

Evolution of the most recent common ancestor of a population with no selection

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Abstract. We consider the evolution of a population of fixed size with no selection. The number of generations G to reach the first common ancestor evolves in time. This evolution can be described by a simple Markov process, which allows one to calculate several characteristics of the time dependence of G . We also study how G is correlated to the genetic diversity.

Keywords: models for evolution (theory), mutational and evolutionary processes (theory), phylogeny (theory)

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1. Introduction

One of the simplest questions one can ask about the history of an evolving population is the age of its most recent common ancestor (MRCA). As the population evolves, the age of this MRCA as well as the genealogical tree keep changing, with an endless appearance of new branches and disappearance of old branches. These perpetual changes in the genealogy are accompanied by sudden jumps of the age of the MRCA, which correspond to the extinction of one of the oldest branches [1]. In the first part of the present paper we try to describe the evolution of this age in one of the simplest models of an evolving population, the Wright–Fisher model [2]–[5] with no selection.

Analysis of the human genome makes possible the precise comparison of the DNA sequences of individuals in a population. The number of differences between the sequences of a group of individuals is a testimony of the time passed since their common ancestors and one may hope to infer the history of the group from the knowledge of its DNA sequences [6]–[8]. The task is however immense as many factors interfere: selection [9], history, demography [7, 8], geography [10, 11], and diploidy [12, 13]. In order to attack the problem of estimating the age of the MRCA from the observed DNA sequences at a given generation, a number of models have been studied [6, 8], where at most few of these factors are included. The goal is always to correlate the observed genetic diversity of the population at a given generation to the age of this MRCA. However, it is difficult to characterize a sample of DNA sequences by a single parameter which would measure its genetic diversity. Ideally the optimal parameter would be to find a measure of the genetic diversity at a given generation which would be as correlated as possible to the age of the MRCA. In practice, one often uses Tajima’s estimator [14], which counts the number of different base pairs between pairs of individuals. But the more precise the characterization of the genetic diversity is, the more difficult the calculations are [6]. Here

we consider in the second part of this paper the simple case of the infinite allele model, where the only information we keep about pairs of individuals is whether they have the same allele or not, and we try to calculate how the distribution of the age of the MRCA is correlated to this information.

The simplest models one can consider consist in defining some stochastic rules which relate each individual (and its genome) to its parent in the previous generation, and the above questions can be formulated as steady state properties of simple non-equilibrium systems: for example, the coalescence process described below can be viewed as a reaction–diffusion process $A + A \rightarrow A$. The coalescing trees observed in genealogies also have striking similarities with the ultrametric structures which emerge in the theory of spin glasses and disordered systems [15, 16]. This is why they motivate a growing interest among statistical physicists [17].

We consider here a population of N individuals evolving according to the Wright–Fisher model (see [4] for a general introduction): successive generations do not overlap, at each new generation all the individuals are replaced by N new ones and each individual has one parent chosen randomly in the previous generation.

Many results are known in the absence of selection, such as the distribution of the age of the MRCA [18, 19] and the stochastic dynamics of the frequency of a gene [20, 21]. In the last part of this introduction, we recall a few known results that we will use in the rest of the paper.

Recently, Serva addressed the problem of the temporal dynamics of the age of the MRCA. In section 2, we show how to describe these dynamics as a simple Markov process, which allows one to calculate all the correlations between these MRCA ages at different generations.

One can associate with each individual a gene (or a genome). In section 3, where we try to correlate the genetic diversity to the age of the MRCA, we will consider the infinite allele case: each mutation creates a new genome, different from all the genomes which had previously appeared in the whole history of the population. At each generation, there is a probability θ/N of mutation in the transmission of each genome. This means that each new individual inherits the genome of its parent with probability $1 - \theta/N$ and receives a new genome with probability θ/N . On average, there are of course θ mutants in the whole population at each generation. The assumptions made in the infinite allele model and their links to phylogenetics are discussed in [5] and [4]: it is an approximation which neglects in particular the possibility that two mutations occur on the same base pair.

The results presented in this article are mostly derived in the limit of a large population. It is well known [4] that, for large N , all the relevant times in the genealogy (for example the age of the MRCA) scale like N . In the rest of this paper, we will therefore count the number G of generations in units of N and define the time by $t = G/N$.

In the remaining part of this introduction we recall some well known properties of the Wright–Fisher model that we will use later [4]. If one considers a finite number n of individuals, the probability that these individuals have only p parents in the previous generation and that they undergo m mutations scales as $1/N^{(n-p)+m}$: therefore, if one goes back one generation, there is a probability $1 - (n(n-1)/2 + n\theta)/N$ that the n individuals have different parents and that their genomes are identical to those of their parents. Moreover, there is a probability $n\theta/N$ of observing a single mutation among these n individuals and there is a probability $n(n-1)/(2N)$ that two among the n individuals

have the same parent. Therefore, when the size N of the population is large and for $n \ll N^{1/2}$, only pairs of branches coalesce along the tree. The time T_n to find the most recent common ancestor to these n individuals can be written as a sum of n independent times τ_i :

$$T_n = \tau_2 + \tau_3 + \cdots + \tau_n$$

where τ_i is the time spent between the i th and the $(i-1)$ th coalescence on the tree. This allows one to calculate the distributions $\rho_i(\tau_i)$, as shown in appendix A:

$$\rho_i(\tau_i) = c_i e^{-c_i \tau_i} \quad (1)$$

where the coefficients c_i are defined by

$$c_i = \frac{i(i-1)}{2}. \quad (2)$$

The generating function of the coalescence time T_n is therefore

$$\langle e^{-\lambda T_n} \rangle = \prod_{i=2}^n \frac{c_i}{\lambda + c_i}. \quad (3)$$

From (3), one can get the average and the variance of T_n :

$$\langle T_n \rangle = 2 \left(1 - \frac{1}{n} \right) \quad \text{and} \quad \langle T_n^2 \rangle - \langle T_n \rangle^2 = \frac{8}{n} - \frac{4}{n^2} - 12 + \sum_{j=1}^n \frac{8}{j^2}. \quad (4)$$

One can notice that the distribution of T_n remains broad even for large n . Although the expressions (4) are derived for fixed $n \ll N$ and in the limit $N \rightarrow \infty$, the limit $n \rightarrow \infty$ in (3) and (4) coincides with what would be obtained by setting $n = N$, i.e. by considering the time T to find the MRCA of the whole population:

$$\langle e^{-\lambda T} \rangle = \prod_{l=2}^{\infty} \frac{c_l}{\lambda + c_l}. \quad (5)$$

It leads to the expressions of the first two moments of the coalescence time,

$$\langle T \rangle = 2 \quad \text{and} \quad \langle T^2 \rangle - \langle T \rangle^2 = \frac{4\pi^2}{3} - 12 \simeq 1.159 \dots$$

and to the following stationary distribution: $\rho_{\text{st}}(T)$:

$$\rho_{\text{st}}(T) = \sum_{p=2}^{\infty} (-1)^p (2p-1) c_p e^{-c_p T}. \quad (6)$$

On the other hand, the stationary distribution of the genomes is given in [5]: the probability that, among n individuals, the first n_1 have the same genome, the next n_2 another genome, and so on until the last n_k which have the k th genome, is given by Ewens' sampling formula [22],

$$P_{\text{groups}}(n_1, \dots, n_k) = \frac{\Gamma(2\theta)}{\Gamma(n+2\theta)} (2\theta)^k \frac{n!}{n_1 n_2 \dots n_k} \quad (7)$$

where $\Gamma(x)$ is the Euler Γ function and θ the mutation rate.

There are several approaches to calculate the statistical properties of the above model: either one can write recursive equations between successive generations and try to solve them, or one can count directly all the possible coalescence and mutation histories of a group. The first approach leads to a hierarchy of equations, whereas the second option reduces to a simple enumeration. Depending on which of these two approaches appeared to us the simpler to implement, we use alternatively both of them in the present paper. A coalescence history as described in appendix A consists in a tree structure, in which each step corresponds to a coalescence of two individuals chosen randomly among the $n' \leq n$ which remain, and in a set of $n - 1$ times τ_i between two successive coalescences. A very important simplification (shown in appendix A) which we will use over and over is that the shape (i.e. the topology) of the trees and the times τ_i are independent random variables.

2. Statistics of the discontinuities of the coalescence time of the population

2.1. Numerical simulations

The Wright–Fisher model implemented for a population of $N = 500$ individuals shows interesting features for the evolution of the coalescence time T (see figure 2 for $G = 5000$ generations, corresponding to a normalized duration of $\Delta t = 10$). The evolution shows periods of linear increase, separated by discontinuous drops. Let us call the duration of the k th linear increase D_k and the height of the drop following it H_k . The distributions of the D_k and H_k , measured over 9169 discontinuities, are shown in figure 3. Similar results were previously reported in [1].

The data of figure 3 indicate that the delays D_k and the heights H_k have an exponential distribution of unit average. The correlations can also be measured (error bars of order of 0.01):

$$\langle D_k D_{k+1} \rangle - \langle D_k \rangle \langle D_{k+1} \rangle \simeq -0.005 \quad (8a)$$

$$\langle H_k H_{k+1} \rangle - \langle H_k \rangle \langle H_{k+1} \rangle \simeq -0.006 \quad (8b)$$

$$\langle H_{k-1} D_k \rangle - \langle H_{k-1} \rangle \langle D_k \rangle \simeq -0.002 \quad (8c)$$

$$\langle H_k D_k \rangle - \langle H_k \rangle \langle D_k \rangle \simeq 0.84 \quad (8d)$$

$$\langle H_k D_{k-1} \rangle - \langle H_k \rangle \langle D_{k-1} \rangle \simeq 0.12. \quad (8e)$$

This indicates that the only correlations seem to be between the H_k and the previous delays D_k . We try to understand these correlations below.

