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Random Trees

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Abstract. The meeting was devoted to *random trees*, a central concept in mathematics that provides a key way of thinking about *relationships* between objects such as particles in a fluid, individuals in a population, or labels in a search algorithm. Particular emphasis was put on the role of random trees in *physics, biology*, and *computer science*.

Mathematics Subject Classification (2000): 05C05, 05C80, 60-xx, 92D15, 82Bxx, 68Wxx.

Introduction by the Organisers

Random trees are a central concept in mathematics, with important applications in a variety of different disciplines. They provide a key way of thinking about *relationships* between objects of various kinds. Typically, these objects are organised randomly in *space* and *time*, such as particles in a fluid, individuals in a population, or labels in a search algorithm. Random trees both qualify and quantify important *phenomena* in these systems, such as phase transitions, genetic extinction, or the breaking of codes. They are capable of revealing important links between these phenomena, often from surprising angles, and as such play a *unifying* role.

The workshop focussed on the role of random trees in *physics*, *biology* and *computer science*. The goal of the workshop was two-fold: (1) to reinforce the link between the *discrete* and the *continuum* parts of the random tree community, through an exposition of common ideas, tools and techniques; (2) to address *emerging connections* between applications of random trees in the three disciplines, centering around a number of core topics. In this way, participants were able to learn about their different approaches and their recent progress.

During the workshop, two types of lectures were given: (a) longer lectures (1.5 hour) in the morning, highlighting specific research areas; (b) shorter lectures (1 hour) in the afternoon, enlarging these areas into a broader spectrum. The following themes were covered:

- *History of branching processes*: Jagers.
- *Geometry of random trees*: Evans, Le Gall.
- *Properties of random trees*: Bertoin, Pfaffelhuber.
- *Random processes on random trees*: Külske, Popovic, Swart.
- *Dynamics of random trees*: Winter.
- *Spin glasses and ultrametricity*: Bovier, de Sanctis.
- *Self-avoiding walk and renormalisation*: Slade.
- *Construction of genealogical processes*: Kurtz.
- *Ancestral selection and statistical inference*: Tavaré, Wakeley.
- *Lambda-coalescents*: Birkner, Blath, Sturm.
- *Random search algorithms*: Chauvin, Devroye, Grübel.

Workshop: Random Trees

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Abstracts

The continuous limit of large random planar maps

Jean-François Le Gall

In the present report, we discuss recent progress towards the study of scaling limits of large random planar maps. This leads to a continuous random metric space called the Brownian map, which can be defined as a quotient space of Aldous' Continuum Random Tree.

Let us recall some basic definitions. A planar map is a proper embedding of a finite connected graph in the two-dimensional sphere $\mathbf{S}^2$. Loops and multiple edges are a priori allowed. The faces of the map are the connected components of the complement of the union of edges. A planar map is rooted if it has a distinguished oriented edge called the root edge. Two rooted planar maps are said to be equivalent if the second one is the image of the first one under an orientation-preserving homeomorphism of the sphere, which also preserves the root edges. Two equivalent rooted planar maps are always identified.

Given an integer $p \geq 3$, a p-angulation is a planar map where each face has degree p, that is p adjacent edges. One should count edge sides, so that if an edge lies entirely inside a face it is counted twice. We denote by $\mathcal{M}_n^p$ the set of all rooted p-angulations with n faces. Thanks to the preceding identification, the set $\mathcal{M}_n^p$ is finite. A 3-angulation is called a triangulation, and a 4-angulation is called a quadrangulation.

Consider a planar map M. Let $V(M)$ denote the vertex set of M. A path in M with length k is a finite sequence $a_0, a_1, \ldots, a_k$ in $V(M)$ such that a_i and a_{i-1} are connected by an edge of the map, for every $i \in \{1, \ldots, k\}$. The graph distance $d_{gr}(a, a')$ between two vertices a and a' is the minimal k such that there exists a path $\gamma = (a_0, a_1, \ldots, a_k)$ with $a_0 = a$ and $a_k = a'$. The set $V(M)$ equipped with the metric d_{gr} is a (finite) metric space.

In order to state our main result, we denote by $\mathcal{T}_{\mathbf{e}}$ the random rooted real tree known as the CRT (Continuum Random Tree). The notation $\mathcal{T}_{\mathbf{e}}$ comes from the fact that the CRT can be defined as the random tree coded by a normalized Brownian excursion $\mathbf{e}$. This coding also makes it possible to define a lexicographical order on the vertices of the CRT: For every $a, b \in \mathcal{T}_{\mathbf{e}}$, one can consider the lexicographical intervals $[a, b]$ and $[b, a]$. Roughly speaking, $[a, b]$ is the set of all vertices of the CRT that are visited when going from a to b in clockwise order around the tree.

We also need to introduce Brownian labels on the CRT. Conditionally given $\mathcal{T}_{\mathbf{e}}$, we consider the centered Gaussian process $(Z_a)_{a \in \mathcal{T}_{\mathbf{e}}}$ with covariance $\mathrm{cov}(Z_a, Z_b) = |a \wedge b|$, where $|a \wedge b|$ stands for the distance between the root of the CRT and the vertex $a \wedge b$ which is the most recent common ancestor of a and b in the tree. The process Z should be understood as Brownian motion indexed by the tree $\mathcal{T}_{\mathbf{e}}$: Z_a is a "label" assigned to vertex a, and this label evolves as linear Brownian motion

when varying a along a line segment of the tree. Finally, we define a random equivalence relation $\approx$ on the CRT by setting

$$a \approx b \qquad \text{iff} \quad Z_a = Z_b = \min\Big(\min_{c\in[a,b]} Z_c, \min_{c\in[b,a]} Z_c \Big).$$

Theorem 1. *[1] Let $p \geq 2$ be a fixed integer. For every integer $n \geq 2$, let M_n be a random planar map, which is uniformly distributed over $\mathcal{M}_n^{2p}$. From every increasing sequence of positive integers, one can extract a subsequence along which the following holds: The random metric spaces $(V(M_n), n^{-1/4} d_{gr})$ converge in distribution to $(\mathcal{T}_{\mathbf{e}}/\approx, D)$, in the sense of the Gromov-Hausdorff distance. Here D is a distance on $\mathcal{T}_{\mathbf{e}}/\approx$, which induces the quotient topology.*

The limiting random metric space $(\mathcal{T}_{\mathbf{e}}/\approx, D)$ is called the Brownian map. To be more precise, we should say that we use the name Brownian map for any of the limiting random metric spaces that can arise in the theorem, when we vary p and the subsequence. The need for a subsequence in the theorem comes from the fact that the limiting random metric D has not been fully characterized, and so there might be different metrics D corresponding to different subsequences. Still one believes that it should not be necessary to take a subsequence, and that the limiting metric space should be the same independently of p (and the same limit should hold for triangulations, etc.). This would imply that the Brownian map is in some sense the universal scaling limit of random planar maps.

We finally state two theorems that give properties of the Brownian map.

Theorem 2. *[1] The Hausdorff dimension of the Brownian map is almost surely equal to 4.*

Theorem 3. *[3] The Brownian map is almost surely homeomorphic to the 2-sphere $\mathbf{S}^2$.*

More information about the Brownian map can be found in the preprint [2], which provides a detailed analysis of geodesics in this random metric space.

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Probability fringe convergence and the eigenvalues of large random trees

Stevan N. Evans
(joint work with Shankar Bhamidi, Erick Matsen, Arnab Sen)

The eigenvalues of the *adjacency matrix* of a graph are of interest because of their intimate connection with many of the graph's "graph-theoretic" properties. The talk described recent research on the eigenvalues of quite general models of (large) random rooted trees, including various of the *preferential attachment schemes* that have recently attracted interest in computer science as models of real-world networks, as well as *random recursive trees*, *Yule trees*, and *uniform random trees*.

Many such ensembles possess the following property of *probability fringe convergence*. Suppose that $\mathcal{T}_n$ is the member of the ensemble with n vertices. Given a vertex v that is at distance h from the root ρ, let $(v = v_0, v_1, \ldots, v_h = \rho)$ denote the path from v to ρ. Write $\mathcal{T}_n^0$ for the subtree rooted at $v_0 = v$ that consists of all vertices for which the path to the root passes through v_0, and for $1 \leq k \leq h$, write $\mathcal{T}_n^k$ for the subtree rooted at v_k that consists of all vertices for which the path from the root passes through v_k but not through v_{k-1}. For $k > h$, define $\mathcal{T}_n^k$ to be $*$, where $*$ is some element adjoined to the space $\mathbb{T}$ of finite rooted trees. The empirical distribution of the sequences $(\mathcal{T}_n^0)_{k=0}^{\infty}$ as v ranges over $\mathcal{T}_n$ is a random probability measure on $(\mathbb{T} \sqcup \{*\})^{\infty}$. We say that $(\mathcal{T}_n)_{n=1}^{\infty}$ converges in the probability fringe sense if this sequence of random probability measures converges in distribution to a deterministic probability measure on $(\mathbb{T} \sqcup \{*\})^{\infty}$ that is concentrated on $\mathbb{T}^{\infty}$. The usual tool for proving probability fringe convergence is to embed the random trees of interest into a suitable continuous time-branching process.

We used fairly simple ideas from linear algebra (primarily the *interlacing inequalities*) to show that if $(\mathcal{T}_n)_{n=1}^{\infty}$ converges in the probability fringe sense, then the empirical distributions of the eigenvalues of the corresponding adjacency matrices converge in distribution to a deterministic limit (in the topology of weak convergence of probability measures). Moreover, the masses assigned by the empirical distributions to individual points also converge in distribution to constants. We conclude for ensembles such as the linear preferential attachment models and the random recursive trees that the limiting spectral distribution has a set of atoms that is dense in the real line. However, we are unable to tell whether the limiting spectral distributions are purely atomic. One technically interesting feature of this work is that the most commonly used tool in random matrix theory, the method of moments, cannot be applied to some natural ensembles, because the expected values of higher moments of the empirical spectral measure diverge.

We were able to get precise asymptotics on the mass assigned to zero by the empirical spectral measures due to the connection between the number of zero eigenvalues of the adjacency matrix of a tree and the cardinality of a *maximal matching* on the tree. In particular, we used a simplified version of an algorithm

due to Karp and Sipser to construct maximal matchings and understand their properties.

We also established the joint convergence in distribution of the suitably normalized k largest eigenvalues of the linear preferential attachment ensemble for any k using a previously known connection between the largest eigenvalues of this model and the largest out-degrees.

Random trees in computer science

Luc Devroye

The purpose of this talk was to survey the study of random trees from the perspective of computer science. There were three interwoven parts in the presentation: the introduction of various random tree models, the motivation for studying certain tree parameters, and the latest probability theoretical results for those models and parameters.

The models. By far the most important tree in computer science is the binary search tree. When constructed on the basis of a uniform random permutation, its shape is distributed like that of a random Yule tree, and also as that of the Kingman coalescent. It is also the tree underlying the popular quicksort method of sorting n elements.

There are various other tree models that matter, but many are simple extensions of random binary search trees. A conveniently wide class of trees are the so-called split trees on n nodes, in which the root node has subtrees of random sizes $N_1, \ldots, N_k$, where $(N_1/n, \ldots, N_k/n)$ is suitably close in some probabilistic sense to a random vector $V = (V_1, \ldots, V_k)$. All splits at lower level nodes are performed independently according to the same law. Special cases of such trees include random quadtrees, random m-ary search trees, random median-of-$(2k-3)$ trees, Dirichlet trees (in which V is Dirichlet), random tries, and random simplex trees.

