i=1}^n \mu_i q_{n-i} = \sum_{i=1}^{\infty} \mu_i q_{n-i} = (\mu * q)_n,$$

where  $*$  denotes the convolution of sequences, recall  $q_n = 0$  if  $n < 0$ . Since  $q_0 = 1$  and the Laplace transform of a convolution is the product of the Laplace transforms, we have

$$\hat{q}(t) = (1 - \hat{\mu})^{-1},$$

and because  $\mu$  is a probability measure,

$$1 - \hat{\mu}(t) = - \int_0^t \hat{\mu}'(x) dx = \int_0^t \sum_{n=1}^{\infty} n \mu_n e^{-xn} dx. \quad (3)$$

We will now repeatedly apply Karamata's Tauberian Theorem (Theorem 1.7.1 of [1]), usually in the form for power series, which is stated in Theorem 1.7.3 of [1]. First, note that

$$\sum_{n=1}^i n \mu_n = \sum_{n=1}^i \mu(\{n, \dots, i\}) = \sum_{n=1}^i \mu(\{n, \dots, \infty\}) - i \mu(\{i+1, \dots, \infty\}).$$

Now by our assumption that  $\mu \in \Gamma_\alpha$ , the implication (1.7.7)  $\Rightarrow$  (1.7.6) of [1] tells us that

$$\sum_{n=1}^i n \mu_n \sim \frac{\alpha}{1-\alpha} \cdot i^{1-\alpha} L(i), \quad i \rightarrow \infty.$$

Applying Karamata's Tauberian Theorem to this sequence plugging into (3) gives

$$1 - \hat{\mu}(t) \sim \frac{\Gamma(2-\alpha)}{1-\alpha} t^\alpha L(1/t), \quad t \searrow 0,$$

and hence,

$$\hat{q}(t) \sim \frac{1-\alpha}{\Gamma(2-\alpha)} t^{-\alpha} L(1/t)^{-1} \quad t \searrow 0. \quad (4)$$

Using Karamata's Tauberian Theorem once more in the converse direction, we obtain

$$\sum_{n=0}^i q_n \sim \frac{1-\alpha}{\Gamma(2-\alpha)\Gamma(1+\alpha)} \cdot i^\alpha L(i)^{-1}, \quad i \rightarrow \infty.$$

(b) For  $\alpha > 1$  this follows from the discrete renewal theorem, see for example [3], which implies  $\lim_{n \rightarrow \infty} q_n = \frac{1}{E[\eta]}$ . In the case  $\alpha \in (1/2, 1)$ , we obtain by Cauchy-Schwarz that  $\hat{q}(t) \leq t^{-1/2} (\sum_{n=0}^{\infty} q_n^2)^{1/2}$ , which together with (4) implies that the sum is infinite if  $\alpha > 1/2$ . That  $\sum_{n=0}^{\infty} q_n^2$  is finite if  $\alpha \in (0, 1/2)$  follows from Parseval's identity once it is shown that the Fourier transform  $\tilde{q}(s) = \sum_{n=0}^{\infty} q_n e^{isn}$  satisfies  $|\tilde{q}(s)| \leq cs^{-\alpha} L(1/t)$ , which follows from Theorem 1 of [5], details see [6].

(c) Equation (4) implies for the convolution

$$(\widehat{q * q})(t) = \hat{q}(t) \hat{q}(t) = \frac{(1-\alpha)^2}{\Gamma(2-\alpha)^2} t^{-2\alpha} \tilde{L}(1/t)^{-1}$$

Again by Karamata's Tauberian Theorem for power series we obtain

$$\sum_{n=0}^i (q * q)(n) \sim \frac{(1-\alpha)^2}{\Gamma(2-\alpha)^2 \Gamma(1+2\alpha)} \cdot i^{2\alpha} L(i), \quad i \rightarrow \infty,$$

which by virtue of the discrete version of the Monotone Density Theorem (the second part of Cor 1.7.3 of [1]) yields (c).  $\square$