2.2. Distribution of delays between two discontinuities

When N is large, simultaneous coalescence between groups of three or more individuals are negligible (order $1/N^2$) at the top of the tree (i.e. for the last n coalescences with $n \ll \sqrt{N}$, only coalescences of pairs occur). Thus, as shown in figure 1, all the population in the present generation is generated by the two individuals A_1 and A_2 reached at the penultimate coalescence and thus it can be divided into two groups according to these two

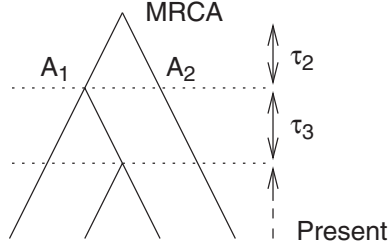


Figure 1. The top of the genealogical tree of a large population. When the size N of the population is large, coalescences at the top of the tree occur only among pairs of individuals and the coalescence times τ_i are independent random variables. One can see that the two ancestors A_1 and A_2 generate all the population in the present generation.

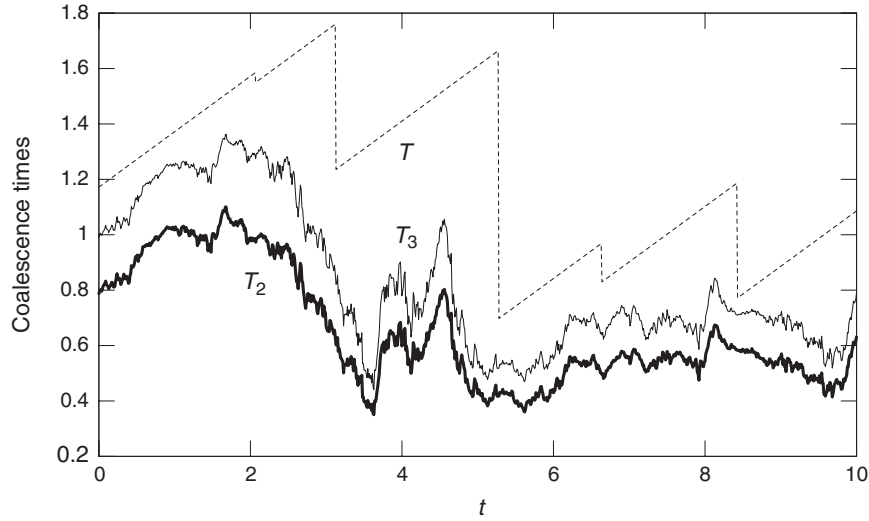


Figure 2. Evolution of the age $T = G/N$ of the MRCA for a population of $N = 500$ individuals in the Wright–Fisher model over a rescaled duration $\Delta t = 10$, i.e. over $N\Delta t = 10N$ generations (dashed line). Thick line, average T_2 over the whole population of the coalescence time of two individuals; thin line, average T_3 over the whole population of the coalescence time of three individuals. One can see that discontinuities are anticipated by the decreases of the average coalescence time of two or three individuals.

ancestors. A discontinuity appears in the age of the MRCA when one of the two groups generated by A_1 and A_2 has no offspring. The dynamics of the sizes N_i was studied in [1] by Serva, who showed numerically that the delays D_i have an exponential distribution:

$$p_{\text{delay}}(D) = e^{-D} \quad (9)$$

consistent with the results of figure 3.

In order to derive (9), let us introduce the probability $P_{\text{same}}(t_0, t)$ that the MRCA of a population is the same at time t_0 and at time t (with $t > t_0$), as in figure 4.

As explained above, the population at time t_0 can be divided into two parts of size $N_1 = xN$ and $N_2 = (1-x)N$ according to the ancestors A_1 and A_2 from which they come.

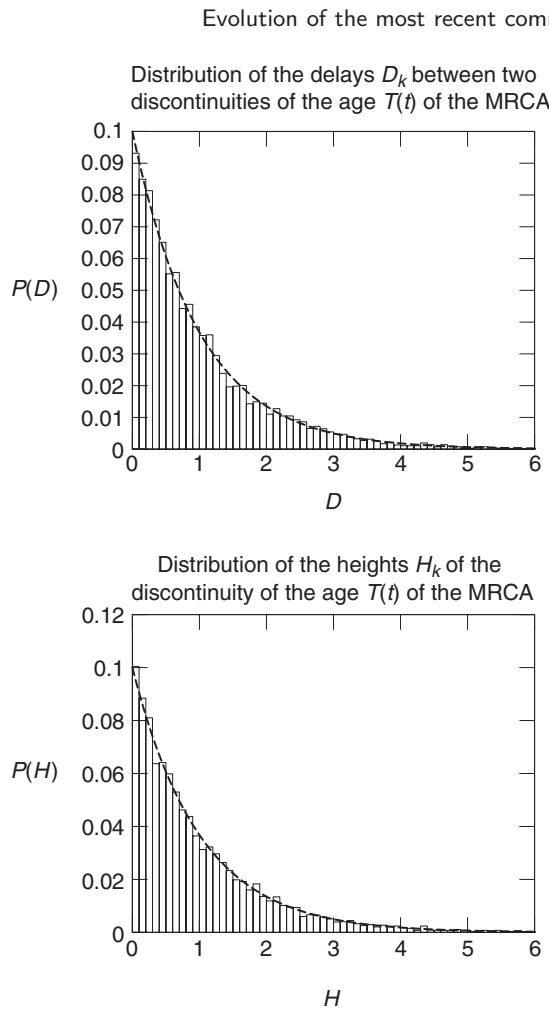


Figure 3. Measured distributions of the discontinuities of the age T of the MRCA for a sample of 9169 discontinuities when the population size is $N = 500$ individuals. Top: histogram of the distribution of the delays D_k between two successive discontinuities; the dashed line is the exponential distribution (9). Bottom: histogram of the distribution of the jumps H_k at the discontinuities of T ; the dashed line is the exponential distribution (31).

The sizes of these two groups are N_1 and $N_2 = N - N_1$ and one can define the densities $x = N_1/N$ and $1 - x = N_2/N$. At a given generation, x is a random variable in $[0, 1]$. Its stochastic evolution is given by the Wright–Fisher rule (see [1] for an analogy with Brownian motion) and its stationary distribution $\rho(x)$ is uniform on $[0, 1]$ for x of order unity (see [1] or appendix A for a short derivation). There are finite size corrections to this uniform distribution near the boundaries for $x = O(1/N)$ and $1 - x = O(1/N)$; we will not discuss them here as they have no incidence on what follows.

The MRCA of the population at time t is the same as the one of the population at time t_0 if and only if the ancestors A_1 and A_2 still have descendants in the population at time t . If m is the number of ancestors at time t_0 of the population at time t , this means that some of these m ancestors should be present in both groups of size N_1 and N_2 coming from A_1 and A_2 (see figure 4). As the probabilities for each of the m to belong to

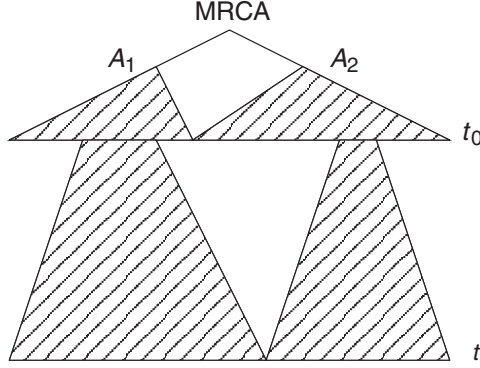


Figure 4. Structure of the genealogical tree of the population when the MRCA is the same at t_0 and t . The population at t must have ancestors at t_0 in each of the two groups generated by A_1 and A_2 .

the first or the second group are x and $1 - x$, the probability that both groups contains at least one of these m ancestors is $1 - (1 - x)^m - x^m$.

If one introduces the probability $z_m(t - t_0)$ that the population at time t has m ancestors in the population at time $t_0 < t$, the probability $P_{\text{same}}(t_0, t)$ is given by

$$P_{\text{same}}(t_0, t) = \int_0^1 dx \sum_{m=2}^{\infty} z_m(t - t_0) (1 - (1 - x)^m - x^m). \quad (10)$$

The functions $z_m(t)$ are known [16]. They satisfy recursive equations: the probability that the number of ancestors at $t_0 < t$ of a population at t is m is the sum of the probability that this number is m at time $t_0 + dt$ with no coalescence among these m during dt and of the probability that there are $m + 1$ ancestors at $t_0 + dt$ with a coalescence between t_0 and $t_0 + dt$. Therefore, the functions z_m satisfy

$$\frac{d}{d\tau} z_m(\tau) = c_{m+1} z_{m+1}(\tau) - c_m z_m(\tau). \quad (11)$$

The function $z_1(\tau)$ is known as it is related to the distribution (6) of the age T of the MRCA:

$$\frac{d}{d\tau} z_1(\tau) = \rho_{\text{st}}(\tau) \quad \text{and} \quad z_1(0) = 0.$$

The solution of (11) is [16]

$$z_m(\tau) = \sum_{p=m}^{\infty} (-1)^{p+m} \frac{(2p-1)(m+p-2)!}{m!(m-1)!(p-m)!} e^{-c_p \tau}. \quad (12)$$

Using the normalization $\sum_{m=1}^{\infty} z_m(\tau) = 1$ and the fact that x is uniformly distributed between zero and unity, one gets

$$\begin{aligned} P_{\text{same}}(t_0, t) &= 1 - z_1(t - t_0) - \sum_{m=2}^{\infty} \frac{2}{m+1} z_m(t - t_0) \\ &= \sum_{p=2}^{\infty} (-1)^p (2p-1) e^{-c_p(t-t_0)} \left[1 - 2 \sum_{m=2}^p \frac{(-1)^m (m+p-2)!}{(m+1)!(m-1)!(p-m)!} \right]. \end{aligned} \quad (13)$$

Using the identity

$$\sum_{m=2}^p \frac{(-1)^m (m+p-2)!}{(m+1)!(m-1)!(p-m)!} = \begin{cases} 1/3 & \text{if } p = 2 \\ 1/2 & \text{if } p \geq 3 \end{cases}$$

one can see that all the exponentials in (13) vanish except the one for $p = 2$, and one obtains

$$P_{\text{same}}(t_0, t) = e^{-(t-t_0)}. \quad (14)$$

This shows that the delays D_k between two successive jumps are distributed according to (9):

$$p_{\text{delay}}(D) = \frac{dP_{\text{same}}}{dt}(0, t = D) = e^{-D}.$$

2.3. The coalescence times τ_i as a Markov process

Figure 5 shows the stochastic dynamics of the coalescence time τ_2 . Actually, all the elementary times τ_i of figure 1 have similar dynamics. The coalescence times τ_i are the waiting times between two successive coalescences in a genealogy (see figure 1) and evolve when extinctions of lineages occur. For example, if the lineage of A_2 in figure 1 becomes extinct, then the new MRCA is A_1 and the new time τ'_2 is the former τ_3 . This change implies a global shift $\tau'_i = \tau_{i+1}$ for $i \geq 2$. On the other hand, if the lineage of A_1 on the left becomes extinct, the MRCA does not change but the τ_i become $\tau'_2 = \tau_2 + \tau_3$ and $\tau'_i = \tau_{i+1}$ for $i \geq 3$.