Recent developments on random networks and web models have propelled other models to the front. Tree models are defined incrementally, with the n-th node making a link to one of the nodes of lower index, selected in some random manner. A simplistic model is given by the uniform random recursive tree: the node with label n selects a link to a uniformly chosen node in $\{1, \ldots, n-1\}$. Barabasi and Albert, and Biggins and Gray, and others introduced the preferential attachment models (or plane-oriented recursive trees): here node n selects a node of lower index with probability proportional to one plus the degree (number of neighbors) of that node. Popular nodes thus attract more links. Both models have been generalized in numerous ways.

The parameters. Search trees are used for searching, and costs are measured with respect to distances from the root. The depth of a node is its path distance from the root, and the height of a tree is the maximal depth of any of its nodes. Both should be small, i.e., the mean and the tails of these random variables matter.

For sorting, the number of comparisons between elements is the usual yardstick. This corresponds to the sum of all depths of nodes in a tree, or, by duality, to the sum of all proper subtree sizes over all nodes in a tree. In general, recursive algorithms give rise to complexities (costs) that are sums of functions of subtree sizes, totaled over all nodes. Such parameters are called toll functions, a term coined by Philippe Flajolet.

The distribution or histogram of the depths, also called the profile, is of some interest as it measures the volatility in the complexities of search times.

The results. For the models described above, a number of different probability theoretical tools are useful. By taking logarithms, one can regard the partition process of split trees as a branching random walk with unit steps in the walk corresponding to $\log V_i$ for the split variables. The height of the tree is more than k if and only if the maximal displacement of the branching random walk (which is started from the value $\log n$) after k steps is more than zero. But maximal displacements of branching random walks are now well understood. Two papers in 2008 by Hu and Shi, and by Addario-Berry and Reed, basically describe the precise asymptotics of the height of random split trees as a function of n: it is in probability proportional to $a \log n - b \log\log n + O(1)$ for some positive constants a and b that depend upon the distribution of V. These results use certain assumptions and idealizations that may not hold for some trees used by computer scientists, but they provide sharp insights into them. It should be noted that first-term asymptotics can easily be obtained following large deviation proofs from the 1970s by Biggins for maximal displacements in Bienaymé trees.

We showed in the talk how many other models, such as the two web models cited above can be reduced to weighted split trees, i.e., trees in which the edges have random weights. The maximal weighted height of these trees is then equal to the weight of the original trees. In this manner, Broutin (2008) studied the weighted height for split trees combining Biggins' ideas and two-dimensional large deviation theory. It is quite generally asymptotic to $a \log n$ in probability for $a > 0$ depending upon the joint distribution of the split vector V and the vector of weights.

The depth of a randomly selected node is studied by following a random path from the root that in weighted by subtree sizes, until it reaches a leaf. Standard renewal theory yields a central limit theorem for the length L_n of this path, which states that $(L_n - \mu \log n)/\sigma\sqrt{\log n}$ tends in law to the standard normal. Here μ and σ are parameters that depend upon the entropy of first and second order, respectively, of the split vector V.

The profile of split trees at a level $\theta \log n$ with $\theta \neq \mu$ has mean $n^{f(\theta)+o(1)}$ for some function f, which, after normalization by the mean, tends to a limit distribution, which is described by a stochastic fixed-point equation. The contraction method used in the proof of these results was pioneered by Rösler in 1989, and has since then seen quite a few striking applications in the study of tree parameters. Additional relevant work is due to Neininger, Rüschendorf, Hwang, Drmota, Chauvin, Janson, Fill, and many others. Perhaps the main open problem solved

by this method is that of the limit law for the properly scaled complexity of quicksort and of toll functions of random trees. Toll functions that are $O(\sqrt{n})$ lead to normal limit laws and can be obtained by Stein's method, as shown by Hwang, Neininger and the speaker. If the toll functions increase faster than linearly with n, then the stochastic fixed-point equation result can be obtained quite trivially without resorting to contraction methods. However, the rates of increase that are squeezed in-between, such as the linear toll function of quicksort, are more difficult—their limit laws require a careful application of the contraction method. A general theorem valid for all split trees and most toll functions was obtained by Neininger.

Limit distributions for m-ary search trees when $m \geq 27$

Brigitte Chauvin
(joint work with Nicolas Pouyanne)

Consider an m-ary search tree process and denote by X_n the $\mathbb{R}^{m-1}$-valued random vector whose coordinates are the number of nodes containing $0, \ldots, m-2$ keys at time n. Since [4, 2, 6] and [7], it is well known that the asymptotics of this vector admits a phase transition:

- if $m \leq 26$, then $(X_n - nv_1)/\sqrt{n}$ converges in law to a Gaussian vector, where v_1 is a deterministic vector;
- if $m \geq 27$, then $X_n = nv_1 + n^\sigma \Re\left(n^{i\tau} W^{DT} v_2\right) + o(n^\sigma)$ where $1/2 < \sigma < 1$, $\tau \in \mathbb{R}$, v_2 is a suitable complex deterministic vector, W^{DT} is a complex random variable[1]. The small o is almost sure and in any $\mathrm{L}^{\geq 1}$-space and the joint moments of W^{DT} and its conjugate can be recursively computed.

The random variable W appears in the proof as a martingale's limit. The present paper deals with the open question of its distribution.

To this effect, we embed the search tree's *node* process in a multi-type branching continuous time process, taking its values in the space of m-ary trees whose leaves have colors (or types) in $\{1, \ldots, m-1\}$: each external node of type $j \in \{1, \ldots, m-1\}$ is equipped with an $\mathcal{E}xp(j)$ distributed clock, every clock being independent from each other. When a clock rings, the corresponding external node is replaced by a node of type $j+1$ when $j \in \{1, \ldots, m-2\}$, or by m nodes of type 1 when $j = m-1$. Besides, all the clocks are then reset to zero. We denote by $X(t)$ the composition vector at time t, i.e. $X(t) = (X(t)^{(j)})_{1 \leq j \leq m-1}$ where $X(t)^{(j)}$ is the number of external nodes of type j alive at time t. The n-th jump time of the continuous-time process is denoted by τ_n.

We prove that the continuous time process, for large values of m, has the following asymptotics: if $m \geq 27$, then

$$X(t) = e^t \xi v_1 + \Re\left(e^{\lambda t} W^{CT} v_2\right) + o\left(e^{\sigma t}\right)$$

[1]The exponent ^{DT} is used to denote random variables concerned with *discrete time* processes, while ^{CT} means *continuous time.*

where ξ is a suitable Gamma-distributed random variable, $\lambda = \sigma + i\tau$ (same notations as above), W^{CT} is a complex random variable, the small o being in the sense of any $\mathrm{L}^{\geq 1}$-space. In the spirit of [7], the method consists in decomposing the infinitesimal generator of this Markov process on spaces of m-variables polynomials.

The discrete time process $(X_n)_{n\geq 0}$ and the stopped continuous time process $(X(\tau_n))_{n\geq 0}$ have the same distribution. This property allows us to connect the asymptotics of both processes. In particular, the complex random variables are related by the a.s. formula

$$W^{CT} = \xi^{\lambda}\ W^{DT}, \tag{1}$$

so that, since ξ^{λ} is invertible, the distribution of W^{DT} is determined by W^{CT}'s one. On the other hand, this relation shows for example that W^{CT} has a density.

Let $(X_k(t))_t$ denote the continuous time process starting from the initial condition $X(0) = (0, \dots, 1, \dots 0)$ where the 1 is placed at the k-th position. We denote by $W_k = W_k^{CT}$ the corresponding martingale limit. The independence gained in the continuous time process and the branching property lead to the dislocation system

$$\left\{ \begin{array}{l} W_1 \stackrel{\mathcal{L}}{=} e^{-\lambda\tau_{(1)}} W_2 \\ \\ W_2 \stackrel{\mathcal{L}}{=} e^{-\lambda\tau_{(2)}} W_3 \\ \\ \dots \\ \\ W_{m-2} \stackrel{\mathcal{L}}{=} e^{-\lambda\tau_{(m-2)}} W_{m-1} \\ \\ W_{m-1} \stackrel{\mathcal{L}}{=} e^{-\lambda\tau_{(m-1)}} [m] W_1 \end{array} \right. \tag{2}$$

where the random variables τ's are all independent of each other and independent of the W's, $\tau_{(j)}$ being $\mathcal{E}xp(j)$ distributed; notation $[m]X$ denotes the sum of m independent copies of the random variable X.

For any $k \in \{1, \dots, m-1\}$, let F_k be the two-dimensional Fourier transform of the complex variable W_k: for any $z \in \mathbb{C}$,

$$F_k(z) = E\left(e^{i\left(z\overline{W} + \overline{z}W\right)}\right).$$

The dislocation system (2), transposed on these characteristic functions, implies that the function F_1 is solution of the integral equation

$$F_1(z) = (m-1)\int_0^{+\infty} F_1^m(ze^{-\lambda u})e^{-u}(1-e^{-u})^{m-2}du;$$

boundary conditions $F_1(0) = 1$ and $F_1'(0) = 1/\Gamma(1+\lambda)$ are also satisfied.

Relations on the formal Laplace series of the W_k's can also be derived from dislocation equations (2). If one denotes them respectively by L_k, namely

$$L_k(T) = \sum_{p \geq 0} \frac{E(W_k)^p}{p!} T^p,$$

then these series are formal solutions of the differential system

$$\left\{ \begin{array}{l} \forall k \in \{1, \ldots, m-2\},\ L_k + \dfrac{\lambda}{k} T L_k' = L_{k+1} \\ L_{m-1} + \dfrac{\lambda}{m-1} T L_{m-1}' = L_1^m. \end{array} \right. \tag{3}$$

together with the same boundary conditions as above. In particular, after a very simple (ramified) change of functions, these formal solutions are related to the solutions of the nonsingular differential equation

$$y^{(m-1)} = y^m. \tag{4}$$

Many properties of W^{CT}'s distribution can be derived from relations (3) and (4).

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Genealogies and ordered approximations for measure-valued processes

Thomas G. Kurtz

Two types of particle representations of measure-valued processes as given in [1, 2, 3, 7] are described. In the first, at each time t, the particle locations $X_1(t), X_2(t), \ldots$ are exchangeable and the state of the measure-valued process is given by the corresponding de Finetti measure $\Phi(t) = \lim_{n\to\infty} \frac{1}{n}\sum_{k=1}^{n} \delta_{X_k}(t)$. In the second, each particle location $X_i(t)$ is assigned a positive "level" $U_i(t)$ in such a way that the random counting measure $\xi(t) = \sum_i \delta_{(X_i(t),U_i(t))}$ is a conditionally Poisson random measure with Cox measure $\Xi(t) \times m$, where $\Xi(t)$ is the state of the measure-valued process and m is Lebesgue measure. The measure-valued state is then obtained as $\Xi(t) = \lim_{K\to\infty} \frac{1}{K}\xi(t, \cdot \times [0, K])$. In the exchangeable representation, we refer to the index of the particle location as the level of the particle.

