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A new model for evolution in a spatial continuum

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Abstract

We investigate a new model for populations evolving in a spatial continuum. This model can be thought of as a spatial version of the Λ-Fleming-Viot process. It explicitly incorporates both small scale reproduction events and large scale extinction-recolonisation events. The lineages ancestral to a sample from a population evolving according to this model can be described in terms of a spatial version of the Λ-coalescent. Using a technique of Evans (1997), we prove existence and uniqueness in law for the model. We then investigate the asymptotic behaviour of the genealogy of a finite number of individuals sampled uniformly at random (or more generally 'far enough apart') from a two-dimensional torus of sidelength L as $L \to \infty$. Under appropriate conditions (and on a suitable timescale) we can obtain as limiting genealogical processes a Kingman coalescent, a more general Λ-coalescent or a system of coalescing Brownian motions (with a non-local coalescence mechanism) .

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1 Introduction

In 1982, Kingman introduced a process called the *coalescent*. This process provides a simple and elegant description of the genealogical (family) relationships amongst a set of neutral genes in a randomly mating (biologists would say *panmictic*) population of constant size. Since that time, spurred on by the flood of DNA sequence data, considerable effort has been spent extending Kingman's coalescent to incorporate things like varying population size, natural selection and spatial (and genetic) structure of populations. Analytic results for these coalescent models can be very hard to obtain, but it is relatively easy, at least in principle, to simulate them and so they have become fundamental tools in sequence analysis. However, models of spatial structure have largely concentrated on subdivided populations and a satisfactory model for the ancestry of a population evolving in a two-dimensional spatial continuum has remained elusive. Our aim in this paper is to present the first rigorous investigation of a new model that addresses some of the difficulties of existing models for spatially extended populations while retaining some analytic tractability. The rest of this introduction is devoted to placing this research in context. The reader eager to skip straight to the model and a precise statement of our main results should proceed directly to Section 2.

Our concern here is with the extension of the coalescent to spatially structured populations. In this setting it is customary to assume that the population is subdivided into *demes* of (large) constant size, each situated at a vertex of a graph G, and model the genealogical trees using the *structured* coalescent. As we trace backwards in time, within each deme the ancestral lineages follow Kingman's coalescent, that is each pair of lineages merges (or *coalesces*) into a single lineage at a constant rate, but in addition lineages can migrate between demes according to a random walk on the graph G. The genealogical trees obtained in this way coincide with those for a population whose forwards in time dynamics are given by Kimura's stepping stone model (Kimura 1953) or, as a special case, if G is a complete graph, by Wright's island model (Wright 1931).

The stepping stone model is most easily described when the population consists of individuals of just two types, a and A say. It can be extended to incorporate selection, but let us suppose for simplicity that these types are selectively neutral. Labelling the vertices of the graph G by the elements of the (finite or countable) set I and writing p_i for the proportion of individuals in deme i of type a, say, we have

$$dp_i(t) = \sum_{j\in I} m_{ji}\left(p_j(t) - p_i(t)\right)dt + \sqrt{\gamma p_i(t)\left(1 - p_i(t)\right)}dW_i(t) \tag{1}$$

where $\{W_i(t); t \geq 0\}_{i\in I}$ is a collection of independent Wiener processes, γ is a positive constant and $\{m_{ij}\}_{i,j\in I}$ specifies the rates of a continuous time random walk on G. The graph G, chosen to caricature the spatial structure of the population, is typically taken to be $\mathbb{Z}^2$ (or its intersection with a two-dimensional torus) and then one sets $m_{ij} = \kappa\mathbf{1}_{\{\|i-j\|=1\}}$, corresponding to simple random walk.

Although the stepping stone model is widely accepted as a model for structured populations, in reality, many populations are not subdivided, but instead are distributed across a spatial continuum. Wright (1943) and Malécot (1948) derived expressions for the probability of identity of two individuals sampled from a population dispersed in a two-dimensional continuum by assuming on the one hand that genes reproduce and disperse independently of one another, and on the other hand that they are scattered in a stationary Poisson distribution. However, these assumptions are incompatible (Felsenstein 1975, Sawyer & Fleischmann 1979). The assumption of independent reproduction will result in ‘clumping’ of the population and some local regulation will be required to control the local population density.

A closely related approach is to assume that the genealogical trees can be constructed from Brownian motions which coalesce at an instantaneous rate given by a function of their separation. The position of the common ancestor is typically taken to be a Gaussian centred on the midpoint between the two lineages immediately before the coalescence event (although other distributions are of course possible). However, the coalescent obtained in this way does not exhibit *sampling consistency*. That is, if we construct the genealogical tree corresponding to a sample of size n and then examine the induced genealogical tree for a randomly chosen subsample of size $k < n$, this will not have the same distribution as the tree we obtain by constructing a system of coalescing lineages directly from the subsample. The reason is that whenever one of the lineages in the subsample is involved in a coalescence event in the full tree it will jump. Furthermore, just as in Malécot’s setting, there is no corresponding *forwards* in time model for the evolution of the population.

Barton et al. (2002) extend the formulae of Wright and Malécot to population models which incorporate local structure. The probability of identity is obtained from a recursion over timeslices of length Δt. Two related assumptions are made. First, the ancestral lineages of genes that are sufficiently well separated are assumed to follow independent Brownian motions (with an effective dispersal rate which will in general differ from the forwards in time dispersal rate) and their chance of coancestry in the previous timeslice is negligible. Second, it must be possible to choose Δt sufficiently large that the changes in the population over successive timeslices are uncorrelated. (For general Δt this will not be the case. The movements of ancestral lineages in one time step may be correlated with their movements in previous steps if, for example, individuals tend to disperse away from temporarily crowded clusters.) Over all but very small scales, the resulting probability of identity can be written as a function of three parameters: the *effective dispersal rate*, the *neighbourhood size* and the *local scale*. However the usefulness of this result is limited due to a lack of explicit models for which the assumptions can be validated and the effective parameters established. Moreover, as explained in Barton et al. (2002), although one can in principle extend the formula to approximate the distribution of genealogies amongst larger samples of well-separated genes, additional assumptions need to be made if such genealogies are to be dominated by pairwise coalescence. If several genes are sampled from one location and neighbourhood size is small then multiple coalescence (by which we mean simultaneous coalescence of *three* or more lineages) could become significant.

Multiple merger coalescents have received considerable attention from mathematicians over the last decade. Pitman (1999) and Sagitov (1999) introduced what we now call Λ-*coalescents*, in which more than two ancestral lineages can coalesce in a single event, but *simultaneous* coalescence events are not allowed. Like Kingman’s coalescent, these processes take their values among partitions of $\mathbb{N}$ and their laws can be prescribed by specifying the restriction to partitions of $\{1,2,\ldots,n\}$ for each $n \in \mathbb{N}$. For our purposes, the Λ-coalescent describes the ancestry of a population whose individuals are labelled by $\mathbb{N}$. Each block in the partition at time t corresponds to a single ancestor at time t before the present, with the elements of the block being the descendants of that ancestor. Tracing backwards in time, the evolution of the Λ-coalescent is as follows: if there are currently p ancestral lineages, then each transition involving j of the blocks merging into one happens at rate

$$\beta^{\Lambda}_{p,j} = \int_{[0,1]} u^{j-2}(1-u)^{p-j}\Lambda(du), \tag{2}$$

and these are the only possible transitions. Here, Λ is a finite measure on $[0,1]$. Kingman's coalescent corresponds to the special case $\Lambda = \delta_0$, the point mass at the origin.

Remark 1.1. *More generally, one can consider processes with simultaneous multiple coalescence events. Such coalescents were obtained as the genealogies of suitably rescaled population models by Möhle & Sagitov (2001). Independently, Schweinsberg (2000) obtained the same class of coalescents and characterised the possible rates of mergers in terms of a single measure Ξ on an infinite simplex. Coalescents which allow* simultaneous *multiple mergers are now generally referred to as* Ξ-coalescents.

Kingman's coalescent can be thought of as describing the genealogy of a random sample from a Fleming-Viot process. In the same way, a Λ-coalescent describes the genealogy of a random sample from a generalised Fleming-Viot process. This process takes its values among probability measures on $[0,1]$. We shall describe it in terms of its generator, $\mathscr{R}$ acting on functions of the form

$$F(\rho) = \int f(x_1,\dots,x_p)\rho(dx_p)\dots\rho(dx_1),$$

where $p \in \mathbb{N}$ and $f : [0,1]^p \to \mathbb{R}$ is measurable and bounded. First we need some notation. If $x = (x_1,\dots,x_p) \in [0,1]^p$ and $J \subseteq \{1,\dots,p\}$ we write

$$x_i^J = x_{\min J} \text{ if } i \in J, \text{ and } x_i^J = x_i \text{ if } i \notin J, \quad i = 1,\dots,p.$$

Then for Λ a finite measure on $[0,1]$, a Λ-Fleming-Viot process has generator

$$\mathscr{R}F(\rho) = \sum_{J\subseteq\{1,\dots,p\},|J|\geq 2} \beta^{\Lambda}_{p,|J|} \int \Big(f(x_1^J,\dots,x_p^J) - f(x_1,\dots,x_p)\Big)\rho(dx_p)\dots\rho(dx_1),$$

where $\beta^{\Lambda}_{p,j}$ is defined in Equation (2). When $\Lambda(\{0\}) = 0$, this can also be written

$$\mathscr{R}F(\rho) = \int_{(0,1]}\int_{[0,1]} \Big(F\big((1-u)\rho + u\delta_k\big) - F(\rho)\Big)\rho(dk)u^{-2}\Lambda(du).$$

(When $\Lambda(\{0\}) > 0$, one must add a second term corresponding to a classical Fleming-Viot process and somehow dual to the Kingman part of the Λ-coalescent.) In this case, an intuitive way to think about the process is to consider a Poisson point process on $\mathbb{R}_+ \times (0,1]$ with intensity measure $dt \otimes u^{-2}\Lambda(du)$, which picks jump times and sizes for $\rho(t)$. At a jump time t with corresponding jump size u, a type k is chosen according to $\rho(t-)$, an atom of mass u is inserted at k and $\rho(t-)$ is scaled down by $(1-u)$ so that the total mass remains equal to one, i.e.,

$$\rho(t) = (1-u)\rho(t-) + u\delta_k. \tag{3}$$

The duality between Λ-coalescents and Λ-Fleming-Viot processes was first proved by Bertoin & Le Gall (2003). Their approach uses a correspondence between the Λ-coalescents and stochastic flows of bridges. The duality can also be understood via the Donnelly & Kurtz (1999) 'modified look-down construction' and indeed is implicit there. An explicit explanation can be found in Birkner et al. (2005).

In recent work (described briefly in Etheridge 2008), Barton & Etheridge have proposed a new class of consistent forwards and backwards in time models for the evolution of allele frequencies in a population distributed in a two-dimensional (or indeed d-dimensional) spatial continuum which, in the simplest setting, can be thought of as spatial versions of the Λ-Fleming-Viot and Λ-coalescent models (although we emphasize that these are not the same as the spatial Λ-coalescents considered by Limic & Sturm 2006). They share many of the advantages of the classical models for spatially structured populations while overcoming at least some of the disadvantages. The idea is simple. Just as in the Λ-Fleming-Viot process, reproduction events are determined by a Poisson point process but now, in addition to specifying a time and a value u, this process prescribes a region of space which will be affected by the event. In what follows, the region will be a ball with random centre and radius. Within that region the effect is entirely analogous to Equation (3).

This approach differs from existing spatial models in three key ways. First, density dependent reproduction is achieved by basing reproduction events on neighbourhoods (whose locations are determined by the Poisson point process), rather than on individuals. Second, the offspring of a single individual can form a significant proportion of the population in a neighbourhood about the parent, capturing the essentially finite nature of the local population size. Third, large scale extinction-recolonisation events are explicitly incorporated. This reflects the large scale fluctuations experienced by real populations in which the movement and reproductive success of many individuals are correlated. For example, climate change has caused extreme extinction and recolonisation events that dominate the demographic history of humans and other species (e.g. Eller et al. 2004).

The spatial Λ-Fleming-Viot process, like its classical counterpart, can be obtained as a limit of individual based models. Those prelimiting models are discussed in Berestycki et al. (2009). In the (backwards in time) spatial Λ-coalescent, ancestral lineages move around according to dependent Lévy processes (in fact they will be compound Poisson processes), jumping whenever they are affected by a reproduction event. Two or more lineages can coalesce if they are all affected by the same reproduction event.

Our first aim here is to provide a precise mathematical description of the spatial Λ-Fleming-Viot process and the corresponding spatial Λ-coalescent model and address questions of existence and uniqueness. This is achieved through adapting the work of Evans (1997). The idea is to first construct the dual (backwards in time) process of coalescing Lévy processes corresponding to a finite sample from the population at time zero, and then to use a functional duality to define the forwards in time model. The principal difference between our setting and that of Evans is that, in his work, ancestral lineages evolve *independently* until they meet.

The system of coalescing Lévy processes that describes the genealogy of a sample from the population, mirrors the system of coalescing random walks that plays the same rôle for the stepping stone model. For systems of coalescing walks a number of studies have investigated conditions under which, when viewed on an appropriate timescale, and for sufficiently well-separated samples, the effect of the geographical structure of the population can be summarised as a single 'effective' parameter and the system of coalescing lineages converges to Kingman's coalescent. One of the first works along these lines is due to Cox (1989), who considers random walks on a torus $\mathbb{T}(L)\cap\mathbb{Z}^d$ of sidelength L with the walks coalescing instantly on meeting. This corresponds to taking $G=\mathbb{T}(L)\cap\mathbb{Z}^d$ and $\gamma=\infty$ in Equation (1). He shows that if one starts walks from any finite number $n\in\mathbb{N}$ of points chosen independently and uniformly at random from $\mathbb{T}(L)\cap\mathbb{Z}^d$, then in suitable time units, as $L\to\infty$, the number of surviving lineages is determined by Kingman's coalescent. For two spatial dimensions, this analysis was extended by Cox & Durrett (2002) and Zähle et al. (2005) to random walks on $\mathbb{T}(L)\cap\mathbb{Z}^2$ with delayed coalescence (corresponding to $\gamma<\infty$). It is natural to ask whether similar results are true here. Our second aim then is to establish conditions under which the genealogy of a sample taken at random from a large torus will converge to a non-spatial coalescent. We shall concentrate on the most difficult, but also most biologically relevant, case of two spatial dimensions. If reproduction events only affect bounded neighbourhoods, then, not surprisingly, we recover a Kingman coalescent limit. However, we also consider the more general situation in which in addition to 'small' events that affect only bounded neighbourhoods we allow 'large' extinction-recolonisation events (see Section 3 for the precise setting). Unless these events affect a non-negligible proportion of the torus, on a suitable timescale, asymptotically we once again recover a Kingman coalescent. The timescale is determined by the relative rates of 'large' and 'small' events. However, if we have extinction-recolonisation events that affect regions with sidelength of order $\mathcal{O}(L)$, then, again depending on the relative rates of 'large' and 'small' events, we can obtain a more general (non-spatial) Λ-*coalescent* limit or a system of coalescing Brownian motions (where the coalescence is non-local).

The rest of the paper is laid out as follows. In Section 2 we define the model. In Section 3, we give a precise statement of the conditions under which we obtain convergence of the genealogy of a random sample from a (two-dimensional) torus of side L as $L \to \infty$. The corresponding convergence results are Theorem 3.3 and Theorem 3.7. In Section 4 we establish existence of the process and prove uniqueness in law. In Section 5 we gather the necessary results on Lévy processes in preparation for our proofs of Theorem 3.3 and Theorem 3.7 in Sections 6 and 7. Finally, Appendices A and B contain the proofs of the technical lemmas stated in Sections 5 and 6.

2 The model

First we describe a prelimiting model. Individuals in our population are assumed to have a *type* taken from $[0,1]$ and a spatial position in a metric space E that we shall usually take to be $\mathbb{R}^2$ (or the torus $\mathbb{T}(L)$ in $\mathbb{R}^2$). Even though it will be clear that existence and uniqueness of the process holds in much greater generality, the model is primarily motivated by considerations for populations evolving in two-dimensional continua. The dynamics are driven by a Poisson point process Π on $\mathbb{R}_+ \times \mathbb{R}^2 \times (0,\infty)$ with intensity $dt \otimes dx \otimes \mu(dr)$. If $(t,x,r) \in \Pi$, the first component represents the time of a reproduction event. The event will affect only individuals in $B(x,r)$, the closed ball of centre x and radius r. We require two more ingredients. The first, m, is a fixed positive constant which we shall refer to as the *intensity* of the model. Second, associated to each fixed radius $r > 0$ there is a probability measure ν_r on $[0,1]$. In the sequel, we assume that the mapping $r \mapsto \nu_r$ is measurable with respect to μ.

For definiteness, suppose that the population is initially distributed according to a spatially homogeneous Poisson process. The dynamics of our prelimiting model are described as follows. Suppose that $(t,x,r) \in \Pi$. Consider the population in $B(x,r)$ at time $t-$. If the ball is empty, then nothing happens. Otherwise, independently for each event:

1. Select a 'parent' uniformly at random from those individuals in $B(x,r)$ at time $t-$ and sample $u \in [0,1]$ at random according to ν_r.

2. Each individual in $B(x,r)$, independently, dies with probability u, otherwise it is unaffected by the reproduction event.

3. Throw down offspring in the ball, with the same type as the selected parent (who may now be

dead), according to an independent Poisson point process with intensity $u\, m\, \mathrm{Leb}|_{B(x,r)}$ where Leb denotes Lebesgue measure.

We shall refer to these events as *reproduction events*, even though they are also used to model large-scale extinction-recolonisation events. Notice that recolonisation is modelled as being instantaneous even after a large scale extinction.

Remark 2.1. *For simplicity we have described only a special version of the model in which, even when the reproduction event affects a large region, recolonisation is through a single founder. This guarantees that if we look at the genealogy of a sample from this population, although we may see more than two lineages coalescing in a single event, we do not see* simultaneous *mergers. More generally it would be natural to take a random number of colonists and then, on passing to the limit, the corresponding model would yield a spatial Ξ-coalescent.*

Any reproductive event has positive probability of leaving the corresponding region empty, but because the neighbourhoods determined by different reproduction events overlap, an empty region can subsequently become recolonised. Provided the measure $\mu(dr)$ decays sufficiently quickly as $r \to \infty$, Berestycki et al. (2009) show that there is a critical value of m above which the population, when started from a translation invariant initial condition, survives with probability one. The difficulty is that it is not easy to find an explicit expression for the distribution of the genealogical trees relating individuals in a sample from the population. Knowing that an ancestral lineage is in a given region of space gives us information about the rate at which that region was hit by reproduction events as we trace backwards in time. On the other hand, simulations reveal that this effect is rarely significant. Mathematically, we overcome this difficulty by considering a model in which the intensity m is infinite, but we preserve some of the signature of a finite local population size by retaining the reproduction mechanism so that a non-trivial proportion of individuals in a neighbourhood are descended from a common ancestor. In particular, this will result in multiple coalescences of ancestral lineages.

Now let us describe the model that arises from letting $m \to \infty$. (That the prelimiting model really does converge to this limit will be proved elsewhere.) At each point $x \in \mathbb{R}^2$, the model specifies a probability measure on type space which we shall write $\rho(t,x,\cdot)$, or sometimes for brevity ρ_x. The interpretation is that if we sample an individual from x, then its type will be determined by sampling from ρ_x. The reproduction mechanism mirrors that for our discrete time model:

Definition 2.2 (Spatial Λ-Fleming-Viot process). *The* spatial Λ-Fleming-Viot process, $\{\rho(t,x,\cdot), x \in \mathbb{R}^2, t \geq 0\}$ *specifies a probability measure on the type space* $[0,1]$ *for every* $t \geq 0$ *and every* $x \in \mathbb{R}^2$. *With the notation above, the dynamics of the process are as follows. At every point* (t,x,r) *of the Poisson point process* Π, *we choose* $u \in [0,1]$ *independently according to the measure* $\nu_r(du)$. *We also select a point* z *at random from* $B(x,r)$ *and a type* k *at random according to* $\rho(t-,z,\cdot)$. *For all* $y \in B(x,r)$,

$$\rho(t,y,\cdot) = (1-u)\rho(t-,y,\cdot) + u\delta_k.$$

Sites outside $B(x,r)$ *are not affected, that is* $\rho(t,y,\cdot) = \rho(t-,y,\cdot)$ *for every* $y \notin B(x,r)$.

Remark 2.3. *There are many variants of this model, some of which are outlined in Etheridge (2008). The model presented here should be regarded as fitting into a general framework in which the key feature is that reproduction events are driven by a Poisson point process determining their times and spatial locations, rather than on individuals. Barton et al. (2009) investigate a version of the model in* *which, instead of replacing a portion u of the population in a disc at the time of a reproduction event, the proportion of individuals affected decays (in a Gaussian distribution) with the distance from the 'centre' x of the event. Whereas in the disc based approach in the prelimiting (individual based) model we had to suppress reproduction events that affected empty regions, this is not necessary in the Gaussian model. Moreover, (in contrast to the disc model) in that setting the prelimiting model has the Poisson point process in* $\mathbb{R}^2$ *with constant intensity m as a stationary distribution. Although the proofs would be rather involved, analogues of our results here should carry over to the Gaussian setting.*

Of course we must impose restrictions on the intensity measure if our process is to exist. To see what these should be, consider first the evolution of the probability measure $\rho(t,x,\cdot)$ defining the distribution of types at the point x. This measure experiences a jump of size $y \in A \subseteq (0,1]$ at rate

$$\int_{(0,\infty)} \int_A \pi r^2 \nu_r(du)\mu(dr).$$

By analogy with the Λ-Fleming-Viot process, we expect to require that

$$\Lambda(du) = \int_{(0,\infty)} u^2 r^2 \nu_r(du)\mu(dr) \tag{4}$$

defines a finite measure on $[0,1]$. In fact, in the spatial setting we require a bit more. To see why, suppose that ψ is a bounded measurable function on $[0,1]$ and consider the form that the infinitesimal generator of the process must take on test functions of the form $\langle \rho(x,dk), \psi(k)\rangle$ (with angle brackets denoting integration). Denoting the generator, if it exists, by G we shall have

$$\begin{aligned} G(\langle \rho,\psi\rangle) &= \int_{\mathbb{R}^2}\int_{(0,\infty)}\int_{[0,1]}\int_{[0,1]} \frac{L_r(x,y)}{\pi r^2}\big(\langle (1-u)\rho(x,\cdot)+u\delta_k,\psi\rangle - \langle \rho(x,\cdot),\psi\rangle\big) \\ &\qquad\qquad\qquad\qquad \rho(y,dk)\nu_r(du)\mu(dr)dy \\ &= \int_{\mathbb{R}^2}\int_{(0,\infty)}\int_{[0,1]} \frac{L_r(x,y)}{\pi r^2} u\big(\langle \rho(y,\cdot),\psi\rangle - \langle \rho(x,\cdot),\psi\rangle\big)\nu_r(du)\mu(dr)dy, \end{aligned}$$

where $L_r(x,y)$ denotes the volume of the set $B(x,r)\cap B(y,r)$. Notice in particular that $L_r(x,y) \le \pi r^2 \mathbf{1}_{\{|x-y|\le 2r\}}$. In the non-spatial case, this term vanishes (set $y = x$), but here if we want the generator to be well-defined on these test functions we make the stronger

Assumption 2.4.

$$\tilde{\Lambda}(du) = \int_{(0,\infty)} u r^2 \nu_r(du)\mu(dr) \tag{5}$$

defines a finite measure on $[0,1]$.

Condition (5) controls the jumps of ρ at a single point. Since we are going to follow Evans (1997) in constructing our process via the dual process of coalescing lineages ancestral to a sample from the population, we should check that such a process is well-defined. First we define the coalescent process more carefully.

In order to make sense of the genealogy of a sample at any time, we extend the Poisson point process Π of reproduction events to the whole time line $(-\infty,+\infty)$. We need some notation for (labelled) partitions.

Notation 2.5 (Notation for partitions).

1. *For each integer $n \geq 1$, let $\mathscr{P}_n$ denote the set of partitions of $\{1, \dots, n\}$, and define a labelled partition of $\{1, \dots, n\}$, with labels from a set E, to be a set of the form $\{(\pi_1, x_{\pi_1}), \dots, (\pi_k, x_{\pi_k})\}$, where $\{\pi_1, \dots, \pi_k\} \in \mathscr{P}_n$ and $(x_{\pi_1}, \dots, x_{\pi_k}) \in E^k$. Let $\mathscr{P}_n^\ell$ be the set of all labelled partitions of $\{1, \dots, n\}$.*
2. *For each $n \in \mathbb{N}$, let $\wp_n$ denote the partition of $\{1, \dots, n\}$ into singletons. Moreover, if E is the space of labels and $\mathbf{x} \equiv (x_1, \dots, x_n) \in E^n$, let $\wp_n(\mathbf{x})$ denote the element $\{(\{1\}, x_1), \dots, (\{n\}, x_n)\}$ of $\mathscr{P}_n^\ell$.*
3. *If $\pi \in \mathscr{P}_n^\ell$ for some $n \in \mathbb{N}$, then $\mathrm{bl}(\pi)$ will refer to the unlabelled partition of $\{1, \dots, n\}$ induced by π and if $a \in \mathrm{bl}(\pi)$, x_a will be our notation for the label of a.*

Our genealogical process will be a labelled partition. As in classical representations of genealogical processes, a block of the partition at genealogical time $t \geq 0$ contains the indices of the initial lineages which share a common ancestor t units of time in the past, and its label gives the current location of this ancestor in $E = \mathbb{R}^2$.

From the description of the forwards-in-time dynamics, the evolution of a sample of ancestral lineages represented by a labelled partition should be the following. We start with a finite collection of lineages at time 0. At each point $(-t, x, r) \in \Pi$ (with $t \geq 0$ here, since genealogical time points towards the past), given that $u \in [0, 1]$ is the result of the sampling according to ν_r each lineage present in the ball $B(x, r)$, independently, is affected (resp., is not affected) with probability u (resp., $1-u$). A site y is chosen uniformly in $B(x, r)$, and the blocks of all affected lineages merge into a single block labelled by y. The other blocks and their labels are not modified. We write $\{\mathscr{A}(t),\ t \geq 0\}$ for the Markov process of coalescing lineages described in this way. Its state space is $\bigcup_{n\geq 1} \mathscr{P}_n^\ell$. Note that $\mathscr{A}$ is constructed on the same probability space as that of the Poisson point process of reproduction events. Writing $\mathbb{P}$ for the probability measure on that space, we abuse notation slightly by writing $\mathbb{P}_A$ to indicate that $\mathscr{A}(0) = A$, $\mathbb{P}_A$-a.s. Now let us verify that our Condition (5) is sufficient to ensure that the process $\{\mathscr{A}(t), t \geq 0\}$ is well-defined. Since two lineages currently at separation $y \in \mathbb{R}^2$ will coalesce if they are *both* involved in a replacement event, which happens at instantaneous rate

$$\int_{(|y|/2,\infty)} L_r(y, 0) \left(\int_{[0,1]} u^2 \nu_r(du) \right) \mu(dr), \tag{6}$$

Condition (5) is more than enough to bound the rate of coalescence of ancestral lineages. To guarantee that we can fit together the measures ρ at different points in a consistent way, we also need to be able to control the spatial motion of ancestral lineages. Consider the (backwards in time) dynamics of a single ancestral lineage. It evolves in a series of jumps with intensity

$$dt \otimes \int_{(|x|/2,\infty)} \int_{[0,1]} \frac{L_r(x, 0)}{\pi r^2} u \nu_r(du) \mu(dr) dx \tag{7}$$

on $\mathbb{R}_+ \times \mathbb{R}^2$. If we want this to give a well-defined Lévy process, then we require

$$\int_{\mathbb{R}^2} (1 \wedge |x|^2) \left(\int_{(|x|/2,\infty)} \int_{[0,1]} \frac{L_r(x, 0)}{\pi r^2} u \nu_r(du) \mu(dr) \right) dx < \infty. \tag{8}$$

But Condition (5) certainly guarantees this. In fact it ensures that the rate of jumps of each ancestral lineage is *finite*. In other words, ancestral lineages follow compound Poisson processes.