More generally, one can consider the top of the genealogical tree of a population where the number of ancestors is less than or equal to n . In this part of the tree, there are $n-1$ coalescence times τ_2, \dots, τ_n . The n leaves of the tree generate all the population in the present generation. The dynamics of the τ_i is controlled by the extinctions of the n lineages coming from these n ancestors: whenever one of them becomes extinct, some of the times τ_i topple.

Actually, the observed dynamics of the τ_i can be described by the large n limit of the following stochastic process: either no extinction occurs and the times τ_i remain unchanged,

$$\tau_j(t+dt) = \tau_j(t) \quad \text{with probability } 1 - \frac{n(n-1)}{2} dt \quad (15)$$

or an extinction occurs and, with probability $p_i dt$ for $2 \leq i \leq n-1$, the times topple at rank i ,

$$\begin{aligned} \tau_j(t+dt) &= \tau_j(t) & \text{for } j < i \\ \tau_i(t+dt) &= \tau_i(t) + \tau_{i+1}(t) \\ \tau_j(t+dt) &= \tau_{j+1}(t) & \text{for } i+1 \leq j \leq n-1 \\ \tau_n(t+dt) &= \epsilon_n(t). \end{aligned} \quad (16)$$

Moreover, with probability $p_1 dt$, for $i = 1$, all the times τ_j are shifted:

$$\begin{aligned} \tau_j(t+dt) &= \tau_{j+1}(t) & \text{for } 2 \leq j \leq n-1 \\ \tau_n(t+dt) &= \epsilon_n(t). \end{aligned} \quad (17)$$

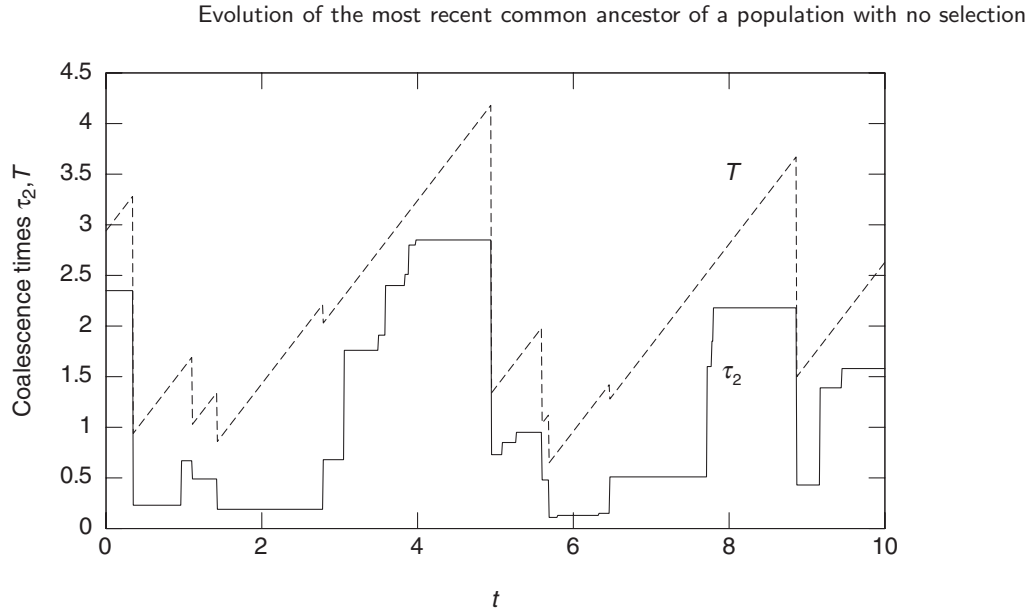


Figure 5. Evolution of the delay τ_2 between the two oldest coalescences at the top of the genealogical tree of a population of 100 individuals at time t . The dashed line corresponds to the age T of the MRCA: its shape is similar to figure 2. The study of the dynamics of τ_2 shows that, at random times depending on extinctions, the time τ_2 either increases by τ_3 or is reset to τ_3 , so that the new τ_2' is given either by $\tau_2 + \tau_3$ or by τ_3 .

In appendix B, we show that the toppling rates p_i are given by

$$p_i = i. \quad (18)$$

To determine the dynamics of τ_n , we need to specify $\epsilon_n(t)$: the $\epsilon_n(t)$ are random numbers uncorrelated in time which must have the same average as τ_n : $\langle \epsilon_n \rangle = \langle \tau_n \rangle = 2/(n(n-1))$. We will see however that, when n is large, the precise form of the distribution of the ϵ_n plays no role as long as $\langle \epsilon_n \rangle = \langle \tau_n \rangle$. This feature can be understood because $c_n = n(n-1)/2$ goes to infinity when n becomes large; therefore, the larger n is, the more often the time τ_n is reset and a new ϵ_n enters the system; in any time interval, the time τ_n is reset so many times with many independent ϵ_n 's entering the system that only $\langle \epsilon_n \rangle$ matters because of the law of large numbers.

The value of $\langle \epsilon_n \rangle$ can also be understood through the stationary conditions: ϵ_n is added to the system with a rate c_n whereas τ_2 is removed with a rate 1. The system can reach a stationary state only if $\langle \epsilon_n \rangle c_n = \langle \tau_2 \rangle = 1$. Another consequence is that the total coalescence time $T(t) = \sum_{i=2}^n \tau_i$ increases on average by $c_n \langle \epsilon_n \rangle \Delta t = \Delta t$ during Δt when no discontinuity occurs, in agreement with the unit slope observed in figures 2 and 5.

These simple dynamics of the times τ_i allow one to determine all the statistical properties of $T(t)$: its correlations at different times, the distribution of its discontinuities H_k and the distribution of the coalescence times T right before a discontinuity.

First, within this picture, it becomes obvious that the distribution of delays between successive discontinuities of T is exponential. The toppling dynamics (16) also imply that, at a given time t , all the $\tau_i(t)$ are sums of the times $\tau_j(0)$ with $j \geq i$ and of the ϵ_n . These sums do not overlap and thus, if the initial times $\tau_i(t)$ are not correlated at $t = 0$, they

remain uncorrelated at any later times. However, any τ_i depends only on previous τ_j with $i \leq j$ such that the only non-zero correlations in this system are the $G_{i,j}(t)$ with $i \leq j$ defined as

$$G_{i,j}(t) = \langle \tau_i(t) \tau_j(0) \rangle - \langle \tau_i(t) \rangle \langle \tau_j(0) \rangle. \quad (19)$$

A consequence of (16) and (17) is that

$$\tau_i(t + dt) = \begin{cases} \tau_i(t) & \text{with probability } 1 - c_{i+1} dt \\ \tau_i(t) + \tau_{i+1}(t) & \text{with probability } i dt \\ \tau_{i+1}(t) & \text{with probability } c_i dt. \end{cases} \quad (20)$$

Therefore, $G_{i,j}$ satisfies the following differential equation:

$$\partial_t G_{i,j}(t) = -c_i G_{i,j}(t) + c_{i+1} G_{i+1,j}(t). \quad (21)$$

The initial conditions correspond to the times τ_i generated according to the stationary distribution (1) and thus one has $G_{i,j}(0) = \delta_{ij}/c_i^2$. We have seen that $G_{i,j}(t) = 0$ if $i \geq j+1$ and this gives immediately the solution of (21) for $i = j$:

$$G_{j,j}(t) = \frac{1}{c_j^2} e^{-c_j t}. \quad (22)$$

More generally, the Laplace transform $\hat{G}_{i,j}(\lambda) = \int_0^\infty e^{-\lambda t} G_{i,j}(t) dt$ is given by the following product:

$$\hat{G}_{i,j}(\lambda) = \frac{1}{c_i c_j^2} \prod_{l=i}^j \frac{c_l}{\lambda + c_l}. \quad (23)$$

In particular, the correlation function of the total coalescence time $T(t) = \tau_2(t) + \tau_3(t) + \dots$ can be written as

$$\begin{aligned} \langle T(t) T(0) \rangle - \langle T(t) \rangle \langle T(0) \rangle &= \sum_{i,j} \langle \tau_i(t) \tau_j(0) \rangle - \langle \tau_i(t) \rangle \langle \tau_j(0) \rangle \\ &= \sum_{i=2}^{\infty} \sum_{j=2}^{\infty} G_{i,j}(t). \end{aligned} \quad (24)$$

In principle, (23) and (24) allow one to extract the explicit expression of the autocorrelation function of T . We will describe later an alternative method to determine this explicit expression.