The measure-valued processes considered arise naturally as limits of finite population models. To obtain the desired representation for the measure-valued process, representations for prelimiting models are constructed in which the behavior of the particles is highly dependent on the level of the particle, but observations of the empirical measure $Z(t) = \sum_{i=1}^{N(t)} \delta_{X_i(t)}$ of the particle locations give no information about the levels of the particles. For discrete levels,

$$E[f(X_1(t), \ldots X_m(t))|\mathcal{F}_t^Z] = \frac{1}{\binom{N(t)}{m}} \sum_{\{x_1,\ldots,x_m\}\subset X(t)} f(x_1, \ldots x_m).$$

The prelimiting models with continuous levels have levels in an interval $[0, r]$ and

$$E[\prod_{i=1}^{N(t)} g(X_i(t), U_i(t))|\mathcal{F}_t^Z] = \prod_{i=1}^{N(t)} \frac{1}{r}\int_0^r g(X_i(t), u)du,$$

that is, conditioned on Z, the levels are iid and uniformly distributed.

In both constructions, the locations of the particles evolve independently between birth and death events. In the discrete-level construction, the population size process N is given a-priori, for example by a birth and death process. If a death occurs, the particle with the highest level is eliminated. To an observer who knows only Z and hence has no information about the levels, it appears that a randomly selected particle has been eliminated. Similarly, when a birth occurs, the lower level particles are more likely to reproduce, but again, to an observer ignorant of the levels, it appears that parents are chosen at random.

For the constructions with continuous levels, the levels change with time, for example, as solutions of an ode of the form

$$\dot{U}_i(t) = a(X_i(t))U_i^2(t) - b(X_i(t))U_i(t).$$

In the prelimiting model, the particle dies when its level hits r. In the infinite population limit, $r \to \infty$, and a particle dies when the level hits infinity.

In the discrete case, if N never hits zero, for example, as might occur if N is a supercritical branching process, then the bottom level particle is never eliminated

since it is never the highest level particle at the time of a death. It should be understood, however, that the bottom level really represents a line of descent that never terminates, not a single individual who lives forever.

In the discrete case, the measure-valued process is given by the limit of a sequence of finite models $\{(X_1^n(t), \ldots, X_{N_n(t)}^n(t))\}$, where the normalized population size, $n^{-1}N_n$, is assumed to converge to a process P and

$$(X_1^n(t), \ldots, X_{N_n(t)}^n(t)) \Rightarrow (X_1(t), X_2(t), \ldots).$$

The limiting model is given by a system of particles that is infinite up until the first time P hits zero. For each t, the sequence of locations is exchangeable, and the state of the limiting measure-valued process is given by $P(t)\Phi(t)$, where $\Phi(t)$ is the de Finetti measure for $\{X_i(t)\}$.

In the continuous case, the limiting sequence of levels $\{U_i(t)\}$ is conditionally a Poisson process whose intensity gives the total mass of the limiting measure-valued process.

The investment made to achieve the complex particle representation is returned in a number of ways. The representations incorporate the limits of the complete genealogies of the finite approximating models, including models whose genealogy corresponds to the Λ-coalescents of Pitman [8], they give insight into a number of conditioning results such as those given in [4, 5, 6], and they provide a powerful tool for proving a variety of limit theorem including ergodicity for the measure-valued processes and weak approximation results.

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Measure-valued processes, multiple merger coalescents and population genetic inference

Jochen Blath and Matthias Birkner
(joint work with Matthias Steinrücken)

Jochen Blath and Matthias Birkner

One of the main problems in mathematical genetics is the inference of evolutionary parameters of a population (such as the mutation rate) based on the observed genetic types in a finite DNA sample. If the population model under consideration is in the domain of attraction of a classical Fleming-Viot process, then the standard means to describe the corresponding genealogy is Kingman's coalescent. For this process, powerful inference methods are well-established. An important feature of this class of models is, roughly speaking, that the number of offspring of each individual is small when compared to the total population size.

Recently, more general population models have been studied, in particular in the domain of attraction of so-called *generalised Lambda Fleming-Viot processes*, as well as their (dual) genealogies, given by the so-called *Lambda-coalescents*. Moreover, Eldon & Wakeley (2006) have provided evidence that such more general coalescents, which allow multiple collisions, might actually be more adequate to describe real populations with extreme reproductive behaviour, in particular many marine species.

We show how Ethier & Griffiths' (1987) recursion for the probability of observed types under the infinitely-many sites model can be extended from the Kingman- to a Lambda-coalescent framework and how it may then be applied to obtain likelihood based inference methods. In particular, we present and compare various Monte Carlo- and Importance Sampling methods, generalizing results by Griffiths & Tavaré (1994), Stephens & Donnelly (2000) and Hobolth et. al. (2008) to the Lambda-case.

Further, we argue that within the (vast) family of Lambda-coalescents, the parametrisable sub-family of Beta$(2-\alpha, \alpha)$-coalescents, where $\alpha \in (1, 2]$, are of particular biological relevance. We apply our inference methods in this case to simulated and several real datasets (taken from Árnason (2004) and various other sources).

We conclude that for populations with extreme reproductive behaviour, the Kingman-coalescent as standard model might have to be replaced by more general coalescents, in particular by Beta$(2-\alpha, \alpha)$-coalescents.

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Spatial coalescents with multiple mergers

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(joint work with Vlada Limic)

The Λ-*coalescent*, sometimes also called the coalescent with multiple mergers, is a Markov process Π whose state space is the set of partitions of the positive integers, $\mathcal{P}$. The *standard* Λ-*coalescent* Π starts at the partition of the positive integers into singletons, and its restriction to $[n] := \{1, \dots, n\}$, denoted by $\Pi|_n \in \mathcal{P}_n$, is the Λ-coalescent starting with n initial partition elements. The measure Λ, which is a finite measure on $[0, 1]$, dictates the rate of coalescence events, as well as how many of the (exchangeable) partition elements, which we will also refer to as *blocks*, may coalesce into one at any such event. More precisely, if we define for $2 \leq k \leq b$, $k, b \in \mathbf{N}$ integers,

$$\lambda_{b,k} := \int_{[0,1]} x^{k-2}(1-x)^{b-k} d\Lambda(x), \tag{1}$$

then the parameter $\lambda_{b,k} \geq 0$ is the rate at which any collection of k blocks coalesces into one new block when the current configuration has b blocks.

The Λ-coalescent was introduced by Pitman [9], and also studied by Schweinsberg [11]. It was obtained as a limit of genealogical trees in Cannings models by Sagitov [10]. The well-known Kingman coalescent [6] corresponds to the Λ-coalescent with $\Lambda(dx) = \delta_0(dx)$, the unit atomic measure at 0. For this coalescent, each pair of current partition elements coalesces at unit rate, independently of other pairs. The survey [1] gives many pointers to the literature. The Λ-coalescent generalizes the Kingman coalescent in the sense that now any number of partition elements may merge into one at a coalescence event, but the rate of coalescence for any k-tuple of partition elements depends still only on k. Alongside a further generalization, *coalescents with simultaneous multiple collisions*, Λ-coalescents have been studied intensely in recent years.

We first extend the notion of the Λ-coalescent to the spatial setting. Here, partition elements migrate in a geographical space, a finite graph $\mathcal{G}$, and may only coalesce while sharing the same location, namely:

(i) at each site blocks coalesce according to the Λ-coalescent,

(ii) the location process of each block is an independent continuous Markov chain on $\mathcal{G}$ with jump rate 1 and transition probabilities $p(g_i, g_j), g_i, g_j \in \mathcal{G}$.

The spatial Λ-coalescent started from a finite configuration $\{(1, i_1), \ldots, (n, i_n)\}$ is a well-defined strong Markov process (chain) with state space being the set of all partitions of $[n] = \{1, \ldots, n\}$ labeled by their location in $\mathcal{G}$, which we call $\mathcal{P}^\ell$. We construct the spatial Λ-coalescents Π^ℓ with general (possibly infinite) initial states and show that this is a càdlàg Feller and strong Markov process on $\mathcal{P}^\ell$.

Earlier works on variants of spatial coalescents, sometimes also referred to as structured coalescents, have all assumed Kingman coalescent-like behavior, and include Notohara [8], Herbots [5], and more recently Barton et al. [2] in the case of finite initial configurations, and Greven et al. [4] with infinite initial states. A related model has been studied by Zähle et al. [12] on two-dimensional tori. Spatial coalescents are related to coalescing random walks, the difference being that for coalescing random walks blocks coalesce *instantaneously* when they enter the same site. Coalescing random walks have been studied extensively, in particular as dual processes to the voter model, see for example Cox [3].

It can be shown that spatial Λ-coalescents describe the genealogy of spatial population models in the limit as the population size of each colony at the sites in $\mathcal{G}$ tends to infinity. One spatial model whose genealogy converges appropriately is a spatial Cannings model. Here, each colony has a fixed large size over time. After reproduction, in which the parent generation is replaced by another generation of offspring, a certain number of individuals is selected at random from each colony and exchanged with individuals from another colony. If the variance of the offspring distribution is relatively large then spatial Λ-coalescents are obtained instead of spatial Kingman coalescents (as in [5]).

After constructing the general spatial Λ-coalescent, we turn to characterizing those that come down from infinity. Denoting by $\#\Pi(t)$ the total number of blocks in $\Pi^\ell(t)$ with any label we show that

$$\sum_{b\geq 2} \frac{1}{\gamma_b} < \infty, \qquad \text{where} \qquad \gamma_b := \sum_{k=2}^{b} \binom{b}{k} (k-1)\lambda_{b,k} \tag{2}$$

implies *coming down from infinity*, namely $P[\#\Pi(t) < \infty, \forall t > 0] = 1$, even if the initial configuration $\Pi^\ell(0)$ contains infinitely many blocks. We also show via a coupling to the non-spatial coalescent that if (2) does not hold, provided $\#\Pi(0) = \infty$ and Λ has no atom at 1, then $P[\#\Pi(t) = \infty, \forall t > 0] = 1$, that is the spatial Λ-coalescent *stays infinite*. Our results extend to the spatial coalescent for which the migration mechanism may be more general, for example non-exponential or depending on the past and in a restricted sense even on the future of the coalescence mechanism. Our results are analogous to those found by Schweinsberg [11] for non-spatial Λ-coalescents. A key result for showing *coming down from infinity*, is the following estimate for $T_n^{(k)}$, the time until there are on average k or

fewer blocks per site if there are initially n blocks per site:

$$\sup_n E[T_n^{(k)}] \leq \sum_{b=k}^{\infty} \frac{1}{\gamma_b} + \frac{k}{\gamma_k}. \tag{3}$$

Note that this estimate, which is uniform not only in n but also in the number of sites of the graph $\mathcal{G}$, relies on the independence of the coalescence and migration mechanisms. For more general migration mechanisms we find a somewhat weaker bound which is however still sufficient for showing coming down from infinity.