Remark 2.6. *At first sight it is disappointing that we have to take Condition (5) and hence obtain a system of coalescing compound Poisson processes rather than more general symmetric Lévy processes that (4) and (8) would allow. However, biologically there is not much loss. The 'gap' between Condition (5) and the weaker Condition (4) is that the latter would allow one to include very large numbers of extremely small jumps (in which only a tiny proportion of the population is affected) as the radius of the area affected by a reproduction event tends to zero. But in our population model, for small r we expect that a* large *proportion of the population in the neighbourhood be replaced.*

Remark 2.7. *Notice that the locations of ancestral lineages are* not *independent of one another. Knowing that one lineage has jumped tells us that a reproduction event has taken place that could have affected other lineages ancestral to our sample. Wilkins & Wakeley (2002) consider a somewhat analogous model in which a linear population evolves in discrete generations (see Wilkins 2004 for a two-dimensional analogue). Each individual in the parental generation scatters an infinite pool of gametes in a Gaussian distribution about themselves, and the next generation is formed by sampling from the pool of gametes at each point. Individuals are assumed to have a finite linear width to avoid the pathologies that arise when common ancestry in a continuum model requires two ancestral lineages to have a physical separation of zero. They observe that "conditional on not coalescing in the previous generation, two lineages are slightly more likely to be further apart than closer together". In their setting a change of coordinates settles the problem: the distance apart and the average position of two lineages do evolve independently. For us the dependencies between lineages are more complex because the presence of a jump contains the information that a reproduction event has taken place, whereas the conditioning obviously tells us nothing about the timing of events in the discrete generation model.*

3 The genealogy of points sampled uniformly from a large torus

We now turn our attention to populations evolving on a two-dimensional torus of sidelength L. Our goal is to describe the genealogy of a finite number of individuals sampled uniformly at random from the torus and subject to events of very different scales, as $L \to \infty$

To this end, we now consider a family of models indexed by $\mathbb{N}$. For each $L \in \mathbb{N}$, we consider a population evolving on the torus $\mathbb{T}(L) \subset \mathbb{R}^2$ of sidelength L. We identify $\mathbb{T}(L)$ with the subset $[-L/2, L/2]^2$ of $\mathbb{R}^2$ and use the Euclidean norm $|\cdot|$ induced on $\mathbb{T}(L)$ by this identification. Although $B_{\mathbb{T}(L)}(x,r)$ will be our notation for the ball in $\mathbb{T}(L)$ centred in x and with radius r, we shall omit the subscript when there is no risk of confusion.

The population will be subject to two different classes of events that we call *small* and *large*. The region affected by each small event will be uniformly bounded (independently of the size of the torus). Large events will affect regions whose diameter is on the order of ψ_L which will be taken to grow with L, but they will be less frequent. We shall assume that the rate at which a given ancestral lineage is affected by a large event is proportional to $1/\rho_L$ with ρ_L also chosen to grow with L.

Now let us make the model more precise. Let $(\psi_L)_{L\geq 1}$ be an increasing sequence such that there exists $\alpha \in (0,1]$ satisfying

$$\lim_{L\to\infty} \frac{\log \psi_L}{\log L} = \alpha, \tag{9}$$

and assume that $|\alpha \log L - \log \psi_L| = o((\log L)^{-1/2})$ as $L \to \infty$.

Remark 3.1. *The latter assumption is not necessary since all our results would still hold with each occurrence of* $(1-\alpha)\log L$ *replaced by* $\log(L\psi_L^{-1})$ *(see the end of the proof of Proposition 6.2), but it is weak and considerably simplifies the presentation.*

Let $(\rho_L)_{L\geq 1}$ be an increasing sequence with values in $(0,+\infty]$, tending to infinity as $L\to\infty$. Finally, let $\mu^s(dr)$ and $\mu^B(dr)$ be two σ-finite Borel measures on $(0,\infty)$, independent of L, such that there exist some positive constants R^s and R^B satisfying

$$\inf\{R:\mu^s\big((R,\infty)\big)=0\}=R^s<\infty \quad\text{and}\quad \inf\{R:\mu^B\big((R,\infty)\big)=0\}=R^B<\infty.$$

(For convenience, we ask that $R^B\leq 1/\sqrt{2}$ if $\alpha=1$.) To every $r\geq 0$, we associate two probability measures $\nu_r^s(du)$ and $\nu_r^B(du)$ on $[0,1]$, and we assume that for $\star\in\{B,s\}$ and for each $\varepsilon\in(0,R^\star)$,

$$\mu^\star\big(\{r\in[R^\star-\varepsilon,R^\star]:\nu_r^\star\neq\delta_0\}\big)>0. \tag{10}$$

If Condition (10) does not hold, we decrease the corresponding radius $R^\star$ since otherwise the largest events never affect a lineage.

Let us suppose that for each $L\geq 1$, the reproduction events of the forwards in time model can be of two types :

- **Small events**, given by a Poisson point process Π_L^s on $\mathbb{R}\times\mathbb{T}(L)\times(0,\infty)$ with intensity measure $dt\otimes dx\otimes\mu^s(dr)$. If (t,x,r) is a point of Π_L^s, then the centre of the reproduction event is x, its radius is r and the fraction of individuals replaced during the event is chosen according to ν_r^s.
- **Large events**, given by a Poisson point process Π_L^B on $\mathbb{R}\times\mathbb{T}(L)\times(0,\infty)$, independent of Π_L^s and with intensity measure $(\rho_L\psi_L^2)^{-1}dt\otimes dx\otimes\mu^B(dr)$. If (t,x,r) is a point of Π_L^B, then the centre of the reproduction event is x, its radius is $\psi_L r$ and the fraction of individuals replaced during the event is chosen according to ν_r^B.

Notice that we allow ρ_L to be infinite, in which case large events do not occur. Since Π_L^s and Π_L^B are independent, the reproduction events could be formulated in terms of a single Poisson point process to fit into the Definition 2.2 of the spatial Λ-Fleming-Viot process. However, our aim here is to disentangle the effects of events of different scales, hence our decomposition into two point processes.

Remark 3.2. *Observe that, although the intensity of* Π_L^B *is proportional to* $(\rho_L\psi_L^2)^{-1}$*, the rate at which a lineage is affected by (that is, jumps because of) a large event is of order* $\mathcal{O}(\rho_L^{-1})$*. Indeed, the volume of possible centres for such an event is proportional to* ψ_L^2*, so that the jump rate of a lineage due to the large events is given by*

$$\frac{1}{\rho_L\psi_L^2}\int_0^{R^B}\int_0^1\pi(\psi_L r)^2u\ \nu_r^B(du)\mu^B(dr)=\frac{\pi}{\rho_L}\int_0^{R^B}\int_0^1 r^2u\ \nu_r^B(du)\mu^B(dr).$$

In order for the genealogical processes, which we now denote by $\mathscr{A}^L$ to emphasize dependence on L, to be well-defined for every $L\in\mathbb{N}$, we assume that Condition (5) is fulfilled. In this setting, the condition can be written

$$\int_0^{R^s}\int_0^1 r^2u\ \nu_r^s(du)\mu^s(dr)+\frac{1}{\rho_L}\int_0^{R^B}\int_0^1 r^2u\ \nu_r^B(du)\mu^B(dr)<\infty.$$

Let us introduce some more notation. We write

$$\Gamma(L,1) \equiv \left\{ x \in \mathbb{T}(L) : |x| \geq \frac{L}{\log L} \right\},$$

and for each integer $n \geq 2$,

$$\begin{aligned}\Gamma(L,n) &\equiv \left\{ \{x_1,\dots,x_n\} \in \mathbb{T}(L)^n : |x_i - x_j| \geq \frac{L}{\log L} \text{ for all } i \neq j \right\}, \\ \Gamma_{\mathscr{A}}(L,n) &\equiv \left\{ \{(a_1,x_{a_1}),\dots,(a_k,x_{a_k})\} \in \mathscr{P}_n^{\ell} : \{x_{a_1},\dots,x_{a_k}\} \in \Gamma(L,k) \right\},\end{aligned}$$

where as before $\mathscr{P}_n^{\ell}$ denotes the labelled partitions of $\{1,\dots,n\}$. When we require an element A of $\Gamma_{\mathscr{A}}(L,n)$ to have exactly n blocks, we shall write $A \in \Gamma_{\mathscr{A}}(L,n)^*$.

In order to obtain a non-trivial limit, we rescale time for the process $\mathscr{A}^L$ by a factor that we denote ϖ_L. Recall that if $A \in \mathscr{P}_n^{\ell}$ for some $n \in \mathbb{N}$, bl(A) stands for the unlabelled partition of $\{1,\dots,n\}$ induced by A. For each $L \in \mathbb{N}$, let us define the (non-Markov) process $\mathscr{A}^{L,u}$ by

$$\mathscr{A}^{L,u}(t) = \mathrm{bl}\big(\mathscr{A}^L(\varpi_L t)\big), \qquad t \geq 0.$$

Note that for each $L \in \mathbb{N}$, if we start $\mathscr{A}^L$ from A_L, a labelled partition of $\{1,\dots,n\}$ with labels from $\mathbb{T}(L)$, then $\mathscr{A}^{L,u}$ takes its values in the Skorohod space $D_{\mathscr{P}_n}[0,\infty)$ of all càdlàg paths with values in $\mathscr{P}_n$ (the set of partitions of $\{1,\dots,n\}$), $\mathbb{P}_{A_L}$-a.s.

Recall the definition of α given in (9). In the absence of large events, our model is similar in many respects to the two-dimensional stepping stone model and so it comes as no surprise that just as for the stepping stone model, the genealogy of a random sample from the torus should converge (on a suitable timescale) to a Kingman coalescent as the size of the torus tends to infinity (see in particular Cox & Griffeath 1986,1990, Cox & Durrett 2002 and Zähle et al. 2005 for precise statements of this result in different contexts). Our first result says that if $\alpha < 1$, then we still obtain a Kingman coalescent, but the *timescale* will be influenced by the large events: the latter reduce the effective population size.

Before stating the result formally, let us try to understand why we should expect something like this to be true. To understand the appropriate timescale we just need to consider two lineages. The time they need to coalesce will be decomposed into two phases. If ρ_L is not too big, the first phase will be the time until they first come within distance $2R^B\psi_L$ and the second will be the additional time required for them to coalesce. During the first phase they evolve according to independent compound Poisson processes. If ρ_L is small enough, the coalescence event that will eventually occur during the second phase will, with probability close to one, be triggered by a large event. For larger values of ρ_L, large events will not be frequent enough to hit the two lineages when they are at a distance that would allow them to coalesce (i.e., less than $2R^B\psi_L$), and coalescence will instead be caused by a small-scale event. The first phase is then taken to be the time until the lineages first come within distance $2R^s$ of one another. The fact that with high probability they will not be hit by the same large-scale event means that once again they evolve (almost) independently of one another during this first phase. The second phase is now the time taken for them to coalesce due to a small event. The transition between these two regimes is when $\rho_L \propto \psi_L^2 \log L$. Now suppose that we start from a sample in $\Gamma(L,n)$. The first phase is then long enough that, when it ends, the spatial location of lineages is no longer correlated with their starting points. Finally, why do large-scale events not lead to multiple mergers? The key point is that, when a pair of lineages ancestral to our sample first comes within $2R^B\psi_L$ of one another, all *other* pairs are still well-separated. So if ρ_L is not too big, this pair will coalesce before a third lineage can come close enough to be affected by a common event. If we take larger ρ_L, the reason is exactly the same but now lineages have to come within distance $2R^s$ and coalescence is driven by small events.

Here then is the formal result which makes explicit the convergence in distribution of our spatial genealogies to a nonspatial coalescent process. In the following, σ_s^2 (resp., $\sigma_B^2\psi_L^2\rho_L^{-1}$) is the variance of the displacement of a lineage during one unit of time due to small (resp., large) events, see (20) below.

Theorem 3.3. *Let $\mathscr{K}$ denote Kingman's coalescent, and recall that for each $n \in \mathbb{N}$, $\wp_n$ denotes the partition of $\{1, \dots, n\}$ into singletons. In the notation of (9), suppose $\alpha < 1$ (and (10) holds). Then, for each integer $n \geq 2$ and any sequence $(A_L)_{L\in\mathbb{N}}$ such that $A_L \in \Gamma_{\mathscr{A}}(L,n)^*$ for every L,*

$$\mathscr{L}_{\mathbb{P}_{A_L}}(\mathscr{A}^{L,u}) \Rightarrow \mathscr{L}_{\mathbb{P}_{\wp_n}}(\mathscr{K}) \qquad \text{as } L \to \infty,$$

where

$$\varpi_L = \begin{cases} \frac{(1-\alpha)\rho_L L^2 \log L}{2\pi\sigma_B^2\psi_L^2} & \text{if } \rho_L^{-1}\psi_L^2 \to \infty, \\ \frac{(1-\alpha)L^2\log L}{2\pi(\sigma_s^2 + b\sigma_B^2)} & \text{if } \rho_L^{-1}\psi_L^2 \to b \in [0,\infty) \text{ and } \frac{\psi_L^2 \log L}{\rho_L} \to \infty, \\ \frac{L^2\log L}{2\pi\sigma_s^2} & \text{if } (\rho_L^{-1}\psi_L^4)_{L\geq 1} \text{ is bounded or } \frac{L^2\log L}{\rho_L} \to 0. \end{cases}$$

Here $\mathscr{L}_{\mathrm{P}}(X)$ denotes the law under the probability measure P *of the random variable X and $\Rightarrow$ refers to weak convergence of probability measures.*

For $\alpha = 1$, things are more complicated. When ψ_L is commensurate with L, large scale events cover a non-negligible fraction of the torus. If they happen too quickly, then they will be able to capture multiple lineages while the locations of those lineages are still correlated with their starting points. For intermediate ranges of ρ_L, lineages will have homogenised their positions on $\mathbb{T}(L)$ through small events, but not coalesced, before the first large event occurs and we can expect a Λ-coalescent limit. If the large events are too rare, then coalescence will be through small events and we shall recover the Kingman coalescent again.

To give a precise result we need to define the limiting objects that arise. In the case $\alpha = 1$, for each $L \in \mathbb{N}$, we set

$$\varpi_L = \begin{cases} \rho_L & \text{if } \rho_L/(L^2\log L) \text{ has a finite limit}, \\ \frac{L^2\log L}{2\pi\sigma_s^2} & \text{if } \rho_L/(L^2\log L) \to +\infty, \end{cases}$$

and define $\mathscr{A}^{L,u}$ as before. Since we shall need to keep track of the labels (spatial positions) of the ancestral lineages in some cases, it will also be convenient to introduce the following rescaling of $\mathscr{A}^L$, evolving on $\mathbb{T}(1)$ for all $L \in \mathbb{N}$:

$$\bar{\mathscr{A}}^L(t) = \frac{1}{L}\,\mathscr{A}^L(\varpi_L t), \qquad t \geq 0,$$

where by this notation we mean that the labels are rescaled by a factor L^{-1}. Similarly, for $\mathbf{x} \in \mathbb{T}(1)^n$ we write $L\mathbf{x}$ for $(Lx_1, \dots, Lx_n) \in \mathbb{T}(L)^n$. Finally, let us introduce the processes which will appear as the limits of our rescaled genealogical processes.

Definition 3.4. *Let $b \in [0,\infty)$ and $c > 0$. We call $\bar{\mathscr{A}}^{\infty,b,c}$ the Markov process with values in $\bigcup_{n\in\mathbb{N}} \mathscr{P}_n^\ell$ (with labels in $\mathbb{T}(1)$) such that*

1. *The labels of the lineages perform independent Brownian motions on $\mathbb{T}(1)$ at speed $b\sigma_s^2$ (if $b = 0$, the labels are constant), until the first large event occurs.*
2. *Large events are generated by a Poisson point process $\overline{\Pi}^B$ on $\mathbb{R} \times \mathbb{T}(1) \times (0, 1/\sqrt{2}]$ with intensity measure $c^{-2} dt \otimes dx \otimes \mu^B(dr)$. At a point (t,x,r) of $\overline{\Pi}^B$, a number $u \in [0,1]$ is sampled from the probability measure ν_r^B, and each lineage whose label belongs to $B_{\mathbb{T}(1)}(x,cr)$ is affected (resp., is not affected) by the event with probability u (resp., $1-u$), independently of each other. A label z is chosen uniformly at random in $B_{\mathbb{T}(1)}(x,cr)$, and all the lineages affected merge into one block which adopts the label z. The other lineages (blocks and labels) remain unchanged.*
3. *The evolution of the labels starts again in the same manner.*

Remark 3.5. *Notice that this process looks like another spatial Λ-coalescent, except that now ancestral lineages perform independent spatial motions in between coalescence events. This process is dual (in the obvious way) to a spatial Λ-Fleming-Viot process in which, during their lifetimes, individuals move around in space according to independent Brownian motions.*

For each $r \in [0, 1/\sqrt{2}]$, let V_r denote the volume of the ball $B_{\mathbb{T}(1)}(0,r)$.

Definition 3.6. *Let $\beta \in [0,\infty)$ and $c > 0$. We use $\Lambda^{(\beta,c)}$ to denote the Λ-coalescent, defined on $\bigcup_{n\in\mathbb{N}} \mathscr{P}_n$, for which if there are currently m ancestral blocks, then each transition involving k of them merging into one happens at rate*

$$\lambda_{m,k}^{(\beta,c)} = c^{-2} \int_0^{(\sqrt{2})^{-1}} \int_0^1 (V_{cr}u)^k (1 - V_{cr}u)^{m-k} \nu_r^B(du) \mu^B(dr) + \beta\ \delta_{\{k=2\}}.$$

Recall the notation $\wp_n$ and $\wp_n(\mathbf{x})$ introduced in Notation 2.5, and $\mathscr{L}_{\mathrm{P}}(X)$ and $\Rightarrow$ introduced in the statement of Theorem 3.3. We can now state the result for $\alpha = 1$.

Theorem 3.7. *Suppose there exists $c > 0$ such that for every $L \in \mathbb{N}$, $\psi_L = cL$. Let $n \in \mathbb{N}$, $\mathbf{x} \in \mathbb{T}(1)^n$ such that $x_i \neq x_j$ whenever $i \neq j$, and let $(A_L)_{L\in\mathbb{N}}$ be such that for every L, $A_L \in \Gamma_{\mathscr{A}}(L,n)^*$. Then, as $L \to \infty$,*

(a) If $\rho_L L^{-2} \to b \in [0,\infty)$,

$$\mathscr{L}_{\mathbb{P}_{\wp_n(L\mathbf{x})}}\big(\bar{\mathscr{A}}^L\big) \Rightarrow \mathscr{L}_{\mathbb{P}_{\wp_n(\mathbf{x})}}\big(\bar{\mathscr{A}}^{\infty,b,c}\big),$$

(b) If $\rho_L L^{-2} \to \infty$, $\frac{2\pi\sigma_s^2\rho_L}{L^2\log L} \to \beta \in [0,\infty)$ and if the total rate of occurrence of large events is finite (i.e., μ^B has finite total mass),

$$\mathscr{L}_{\mathbb{P}_{A_L}}\big(\mathscr{A}^{L,u}\big) \Rightarrow \mathscr{L}_{\mathbb{P}_{\wp_n}}\big(\Lambda^{(\beta,c)}\big).$$

(c) If $\frac{\rho_L}{L^2\log L} \to \infty$,

$$\mathscr{L}_{\mathbb{P}_{A_L}}\big(\mathscr{A}^{L,u}\big) \Rightarrow \mathscr{L}_{\mathbb{P}_{\wp_n}}\big(\mathscr{K}\big).$$

Notice that the case (a) differs from all other cases in that the influence of space does not disappear as $L \to \infty$ and the evolution of the limiting genealogy still depends on the precise locations of the lineages.

The intuition behind Theorem 3.7 is as follows. If $\psi_L \propto L$ large events cover a non-negligible fraction of the torus, and so only a few large events are sufficient to gather two lineages at a distance at which they can coalesce. However, a local central limit theorem will give us that on a timescale of order at most $\mathcal{O}(L^2)$, a lineage subject to only small events behaves approximately like Brownian motion, whereas after a time $t_L \gg L^2$, its distribution is nearly uniform on $\mathbb{T}(L)$ (for L large enough, see Lemma 5.4). Since the mean time before a large event affects a lineage is of order $\mathcal{O}(\rho_L)$, the limiting genealogical process (when we include both large and small reproduction events) will depend on how ρ_L scales with L^2. If ρ_L is of order at most $\mathcal{O}(L^2)$, then space matters and the process $\mathcal{A}^L$ rescaled to evolve on $\mathbb{T}(1)$ on the timescale ρ_L converges to a system of coalescing Brownian motions, whereas if $\rho_L \gg L^2$, the homogenisation of the labels/locations of the lineages before the occurrence of the first large event which affects them leads to a limiting unlabelled genealogical process given by an exchangeable coalescent with multiple mergers.

Remark 3.8. *It is somehow disappointing that we must impose a finite rate of large events to obtain the convergence of Theorem 3.7(b). Indeed, it seems that case (a) should give us the right picture: in the limit, in between large events lineages perform Brownian motions on the torus of sidelength 1 due to small events, except that now the time required for at least one lineage to be affected by a large event is so long that lineages exhaust space and their locations become uniformly distributed over the torus before they are taken by a coalescence event. However, when* μ^B *has infinite mass, lineages are infinitely often in the (geographical) range of a large reproduction event over any interval of time, and we need good control of their complete paths to actually be able to say something about the epoch and outcome of the first potential coalescence event. Now, observe that Equation (54) can only be generalized to the finite-dimensional distributions of these paths, and does not guarantee that a large event cannot capture some of the lineages at a time when they are not uniformly distributed over* $\mathbb{T}(1)$.

Theorem 3.7 deals with the case where ψ_L is proportional to L. Let us now comment on the remaining cases, in which $\alpha = 1$ but $\psi_L \ll L$. First, it is easy to see that the convergence in (c) still holds, since it is based on the fact that large events are so rare that none of them occurs before small events reduce the genealogical process to a single lineage.

Second, since the total rate of large events on the timescale ρ_L is $\mu^B(\mathbb{R}_+)L^2/\psi_L^2$, it cannot be bounded unless $\mu^B \equiv 0$ (a situation we excluded in (10)). On the other hand, for the reason expounded in Remark 3.8 we are unable to derive a limiting behaviour for the genealogy when large events can accumulate, and so the result of Theorem 3.7(b) has no counterpart when $\psi_L \ll L$.

Third, as explained above, when $\rho_L \leq bL^2$ any limiting process will necessarily have a spatial component. Now, because we start with lineages at distance $\mathcal{O}(L)$ of each other, we need to rescale space by L in order to obtain a non trivial initial condition. The last parameter we need is the timescale ϖ_L on which to consider the genealogical process. But a separation of timescales will not occur here, and so the computations done in Section 5 will show that the suitable choice of ϖ_L depends on the precise behaviour of ρ_L/L^2 and ρ_L/ψ_L^2. Several limiting processes are thus possible, and since all the arguments needed to derive these limits are scattered in Sections 5 and 7, we chose not to detail them here.

4 Existence and uniqueness of the forwards-in-time process

Our spatial Λ-Fleming-Viot process associates a probability measure on type space to each point in $\mathbb{R}^2$. In other words, it takes its values among functions from $\mathbb{R}^2$ to $\mathscr{M}_1([0,1])$. Evans (1997) uses duality with a system of coalescing Borel right processes on a Lusin space E to construct a family of Markov processes with values in the set of functions from E to $\mathscr{M}_1(\{0,1\}^{\mathbb{N}})$ (or equivalently, to $\mathscr{M}_1([0,1])$). He also obtains uniqueness in distribution of the process. In his setting, coalescing particles evolve independently until they meet, at which point they instantly coalesce. In our case, the particles in the candidate dual do not move independently and nor do two particles hit by the same reproduction event necessarily coalesce, but nonetheless the key ideas from his construction remain valid. Note that, although we present the result in two dimensions, the proof carries over to other dimensions.

First we give a formal description of the coalescing dual and then we use the Evans' construction to give existence and uniqueness in law of a process ρ which assigns a probability measure on $[0,1]$ to each point in $\mathbb{R}^2$. We then identify ρ as the spatial Λ-Fleming-Viot process in which we are interested.

4.1 State-space of the process and construction via duality

We shall only present the main steps of the construction, and refer to Evans (1997) for more details. Let us define $\tilde{\Xi}$ as the space of all Lebesgue-measurable maps $\rho : \mathbb{R}^2 \to \mathscr{M}_1([0,1])$. Two elements ρ_1 and ρ_2 of $\tilde{\Xi}$ are said to be equivalent if $\mathrm{Leb}(\{x \in \mathbb{R}^2 : \ \rho_1(x) \neq \rho_2(x)\}) = 0$. Let Ξ be the quotient space of $\tilde{\Xi}$ by this equivalence relation. If E is a compact space, let us write $C(E)$ for the Banach space of all continuous functions on E, equipped with the supremum norm $\|\cdot\|_\infty$. For each $n \in \mathbb{N}$, let $L^1(C([0,1]^n))$ be the Banach space of all Lebesgue-measurable maps $\Phi : (\mathbb{R}^2)^n \to C([0,1]^n)$ such that $\int_{(\mathbb{R}^2)^n} \|\Phi(x)\|_\infty \, dx < \infty$. A remark in Section 3 of Evans (1997) tells us that the separability of $L^1(C([0,1]))$ and a functional duality argument guarantee that Ξ, equipped with the relative weak* topology, is a (compact) metrisable space. Finally, if λ is a measure on a space E', let us write $L^1(\lambda)$ for the set of all measurable functions $f : E' \to \mathbb{R}$ such that $\int_{E'} |f(e)| \lambda(de) < \infty$.

Let $n \in \mathbb{N}$. Given $\Phi \in L^1(C([0,1]^n))$, let us define a function $I_n(\cdot\,;\Phi) \in C(\Xi)$ by

$$I_n(\rho;\Phi) \equiv \int_{(\mathbb{R}^2)^n} \Big\langle \bigotimes_{1\leq i\leq n} \rho(x_i), \Phi(x_1,\dots,x_n) \Big\rangle \, dx_1 \dots dx_n,$$

where as before the notation $\langle \nu, f \rangle$ stands for the integral of the function f against the measure ν. We have the following lemma, whose proof is essentially that of Lemma 3.1 in Evans (1997).