The dynamics (16) also gives the statistical properties of the τ_i at the time of the discontinuity. In particular, we are going to show that the distribution of the total coalescence time $T(t)$ right before a discontinuity is equal to the stationary distribution (6).

First, we remark from (16) that a discontinuity occurs when τ_2 is thrown out of the system. More precisely, the height H_k is equal to this τ_2 just before the discontinuity and the distribution of each τ_i just after the jump is the distribution of τ_{i+1} before the jump. Moreover, if the process is started at time zero just after a discontinuity (i.e. we choose a discontinuity of T as origin of time), one can introduce a variable $\eta(t)$ defined as

$$\eta(t) = \begin{cases} 1 & \text{before the next discontinuity of } T \\ 0 & \text{after the next discontinuity of } T. \end{cases} \quad (25)$$

The dynamics (16) implies that the average $\langle \eta \rangle$ decays exponentially as $\langle \eta(t) \rangle = e^{-t}$. The introduction of η allows us to study what happens between discontinuities. In particular, the generating function $G^{(-)}(\lambda) = \langle e^{-\lambda T} \rangle_{\text{before}}$ of the coalescence time $T(t)$ right *before* a discontinuity takes the form

$$G^{(-)}(\lambda) = \langle e^{-\lambda T} \rangle_{\text{before}} = \int_0^\infty \langle \eta(t) e^{-\lambda T(t)} \rangle dt. \quad (26)$$

From (16), the correlation function $\langle \eta(t) e^{-\lambda T(t)} \rangle$ satisfies

$$\partial_t \langle \eta(t) e^{-\lambda T(t)} \rangle = -c_n \langle \eta(t) e^{-\lambda T(t)} \rangle + (c_n - 1) \langle \eta(t) e^{-\lambda T(t)} \rangle \langle e^{-\lambda \epsilon_n} \rangle.$$

Integrating over t , one gets for $G^{(-)}(\lambda)$ from (26)

$$G^{(-)}(\lambda) = \frac{1}{c_n - (c_n - 1) \langle e^{-\lambda \epsilon_n} \rangle} G^{(+)}(\lambda) \quad (27)$$

where $G^{(+)}(\lambda) = \langle e^{-\lambda T} \rangle_{\text{after}}$ is the generating function of the total coalescence time right *after* the discontinuity.

On the other hand, the stationary distribution can also be written in terms of $G^{(+)}$. The generating function $\langle e^{-\lambda T(t)} \rangle$ of $T(t)$ satisfies

$$\langle e^{-\lambda(T(t)+dt)} \rangle = (1 - c_n dt) \langle e^{-\lambda T(t)} \rangle + dt \langle e^{-\lambda T(t)} \rangle_{\text{after}} + (c_n - 1) \langle e^{-\lambda T(t)} \rangle \langle e^{-\lambda \epsilon_n} \rangle. \quad (28)$$

Thus, the stationary generating function is given by

$$G_{\text{st}} = \langle e^{-\lambda T(t)} \rangle_{\text{st}} = \frac{1}{c_n - (c_n - 1) \langle e^{-\lambda \epsilon_n} \rangle} G^{(+)}(\lambda). \quad (29)$$

Comparing (27) and (29), we see that

$$G^{(-)}(\lambda) = \langle e^{-\lambda T} \rangle_{\text{before}} = \langle e^{-\lambda T(t)} \rangle_{\text{st}} = G_{\text{st}}(\lambda). \quad (30)$$

This result, which we checked in our simulations, looks paradoxical: although $T(t)$ reaches a local maximum when the MRCA changes, the distribution of T at these local maxima is the same as the distribution of $T(t)$ over the whole range of time. In fact, one can show by similar calculations that the same is true for all the τ_i : their distributions right before a discontinuity of T are the same as the stationary ones. The case of τ_2 explains the properties of the drops H_k at the discontinuities of T , since the value of H_k is the value of τ_2 just before the discontinuity. Their distribution is exponential:

$$p_{\text{height}}(H) = e^{-H} \quad (31)$$

which is in agreement with the data of figure 3. Moreover, the H_k are not correlated in agreement with (8b), as if $H_k = \tau_2$, then H_{k+1} is made of some τ_j with $j \geq 3$ at the time of the previous discontinuity.

One also sees from (16) that, just after the discontinuity, τ_i is replaced by τ_{i+1} just before the discontinuity, which was distributed according to the stationary distribution (1). Thus the distribution $G^{(+)}$ should be given by a formula similar to (5) starting only at $l = 3$. The comparison with (29) implies that the factor $1/(c_n - (c_n - 1) \langle e^{-\lambda \epsilon_n} \rangle)$ should become $1/(\lambda + 1)$ for the large n limit. This is easily checked as $\epsilon_n \sim 1/n^2$ and for large n

$$\langle e^{-\lambda \epsilon_n} \rangle = 1 - \lambda \langle \epsilon_n \rangle + o(1/n^2).$$

This in particular shows that for large n only the average of $\langle \epsilon_n \rangle$ matters.

The analytical value of (8d) can also be obtained using the toppling dynamics of the τ_i . Using the variable $\eta(t)$ defined in (25), the delay D_k is the time at which $\eta(t)$ goes to zero and the height H_k is the time τ_2 right before the drop. The correlation coefficient is given by

$$\langle D_k H_k \rangle = \int_0^\infty t \langle \eta(t) \tau_2(t) \rangle dt.$$

This suggests considering the functions $\psi_i(\lambda) = \int_0^\infty e^{-\lambda t} \langle \eta(t) \tau_i(t) \rangle dt$, as the correlation coefficient is $\langle DH \rangle = -d\psi_2/d\lambda$ for $\lambda = 0$. The coefficients $\langle \eta(t) \tau_i(t) \rangle$ satisfy the following differential equation derived from (16) and (20):

$$\frac{d}{dt} \langle \eta(t) \tau_i(t) \rangle = -c_i \langle \eta(t) \tau_i(t) \rangle + (c_{i+1} - 1) \langle \eta(t) \tau_{i+1}(t) \rangle. \quad (32)$$

At $t = 0$, $\eta(t) = 1$ and τ_i is distributed according to ρ_{i+1} given by (1), since we saw in (17) that there is a global shift of the τ_i at each discontinuity of T . This implies that the functions ψ_i satisfy the following recursion:

$$\lambda \psi_i(\lambda) - \frac{1}{c_{i+1}} = -c_i \psi_i(\lambda) + (c_{i+1} - 1) \psi_{i+1}(\lambda). \quad (33)$$

As we need the first derivative of ψ_2 in zero, we can expand ψ_i in powers of λ :

$$\psi(\lambda) = \frac{2}{i(i+1)} (u_i - \lambda v_i + O(\lambda^2)). \quad (34)$$

The coefficients u_i and v_i satisfy the following simple recursion derived from (33):

$$u_i = \frac{2}{i(i-1)} + u_{i+1} \quad (35a)$$

$$v_i = \frac{u_i}{i(i-1)} + v_{i+1}. \quad (35b)$$

The term ψ_{n+1} is linked to the boundary condition ϵ_n and one has $\psi_{n+1}(\lambda) = \langle \epsilon_n \rangle / (1 + \lambda)$ so that $u_{n+1} = \langle \epsilon_n \rangle (n+1)(n+2)/2$ and $v_{n+1} = \langle \epsilon_n \rangle (n+1)(n+2)/2$ (which are not negligible when $n \rightarrow \infty$). Equations (35a) and (35b) lead to simple summation formulae for u_i and v_i :

$$u_i = \sum_{j=i}^n \frac{2}{j(j-1)} + \langle \epsilon_n \rangle (n+1)(n+2)/2 \xrightarrow{n \rightarrow \infty} \frac{2}{i-1} + 1 \quad (36a)$$

$$v_i = \sum_{j=1}^n \frac{u_j}{j(j-1)} + \langle \epsilon_n \rangle (n+1)(n+2)/2 \xrightarrow{n \rightarrow \infty} \frac{2\pi^2}{3} + 1 - \frac{2}{i-1}. \quad (36b)$$

Finally, the expansion of ψ_2 around $\lambda = 0$ gives the following correlation coefficient in good agreement with the measured value (8d):

$$\langle D_k H_k \rangle - \langle D_k \rangle \langle H_k \rangle = \frac{2\pi^2}{9} - \frac{4}{3} \simeq 0.8599 \dots \quad (37)$$

2.4. Correlation functions of the coalescence times between a few individuals

Consider a pair (i, j) of individuals at generation t . One can define the time $T^{(i,j)}(t)$ to find their first common ancestor (i.e. $NT^{(i,j)}(t)$ is the number of generations to reach their first common ancestor). Similarly, one may consider three individuals (i, j, k) at generation t and define the time $T^{(i,j,k)}(t)$ to find their first common ancestor. One can average these times over the whole population:

$$T_2(t) = \frac{1}{N^2} \sum_{i,j} T^{(i,j)}(t) \quad (38)$$

$$T_3(t) = \frac{1}{N^3} \sum_{i,j,k} T^{(i,j,k)}(t). \quad (39)$$

Figure 2 shows the stochastic evolution of these averages $T_2(t)$ and $T_3(t)$. We are now going to determine the correlation functions of these times (in order to avoid confusion, we will use lower case letters t for the usual time (oriented towards the future) and upper case letter T for ages (i.e. oriented towards the past)).

To understand the correlations of $T_2(t)$ and $T_3(t)$, let us look at two individuals i and j at generation t and two individuals k and l at generation 0. Their coalescence times are defined as $T^{(i,j)}(t)$ and $T^{(k,l)}(0)$. There are two possibilities:

- either $T^{(i,j)}$ is smaller than t and the coalescence times $T^{(i,j)}(t)$ and $T^{(k,l)}(0)$ are independent,
- $T^{(i,j)}$ is larger than t and the entanglement between lineages creates a correlation between $T^{(k,l)}(0)$ and $T^{(i,j)} - t$. In the large population limit $N \rightarrow \infty$, the probability that the ancestors of i and j are k or l goes to zero as $1/N$; thus, in the second case, the quantity $\langle (T^{(i,j)}(t) - t)T^{(k,l)}(0) \rangle$ is the average of the product of the coalescence times of two distinct pairs of individuals at the generation 0.