Finally, we study space-time asymptotic properties of Λ-coalescents that come down from infinity uniformly in the sense of (3) on large finite tori at time scales on the order of the volume. Thus, we consider $\mathcal{G}$ to be the d-dimensional torus $T^N = [-N, N]^d$ for some $N \in \mathbf{N}$, where $d \geq 3$ is fixed. The migration is given by $p(x, y) \equiv \sum_{\{z:(z-y) \bmod N=0\}} \tilde{p}(z - x)$, such that $\sum_x |x|^2 \tilde{p}(x) < \infty$ and $G := \sum_{k=0}^{\infty} \tilde{p}_k(0) < \infty$. In [4], this asymptotic behavior was studied for the spatial Kingman coalescent where $\Lambda = \gamma\delta_0$ for some $\gamma > 0$. It is interesting that on appropriate space-time scales, the scaling limit is again (as in [4]) the Kingman coalescent, with only its starting configuration (and time scale) depending on the specific properties of the underlying Λ-coalescent: Let K_π be a *non-spatial* Kingman coalescent with $K_\pi(0) = \pi$. Set

$$\kappa = \frac{2}{G + 2/\lambda_{2,2}}, \qquad \lambda_{2,2} = \Lambda([0, 1]).$$

We obtain a functional limit theorem for the partition structure.

Theorem *Assume that for $n \geq 1$ and all large N,*

$$\Pi^{N,\ell}(0)|_n = \Pi^{N+1,\ell}(0)|_n.$$

Then for each $n \in \mathbf{N}$, we obtain as $N \to \infty$, convergence of the (unlabeled) partition processes:

$$(\Pi^N|_n(t(2N + 1)^d))_{t\geq 0} \Rightarrow (K_{\Pi^{\mathbf{Z}^d}|_n(\infty)}(\kappa t))_{t\geq 0},$$

on the càdlàg space $D(\mathbf{R}_+, \mathcal{P}_n)$. where both $\Pi^{N,\ell}|_n$ and $\Pi^{\mathbf{Z}^d,\ell}|_n$ are started from $\Pi^{N,\ell}(0)|_n \in \mathcal{P}_n^\ell$. Here, $\Pi^{\mathbf{Z}^d}|_n(\infty)$ is the limiting partition for the n-coalescent on $\mathbf{Z}^d$ and " $\Rightarrow$ " denotes weak convergence.

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The allelic partition of Galton-Watson trees

Jean Bertoin

We consider a Galton-Watson process, i.e. a population model with asexual reproduction such that at every generation, each individual gives birth to a random number of children according to a fixed distribution, and independently of the other individuals in the population. We are interested in the situation where a child can be either a clone, that is of the same type (or allele) as its parent, or a mutant, that is of a new type. We stress that each mutant has a distinct type and in turn gives birth to clones of itself and to new mutants according to the same statistical law as its parent, even though it bears a different allele. In other words, we are working with an infinite alleles model where mutations are neutral for the population dynamics. We might as well think of a spatial population model in which children either occupy the same location as their parents or migrate to new places and start growing colonies on their own.

We are interested in the partition of the population into clusters of individuals having the same allele, which will be referred to as the *allelic partition*. Statistics of the allelic partition of a random population model with neutral mutations have been first determined in a fundamental work of Ewens [3] for the Wright-Fisher model (more precisely this concerns the partition of the population at a fixed generation).

This talk is based on [1] whose main purpose is to describe explicitly the structure of the allelic partition of the entire population for Galton-Watson processes with neutral mutations. We will always assume that the Galton-Watson process is critical or sub-critical, so the descent of any individual becomes eventually extinct, and in particular the allelic clusters are finite a.s. We suppose that every ancestor (i.e. individual in the initial population) bears a different allele; it is convenient to view each ancestor as a mutant of the zero-th kind. We then call mutant of the first kind a mutant-child of an individual of the allelic cluster of an ancestor, and the set of all its clones (including that mutant) a cluster of the first kind. By iteration, we define mutants and clusters of the k-th kind for any integer $k \geq 0$.

In order to describe the statistics of the allelic partition, we distinguish an ancestor which will then be referred to as *Eve*, and focus on its descent. The set of all individuals bearing the same allele as Eve is called the *Eve cluster*. The Eve cluster has obviously the genealogical structure of a Galton-Watson tree with reproduction law given by the distribution of the number of clone-children of a typical individual. Informally, the branching property indicates that the same holds for the other clusters of the allelic partition. Further, it should be intuitively clear that the process which counts the number of clusters of the k-th kind for $k \geq 0$ is again a Galton-Watson process whose reproduction law is given by the distribution of the number of mutants of the first kind; this phenomenon has already been pointed at in the work of Taïb [6]. That is to say that, in some loose sense, the allelic partition inherits branching structures from the initial Galton-Watson process. Of course, these formulations are only heuristic, and precise statements will be given later on. We also stress that the forest structure which connects clusters of different kinds and the genealogical structure on each cluster are not independent since, typically, the number of mutants of the first kind who stem from the Eve cluster is statistically related to the size of the Eve cluster.

Our approach essentially relies on a variation of the well-known connection due to Harris [4, 5] between ordinary Galton-Watson processes and sequences of i.i.d. integer valued random variables. Specifically, we incorporate neutral mutations in Harris representation and by combination with the celebrated ballot theorem (which is another classical tool in this area, see [7]), we obtain expressions for the joint distribution of various natural variables (size of the total descent of an ancestor, number of alleles, size and number of mutant-children of an allelic cluster) in terms of the transition probabilities of the two-dimensional random walk which is generated by the numbers of clone-children and of mutant-children of a typical individual. These formulas can be viewed as extensions of that of Dwass [2] for the total population of a Galton-Watson process.

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Catalytic Branching Models

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(joint work with Andreas Greven, Anita Winter)

It is well-known that Feller's branching diffusion and continuous state branching processes appear as weak limits of a broad range of suitably rescaled Galton-Watson processes. Provided one introduces a suitable topology the rescaled family forests of these Galton Watson processes converge to limit forests which can be represented by paths of a reflected Brownian motion, and a reflected Levy process without negative jumps [1, 2]. These invariance principles are the main tool for analyzing the asymptotic behavior of genealogies of Galton-Watson processes.

One of the next important steps is to investigate genealogies of multitype branching models with possible interactions between populations. For neutral two-type branching models there are three universality classes of behavior: independent branching, (one-sided) catalytic branching and mutually catalytic branching. Loss of independence in the two latter models generates many new features as well as some new technical difficulties for its analysis.

We describe in this talk the genealogy of a catalytic branching diffusion. This is the many individual fast branching limit of an interacting branching particle model involving two populations, in which one population, the "catalyst", evolves autonomously according to a continuous time critical branching process with constant branching rate, while the other population, the "reactant", evolves according to a continuous time critical branching process whose rate depends on the current mass of catalyst particles.

We show that the sequence of suitably rescaled family forests for the reactant population converges in Gromov-Hausdorff topology to a limit forest and we characterize the distribution of this limit. We first describe the limit of the reactant family forest cut off at a height where the catalyst falls below a certain threshold. We show that its contour process is given by a path of a reflected diffusion process. From that path we derive a collection of point processes each describing the mutual genealogical distances between all individuals in the population alive at a certain time. Such point-processes were introduced in [4] and provide a convenient

structure for recording the mutual distance between pairs of extant individuals via a Poisson intensity measure.

Our analysis from a "quenched" point of view, i.e., by fixing a realization of the catalyst population as an autonomous branching process, and considering the reactant population as a branching process in a given medium. One can then change to an "annealed" point of view and show that the joint law of the rescaled catalyst and the reactant population converges to a limit.

In the end we draw conclusions about the differences between the reactant limit forest and the classical continuum random forest which is known to be associated with a reflected Brownian motion. The point processes exhibit the difference in genealogical structure between the reactant population family forests and the classical Brownian continuum random tree. The differences are due to two different effects: the vanishing branching rate once the catalyst becomes extinct, and the temporal inhomogeneity of the branching rates. The differences are roughly as follows. If we pick from the population of the reactant at time t two individuals at random, their mean genealogical distance is smaller than in the classical case (with a suitable choice of the branching rate). Furthermore the total tree length becomes infinite in a stronger sense, namely instead of having Hausdorff dimension 2 with finite Hausdorff measure function, we now have a Hausdorff measure function that grows faster than a square. As a consequence, with positive probability the reactant limit forest can not be associated with the path of a diffusion.

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The length of Kingman's coalescent: asymptotics and dynamical properties

Peter Pfaffelhuber

(joint work with Anton Wakolbinger, Heinz Weisshaupt)

1. Introduction

The classical Moran model describes the evolution of a constant size population. The population consists of N individuals. Any (unordered) pair of individuals resamples at constant rate 1. In a resampling event one individual dies and the other individual reproduces. Neutral evolution refers to the case when both events

have probability $\frac{1}{2}$. Looking back in time, any pair of individuals has a common ancestor some exponential-(rate 1)-time ago. More generally, for any time t, a random tree describes the genealogy of all individuals alive at time t. This tree is known as Kingman's N-coalescent [Kin82]. As $\mathrm{N} \to \infty$, the N-coalescent converges to a random tree which we refer to as the *full coalescent*. We are interested in (asymptotics of) the total length of the N coalescent, i.e. the sum of all branch lengths. Interesting questions arise both, for fixed and varying t, leading to a study of the length of an evolving coalescent. All details of the presentation can be found in [PWW09].

2. The tree length for fixed t

The total sum of all branch lengths in Kingman's N-coalescent is easily described. Let X_i be the amount of time the tree has i lines, $i = 2, ..., \mathrm{N}$ and $\mathscr{L}_t^{\mathrm{N}}$ the length of the genealogy of the population at time t. If there are k lines in the coalescent, there are $\binom{k}{2}$ pairs, each coalescing independently at rate 1. Hence, the time to the next coalescence event is $X_k \stackrel{d}{=} \mathcal{EXP}\binom{k}{2}$ and $\mathscr{L}_t^{\mathrm{N}} \stackrel{d}{=} \sum_{k=2}^{\mathrm{N}} kX_k$. It is straightforward to write

$$\tfrac{1}{2}\mathscr{L}_t^{\mathrm{N}} \stackrel{d}{=} \tfrac{1}{2}\sum_{k=2}^{\mathrm{N}} k \cdot \mathcal{EXP}\binom{k}{2} \stackrel{d}{=} \sum_{k=1}^{\mathrm{N}-1} \mathcal{EXP}(k) \stackrel{d}{=} \max_{1\le k\le \mathrm{N}-1} \mathcal{E}(1)$$

and consequently, $\frac{1}{2}(\mathscr{L}_t^{\mathrm{N}} - \log \mathrm{N}) \stackrel{\mathrm{N}\to\infty}{\Longrightarrow} G$, where G is Gumbel distributed. This argument dates back to [Tav84]; see also [Wak08]. The convergence statement can readily be extended to an L^2*–version*: Consider a full coalescent which has intercoalescent times $X_k, k = 1, 2, ...$ and take a sample of size N from the infinitely many lines in the coalescent. Then, the sample tree is a subset of the full coalescent. More exactly, let K_i^{N} be the number of lines in the sample coalescent while the full coalescent has i lines, $i = 2, 3, ...$ Then, $\mathscr{L}_t^{\mathrm{N}} \stackrel{d}{=} \sum_{i=2}^{\infty} K_i^{\mathrm{N}} X_i$. It is possible to show that there is a Gumbel distributed random variable G with

$$\tfrac{1}{2}\sum_{i=2}^{\infty} K_i^{\mathrm{N}} X_i - \log \mathrm{N} \xrightarrow{\mathrm{N}\to\infty} G \text{ in } L^2 \tag{1}$$