Lemma 4.1. *The linear subspace spanned by the constant functions and functions of the form $I_n(\cdot\,;\Phi)$, with $\Phi = \psi \otimes \big(\prod_{i=1}^n \chi_i\big)$, $\psi \in L^1(dx^{\otimes n}) \cap C((\mathbb{R}^2)^n)$ and $\chi_i \in C([0,1])$ for all $1 \leq i \leq n$ is dense in $C(\Xi)$.*

We need a last definition before stating the existence and uniqueness result. Let $n \in \mathbb{N}$. For any $\rho \in \Xi$, $\pi \in \mathscr{P}_n^\ell$ such that $\mathrm{bl}(\pi) = \{a_1,\dots,a_k\}$, and any bounded measurable function $F : [0,1]^n \to \mathbb{R}$, we set

$$\Upsilon_n(\rho;\pi;F) \equiv \int_{[0,1]^k} F(\nu_{a^{-1}(1)},\dots,\nu_{a^{-1}(n)}) \rho(x_{a_1})(d\nu_{a_1}) \dots \rho(x_{a_k})(d\nu_{a_k}),$$

where $a^{-1}(i)$ is the (unique) block a_j which contains i and v_{a_j} is the variable used for the measure $\rho(x_{a_j})$. In words, we assign the same variable to all coordinates which belong to the same block in the partition π. (Recall that x_a is our notation for the label of block a.) Recall also the notation $\wp_n(\mathbf{x})$ and $\mathscr{A}$ introduced in Notation 2.5 and the following paragraph.

Theorem 4.2. *There exists a unique, Feller, Markov semigroup $\{Q_t, t \geq 0\}$ on Ξ such that for all $n \in \mathbb{N}$ and $\Phi \in L^1(C([0,1]^n))$, we have*

$$\int Q_t(\rho, d\rho') I_n(\rho';\Phi) = \int_{(\mathbb{R}^2)^n} \mathbb{E}_{\wp_n(\mathbf{x})}\big[\Upsilon_n\big(\rho;\mathscr{A}(t);\Phi(x_1,\dots,x_n)\big)\big]\,dx_1\dots dx_n. \tag{11}$$

Consequently, there exists a Hunt process $\{\rho(t), t \geq 0\}$ with state-space Ξ and transition semigroup $\{Q_t, t \geq 0\}$.

Before proving Theorem 4.2, let us make two comments on this result. First, since the Ξ-valued process we obtain is a Hunt process it is càdlàg and quasi-left continuous, that is, it is almost surely left-continuous at any previsible stopping time (see e.g. Rogers & Williams 1987 for a definition of quasi-left continuous filtrations). However, more precise statements on its space-time regularity seem to be a delicate question, which will require a thorough investigation.

Second, as in Kimura's stepping stone model introduced in (1), the duality relation (11) can be interpreted in terms of genealogies of a sample of individuals. Indeed, recall the stepping stone model is dual to the system $(\{n_i(t);\ i \in I\})_{t\geq 0}$ of particles migrating from deme i to deme j at rate m_{ji} and coalescing in pairs at rate $1/N_e$ when in the same deme: for any $t \geq 0$, we have

$$\mathbb{E}\Big[\prod_{i\in I} p_i(t)^{n_i(0)}\Big] = \mathbb{E}\Big[\prod_{i\in I} p_i(0)^{n_i(t)}\Big].$$

These equations show that a function (here the $n_i(0)$-th moments) of the frequencies at different sites of $\mathbb{Z}^2$ and at (forward) time t can be expressed in terms of the genealogy of a sample made of $n_i(0)$ individuals in deme i for every $i \in I$, and run for a (backward) time t: all lineages having coalesced by time t necessarily carry the same type, whose law is given by the type distribution at the site where their ancestor lies at backward time t (or forward time 0). Equation (11) can be interpreted in exactly the same manner, but holds for a much wider collection of functions of ρ and $\mathscr{A}$.

Proof of Theorem 4.2: The observation that the construction of Evans (1997) can also be justified in our setting follows from Remark (a) at the end of his Section 4.

Existence and uniqueness of $\mathscr{A}$ are easy from Assumptions (6) and (8). Next, we must verify consistency of $\mathscr{A}$ in the sense of his Lemma 2.1. In fact, this is the 'sampling consistency' described in the introduction and was a primary consideration in writing down our model. It follows since the movement of the labels of a collection of blocks does not depend on the blocks themselves and from the fact that a coalescence event of the form $\{(\{1\},x_1),(\{2\},x_2)\} \to \{(\{1,2\},x)\}$ for a pair of particles corresponds to a jump $\{(\{1\},x_1)\} \to \{(\{1\},x)\}$ onto the same site $x \in \mathbb{R}^2$ if we restrict our attention to the first particle.

The next property needed in the construction is that provided it is true at $t = 0$, for every $t > 0$ the distribution of the labels in $\mathscr{A}(t)$ has a Radon-Nikodym derivative with respect to Lebesgue measure, and furthermore an analogue of Evans' Equation (4.2) holds. In the setting of Evans (1997), the first requirement stems from the independence of the spatial motions followed by different labels and the corresponding result for a single label. Here, since the motion of all lineages is driven by the same Poisson process of events, their movements are correlated. However, the desired property is still satisfied. To see this, note that each jump experienced by a lineage in the interval $[-t,0]$ takes it to a position that is uniformly distributed over the open ball affected by the corresponding reproduction event. Thus, if $\mathscr{A}(t)$ has k blocks and $D\subset(\mathbb{R}^2)^k$ has zero Lebesgue measure, the probability that the labels of the blocks of $\mathscr{A}(t)$ belong to D is equal to 0. Equation (4.2) of Evans (1997) then still holds, without Evans' additional assumption of the existence of a dual process for the motion of one lineage (which anyway is satisfied since our lineages perform symmetric Lévy processes).

The last step is to check the strong continuity of the semigroup $\{Q_t, t\geq 0\}$, but this readily follows from the relation (11) and the Feller property of $\mathscr{A}$ (which is itself evident since jumps do not accumulate in our dual process).

The desired conclusion now follows from Theorem 4.1 in Evans (1997). □

4.2 Identification of the process

We can use (11) to derive an expression for the infinitesimal generator of $\{\rho(t), t\geq 0\}$ acting on the functions $I_n(\cdot\,;\Phi)$ considered in Lemma 4.1. This lemma and the uniqueness result stated in Theorem 4.2 guarantee that it will be sufficient to characterize the process ρ and to show that it corresponds to the evolution we described in Section 2 in terms of a Poisson point process of reproduction events.

Let $n\in\mathbb{N}$ and $\Phi\in C(\Xi)$ be such that $\Phi=\psi\otimes\big(\prod_{i=1}^n\chi_i\big)$, where $\psi\in L^1(dx^{\otimes n})\cap C((\mathbb{R}^2)^n)$ and $\chi_i\in C([0,1])$ for all $1\leq i\leq n$. Writing G for the generator of the process ρ and $\mathscr{G}_n$ for the generator of the coalescing Lévy processes $\mathscr{A}$ acting on functions of $\mathscr{P}_n^\ell$, we obtain from (11) that

$$\begin{aligned}
GI_n(\,\rho\,;\Phi) &= \lim_{t\to 0}\frac{\mathbb{E}_\rho[I_n(\rho(t),\Phi)]-I_n(\rho,\Phi)}{t}\\
&= \lim_{t\to 0}\frac{1}{t}\int_{(\mathbb{R}^2)^n}\psi(x_1,\ldots,x_n)\bigg\{\mathbb{E}_{\wp_n(\mathbf{x})}\Big[\Upsilon_n\Big(\rho;\mathscr{A}(t);\prod_{i=1}^n\chi_i\Big)\Big]-\prod_{i=1}^n\langle\rho(x_i),\chi_i\rangle\bigg\}\,dx^{\otimes n}\\
&= \int_{(\mathbb{R}^2)^n}\psi(x_1,\ldots,x_n)\,\mathscr{G}_n\Big[\Upsilon_n\Big(\rho;\,\cdot\,;\prod_{i=1}^n\chi_i\Big)\Big](\wp_n(\mathbf{x}))\,dx^{\otimes n}. \qquad (12)
\end{aligned}$$

Note that the quantity on the right-hand side of (12) is well-defined (and the interchange of limit and integral is valid) since ψ belongs to $L^1(dx^{\otimes n})$ and the rate at which at least one of $k\leq n$ blocks is affected by a reproduction event is bounded by n times the integral in (5), so that $\mathscr{A}$ is a jump-hold process and its generator satisfies

$$\Big\|\mathscr{G}_n\Big[\Upsilon_n\Big(\rho;\,\cdot\,;\prod_{i=1}^n\chi_i\Big)\Big]\Big\|_\infty\leq 2Cn\,\Big\|\Upsilon_n\Big(\rho;\,\cdot\,;\prod_{i=1}^n\chi_i\Big)\Big\|_\infty\leq 2Cn\prod_{i=1}^n\|\chi_i\|_\infty<\infty$$

for a given constant $C<\infty$.

Using the description of the evolution of $\mathscr{A}$ in terms of events in Π, the right-hand side of (12) is equal to

$$\int_{(\mathbb{R}^2)^n} dx^{\otimes n}\psi(x_1,\dots,x_n)\int_{\mathbb{R}^2} dy\int_0^\infty \mu(dr)\int_0^1 \nu_r(du)\int_{B(y,r)}\frac{dz}{\pi r^2}$$
$$\times\sum_{I\subset\{1,\dots,n\}}\Big[\prod_{i\in I}\mathbf{1}_{B(y,r)}(x_i)\prod_{i'\notin I}\mathbf{1}_{B(y,r)^c}(x_{i'})\Big]$$
$$\times\sum_{J\subset I}u^{|J|}(1-u)^{|I|-|J|}\Big[\prod_{i\notin J}\langle\rho(x_i),\chi_i\rangle\Big]\Big[\Big\langle\rho(z),\prod_{j\in J}\chi_j\Big\rangle-\prod_{j\in J}\langle\rho(x_j),\chi_j\rangle\Big], \tag{13}$$

where $|\cdot|$ stands for cardinality. Indeed, given $x_1,\dots,x_n$ in (13), only one term in the sum over $I\subset\{1,\dots,n\}$ is non-zero. For this particular term, each of the $|I|$ blocks whose labels lie in $B(y,r)$ belong to the set J of the blocks affected by the event with probability u (independently of one another), and the affected blocks adopt the label z. After some algebra and several uses of Fubini's theorem, we obtain that (13) is equal to

$$\int_{\mathbb{R}^2} dy\int_0^\infty \mu\,(dr)\int_0^1 \nu_r(du)\int_{B(y,r)}\frac{dz}{\pi r^2}\int_0^1 \rho_z(dk)\int dx_1\dots dx_n\;\psi(x_1,\dots,x_n)$$
$$\times\sum_{I\subset\{1,\dots,n\}}\prod_{j\notin I}\{\mathbf{1}_{B(y,r)^c}(x_j)\langle\rho_{x_j},\chi_j\rangle\}\prod_{i\in I}\mathbf{1}_{B(y,r)}(x_i)$$
$$\times\Big(\prod_{i\in I}\langle(1-u)\rho_{x_i}+u\delta_k,\chi_i\rangle-\prod_{i\in I}\langle\rho_{x_i},\chi_i\rangle\Big), \tag{14}$$

which is precisely the generator of the forwards in time process of Section 2. Using Theorem 4.2, we arrive at the following result.

Proposition 4.3. *The martingale problem associated to the operator G defined by (14) on functions of the form given in Lemma 4.1 is well-posed. Furthermore, the spatial Λ-Fleming-Viot process ρ of Theorem 4.2 is the solution to it.*

5 Some estimates for symmetric Lévy processes

In this section, we gather some results on symmetric Lévy processes that we shall need to call upon in our proofs of Theorem 3.3 and Theorem 3.7. For the sake of clarity, the proofs of the three lemmas are given in Appendix A.

First, we introduce some notation that we shall use repeatedly.

Notation 5.1. *1. In the following, we shall suppose that all the random objects considered are constructed on the same probability space $(\Omega,\mathscr{F},\mathbb{P})$, and if X is a process defined on Ω with state-space E and $x\in E$, we shall write $\mathbb{P}_x$ for the probability measure on Ω under which $X(0)=x$ a.s.*

2. For a stochastic process $\{X_t\}_{t\geq 0}$ evolving in $\mathbb{T}(L)$, we shall write $T(R,X)$ for the first entrance time *of X into $B_{\mathbb{T}(L)}(0,R)$. When there is no ambiguity, we write simply $T(R)$.*

Let $(\ell^L)_{L\geq 1}$ be a sequence of Lévy processes such that for each $L \in \mathbb{N}$, ℓ^L evolves on the torus $\mathbb{T}(L)$ and $\ell^L(1) - \ell^L(0)$ has a covariance matrix of the form $\sigma_L^2\mathrm{Id}$. Assume that the following conditions hold.

Assumption 5.2. (i) *There exists $\sigma^2 > 0$ such that $\sigma_L^2 \to \sigma^2$ as $L \to \infty$.*

(ii) *$\mathbb{E}_0\big[|\ell^L(1)|^4\big]$ is bounded uniformly in L.*

Our first lemma describes the time ℓ^L needs to reach a ball of radius $d_L \ll L$ around 0, when it starts at distance $\mathcal{O}(L)$ of the origin (recall the definition of $\Gamma(L,1)$ given in Section 3).

Lemma 5.3. *Let $(d_L)_{L\geq 1}$ be such that $\liminf_{L\to\infty} d_L > 0$ and $\frac{\log^+(d_L)}{\log L} \to \gamma \in [0,1)$ as $L \to \infty$. Then,*

$$\lim_{L\to\infty} \sup_{t\geq 0} \sup_{x_L\in\Gamma(L,1)} \left| \mathbb{P}_{x_L}\left[T(d_L,\ell^L) > \frac{(1-\gamma)L^2\log L}{\pi\sigma^2}\, t \right] - e^{-t} \right| = 0. \tag{15}$$

The proof of Lemma 5.3 follows that of Theorem 2 in Cox & Durrett (2002). In particular, we shall use the following local central limit theorem (which is the counterpart in our setting of Lemma 3.1 in Cox & Durrett 2002). Let $\lfloor z \rfloor$ denote the integer part of $z \in \mathbb{R}$, and write $p^L(x,t)$ for $\mathbb{P}_x[\ell^L(t) \in B(0,d_L)]$.

Lemma 5.4. *(a) Let $\varepsilon_L = (\log L)^{-1/2}$. There exists a constant $C_1 < \infty$ such that for every $L \geq 2$,*

$$\sup_{t\geq\lfloor\varepsilon_L L^2\rfloor} \sup_{x\in\mathbb{T}(L)} \frac{\lfloor \varepsilon_L L^2 \rfloor}{d_L^2}\, p^L(x,t) \leq C_1. \tag{16}$$

(b) If $v_L \to \infty$ as $L \to \infty$, then

$$\lim_{L\to\infty} \sup_{t\geq\lfloor v_L L^2\rfloor} \sup_{x\in\mathbb{T}(L)} \frac{L^2}{d_L^2} \left| p^L(x,t) - \frac{\pi d_L^2}{L^2} \right| = 0. \tag{17}$$

(c) If $u_L \to \infty$ as $L \to \infty$ and $I(d_L,x) \equiv 1 + (|x|^2 \vee d_L^2)$, then

$$\lim_{L\to\infty} \sup_{x\in\mathbb{T}(L)} \sup_{u_L I(d_L,x)\leq t\leq\varepsilon_L L^2} \left| \frac{2\sigma_L^2 t}{d_L^2}\, p^L(x,t) - 1 \right| = 0. \tag{18}$$

(d) There exists a constant $C_2 < \infty$ such that for every $L \geq 1$,

$$\sup_{t\geq 0} \sup_{x\in\mathbb{T}(L)} \left(1 + \frac{|x|^2}{d_L^2} \right) p^L(x,t) \leq C_2. \tag{19}$$

In essence, Lemma 5.4 says that on the timescale $d_L^2 \ll t \ll L^2$, the Lévy process ℓ^L behaves like two-dimensional Brownian motion, whereas at any given time $t \gg L^2$, its location is roughly uniformly distributed over $\mathbb{T}(L)$.

Another consequence of Lemma 5.4 is the following result, which bounds the probability that ℓ^L hits a ball of bounded radius during a 'short' interval of time in the regime $t \gg L^2$.

Lemma 5.5. *Fix $R > 0$. Let $(U_L)_{L\geq 1}$ and $(u_L)_{L\geq 1}$ be two sequences increasing to infinity such that $U_L L^{-2} \to \infty$ as $L \to \infty$ and $2u_L \leq L^2(\log L)^{-1/2}$ for every $L \geq 1$. Then, there exist $C > 0$ and $L_0 \in \mathbb{N}$ such that for every sequence $(U_L')_{L\geq 1}$ satisfying $U_L' \geq U_L$ for each L, every $L \geq L_0$ and all $x \in \mathbb{T}(L)$,*

$$\mathbb{P}_x\Big[T(R,\ell^L) \in [U_L' - u_L, U_L'] \Big] \leq \frac{C u_L}{L^2}.$$

6 Proof of Theorem 3.3

Armed with the estimates of Section 5, we can now turn to the proofs of our main results.

Notation 6.1. *For each* $L \geq 1$*, let* $\{\xi^L(t), t \geq 0\}$ *be the Lévy process on* $\mathbb{T}(L)$ *whose distribution is the same as that of the motion of a single lineage subject to the large and small reproduction events generated by* Π_L^s *and* Π_L^B*.*

In the rest of this section, we assume that the assumptions of Theorem 3.3 are satisfied.

6.1 Coalescence time for two lineages

We begin by studying the genealogical process of a pair of lineages starting at distance $\mathcal{O}(L)$ from each other. Since the motions ξ_1^L and ξ_2^L of the lineages are distributed like two independent copies of the process ξ^L until the random time T_L at which they come at distance less than $2R^B\psi_L$, the difference

$$X^L(t) \equiv \xi_1^L(t) - \xi_2^L(t), \qquad 0 \leq t \leq T_L$$

has the same distribution as $\left\{\xi^L(2t),\ 0 \leq t \leq \frac{1}{2}\ T(2R^B\psi_L, \xi^L)\right\}$. We shall use Lemma 5.3 to derive the limiting distribution of T_L, but first we need to introduce the relevant variances. Consider a single lineage. Because it jumps at a finite rate owing to small and large events, the following two quantities are well-defined and finite :

$$\sigma_s^2 \equiv \int y^2\ \chi^s(dy, dz) \qquad \text{and} \qquad \sigma_B^2 \equiv \int y^2\ \chi^B(dy, dz), \tag{20}$$

where χ^s stands for the intensity measure of the small jumps experienced by the lineage and χ^B for that of the large jumps renormalised by ψ_L^{-1} (the form of these two measures is given in (7)). We now have all the ingredients we need to describe the asymptotic 'gathering time' of two lineages.

Proposition 6.2. (a) *If* $\rho_L^{-1}\psi_L^2 \to \infty$ *as* $L \to \infty$*, then*

$$\lim_{L\to\infty} \sup_{t\geq 0} \sup_{A_L \in \Gamma_{\mathscr{A}}(L,2)^*} \left| \mathbb{P}_{A_L}\left[T_L > \frac{(1-\alpha)\rho_L L^2 \log L}{2\pi\sigma_B^2\psi_L^2}\ t \right] - e^{-t} \right| = 0.$$

(b) *If* $\rho_L^{-1}\psi_L^2 \to b \in [0,\infty)$ *as* $L \to \infty$*, then*

$$\lim_{L\to\infty} \sup_{t\geq 0} \sup_{A_L \in \Gamma_{\mathscr{A}}(L,2)^*} \left| \mathbb{P}_{A_L}\left[T_L > \frac{(1-\alpha)L^2 \log L}{2\pi(\sigma_s^2 + b\sigma_B^2)}\ t \right] - e^{-t} \right| = 0.$$

Proof of Proposition 6.2: Let us first recall two results on Poisson point processes, which are consequences of the exponential formula given, for instance, in Section 0.5 of Bertoin (1996). Following Bertoin's notation, let $\{e(t), t \geq 0\}$ be a Poisson point process on $\mathbb{R} \times \mathbb{R}_+$ with intensity measure $\kappa(dy) \otimes dt$, where the Borel measure κ satisfies

$$\int_{\mathbb{R}} |1 - e^y|\kappa(dy) < \infty \qquad \text{and} \qquad \int_{\mathbb{R}} y^m \kappa(dy) = 0, \quad m \in \{1,3\}. \tag{21}$$

Under these conditions, we have for each fixed $t > 0$

$$\mathbb{E}\Big[\Big(\sum_{s\leq t} e(s)\Big)^2\Big] = t\int_{\mathbb{R}} y^2\kappa(dy), \tag{22}$$

$$\mathbb{E}\Big[\Big(\sum_{s\leq t} e(s)\Big)^4\Big] = 3t^2\Big(\int_{\mathbb{R}} y^2\kappa(dy)\Big)^2 + t\int_{\mathbb{R}} y^4\kappa(dy). \tag{23}$$

These properties will be useful in computing the variances and fourth moments of the random variables considered below.

Let us start with the proof of (a). Consider the process ℓ^L defined by: for every $t \geq 0$,

$$\ell^L(t) = \frac{1}{\psi_L}\,\xi^L(2\rho_L t).$$

This process evolves on the torus of sidelength $\psi_L^{-1}L$, and makes jumps of size $\mathcal{O}(\psi_L^{-1})$ at a rate of order $\mathcal{O}(\rho_L)$, as well as jumps of size $\mathcal{O}(1)$ at a rate of order $\mathcal{O}(1)$.

Let us check that ℓ^L satisfies the assumptions of Lemma 5.3. To this end, we view $\ell^L(1)$ starting at 0 as the sum of its jumps and adapt the problem to use the results on Poisson point processes given above. First, let us define $\hat{\ell}^L$ as the Lévy process on $\mathbb{R}^2$ evolving like ℓ^L (but without periodic conditions). For $i \in \{0,1\}$ and each $L \geq 1,\ t \geq 0$, let $\hat{\ell}^{L,i}(t)$ denote the i-th coordinate of $\hat{\ell}^L(t)$. Note that the distance reached by ℓ^L up to a given time t is less than or equal to the distance at which $\hat{\ell}^L$ traveled up to t, and so we can write

$$\begin{aligned}\mathbb{E}_0\big[|\ell^L(1)|^4\big] \leq \mathbb{E}_0\big[|\hat{\ell}^L(1)|^4\big] &= \mathbb{E}_0\Big[\Big\{\hat{\ell}^{L,1}(1)^2 + \hat{\ell}^{L,2}(1)^2\Big\}^2\Big]\\ &\leq 2\Big\{\mathbb{E}_0\big[\hat{\ell}^{L,1}(1)^4\big] + \mathbb{E}_0\big[\hat{\ell}^{L,2}(1)^4\big]\Big\}.\end{aligned}$$

By symmetry, we need only bound $\mathbb{E}_0\big[\hat{\ell}^{L,1}(1)^4\big]$. Let us denote by $a_1, a_2, \ldots \in [-2R^s/\psi_L,\, 2R^s/\psi_L]^2$ (resp., $b_1, b_2, \ldots \in [-2R^B, 2R^B]^2$) the sequence of the jumps of $\hat{\ell}^{L,1}$ before time 1 due to small (resp., large) events. Using the convexity of $y \mapsto y^4$, we have

$$\mathbb{E}_0\big[\hat{\ell}^{L,1}(1)^4\big] = \mathbb{E}_0\Big[\Big(\sum_i a_i + \sum_j b_j\Big)^4\Big] \leq 8\ \mathbb{E}_0\Big[\Big(\sum_i a_i\Big)^4 + \Big(\sum_j b_j\Big)^4\Big]. \tag{24}$$

Applying (23) to each term on the right-hand side of (24) yields

$$\mathbb{E}_0\big[(\hat{\ell}^{L,1}(1))^4\big] \leq 96\frac{\rho_L^2}{\psi_L^4}\,\sigma_s^4 + 16\frac{\rho_L}{\psi_L^4}\int y^4\chi^s(dy,dz) + 96\sigma_B^4 + 16\int y^4\chi^B(dy,dz), \tag{25}$$

which is bounded uniformly in L since $\rho_L\psi_L^{-2}$ vanishes as L grows to infinity, and each integral is finite. Coming back to the original problem, we obtain that Assumption 5.2 (ii) holds for the sequence of processes $(\ell^L)_{L\geq 1}$.

Concerning Assumption 5.2 (i), observe that σ_L^2 is simply the variance of $\ell^{L,1}(1)$. To obtain the asymptotic behaviour of σ_L^2, we show that up to time 1, ℓ^L does not see that it is on a torus. Hence, with high probability $\ell^{L,1}(1)^2 = \hat{\ell}^{L,1}(1)^2$ and so

$$\mathbb{E}_0\big[\ell^{L,1}(1)^2\big] \approx \mathbb{E}_0\big[\hat{\ell}^{L,1}(1)^2\big] = 2\frac{\rho_L}{\psi_L^2}\int y^2\chi^s(dy,dz) + 2\int y^2\chi^B(dy,dz) = 2\sigma_B^2 + o(1)$$

as $L \to \infty$, where the second equality uses (22). To make the first equality rigorous, we apply Doob's maximal inequality to the submartingale $|\hat{\ell}^L|^4$. This yields, with a constant $C > 0$ which may change from line to line,

$$\mathbb{P}_0\left[\sup_{0\le s\le 1} |\hat{\ell}^L(s)| > \frac{L}{3\psi_L}\right] \le \frac{C\psi_L^4}{L^4}\,\mathbb{E}_0\left[|\hat{\ell}^L(1)|^4\right].$$

But the calculation in (25) shows that the latter expectation is finite, and so

$$\mathbb{P}_0\left[\sup_{0\le s\le 1} |\hat{\ell}^L(s)| > \frac{L}{3\psi_L}\right] \le C\frac{\psi_L^4}{L^4}. \tag{26}$$

On the event $\mathscr{E}_L \equiv \left\{\sup_{0\le s\le 1} |\hat{\ell}^L(s)| \le \frac{L}{3\psi_L}\right\}$, the paths of ℓ^L and $\hat{\ell}^L$ can be coupled so that $\ell^L(s) = \hat{\ell}^L(s)$ for every $s \in [0,1]$, and since these quantities are bounded for each L we can write

$$\begin{aligned}\mathbb{E}_0\left[(\ell^{L,1}(1))^2\right] &= \mathbb{E}_0\left[(\hat{\ell}^{L,1}(1))^2\,\mathbf{1}_{\mathscr{E}_L}\right] + \mathbb{E}_0\left[(\ell^{L,1}(1))^2\,\mathbf{1}_{\mathscr{E}_L^c}\right]\\ &= \mathbb{E}_0\left[(\hat{\ell}^{L,1}(1))^2\right] - \mathbb{E}_0\left[(\hat{\ell}^{L,1}(1))^2\,\mathbf{1}_{\mathscr{E}_L^c}\right] + \mathbb{E}_0\left[(\ell^{L,1}(1))^2\,\mathbf{1}_{\mathscr{E}_L^c}\right].\end{aligned} \tag{27}$$

By (26) and the fact that ℓ^L evolves on the torus of size $L\psi_L^{-1}$, the last term on the right-hand side of (27) is bounded by

$$C\,\frac{L^2}{\psi_L^2} \times \frac{\psi_L^4}{L^4} = C\,\frac{\psi_L^2}{L^2} \to 0 \qquad \text{as } L \to \infty.$$

For the second term on the right-hand side of (27), let $\hat{s}_L(1) \equiv \sup_{0\le s\le 1} |\hat{\ell}^L(s)|$. Using Fubini's theorem on the second line, we have

$$\begin{aligned}\mathbb{E}_0\left[(\hat{\ell}^{L,1}(1))^2\,\mathbf{1}_{\mathscr{E}_L^c}\right] &\le \mathbb{E}_0\left[\hat{s}_L(1)^2\,\mathbf{1}_{\mathscr{E}_L^c}\right]\\ &= \int_0^\infty \mathbb{P}_0\left[\hat{s}_L(1) > \frac{L}{3\psi_L} \vee \sqrt{y}\right] dy\\ &= \frac{L^2}{9\psi_L^2}\,\mathbb{P}_0\left[\hat{s}_L(1) > \frac{L}{3\psi_L}\right] + \int_{\frac{L^2}{9\psi_L^2}}^\infty \mathbb{P}_0\left[\hat{s}_L(1) > \sqrt{y}\right] dy.\end{aligned} \tag{28}$$

Now, by the argument leading to (26), $\mathbb{P}_0[\hat{s}_L(1) > \sqrt{y}]$ is bounded by Cy^{-2} for each $y > 0$, where C is a constant independent of y. Consequently, the right-hand side of (28) is bounded by

$$C'\,\frac{\psi_L^2}{L^2} + C\int_{L^2/(9\psi_L^2)}^\infty \frac{dy}{y^2} \;\to\; 0 \qquad \text{as } L \to \infty.$$

Coming back to (27), we can conclude that

$$\sigma_L^2 = 2\sigma_B^2 + o(1) \qquad \text{as } L \to \infty.$$

If we now recall the equality in distribution described at the beginning of the section, we can use Lemma 5.3 applied to ℓ^L on the torus of size $L\psi_L^{-1}$ and the entrance time into $B(0, 2R^B)$ to write that

$$\lim_{L\to\infty}\sup_{t\ge 0}\sup_{A_L\in\Gamma_{\mathscr{A}}(L,2)^*}\left|\mathbb{P}_{A_L}\left[T_L > \frac{\rho_L(L/\psi_L)^2\log(L/\psi_L)}{2\pi\sigma_B^2}\,t\right] - e^{-t}\right| = 0. \tag{29}$$

By the assumption on $|\alpha \log L - \log(\psi_L)|$ introduced just after (9) and Lemma 5.5 applied to ℓ^L to bound the probability that T_L lies between $\frac{\rho_L L^2 \log(L/\psi_L)}{2\pi\sigma_B^2\psi_L^2}$ and $\frac{(1-\alpha)\rho_L L^2 \log L}{2\pi\sigma_B^2\psi_L^2}$, (a) of Proposition 6.2 follows from (29).