As a result, the average over the population $T_2(t)$ of the coalescences times of two individuals $T_2^{(i,j)}$ satisfies

$$\langle T_2(t)T_2(0) \rangle_{N \rightarrow \infty} = \int_0^t \rho_2(\tau_2)\tau_2 d\tau_2 \times \langle T_2(0) \rangle + e^{-t}(t\langle T_2(0) \rangle + \langle T^{(1,2)}(0)T^{(3,4)}(0) \rangle). \quad (40)$$

The coefficient $\langle T^{(1,2)}(0)T^{(3,4)}(0) \rangle$ can be calculated by looking at the genealogy of only four individuals. Following appendix A, the coalescence times $T^{(1,2)}(0)$ and $T^{(3,4)}(0)$ are sums of the three elementary coalescences times τ_2 , τ_3 and τ_4 . These decompositions are shown in figure 6. Averaging over the tree structures and the times τ_i leads to

$$\langle T_2(t)T_2(0) \rangle = 1 + \frac{2}{9}e^{-t}. \quad (41)$$

A similar calculation of the coalescence time of three individuals leads to

$$\langle T_3(t)T_3(0) \rangle = \frac{16}{9} + \frac{29}{60}e^{-t} - \frac{13}{900}e^{-3t}. \quad (42)$$

More generally, the correlation functions of coalescence times T_m would be a linear combination of $e^{-c_p t}$ weighted by coefficients. The calculation of the correlation function of the T_m becomes however more and more complicated with increasing m . We have only been able to determine the correlation function $\langle T(t)T(0) \rangle - \langle T(t) \rangle \langle T(0) \rangle$ of the

Evolution of the most recent common ancestor of a population with no selection


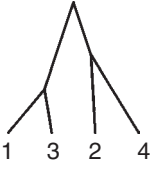

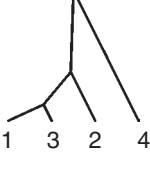
Tree structure	$T(1,2)$	$T(3,4)$	Symmetry factor
	τ_4	$\tau_4 + \tau_3$	$\frac{2}{18}$
	$\tau_4 + \tau_3 + \tau_2$	$\tau_4 + \tau_3 + \tau_2$	$\frac{4}{18}$
	τ_4	$\tau_4 + \tau_3 + \tau_2$	$\frac{4}{18}$
	$\tau_4 + \tau_3$	$\tau_4 + \tau_3 + \tau_2$	$\frac{8}{18}$

Figure 6. Genealogical trees of four individuals 1, 2, 3 and 4 and the corresponding decomposition of the coalescence times of individuals 1 and 2 on one hand, and 3 and 4 on the other hand. Up to symmetries, there are only these four types of decomposition: any other tree leads to the same type of decomposition (up to permutations of the labels or of the roles of (1, 2) and (3, 4)). The symmetry factors count these relabellings.

coalescence time of the whole population represented in figure 2. As for T_2 , one has to consider two cases: either the MRCA of the population at t is reached between 0 and t so that $T(t) < t$, or the number of ancestors at 0 is $m \geq 2$ so that $T(t) = t + T_m(0) > t$. If $z_m(\tau)$ is the probability (12) that the number of ancestors of the population after a duration τ in the past is m , we have the following decomposition:

$$\langle T(t)T(0) \rangle = \int_0^t \tau z'_1(\tau) d\tau \times \langle T(0) \rangle + \sum_{m \geq 2} z_m(t) \langle (t + T_m(0))T(0) \rangle \quad (43)$$

where $z'_1(\tau) = \rho_{st}(\tau) = \text{Prob}(T = \tau)$ is the probability that the MRCA is reached at τ .

The coefficients $\langle T_m(0)T(0) \rangle$ can be decomposed in a tree-dependent combination of the elementary times τ_i (see section 1 and appendix A) with

$$T_m(0) = \sum_{i=q+1}^{\infty} \tau_i \quad \text{and} \quad T(0) = \sum_{i=2}^{\infty} \tau_i \quad (44)$$

where q is the number of ancestors left from the whole population when the subgroup of size m has just coalesced. If $a_{m,\infty}(q)$ is the probability distribution of q , then one has

$$\langle T_m(0)T(0) \rangle = \sum_{q=1}^{\infty} a_{m,\infty}(q) \sum_{i=q+1}^{\infty} \sum_{j=2}^{\infty} \langle \tau_i \tau_j \rangle = \sum_{i=2}^{\infty} \left[\sum_{j=2}^{\infty} \langle \tau_i \tau_j \rangle \right] \left[\sum_{q=1}^{i-1} a_{m,\infty}(q) \right] \quad (45)$$

where the τ_i are independent random variables with exponential distribution (1).

Let us define $a_{m,n}(q)$ as the probability that the number of ancestors of a group of size $m+n$ is q at the time when the first subgroup of m individuals has just coalesced into a single ancestor. Writing all the possibilities for the first coalescence of the group of size $m+n$ leads to the following recursive equation:

$$a_{m,n}(q) = \frac{c_m a_{m-1,n}(q) + (c_n + nm) a_{m,n-1}(q)}{c_{n+m}}. \quad (46)$$

The boundary conditions are the probability that coalescences occur only among the first m if $q = n+1$,

$$a_{m,n}(n+1) = \prod_{i=2}^m \frac{c_i}{c_{i+n}} = \frac{m!(m-1)!n!(n+1)!}{(m+n)!(m+n-1)!}$$

and the probability for $m=2$ that two individuals coalesce once the n others are reduced to q ,

$$a_{2,n}(q) = \frac{c_2}{c_{q+1}} \prod_{j=q}^n \frac{c_j + 2j}{c_{j+2}} = \frac{2}{(q+2)(q+1)} \frac{n+3}{n+1}.$$

With these boundary conditions, one gets for the solution of (46)

$$a_{m,n}(q) = \frac{m!n!q!(m+n-q-1)!(m-1)(m+n+1)}{(q+m)!(m+n-1)!(n-q+1)!} \quad (47)$$

and in the limit $n \rightarrow \infty$

$$a_{m,\infty}(q) = \frac{q!m!(m-1)}{(m+q)!}. \quad (48)$$

One can check easily that

$$\sum_{q=1}^{i-1} a_{m,\infty}(q) = 1 - \frac{i!m!}{(m+i-1)!}. \quad (49)$$

Moreover, using (1), the correlation between τ_i and τ_j is

$$\langle \tau_i \tau_j \rangle = \frac{1}{c_i c_j} (1 + \delta_{ij}). \quad (50)$$

Using (50) and (49), the permutation of the sums in (45) gives the correlation coefficients $\langle T_m(0)T(0) \rangle$:

$$\begin{aligned} \langle T_m(0)T(0) \rangle &= \sum_{i=2}^{\infty} \left[\frac{1}{c_i^2} + \frac{2}{c_i} \right] \left[1 - \frac{i!m!}{(m+1-i)!} \right] \\ &= \sum_{i=2}^{\infty} \left(\frac{1}{c_i^2} + \frac{2}{c_i} \right) - 4 \sum_{i=2}^{\infty} \frac{m!(i-2)!}{(m+i-1)!} - \sum_{i=2}^{\infty} \frac{4m!i!}{i^2(i-1)^2(m+i-1)!}. \end{aligned}$$

The calculations of the first two sums give

$$\sum_{i=2}^{\infty} \left(\frac{1}{c_i^2} + \frac{2}{c_i} \right) = \frac{4\pi^2}{3} - 8$$

$$\sum_{i=2}^{\infty} \frac{m!(i-2)!}{(m+i-1)!} = \frac{1}{m}$$

and $\langle T_m(0)T(0) \rangle$ becomes

$$\langle T_m(0)T(0) \rangle = \frac{4\pi^2}{3} - 8 - \frac{4}{m} - \sum_{i=2}^{\infty} \frac{4m!i!}{i^2(i-1)^2(m+i-1)!}. \quad (51)$$

Finally, using the normalization $\sum_{m=1}^{\infty} z_m(t) = 1$ and the fact that $\langle T(0) \rangle = 2$, the integration of the first term of (43) leads to

$$\langle T(t)T(0) \rangle = 2 \int_0^t (1 - z_1(t)) dt + \sum_{m=2}^{\infty} \langle T_m(0)T(0) \rangle z_m(t).$$

By multiplying (11) by $1/m$ and summing over m , one gets

$$\frac{d}{d\tau} \left(\sum_{m=2}^{\infty} \frac{1}{m} z_m(\tau) \right) = -\frac{d}{d\tau} z_1(\tau) + \frac{1}{2}(1 - z_1(\tau)). \quad (52)$$

Since the sum $\sum_{m=2}^{\infty} z_m(\tau)/m$ must vanish for large τ , the solution of (52) is

$$\sum_{m=2}^{\infty} \frac{1}{m} z_m(t) = (1 - z_1(t)) - \frac{1}{2} \int_t^{\infty} (1 - z_1(t)) dt. \quad (53)$$

Using (51) and (53) one gets

$$\langle T(t)T(0) \rangle = 4 + \left(\frac{4\pi^2}{3} - 12 \right) (1 - z_1(t)) - \sum_{m=2}^{\infty} \sum_{i=2}^{\infty} \frac{4m!i!}{i^2(i-1)^2(m+i-1)!} z_m(t).$$