3. The evolution of tree lengths

When the population evolves, genealogical relationships evolve as well. For a Moran model of size N, the total tree length at time t can e.g. be read off from its graphical representation. The evolution of the tree length consists of two mechanisms: in between resampling events, the tree grows by Ndt during time dt. In addition, by resampling events, a randomly chosen external branch breaks off from the coalescent. If J^{N} is an external branch of a coalescent of size N, recent results of [CNKR07] show that $\mathrm{N} \cdot J^{\mathrm{N}} \stackrel{\mathrm{N}\to\infty}{\Longrightarrow} J$, where $\mathbb{E}[J] = \frac{2}{\mathrm{N}}$ and $\mathbb{V}[J] = \infty$. The expectation is not surprising since during one time unit, the tree grows by N units which must be compensated by $\binom{\mathrm{N}}{2}$ jumps. Hence, each jump must approximately be of size $\frac{2}{\mathrm{N}}$ on average. However, the infinite variance of J implies that typical

jumps of the process may create paths without quadratic variation. Indeed, we can prove the following Theorem:

Theorem 1. *Let $\mathscr{L}^{\mathrm{N}} = (\mathscr{L}^{\mathrm{N}}_t)_{t\in\mathbb{R}}$ be the tree length process of a Moran model of size* N. *There is a process $\mathscr{L} = (\mathscr{L}_t)_{t\in\mathbb{R}}$ with sample paths in $\mathcal{D}(\mathbb{R};\mathbb{R})$such that*

$$\mathscr{L}^{\mathrm{N}} \overset{\mathrm{N}\to\infty}{\Longrightarrow} \mathscr{L}.$$

The process $\mathscr{L}$ has infinite quadratic variation; in particular,

$$\frac{1}{t|\log t|}\mathbb{E}[(\mathscr{L}_t - \mathscr{L}_0)^2] \xrightarrow{t\to 0} 2. \tag{2}$$

To prove the Theorem one has to show convergence of finite dimensional distributions as well as tightness of $(\mathscr{L}^{\mathrm{N}})_{\mathrm{N}\in\mathbb{N}}$. The former is a corollary of the L^2–version of the convergence (1), extended to a finite number of time points. Tightness, however, requires at least to show that

$$\limsup_{\mathrm{N}\to\infty} \mathbb{V}[\mathscr{L}^{\mathrm{N}}_\varepsilon - \mathscr{L}^{\mathrm{N}}_0] \xrightarrow{\varepsilon\to 0} 0. \tag{3}$$

As Figure 1 shows, one can represent

$$\mathscr{L}^{\mathrm{N}}_\varepsilon - \mathscr{L}^{\mathrm{N}}_0 \overset{d}{=} A^{\mathrm{N}}_{0,\varepsilon} - B^{\mathrm{N}}_{0,\varepsilon}, \tag{4}$$

where $A^{\mathrm{N}}_{0,\varepsilon}$ and $B^{\mathrm{N}}_{0,\varepsilon}$ are explained in the caption of that figure. If $S^{\mathrm{N}}_{s,t}$ is the number of time-s-ancestors of the population of size N at time t, we may write

$$A^{\mathrm{N}}_{0,\varepsilon} = \int_0^\varepsilon S^{\mathrm{N}}_{t,\varepsilon} dt.$$

Using results obtained in [Ald99, (35)], we obtain

$$\lim_{\mathrm{N}\to\infty} \mathbb{V}[A^{\mathrm{N}}_{0,\varepsilon}] \overset{t\to 0}{\sim} t. \tag{5}$$

To bound the variance of $B^{\mathrm{N}}_{0,\varepsilon}$, consider an M-coalescent embedded in an N-coalescent, with $\mathrm{M} < \mathrm{N}$. We write $K_i^{\mathrm{M,N}}$ for the number of lines in the M-coalescent at times the N-coalescent has i lines. It is then clear that

$$B^{\mathrm{N}}_{0,t} \overset{d}{=} \sum_{i=2}^{\mathrm{N}} (i - K_i^{S^{\mathrm{N}}_{0,\varepsilon},\mathrm{N}}) X_i$$

where $X_i \overset{d}{=} \mathcal{EXP}\binom{i}{2}$ and $S^{\mathrm{N}}_{0,\varepsilon}$ are independent. Using that $S^{\mathrm{N}}_{0,\varepsilon} \approx \frac{2}{\varepsilon}$ for small ε and that $(K_i^{\mathrm{M,N}})_{i=\mathrm{N},\mathrm{N}-1,\ldots}$ is a Markov Chain, we can show that

$$\lim_{\mathrm{N}\to\infty} \mathbb{V}[B^{\mathrm{N}}_{0,\varepsilon}] \overset{\varepsilon\to 0}{\sim} 2\varepsilon|\log\varepsilon|. \tag{6}$$

Combining (6) and (5) immediately shows (3). A refinement of these arguments, using [EK86, Lemma 3.4.3], leads to a proof of tightness of the family $(\mathscr{L}^{\mathrm{N}})_{\mathrm{N}\in\mathbb{N}}$.

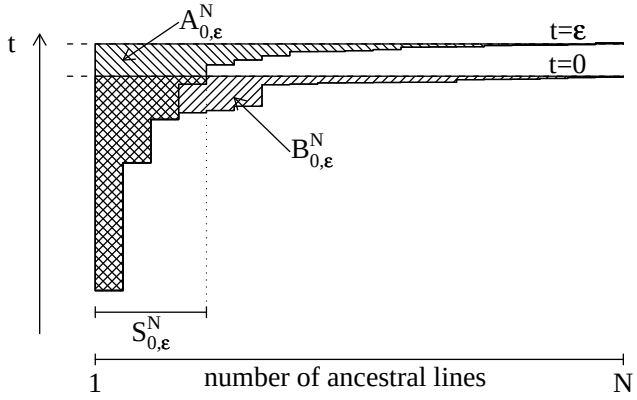

FIGURE 1. Schematic picture of tree change between two times 0 and ε for a population of size N. Tree topology is ignored in the figure and only the number of ancestral lines are given. The population at time ε has $S^N_{0,\varepsilon}$ ancestors at time 0. The genealogical tree at time ε overlaps with the tree at time 0. The part of length $A^N_{0,\varepsilon}$ belongs to the tree at time ε but not to the tree at time 0. The part of length $B^N_{0,\varepsilon}$ is lost between time 0 and ε.

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Notes on the history of branching processes

Peter Jagers

First I make some remarks about the early history of the family extinction problem, in particular about the discussion of that time about Galton's and Watson's mistaken conclusion that all families must die out. I move on to the rebirth of the theory in the early 20th Century, largely motivated by genetics, and the correct solution of the extinction problem then.

After the 2nd World War, the connection to nuclear physics steps into the foreground. So called age-dependent, but still splitting processes are introduced. Then for some decades pure mathematical research, largely analytical, dominates. In the late 60's general branching processes are introduced, where individuals can have arbitrary lifespans and give birth also during their lives, but individuals still lead independent lives, once born.

Thus, finally, branching processes encompass realistic frameworks for animal and plant, and even human population dynamics. A further step is taken by the letting individuals be of various (geno)types, so that individual lives need not be identically distributed. Thereby a structure that is Markov over the population tree, but not in real time arises. It can be studied with a combination of martingale and Markov renewal methods. In particular, in the 80's the doubly infinite limiting tree structure of non-extinct single, and later multi-type, general branching processes was established. Through this, relational properties and the history of individuals chosen at random (typical individuals) can be investigated. Examples of this are the probability of being first-born and the time back to a given ancestor.

What remains is now to broaden the perspective so as to allow interaction between individuals, while keeping in mind that the very definition of a population implies that changes are effectuated by individuals; in this non-precise sense they are the agents of change.

This perspective, mine, is basically theoretical biological, and stresses the interplay of the theory with society, science in general, and even culture. During the last two decades branching processes have however also been stimulated by influences from computer science and theoretical probability, and also used to interpret non-linear partial differential equations. But these aspects are not discussed in the lecture [1].

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A renormalisation group analysis of the 4-dimensional self-avoiding walk

Gordon Slade
(joint work with David C. Brydges)

Self-avoiding walks on $\mathbb{Z}^d$ are simple-random walk paths without self-intersections. Self-avoiding walks of the same length are declared to be equally likely. Basic questions are: (1) how many self-avoiding walks are there of length n (started from the origin), and (2) how far on average is their endpoint from the origin? In dimensions 5 and higher, these questions have been answered using the lace expansion. For $d = 2$, SLE appears to hold the key to the answer, but so far no one has understood how to unlock the door. For $d = 3$, there are only numerical results.

In this lecture, I described work in progress with David Brydges [6] for the case $d = 4$ (see also [1]). Our immediate goal is to prove that the critical two-point function (Green function) for a particular spread-out model of self-avoiding walks on $\mathbb{Z}^4$ decays like $|x|^{-2}$ at large distances, as it does for simple random walk, and that the same is true for the nearest-neighbour weakly self-avoiding walk if the repulsion is sufficiently small. The latter extends previous results of [2] (see also [4, 5]) that were obtained for weakly self-avoiding walk on a 4-dimensional hierarchical lattice.

We begin with an exact representation (due to John Imbrie [7]) of the two-point function for self-avoiding walks as the two-point function of a certain supersymmetric field theory involving both bosons and fermions. In the first part of the lecture, I explained this representation. Given the representation, we forget about the walks, and perform a renormalisation group analysis of the field theory. In the second part of the lecture, I described some of the ingredients in the renormalisation group analysis, of which the first is the finite-range covariance decomposition of [3].

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Extremality of Tree-indexed Markov chains in equilibrium

Christof Külske
(joint work with Marco Formentin)

We provide a method to prove extremality of tree-indexed Markov chains obtained by broadcasting a signal from the root with a given transition matrix. This is equivalent to proving that it is impossible to reconstruct the state of the root from observing a typical signal at a large distance. The method is based on the use of symmetric entropy as a Lyapunov function to control the contractivity of a stochastic recursion relation.

1. The result

Consider an infinite rooted tree T having no leaves. For $v, w \in T$ we write $v \to w$, if w is the child of v, and denote by $|v|$ the distance of a vertex v to the root. We write T^N for the subtree of all vertices with distances $\leq N$ to the root.

To each vertex v there is associated a spin variable $\sigma(v) \in \{1, 2, \dots, q\}$. Our model will be defined in terms of the stochastic matrix with non-zero entries

$$M = (M(v, w))_{1 \leq v, w \leq q}$$

By the Perron-Frobenius theorem there is a unique single-site measure $\alpha = (\alpha(j))_{j=1,\dots,q}$ which is invariant under the application of the transition matrix M, meaning that $\sum_{i=1}^{q} \alpha(i) M(i, j) = \alpha(j)$.

Then the object our study is the corresponding *tree-indexed Markov chain in equilibrium*. This is the probability distribution $\mathbb{P}$ on $\{1, \dots, q\}^T$ whose restrictions $\mathbb{P}_{T^N}$ to the state spaces of finite trees $\{1, \dots, q\}^{T^N}$ are given by

$$\mathbb{P}_{T^N}(\sigma_{T^N}) = \alpha(\sigma(0)) \prod_{\substack{v, w: \\ v \to w}} M(\sigma(v), \sigma(w)) \tag{1}$$

The notion equilibrium refers to the fact that all single-site marginals are given by the invariant measure α.