Let us now turn to the proof of (b). This time, we define ℓ^L for every $t \geq 0$ by

$$\ell^L(t) = \frac{1}{\psi_L}\, \xi^L(2\psi_L^2 t).$$

Similar calculations give, as $L \to \infty$,

$$E_0\left[|\ell^L(1)|^2\right] = 2\sigma_s^2 + 2b\sigma_B^2 + o(1) \qquad \text{if } \rho_L^{-1}\psi_L^2 \to b \in [0,\infty).$$

and $E_0\left[|\ell^L(1)|^4\right]$ is bounded uniformly in L. We can therefore apply Lemma 5.3 to ℓ^L as above. □

Having established the time that it takes for two lineages starting from distance L apart to come close enough together that they have a chance to coalesce, we now calculate the additional time required for them to actually do so. We shall have to distinguish between several regimes, depending on whether large or small events prevail in the evolution of the pair of lineages. Our goal in the rest of this section is to prove the following result.

Theorem 6.3. *For each $L \in \mathbb{N}$, let t_L denote the coalescence time of the pair of lineages under consideration. Then,*

(a) *If $\frac{\psi_L^2}{\rho_L} \to \infty$ as $L \to \infty$,*

$$\lim_{L\to\infty} \sup_{t\geq 0} \sup_{A_L \in \Gamma_{\mathscr{A}}(L,2)^*} \left| \mathbb{P}_{A_L}\left[t_L > \frac{(1-\alpha)\rho_L L^2 \log L}{2\pi\sigma_B^2\psi_L^2}\, t \right] - e^{-t} \right| = 0.$$

(b) *If $\frac{\psi_L^2}{\rho_L} \to b \in [0,\infty)$ and $\frac{\psi_L^2 \log L}{\rho_L} \to \infty$ as $L \to \infty$,*

$$\lim_{L\to\infty} \sup_{t\geq 0} \sup_{A_L \in \Gamma_{\mathscr{A}}(L,2)^*} \left| \mathbb{P}_{A_L}\left[t_L > \frac{(1-\alpha) L^2 \log L}{2\pi(\sigma_s^2 + b\sigma_B^2)}\, t \right] - e^{-t} \right| = 0.$$

(c) *If $(\frac{\psi_L^4}{\rho_L})_{L\geq 1}$ is bounded or $\frac{L^2 \log L}{\rho_L} \to 0$ as $L \to \infty$ (and so $\frac{\psi_L^2 \log L}{\rho_L} \to 0$), then*

$$\lim_{L\to\infty} \sup_{t\geq 0} \sup_{A_L \in \Gamma_{\mathscr{A}}(L,2)^*} \left| \mathbb{P}_{A_L}\left[t_L > \frac{L^2 \log L}{2\pi\sigma_s^2}\, t \right] - e^{-t} \right| = 0.$$

The cases (a) and (b) are separated only because the timescales of interest are not of the same order, but the reasons why they hold are identical: in both cases, large jumps are frequent enough that, once the lineages have been gathered at distance $2R^B\psi_L$, they coalesce in a time negligible compared to T_L. In contrast, in (c) we assume that the rate at which the lineages are affected by large events is so slow that we have to wait for the lineages to be gathered at distance less than $2R^s$ before they have a chance to coalesce (and they do so in a negligible time compared to $L^2 \log L$). If none of the above conditions hold, then the proof of (c) will show that, also in this case, the probability that a large event affects the lineages when they are at distance less than $2R^B\psi_L$ and before a time of order $\mathcal{O}(L^2\log L)$ vanishes as L tends to infinity. However, we are no longer able to describe precisely the limiting behaviour of t_L, see Remark 6.8.

Let us first make more precise the sense in which the additional time to coalescence is negligible once the lineages have been gathered at the right distance.

Proposition 6.4. *Let $(\Phi_L)_{L\geq 1}$ be a sequence tending to infinity as $L\to\infty$.*
(a) If $(\Phi_L)_{L\geq 1}$ is such that $\frac{\rho_L}{\psi_L^2\log\Phi_L}\to 0$ as $L\to\infty$, we have

$$\lim_{L\to\infty}\sup_{A_L}\ \mathbb{P}_{A_L}\big[t_L>\Phi_L\rho_L\big]=0, \tag{30}$$

where the supremum is taken over all samples $A_L=\big\{(\{1\},x_1^L),(\{2\},x_2^L)\big\}$ such that $|x_1^L-x_2^L|\leq 2R^B\psi_L$.
(b) Under no additional condition, we have

$$\lim_{L\to\infty}\sup_{A_L'}\ \mathbb{P}_{A_L'}\big[t_L>\Phi_L\big]=0, \tag{31}$$

where the supremum is now taken over all samples $A_L'=\big\{(\{1\},x_1^L),(\{2\},x_2^L)\big\}$ such that $|x_1^L-x_2^L|\leq 2R^s$.

Taking $\Phi_L=\frac{L^2}{\rho_L\log L}(1\wedge\rho_L\psi_L^{-2})$, the result in (a) shows that when $\frac{\psi_L^2\log L}{\rho_L}\to\infty$, the coalescence time of two lineages at distance at most $2R^B\psi_L$ is indeed much smaller than T_L (which is of order $L^2\log L\times\big(1\wedge\rho_L\psi_L^{-2}\big)$ by Proposition 6.2).

Proof of Proposition 6.4: Recall that for each $L\in\mathbb{N}$, we defined X^L as the difference between the locations of the lineages ξ_1^L and ξ_2^L on the torus $\mathbb{T}(L)$. In the following, if both lineages are affected by the same event, we shall consider that X^L hits 0 but the number of lineages remains equal to 2, which means that they can separate again later (if the measures ν_r^s and ν_r^B are not all the point mass at 1). However, it is the first time at which such an event occurs which will be of interest, and we keep the notation t_L to denote this time. As we already noticed, X^L behaves like $\{\xi^L(2t),\ t\geq 0\}$ outside $B\big(0,2R^B\psi_L\big)$, whereas inside the ball it can hit 0 owing to reproduction events affecting both lineages ξ_1^L and ξ_2^L.

Case (a)**.** For each $L\in\mathbb{N}$, set $q_0^L=Q_0^L\equiv 0$ and for every $i\geq 1$,

$$Q_i^L\equiv\inf\Big\{t>q_{i-1}^L:\ X^L(t)\notin B\Big(0,\frac{7}{4}R^B\psi_L\Big)\Big\}$$

and

$$q_i^L\equiv\inf\Big\{t>Q_i^L:\ X^L(t)\in B\Big(0,\frac{3}{2}R^B\psi_L\Big)\Big\},$$

with the convention that $\inf\emptyset=+\infty$. We shall use the following lemmas, which will enable us to describe how X^L wanders around in $\mathbb{T}(L)$, independently of whether it ever hits 0 or not.

Lemma 6.5. *There exist a function $g:\mathbb{R}_+\to\mathbb{R}_+$ vanishing at infinity, $C_q>0$, $u_q>1$ and $L_q\in\mathbb{N}$ such that for every $L\geq L_q$ and $u\geq u_q$,*

$$\sup_{x\in B(0,4R^B)\setminus B(0,(7/4)R^B)}\mathbb{P}_{\psi_L x}\big[q_1^L>\rho_L u\big]\leq g(u)\qquad\text{if }\rho_L=\mathcal{O}(\psi_L^2),$$

$$\sup_{x\in B(0,4R^B)\setminus B(0,(7/4)R^B)} \mathbb{P}_{\psi_L x}\left[q_1^L > \psi_L^2 u\right] \le \frac{C_q}{\log u} \qquad \text{if } \rho_L^{-1}\psi_L^2 \to 0.$$

Lemma 6.5 will give us good control of the probability of a long excursion outside $B(0,(3/2)R^B\psi_L)$.

Lemma 6.6. *Suppose that*

$$\mathrm{Leb}\big(\{r\in[0,R^B]:\ \nu_r^B \notin \{\delta_0,\delta_1\}\}\big) > 0. \tag{32}$$

Then, there exists a constant $C_Q<\infty$ such that for each $L\ge 1$,

$$\sup_{x\in B(0,(3/2)R^B)} \frac{1}{\rho_L}\,\mathbb{E}_{\psi_L x}\left[Q_1^L\right] < C_Q.$$

Condition (32) guarantees that, whenever X^L hits 0, it has a chance not to remain stuck at this value for all times. Lemma 6.6 then tells us that X^L starting within $B((3/2)R^B\psi_L)$ needs an average time of order $\mathcal{O}(\rho_L)$ to reach distance $(7/4)R^B\psi_L$ from the origin.

Lemma 6.7. *Suppose that $\rho_L\psi_L^{-2}$ remains bounded as $L\to\infty$. Then, there exists $\theta_1\in(0,1)$ such that for every $L\ge 1$,*

$$\inf_{x\in B(0,(3/2)R^B)} \mathbb{P}_{\psi_L x}\left[X^L \text{ hits 0 before leaving } B\big(0,(7/4)R^B\psi_L\big)\right] \ge \theta_1. \tag{33}$$

If $\liminf_{L\to\infty}\rho_L^{-1}\psi_L^2=0$, there exist $\theta_2\in(0,1)$ and $\theta_3>0$ such that

$$\begin{aligned}\inf_{x\in B(0,(3/2)R^B)} &\mathbb{P}_{\psi_L x}\left[X^L \text{ hits 0 before leaving } B\ \big(0,(7/4)R^B\psi_L\big)\right]\\ &\ge \theta_2\left(1-\exp\left\{-\theta_3\frac{\psi_L^2}{\rho_L}\right\}\right).\end{aligned} \tag{34}$$

The proofs of these lemmas are given in Appendix B.

The following technique is inspired by that used in Cox & Durrett (2002) and Zähle et al. (2005), although the motions of the lineages and the mechanism of coalescence here are more complex and require slightly more work. Our plan is first to find a good lower bound on the number of times the lineages meet at distance less than $(3/2)R^B\psi_L$ (and then separate again) before time $\Phi_L\rho_L$. In a second step, we use the estimates on the probability that during such a gathering the lineages merge before separating again derived in Lemma 6.7, and obtain that coalescence does occur before $\Phi_L\rho_L$ with probability tending to 1. For the sake of clarity, we show (30) in the case where $\rho_L\psi_L^{-2}$ remains bounded, and then comment on how to adapt the arguments in the general case.

Assume first that Condition (32) holds. Recall the definition of Q_i^L and q_i^L given above, and define k_L by

$$k_L \equiv \max\{n:\ Q_n^L \le \Phi_L\rho_L\}.$$

By Lemma 6.7, there exists a positive constant θ_1 such that for every $L\ge1$ and $x\in B(0,(3/2)R^B\psi_L)$,

$$\mathbb{P}_x\left[X^L \text{ hits 0 before leaving } B\big(0,(7/4)R^B\psi_L\big)\right] \ge \theta_1.$$

Hence, for every $x \in B\big(0, 2R^B\psi_L\big)$, we have

$$\mathbb{P}_x\big[t_L > \Phi_L\rho_L\big] \le \mathbb{P}_x\big[t_L > Q^L_{k_L}\big] \le \mathbb{E}_x\big[(1-\theta_1)^{k_L}\big]. \tag{35}$$

Let us fix $x \in B\big(0, 2R^B\psi_L\big)$ and show that $k_L \to \infty$ as $L \to \infty$, in $\mathbb{P}_x$-probability. The fact that the bounds obtained below do not depend on $x \in B\big(0, 2R^B\psi_L\big)$ will then give us the desired uniformity. Let $M \in \mathbb{N}$. We have

$$\begin{aligned}
\mathbb{P}_x\big[k_L < M\big] &= \mathbb{P}_x\big[Q^L_M > \Phi_L\rho_L\big] \\
&= \mathbb{P}_x\left[\sum_{i=1}^{M}(Q^L_i - q^L_{i-1}) + \sum_{i=1}^{M-1}(q^L_i - Q^L_i) > \Phi_L\rho_L\right] \\
&\le \sum_{i=1}^{M}\mathbb{P}_x\left[Q^L_i - q^L_{i-1} > \frac{\Phi_L\rho_L}{2M}\right] + \sum_{i=1}^{M-1}\mathbb{P}_x\left[q^L_i - Q^L_i > \frac{\Phi_L\rho_L}{2(M-1)}\right],
\end{aligned} \tag{36}$$

where the last inequality uses the fact that at least one of the $2M-1$ terms of the sums on the second line must be larger than a fraction $(2M-1)^{-1}$ of the total time. Now, using the Markov inequality, the strong Markov property at time q^L_{i-1} and then Lemma 6.6, we can write for each i

$$\begin{aligned}
\mathbb{P}_x\left[Q^L_i - q^L_{i-1} > \frac{\Phi_L\rho_L}{2M}\right] &\le \frac{2M}{\Phi_L\rho_L}\,\mathbb{E}_x\big[Q^L_i - q^L_{i-1}\big] \\
&\le \frac{2M}{\Phi_L\rho_L}\sup_{y\in B(0,(3/2)R^B)}\mathbb{E}_{\psi_L y}\big[Q^L_1\big] \\
&\le \frac{2MC_Q}{\Phi_L}.
\end{aligned}$$

If we now apply the strong Markov property to X^L at time Q^L_i and use Lemma 6.5 together with the fact that $X^L(Q^L_i) \in B(0, 4R^B\psi_L)$ with probability one, we obtain for each i, and L large enough

$$\mathbb{P}_x\left[q^L_i - Q^L_i > \frac{\Phi_L\rho_L}{2(M-1)}\right] \le g\left(\frac{\Phi_L}{2(M-1)}\right).$$

Coming back to (36), we arrive at

$$\mathbb{P}_x\big[k_L < M\big] \le \frac{2M^2C_Q}{\Phi_L} + (M-1)g\left(\frac{\Phi_L}{2(M-1)}\right) \to 0, \qquad \text{as } L \to \infty.$$

To complete the proof of (a) when Condition (32) holds and $\rho_L\psi_L^{-2}$ remains bounded, let $\varepsilon > 0$ and fix $M = M(\varepsilon) \in \mathbb{N}$ such that

$$(1-\theta_1)^M < \varepsilon.$$

Splitting the expectation in (35) into the integral over $\{k_L \ge M\}$ and $\{k_L < M\}$ yields

$$\limsup_{L\to\infty}\sup_{x\in B(0,2R^B\psi_L)}\mathbb{P}_x\big[t_L > \Phi_L\rho_L\big] \le \varepsilon + \limsup_{L\to\infty}\sup_{x\in B(0,2R^B\psi_L)}\mathbb{P}_x\big[k_L < M\big] = \varepsilon,$$

and since ε was arbitrary, the desired result follows.

When Condition (32) is fulfilled but $\rho_L \psi_L^{-2}$ is unbounded as $L \to \infty$, we can apply the same technique to obtain (30). This time, using the second result of Lemma 6.7 we can write as in (35) that, for every $x \in B\big(0, 2R^B \psi_L\big)$,

$$\mathbb{P}_x\big[t_L > \Phi_L \rho_L\big] \leq \mathbb{E}_x\bigg[\bigg(1 - \theta_2\Big(1 - \exp\Big\{-\theta_3 \frac{\psi_L^2}{\rho_L}\Big\}\Big)\bigg)^{k_L}\bigg].$$

The same arguments as above (using the second part of Lemma 6.5) yield, for L large enough,

$$\sup_{x \in B(0, 2R^B \psi_L)} \mathbb{P}_x\bigg[k_L < M \frac{\rho_L}{\psi_L^2}\bigg] \leq \frac{2C_Q M^2 \rho_L^2}{\psi_L^4 \Phi_L} + \frac{C_q M \rho_L}{\psi_L^2 \log(\Phi_L/2M)},$$

which tends to 0 as L tends to infinity by our assumption of $(\Phi_L)_{L \geq 1}$. We conclude in the same manner, using the fact that when $\psi_L^2/\rho_L \to \infty$,

$$\bigg(1 - \theta_2\Big(1 - \exp\Big\{-\theta_3 \frac{\psi_L^2}{\rho_L}\Big\}\Big)\bigg)^{M\rho_L/\psi_L^2} \sim e^{-\theta_2\theta_3 M}.$$

Let us finish the proof of (a) by removing the assumption (32). In the preceding proof, the main idea is that each time X^L passes through $B\big(0, (3/2)R^B \psi_L\big)$, the two lineages have an opportunity to try to coalesce and their success probability is bounded from below by the quantity obtained in Lemma 6.7. However, if we do not assume that (32) holds, X^L may become stuck at 0 once it has hit it, and so the number k_L of such sojourns in $B\big(0, (3/2)R^B \psi_L\big)$ may be finite. This makes our arguments break down. Nevertheless, X^L can only hit 0 through a coalescence event, and so this issue is merely an artefact of the technique of the proof. To overcome it, let us increase the rate of reproduction events by a factor 2, but divide each probability to be affected by 2. Overall, coalescence will take a longer time in this new setting, but the motions of the lineages before their coalescence time will remain identical in distribution.

More precisely, assume that (32) does not hold. Define $\hat{\Pi}_L^B$ as a Poisson point process on $\mathbb{R} \times \mathbb{T}(L) \times (0, \infty)$, independent of Π_L^s and Π_L^B and with intensity measure $2(\rho_L \psi_L^2)^{-1} dt \otimes dx \otimes \mu^B(dr)$, and for each $r > 0$ such that $\nu_r^B = \delta_1$, set $\hat{\nu}_r^B \equiv \delta_{1/2}$. Let also $\hat{\Pi}_L^s$ be a Poisson point process with the same distribution as Π_L^s and independent of all the other point processes. Call $\hat{X}^L$ the process defined in the same manner as X^L but with Π_L^B (resp., Π_L^s, ν_r^B) replaced by $\hat{\Pi}_L^B$ (resp., $\hat{\Pi}_L^s$, $\hat{\nu}_r^B$). By computing the intensity of the jumps of a single lineage, one can observe that it is equal to

$$dt \otimes \bigg(\frac{2}{\rho_L} \int_{|x|/2}^{R^B} \frac{L_r(x)}{2\pi r^2}\, \mathbf{1}_{\{\nu_r^B = \delta_1\}} \mu^B(dr) d(\psi_L x) + \int_{|x|/2}^{R^s} \int_0^1 \frac{L_r(x)}{\pi r^2}\, u\, \nu_r^s(du) \mu^s(dr) dx\bigg),$$

which is precisely that of ξ^L. Here, $L_r(x)$ stands for the volume of $B(0, r) \cap B(x, r)$. If we now compute the coalescence rate of two lineages at distance $z \in [0, 2R^B \psi_L]$, we obtain the same term due to small events for X^L and $\hat{X}^L$, to which is added the respective contributions of large events

$$\frac{1}{\rho_L} \int_{z/2}^{R^B} L_r(z) \mathbf{1}_{\{\nu_r^B = \delta_1\}} \mu^B(dr) \qquad \text{and} \qquad \frac{1}{2\rho_L} \int_{z/2}^{R^B} L_r(z) \mathbf{1}_{\{\nu_r^B = \delta_1\}} \mu^B(dr).$$

Hence, the evolutions of both processes follow the same law outside $B(0, 2R^B \psi_L)$, the contribution of large events whose area encompasses only one of the two lineages is identical even within

$B(0,2R^B\psi_L)$, and coalescence occurs at a higher rate for X^L than for $\hat{X}^L$. This gives us for every $L \geq 1$ and $x \in \mathbb{T}(L)$,

$$\mathbb{P}_x\big[t_L > \Phi_L\rho_L\big] \leq \mathbb{P}_x\big[\hat{t}_L > \Phi_L\rho_L\big],$$

where $\hat{t}_L$ is defined in an obvious manner. But Condition (32) holds for $\hat{X}^L$, and so we can use the result obtained in the previous paragraph to complete the proof of (a) when (32) does not hold.

Case (b)**.** The arguments are essentially the same. First of all, since we assumed that ρ_L grows to infinity as $L \to \infty$, and because

$$\mathbb{P}_x\big[t_L > \Phi_L\big] \leq \mathbb{P}_x\big[t_L > \Phi'_L\big]$$

whenever $\Phi_L \geq \Phi'_L$, we can restrict our attention to sequences $(\Phi_L)_{L\geq 1}$ such that $\rho_L^{-1}\Phi_L \to 0$ as $L \to \infty$. Let $\mathscr{E}_L$ denote the event that no large events affected any of the lineages before time Φ_L. Let $\theta_{\max} \in (0,\infty)$ be such that the maximal rate at which at least one of the two lineages of the sample is affected by a large event is less than $\theta_{\max}\rho_L^{-1}$ (recall that the total rate at which at least one of two lineages is affected is smaller than twice the corresponding rate for a single lineage, which is finite and independent of the location of the lineage). For each $L \in \mathbb{N}$, define e_L as an exponential random variable, with parameter $\theta_{\max}\rho_L^{-1}$. By our assumption on Φ_L, we can write

$$\mathbb{P}_x[\mathscr{E}_L^c] \leq \mathbb{P}[e_L \leq \Phi_L] = 1 - \exp\left\{-\frac{\theta_{\max}\Phi_L}{\rho_L}\right\} \to 0, \quad \text{as } L \to \infty.$$

The distribution of the process X^L up to the first time at which it is affected by a large event is equal to that of $\tilde{X}^L$ (defined as the process experiencing only small events) up to the random time $e(\tilde{X}^L)$, so that if $\rho_L^{-1}\theta_{B,L}(x)$ is the rate at which at least one of two lineages at separation $x \in \mathbb{T}(L)$ is affected by a large event, then for each $t \geq 0$ and $y \in \mathbb{T}(L)$

$$\mathbb{P}_y\big[e(\tilde{X}^L) > t\big] = \mathbb{E}_y\left[\exp\left\{-\int_0^t \frac{\theta_{B,L}\big(\tilde{X}^L(s)\big)}{\rho_L}\,ds\right\}\right].$$

By the definition of $\theta_{\max}$, for each $L \in \mathbb{N}$ the variable e_L is stochastically bounded by $e(\tilde{X}^L)$. Consequently, if $\tilde{t}_L$ denotes the coalescence time associated to $\tilde{X}^L$ (or, more precisely, to the model where lineages are affected only by small events), we have for each $x \in B(0,2R^s)$

$$\begin{aligned}\mathbb{P}_x\big[t_L \geq \Phi_L\big] &\leq \mathbb{P}_x\big[t_L \geq \Phi_L;\ \mathscr{E}_L\big] + \mathbb{P}_x\big[\mathscr{E}_L^c\big]\\ &\leq \mathbb{P}_x\big[\tilde{t}_L \geq \Phi_L\big] + o(1) \quad \text{as } L \to \infty,\end{aligned}$$

where the remaining terms converge to 0 uniformly in $x \in \mathbb{T}(L)$. Then, an easy modification of the proof of (a) with "$\psi_L = \rho_L = 1$" yields the desired result and completes the proof of Proposition 6.4. □

We can now turn to the proof of Theorem 6.3.