If one collects the exponential terms $e^{-c_p t}$ using (12), the correlation function takes the following form:

$$\langle T(t)T(0) \rangle - \langle T(t) \rangle \langle T(0) \rangle = \sum_{p=2}^{\infty} (-1)^p (2p-1) A_p e^{-c_p t} \quad (54)$$

with coefficients A_p given by

$$A_p = \frac{4\pi^2}{3} - 12 - \sum_{i=2}^{\infty} \sum_{m=2}^p \frac{4i!(-1)^m(m+p-2)!}{i^2(i-1)^2(m+i-1)!(m-1)!(p-m)!}. \quad (55)$$

One can show that the sum over m is given by

$$\sum_{m=2}^p \frac{(m+p-2)!(-1)^m}{(m+i-1)!(m-1)!(p-m)!} = \frac{1}{i!} - \begin{cases} 0 & \text{for } p > i \\ \frac{(i-1)!}{(p+i-1)!(i-p)!} & \text{for } i \geq p. \end{cases}$$

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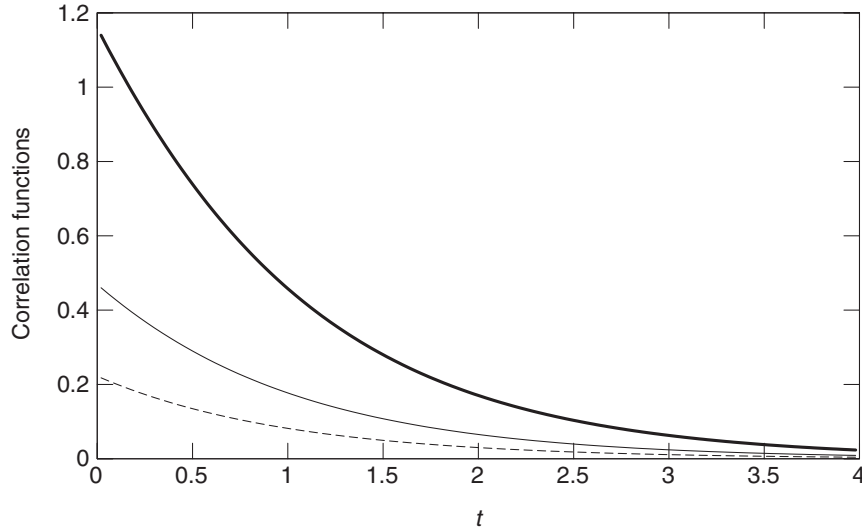


Figure 7. Correlation functions of the average over the population $T_2 = 1/(N^2) \sum_{i,j} T^{(i,j)}$ of the age of the MRCA for $n = 2$ individual (dashed), of the average $T_3 = 1/(N^3) \sum_{i,j,k} T^{(i,j,k)}$ of the age of the MRCA of $n = 3$ individuals (thin) and of the age $T(t)$ of the MRCA of the whole population (thick).

This identity gives finally the coefficient A_p :

$$A_p = 4 \sum_{i=p}^{\infty} \frac{(i-2)!^2}{i(i+p-1)!(i-p)!}. \quad (56)$$

One can notice that $A_p \rightarrow 0$ when $p \rightarrow \infty$. The correlation functions $\langle T_2(t)T_2(0) \rangle - \langle T_2(t) \rangle \langle T_2(0) \rangle$, $\langle T_3(t)T_3(0) \rangle - \langle T_3(t) \rangle \langle T_3(0) \rangle$ and $\langle T(t)T(0) \rangle - \langle T(t) \rangle \langle T(0) \rangle$ are shown in figure 7.

By a calculation not shown here, one can check that expressions (54) and (56) coincide with the one obtained from (24) and this confirms the validity of the Markov process defined in (16) and (17).

3. Correlation between the coalescence time and the genomic diversity

So far we have only considered the statistical properties of the coalescence times along the tree. We are going to study now how these times are correlated to the genetic diversity.

The genetic diversity can be measured by different quantities according to the model one considers (see for example Tajima's estimator for the infinite site model [14]). We consider here the case of an infinite number of alleles: any mutation creates a new allele which has never occurred before. Thus, for two individuals chosen at random in the population, there are only two possibilities: either they have the same allele or they have different ones. Now we want to calculate the average age of the MRCA, conditioned on the fact that the two individuals chosen at random have (or not) the same genome.

More generally, the population is divided into groups of individuals sharing the same genome, whose sizes characterize the genetic diversity of the population. The

determination of the distribution of the age of the MRCA, given the size of these groups, is a difficult problem that we could not solve. Here we address a simpler version of this problem: suppose we have some information about the genes of a few individuals chosen at random in the population; what can be said about the age of the MRCA?

In the present case, we consider a group of $n \ll N$ individuals and we suppose that the first m of them have identical genomes. Of course, the $n - m$ others may have the same genome or different ones: we suppose that we have no information about them. Knowing this partial information about the present generation, we look at the coalescence time of the whole group of n individuals.

We first consider the probability distribution $p_{m,n}(T_n)$ of observing a group of size n whose coalescence time is equal to T_n and in which the first m individuals have the same genome. The coalescence time T_n of such a group of size n is the coalescence time of their parents at the previous generation plus one generation. The group of the parents is a group of size $n' \leq n$. At first order in $1/N$, the only possible events which may occur are a coalescence ($n' = n - 1$) or a mutation ($n' = n$). The probability of a coalescence among the first m individuals is $c_m/N = m(m - 1)/2N$; in this case, the probability distribution of the coalescence time of the parents is $p_{m-1,n}$. For other coalescences (probability $(c_n - c_m)/N$), it is $p_{m,n-1}$. Moreover, no mutation must affect the first m individuals. Consequently, the probability distribution $p_{m,n}(T)$ satisfies the following recursive equation:

$$\frac{d}{dT} p_{m,n}(T) = c_m p_{m-1,n-1}(T) + (c_n - c_m) p_{m,n-1}(T) - (c_n + m\theta) p_{m,n}(T) \quad (57)$$

where the c_n are the binomial coefficient (2).

For $m = 1$, the distribution $p_{1,n}$ is just the stationary distribution of T_n related to (3). For $n = m$, $p_{m,m}$ is the distribution of the coalescence time of a group of m individuals with the same genome. Its Laplace transform is [4]

$$\hat{p}_{m,m}(s) = \int_0^\infty p_{m,m}(t) e^{-st} dt = \prod_{i=2}^m \frac{c_i}{s + c_i + i\theta}. \quad (58)$$

The general solution of (57), which we will give below in (66), is difficult to handle in general. Let us consider first the simple case $m = 2$ and define the parameter Y related to the genomic diversity as

$$Y = \frac{1}{N(N-1)} \sum_{i \neq j} \delta_{g(i),g(j)} \quad (59)$$

where $g(i)$ is the genome of the individual i . Y does not count the number of differences between two sequences (as does Tajima's estimator [14]), since we do not suppose any information about the structure of the genome, but just detects whether at least one mutation has occurred or not, and can be interpreted as the fraction of pairs of individuals having the same genome. When Y is close to unity the population is very homogeneous and all the individuals have very similar genomes, whereas Y close to zero corresponds to a population where the genetic diversity is very large. From the definition of $p_{m,n}$, one gets

$$\hat{p}_{2,\infty}(s) = \langle Y e^{-sT} \rangle \quad (60)$$

where $\hat{p}_{2,\infty}(s)$ is the limit for large n of the generating functions $\hat{p}_{2,n}(s)$ that satisfy a recursion directly deduced from (57):

$$\hat{p}_{2,n}(s) = \frac{1}{s + c_n + 2\theta} (\hat{p}_{n-1}(s) + (c_n - 1)\hat{p}_{2,n-1}(s)) \quad (61)$$

where $\hat{p}_n(s) = \langle e^{-sT_n} \rangle$ is the generating function with no information (3). The solution of (61) (which is a particular case of the general solution (66) given below) is

$$\hat{p}_{2,\infty}(s) = \langle Y e^{-sT} \rangle = \sum_{q=1}^{\infty} \frac{2}{(q+2)(q+1)} \prod_{i=2}^q \frac{c_i}{s + c_i} \prod_{j=q+1}^{\infty} \frac{c_j}{s + c_j + 2\theta}. \quad (62)$$

It allows one to determine the distribution of the coalescence time of the whole population, conditioned on the fact that two individuals chosen at random have the same genome. Moreover, taking successive derivations of (62) at $s = 0$ gives all the correlation coefficients $\langle Y T^k \rangle$. The following computation focuses on the properties of the average coalescence time $\langle T | 2 \text{ id} \rangle$ knowing that two individuals chosen at random have the same genome.