**Proof of Theorem 2.1.** (a) Without loss of generality, assume  $i_v = i_w = 0$ . Denote by  $(R_n)$  and  $(R'_n)$  the sequences of renewal times of the renewal processes corresponding to  $v$  and  $w$  respectively. In other words,  $R_n = 1$  if and only if  $v$  has an ancestor in generation  $-n$ . Let

$$T := \inf\{n : R_n = R'_n = 1\}$$

denote the coupling time of the two renewal processes. Since each time  $v$  and  $w$  have an ancestor in the same generation, these ancestors are the same with probability  $N$ , we get

$$E[\tau] = NE[T].$$

But if  $\alpha > 1$ , we have that  $E[\eta] < \infty$ , and therefore by Proposition 2 of [10],  $E[T] < \infty$ . This proves part (a).

(b) We note that  $v$  and  $w$  both have an ancestor in generation  $n \in \mathbb{N}$  if and only if  $R_n R'_n = 1$ . For independent samples  $R$  and  $R'$ , the expected number of generations where both individuals have an ancestor, is given by

$$E\left[\sum_{n=0}^{\infty} R_n R'_n\right] = \sum_{n=0}^{\infty} E[R_n]E[R'_n] = \sum_{n=0}^{\infty} q_n^2,$$

which is infinite if  $\alpha > 1/2$  due to Lemma 3.1 (b). Again, each of these times the ancestors are the same with probability  $1/N$ , therefore with probability one  $A(v)$  and  $A(w)$  eventually meet. However, the expected time until this event is bounded from below by the expectation of the step size,

$$E_\mu^N[\tau] \geq E[\eta] = \infty$$

if  $\alpha < 1$ .

(c) In this case,  $E\left[\sum_{n=0}^{\infty} R_n R'_n\right] = \sum_{n=0}^{\infty} q_n^2 < \infty$ , and therefore

$$P\left(\sum_{n=0}^{\infty} R_n R'_n = \infty\right) = 0,$$

which implies that the probability that  $A(v)$  and  $A(w)$  never meet is positive.  $\square$

We prove now Theorem 2.6. Let us assume  $\lambda = \lambda_p$ . We define  $Y_v := 1_{\{X_v=a\}}$ .

**Lemma 3.2.** *If  $\lambda = \lambda_p$ , then*

$$\text{cov}_\lambda(Y_v, Y_w) = p(1-p)P_\mu^N(A(v) \cap A(w) \neq \emptyset).$$

**Proof.** We have

$$E_\lambda^N(Y_v Y_w) = \lambda(X_v = X_w = a) = pP_N^\mu(A(v) \cap A(w) \neq \emptyset) + p^2(1 - P_N^\mu(A(v) \cap A(w) \neq \emptyset))$$

and  $E_\lambda^N(X_v)E_\lambda^N(X_w) = p^2$ .  $\square$

Hence we need to compute  $P_N^\mu(A(v) \cap A(w) \neq \emptyset)$ .

**Lemma 3.3.** *Let  $\alpha \in (0, 1/2)$ . If  $v \neq w, i_v \geq i_w$ , then*

$$P_N^\mu(A(v) \cap A(w) \neq \emptyset) = \frac{\sum_{n=1}^{\infty} q_n q_{n+i_v-i_w}}{\sum_{n=0}^{\infty} q_n^2}.$$

**Proof.** Let  $S_n, S'_n$  denote two independent samples of the renewal process, with  $S_0 = i_v, S'_0 = i_w$ . Note that this implies for the times of the renewals that

$$P(R_n = 1) = q_{n+i_v}.$$

Recall that the renewal process is running forward in time, whence the ancestral lines are traced backwards. Let  $A_v$  and  $A_w$  denote two independent samples of the ancestral lines of  $v$  and  $w$ ,

using the processes  $S$  and  $S'$  respectively, without coupling the processes. Then the expected number of intersections of  $A_v$  and  $A_w$  is given by

$$\begin{aligned} E[|A_v \cap A_w|] &= \frac{1}{N} E\left[\sum_{n=-i_w}^{\infty} R_n R'_n\right] = \frac{1}{N} \sum_{n=-i_w}^{\infty} q_{n+i_v} q_{n+i_w} \\ &= \frac{1}{N} \sum_{n=0}^{\infty} q_n q_{n+i_v-i_w}, \end{aligned} \quad (5)$$