Proof of Theorem 6.3:

Cases (a) **and** (b)**.** For (a), let us define Φ_L for each $L \in \mathbb{N}$ by

$$\Phi_L = \frac{\rho_L L^2}{\psi_L^2 \log L}.$$

Let $t > 0$ and $(A_L)_{L\geq 1}$ be such that $A_L \in \Gamma_{\mathscr{A}}(L,2)^*$ for each $L \in \mathbb{N}$. Introducing the time T_L needed for the two lineages of the sample to come at distance less than $2R^B\psi_L$, we can write

$$\begin{aligned}
&\mathbb{P}_{A_L}\left[\, t_L > \frac{(1-\alpha)\rho_L L^2 \log L}{2\pi\sigma_B^2\psi_L^2}\, t\right] \\
&\quad = \mathbb{P}_{A_L}\left[t_L > \frac{(1-\alpha)\rho_L L^2 \log L}{2\pi\sigma_B^2\psi_L^2}\, t;\ T_L > \frac{(1-\alpha)\rho_L L^2 \log L}{2\pi\sigma_B^2\psi_L^2}\, t - \Phi_L\right] \qquad (37)\\
&\quad\quad + \mathbb{P}_{A_L}\left[t_L > \frac{(1-\alpha)\rho_L L^2 \log L}{2\pi\sigma_B^2\psi_L^2}\, t;\ T_L \leq \frac{(1-\alpha)\rho_L L^2 \log L}{2\pi\sigma_B^2\psi_L^2}\, t - \Phi_L\right]. \qquad (38)
\end{aligned}$$

Using the strong Markov property at time T_L and the uniform convergence derived in Proposition 6.4(a), we obtain that the expression in (38) tends to 0 as $L \to \infty$ independently of the choice of $t > 0$ and $(A_L)_{L\in\mathbb{N}}$. For (37), note that

$$\begin{aligned}
&\Bigg|\,\mathbb{P}_{A_L}\left[\, t_L > \frac{(1-\alpha)\rho_L L^2 \log L}{2\pi\sigma_B^2\psi_L^2}\, t;\ T_L > \frac{(1-\alpha)\rho_L L^2 \log L}{2\pi\sigma_B^2\psi_L^2}\, t - \Phi_L\right] \\
&\qquad - \mathbb{P}_{A_L}\left[T_L > \frac{(1-\alpha)\rho_L L^2 \log L}{2\pi\sigma_B^2\psi_L^2}\, t\right]\Bigg| \\
&\qquad \leq \mathbb{P}_{A_L}\left[\frac{(1-\alpha)\rho_L L^2 \log L}{2\pi\sigma_B^2\psi_L^2}\, t - \Phi_L \leq T_L \leq \frac{(1-\alpha)\rho_L L^2 \log L}{2\pi\sigma_B^2\psi_L^2}\, t\right]. \qquad (39)
\end{aligned}$$

Since X^L (defined at the beginning of Section 6.1) has the same law as $\{\xi^L(2t), t \geq 0\}$ until the random time T_L, we can bound the quantity in (39) by working directly with the latter process. In order to apply Lemma 5.5 to $\{\psi_L^{-1}\xi^L(2\rho_L t), t \geq 0\}$, with

$$U_L = \frac{(1-\alpha)L^2 \log L}{4\pi\sigma_B^2\psi_L^2}, \quad u_L = \frac{\Phi_L}{2\rho_L} = \frac{L^2}{2\psi_L^2 \log L} \quad \text{and } R = 2R^B,$$

we need to check that $U_L\psi_L^2 L^{-2} \to \infty$ and $u_L \leq \frac{L^2}{\psi_L^2\sqrt{\log(L/\psi_L)}}$ (recall that this process evolves on the torus of size $\psi_L^{-1}L$.) Both conditions are fulfilled here, and so by Lemma 5.5, the right-hand side of (39) is bounded by

$$\frac{C\Phi_L\psi_L^2}{\rho_L L^2} = \frac{C}{\log L} \to 0 \qquad \text{as } L \to \infty.$$

Hence, coming back to (37), we can use the result of Proposition 6.2 and the uniformity in $t > 0$ and $(A_L)_{L\geq 1}$ of our estimates to obtain

$$\lim_{L\to\infty} \sup_{t\geq 0} \sup_{A_L \in \Gamma_{\mathscr{A}}(L,2)^*} \left|\mathbb{P}_{A_L}\left[t_L > \frac{(1-\alpha)\rho_L L^2 \log L}{2\pi\sigma_B^2\psi_L^2}\, t\right] - e^{-t}\right| = 0.$$

The proof of (b) follows exactly the same lines, with $\Phi_L \equiv L^2(\log L)^{-1}$ and Lemma 5.5 applied to $\psi_L^{-1}\xi^L(2\psi_L^2\cdot)$.

Case (c)**.** In contrast with the two previous cases, where coalescence in the limit is due to large events only, here the pair of lineages can coalesce only through a small event. To see this, let us define T_L^* as the first time at which the two lineages (indexed by L) come at distance less than $2R^s$ from each other, and τ_L as the first time at which at least one of them is affected by a large event while they are at distance less than $2R^B\psi_L$ (i.e., while $X^L \in B(0, 2R^B\psi_L)$). Note that for each L, T_L^* and τ_L are stopping times with respect to the filtration $\{\mathscr{F}_t,\ t \geq 0\}$ associated to $\Pi_L^s \cup \Pi_L^B$ as we trace backwards in time. In addition, define $\tilde{T}_L^*$ as the entrance time of ξ^L into $B(0, 2R^s)$ and $\tilde{\tau}_L$ as the first time ξ^L makes a jump of size $\mathscr{O}(\psi_L)$ while it is lying in $B(0, 2R^B\psi_L)$. These two random times are stopping times with respect to the filtration $\{\tilde{\mathscr{F}}_t,\ t \geq 0\}$ associated to ξ^L. We claim that for each $L \in \mathbb{N}$,

$$\{X^L(t),\ t < \tau_L \wedge T_L^*\} \overset{(d)}{=} \{\xi^L(2t),\ 2t < \tilde{\tau}_L \wedge \tilde{T}_L^*\}, \tag{40}$$

where the notation $\overset{(d)}{=}$ refers to equality in distribution. Indeed, as long as X^L has not entered $B(0, 2R^s)$ and no large event has affected it while it lay in $B(0, 2R^B\psi_L)$, coalescence events are impossible and the rates and distributions of the jumps of both processes are identical. We cannot include the terminal times in (40) since the values of the processes will differ if $\tau_L \wedge T_L^* = \tau_L$ and the corresponding event is a coalescence, but since X^L and ξ^L are jump processes with finite rates, we can easily see that the event $\{\tau_L \wedge T_L^* = \tau_L\}$ (resp., $\tilde{\tau}_L \wedge \tilde{T}_L^* = \tilde{\tau}_L$) is $\mathscr{F}_{(\tau_L \wedge T_L^*)-}$ (resp., $\tilde{\mathscr{F}}_{(\tilde{\tau}_L \wedge \tilde{T}_L^*)-}$) -measurable. Hence, for each $L \in \mathbb{N}$, $A = \wp_2(x_1, x_2)$ and $x \equiv x_1 - x_2 \in \mathbb{T}(L)$, we have

$$\mathbb{P}_A\big[\tau_L < T_L^*\big] = \mathbb{P}_x\big[\tilde{\tau}_L < \tilde{T}_L^*\big]. \tag{41}$$

Let us now bound the right-hand side of (41) under the assumption that $(\rho_L^{-1}\psi_L^4)_{L\in\mathbb{N}}$ is bounded. Analogous computations to those in the proof of Proposition 6.2 show that $\{\xi^L(2t), t \geq 0\}$ itself satisfies Assumption 5.2 with $\sigma_L^2 = 2\sigma_s^2 + o(1)$ as $L \to \infty$. Hence, Lemma 5.3 applied with $d_L = 2R^s$ gives us

$$\lim_{L\to\infty} \sup_{t\geq 0} \sup_{x_L \in \Gamma(L,1)} \left| \mathbb{P}_{x_L}\left[\tilde{T}_L^* > \frac{L^2 \log L}{2\pi\sigma_s^2}\, t\right] - e^{-t} \right| = 0. \tag{42}$$

Let $\theta_{\max} < \infty$ be such that for every $L \in \mathbb{N}$, the rate at which ξ^L makes a jump of size $\mathscr{O}(\psi_L)$ is bounded by $\theta_{\max}/\rho_L$. Fixing $\varepsilon > 0$ and $K > 0$ such that $e^{-2\pi\sigma_s^2 K} < \varepsilon$, we have for L large enough and any sequence $(x_L)_{L\geq 1}$ such that $x_L \in \Gamma(L, 1)$ for every L:

$$\begin{aligned}
&\mathbb{P}_{x_L}\big[\,\tilde{\tau}_L < \tilde{T}_L^*\big] \\
&\quad = \mathbb{P}_{x_L}\big[\tilde{\tau}_L < \tilde{T}_L^* \leq KL^2 \log L\big] + \mathbb{P}_{x_L}\big[\tilde{\tau}_L < \tilde{T}_L^*\ ;\ \tilde{T}_L^* > KL^2 \log L\big] \\
&\quad \leq \mathbb{P}_{x_L}\big[\tilde{\tau}_L < KL^2 \log L\big] + \mathbb{P}_{x_L}\big[\tilde{T}_L^* > KL^2 \log L\big] \\
&\quad \leq \mathbb{E}_{x_L}\left[1 - \exp\left\{-\frac{\theta_{\max}}{\rho_L} \int_0^{KL^2 \log L} \mathbf{1}_{B(0,2R^B\psi_L)}\big(\xi^L(2s)\big)\, ds\right\}\right] + \varepsilon.
\end{aligned} \tag{43}$$

Splitting the integral below into the sum $\int_0^{\psi_L^2\sqrt{\log L}} + \int_{\psi_L^2\sqrt{\log L}}^{L^2/\sqrt{\log L}} + \int_{L^2/\sqrt{\log L}}^{L^2\sqrt{\log L}} + \int_{L^2\sqrt{\log L}}^{KL^2\log L}$ and using the four results of Lemma 5.4, there exists $L_0 \in \mathbb{N}$, and $a_1, a_2 > 0$ independent of L, $(x_L)_{L\geq 1}$ and $K > 0$, such that for every $L \geq L_0$,

$$\mathbb{E}_{x_L}\left[\int_0^{KL^2 \log L} \mathbf{1}_{B(0,2R^B\psi_L)}\big(\xi^L(2s)\big)\, ds\right] \leq (a_1 + a_2 K)\psi_L^2 \log L.$$

Hence, the first term on the right-hand side of (43) is bounded by

$$\mathbb{E}_{x_L}\left[\frac{\theta_{\max}}{\rho_L}\int_0^{KL^2\log L}\mathbf{1}_{B(0,2R^B\psi_L)}\big(\xi^L(2s)\big)\,ds\right]\le\theta_{\max}(a_1+a_2K)\frac{\psi_L^2\log L}{\rho_L},$$

which tends to 0 as $L\to\infty$, independently of the sequence $(x_L)_{L\geq 1}$ considered. As ε in (43) is arbitrary, we can conclude that

$$\lim_{L\to\infty}\sup_{x_L\in\Gamma(L,1)}\mathbb{P}_{x_L}\big[\tilde{\tau}_L<\tilde{T}_L^*\big]=0,$$

and by (41), the same result holds for X^L and any sequence $(A_L)_{L\in\mathbb{N}}$ such that $A_L\in\Gamma_{\mathscr{A}}(L,2)^*$ for every L. In words, we have obtained that with probability tending to 1, any pair of lineages starting at distance $\mathcal{O}(L)$ from each other gather at distance $2R^s$ before having a chance to coalesce through a large reproduction event. By using the same method as in (a) but this time with the result of Proposition 6.4 (b) and with Proposition 6.2 replaced by (42), we obtain the desired conclusion under the assumption that $(\rho_L^{-1}\psi_L^4)_{L\in\mathbb{N}}$ is bounded.

When $\rho_L\gg L^2\log L$, with probability increasing to 1 no large events at all affect any of the lineages by the time they are gathered at distance $2R^s$ by small events. The result then follows from the same arguments, with ξ^L replaced by the motion of a single lineage subject to only small reproduction events. □

Remark 6.8. *Let us comment on the cases not covered by the theorem, that is $\psi_L^4\gg\rho_L$, ρ_L is of order at most $L^2\log L$ and $\rho_L^{-1}\psi_L^2\log L$ has a finite limit (possibly 0). When the latter limit is positive, from the results obtained so far coalescence events due to small and to large reproduction events occur on the same timescale and depend on the precise paths of the two lineages. Therefore, we do not expect t_L to be exponentially distributed (with a deterministic parameter). When $\rho_L^{-1}\psi_L^2\log L$ tends to 0, the same reasoning as in the proof of (c) gives us that the probability that a large reproduction event causes the two lineages to coalesce before a time of order $L^2\log L$ vanishes as $L\to\infty$. However, X^L does not satisfy the conditions of Section 5 (Assumption 5.2) as it does when the assumptions of (c) hold. Using instead $\ell^L\equiv\psi_L^{-1}X^L(\psi_L^2\cdot)$, the time needed for the lineages to come at distance less than $2R^s$ translates into $T(\ell^L,2R^s/\psi_L)$, which is not covered by Lemma 5.3 and requires estimates of the entrance time of the jump process into a ball of shrinking radius, which we have been unable to obtain.*

6.2 Convergence to Kingman's coalescent

To complete the proof of Theorem 3.3, we now turn to the genealogy of a finite sample, starting at distance $\mathcal{O}(L)$ from each other on $\mathbb{T}(L)$.

We can already see from our analysis for a single pair of lineages that our spatial Λ-coalescent is similar in several respects to the coalescing random walks dual to the two-dimensional voter and stepping-stone models with short-range interactions (see e.g. Cox & Griffeath 1986, 1990 for a study on $\mathbb{Z}^2$, and Cox 1989 or Zähle et al. 2005 for examples on the torii $\mathbb{T}(L)\cap\mathbb{Z}^2$). It will therefore be no surprise that the analogy carries over to larger samples. In most of the papers cited above, the authors are interested in the sequence of processes giving the number of blocks in the ancestral partition. They show that, when the initial distance between the lineages grows to infinity, the finite-dimensional distributions of these counting processes converge to those of a pure death process corresponding to a time-change of the number of blocks of Kingman's coalescent. In Cox & Griffeath (1990), more elaborate arguments yield the convergence of the finite-dimensional distributions of the unlabelled genealogical processes to those of Kingman's coalescent. Instead of adding a new instance of such proofs to the literature, we shall simply explain why the same method applies to our case. This will also enable us to prove the tightness of the unlabelled genealogical processes.

Proof of Theorem 3.3: **(i) Convergence of the finite-dimensional distributions.**

We follow here the proofs in Cox & Griffeath (1986) (for the number of blocks of the ancestral partition) and Cox & Griffeath (1990) (for the unlabelled genealogical process of a system of coalescing simple random walks on $\mathbb{Z}^2$). Notice that, since we work on the torii $\mathbb{T}(L)$, our rescaling of time differs from Cox and Griffeath's. Another significant difference is the fact that, in their model, lineages move independently of each other until the first time two of them are on the same site, upon which they coalesce instantaneously. In our setting, the movements of lineages are defined from the same Poisson point processes, and two lineages having reached a distance that enables them to coalesce can separate again without coalescing.

Despite these differences, Lemma 6.9 below shows that a key ingredient of their proof is still valid here: at the time when two lineages coalesce, the others are at distance $\mathcal{O}(L)$ from each other and from the coalescing pair. To state this result, we need some notation. Let τ_{ij} be the first time lineages i and j come within distance less than $2R^B\psi_L$ (resp., $2R^s$) if $\rho_L \ll \psi_L^2 \log L$ (resp., $\rho_L \gg \psi_L^2 \log L$) and τ be the minimum of the τ_{ij}'s over all pairs considered. Let also τ_{ij}^* be the coalescence time of the ancestral lines of i and j, and τ^* be the minimum of the τ_{ij}^* over all lineages considered. Finally, for each i we shall denote the motion in $\mathbb{T}(L)$ of the block containing i by ξ_i^L.

Lemma 6.9. *Under the conditions of Theorem 3.3, we have*

$$\lim_{L\to\infty} \sup_{A_L\in\Gamma_{\mathscr{A}}(L,4)^*} \mathbb{P}_{A_L}\left[\tau^* = \tau_{12}^* \ ; \ |\xi_1^L(\tau^*) - \xi_3^L(\tau^*)| \le \frac{L}{\log L}\right] = 0, \tag{44}$$

$$\lim_{L\to\infty} \sup_{A_L\in\Gamma_{\mathscr{A}}(L,4)^*} \mathbb{P}_{A_L}\left[\tau^* = \tau_{12}^* \ ; \ |\xi_3^L(\tau^*) - \xi_4^L(\tau^*)| \le \frac{L}{\log L}\right] = 0. \tag{45}$$

The proof of Lemma 6.9 is deferred to Appendix B.

The other ingredients required to apply Cox and Griffeath's techniques are a control on the probability of "collision" for two lineages during a short interval of time, obtained here in Lemma 5.5, and the uniform convergence of the coalescence time of two lineages, which constitutes our Theorem 6.3. With these estimates, one can obtain the limiting rates of decrease of the number of blocks of $\mathscr{A}^{L,u}$ (namely those of the number of blocks in Kingman's coalescent), and the fact that mergers are only binary as in Cox & Griffeath (1986). In particular, the counterpart of their Proposition 2 here gives us that for each $n \in \mathbb{N}$,

$$\lim_{L\to\infty} \sup_{t\ge 0} \sup_{A_L\in\Gamma_{\mathscr{A}}(L,n)^*} \left| \mathbb{P}_{A_L}\left[|\mathscr{A}^{L,u}(t)| = n\right] - \exp\left\{-\frac{n(n-1)}{2}\, t\right\}\right| = 0, \tag{46}$$

which we state here because we shall need it for the case $\alpha = 1$ (observe that our L corresponds to their t). Note that in Proposition 2 of Cox & Griffeath (1986), the right-hand side of their equation gives the probability that the number of blocks is less than n, instead of equal to n as it is stated.

Furthermore, in (46) the supremum is over $t \geq 0$ instead of $t \in [0, T]$ for some $T > 0$ (as in Cox & Griffeath 1986). Our argument for this modification is the fact that the two quantities we are comparing are monotone decreasing in t and both tend to 0.

Then, the same arguments lead to the proof that any pair of lineages is equally likely to be the first one to coalesce, as in Lemma 1 of Cox & Griffeath (1990). The uniformity of the estimates obtained enables us to proceed by induction to show the uniform convergence (on a compact time-interval) of the one-dimensional distributions of $\mathscr{A}^{L,u}$ to those of $\mathscr{K}$, which translate into the uniform convergence of the finite-dimensional distributions, still on intervals of the form $[0, T]$. We refer to Cox & Griffeath (1990) for the complete proof of these results.

(ii) Tightness.

This follows easily from the fact that the labelled partition $\mathscr{A}^L$ with initial value in $\Gamma_{\mathscr{A}}(L,n)^*$ for some $n \in \mathbb{N}$ lies in $\Gamma_{\mathscr{A}}(L,n)$ immediately after each coalescence event, with probability tending to 1. Indeed, for each $L \in \mathbb{N}$, let $\gamma_1^L < \ldots < \gamma_{n-1}^L$ be the ranked epochs of jumps of $\mathscr{A}^{L,u}$ (if less than $n-1$ jumps occur, then the last times are equal to $+\infty$ by convention). Let also $n \in \mathbb{N}$, $A_L \in \Gamma_{\mathscr{A}}(L,n)^*$ for every $L \geq 1$, and following Ethier & Kurtz (1986), for every $\delta, T > 0$ let $w'(\mathscr{A}^{L,u}, T, \delta)$ denote the modulus of continuity of the process $\mathscr{A}^{L,u}$ on the time interval $[0, T]$ and with time-step δ. Let $\varepsilon > 0$. With the convention that $(+\infty) - (+\infty) = +\infty$, we have

$$\mathbb{P}_{A_L}\big[w'(\mathscr{A}^L, T, \delta) > \varepsilon\big] \leq \sum_{k=2}^{n} \mathbb{P}_{A_L}[\gamma_k^L - \gamma_{k-1}^L < \delta]. \tag{47}$$

An easy recursion using the fact that we consider only finitely lineages and the uniform bounds obtained in Lemma 6.9 enables us to write that for all $k \in \{1, \ldots, n-1\}$,

$$\sup_{A'_L \in \Gamma_{\mathscr{A}}(L,n)^*} \mathbb{P}_{A'_L}[\gamma_k^L < \infty \, ; \, \mathscr{A}^L(\varpi_L \gamma_k^L) \notin \Gamma_{\mathscr{A}}(L,n)] \to 0, \qquad \text{as } L \to \infty.$$

This result and an application of the strong Markov property at time γ_{k-1}^L yield

$$\begin{aligned}\mathbb{P}_{A_L}[\gamma_k^L - \gamma_{k-1}^L < \delta] &= \mathbb{E}_{A_L}[\mathbf{1}_{\{\mathscr{A}^L(\varpi_L \gamma_{k-1}^L) \in \Gamma_{\mathscr{A}}(L,n)\}} \mathbb{P}_{\mathscr{A}^L(\varpi_L \gamma_{k-1}^L)}[\gamma_1^L < \delta]] + o(1) \\ &\leq \frac{(n-k)(n-k-1)}{2} \sup_{A'_L \in \Gamma_{\mathscr{A}}(L,2)^*} \mathbb{P}_{A'_L}[\gamma_1^L < \delta] + o(1)\end{aligned} \tag{48}$$

as $L \to \infty$, where the last line uses the consistency of the genealogy to bound the probability that a first coalescence event occurs to the sample of lineages before δ by the sum over all pairs of lineages of this sample of the probability that they have coalesced by time δ (note that there are at most $(n-k)(n-k-1)/2$ possible pairs just after γ_{k-1}^L). But these probabilities converge uniformly to $1 - e^{-\delta}$ by Theorem 6.3, and so for δ small enough, we can make the right-hand side of (48) less than $\varepsilon/(n^3)$ for L large enough (n is fixed here). Coming back to (47), this gives us

$$\limsup_{L \to \infty} \mathbb{P}_{A_L}[w'(\mathscr{A}^L, T, \delta) > \varepsilon] \leq \varepsilon.$$

Since $\mathscr{P}_n$ is a compact metrisable space, we can apply Corollary 3.7.4 in Ethier & Kurtz (1986) to complete the proof. $\square$

7 Proof of Theorem 3.7

We now turn to the case $\psi_L \propto L$. We still have small reproduction events of size $\mathcal{O}(1)$, but now large events have sizes $\mathcal{O}(L)$ (and rate $\mathcal{O}(\rho_L^{-1})$), so that they cover a non-negligible fraction of the torus $\mathbb{T}(L)$. By Lemma 5.4, if the lineages were only subject to small reproduction events, the location of a single lineage would be nearly uniformly distributed on $\mathbb{T}(L)$ after a time $t_L \gg L^2$. This suggests several limiting behaviours for the genealogical process $\mathscr{A}^L$, according to how ρ_L scales with L^2:

- If ρ_L is order at most $\mathcal{O}(L^2)$, then large reproduction events occur at times when the locations of the lineages are still correlated with their starting points, and so we expect space (i.e., labels in the representation we adopted) to matter in the evolution of $\mathscr{A}^L$.
- If $L^2 \ll \rho_L \ll L^2 \log L$, then the lineages have the time to homogenise their locations over $\mathbb{T}(L)$ before the first large event occurs, but not to come at distance $2R^s$ from each other. Hence, large events should affect lineages independently of each other, and bring the genealogy down to the common ancestor of the sample before any pair of lineages experiences a coalescence due to small events.
- If $\rho_L \approx L^2 \log L$, the fact that pairs of lineages have now the time to gather at distance $2R^s$ should add a Kingman part (i.e., almost surely binary mergers) to the genealogical process obtained in the previous point.
- If $\rho_L \gg L^2 \log L$, Kingman's coalescent due to small reproduction events should bring the ancestry of a sample of lineages down to a single lineage before any large event occurs, so that the limiting genealogy will not see these large events.

Proof of Theorem 3.7: For (a), let us write down the generator $\overline{\mathscr{G}}_L$ of $\bar{A}^L$ applied to functions of the $\mathbb{T}(1)$-labelled partitions of $\{1,\dots,n\}$. Recall the notation x_a for the label of the block a of a labelled partition $A \in \mathscr{P}_n^\ell$ (introduced in Notation 2.5), and write $|A|$ for the number of blocks of A. For each $L \geq 1$, f of class C^3 with respect to the labels and $A \in \mathscr{P}_n^\ell$ such that any pair (a_1, a_2) of blocks of A satisfies $|x_{a_1} - x_{a_2}| \geq (2R^s)/L$, we have

$$\overline{\mathscr{G}}_L f(A) = \rho_L \sum_{i=1}^{|A|} \int_{\mathbb{T}(L)} dy \int_0^{R^s} \mu^s(dr) \frac{L_r(y)}{\pi r^2} \int_0^1 \nu_r^s(du) u \\ \times \left[f\left(A \setminus \{(a_i, x_{a_i})\} \cup \left\{ \left(a_i, x_{a_i} + \frac{y}{L} \right) \right\} \right) - f(A) \right] + \mathscr{G}^{(B)}(A), \tag{49}$$

where we wrote $A = \{(a_1, x_{a_1}), \dots, (a_{|A|}, x_{a_{|A|}})\}$ and

$$\begin{aligned} &\mathscr{G}^{(B)}(A) \\ &= \frac{1}{c^2} \int_{\mathbb{T}(1)} dz \int_0^{(\sqrt{2})^{-1}} \mu^B(dr) \int_{B(z,cr)} \frac{dy}{V_{cr}} \sum_{I \subset \{1,\dots,|A|\}} \prod_{i \in I} \mathbf{1}_{\{x_i \in B(z,cr)\}} \prod_{j \notin I} \mathbf{1}_{\{x_j \notin B(z,cr)\}} \\ &\times \sum_{J \subset I} \int_0^1 u^{|J|} (1-u)^{|I|-|J|} \nu_r^B(du) \left[f\left(A \setminus \left(\bigcup_{i \in J} \{(a_i, x_{a_i})\} \right) \cup \left\{ \left(\bigcup_{i \in J} a_i, y \right) \right\} \right) - f(A) \right] \end{aligned}$$

is the generator of the coalescence events due to large reproduction events (recall V_r is the volume of the ball $B_{\mathbb{T}(1)}(0, r)$). Note that $\mathscr{G}^{(B)}$ does not depend on L. Let us look at a particular term in the sum on the right-hand side of (49). Since f is of class C^3 with respect to the labels of the blocks, a Taylor expansion and the symmetry of the jumps due to small events give us

$$\begin{aligned}\rho_L \int dy \int_0^{R^s} \mu^s(dr)\frac{L_r(y)}{\pi r^2}\int_0^1 \nu_r(du)u\Big[f\Big(A\setminus\{(a_i,x_{a_i})\}\cup\Big\{\Big(a_i,x_{a_i}+\frac{y}{L}\Big)\Big\}\Big)-f(A)\Big]\\ =\frac{\rho_L}{L^2}\,\frac{\sigma_s^2}{2}\,\Delta_i f(A)+\mathscr{O}\Big(\frac{\rho_L}{L^3}\Big),\end{aligned}$$

where Δ_i is the Laplacian operator on $\mathbb{T}(1)$ applied to the label of the block a_i only. Since $\rho_L L^{-2}\to b\in[0,\infty)$ by assumption and because f is continuous on a compact space, we obtain that $\overline{\mathscr{G}}_L f$ defined on the compact set $E_L\equiv\{A\in\mathscr{P}_n^\ell : L|x_{a_i}-x_{a_j}|\geq 2R^s\ \forall i\neq j\}$ converges uniformly towards

$$\overline{\mathscr{G}}f(A)\equiv\frac{b\sigma_s^2}{2}\sum_{i=1}^{|A|}\Delta_i f(A)+\mathscr{G}^{(B)}f(A).$$

Now, by the same technique as in Section 5, one can prove that the gathering time at distance $2R^s$ of two lineages starting at distance $\mathscr{O}(L)$ on $\mathbb{T}(L)$ and subject only to small events converges uniformly on the time scale $\frac{L^2\log L}{\pi\sigma_s^2}$ to an Exp(1) random variable (in the sense of Lemma 5.3). In addition, since the new location of a lineage affected by a large event is chosen uniformly over a ball of $\mathbb{T}(L)$ whose radius is of order $\mathscr{O}(L)$, if a large event affects a pair of lineages but does not lead to their coalescence, then the probability that the lineages are at distance less than $L(\log L)^{-1}$ just after the event vanishes as $L\to 0$. If we call $\check{T}_L^*$ the first time at which two lineages on $\mathbb{T}(L)$ are gathered at distance $2R^s$ and t_L^* their coalescence time in the original timescale, we readily obtain that for any $u>0$, and $x_1'\neq x_2'\in\mathbb{T}(1)^2$,

$$\lim_{L\to\infty}\mathbb{P}_{\wp_2(Lx_1',Lx_2')}\big[t_L^*>\check{T}_L^*\ ;\ \check{T}_L^*\leq\rho_L u\big]=0.$$

Indeed, as we already mentioned, if a large event does not make the lineages coalesce then with probability tending to one, the latter start at separation $\mathscr{O}(L)$ and do not have the time to meet at distance $2R^s$ before the next large event. Now, the number of large reproduction events that the pair of lineages experiences before time $\rho_L u$ can be stochastically bounded by a Poisson random variable whose parameter is finite and independent of L. Hence, if none of them leads to a coalescence then with probability tending to 1, $\check{T}_L^*>\rho_L u$. It follows that, if $u>0$ is fixed, we can use the consistency of the genealogy and write

$$\mathbb{P}_{\wp_n(L\mathbf{x})}[\exists t\in[0,u]:\bar{\mathscr{A}}^L(t)\notin E_L]\leq\sum_{i<j=1}^{n}\mathbb{P}_{\{(\{i\},Lx_i),(\{j\},Lx_j)\}}\big[t_L^*>\check{T}_L^*;\check{T}_L^*\leq\rho_L u\big]\to 0.$$

Consequently, one can use Corollary 4.8.7 in Ethier & Kurtz (1986) (with E_L as the subspace of interest in condition (f)) to conclude that the law under $\mathbb{P}_{\wp_n(L\mathbf{x})}$ of $\bar{A}^L$ converges to that of $\bar{\mathscr{A}}^{\infty,b,c}$ as processes in the Skorohod space of all càdlàg paths with values in the $\mathbb{T}(1)$-labelled partitions of $\{1,\dots,n\}$.