A probability measure μ on $\{1, 2, \dots, q\}^T$ is called a *Gibbs measure* if it is has the same finite volume conditional probabilities. This means that, for all finite subsets $V \subset T$, we have for all N sufficiently large

$$\mu(\sigma_V | \sigma_{V^c}) = \mathbb{P}_{T^N}(\sigma_V | \sigma_{\partial V})$$

μ-almost surely. The Gibbs measures, being defined in terms of a linear equation, form a simplex, and we would like to understand its structure, and exhibit its extremal elements [3]. Multiple Gibbs measures (phase transitions) may occur if the loss of memory in the transition described by M is small enough compared and there are sufficiently many offspring along the tree T. Uniqueness of the Gibbs measure trivially implies extremality of the measure $\mathbb{P}$, but interestingly the converse is not true. Parameterizing M by a temperature-like parameter may lead to two different transition temperatures, one where $\mathbb{P}$ becomes extremal and one where the Gibbs measure becomes unique. Broadly speaking, statistical mechanics

models with two transition temperatures are peculiar to trees (and more generally models indexed by non-amenable graphs [5]). This is one of the reasons for the interest in models on trees compared to models on lattices.

Now, our present aim is to provide a general theorem which is able to cover such cases, yielding computable bounds on parameter regions for given models. To formulate our result we need the following notations.

We write for the simplex of length-q probability vectors

$$P = \{(p(i))_{i=1,\dots,q}, p(i) \geq 0 \ \forall i, \ \sum_{i=1}^{q} p(i) = 1\}$$

and we denote the relative entropy between probability vectors $p, \alpha \in P$ by $S(p|\alpha) = \sum_{i=1}^{q} p(i) \log \frac{p(i)}{\alpha(i)}$. We introduce the *symmetrized entropy* between p and α and write

$$L(p) = S(p|\alpha) + S(\alpha|p) = (p - \alpha) \log \frac{dp}{d\alpha}$$

While the symmetrized entropy is not a metric since (the triangle inequality fails) it serves us as a "distance" to the invariant measure α.

Let us define the constant

$$C_1 = \sup_{p \in P} \frac{L(pM^{\mathrm{rev}})}{L(p)}$$

where $M^{\mathrm{rev}}(i,j) = \frac{\alpha(j)M(j,i)}{\alpha(i)}$ is the transition matrix of the reversed chain. Note that numerator and denominator vanish when p takes the invariant distribution α. Consider a random tree with i.i.d. offspring distribution concentrated on $\{1, 2, \dots\}$ and denote the corresponding expected number of offspring by $\mathbb{E}d$.

Here is our main result.

Theorem 1. *If $(\mathbb{E}d)C_1 < 1$ then the tree-indexed Markov chain $\mathbb{P}$ on the random tree T is extremal for almost every tree T.*

For the specific example of the q-state Markov chain corresponding to the Potts model the proof can be found in [2](2), the proof in the general case is given in a forthcoming paper.

2. Discussion

Non-uniqueness of the Gibbs measures corresponds to the existence of boundary conditions which will cause the corresponding finite volume conditional probabilities to converge to different limits. Extremality of the measure $\mathbb{P}$ means that conditioning the measure $\mathbb{P}$ to acquire a configuration ξ at a distance larger than N will cease to have an influence on the state at the root if ξ is chosen according to the measure $\mathbb{P}$ itself and N is tending to infinity. In the language of information theory this is called non-reconstructability (of the state at the origin on the basis of noisy observations far away).

The bound given in the theorem is sharp (on a regular tree) for the symmetric Ising model and reproduces the known results of [1, 4]. The bound is not sharp

(but close to the true values [9]) for the symmetric Potts model with more than 2 states, and provides an explicit parameter regime where $\mathbb{P}$ is extremal but the Gibbs measure is not unique.

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Spin models on sparse random graphs: results and puzzles

Luca De Sanctis

We want to illustrate some results and some puzzles in the statistical mechanics of spin systems on graphs (sparse or complete). The models we consider are physically known as ferromagnets, glasses, antiferromagnets. We mainly focus on the variational principles providing the free energy of the models.

Given a set of N points, our models are defined for configurations $\sigma : i \to \pm 1$, $i = 1, \dots, N$ of Ising spins. The simplest model we consider is mean field ferromagnet on the complete graph, with N vertices and N^2 edges, defined by the Curie-Weiss (CW) Hamiltonian

$$H_N^{CW}(\sigma) = -\frac{1}{N} \sum_{i<j}^{1,N} \sigma_i \sigma_j = -N \frac{1}{2} m^2(\sigma) \ ,$$

where the magnetization of configuration σ is by definition $m(\sigma) = \sum_{i=1}^N \sigma_i / N$. More generally, we could consider a ferromagnetic Hamiltonian with a concave dependence on the magnetization: $H_N^{CW}(\sigma) = -N f(m)$, f convex. With $Z_N^{CW}(\beta) =$

$\sum_{\{\sigma\}} \exp(-\beta H_N^{CW}(\sigma))$ and $\beta \geq 0$, one is interested in computing the pressure

$$p^{CW}(\beta) = \lim_{N\to\infty} p_N^{CW}(\beta) = \lim_{N\to\infty} \frac{1}{N} \ln Z_N(\beta) \ .$$

An estimate of the pressure can be immediately found simply using the inequality

$$f(m) \geq f(\tilde{m}) + (m - \tilde{m}) f'(\tilde{m})$$

holding for any numerical trial magnetization $\tilde{m}$. Plugging this approximation into the pressure one obtains a trial function in the form

$$g^{CW}(\beta; \tilde{m}) = \frac{1}{N} \ln \left[\exp(-\beta N \tilde{m} f'(\tilde{m})) \sum_{\sigma} \exp(\beta N m f'(\tilde{m})) \right] + \beta f(\tilde{m})$$

which is independent of N and is easy to compute explicitly and to optimize over the possible choices for $\tilde{m}$. An additional argument shows that the bound is optimal in the thermodynamic limit, i.e.

$$p^{CW}(\beta) = \sup_{\tilde{m}} g^{CW}(\beta; \tilde{m}) = g^{CW}(\beta; \ barm_\beta) \ , \ \bar{m}_\beta : \tanh(\beta \bar{m}_\beta) = \bar{m}_\beta$$

Hence the pressure is obtained through a variational principle in agreement with the predicament of statistical mechanics: as a supremum over a space of trial states (here in terms of trial order parameters of clear physical meaning: the trial magnetization representing a trial state). It is not difficult to see that the second term of $g^{CW}(\beta; \tilde{m})$ is minus β times the internal energy per spin $-\partial_\beta p^{CW}(\beta)$, in the state $\tilde{m}$. Therefore one expects the other term to be the entropy $s(\tilde{m})$. Unfortunately this term depends on the form of the interaction through f' and not on the state only, so preventing the classical Legendre structure [4]. But if one takes the infimum $\inf_{f'}$ of this term over the possible forms of the interactions, then the expression does not depend on f' anymore and it actually coincides with the entropy $s(\tilde{m})$ of a spin with average magnetization $\tilde{m}$: $s(\tilde{m}) = -\mu_+ \ln \mu_+ - \mu_- \ln \mu_-$, with $\mu_\pm = (1 \pm \tilde{m})/2$. Then one can optimize over $\tilde{m}$ recovering the classical Legendre structure: $p^{CW}(\beta) = \sup_{\tilde{m}} \{s(\tilde{m}) + \beta f(\tilde{m})\}$.

We want to study to what extent all this can be reproduced for models on s parse random graphs, both in the case of ferromagnetic interactions and in the case of random interactions.

By $\{i_\nu, j_\nu, k_\nu, l_\nu\}$, $\nu \in \mathbb{N}$, we will denote families independent random variables all uniformly distributed on $1, \ldots, N$. The Hamiltonian of the dilute ferromagnet and the one of the Viana-Bray (VB) model of dilute spin glass are

$$H_N(\sigma; \mathcal{J}) = -\sum_{i,j}^{1,N} K_{ij} \sigma_i \sigma_j \ ; \ H_N^{VB}(\sigma; \mathcal{J}) = -\sum_{i,j}^{1,N} J_{ij} K_{ij} \sigma_i \sigma_j$$

where K_{ij} are independent Poisson random variables of mean α/N, for some given *connectivity* $\alpha \in \mathbb{R}_+$. So the models are defined on a graph with N vertices and each on the N^2 possible edges has a Poisson random weight. The (so called *quenched*) expectation with respect to the Poisson random variables is denoted by $\mathbb{E}$ and $p_N(\alpha, \beta) = \frac{1}{N} \mathbb{E} \ln \sum_\sigma \exp(-\beta H_N(\sigma))$ is the pressure (analogously for the VB model). A first theorem that can be proven states that the pressure of

both models is not altered if the variables K_{ij} are Bernoulli with same mean, like in the most standard choice for the underlying graph. A second theorem states that the pressure of the dilute ferromagnet does not change if the model is put on any locally tree-like rooted tree [1]. A third theorem states that if $\alpha \to \infty$ and $\beta \to 0$ with $2\alpha \tanh \beta = \beta'$ kept constant, then $p_N(\alpha, \beta) \to p_N^{CW}(\beta')$, and similarly for the VB model whose pressure tends to that of the (Gaussian) model on the complete graph (the Sherrington-Kirkpatrick model). In the case of the VB model, the existence of the thermodynamic limit of the pressure per spin is ensured by the inequality $\ln Z_{N+M}^{VB} \geq \ln Z_N^{VB} + \ln Z_M^{VB}$, easy to prove by interpolation on the connectivity, which has the opposite verse as compared to the CW model. The fact that the natural interpolation is on the connectivity and the verse of the inequality have major consequences. The generalization [2] to spin glasses on sparse random graphs of the method illustrated for the CW model is expressed in the next variational principle

$$p^{VB}(\alpha, \beta) = \lim_{N \to \infty} p_N^{VB}(\alpha, \beta) = \inf_{\mathcal{R}} g^{VB}(\mathcal{R}; \alpha, \beta) = \inf_{\mathcal{R}} \mathbb{E} \ln \frac{\Omega[\sum_\sigma \exp(-\beta \tilde{h} \sigma)]}{\Omega[\exp(-\beta \hat{H})]}$$

where $\mathcal{R}$ consists in a set of random probability weights (the expectation with respect to which is denoted by Ω) defined on some discrete space Σ and a positive semi-definite multi-overlap kernel $\{q_{2n}\}_{n \in \mathbb{N}} : \Sigma^{2n} \to [0, 1]$, which provides a constraints on the random fields $\tilde{h}$ and $\hat{H}$ (see [2] for details). Now, the trial pressure is again the difference between two competing terms, and the denominator in g^{VB} can be seen to be essentially the derivative of the pressure with respect to α [2]. Two deep problems arise. A first one is well known since it emerged in the spin glass theory on the complete graph: the infimum as opposed to the supremum appearing in the standard statistical mechanics. The second problem is instead due to the sparse nature of the graph: since the two terms come basically from a differentiation with respect to α, they cannot be interpreted as internal energy and entropy. The main current open problem is however proving that the conjecture from theoretical physics (which corresponds to a particular $\mathcal{R}$ associated to a GREM) is correct. Another interesting question is whether the numerator can be given in terms of a differential equation like the Parisi one in the case of the complete graph. Among the various other questions one may pose, let us only recall that a Legendre structure in principle can be found for this model, but the interpretation of the various terms remains obscure.