On the other hand, conditioning on the event that the ancestral lines meet, and then restart the renewal processes in the generation of the first common ancestor, which is the same as sampling two ancestral lines starting at  $(0, 0)$ ,

$$\begin{aligned} E[|A_v \cap A_w|] &= E[|A_v \cap A_w| \mid A_v \cap A_w \neq \emptyset] P(A_v \cap A_w \neq \emptyset) \\ &= P(A_v \cap A_w \neq \emptyset) E[|A_0 \cap A_0|] \\ &= P(A_v \cap A_w \neq \emptyset) \frac{1}{N} \sum_{n=0}^{\infty} q_n^2. \end{aligned}$$

This proves the Lemma. □

**Proof of Theorem 2.6.** (a) Follows immediately from the definition of  $\lambda_N^p$ , as this implies  $\lambda_N^p(Y_{i,k} = 1) = p$ .

(b) By the above Lemmas, we get for  $v$  and  $w$  in the same generation,  $v \neq w$ ,

$$\text{cov}_\lambda(Y_v, Y_w) = p(1-p) \frac{\sum_{n=1}^{\infty} q_n^2}{\sum_{n=0}^{\infty} q_n^2} = p(1-p) \left(1 - \frac{1}{\sum_{n=0}^{\infty} q_n^2}\right),$$

and for the variance we obtain

$$\text{var}_\lambda(Y_v) = p(1-p).$$

This implies

$$\text{var}_\lambda(Y_N(i)) = \frac{1}{N^2} \sum_{k,j=1}^N \text{cov}_\lambda(Y_{(i,k)}, Y_{(i,j)}) = p(1-p) \left(1 - \frac{1}{\sum_{n=0}^{\infty} q_n^2}\right) + \frac{p(1-p)}{N \sum_{n=0}^{\infty} q_n^2}.$$

Letting  $N$  tend to infinity proves (b).

For (c) let  $i_v - i_w = i$ , and get from the above lemma

$$\text{cov}_\lambda(Y_v, Y_w) = p(1-p) \frac{\sum_{n=1}^{\infty} q_n q_{n+i}}{\sum_{n=0}^{\infty} q_n^2}.$$

Since  $q_n = 0$  if  $n < 0$ , for  $i \geq 1$ ,

$$\sum_{n=1}^{\infty} q_{n+i} q_n = \sum_{n=0}^{\infty} q_{n-i} q_n = (q * q)(i).$$

The result now follows from Lemma 3.1 (c). □

## A Appendix: Characterisation of the extremal Gibbs measures

We give now the proof of Proposition 2.5. This follows closely the Propostion 1 of [6], and we refer the reader to this work for details. For the sake of completeness, we still sketch the complete argument, and indicate the adaptations that have to be made. Note that part (b) follows immediately from Theorem 2.1, as this implies that all individuals have the same type almost surely.

**Lemma A.1.** *Let  $\mu$  be a measure on the positive integers. Assume that the greatest common divisor of its support is equal to one. Then  $G \in \mathcal{T}_N^\mu$  has either one component almost surely, or infinitely many components almost surely.*

**Proof.** This proof works as in [6], Lemma 2.1, with some obvious modifications.

**Lemma A.2.** *For all  $N \in \mathbb{N}$ , the set of  $\mu$ -Gibbs measures is non-empty and convex.*

**Proof.** Due to Lemma A.1 it is easy to see that  $\lambda_N^p$  is a  $\mu$ -Gibbs measure. This proves the existence. Convexity of the set of Gibbs measures is clear from the definition.  $\square$

We define the **extremal** Gibbs measures to be the extremal points of the set of  $\mu$ -Gibbs measures.