Let us now prove (b). Recall the assumption that the total rate at which large events occur is finite, that is $M\equiv c^{-2}\mu^B([0,(\sqrt{2})^{-1}])<\infty$. Let us first analyse what happens during the first event which may affect the unlabelled ancestral partition.

Define for each $L \geq 1$ the stopping time e_1^L by the following property: $\rho_L e_1^L$ is the first time on the original timescale at which either a large event occurs, or $\mathscr{A}^L$ undergoes a coalescence event due to small reproduction events. Since large and small reproduction events are independent, $\rho_L e_1^L$ has the same distribution as the minimum of two following independent random times:

- the first time of occurrence of a large event, that is an $\mathrm{Exp}\big(M/\rho_L\big)$-random variable.
- the time t_L^* at which a first coalescence event occurs between lineages of the genealogical process $\tilde{\mathscr{A}}^L$ evolving only owing to small reproduction events.

By (46) applied to the case $\rho_L \equiv +\infty$ (i.e., no large events occur), $\frac{2\pi\sigma_s^2}{L^2 \log L}\ t_L^*$ converges to an $\mathrm{Exp}\big(n(n-1)/2\big)$-random variable under $\mathbb{P}_{A_L}$, uniformly in $(A_L)_{L\in\mathbb{N}}$ such that $A_L \in \Gamma_{\mathscr{A}}(L,n)^*$ for every L. It is then straightforward to obtain

$$\lim_{L\to\infty} \sup_{t\geq 0} \sup_{A_L \in \Gamma_{\mathscr{A}}(L,n)^*} \left| \mathbb{P}_{A_L}[e_1^L > t] - \exp\Big(-\Big\{M + \beta\frac{n(n-1)}{2}\Big\}t\Big)\right| = 0, \tag{50}$$

where the formulation is also valid for $\beta = 0$. Also, by the independence of Π_L^s and Π_L^B, for every $(A_L)_{L\in\mathbb{N}}$ as above we have (with an abuse of notation)

$$\mathbb{P}_{A_L}\big[\rho_L e_1^L = t_L^*\big] = \mathbb{E}_{A_L}\Big[\exp\Big\{-\frac{M}{\rho_L}\ t_L^*\Big\}\Big].$$

Using Fubini's theorem and a change of variable, we can write

$$\begin{aligned}
\mathbb{E}_{A_L}\Big[\exp\Big\{-\frac{M}{\rho_L}\ t_L^*\Big\}\Big] &= \int_0^1 \mathbb{P}_{A_L}\Big[\exp\Big\{-\frac{M}{\rho_L}\ t_L^*\Big\} > s\Big]ds \\
&= \int_0^1 \mathbb{P}_{A_L}\Big[\frac{2\pi\sigma_s^2}{L^2\log L}\ t_L^* < -\frac{2\pi\sigma_s^2\rho_L}{ML^2\log L}\ \log s\Big]ds \\
&= \frac{ML^2\log L}{2\pi\sigma_s^2\rho_L}\int_0^\infty e^{-\frac{ML^2\log L}{2\pi\sigma_s^2\rho_L}u}\ \mathbb{P}_{A_L}\Big[\frac{2\pi\sigma_s^2}{L^2\log L}\ t_L^* < u\Big]du \\
&= 1 - \frac{ML^2\log L}{2\pi\sigma_s^2\rho_L}\int_0^\infty e^{-\frac{ML^2\log L}{2\pi\sigma_s^2\rho_L}u}\ \mathbb{P}_{A_L}\Big[\frac{2\pi\sigma_s^2}{L^2\log L}\ t_L^* \geq u\Big]du.
\end{aligned}$$

When $\beta > 0$, we have $\frac{ML^2\log L}{2\pi\sigma_s^2\rho_L} \to \frac{M}{\beta}$ and so we can use the uniform convergence derived in (46) and the fact that the distribution of t_L^* does not charge points to conclude that

$$\lim_{L\to\infty} \sup_{A_L\in\Gamma_{\mathscr{A}}(L,n)^*}\left|\mathbb{P}_{A_L}\big[\rho_L e_1^L = t_L^*\big] - \frac{\beta n(n-1)}{\beta n(n-1) + 2M}\right| = 0.$$

The limit holds also for $\beta = 0$ by a trivial argument. A byproduct of this result is the existence of a constant $C_0 > 0$ and $L_0 \in \mathbb{N}$ such that, for all $L \geq L_0$ and $(A_L)_{L\in\mathbb{N}}$ as above, $\mathbb{P}_{A_L}[\rho_L e_1^L < t_L^*] \geq C_0$. We shall need this fact in the next paragraph.

By Theorem 3.3 in the case $\rho_L \equiv \infty$, up to an error term tending uniformly to 0, on the event $\{\rho_L e_1^L = t_L^*\}$ the transition occurring to $\mathscr{A}^{L,u}$ at time $\rho_L e_1^L$ is the coalescence of a pair of blocks, each pair having the same probability to be the one which coalesces. Let us show that, conditioned on $\{\rho_L e_1^L < t_L^*\}$, the locations of the lineages at time $(\rho_L e_1^L)-$ are approximately distributed as n independent uniform random variables on $\mathbb{T}(L)$. We use again the notation τ_{ij}, τ_{ij}^* and $\tau, \tau^*(= t_L^*$ here) introduced in the proof of Theorem 3.3 for the gathering time at distance $2R^s$ and the coalescence time of lineages i and j, and their minima (once again on the original timescale). These quantities depend on L but, for the sake of clarity, we do not reflect that in our notation. In order to use our results on Lévy processes, we need to make sure that no pairs of lineages have come at distance less than $2R^s$ before time $\rho_L e_1^L$. We have for each $L \in \mathbb{N}$

$$\mathbb{P}_{A_L}\left[\tau < \rho_L e_1^L \middle| \, \rho_L e_1^L < t_L^*\right] \leq \sum_{i<j=1}^{n} \mathbb{P}_{A_L}\left[\tau_{ij} < \rho_L e_1^L \middle| \, \rho_L e_1^L < t_L^*\right], \tag{51}$$

Each term (i,j) on the right-hand side of (51) is bounded by

$$\begin{aligned}
&\mathbb{P}_{A_L}\left[\,\tau_{ij} < \rho_L e_1^L - \log L \middle| \, \rho_L e_1^L < t_L^*\right] \\
&\qquad\qquad + \mathbb{P}_{A_L}\left[\rho_L e_1^L - \log L \leq \tau_{ij} < \rho_L e_1^L \middle| \, \rho_L e_1^L < t_L^*\right] \\
&\qquad \leq C_0^{-1}\Big\{\mathbb{P}_{A_L}\left[\tilde{\tau}_{ij}^* > \tilde{\tau}_{ij} + \log L\right] + \mathbb{P}_{A_L}\left[\tilde{\tau}_{ij} \in [\varsigma_L - \log L, \varsigma_L)\right]\Big\},
\end{aligned} \tag{52}$$

where for each $L \in \mathbb{N}$, ς_L is an $\mathrm{Exp}(M/\rho_L)$-random variable independent of all other variables, and $\tilde{\tau}_{ij}$ and $\tilde{\tau}_{ij}^*$ are defined as above, but for the process $\tilde{\mathscr{A}}^L$. By the strong Markov property applied at time $\tilde{\tau}_{ij}$ and the result of Proposition 6.4 (b), the first term on the right-hand side of (52) converges to 0 uniformly in $A_L \in \Gamma_{\mathscr{A}}(L,n)^*$. By a simple change of variable, the second term is equal to

$$M \int_0^\infty e^{-Ms}\, \mathbb{P}_{A_L}\left[\tilde{\tau}_{ij} \in [\rho_L s - \log L, \rho_L s)\right] ds \leq M \int_0^\infty e^{-Ms}\, C\, \frac{\log L}{L^2}\, ds \;\to\; 0,$$

where the inequality comes from Lemma 5.5. Therefore, back to (51) we obtain that

$$\lim_{L\to\infty} \sup_{A_L \in \Gamma_{\mathscr{A}}(L,n)^*} \mathbb{P}_{A_L}\left[\tau < \rho_L e_1^L \middle| \, \rho_L e_1^L < t_L^*\right] = 0. \tag{53}$$

Now, let $D_1, \ldots, D_n$ be n measurable subsets of $\mathbb{T}(1)$, and for each $i \in \{1, \ldots, n\}$ and $L \geq 1$, let $LD_i \subset \mathbb{T}(L)$ be the dilation of D_i by a factor L. Let us show that

$$\begin{aligned}
\lim_{L\to\infty} \sup_{A_L \in \Gamma_{\mathscr{A}}(L,n)^*} \Bigg| \, \mathbb{P}_{A_L}\Big[\,(\xi_1^L, \ldots, \xi_n^L)(\rho_L e_1^L -) \in (LD_1) \times \ldots \times (LD_n) \Big| \rho_L e_1^L < t_L^*\Big] \\
- \prod_{i=1}^{n} \mathrm{Leb}(D_i) \Bigg| = 0,
\end{aligned} \tag{54}$$

where $\xi_i^L(t)$ denotes the location of the i-th lineage of $\mathscr{A}^L$ at time t. To do so, let us use the fact that on the event $\{\rho_L e_1^L < t_L^*\}$, the genealogical process $\mathscr{A}^L$ up to time $\rho_L e_1^L$ has the same distribution as $\tilde{\mathscr{A}}^L$ up to time ς_L and on the event $\{\tilde{\tau}^* > \varsigma_L\}$. We have

$$\begin{aligned}
&\mathbb{P}_{A_L}\Big[(\xi_1^L,\dots,\xi_n^L)(\rho_L e_1^L-)\in\prod_{i=1}^n(LD_i)\Big|\rho_L e_1^L<t_L^*\Big]\\
&=\ \frac{1}{\mathbb{P}_{A_L}[\rho_L e_1^L<t_L^*]}\,\mathbb{P}_{A_L}\Big[(\xi_1^L,\dots,\xi_n^L)(\rho_L e_1^L-)\in\prod_{i=1}^n(LD_i);\ \rho_L e_1^L<t_L^*\Big]\\
&=\ \frac{1}{\mathbb{P}_{A_L}[\rho_L e_1^L<t_L^*]}\,\mathbb{P}_{A_L}\Big[(\tilde{\xi}_1^L,\dots,\tilde{\xi}_n^L)(\varsigma_L-)\in\prod_{i=1}^n(LD_i);\ \varsigma_L<\tilde{\tau}^*\Big]\\
&=\ \frac{1}{\mathbb{P}_{A_L}[\rho_L e_1^L<t_L^*]}\,\mathbb{P}_{A_L}\Big[(\tilde{\xi}_1^L,\dots,\tilde{\xi}_n^L)(\varsigma_L-)\in\prod_{i=1}^n(LD_i);\ \varsigma_L<\tilde{\tau}\Big]+\eta_L(A_L)\\
&=\ \frac{M}{\mathbb{P}_{A_L}[\rho_L e_1^L<t_L^*]}\int_0^\infty ds\ e^{-Ms}\mathbb{P}_{A_L}\Big[(\tilde{\xi}_1^L,\dots,\tilde{\xi}_n^L)(\rho_L s-)\in\prod_{i=1}^n(LD_i);\\
&\qquad\qquad\qquad\qquad\qquad\qquad\qquad\qquad\qquad\tilde{\tau}>\rho_L s\Big]+\eta_L(A_L),
\end{aligned}\tag{55}$$

where $\eta_L(A_L)$ tends to 0 uniformly in $(A_L)_{L\in\mathbb{N}}$ by (53) and the fact that $\mathbb{P}_{A_L}\big[\rho_L e_1^L<t_L^*\big]$ does not vanish.

Let us fix $s>0$ for a moment, and consider the corresponding probability within the integral. Up to time $\tilde{\tau}$, the movements of the lineages are distributed as n independent copies $\hat{\xi}_1^L,\dots,\hat{\xi}_n^L$ of the motion of a single lineage, for which an easy modification of Lemma 5.4 (b) tells us that, if $(\varepsilon_L)_{L\in\mathbb{N}}$ is such that $\varepsilon_L\to 0$ but $\varepsilon_L\rho_L\gg L^2$ as $L\to\infty$,

$$\lim_{L\to\infty}\ \sup_{v\geq\varepsilon_L}\ \sup_{x\in\mathbb{T}(L)}\Big|\mathbb{P}_x\big[\hat{\xi}^L(v\rho_L)\in(LD)\big]-\mathrm{Leb}(D)\Big|=0.\tag{56}$$

However, it is not entirely clear that this convergence will still hold for n independent lineages on the event $\{\hat{\tau}>\rho_L s\}$ (where $\hat{\tau}$ is the first time at which at least two of them come at distance less than $2R^s$). Keeping the notation A_L for the initial value of the set of lineages and denoting the set of n (non-coalescing) motions by $\hat{\mathscr{A}}^L$, we have

$$\begin{aligned}
&\mathbb{P}_{A_L}\ \big[(\hat{\xi}_1^L,\dots,\hat{\xi}_n^L)(\rho_L s-)\in(LD_1)\times\ldots\times(LD_n);\ \hat{\tau}\leq\rho_L s\big]\\
&=\ \mathbb{E}_{A_L}\bigg[\mathbf{1}_{\{\hat{\tau}\leq\rho_L s\}}\ \mathbb{P}_{\hat{\mathscr{A}}^L(\hat{\tau})}\Big[(\hat{\xi}_1^L,\dots,\hat{\xi}_n^L)\big((\rho_L s-\hat{\tau})-\big)\in(LD_1)\times\ldots\times(LD_n)\Big]\bigg].
\end{aligned}$$

Splitting the preceding integral into $\big\{\rho_L(s-\varepsilon_L)\leq\hat{\tau}\leq\rho_L s\big\}$ and $\big\{\hat{\tau}<\rho_L(s-\varepsilon_L)\big\}$, we can use (56) in the latter case to write

$$\begin{aligned}
&\mathbb{E}_{A_L}\bigg[\ \mathbf{1}_{\{\hat{\tau}\leq\rho_L s\}}\ \mathbb{P}_{\hat{\mathscr{A}}^L(\hat{\tau})}\Big[(\hat{\xi}_1^L,\dots,\hat{\xi}_n^L)\big((\rho_L s-\hat{\tau})-\big)\in\prod_{i=1}^n(LD_i)\Big]\bigg]\\
&\quad=\mathbb{E}_{A_L}\bigg[\mathbf{1}_{\{\rho_L(s-\varepsilon_L)\leq\hat{\tau}\leq\rho_L s\}}\ \mathbb{P}_{\hat{\mathscr{A}}^L(\hat{\tau})}\Big[(\hat{\xi}_1^L,\dots,\hat{\xi}_n^L)\big((\rho_L s-\hat{\tau})-\big)\in\prod_{i=1}^n(LD_i)\Big]\bigg]\\
&\quad\quad+\Big(\prod_{i=1}^n\mathrm{Leb}(D_i)\Big)\mathbb{P}_{A_L}[\hat{\tau}<\rho_L(s-\varepsilon_L)]+\delta_L(A_L),
\end{aligned}\tag{57}$$

where $(\delta_L(A_L))_{L\in\mathbb{N}}$ tends to zero uniformly in $(A_L)_{L\in\mathbb{N}}$ as L tends to infinity (we still impose that $A_L \in \Gamma_{\mathscr{A}}(L,n)^*$ for every L). By the convergence of the distribution function of $\frac{\tilde{\tau}}{L^2\log L}$ to that of an exponential random variable, uniformly in the time variable and in $(A_L)_{L\in\mathbb{N}}$, we obtain that $\mathbb{P}_{A_L}[\rho_L(s-\varepsilon_L) \le \hat{\tau} \le \rho_L s]$ converges to 0 uniformly in $(A_L)_{L\in\mathbb{N}}$ (which is also true if $\beta = 0$, i.e., $\rho_L \ll L^2\log L$). Hence, we can find a sequence $(\delta'_L(A_L))_{L\in\mathbb{N}}$ decreasing to 0 uniformly in $(A_L)_{L\in\mathbb{N}}$, such that the whole sum on the right-hand side of (57) is equal to

$$\Big(\prod_{i=1}^{n}\mathrm{Leb}(D_i)\Big)\mathbb{P}_{A_L}[\hat{\tau} \le \rho_L s] + \delta'_L(A_L).$$

Likewise, we can find another sequence $(\delta''_L)_{L\in\mathbb{N}}$ decreasing to zero uniformly in $(A_L)_{L\in\mathbb{N}}$ such that

$$\mathbb{P}_{A_L}\big[(\hat{\xi}^L_1,\dots,\hat{\xi}^L_n)(\rho_L s-) \in (LD_1)\times\ldots\times(LD_n)\big] = \prod_{i=1}^{n}\mathrm{Leb}(D_i) + \delta''_L(A_L).$$

Subtracting the two last equalities, we obtain

$$\mathbb{P}_{A_L}\Big[(\hat{\xi}^L_1,\dots,\hat{\xi}^L_n)(\rho_L s-) \in \prod_{i=1}^{n}(LD_i);\, \hat{\tau} > \rho_L s\Big] = \Big\{\prod_{i=1}^{n}\mathrm{Leb}(D_i)\Big\}\mathbb{P}_{A_L}[\hat{\tau} > \rho_L s] + o(1),$$

where the remainder decreases to 0 uniformly in $s > 0$ and $(A_L)_{L\ge 1}$ such that $A_L \in \Gamma_{\mathscr{A}}(L,n)^*$ for each L. Coming back to (55), we obtain that it is equal to

$$\begin{aligned}\frac{M}{\mathbb{P}_{A_L}[\rho_L e^L_1 < t^*_L]}\int_0^\infty ds\, e^{-Ms}\Big\{\Big(\prod_{i=1}^{n}\mathrm{Leb}(D_i)\Big)\mathbb{P}_{A_L}[\hat{\tau} > \rho_L s] + o(1)\Big\} \\ = \frac{\mathbb{P}_{A_L}[\tilde{\tau} > \varsigma_L]}{\mathbb{P}_{A_L}[\tilde{\tau}^* > \varsigma_L]}\prod_{i=1}^{n}\mathrm{Leb}(D_i) + o(1) \\ = \frac{\mathbb{P}_{A_L}[\tilde{\tau}^* > \varsigma_L] + o(1)}{\mathbb{P}_{A_L}[\tilde{\tau}^* > \varsigma_L]}\prod_{i=1}^{n}\mathrm{Leb}(D_i) + o(1),\end{aligned}$$

where the last line uses (53). We can thus conclude that (54) holds.

Condition on the first event being a large reproduction event. By the description of such an event, the result for the genealogical process is the merger of at most one group of blocks into a bigger block. Furthermore, the transitions depend only on the number of blocks and their labels, so for convenience we derive the transition probabilities for A_L of the form $\wp_n(\mathbf{x})$ only, although we shall use the result later for more general labelled partitions. Let π be a partition of $\{1,\dots,n\}$ such that π has exactly one block of size greater than 1, which we call J. Then if the large event has centre x and radius cr in $\mathbb{T}(1)$, the probability that the transition undergone by $\mathscr{A}^{L,u}$ is $\wp_n \to \pi$ is the probability that at this time, at least all the lineages in J have labels in $B(x,cr)$ and are really affected by the event, and all the other lineages present in $B(x,cr)$ are not affected by the event. Summing over all possible choices $I \subset \{1,\dots,n\}\setminus J$ for these "other lineages" (I can be empty) and using (54), the probability of the transition $\wp_n \to \pi$ up to a vanishing error is given by

$$\begin{aligned}
\sum_I V_{cr}^{|J|+|I|}(1-V_{cr})^{n-|J|-|I|}\int_0^1 u^{|J|}(1-u)^{|I|}\nu_r^B(du)& \\
= & \int_0^1 (uV_{cr})^{|J|}\sum_{i=0}^{n-|J|}\binom{n-|J|}{i}V_{cr}^i(1-V_{cr})^{n-|J|-i}(1-u)^i\nu_r^B(du) \\
= & \int_0^1 (uV_{cr})^{|J|}((1-u)V_{cr}+1-V_{cr})^{n-|J|}\nu_r^B(du) \\
= & \int_0^1 (uV_{cr})^{|J|}(1-uV_{cr})^{n-|J|}\nu_r^B(du). \qquad (58)
\end{aligned}$$

We now have the results we need to show (b). For every $L\in\mathbb{N}$, let us consider again the time e_1^L introduced earlier, and define for each integer $i\geq 2$,

$$\begin{aligned}
e_i^L = \inf\big\{t > e_{i-1}^L\ :\ \rho_L t\in\Pi_L^B \text{ or } \rho_L t \text{ is the epoch of a coalescence}& \\
\text{due to small events}\big\}.&
\end{aligned}$$

Let us also define similar times corresponding to $\Lambda^{(\beta,c)}$. From the expression of its rates given in Definition 3.6, $\Lambda^{(\beta,c)}$ is composed of a Kingman part (i.e., only binary mergers) run at rate β, and of a set of multiple mergers due to the part $\Lambda^{(0)}$ of its Λ-measure with the atom at 0 removed. Furthermore, the finite measure $\Lambda^{(0)}$ on $[0,1]$ is given by

$$\begin{aligned}
\Lambda^{(0)}(dv) &= c^{-2}v^2\int_0^{(\sqrt{2})^{-1}} \nu_r^B\big(\{u:\ uV_{cr}\in dv\}\big)\mu^B(dr) \\
&= c^{-2}v^2\int_0^{(\sqrt{2})^{-1}} \mathbf{1}_{\{V_{cr}\geq v\}}\nu_r^B\Big(d\frac{v}{V_{cr}}\Big)\mu^B(dr).
\end{aligned}$$

Following Pitman's Poissonian construction of a coalescent with multiple mergers (whose Λ-measure has no atom at 0, see Pitman 1999), let us define Π as a Poisson point process on $\mathbb{R}_+\times[0,1]$ with intensity $dt\otimes v^{-2}\Lambda^{(0)}(dv)$. Note that because of our assumption on M, $v^{-2}\Lambda^{(0)}(dv)$ is also a finite measure, with total mass M. The atoms of Π constitute the times at which $\Lambda^{(\beta,c)}$ acting on the partitions of $\mathbb{N}$ experiences a multiple collision, and the probabilities that any given lineage is affected by the event. The Kingman part of $\Lambda^{(\beta,c)}$ is superimposed on this construction by assigning to all pairs of blocks of the current partition independent exponential clocks with parameter β, giving the time at which the corresponding pair merges into one block.

From now on, we consider only the restriction of $\Lambda^{(\beta,c)}$ to $\mathscr{P}_n$, although we do not make it appear in the notation. Let e_1 be the minimum of the first time a pair of blocks of $\Lambda^{(\beta,c)}$ merges due to the Kingman part and of the time corresponding to the first point of Π. Define e_i in a similar manner for all $i\geq 2$, so that $(e_i)_{i\in\mathbb{N}}$ is an increasing sequence of random times at which $\Lambda^{(\beta,c)}$ may undergo a transition. Our goal is to show that the finite-dimensional distributions of $\big\{(e_i^L, \mathscr{A}^{L,u}(e_i^L)),\ i\in\mathbb{N}\big\}$ under $\mathbb{P}_{A_L}$ converge to those of $\big\{(e_i,\Lambda^{(\beta,c)}(e_i)),\ i\in\mathbb{N}\big\}$ under $\mathbb{P}_{\wp_n}$, as $L\to\infty$. Since $\mathscr{A}^{L,u}$ (resp., $\Lambda^{(\beta,c)}$) can jump only at the times e_i^L (resp., e_i), the fact that only finitely many jumps occur to $\Lambda^{(\beta,c)}$ in any compact time interval, together with Proposition 3.6.5 in Ethier & Kurtz (1986) enable us to conclude that this convergence yields (b). We proceed by induction, by showing that for each $i\in\mathbb{N}$:

$H(i)$: if $a_L \in \Gamma_{\mathscr{A}}(L,n)$ for each L and there exists $\pi_0 \in \mathscr{P}_n$ such that for all $L \in \mathbb{N}$, $\mathrm{bl}(a_L) = \pi_0$, then as $L \to \infty$

$$\mathscr{L}_{\mathbb{P}_{a_L}}\big(\{(e_1^L, \mathscr{A}^{L,u}(e_1^L)), \dots, (e_i^L, \mathscr{A}^{L,u}(e_i^L))\}\big) \Rightarrow \mathscr{L}_{\mathbb{P}_{\pi_0}}\big(\{(e_1, \Lambda^{(\beta,c)}(e_1)), \dots, (e_i, \Lambda^{(\beta,c)}(e_i))\}\big).$$

(Note that a_L can have less than n blocks).