The average coalescence time T_n of n individuals conditioned on the fact that two individuals chosen at random among these n have the same genome can also be obtained from (57). The Laplace transform $\hat{p}_{m,n}(s) = \int_0^{\infty} e^{-sT} p_{m,n}(T) dT$ for $s = 0$ gives the probability that the first m individuals of the group of size n have the same genome (see (7)). Thus the normalized quantity $\hat{p}_{m,n}(s)/\hat{p}_{m,n}(0)$ is the generating function of the coalescence time of n individuals conditioned on the fact that m individuals chosen at random among them have the same genome. For $m = 2$, one has $\hat{p}_{2,n}(0) = 1/(1 + 2\theta)$. The average conditioned time is the derivative of $\hat{p}_{m,n}(s)/\hat{p}_{m,n}(0)$ for $s = 0$:

$$u_n(\theta) = \langle T_n | 2 \text{ id} \rangle = -(1 + 2\theta) \left. \frac{d}{ds} \hat{p}_{2,n}(s) \right|_{s=0}.$$

By taking the derivative of (61) one gets

$$u_n(\theta) = \frac{1}{c_n + 2\theta} \left(1 + 2(1 + 2\theta) \frac{n-2}{n-1} + (c_n - 1)u_{n-1}(\theta) \right). \quad (63)$$

The initial condition is given by the coalescence time of two individuals with the same genome:

$$u_2(\theta) = \frac{1}{1 + 2\theta}.$$

The general solution of (63) is given by

$$u_n(\theta) = \frac{2(n-2)}{n-1} + \frac{1}{1+2\theta} + \sum_{p=3}^n \frac{(-1)^p}{c_p + 2\theta} \frac{(n+1)!(n-2)!}{(n+p-1)!(n-p)!} \frac{(2p-1)(p+1)(p-2)}{2}. \quad (64)$$

If $\theta = 0$, all the individuals have the same genome and the value of $u_n(\theta)$ for $\theta = 0$ is just $2(n-1)/n$ as given by (4). The large n limit of (64) (performed by considering $u_n(\theta) - u_n(0)$ to regularize the series) leads for the average coalescence time $\langle T | 2 \text{ id} \rangle$ of

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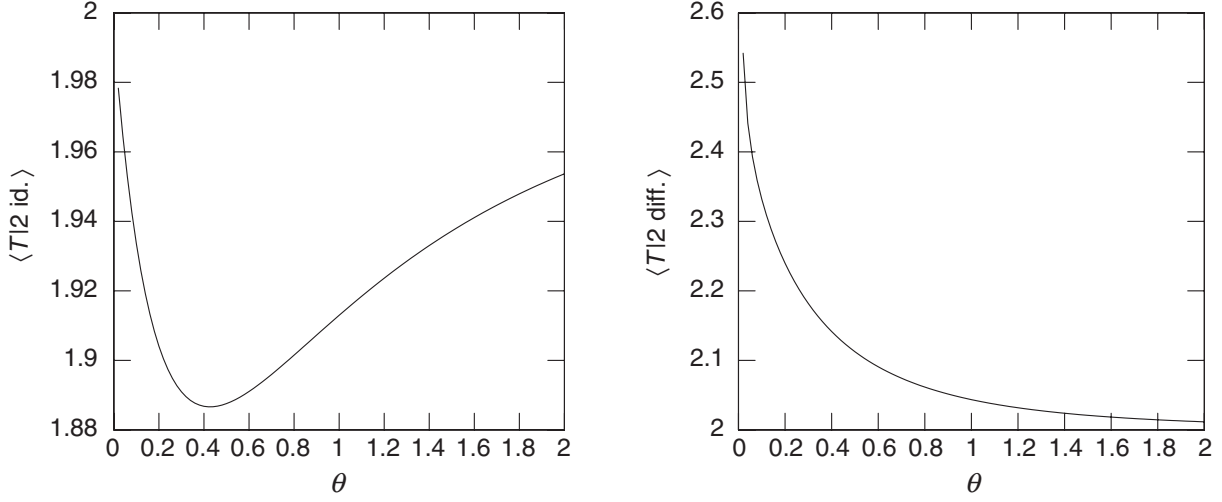


Figure 8. Average coalescence time of a whole population of large size knowing that two individuals chosen at random have the same genome (left) or different genomes (right). Without conditioning on the genomes of the two individuals, the average coalescence time would be $\langle T \rangle = 2$.

a whole population conditioned on the fact that two individuals chosen at random have identical genomes to

$$\langle T|2 \text{ id} \rangle = 1 + \frac{1}{1+2\theta} - 2\theta \sum_{p=3}^{\infty} \frac{(2p-1)(p+1)(p-2)}{2} \frac{(-1)^p}{c_p(c_p+2\theta)}. \quad (65)$$

The θ dependence of this average coalescence time is shown in figure 8. Although Y is a rough estimator of the genetic diversity and we consider only information about two individuals, $\langle T|2 \text{ id} \rangle$ is shifted up to 5% compared to the case of no information.

One can write down a general expression for the Laplace transform $\hat{p}_{m,n}(s) = \int_0^\infty p_{m,n}(t)e^{-st} dt$ of the solution of (57):

$$\hat{p}_{m,n}(s) = \sum_{1 \leq n_1 < \dots < n_m = n} \left(\frac{B_{n,m}(n_j)}{S(n)} \right) \times \left(\prod_{i=2}^n \hat{f}_i(\{n_j\}, s) \right) \quad (66)$$

with functions $f_i(\{n_j\}, s)$ defined as

$$\hat{f}_i(n_j, s) = \begin{cases} \frac{c_i}{s + c_i + j\theta} & \text{for } n_j \geq i \geq n_{j-1} + 1 \text{ and } j \geq 1, \\ \frac{c_i}{s + c_i} & \text{for } n_1 \geq i \end{cases} \quad (67)$$

and amplitudes

$$B_{n,m}(n_j) = \frac{S(m)(n+m-1)!(n-m)!}{2^{n-1}} \prod_{j=1}^{m-1} \frac{1}{c_{n_j+j+1}}.$$

This result can be obtained by counting trees and averaging on coalescence times τ_i as shown in appendix A. Let us sketch briefly the derivation of (66). The genealogy of the

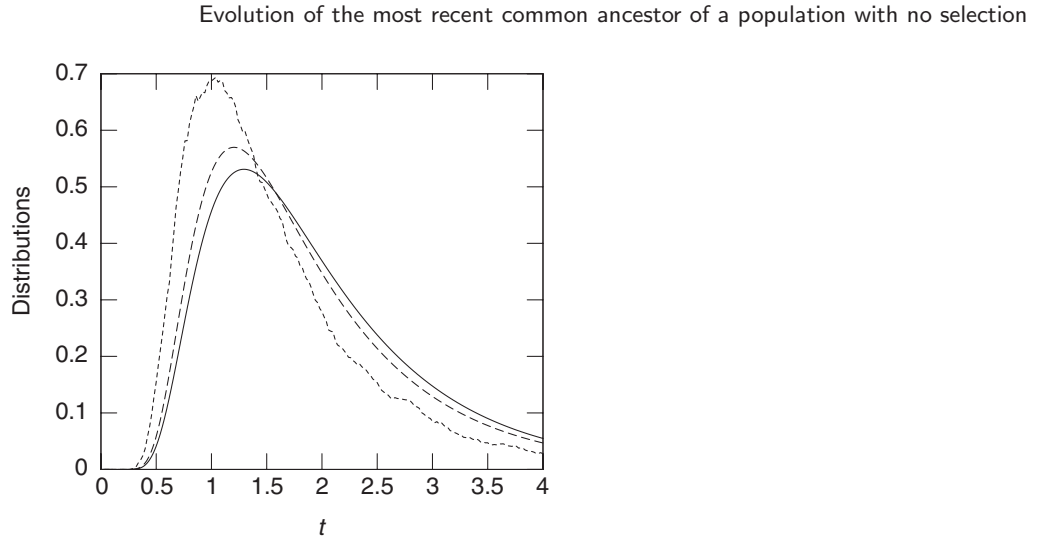


Figure 9. Probability distribution of the coalescence time of a group of individuals knowing that the first m of them have the same genome. Solid line: stationary distribution for a large group without information. Dashed (long): $\theta = 0.5$ and $m = 2$ in a large group. Dashed (short): $\theta = 0.5$ and $m = 5$ (numerical simulations for a population of 50 individuals).

group of n individuals can be divided into several parts, which correspond to a constant number of ancestors of the subgroup of m individuals, i.e. the parts are separated by coalescences *among* the ancestors of the m individuals. The indices n_j in (66) are the number of ancestors of the n individuals at the times of these coalescences, i.e. when the number of ancestors of the m individuals decreases from $j + 1$ to j due to a coalescence. The quantity $B_{n,m}(n_j)S(n + m)$ counts the number of trees sharing the same parameters n_j and thus the sum over the n_i in (66) is an average over the shape of the trees. The value of $B_{n,m}(n_j)$ can be obtained by counting at each coalescence the number of possibilities compatible with the value n_j .

Given a set of parameters n_i , we now consider the distribution of the coalescence times τ_i conditioned by the shape of the tree and the genomes of the subgroup of m individuals. Mutations are forbidden in the subtree of the m individuals. Thus, if the number of ancestors of the m individuals is j during τ_i , the probability that no mutations occur is $e^{-j\theta\tau_i}$. If one introduces the parameters n_i , the probability that the delay between the $(i - 1)$ th coalescence and the i th is τ_i and that no mutations occur on the lineages of the m individuals with the same genome is $f_i(n_j, t)$ defined as

$$f_i(n_j, \tau_i) = \begin{cases} c_i e^{-(c_i + j\theta)\tau_i} & \text{for } n_j \geq i \geq n_{j-1} + 1 \text{ and } j \geq 1, \\ c_i e^{-c_i \tau_i} & \text{for } n_1 \geq i. \end{cases} \quad (68)$$

The Laplace transform of these expressions gives the result (67) and the product of the \hat{f}_i in (66) corresponds to the average on the τ_i .

Figure 9 shows the distribution $p_{2,\infty}(t)/\hat{p}_{2,\infty}(0)$ of the conditioned coalescence time T obtained from (62). It also shows numerical results on a population of 50 individuals which agree with analytical calculations showing how information about five individuals modifies the coalescence time of the whole population significantly.

4. Conclusion

In the present paper, we have shown that the evolution of all the coalescence times at the top of the genealogical tree can be described by a Markov process (section 2.3). This Markov process allowed us to calculate various properties (24), (27), (30), (37) of the age of the MRCA, in particular its autocorrelation function (54), (56). We have also shown how to calculate the correlation between the age of the MRCA and a parameter representing the genetic diversity (section 3). Our general formula (66), correlating the age of the MRCA of n individuals knowing that a sample of p of them chosen at random have the same allele, is not easy to manipulate. Its interpretation as a weighted sum over a large number of tree configurations may however allow numerical simulations with Monte-Carlo methods [8] by sampling efficiently the terms of the sum.