**Lemma A.3.** *Any extremal  $\mu$ -Gibbs measure is translation invariant.*

**Proof.** Clear from the construction, since  $P_N^\mu$  is translation invariant.  $\square$

A crucial propety of extremal Gibbs measures is their tail-triviality. Let  $\sigma_{-\infty} := \bigcap_{n \geq 0} \sigma_{-n}$  denote the tail-sigma algebra of the past.

**Lemma A.4.**  *$\lambda$  is an extremal  $\mu$ -Gibbs measure if and only if  $\lambda$  is tail-trivial, that is, for every  $A \in \sigma_{-\infty}$ , we have  $\lambda(A) \in \{0, 1\}$ .*

**Proof.** This is a general fact, but we give a proof here for the “if” direction, which is the one we will use. Let  $\lambda$  be an extremal  $\mu$ -Gibbs measure, and assume we find  $A \in \sigma_{-\infty}$  such that  $0 < \lambda(A) < 1$ . In that case we can define probability measures  $\nu$  and  $\nu'$  as

$$\nu(\cdot) := \lambda(\cdot|A), \quad \nu'(\cdot) := \lambda(\cdot|A^c).$$

Clearly,  $\nu \neq \nu'$ , and  $\lambda = \lambda(A)\nu + (1 - \lambda(A))\nu'$ . So, if we show that  $\nu$  and  $\nu'$  are both  $\mu$ -Gibbs measures, we are done, because then we have found a contradiction to the extremality of  $\lambda$ . We check that for any measurable function  $f$ , and for any  $i$  we have

$$\int f d\lambda = \int \int f(x \vee \xi) \lambda_{N,i}^\xi(dx) \lambda(d\xi). \quad (6)$$

To see this, observe that  $\frac{d\nu}{d\lambda} = \frac{1_A}{\lambda(A)}$ , and

$$\int f d\nu = \frac{1}{\lambda(A)} \int f 1_A d\lambda = \frac{1}{\lambda(A)} \int 1_A \int f(x \vee \xi) \lambda_{N,i}^\xi(dx) \lambda(d\xi), \quad (7)$$

where we used the fact that  $A \in \sigma_{-\infty}$ , hence  $1_A$  does not depend on  $x \in \{i+1, \dots\}$ . This implies (6). The argument for  $\nu'$  is exactly the same, and we are done.  $\square$

**Corollary A.5.** For an extremal  $\mu$ -Gibbs measure  $\lambda$  we have  $\lambda = \lambda(\cdot|\sigma_{-\infty})$   $\lambda$ -a.s., and if for an event  $A$  the sequence  $\lambda(A|\sigma_{-n})$  converges as  $n \rightarrow \infty$  in  $L^1(\lambda)$  to some random variable  $Y$ , then  $Y = \lambda(A)$   $\lambda$ -a.s.

**Proof.** The first statement follows directly from the above lemma, and the second one by dominated convergence.  $\square$

The crucial step in the proof of part (a) of the proposition is the following Lemma.

**Lemma A.6.** Let  $\lambda$  be a extremal  $\mu$ -Gibbs measure. Then there exist  $p \in [0, 1]$  such that for all  $v = (i_v, k_v) \in V_N$

$$\lim_{m \rightarrow \infty} \lambda(X_v = a|\sigma_{-m}) = p \quad \lambda - a.s.$$

**Proof.** To prove existence of the limit, we use the backward martingale convergence theorem which is stated in [7], page 233, as follows: Let  $(X_{-n}, F_{-n})$  be a backwards martingale and  $F_{-\infty} = \bigcap_{n=0}^{\infty} F_{-n}$ . The sequence  $(X_{-n})$  converges a.s. and in  $L^1$  to a limit  $X$  as  $n$  goes to infinity. Furthermore,  $X$  is finite and integrable. Applying this to our situation,  $F_{-n} = \sigma_{-n}$ , and  $X_{-n} = \lambda(X_v = a|\sigma_{-n})$ . Then the backwards martingale theorem states that  $\lim_{n \rightarrow \infty} \lambda(X_v = a|\sigma_{-n})$  exists. The limit is the conditional expectation,  $X = \lambda(X_v = a|\sigma_{-\infty})$ , which by Corollary A.5 is almost surely a constant that we denote by  $p_v$ .