Let us start by $H(1)$. Let $t \geq 0$, $\pi \in \mathscr{P}_n$ and write n_0 for the number of blocks of π_0. We have, in the notation used in the previous paragraph (and with $\tilde{\mathscr{A}}^{L,u}$ defined as the unlabelled partition induced by $\tilde{\mathscr{A}}^L$ on the timescale ρ_L),

$$\begin{aligned}
&\mathbb{P}_{a_L}\left[e_1^L \leq t;\ \mathscr{A}^{L,u}(e_1^L) = \pi\right] \\
&= \mathbb{P}_{a_L}\big[e_1^L \leq t;\ \mathscr{A}^{L,u}(e_1^L) = \pi;\ \rho_L e_1^L = t_L^*\big] + \mathbb{P}_{a_L}\big[e_1^L \leq t;\ \mathscr{A}^{L,u}(e_1^L) = \pi;\ \rho_L e_1^L < t_L^*\big] \\
&= \mathbb{P}_{a_L}\big[t_L^* \leq \rho_L t;\ \tilde{\mathscr{A}}^{L,u}(t_L^*/\rho_L) = \pi;\ t_L^* < \zeta_L\big] \qquad (59)\\
&\quad + \mathbb{P}_{a_L}\big[e_1^L \leq t;\ \mathscr{A}^{L,u}(e_1^L) = \pi \big|\ \rho_L e_1^L < t_L^*\big]\mathbb{P}_{a_L}\big[\rho_L e_1^L < t_L^*\big]. \qquad (60)
\end{aligned}$$

By Theorem 3.3 applied with $\rho_L \equiv +\infty$, $\tilde{\mathscr{A}}^{L,u}$ with initial value a_L converges as $L \to \infty$ to Kingman's coalescent $\mathscr{K}^{(\beta)}$ started at π_0 and run at rate β, as a process in $D_{\mathscr{P}_n}[0,\infty)$ (if $\beta = 0$, then $\tilde{\mathscr{A}}^{L,u}$ converges to the constant process equal to π_0). Hence, by the independence of $\tilde{\mathscr{A}}^L$ and ζ_L for every L and a simple time-change, the quantity in (59) tends to that corresponding to $\mathscr{K}^{(\beta)}$, that is

$$\mathbb{P}_{\pi_0}\big[\mathscr{K}^{(\beta)}(e_1^{\mathscr{K}}) = \pi\big]\mathbb{P}_{\pi_0}\big[e_1^{\mathscr{K}} < t \wedge \zeta\big], \qquad (61)$$

where $e_1^{\mathscr{K}}$ is distributed like an $\mathrm{Exp}\big(\beta\frac{n_0(n_0-1)}{2}\big)$-random variable and stands for the epoch of the first event occurring to $\mathscr{K}^{(\beta)}$, and ζ is an $\mathrm{Exp}(M)$-random variable. By the construction of $\Lambda^{(\beta,c)}$ given in the last paragraph, (61) is the probability that the first event occurring to $\Lambda^{(\beta,c)}$ happens before time t, is due to the Kingman part of the coalescent and leads to the transition $\pi_0 \to \pi$. For (60), note first that because Π_L^B and Π_L^s are independent, if we condition on $\rho_L e_1^L$ being the time of the first point (t_1^L, x_1^L, r_1^L) of Π_L^B, then e_1^L and the pair (x_1^L, r_1^L) are independent. Hence, we have for each $L \geq 1$

$$\begin{aligned}
&\mathbb{P}_{a_L}\big[e_1^L \leq t\ ;\ \mathscr{A}^{L,u}(e_1^L) = \pi \big|\ \rho_L e_1^L < t_L^*\big] \\
&\qquad = \mathbb{P}_{a_L}\big[e_1^L \leq t \big|\ \rho_L e_1^L < t_L^*\big]\mathbb{P}_{a_L}\big[\mathscr{A}^{L,u}(e_1^L) = \pi \big|\ \rho_L e_1^L < t_L^*\big].
\end{aligned}$$

Using (50) and the same reasoning as for (59), we can write

$$\begin{aligned}
&\mathbb{P}_{a_L}\big[e_1^L \leq t \big|\ \rho_L e_1^L < t_L^*\big]\ \mathbb{P}_{a_L}\ \big[\rho_L e_1^L < t_L^*\big] \\
&\qquad = \mathbb{P}_{a_L}\big[e_1^L \leq t;\ \rho_L e_1^L < t_L^*\big] \\
&\qquad = \mathbb{P}_{a_L}\big[e_1^L \leq t\big] - \mathbb{P}_{a_L}\big[e_1^L \leq t;\ \rho_L e_1^L = t_L^*\big] \\
&\qquad \to \exp\Big\{-\Big(M + \beta\frac{n_0(n_0-1)}{2}\Big)t\Big\} - \mathbb{P}_{\pi_0}\big[e_1^{\mathscr{K}} \leq t \wedge \zeta\big] \\
&\qquad = \mathbb{P}_{\pi_0}\big[\zeta < t \wedge e_1^{\mathscr{K}}\big],
\end{aligned}$$

where the last equality comes from the fact that an $\mathrm{Exp}\big(\beta\frac{n_0(n_0-1)}{2} + M\big)$-random variable has the same distribution as the minimum of an $\mathrm{Exp}\big(\beta\frac{n_0(n_0-1)}{2}\big)$- and an $\mathrm{Exp}(M)$-random variables, independent of each other. In addition, by the calculation done in (58),

$$\mathbb{P}_{a_L}\big[\mathscr{A}^{L,u}(e_1^L) = \pi \big|\ \rho_L e_1^L < t_L^*\big] \to \mathbb{P}_{\pi_0}\big[\Lambda^{(0)}(e_1^{\Lambda}) = \pi\big], \qquad \text{as } L \to \infty,$$

where e_1^Λ is the time of the first event of Π. Combining the above, and recognizing the transition probability of $\Lambda^{(\beta,c)}$ through the decomposition obtained, we can write

$$\lim_{L\to\infty} \mathbb{P}_{a_L}\big[e_1^L \le t;\ \mathscr{A}^{L,u}(e_1^L) = \pi\big] = \mathbb{P}_{\pi_0}\big[e_1 \le t;\ \Lambda^{(\beta,c)}(e_1) = \pi\big].$$

Since this result holds for each $t \geq 0$ and $\pi_0 \in \mathscr{P}_n$, using a monotone class argument we can conclude that the distribution of $\big(e_1^L, \mathscr{A}^{L,u}(e_1^L)\big)$ under $\mathbb{P}_{a_L}$ converges to the distribution of $(e_1, \Lambda^{(\beta,c)}(e_1))$ under $\mathbb{P}_{\pi_0}$ as $L \to \infty$. This proves $H(1)$.

Suppose that $H(i-1)$ holds for some $i \geq 2$. Let $D \subset (\mathbb{R}_+)^{i-1}$, $t \geq 0$ and $\pi_1, \dots, \pi_i \in \mathscr{P}_n$. Let also $L \in \mathbb{N}$. By the strong Markov property applied to $\mathscr{A}^L$ at time $\rho_L e_{i-1}^L$, we have

$$\begin{aligned}\mathbb{P}_{a_L}\big[(e_1^L, \dots, e_{i-1}^L) \in D;\ e_i^L - e_{i-1}^L \le t;\ \mathscr{A}^{L,u}(e_1^L) = \pi_1, \dots, \mathscr{A}^{L,u}(e_i^L) = \pi_i\big]&\\ = \mathbb{E}_{a_L}\Big[\ \mathbf{1}_{\{(e_1^L,\dots,e_{i-1}^L)\in D\}}\ \mathbf{1}_{\{\mathscr{A}^{L,u}(e_1^L)=\pi_1,\dots,\mathscr{A}^{L,u}(e_{i-1}^L)=\pi_{i-1}\}}&\\ \times \mathbb{P}_{\mathscr{A}^L(\rho_L e_{i-1}^L)}\big[e_1^L \le t;\ \mathscr{A}^{L,u}(e_1^L) = \pi_i\big]\Big]&.\end{aligned}$$

First, using arguments analogous to those leading to Lemma 6.9, up to an error term vanishing uniformly in $(a_L)_{L\in\mathbb{N}}$ such that $a_L \in \Gamma(L,n)$ for every $L \in \mathbb{N}$, we can consider that $\mathscr{A}^L(\rho_L e_{i-1}^L) \in \Gamma_{\mathscr{A}}(L,n)$. As $\mathrm{bl}\big(\mathscr{A}^L(\rho_L e_{i-1}^L)\big) = \pi_{i-1}$ for each L, we can therefore use $H(1)$ to write that

$$\lim_{L\to\infty} \mathbb{P}_{\mathscr{A}^L(\rho_L e_{i-1}^L)}\big[e_1^L \le t;\ \mathscr{A}^{L,u}(e_1^L) = \pi_i\big] = \mathbb{P}_{\pi_{i-1}}\big[e_1 \le t;\ \Lambda^{(\beta,c)}(e_1) = \pi_i\big],$$

and so dominated convergence and $H(i-1)$ give us

$$\begin{aligned}&\lim_{L\to\infty} \mathbb{P}_{a_L}\big[(e_1^L, \dots, e_{i-1}^L) \in D;\ e_i^L - e_{i-1}^L \le t;\ \mathscr{A}^{L,u}(e_1^L) = \pi_1, \dots, \mathscr{A}^{L,u}(e_i^L) = \pi_i\big]\\ &= \mathbb{E}_{\pi_0}\Big[\ \mathbf{1}_{\{(e_1,\dots,e_{i-1})\in D\}}\ \mathbf{1}_{\{\Lambda^{(\beta,c)}(e_1)=\pi_1,\dots,\Lambda^{(\beta,c)}(e_{i-1})=\pi_{i-1}\}} \mathbb{P}_{\pi_{i-1}}\big[e_1 \le t;\ \Lambda^{(\beta,c)}(e_1) = \pi_i\big]\Big]\\ &= \mathbb{P}_{\pi_0}\big[(e_1, \dots, e_{i-1}) \in D;\ e_i - e_{i-1} \le t;\ \Lambda^{(\beta,c)}(e_1) = \pi_1, \dots, \Lambda^{(\beta,c)}(e_i) = \pi_i\big],\end{aligned}$$

which again yields $H(i)$ by standard arguments. The induction is now complete, and so we can conclude that the finite-dimensional distributions of the embedded Markov chain and the holding times of $\mathscr{A}^{L,u}$ under $\mathbb{P}_{a_L}$ converge as $L \to \infty$ towards those of $\Lambda^{(\beta,c)}$ under $\mathbb{P}_{\pi_0}$. The proof of (b) is then complete.

To finish, suppose that $\rho_L \gg L^2 \log L$. Then, we can find a sequence Φ_L increasing to $+\infty$ such that

$$\sup_{A\in\Gamma_{\mathscr{A}}(L,n)} \mathbb{P}_A[\text{ a large event affects at least one lineage before time } \Phi_L L^2 \log L] \to 0$$

as $L \to \infty$. Hence, we can couple $\mathscr{A}^L$ with the process $\tilde{\mathscr{A}}^L$ which experiences only small events, so that the time by which they differ at step L is larger than Φ_L with probability tending to one, uniformly in the sequence $(A_L)_{L\geq 1}$ chosen as above. By the results obtained in Section 6 with $\rho_L \equiv +\infty$, we know that $\tilde{\mathscr{A}}^{L,u}$ converges in distribution towards $\mathscr{K}$, as a process in $D_{\mathscr{P}_n}[0,\infty)$. Since the sample size n is finite and under Kingman's coalescent, a sample of n lineages reaches a common ancestor in finite time almost surely, (c) follows. $\square$

A Proofs of the results of Section 5

Since the proofs of Lemmas 5.3 and 5.4 are highly reminiscent of those of Theorem 2 and Lemma 3.1 in Cox & Durrett (2002), we shall only give the arguments we need to modify and refer to their paper for more extensive proofs.

Proof of Lemma 5.4: Since ℓ^L is a Lévy process, for any integers n and L one can decompose $\ell^L(n)$ into

$$\ell^L(n) = \ell^L(0) + \sum_{k=1}^{n} \{\ell^L(k) - \ell^L(k-1)\},$$

where the n terms in the sum are i.i.d. random variables whose common distribution is that of $\ell^L(1)$ under $\mathbb{P}_0$. Using Bhattacharya's local central limit theorem (see Theorem 1.5 in Bhattacharya 1977) and the boundedness assumption on $\mathbb{E}_0[|\ell^L(1)|^4]$, we can control the deviation of $p^L(x,n)$ from the corresponding probabilities for Brownian motion up to an error of order $o(n^{-1})$ independent of L. Following Cox and Durrett's arguments, we obtain the desired results for integer times. For arbitrary times t, the Markov property applied to ℓ^L at time $\lfloor t \rfloor$ (plus, for (d), the fact that the variations of ℓ^L are bounded on a time interval $[n, n+1]$) completes the proof. □

Proof of Lemma 5.3: To simplify notation, we shall write $T(d_L)$ instead of $T(d_L, \ell^L)$ in the rest of the proof. For every $L \geq 1$, $x \in \mathbb{T}(L)$ and $\lambda > 0$, let us define the following quantities :

$$\begin{aligned} F_L(x,\lambda) &= \mathbb{E}_x\big[\exp(-\lambda T(d_L))\big], \\ G_L(x,\lambda) &= \int_0^\infty e^{-\lambda t} p^L(x,t)dt = \mathbb{E}_x\left[\int_0^\infty e^{-\lambda t}\, \mathbf{1}_{\{\ell^L(t)\in B(0,d_L)\}} dt\right]. \end{aligned}$$

Applying the strong Markov property to ℓ^L at time $T(d_L)$ and using a change of variables, we obtain (for any x_L)

$$G_L(x_L,\lambda) = \mathbb{E}_{x_L}\left[e^{-\lambda T(d_L)} G_L\big(\ell^L(T(d_L)),\lambda\big)\right]. \tag{62}$$

From the results of Lemma 5.4, we can derive the asymptotic behaviour of $G_L(x_L,\lambda)$. To this end, let $(v_L)_{L\geq 1}$ and $(u_L)_{L\geq 1}$ be two sequences growing to infinity such that $v_L(\log L)^{-1/2} \to 0$ and $u_L(\log L)^{-1} \to 0$ as $L \to \infty$. Splitting the integral in the definition of $G_L\big(x_L, \frac{\lambda}{L^2 \log L}\big)$ into four pieces, we obtain first by (b) of Lemma 5.4

$$\begin{aligned} &\frac{1}{d_L^2 \log L}\int_{v_L L^2}^\infty \exp\left(-\frac{\lambda t}{L^2 \log L}\right) p^L(x_L,t)dt \\ &\qquad = \frac{1}{d_L^2 \log L}\int_{v_L L^2}^\infty \exp\left(-\frac{\lambda t}{L^2 \log L}\right) \frac{\pi d_L^2}{L^2}\,(1+\delta_{L,1})\,dt \\ &\qquad = \frac{\pi}{\lambda}\,\exp\left(-\frac{\lambda v_L}{\log L}\right)(1+\delta_{L,1}) = \frac{\pi}{\lambda}\,(1+\delta'_{L,1}) \end{aligned}$$

as $L \to \infty$, where $\delta_{L,1}, \delta'_{L,1} \to 0$ uniformly in $x \in \mathbb{T}(L)$. By (a) of Lemma 5.4, we have

$$\begin{aligned} \frac{1}{d_L^2 \log L}\int_{\varepsilon_L L^2}^{v_L L^2} \exp\left(-\frac{\lambda t}{L^2 \log L}\right) p^L(x_L,t)\,dt \;&\leq\; \frac{1}{d_L^2 \log L}\frac{C_1 d_L^2}{\lfloor L^2 \varepsilon_L\rfloor}\,v_L L^2 \\ &\sim\; \frac{C_1 v_L}{\sqrt{\log L}} \to 0, \quad \text{as } L \to \infty \end{aligned}$$

by our assumption on v_L. By (c) of Lemma 5.4,

$$\begin{aligned}
\frac{1}{d_L^2\log L}\quad &\int_{u_L(1+|x_L|^2\vee d_L^2)}^{\varepsilon_L L^2}\exp\left(-\frac{\lambda t}{L^2\log L}\right)p^L(x_L,t)\,dt\\
&=\frac{1}{d_L^2\log L}\int_{u_L(1+|x_L|^2\vee d_L^2)}^{\varepsilon_L L^2}\frac{d_L^2}{2\sigma_L^2 t}\,(1+\delta_{L,2})\,dt\\
&=\frac{1}{2\sigma_L^2\log L}\,\Big(2\log L-\log(1+|x_L|^2\vee d_L^2)+\log\varepsilon_L-\log u_L\Big)(1+\delta_{L,2})\\
&=\frac{1-\beta\vee\gamma}{\sigma^2}\,(1+\delta'_{L,2}),
\end{aligned}$$

whenever $\frac{\log^+|x_L|}{\log L}\to\beta$ as L grows to infinity. Here again, $\delta_{L,2},\delta'_{L,2}\to 0$ uniformly in $x\in\mathbb{T}(L)$ as $L\to\infty$. Finally, by (d) of Lemma 5.4, we can write

$$\begin{aligned}
\frac{1}{d_L^2\log L}\int_0^{u_L(1+|x_L|^2\vee d_L^2)}&\exp\left(-\frac{\lambda t}{L^2\log L}\right)p^L(x_L,t)dt\\
&\leq\frac{C_2}{d_L^2\log L}\frac{u_L(1+|x_L|^2\vee d_L^2)}{1+d_L^{-2}|x_L|^2}\to 0,
\end{aligned}$$

independently of $(x_L)_{L\geq 1}$ since d_L does not vanish and $u_L(\log L)^{-1}\to 0$.

Combining the above, we obtain that if $\frac{\log^+|x_L|}{\log L}\to\beta$, then

$$\frac{1}{d_L^2\log L}\,G_L\Big(x_L,\frac{\lambda}{L^2\log L}\Big)=\frac{\pi}{\lambda}+\frac{1-(\beta\vee\gamma)}{\sigma^2}+o(1),\qquad\text{as } L\to\infty,$$

where the remainder does not depend on $(x_L)_{L\geq 1}$. Coming back to (62) with $x_L\in\Gamma(L,1)$, the uniform convergence obtained above, together with the fact that $\ell^L(d_L)\in B(0,d_L)$ a.s. yield

$$\lim_{L\to\infty}\mathbb{E}_{x_L}\left[\exp\left(-\frac{\lambda\pi\sigma^2\,T(d_L)}{(1-\gamma)L^2\log L}\right)\right]=\frac{(1-\gamma)/(\sigma^2\lambda)}{(1-\gamma)/(\sigma^2\lambda)+(1-\gamma)/\sigma^2}=\frac{1}{1+\lambda},\tag{63}$$

which we recognize as the Laplace transform of an Exp(1)-random variable. Since the left-hand side of (63) is monotone in λ and the function $\lambda\mapsto(1+\lambda)^{-1}$ is continuous, this convergence is in fact uniform in $\lambda\geq 0$. By standard approximation arguments (see for instance the proof of Theorem 4 in Cox 1989), we obtain that for any fixed $t>0$,

$$\lim_{L\to\infty}\sup_{x_L\in\Gamma(L,1)}\left|\mathbb{P}_{x_L}\left[\frac{\lambda\pi\sigma^2}{(1-\gamma)L^2\log L}\,T(d_L)>t\right]-e^{-t}\right|=0,$$

and, by monotonicity and the fact that all the quantities involved tend to 0 as $t\to\infty$, this convergence is uniform in $t\geq 0$. The interested reader will find all the missing details in the appendix of Cox & Durrett (2002). □

Proof of Lemma 5.5: Let $x \in \mathbb{T}(L)$ and $(U'_L)_{L\in\mathbb{N}}$ be as in the statement of Lemma 5.5. Using the strong Markov property at time $T(R,\ell^L)$, we can write

$$\begin{aligned}\mathbb{P}_x\big[\ell^L(U'_L+u_L)\in B(0,R)\big]&\\ \geq \int_{U'_L-u_L}^{U'_L}\int_{B(0,R)} &\mathbb{P}_x\big[T(R,\ell^L)\in ds, \ell^L(s)\in dy\big]\mathbb{P}_y\big[\ell^L(U'_L+u_L-s)\in B(0,R)\big]. \qquad (64)\end{aligned}$$

Note that, on the right-hand side of (64), the quantity U'_L+u_L-s lies in $[u_L,2u_L]$. We assumed that $2u_L \leq L^2(\log L)^{-1/2}$, and so we can use (c) of Lemma 5.4 with $d_L\equiv R$ and write

$$\lim_{L\to\infty}\ \sup_{y\in B(0,R)}\ \sup_{u_L\leq t\leq 2u_L}\left|\frac{2\sigma_L^2 t}{R^2}\,\mathbb{P}_y\big[\ell^L(t)\in B(0,R)\big]-1\right|=0,$$

which gives us the existence of a constant C_0 and of an index L_0 such that for each $L\geq L_0$, $y\in B(0,R)$ and $t\in[u_L,2u_L]$,

$$\mathbb{P}_y\big[\ell^L(t)\in B(0,R)\big]\geq\frac{C_0}{t}\geq\frac{C_0}{2u_L}.$$

Furthermore, since $U_L L^{-2}\to\infty$, we can use (b) of Lemma 5.4 to obtain the existence of $L_1\in\mathbb{N}$ and a constant $C_1>0$ depending only on $(U_L)_{L\geq1}$ such that for every $L\geq L_1$,

$$\sup_{t\geq U_L}\ \sup_{y\in\mathbb{T}(L)}\left|\mathbb{P}_y\big[\ell^L(t+u_L)\in B(0,R)\big]-\frac{\pi R^2}{L^2}\right|\leq\frac{C_1}{L^2}.$$

Using these two inequalities in (64), we have for L large enough and for all $x\in\mathbb{T}(L)$

$$\frac{C_1+\pi R^2}{L^2}\geq\mathbb{P}_x\big[T(R,\ell^L)\in[U'_L-u_L,U'_L]\big]\times\frac{C_0}{2u_L},$$

which gives us the desired result. □

B Proof of the technical points of Section 6

Proof of Lemma 6.5: Let us start with the case $\rho_L=\mathcal{O}(\psi_L^2)$ as $L\to\infty$. The rate of decay of the probability of a long excursion is known for simple random walks and Brownian motion (see Ridler-Rowe 1966), and so the proof of Proposition 6.2 suggests that we should consider the process $\hat{\ell}^L\equiv\psi_L^{-1}X^L(\rho_L\cdot)$. But $\hat{\ell}^L$ here is not a Lévy process, since X^L is the difference of the locations of two lineages whose motions are not independent in $B(0,2R^B\psi_L)$. However, it is not difficult to convince oneself that for each $y\in B(0,(7/4)R^B)^c$, the return time into $B(0,(3/2)R^B)$ of $\hat{\ell}^L$ starting at y is smaller than or equal to that of ℓ^L defined as the rescaled process $\psi_L^{-1}\xi^L(\rho_L\cdot)$ also starting at y. Indeed, the rate at which reproduction events affect at least one of the lineages is bounded from below by the rate at which a single lineage is affected, the distribution of the jumps of $\hat{\ell}^L$ and ℓ^L are identical outside $B(0,2R^B)$ and inside this ball, coalescence events make it easier for $\hat{\ell}^L$ to enter $B(0,(3/2)R^B)$. Hence, we shall establish the desired bound for ℓ^L. In addition, we shall consider that ℓ^L evolves on $\mathbb{R}^2$ instead of $\mathbb{T}(L)$, since the return time here can only increase with the available space.

For each $L \in \mathbb{N}$, set $\sigma_0^L = 0$ and let $(\sigma_i^L)_{i\in\mathbb{N}}$ be the sequence of jump times of ℓ^L. Let $\rho_L\theta_s$ (resp., θ_B) be the jump rate of ℓ^L due to small events (resp., due to large events). The quantities θ_s and θ_B do not depend on L since μ^B, μ^s and the probability measures $\nu_r^{B,s}$ do not. For each $t \geq 0$, we have $\ell^L(t) = \ell^L(0) + \sum_{i:\sigma_i^L \leq t} \{\ell^L(\sigma_i^L) - \ell^L(\sigma_{i-1}^L)\}$, where $\big(\ell^L(\sigma_i^L) - \ell^L(\sigma_{i-1}^L)\big)_{i\in\mathbb{N}}$ is a sequence of i.i.d. random variables with covariance matrix of the form $\upsilon_L \mathrm{Id}$. Using the distribution of a single small or large jump and the fact that a given jump is a small one with probability $\theta_s\rho_L/(\theta_s\rho_L + \theta_B)$, we easily check that there exists $V > 0$, independent of L, such that $\upsilon_L \sim V/\rho_L$ as $L \to \infty$ (recall our assumption $\rho_L = \mathcal{O}(\psi_L^2)$).

Let x in $B(0,4R^B) \setminus B(0,(7/4)R^B)$ and let W be a two-dimensional Brownian motion starting at x. For each $L \in \mathbb{N}$, by the Skorohod Embedding Theorem (see, e.g., Billingsley 1995) one can construct a sequence $(s_i^L)_{i\in\mathbb{N}}$ of stopping times such that the $W(s_i^L)$ have the same joint distributions as the $\ell^L(\sigma_i^L)$: for every $i \in \mathbb{N}$, conditionally on $W(s_{i-1}^L)$, s_i^L is the first time greater than s_{i-1}^L at which W leaves $B\big(W(s_{i-1}^L), r_i^L\big)$, where r_i^L is a random variable independent of W and of $\{s_j^L, j < i\}$ having the same distribution as the length of the first jump of ℓ^L. Now, we claim that there exists $\gamma > 0$ independent of L and x, such that each time W visits $B(0,R^B/2)$ and then leaves $B(0,(3/2)R^B)$, the probability that one of the s_i^L's falls into the corresponding period of time that W spends within $B(0,(3/2)R^B)$ is at least γ. Indeed, set $T_0(W) = \breve{T}_0(W) = 0$ and define the sequences of stopping times $\{T_k(W), k \geq 1\}$ and $\{\breve{T}_k(W), k \geq 1\}$ by induction in the following manner:

$$\begin{aligned} T_k(W) &= \inf\{t > \breve{T}_{k-1}(W) :\ W(t) \in B(0,R^B/2)\}, \\ \breve{T}_k(W) &= \inf\{t > T_k(W) :\ W(t) \notin B(0,(3/2)R^B)\}. \end{aligned}$$

(Note that each T_k is a.s. finite due to the recurrence of two-dimensional Brownian motion.) Then for each $k \in \mathbb{N}$, if j is the index of the last s_i^L before $T_k(W)$ and s_j^L corresponds to a small event, by construction we have $\left|W(s_j^L) - W(T_k(W))\right| < 2R^s\psi_L^{-1}$ and so $W(s_j^L) \in B(0,(3/2)R^B)$ for L large enough. If s_j^L is due to a large event and $W(s_j^L) \notin B(0,(3/2)R^B)$, then necessarily $W(s_j^L) \in B(0,(5/2)R^B)$. But the exit point from a ball B of Brownian motion started at the centre of this ball is uniformly distributed over the boundary of B, and so one can define γ as the minimum over (y,r) with $|y| \geq 3R^B/2$ and $|y| - R^B/2 < r \leq 2R^B$ of the probability that W started at y escapes $B(y,r)$, through the part of its boundary which lies within $B(0,(3/2)R^B)$. Hence, if we define for each $t \geq 0$ the random variable $N(t)$ as the maximal integer k such that $\breve{T}_k(W) \leq t$, we can write for each L

$$\mathbb{P}_{\psi_L x}\big[q_1^L > \rho_L u\big] = \mathbb{P}_x\big[\ell^L(\sigma_j^L) \notin B(0,(3/2)R^B),\ \forall\, j \leq i(u,L)\big] \leq \mathbb{E}_x\big[(1-\gamma)^{N(s_{i(u,L)}^L)}\big],$$

where $i(u,L) = \max\{j :\ \sigma_j^L \leq u\}$. Since N is a.s. a non-decreasing function of t, we have for any given $m \in \mathbb{R}_+$

$$\mathbb{P}_{\psi_L x}\big[q_1^L > \rho_L u\big] \leq \mathbb{E}_x\big[(1-\gamma)^{N(mu)}\big] + \mathbb{P}_x\big[s_{i(u,L)}^L < mu\big]. \tag{65}$$

Now, $i(u,L)$ is the number of points of the Poisson point processes Π_L^s and Π_L^B which fall into the time interval $[0,u\rho_L]$ on the original timescale, it is therefore a Poisson random variable with parameter $u(\theta_s\rho_L + \theta_B)$. If $a > 0$, then by the Markov inequality

$$\mathbb{P}_x\big[i(u,L) \leq au\theta_s\rho_L\big] \leq e^{au\theta_s\rho_L}\mathbb{E}\big[e^{-i(u,L)}\big] = \exp\{u\theta_s\rho_L(a + e^{-1} - 1) + u\theta_B(e^{-1} - 1)\},$$

so that this quantity converges exponentially fast to 0 for $a > 0$ small enough. On the event $\{i(u,L) > au\theta_s\rho_L\}$, $s_{i(u,L)}^L$ is the sum of at least $au\theta_s\rho_L$ i.i.d. random variables, each of which corresponds to the exit time of Brownian motion from a ball of radius at most $2R^s/\psi_L$ with probability $\theta_s\rho_L/(\theta_s\rho_L+\theta_B)$ and to the exit time of Brownian motion from a ball of radius at most $2R^B$ otherwise. Therefore, one can find $V'>0$ independent of L such that $\mathbb{E}[s_1^L]\sim V'\rho_L^{-1}$ as $L\to\infty$. Using the same technique as above then gives us that for $m>0$ small enough, there exists $\kappa(m)>0$ and $L(m)\in\mathbb{N}$ such that for all $L\geq L(m)$ and $u\geq 0$,

$$\mathbb{P}_x\big[i(u,L)>au\theta_s\rho_L,\ s_{i(u,L)}^L<mu\big]\leq e^{-\kappa(m)\rho_L u}.$$

Let us now prove that

$$\mathbb{P}_x[N(mu)\leq K\log\log u]\leq C\,\frac{\log\log u}{\log u}$$

for a constant $C>0$ independent of $x\in B(0,4R^B)\setminus B(0,(7/4)R^B)$ and u large enough (again independently of x). The reasoning is identical to that made to arrive at (36), with q_i^L (resp., Q_i^L) replaced by $T_i(W)$ (resp., $\breve{T}_i(W)$). Using the fact that $C_1\equiv\sup_{x\in B(0,R^B/2)}\mathbb{E}_x[\breve{T}_1(W)]<\infty$ and

$$\sup_{y\in B(0,4R^B)}\mathbb{P}_x\big[T_1(W)>u\big]\leq\frac{C_2}{\log u}\tag{66}$$

for a constant C_2 and u large enough (see Theorem 2 in Ridler-Rowe 1966), we can conclude that for each $x\in B(0,4R^B)\setminus B(0,(7/4)R^B)$, and u large enough,

$$\mathbb{P}_x\big[N(mu)\leq\log\log u\big]\leq\frac{2C_1(\log\log u)^2}{mu}+\frac{C_2\log\log u}{\log\big(mu/(2\log\log u)\big)}\leq\frac{C'\log\log u}{\log u},$$

again for $C'>0$ and u large enough independently of x. Coming back to (65), we obtain for a constant $C''>0$ and for all $x\in B(0,4R^B)\setminus B(0,(7/4)R^B)$,

$$\begin{aligned}\mathbb{P}_{\psi_L x}\big[q_1^L>\rho_L u\big]&\leq(1-\gamma)^{\log\log u}+\mathbb{P}_x\big[N(mu)\leq\log\log u\big]+e^{-C''u}\\&\leq(1-\gamma)^{\log\log u}+\frac{C'\log\log u}{\log u}+e^{-C''u}.\end{aligned}\tag{67}$$

Define $g(u)$ as the expression on the right-hand side of (67) to obtain the result.