The Markov property of the genealogies is the most promising result of this paper and one may hope to construct more general Markov processes of this type. A first direction would be to try to incorporate the genetic diversity in the Markov process: whereas section 3 leads only to the stationary correlation coefficients $\langle YT^k \rangle$, the construction of a joint Markov process for the times τ_i and the sizes of the families may lead to correlations at different times and establish links between extinctions and variations of the genetic diversity. Moreover, this could be related to works such as [23] in the case where sampling the DNA of individuals at different times is possible.

Extensions of the Markov process to more realistic models would also be interesting, but many aspects of the calculations may differ. For example, the shape of the genealogical trees changes in the presence of selection, since multiple coalescences [24]–[26] have to be included and this should change the weights of the trees and the probabilities of extinctions of families. The study of structured populations [10, 11] shows that demographic and geographic effects are important: it would be interesting to know if the Markov property of the coalescence times persists, up to changes in the transition rates. Diploidy [12, 13] is more problematic since it has more radical effects (e.g. the age of the MRCA scales as $\log N$ and not as N anymore) because genealogical trees have a more complicated structure with loops.

Lastly, it would be interesting to see how more detailed information about the genomes could lead to a more accurate estimation of the age of the MRCA. Analysis of section 3 deals with only one gene. Distinct genes may evolve in different ways since the MRCA and, in the present generation, one is left with different parameters Y for each gene. Information about the genetic diversities for different genes would modify the distribution of the times τ_i in order to account for possible differences in the number of mutations of each gene. Moreover, in real cases, the observation of different genes along a DNA sequence would be incomplete if recombination [4, 27, 28] were not taken into account. Recombination acts as if the two genes of a given individual are not inherited from the same parent. It implies that the genealogical trees of the two genes will have some different branches and the MRCA may be different for the two genes, and the difference of ages between these ancestors may be worth further investigations.

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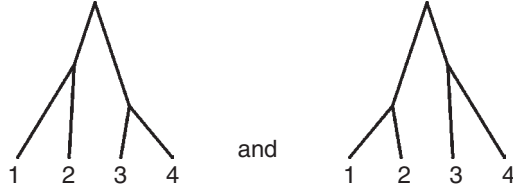


Figure A.1. Two genealogical trees. Their topologies are identical but the chronology is different.

Appendix A: Measure on genealogies

In this appendix we recall briefly the derivation of the statistics [15, 18, 19] of the coalescence times in the genealogies of a set of individuals. The problem can be divided into two aspects: the distribution of the coalescence times and the shape of the tree.

We consider a group of n individuals undergoing coalescences until they reach their MRCA. Each coalescence is characterized by two quantities: the waiting time until it occurs and the pair of individuals which coalesce.

For a large size N of the population, coalescences occur one after another. At each generation, the probability of a coalescence between a given pair of individuals is $1/N$ and the total probability of observing a coalescence is c_n/N for a group of n individuals, where the coefficient c_n is defined as $c_n = n(n-1)/2$ (see (2)). The probability of observing the first coalescence at generation G in the past is then $\rho_n(G) = c_n/N(1 - c_n/N)^G$, which becomes for the rescaled time $\tau = G/N$

$$\rho_n(\tau) = c_n e^{-c_n \tau}. \quad (\text{A.1})$$

After this coalescence, we are left with $n-1$ individuals and the rescaled time τ_{n-1} before the next coalescence is then given by $\rho_{n-1}(\tau_{n-1})$ and so on. So, the distribution of the $(n-1)$ waiting times τ_i between two successive coalescences for a group of n individuals is

$$P_n(\tau_n, \dots, \tau_2) = \prod_{i=2}^n c_i e^{-c_i \tau_i}. \quad (\text{A.2})$$

Consequently, the total coalescence time can be written as a sum of $n-1$ independent variables:

$$T_n = \sum_{i=2}^n \tau_i. \quad (\text{A.3})$$

Once the dates of the coalescences are known, we have to decide which branches coalesce at each step. We will consider here that a tree \mathcal{T} is completely characterized by its topology *and* the chronological order of these $n-1$ coalescences. With this definition, which is convenient for our calculations, the two trees shown in figure A.1 are distinct.

The total number of such ordered trees is thus

$$S(n) = \prod_{i=2}^n c_i = \frac{n!(n-1)!}{2^{n-1}} \quad (\text{A.4})$$

and they are all equally likely. The probability measure μ_n of a given genealogy factorizes as

$$\mu_n(\mathcal{T}, \{\tau_i\}) = \frac{1}{S(n)} \rho_n(\tau_n) \rho_{n-1}(\tau_{n-1}) \dots \rho_2(\tau_2). \quad (\text{A.5})$$

For a given tree, one can determine from (A.5) for each ancestor on a branch of the tree the distribution of its number of descendants in the present generation. For example, right before the last coalescence, the ancestors of the group of size n consist of two parents who have in the present generation p and $n-p$ descendants respectively. The sizes p and $n-p$ of these two groups can be obtained by counting the number $s(n, p)$ of trees satisfying this constraint. The probability $\rho_n(p)$ of observing the subdivision $(p, n-p)$ with $1 \leq p \leq n-1$ is given by

$$\rho_n(p) = \frac{s(n, p)}{S(n)} = \frac{1}{S(n)} S(p) S(n-p) \binom{n}{p} \binom{n-2}{p-1}. \quad (\text{A.6})$$

The binomial coefficient $\binom{n}{p}$ counts the number of ways of making the groups of p and $n-p$ individuals, the coefficients $S(p)$ and $S(n-p)$ count the number of subtrees for each groups and the factor $\binom{n-2}{p-1}$ counts the ways of organizing the chronological order between the coalescences of the two subtrees. The dependence on p disappears in (A.6) and $\rho_n(p)$ is the uniform distribution:

$$\rho_n(p) = \frac{1}{n-1}. \quad (\text{A.7})$$

One should notice that this result is obtained for a large population N and a group of size $n \ll N^{1/2}$, such that coalescences occur only between pairs of individuals and not more. However, if n is large enough and if we define the density $x = p/n$, the corresponding distribution $\rho(x)$ is uniform on $[0, 1]$.

For a branch of length τ , the number m of mutations has a Poisson distribution:

$$P(\tau, m) = \frac{(\theta\tau)^m}{m!} e^{-\theta\tau}.$$

So the probability of observing no mutation on this branch, which is the only relevant quantity in the infinite allele case, is given by

$$P_{\text{no mut}}(\tau) = e^{-\theta\tau}. \quad (\text{A.8})$$

Appendix B: Dynamics of the times τ_i

Figure 5 shows the stochastic dynamics of the coalescence time τ_2 . Actually, all the elementary coalescence times τ_i of figure 1 defined in appendix A have similar dynamics: either they increase by τ_{i+1} or they are reset to τ_{i+1} .

If one considers a generic tree as shown in figure 1 truncated below τ_n , one sees that the times τ_i topple when some lineages coming from the n ancestors at the ‘leaves’ of the truncated tree disappear. Let us assume that the lineage of a given ancestor among these n disappears and that this ancestor is directly connected to the j th coalescence, i.e. the coalescence separating τ_j and τ_{j+1} . For example, if $j = 1$ the ancestor is directly connected to the MRCA, and if $j = 2$ it is directly connected to A_1 in figure 1. If the

lineage of this ancestor in the present generation disappears, the times τ_i topple at rank $j + 1$, i.e. they are redefined as

$$\begin{aligned}\tau'_i &= \tau_i & \text{for } i < j \\ \tau'_j &= \tau_j + \tau_{j+1} \\ \tau'_i &= \tau_{i+1} & \text{for } i > j.\end{aligned}$$

Let us call $P_{\text{node}}(n, j)$ the probability that a given ancestor among the n is directly connected to the node of the j th coalescence, i.e. the lineage of this ancestor does not participate at any coalescence until the number of ancestors reaches j . With these notations, the probability $p_j dt$ defined in (18) that the times topple at rank j is the probability that the lineage which disappears during dt (probability $\alpha_n dt$) is the lineage connected to the j th coalescence and thus it is given by

$$p_j dt = P_{\text{node}}(n, j) \alpha_n dt. \quad (\text{B.1})$$

The value of α_n can be derived by introducing the probability $Q_t(n, t_0)$ that the number of ancestors at time $t_0 < t$ of the whole population at time t is n . These n ancestors at time t_0 generate all the population at time t , which can be divided in n groups, each depending on the ancestor they come from. At time $t + dt$, either one of these groups becomes extinct (probability $\alpha_n dt$) and the number of ancestors at t_0 of the population at $t + dt$ is $n - 1$, or this number is still equal to n . The probabilities $Q_t(n, t_0)$ satisfy the following equations:

$$Q_{t+dt}(n - 1, t_0) = Q_t(n, t_0) \alpha_n dt + Q_t(n - 1, t_0) (1 - \alpha_{n-1} dt).$$

It gives the differential equation

$$\frac{d}{dt} Q_t(n, t_0) = Q_t(n, t_0) \alpha_n - Q_t(n - 1, t_0) \alpha_{n-1}. \quad (\text{B.2})$$

In the stationary regime, this probability is $Q_t(m, t - \tau) = z_n(\tau)$, where the z_m have been defined in section 2.3 and satisfy (11). Comparing (B.2) and (11) leads to

$$\alpha_n = c_n. \quad (\text{B.3})$$

The probability $P_{\text{node}}(n, j)$ is the probability that, in the genealogy of a group of n individuals, the lineage of a given individual among the n is directly connected to the node of the j th coalescence, i.e. that coalescences do not involve its lineage until the number of ancestors of the group is reduced to $j + 1$. Counting the number of possibilities for each coalescence gives

$$P_{\text{node}}(n, j) = \frac{j}{c_{j+1}} \prod_{k=j+2}^n \frac{c_k - (k - 1)}{c_k} = \frac{j}{c_n}. \quad (\text{B.4})$$

Putting (B.4) and (B.3) in (B.1) gives the toppling rates presented in (18):

$$p_i = \frac{i}{c_n} \times c_n = i. \quad (\text{B.5})$$

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