Hence we need to prove that  $p_{v_1} = p_{v_2}$  for an arbitrary pair of points  $v_1, v_2 \in V_N$ . This is done via a coupling of the ancestral lines of  $v_1$  and  $v_2$ . Define  $i(v) = i_v$  for all  $v \in V_N$ , and  $k(v) = k_v$ . Define  $A_j(\omega)$ ,  $j \in 1, 2$  to be a realization of the ancestral line of  $v_j$ , i.e.  $A_j(\omega) = (A_j^0(\omega) = v_j, A_j^1(\omega), A_j^2(\omega) \dots)$ , where  $A_j^1$  is the unique ancestor of  $v_j$ , and  $A_j^2$  the unique ancestor of  $A_j^1$ , etc. Define

$$\tau_m = \tau_m(A_j) := \inf\{n \geq 0 : i(A_j^n) \leq m\}$$

the first time that the ancestral line of  $v_j$  crosses the level  $m$ . It is clear that  $\lambda(X_{v_i} = a|\sigma_m) = \lambda(A_i^{\tau_n} = a|\sigma_m)$  as  $m \rightarrow -\infty$ . The idea is now to construct a process  $B$ , such that

$$B \stackrel{d}{=} A_1 \quad \text{and} \quad P_N^\mu(\exists n : B^{\tau_n} = A_2^{\tau_n}) = 1. \quad (8)$$

Assume such a process  $B$  exists. Then

$$\lim_{m \rightarrow \infty} \lambda(X_{v_1} = a|\sigma_{-m}) = \lim_{m \rightarrow \infty} \lambda(A_1^{\tau_n} = a|\sigma_{-m}) = \lim_{m \rightarrow \infty} \lambda(B_1^{\tau_n} = a|\sigma_{-m}) \quad (9)$$

$$= \lim_{m \rightarrow \infty} \lambda(A_2^{\tau_n} = a|\sigma_{-m}) = \lim_{m \rightarrow \infty} \lambda(X_{v_2} = a|\sigma_{-m}) \quad \lambda\text{-a.s.} \quad (10)$$

So the existence of  $B$  would imply the claim of the lemma.

The construction of  $B$  is done as in [6] with one additional rule. Let  $a, b \in \text{Supp}(\mu)$ , with  $a \neq b$  fixed. Let us assume first that  $|i(v_1) - i(v_2)| = k|b - a|$  for some  $k \in \mathbb{Z}$ . Define  $B$  depending on  $A_2$  by this relation: Let  $B^0 = A_1^0$ . Given  $A_2^1$ , define  $B^1$  by  $k(B^1) = k(A_2^1)$ , and  $i(B^1)$  given by the following prescription:

1. if  $|i(A_2^0) - i(A_2^1)| \neq a$  and  $|i(A_2^0) - i(A_2^1)| \neq b$ , then  $i(B^1)$  is such that  $i(A_2^0) - i(A_2^1) = i(B^0) - i(B^1)$ .
2. if  $|i(A_2^0) - i(A_2^1)| = a$  or  $|i(A_2^0) - i(A_2^1)| = b$ , then  $i(B^1)$  is such that  $P_\mu(i(B^0) - i(B^1) = a) = \frac{\mu(a)}{\mu(a)+\mu(b)}$  and  $P_\mu(i(B^0) - i(B^1) = b) = \frac{\mu(b)}{\mu(a)+\mu(b)}$ , that is, the probability under  $\mu$  of the increment being equal to  $a$  resp.  $b$  conditional of being either of the two.

We claim that this process satisfies (8). It is straightforward to check  $B \stackrel{d}{=} A_1$ .