When $\psi_L^2\rho_L^{-1}\to 0$, the probability that a large event occurs by time $u\psi_L^2$ is given by

$$1-\exp\Big\{-\theta_B u\frac{\psi_L^2}{\rho_L}\Big\}\to 0\qquad\text{as }L\to\infty.$$

On the event that no large events occur by time $u\psi_L^2$, the first visit of W into $B(0,R^B/2)$ will produce a time s_i^L such that $W(s_i^L)\in B(0,(3/2)R^B)$ with probability 1 for the reason expounded above, and so the first term on the right-hand side of (65) is now the probability that $T_1(W)$ is greater than mu. The inequality in (66) and the exponential decay of $\mathbb{P}_x[s_{i(u,L)}^L<mu]$ now imply the result. □

Proof of Lemma 6.6: The arguments are slightly different according to whether $\rho_L\psi_L^{-2}$ is bounded or tends to infinity as $L\to\infty$. Let us consider the first case. Recall the definition of $\rho_L^{-1}\theta_B$ given in the proof of Lemma 6.5 as the maximal rate at which a lineage is affected by a large event. The coalescence rate of two lineages is then bounded by $2\rho_L^{-1}\theta_B$, regardless of their locations. By our assumption (32), there exist $r\in(0,R^B)$ and $\delta>0$ such that $\mathrm{Leb}\big(\{r'\in[r,r+\delta]:\ \nu_{r'}^B\notin$

$\{\delta_0,\delta_1\}\}) > 0$. We shall use these events to send the two lineages at distance at least $(7/4)R^B\psi_L$ from each other, whatever their initial separation was. The proof is quite natural, so we just give the main arguments. If only large jumps occurred, then if a sequence of at least $7R^B/(2r)$ large events increased $|X^L|$ by at least $(r/2)\psi_L$ each before the first coalescence happened, X^L starting within $B(0,(3/2)R^B\psi_L)$ would certainly leave $B(0,(7/4)R^B\psi_L)$. Moreover, a large event affecting X^L and conditioned on not leading to a coalescence biases the jump towards increasing $|X^L|$ (we do not allow some centres that are too close to both lineages). This remark and (32) guarantee that the rate at which these separating events occur (that is, events increasing $|X^L|$ by at least $(r/2)\psi_L$) is bounded from below by $\rho_L^{-1}\theta_{\text{sep}}$, where θ_{sep} is a positive constant. The total rate at which large events affect X^L is bounded by $2\rho_L^{-1}\theta_B$, and so there is a positive probability p_{sep}, independent of the starting point of X^L, that X^L leaves $B(0,(7/4)R^B\psi_L)$ before coming back to 0 through a (large) coalescence event. As regards the effect of small events, recall that we assumed that $\rho_L\psi_L^{-2}$ is bounded. Hence, the probability that X^L starting from $B(0,r\psi_L/2)^c$ does not enter $B(0,2R^s)$ after a time of order $\mathcal{O}(\rho_L)$ only through small jumps is bounded from below and by the symmetry of these small jumps, with probability at least $1/2$ the radius of X^L increases between two large jumps. Hence, up to modifying p_{sep} to take into account the effect of the small jumps, the probability that X^L leaves $B(0,(7/4)R^B\psi_L)$ before coming back to 0 is still bounded from below by $p_{\text{sep}} > 0$.

By the definition of R^B and Assumption (10), large events of size close to R^B occur at a positive rate and lead to the coalescence of the lineages with positive probability, so that the waiting time for the coalescence of two lineages at distance at most $(7/4)R^B\psi_L$ is bounded by ρ_L times an exponential with positive parameter γ. This gives us that $\rho_L^{-1}Q_1^L$ is stochastically bounded by $\sum_{i=1}^k N_i$, where k is geometric with success probability $p_{\text{sep}} > 0$ and $\{N_i, i\in\mathbb{N}\}$ is a sequence of i.i.d. $\text{Exp}(\gamma)$ random variables, all of them independent of the initial value $x\in B(0,(3/2)R^B\psi_L)$ of X^L. We can therefore choose $C_Q = (\gamma p_{\text{sep}})^{-1}$.

When $\rho_L^{-1}\psi_L^2 \to 0$, if we use the same reasoning as above there is a positive probability that a large event separates the two lineages at distance at least $r\psi_L$, regardless of their separation just before this event. In addition, the rate of these separating events is at least equal to $\rho_L^{-1}\theta_{\text{sep}} > 0$. Between two large events, X^L only does small jumps, and as long as $X^L \notin B(0,2R^s)$, the Skorohod Embedding Theorem (see the proof of Lemma 6.5) enables us to assert that X^L will leave $B(0,(7/4)R^B\psi_L)$ in a time of order $\mathcal{O}(\psi_L^2)$. Moreover, for $\varepsilon > 0$ small, the same argument shows that the probability that X^L leaves $B(0,(7/4)R^B\psi_L)$ before entering $B(0,\varepsilon\psi_L)$ is bounded from below by a constant $p_{\text{esc}} > 0$ independent of L and of the value $y\in B(0,r\psi_L)^c$ of X^L just after the large jump described above. A fortiori, p_{esc} is also a lower bound for the probability that X^L started at y leaves $B(0,(7/4)R^B\psi_L)$ before entering $B(0,2R^s)$ only through small jumps, and so we obtain that between two large events such that the first large jump sends (or keeps) X^L out of $B(0,r\psi_L)$, X^L escapes $B(0,(7/4)R^B\psi_L)$ with probability at least p_{esc} (recall that the total rate of large events affecting at least one of the lineages is bounded by $2\theta_B\rho_L^{-1}$ and $\rho_L \gg \psi_L^2$). Consequently, Q_1^L is this time stochastically bounded by $\sum_{i=1}^k N_i(L)$, where k is a geometric random variable with success probability $p_{\text{esc}} > 0$ and for each $L\in\mathbb{N}$, $\{N_i(L), i\in\mathbb{N}\}$ is a sequence of i.i.d. $\text{Exp}(\rho_L^{-1}\theta_{\text{sep}})$ random variables, all of them independent of the initial value $x\in B(0,(3/2)R^B\psi_L)$ of X^L. The desired result follows, with $C_Q = (\theta_{\text{sep}}p_{\text{esc}})^{-1}$. □

Proof of Lemma 6.7: The inequality in (33) can be restated as in (34) (the quantity inside the brackets then tends to 1), so we prove both inequalities using this form. Let θ_c be such that $\rho_L^{-1}\theta_c$ is the minimum rate at which two lineages at distance at most $(1+\delta)R^B\psi_L$ from each other coalesce (where $\delta > 0$ is defined at the beginning of the proof of Lemma 6.6). By the definition of R^B

and assumption (10), the rate at which a reproduction event of radius $r \in \left[R^B(1-\frac{\delta}{4})\psi_L, R^B\psi_L\right]$ occurs and leads to the coalescence of the lineages does not vanish as L tends to infinity (when multiplied by ρ_L), and so $\theta_c > 0$. Let us show that if $\eta > 0$ is small enough, the probability that X^L starting within $B(0, R^B\psi_L)$ does not leave $B(0,(1+\delta)R^B\psi_L)$ through only small jumps by time $\eta\psi_L^2$ is bounded from below by a positive constant, independent of L large. The term inside the brackets in (34) will then come from the probability that a large event occurs before time $\eta\psi_L^2$ and the first such event leads to the coalescence of the lineages (i.e., a jump onto 0 for X^L).

Let $\eta > 0$ and $x \in B(0, R^B\psi_L)$, and let τ_B^L denote the epoch of the first large event affecting X^L. By the argument given above, the probability that X^L starting at x hits 0 before leaving $B(0,(1+\delta)R^B\psi_L)$ is bounded from below by the probability that X^L started at x stays within this ball until τ_B^L, τ_B^L is less than or equal to $\eta\psi_L^2$ and the first large event leads to the coalescence of the lineages. Writing $\mathscr{E}_{L,\eta}$ for the event that X^L stays within $B(0,(1+\delta)R^B\psi_L)$ before τ_B^L and $\tau_B^L \le \eta\psi_L^2$, this probability is equal to

$$\mathbb{P}_x\left[\text{the first large event is a coalescence} \mid \mathscr{E}_{L,\eta}\right]\mathbb{P}_x\left[\mathscr{E}_{L,\eta}\right]. \tag{68}$$

If, for each $L \in \mathbb{N}$, $\rho_L^{-1}E < \infty$ denotes the rate at which a single lineage on $\mathbb{T}(L)$ is affected by a large reproduction event, then the rate at which at least one of two lineages are affected is bounded by twice this quantity, and so the first probability in (68) is bounded from below by $\theta_c/(2E)$. Now, X^L experiences no large reproduction event before time τ_B^L, and so we can again use the equality in distribution stated in the proof of Proposition 6.4 (b) (we also keep the notation introduced there). Write t_{exit} for the first time X^L leaves $B(0,(1+\delta)R^B\psi_L)$, and $\tilde{t}_{\text{exit}}$ for the corresponding time for $\tilde{X}^L$ (which sees only small events). We have

$$\begin{aligned}\mathbb{P}_x\left[\mathscr{E}_{L,\eta}\right] &= \mathbb{P}_x\left[t_{\text{exit}} \ge \tau_B^L;\ \tau_B^L \le \eta\psi_L^2\right]\\ &= \mathbb{P}_x\left[\tilde{t}_{\text{exit}} \ge e(\tilde{X}^L);\ e(\tilde{X}^L) \le \eta\psi_L^2\right]\\ &\ge \mathbb{P}_x\left[\tilde{t}_{\text{exit}} \ge \eta\psi_L^2;\ e(\tilde{X}^L) \le \eta\psi_L^2\right]\\ &= \mathbb{P}_x\left[e(\tilde{X}^L) \le \eta\psi_L^2 \;\middle|\; \tilde{t}_{\text{exit}} \ge \eta\psi_L^2\right]\mathbb{P}_x\left[\tilde{t}_{\text{exit}} \ge \eta\psi_L^2\right].\end{aligned} \tag{69}$$

Since a pair of lineages is affected by a large event at rate at least $\rho_L^{-1}E$, the first probability on the right-hand side of (69) is bounded below for all $x \in B(0, R^B\psi_L)$ by

$$1 - \exp\left\{-\eta E\frac{\psi_L^2}{\rho_L}\right\}.$$

Now, if $\tilde{X}^L$ starts within $B(0, R^B\psi_L)$, it needs to cover a distance of at least $\delta R^B\psi_L$ to exit $B(0,(1+\delta)R^B\psi_L)$. Furthermore, coalescence events tend to keep $\tilde{X}^L$ within $B(0,(1+\delta)R^B\psi_L)$, and so for each x, the second probability on the right-hand side of (69) is larger than $\mathbb{P}_0[\hat{t}_{\text{exit}} \ge \eta\psi_L^2]$, where $\hat{t}_{\text{exit}}$ is the exit time from $B(0,\delta R^B\psi_L)$ of the process $\{\hat{\xi}^L(2t), t \ge 0\}$ which experiences only small jumps. Decomposing this Lévy process into the sum of its jumps and applying Doob's maximal inequality to the submartingale $|\hat{\xi}^L|^2$, we obtain

$$\mathbb{P}_0\left[\sup_{0\le t\le \eta\psi_L^2/2}|\hat{\xi}^L(2t)|^2 > (\delta R^B\psi_L)^2\right] \le \frac{1}{(\delta R^B\psi_L)^2}\,\mathbb{E}_0\left[|\hat{\xi}^L(\eta\psi_L^2)|^2\right] = \frac{2\eta\sigma_s^2}{\delta^2(R^B)^2},$$

where the last equality comes from (22). Choosing $\eta > 0$ small enough so that the quantity above is less than 1, we obtain that for all $x \in B(0, R^B\psi_L)$

$$\mathbb{P}_x\left[\tilde{t}_{\text{exit}} \ge \eta\psi_L^2\right] \ge \mathbb{P}_0\left[\hat{t}_{\text{exit}} \ge \eta\psi_L^2\right] \ge 1 - \frac{2\eta\sigma_s^2}{\delta^2(R^B)^2} \equiv \theta_4 > 0.$$

Combining the above and choosing $\theta_2 = \theta_4\theta_c/(2E)$ and $\theta_3 = \eta E$, we obtain (34). $\square$

Proof of Lemma 6.9: If we were considering the times τ_{ij} rather than τ^*_{ij}, Lemma 6.9 would follow from the same arguments as in Cox & Griffeath (1986) (see Lemma 1). Here, we have to work a bit harder and decompose the event in (44) into more cases. Recall the definition of ϖ_L given in the statement of Theorem 3.3. For each $L \in \mathbb{N}$, the probability in (44) is bounded by

$$\mathbb{P}_{A_L}\Big[\tau < \frac{\varpi_L}{\sqrt{\log L}}\Big] + \mathbb{P}_{A_L}\Big[\tau \geq \frac{\varpi_L}{\sqrt{\log L}}\ ;\ \tau^* = \tau^*_{12}\ ;\ \tau \neq \tau_{12}\Big] \tag{70}$$

$$+\,\mathbb{P}_{A_L}\Big[\tau^* = \tau^*_{12}\ ;\ \frac{\varpi_L}{\sqrt{\log L}} \leq \tau = \tau_{12} < \tau^*_{12} - \frac{\varpi_L}{(\log L)^2}\Big] \tag{71}$$

$$+\,\mathbb{P}_{A_L}\Big[\tau^* = \tau^*_{12}; \frac{\varpi_L}{\sqrt{\log L}} \leq \tau = \tau_{12}; \tau_{12} \geq \tau^*_{12} - \frac{\varpi_L}{(\log L)^2}; \exists i \in \{1,2\}, \tau_{i3} \in (\tau_{12}, \tau^*_{12}]\Big] \tag{72}$$

$$+\,\mathbb{P}_{A_L}\Big[\tau^* = \tau^*_{12}; \frac{\varpi_L}{\sqrt{\log L}} \leq \tau = \tau_{12}; \forall i \in \{1,2\}, \tau_{i3} > \tau^*_{12}; |\xi^L_1(\tau^*) - \xi^L_3(\tau^*)| \leq \frac{L}{\log L}\Big]. \tag{73}$$

Suppose first that $\rho_L \ll \psi_L^2 \log L$. The first term in (70) is bounded by the sum over $i \neq j \in \{1,\ldots,4\}^2$ of $\mathbb{P}_{A_L}[\tau_{ij} < \varpi_L(\log L)^{-1/2}]$, which tends to 0 uniformly in A_L by Proposition 6.2 and the consistency of the genealogy. The quantity in (71), expressing the probability that the first pair to meet is the pair $(1,2)$ but then coalescence of these lineages takes longer than $\varpi_L/(\log L)^2$ units of time, is therefore bounded by

$$\mathbb{P}_{A_L}\Big[\tau^*_{12} - \tau_{12} > \frac{\varpi_L}{(\log L)^2}\Big],$$

which converges to zero as $L \to \infty$, uniformly in A_L (apply the strong Markov property at time τ_{12} and use (a) of Proposition 6.4). The expression in (72) corresponds to the event in which $(1,2)$ is the first pair to meet and "quickly" merge, but another pair of lineages manages to meet between τ_{12} and τ^*_{12}. It is thus bounded by

$$\mathbb{P}_{A_L}\Big[\frac{\varpi_L}{\sqrt{\log L}} \leq \tau = \tau_{12}\ ;\ \tau_{13} \in \Big(\tau_{12}, \tau_{12} + \frac{\varpi_L}{(\log L)^2}\Big]\Big]$$
$$+\mathbb{P}_{A_L}\Big[\frac{\varpi_L}{\sqrt{\log L}} \leq \tau = \tau_{12}\ ;\ \tau_{23} \in \Big(\tau_{12}, \tau_{12} + \frac{\varpi_L}{(\log L)^2}\Big]\Big].$$

Applying the strong Markov property at time τ_{12} and using Lemma 5.5 with $(\ell^L(t))_{t\geq 0} \equiv (\psi_L^{-1}\{\xi^L_i - \xi^L_3\}((\psi_L^2 \wedge \rho_L)t))_{t\geq 0}$ for each $i \in \{1,2\}$ (as in the proof of Theorem 6.3), we can conclude that each of the above terms tends to 0 uniformly in A_L. On the event described by (73), that is $(1,2)$ is the first pair to meet and merge, no other pair meets in between but the distance between lineages 1 and 3 at time τ^* is smaller than $L/\log L$, the differences $\{\xi^L_1 - \xi^L_2\}$ and $\{\xi^L_1 - \xi^L_3\}$ have the same distribution as two independent copies $\hat{\xi}^L$ and $\check{\xi}^L$ of the process ξ^L run at speed 2 up until τ, and so if we write $\hat{T}_L$ (resp., $\check{T}_L$) for the entrance time of $\hat{\xi}^L$ (resp., $\check{\xi}^L$) into $B(0, 2R^B\psi_L)$, with a slight abuse of notation for the initial value to simplify the notation, (73) is bounded by

$$\mathbb{P}_{A_L}\Big[\check{T}_L > \hat{T}_L \geq \frac{\varpi_L}{\sqrt{\log L}}; \big|\check{\xi}^L(\hat{T}_L)\big| \leq \frac{L}{\log L}\Big] \leq \mathbb{P}_{A_L}\Big[\hat{T}_L \geq \frac{\varpi_L}{\sqrt{\log L}}; \big|\check{\xi}^L(\hat{T}_L)\big| \leq \frac{L}{\log L}\Big].$$

A straightforward application of Lemma 5.4 (b) with $(\ell^L(t))_{t\geq 0} \equiv (\psi_L^{-1}\check{\xi}^L((\rho_L \wedge \psi_L^2)t))_{t\geq 0}$ yields the uniform convergence of the last term to 0. Finally, the second term in (70), i.e., the probability that $(1,2)$ is the first pair to meet but not to merge, is bounded by the sum over all pairs $\{i,j\} \in \{1,\ldots,4\}^2$ such that $i \neq j$ and $\{i,j\} \neq \{1,2\}$ of

$$\mathbb{P}_{A_L}\Big[\tau \geq \frac{\varpi_L}{\sqrt{\log L}}; \tau^* = \tau^*_{12}; \tau = \tau_{ij}\Big] \leq \mathbb{P}_{A_L}\Big[\frac{\varpi_L}{\sqrt{\log L}} \leq \tau = \tau_{ij} < \tau^*_{12} - \frac{\varpi_L}{(\log L)^2}; \tau^*_{ij} > \tau^*_{12}\Big]$$
$$+\mathbb{P}_{A_L}\Big[\tau^* = \tau^*_{12} \geq \frac{\varpi_L}{\sqrt{\log L}}; \tau_{ij} \in \Big[\tau^*_{12} - \frac{\varpi_L}{(\log L)^2}, \tau^*_{12}\Big]\Big].$$

We can now conclude as we did for (71) and (72).

When $\rho_L \gg \psi_L^2 \log L$, we saw in the proof of Theorem 6.3 that with probability increasing to 1, a pair of lineages will not be affected by a large event during the periods of time when the lineages are at distance less than $2R^B\psi_L$ from each other, until they come at distance less than $2R^s$. Consequently, we could consider the evolution of the lineages to be independent until their gathering time at distance $2R^s$. Because we are still considering a finite number of lineages, the arguments we used are applicable here again, and the proof of the last paragraph also yields (44) in this case. The proof of (45) is analogous, and is therefore omitted. □

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References

Barton, N. H., Depaulis, F., and Etheridge, A. M. (2002). Neutral evolution in spatially continuous populations. *Theor. Pop. Biol.*, 61:31–48.

Barton, N. H., Kelleher, J., and Etheridge, A. M. (2009). A new model for large-scale population dynamics: quantifying phylogeography. *Preprint*.

Berestycki, N., Etheridge, A. M., and Hutzenthaler, M. (2009). Survival, extinction and ergodicity in a spatially continuous population model. *Markov Process. Related Fields*, 15:265–288. MR2554364

Bertoin, J. (1996). *Lévy Processes*. Cambridge University Press. MR1406564

Bertoin, J. and Le Gall, J.-F. (2003). Stochastic flows associated to coalescent processes. *Probab. Theory Related Fields*, 126:261–288. MR1990057

Bhattacharya, R. N. (1977). Refinements of the multidimensional central limit theorem and applications. *Ann. Probab.*, 5:1–27. MR0436273

Billingsley, P. (1995). *Probability and Measure*. Wiley. MR1324786

Birkner, M., Blath, J., Capaldo, M., Etheridge, A. M., Möhle, M., Schweinsberg, J., and Wakolbinger, A. (2005). Alpha-stable branching and Beta-coalescents. *Electron. J. Probab.*, 10:303–325. MR2120246

Cox, J. T. (1989). Coalescing random walks and voter model consensus times on the torus in $\mathbb{Z}^d$. *Ann. Probab.*, 17:1333–1366. MR1048930

Cox, J. T. and Durrett, R. (2002). The stepping stone model: new formulas expose old myths. *Ann. Appl. Probab.*, 12:1348–1377. MR1936596

Cox, J. T. and Griffeath, D. (1986). Diffusive clustering in the two-dimensional voter model. *Ann. Probab.*, 14:347–370. MR0832014

Cox, J. T. and Griffeath, D. (1990). Mean field asymptotics for the planar stepping stone model. *Proc. London Math. Soc.*, 61:189–208. MR1051103

Donnelly, P. J. and Kurtz, T. G. (1999). Particle representations for measure-valued population models. *Ann. Probab.*, 27:166–205. MR1681126

Eller, E., Hawks, J., and Relethford, J. H. (2004). Local extinction and recolonization, species effective population size, and modern human origins. *Human Biology*, 76(5):689–709.

Etheridge, A. M. (2008). Drift, draft and structure: some mathematical models of evolution. *Banach Center Publ.*, 80:121–144. MR2433141

Ethier, S. N. and Kurtz, T. G. (1986). *Markov processes: characterization and convergence*. Wiley. MR0838085

Evans, S. N. (1997). Coalescing Markov labelled partitions and a continuous sites genetics model with infinitely many types. *Ann. Inst. H. Poincaré Probab. Statist.*, 33:339–358. MR1457055

Felsenstein, J. (1975). A pain in the torus: some difficulties with the model of isolation by distance. *Amer. Nat.*, 109:359–368.

Kimura, M. (1953). Stepping stone model of population. *Ann. Rep. Nat. Inst. Genetics Japan*, 3:62–63.

Kingman, J. F. C. (1982). The coalescent. *Stochastic Process. Appl.*, 13:235–248. MR0671034

Limic, V. and Sturm, A. (2006). The spatial Lambda-coalescent. *Electron. J. Probab.*, 11(15):363–393. MR2223040

Malécot, G. (1948). *Les Mathématiques de l'hérédité*. Masson et Cie, Paris. MR0027490

Möhle, M. and Sagitov, S. (2001). A classification of coalescent processes for haploid exchangeable population models. *Ann. Probab.*, 29:1547–1562. MR1880231

Pitman, J. (1999). Coalescents with multiple collisions. *Ann. Probab.*, 27:1870–1902. MR1742892

Ridler-Rowe, C. J. (1966). On first hitting times of some recurrent two-dimensional random walks. *Z. Wahrsch. verw. Geb.*, 5:187–201. MR0199901

Rogers, L.C.G. and Williams, D. (1987). *Diffusions, Markov processes, and martingales: Itô calculus*. Wiley. MR0921238

Sagitov, S. (1999). The general coalescent with asynchronous mergers of ancestral lines. *J. Appl. Probab.*, 26:1116–1125. MR1742154

Sawyer, S. and Fleischmann, J. (1979). The maximal geographical range of a mutant allele considered as a subtype of a Brownian branching random field. *Proc. Natl. Acad. Sci. USA*, 76(2):872–875.

Schweinsberg, J. (2000). Coalescents with simultaneous multiple collisions. *Electron. J. Probab.*, 5:1–50. MR1781024

Wilkins, J. F. (2004). A separation of timescales approach to the coalescent in a continuous population. *Genetics*, 168:2227–2244.

Wilkins, J. F. and Wakeley, J. (2002). The coalescent in a continuous, finite, linear population. *Genetics*, 161:873–888.

Wright, S. (1931). Evolution in Mendelian populations. *Genetics*, 16:97–159.

Wright, S. (1943). Isolation by distance. *Genetics*, 28:114–138.

Zähle, I., Cox, J. T., and Durrett, R. (2005). The stepping stone model II: genealogies and the infinite sites model. *Ann. Appl. Probab.*, 15:671–699. MR2114986