Getting back to the ferromagnet on a sparse graph, which is expected to be simpler than spin glasses and the exact rigorous expression of its pressure is known [1], it is somewhat surprising that many basic features still escape good understanding. For instance, is there a direct proof that $\ln Z_{N+M} \leq \ln Z_N + \ln Z_M$? Such a proof was given in [3] for low enough β and for $\beta \to \infty$ only. How can one formulate a variational principle for the pressure using proper trial order parameters? Is there a way to find a trial pressure as the difference between entropy and internal energy? Is there Legendre structure?

Notice that in the case of ferromagnetic interaction the variational principle has the right verse (sup) and the pressure is sub-additive, while in the case of spin glasses and antiferromagnets the variational principle has the opposite verse (inf) and the pressure is super-additive. In fact, one can introduce a model [4] interpolating between a ferromagnet and an antiferromagnet, with spin glass at intermediate value of the interpolating parameter. For this model, even on a sparse graph, one can identify the high temperature region and relative pressure, and also formulate for instance a replica symmetric approach. It would be very interesting to study the additivity property of the pressure and obtain a variational principle, as there should emerge a cross-over between super-additivity and sub-additivity, and between sup and inf in the variational principle as the interpolating parameter varies. So one may aim at finding a quantitative control of the thermodynamic limits and of the pressure not relying on bounds in a specific verse, and the study of this interpolating model may offer insights on the Hopfield model of neural networks too, since it also lacks a proof of the existence of the thermodynamic limit of the pressure density.

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Martin boundary for randomly growing binary trees

Rudolf Grübel

(joint work with Steven N. Evans, Anton Wakolbinger)

Half a century ago Doob [1] introduced a general method of compactifying the countable state space S of a transient Markov chain $(X_n)_{n\in\mathbb{N}_0}$ in such a way that X_n converges almost surely to a limit random variable X_∞ in the enlarged space $\bar{S}$. We apply Doob's method to specific Markov chains with values in the set of finite binary trees.

Let $N := \{0,1\}^\star$ be the set of finite sequences of 0's and 1's. The elements of N represent the nodes of the tree t, which can thus be regarded as a prefix-stable subset of N. By a randomly growing sequence $(X_n)_{n\in\mathbb{N}}$ of binary trees we then mean a sequence of random binary trees with the property that $X_n \subset X_{n+1}$, $\#X_n = n$ for all $n \in \mathbb{N}$. Such tree sequences that grow by one node at a time arise by applying algorithms for searching and sorting to random input, for example. Typically, the input is a sequence $(\xi_n)_{n\in\mathbb{N}}$ of independent and identically

distributed real random variables and X_n is the tree associated with $\xi_1, \ldots, \xi_n$. It turns out that two standard algorithms, digital search tree (DST) and binary search tree (BST), lead to the same compactification $\bar{S}$ but have different exit laws, and that these Markov processes are related in the sense that the DST chain is an h-transform of the BST chain. The Martin boundary $\partial S = \bar{S} \setminus S$ consists of the set of probability measures μ on the set $\{0,1\}^\infty$ of 'ends' of the complete binary tree $t_\infty = N$. Conditionally on an exit via μ, i.e. $X_\infty = \mu$, the BST chain is identical in distribution to a DST chain with base parameter μ. Ignoring binary rationals this parameter can in turn be identified with the distribution of the input random variables ξ_n, $n \in \mathbb{N}$, for the DST algorithm.

For X_n's that are uniformly distributed on the set of binary trees with n nodes, for all $n \in \mathbb{N}$, we use the Markovianization obtained by Luczak and Winkler [3]. This process of randomly growing binary trees leads to a different compactification, which reflects the well-known qualitative difference between the uniform and the search tree cases. In both cases, however, the compactification can be based on an embedding that uses the subtree size functional, which associates with a tree t the function $\psi(t,\cdot) : N \to \mathbb{N}_0$, where $\psi(t,u)$ is the size of the subtree of t rooted at the node u. In the case of search trees we need a standardization, for uniformly distributed trees we use the subtree size functional in its raw form.

For these results information on the respective Martin kernel is important. For this we relate the trees to urn models, using the well known fact that the BST chain behaves locally like the famous Pólya urn. We also obtain the exit distributions in the search tree and in the uniform case. The latter turns out to be concentrated on a specific set of infinite binary trees, which we identify, thereby providing an alternative proof for a result of Janson [2].

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The CRT-valued limit dynamics of the Aldous move on cladograms

Anita Winter

(joint work with Leonid Mytnik)

A *N-phylogenetic tree* is a semi-labeled, un-rooted and binary tree with $N \geq 4$ *leaves* labeled $\{1, 2, ..., N\}$ and with $N - 2$ unlabeled internal leaves and positive edge lengths representing the time spans between common ancestors. In biological

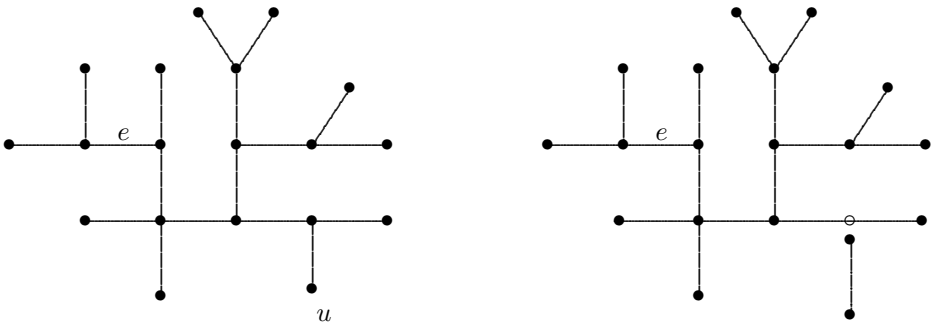

FIGURE 1

systematics *N-phylogenetic trees* are used to represent the revolutionary relationship between N species. If one focuses only on the kingship (that is, taking all edge length of unit length), a more precise term is the *cladogram*.

Markov chains that move through a space of finite trees are an important ingredient for several algorithms in phylogenetic analysis. Usually, such chains are based on a set of simple rearrangements that transform a tree into a "neighboring" tree. One such Markov chain is based on the so-called *Aldous move on cladograms* (introduced in [Ald00]) which is a finite tree-valued Markov chain that has the uniform distribution on all cladograms with a fixed number of vertices as its stationary distribution. The discrete time version has the following transition dynamics (compare Figures 1 and 2).

- Pick a leaf u at random,
- erase the unique edge which connects u with the sub-tree spanned by all leaves but u,
- pick then an edge from the remaining sub-tree at random, and split it into two pieces.
- reintroduce the above edge at the split point.

Since the Aldous move is symmetrically defined and each cladogram can be reached after a finite number of steps classical Markov chain theory implies that the Aldous move approaches the uniform distribution as time goes to infinity. In [Ald00] David Aldous showed that the inverse of the spectral gap (as a measurement for the relaxation time) is at least of order of magnitude N^2 and not greater that $\mathcal{O}(N^3)$. The latter upper bound was improved by Jason Schweinsberg in [Sch02] to the effect that the mixing time is of the order $\mathcal{O}(N^2)$.

On the other hand, David Aldous gives in [Ald93] a notion of convergence of cladograms which shows that the uniform cladogram with N leaves and edge length re-scaled by a factor of $\frac{1}{\sqrt{N}}$ converges to the so-called Brownian continuum

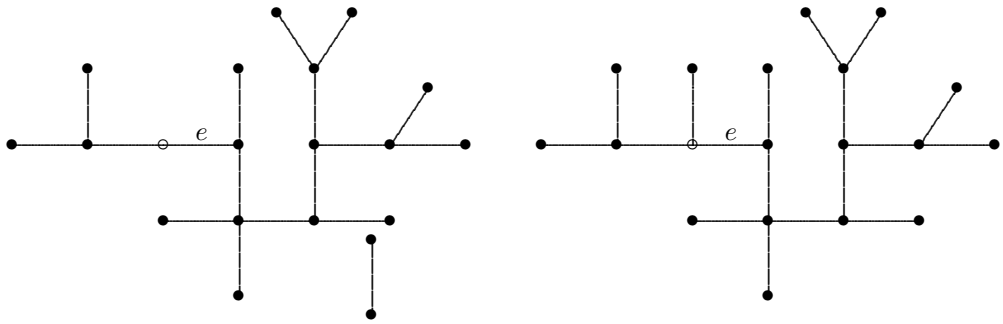

FIGURE 2

random tree (CRT) which is the tree "below" a standard Brownian excursion and can be thought of as the uniform compact real tree.

These two results suggest that if we re-scale edge lengths by a factor of $\frac{1}{\sqrt{N}}$ and speeding up time by a factor N^2 the Aldous move on cladograms converges in some sense to a continuous tree-valued diffusion.

The main emphasis of the talk is to give first precise statements towards that direction. To make life easier we ignore the labels on the leaves. This allows to code a cladogram with N-leaves as 0-hyperbolic metric spaces which are equipped with a probability measure (assigning mass $\frac{1}{N}$ to each point representing a leaf) and use the *Gromov-weak topology* on spaces of metric measure spaces as introduced in [GPW06[.

The main result presented in the talk is the following: If $(T_N, r_N, \mu_N)_{N\in\mathbb{N}}$ is the uniform N-cladogram (ignoring the labels), Ω^N the operator describing the changes in the Aldous move (run at unit time) and

$$\Phi\big((T,r,\mu)\big) := \int_{T^2} \mu^{\otimes 2}(\mathrm{d}(u_1,u_2))\,\phi\big(r(u_1,u_2)\big),$$

then in probability,

$$N^{\frac{3}{2}}\Omega^N\Phi\big((T_N, \tfrac{1}{\sqrt{N}}r_N, \mu_N)\big)$$

$$\underset{N\to\infty}{\longrightarrow} \tfrac{1}{2}\int_{T^2} \mu^{\otimes 2}(\mathrm{d}(u,u'))\Big\{\phi'\big(r(u,u')\ big\big)\big(1-\tfrac{1}{2}r^2(u,u')\big) + r(u,u')\cdot\phi''\big(r(u,u')\big)\Big\}$$

provided $(T_N, \frac{1}{\sqrt{N}}, \mu_N) \underset{N\to\infty}{\longrightarrow} (T,r,\mu)$, in probability.

Note that the slower time scale ($N^{\frac{3}{2}}$ rather than N^2) reflects the fact that our approach does not follow the distance of two initially specified leaves but rather considers the evolution of the averaged distance between any two points. Notice also that the action of the generator on the test function ϕ implies that in equilibrium the distance of two randomly samples leaves has a Rayleigh distribution which supports the conjecture that the uniform distribution on metric probability

measure spaces will turn out to be the unique stationary distribution of the limit diffusion under construction.

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The contact process seen from a typical infected site

Jan M. Swart

1. Contact processes on Cayley graphs

Let Λ be a countable, finitely generated group, with group action denoted by $(i,j) \mapsto ij$ and unit element (origin) 0, and let $\Delta \subset \Lambda$ be a finite symmetric generating set for Λ. Then the (left) *Cayley graph* $\mathcal{G}(\Lambda, \Delta)$ associated with Λ and Δ is the graph with vertex set Λ, where there is an edge connecting $i, j \in \Lambda$ if and only if $j = ki$ for some $k \in \Delta$. Examples of Cayley graphs are $\mathbb{Z}^d$, equipped with the usual nearest-neighbor structure, or the regular tree $\mathbb{T}_d$ in which each site has $d+1$ neighbors.