To show that  $P_N^\mu(\exists n : B^{\tau_n} = A_2^{\tau_n}) = 1$ , define the process  $W_n = |i(A_2^n) - i(B^n)|$  and note that  $W_n$  is a symmetric random walk with independent jumps in  $|a - b|\mathbb{Z}$  with one absorbing state 0. The transitions are one:

$$P_\mu(W_i - W_{i+1} = 0) = 1 - 2 \frac{\mu(a)\mu(b)}{\mu(a) + \mu(b)}$$

$$P_\mu(W_i - W_{i+1} = |a - b|) = \frac{\mu(a)\mu(b)}{\mu(a) + \mu(b)}$$

$$P_\mu(W_i - W_{i+1} = -|a - b|) = \frac{\mu(a)\mu(b)}{\mu(a) + \mu(b)}$$

Clearly,  $W_i$  gets absorbed by zero with probability one, which in our language means that  $B^{\tau_m}(\omega) = A_2^{\tau_m}(\omega)$  for some  $m \in \mathbb{Z}$  with probability one.

The case where  $|i(v_1) - i(v_2)| \neq k|b - a|$  is reduced to the first case as follows: We define  $B$  similarly, as in the first case, with just one extra rule: Given  $A_2^0, A_2^1 \dots A_2^n$ ,  $B^n$  is defined by  $k(B^n) = k(A_2^n)$ , and  $i(B^n)$  given by

1. if  $|i(A_2^{n-1}) - i(A_2^n)| \neq a$  and  $|i(A_2^{n-1}) - i(A_2^n)| \neq b$ , then  $i(B^n)$  is such that  $i(A_2^{n-1}) - i(A_2^n) = i(B^{n-1}) - i(B^n)$ .
2. if  $|i(A_2^{n-1}) - i(A_2^n)| = a$  or  $|i(A_2^{n-1}) - i(A_2^n)| = b$ , then  $P_\mu(i(B^{n-1}) - i(B^n) = a) = \frac{\mu(a)}{\mu(a) + \mu(b)}$  and  $P_\mu(i(B^{n-1}) - i(B^n) = b) = \frac{\mu(b)}{\mu(a) + \mu(b)}$
3. if  $B^{n-1} = A_2^{n-1}$  then  $B^n = A_2^n$ .

Define the stopping time  $j := \inf\{k \in \mathbb{N} : |b - a| \text{ divides } |i(A_1^k) - i(A_2^k)|\}$ . Note that  $j$  is almost surely finite as the greatest common divisor of  $\text{supp}(\mu) = 1$ . Sample independently  $\{A_1^0, A_1^1, \dots, A_1^j\}$  and  $\{A_2^0, A_2^1, \dots, A_2^j\}$ . Given  $A_1^j$  and  $A_2^j$  we are back in the case 1.  $\square$

We give now the rest of the proof of Theorem 2.5. Our presentation differs slightly from [6], but the arguments are the same.

**Proof of Theorem 2.5.** The existence follows from the fact that  $\lambda_p$  satisfies the conditions, so we just need to prove the uniqueness. Let  $\lambda$  be an extremal  $\mu$ -Gibbs measure on  $S_N^\mathbb{Z}$ , such that  $\lim_{m \rightarrow -\infty} \lambda(X_v = a | \sigma_m) = p$  for all  $v \in \mathbb{Z} \times N$ . This property can be written in a slightly different way: Let

$$g_k : S_N^{\{-\infty, \dots, k\}} \rightarrow [0, 1] : \xi \mapsto \lambda_{N,k}^\xi(X_v = a)$$

(compare Definition 2.4). Define

$$\Omega_{k,v}^\varepsilon := g_k^{-1}(p - \varepsilon, p + \varepsilon) \in \sigma_k.$$

Then  $\lim_{m \rightarrow -\infty} \lambda(X_v = a | \sigma_m) = p$  for all  $v \in \mathbb{Z} \times N$  is the same as saying that for every  $\varepsilon > 0$ ,

$$\lim_{k \rightarrow \infty} \lambda(\Omega_{k,v}^\varepsilon) = 1$$

for all  $\varepsilon > 0$  and all  $v \in V_N$ . It is important to note that also  $\lim_{k \rightarrow \infty} \lambda_p(\Omega_{k,v}^\varepsilon) = 1$ , since by definition  $\lambda_{N,k}^\xi$  is also a version of the conditional probability under  $\lambda_p$  given the past up to time  $k$ .

We will prove the lemma by showing that for every finite set  $L \subset V_N$ ,  $L = \{v_1, \dots, v_{|L|}\}$  and for all  $x \in \{a, A\}^{1,2,\dots,|L|}$

$$\lambda((X_{v_1}, X_{v_2}, \dots, X_{v_{|L|}}) = x) = \lambda_p((X_{v_1}, X_{v_2}, \dots, X_{v_{|L|}}) = x).$$

Note that this fact follows straightforward from Lemma A.6 in the case  $|L| = 1$

Suppose  $|L| > 1$ . Roughly speaking, we are going to show is that given a “very far” past  $m \ll 0$ , regarding  $\lambda(X_{v_1}, X_{v_2}, \dots, X_{v_{|L|}} | \sigma_m)$  as sampling  $G$  and assigning to each  $X_v$  the value of the most recent ancestor before time  $m$  is the same as assigning to each component of  $G$  type  $a$  (or  $A$ ) with probability  $p$  (or  $1 - p$ ). Here by “almost” we mean that the equality holds on a set of probability one when  $m$  goes to infinity, since in view of Corollary A.5, what we need to show is that  $\lambda$  and  $\lambda_p$  are non-singular on  $\sigma_{-\infty}$ . We will prove the following: For all  $\varepsilon > 0$ , for all  $L \subset V_N$  finite, there exists  $J_{\varepsilon, L} < \infty$  and  $\Omega_\varepsilon \in \sigma_{-J_{\varepsilon, L}}$  such that

$$\lambda(\Omega_\varepsilon) \geq 1 - \varepsilon|L| \quad \text{and} \quad \lambda_p(\Omega_\varepsilon) \geq 1 - \varepsilon|L|$$

and

$$|\lambda(X_{v_1}, X_{v_2}, \dots, X_{v_{|L|}} = x | \Omega_\varepsilon) - \lambda_p(X_{v_1}, X_{v_2}, \dots, X_{v_{|L|}} = x | \Omega_\varepsilon)| \leq 4\varepsilon|L|. \quad (11)$$

As the sets of the form  $\{(X_{v_1}, X_{v_2}, \dots, X_{v_k}) = x\}$  for  $k \in \mathbb{N}$  and  $x \in \{a, A\}^k$  generate the cylinder sets of  $\{a, A\}^{\mathbb{Z} \times N}$  with the product topology, letting  $\varepsilon \rightarrow 0$ , implies the claim  $\lambda = \lambda_p$ . We are now going to construct  $J_{\varepsilon, L}$  and  $\Omega_\varepsilon$ . Consider  $v \in V_n$  and  $k \in \mathbb{Z}$ ,  $k < i(v)$ . Let  $A_v$  be the ancestral line of  $v$ . Define

$$F_{v, k} := \{v' \in A_v : i(v') = \sup\{i(v'') : v'' \in A_v, i(v'') \leq k\}\}$$

In words,  $F_{v, k}$  is the most recent ancestor of  $v$  that is in the generation  $k$  or older.

Now we want to extend this concept from an individual  $v$  to a set of individuals  $L$ . Let  $L \subset V_N$  and  $k \in \mathbb{Z}$ ,  $k < \min\{i(v) : v \in L\}$ . Define

$$F_{L, k} := \{F_{v, k} : v \in L\}.$$

This set is the set of ancestors of the individuals in  $L$ . Note that for two individuals in  $L$  it is possible to have a common ancestor before generation  $k$ , so  $P_\mu(|F_{L, k}| \leq |L|) = 1$ . Indeed when  $|F_{L, k}| < |L|$ , two or more elements have a common ancestor before time  $k$ . Clearly,  $\{|F_{L, -k}|\}_{k > -\min\{z(v) : v \in L\}}$  is a decreasing process. Moreover, defining  $C_L$  to be the number of components of  $G_\mu$  that intersect  $L$ , it follows that  $|F_{L, -k}| \rightarrow C_L$   $P_\mu$ -a.s. As the convergence occurs in  $\mathbb{N}$  (which is a discrete topological space), after some random time  $T$  we have  $|F_{L, -k}| = C_L$ . Define the function of the realization of the random graph  $G_\mu$ . Note that  $T$  is almost surely finite by the fact that for all possible realization of  $G$  it is finite.  $T$  is the first time that all pairs of elements of  $L$  that live in a common component on  $G$  have reached a common ancestor. Define