The contact process with infection rate λ on a Cayley graph $\mathcal{G}(\Lambda, \Delta)$ is a Markov process $(\eta_t)_{t\geq 0}$ taking values in the subsets of Λ. If $i \in \eta_t$ then we say that the site i is infected at time $t \geq 0$; otherwise we say that the site is healthy. Infected sites infect healthy neighboring sites with rate λ, and infected sites become healthy with recovery rate 1. We let $(\eta_t^A)_{t\geq 0}$ denote the contact process started from the initial state $A \subset \Lambda$.

Let

$$\theta(\lambda) := \mathbb{P}\big[\eta_t^{\{0\}} \neq \emptyset \ \forall t \geq 0\big] = \mathbb{P}\big[(0,0) \to \infty\big]$$

denote the probability that the process started with one infected site survives. Then $\lambda_{\mathrm{c}} := \inf\{\lambda > 0 : \theta(\lambda) > 0$ is the *critical infection rate*. In the celebrated paper of Bezuidenhout and Grimmett [1], it is proved that $\theta(\lambda_{\mathrm{c}}) = 0$ for the process on $\mathbb{Z}^d$ in all dimensions $d \geq 1$. The analogue result for trees has been proved by Morrow, Schinazi, and Zhang in [3]. The next result generalizes this, in the spirit of [2], to any nonamenable Cayley graph:

Theorem 1. **[4]** *Assume that Λ is nonamenable. Then $\theta(\lambda_{\mathrm{c}}) = 0$.*

2. The exponential growth rate

Theorem 1 is proved by looking at the exponential growth rate of contact processes. A simple subadditivity argument shows that each contact process on a Cayley graph has a well-defined exponential growth rate, i.e., there exists a real constant $r = r(\lambda)$ such that the process started in any finite nonzero initial state satisfies:

$$\lim_{t\to\infty} \frac{1}{t} \log \mathbb{E}\big[|\eta_t|\big] = r.$$

On Cayley graphs of subexponential growth, e.g. on $\mathbb{Z}^d$, it is not hard to show that $r \leq 0$. On the other hand, on graphs with exponential growth, it is possible that $r > 0$. Theorem 1 is a consequence of the following proposition.

Proposition 2. *For any Cayley graph $\mathcal{G}(\Lambda, \Delta)$:*

- **(a)** *The function $\lambda \mapsto r(\lambda)$ is Lipschitz continuous.*
- **(b)** *$r(\lambda) > 0$ implies $\theta(\lambda) > 0$.*
- **(c)** *If Λ is nonamenable and $\theta(\lambda) > 0$, then $r(\lambda) > 0$.*

3. The process seen from a typical site

Proposition 2 (c) is proved by relating the exponential growth rate r to the configuration seen from a typical infected site at a typical late time.

Set $\mathcal{P}_+(\Lambda) := \{A \in \mathcal{P}(\Lambda) : A \neq \emptyset\}$, and define locally finite measures μ_t on $\mathcal{P}_+(\Lambda)$ by

$$\mu_t := \sum_{i\in\Lambda} \mathbb{P}[\eta_t^{\{i\}} \in \cdot\,]\big|_{\mathcal{P}_+(\Lambda)} \qquad (t \geq 0),$$

where $|_{\mathcal{P}_+(\Lambda)}$ denotes restriction of a measure to $\mathcal{P}_+(\Lambda)$. Think of μ_t as the law at time t of the process started with one infected site, distributed according to the uniform distribution on Λ. Conditioning μ_t on the origin being infected is equivalent to starting with one infected site, and then looking at the process at time t as seen from a 'typical' infected site, chosen according to a Campbell law.

We set

$$\hat{\mu}_\alpha := \frac{1}{Z_\alpha} \int_0^\infty \mu_t\, e^{-\alpha t} \mathrm{d}t \qquad (\alpha > r),$$

where Z_α is a normalization constant such that $\hat{\mu}_\alpha\{A : 0 \in A\} = 1$.

Proposition 3. *The measures $\{\hat{\mu}_\alpha : \alpha > r\}$ are tight in the topology of vague convergence, and each vague limit as $\alpha \downarrow r$ yields an 'eigenmeasure' with eigenvalue r, i.e., a locally finite measure μ on $\mathcal{P}_+(\Lambda)$ such that*

$$\int \mu(\mathrm{d}A)\, \mathbb{P}\big[\eta_t^A \in \cdot\,\big]\big|_{\mathcal{P}_+(\Lambda)} = e^{rt}\mu \qquad (t \geq 0).$$

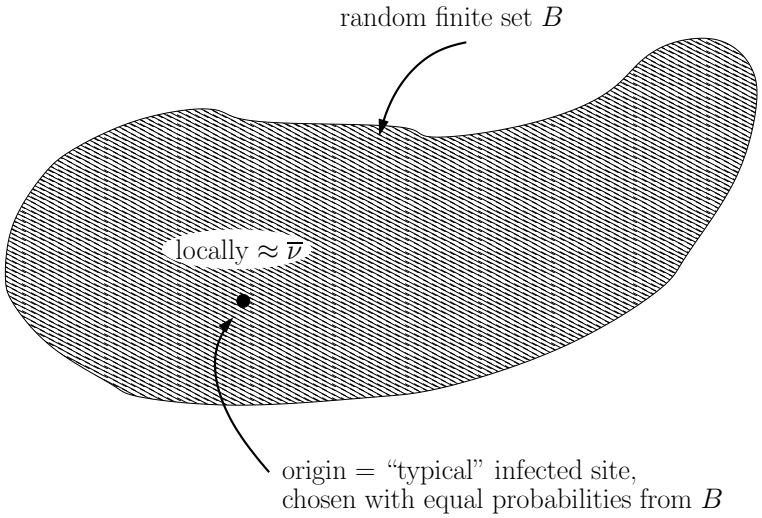
4. Proof of Proposition 2 (c) (sketch)

Recall that each contact process has an upper invariant law $\overline{\nu}$, which is the long-time limit law of the process started with all sites infected. There exists a classical proof, based on duality, which shows that if a contact process survives, then $\overline{\nu}$ is its unique nontrivial spatially homogeneous invariant law. In a similar fashion, one can prove the following, stronger fact:

Proposition 4. *If a contact process on a Cayley graph survives, then, up to a multiplicative constant, the upper invariant law $\overline{\nu}$ is the only spatially homogeneous eigenmeasure with eigenvalue zero.*

Now assume that a contact process on a Cayley graph survives, and its exponential growth rate $r(\lambda)$ is zero. Then, by Propositions 3 and 4, the vague limit $\lim_{\alpha \downarrow 0} \hat{\mu}_\alpha$ exists and is up to a multiplicative constant equal to $\overline{\nu}$.

Consider the law $\hat{\mu}_\alpha$, conditioned on the event $\{A : 0 \in A\}$. By our previous remarks, for α close to zero, this law describes a random finite set B, containing the origin, that looks something like this:



Since seen from the origin, we see something that looks like the spatially homogeneous law $\overline{\nu}$, we conclude that 0 lies with high probability far from the outer boundary of B. Since 0 is a 'typical' site, this contradicts nonamenability, which says that in any finite set B, a positive fraction of the sites must lie near the boundary.

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The conditional ancestral selection graph with strong balancing selection

John Wakeley
(joint work with Ori Sargsyan)

The Ancestral Selection Graph (ASG) was introduced by Claudia Neuhauser and Stephen Krone in 1997 [2] as a model for the joint sampling process of gene genealogies and genetic types at a locus under the influence of mutation, selection, and random genetic drift. In the ten or so years since its introduction, the ASG has not led to many new analyses or results, and has also proven very difficult to simulate efficiently. The reason for this is that the ASG requires a large graph to be generated—prohibitively large when selection is strong—even though the gene genealogy of a sample is always a binary tree.

Somewhat later, Slade [4] described the conditional ASG, which assumes that the genetic types of the sample are known. The conditional ASG is more efficient than the original ASG because conditioning on the types allows a much smaller graph to be generated. A recent general reference for the conditional ASG is the paper by Stephens and Donnelly [5], upon which the work we present here is based.

We imagine a well-mixed haploid population of size N containing two allelic types, A_1 and A_2. The population reproduces with some stochasticity, as in the Wright-Fisher model or the Moran model. There is mutation both from A_1 to A_2 and from A_2 to A_1, with probabilities proportional to θ/N per reproduction event. Finally, selection is in the form of symmetric heterozygote advantage; specifically, when an individual dies in the population, the allele that replaces it is chosen randomly from a pair of alleles sampled at random from the population (A_1A_1, A_1A_2, A_2A_1, or A_2A_2) in proportion to their relative fitness: 1 for A_1A_1 or A_2A_2, and $1+\sigma/N$ for A_1A_2 or A_2A_1. This type of selection will tend to maintain both alleles in the population.

A diffusion approximation for the frequency x of allele A_1 exists in the limit $N \to \infty$ with θ and σ constant. The conditional ASG assumes that the population is at equilibrium with respect to the above processes, so that the frequency of A_1 follows a stationary distribution denoted $\phi_{\theta,\sigma}(x)$. The ancestral process, which generates the gene genealogy of a sample, will depend on the allelic types of the sample as well as on θ and σ, *e.g.* though $\phi_{\theta,\sigma}(x)$. In particular, the conditional ASG is a time-reversed Markov process that gives the rates of common-ancestor (or

coalescent) events, mutation events, and branching events (which create a graph rather than a tree) along the ancestral lineages of the sample; and is derived under the assumption of stationarity with equilibrium probability $\phi_{\theta,\sigma}(x)$ of allele A_1.

The rates of events in the conditional ASG involve ratios of sampling probabilities, which have the form $\int_0^1 x^{n_1}(1-x)^{n_2}\phi_{\theta,\sigma}(x)dx$ for a sample of n_1 alleles of type A_1 and n_2 alleles of type A_2. The rates also depend directly on θ and σ. We are interested the ancestral process when σ is very large. Following a recent study of directional selection in favor of one allele [6], we expect a limiting $\sigma \to \infty$ ancestral process to exist. Based on previous work using a different approach we expect the limiting ancestral process under symmetric heterozygote advantage to be a simple structured coalescent process between the two subpopulations, corresponding to the two allelic types, whose frequencies will be held nearly constant when selection is very strong [1].

Using a heuristic separation-of-time-scales argument, based on the work of Möhole [3], we describe the behavior of the conditional ancestral selection graph with very strong symmetric heterozygote advantage between a pair of alleles. To illustrate our approach, we present a more rigorous demonstration that the neutral conditional ancestral process converges to a simple coalescent in the limit as the mutation rate θ tends to infinity. In the limit as the strength of selection σ tends to infinity, we find that the ancestral process does indeed converge to a neutral structured coalescent, with two subpopulations representing the two alleles and with mutation playing the role of migration. This agrees with a previous result of Kaplan et al. [1]. We present the results of computer simulations to support our heuristic mathematical results. This work is described further in a paper to appear [7].

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