$$F = F_{L, -T}$$

which is well defined as  $T$  is finite, and which stands for the most recent ancestors of the individuals in  $L$ , that live in different components of  $G$ . Now define

$$-J_{\varepsilon, L} := \sup\{k < \inf\{i(v) : v \in L\} : \lambda(\Omega_{k, v}^\varepsilon) > 1 - \varepsilon \text{ and } \lambda_p(\Omega_{k, v}^\varepsilon) > 1 - \varepsilon \text{ for all } v \in L\}.$$

$J_{\varepsilon, L}$  is almost surely finite by hypothesis and by finiteness of  $L$ . Define

$$\Omega_\varepsilon := \bigcap_{v \in F} \Omega_{J_{\varepsilon, L}, v}^\varepsilon \in \sigma_{-J_{\varepsilon, L}}.$$

It remains to check (11). Let  $x_0 \in \{0, 1\}^{|L|}$ ,  $m < \inf\{i(v), v \in F\}$  and  $m < J_{\varepsilon, L}$ . Once we have sampled  $G_\mu$ , we say that  $x_0$  is “allowed” if the  $i$ -th entry is equal to the  $j$ -th every time that  $F_{v_i}$  and  $F_{v_j}$  are in the same component. Clearly  $\lambda_p((X_{v_1}, X_{v_2}, \dots, X_{v_{|L|}}) = x_0) = 0$  if  $x_0$  is not allowed. If  $x_0$  is allowed, it induces some  $x_1$  which stands for the values of the elements of  $F$ , i.e.  $x_1 \in \{0, 1\}^{|F|}$ . Suppose  $x_1$  has  $k \leq |F|$  type  $a$ s, and  $|F| - k$  type  $A$ s, then

$$\lambda_p((X_{v_1}, X_{v_2}, \dots, X_{v_{|L|}}) = x_0) = p^k(1-p)^{|F|-k}$$

where  $p^k(1-p)^{|F|-k}$  arise by independently assigning the types  $a$  and  $A$  to each component with probability  $p$  and  $1-p$ . It follows

$$p^k(1-p)^{|F|-k} - \varepsilon|L| \leq \lambda_p((X_{v_1}, X_{v_2}, \dots, X_{v_{|L|}}) = x_0 | \Omega_\varepsilon) \leq p^k(1-p)^{|F|-k} + \varepsilon|L|.$$

If  $x_1$  is not allowed, we again have  $\lambda((X_{v_1}, X_{v_2}, \dots, X_{v_{|L|}}) = x_0 | \Omega_\varepsilon) = 0$ . Otherwise

$$\lambda((X_{v_1}, X_{v_2}, \dots, X_{v_{|L|}}) = x_0 | \Omega_\varepsilon) + |L|\varepsilon \leq (p + \varepsilon)^k(1 - p + \varepsilon)^{|F|-k} + |L|\varepsilon$$

and

$$\lambda((X_{v_1}, X_{v_2}, \dots, X_{v_{|L|}}) = x_0 | \Omega_\varepsilon) - |L|\varepsilon \geq (p - \varepsilon)^k(1 - p - \varepsilon)^{|F|-k} - |L|\varepsilon$$

as to determine the labels of the elements of  $L$  is enough to determine the labels of the elements of  $F$ . As this is true for every  $\varepsilon > 0$  we conclude

$$|\lambda(X_{v_1}, X_{v_2}, \dots, X_{v_{|L|}} = x | \Omega_\varepsilon) - \lambda_p(X_{v_1}, X_{v_2}, \dots, X_{v_{|L|}} = x | \Omega_\varepsilon)| \leq 4\varepsilon|L|.$$

□

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