Evolving coalescents

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WBPA, Badajoz April 07 – 10, 2015



Part of Schweinsberg's result (2003):

Let $N \in \mathbb{N}$.

Let X_{im} , i = 1, ..., N be the offspring numbers in generation m of a "supercritical Galton-Watson genealogy" with constant population size N.

Thus:

- Constant population size:
$$\sum_{i=1}^{N} X_{im} = N$$
 for all m

- Independence between generations: (X_{1m}, \ldots, X_{Nm}) are iid for different m

- Distribution of (X_{10}, \ldots, X_{N0}) :

Let $\xi_i \ge 1$ be the iid offspring numbers of the individuals $1, \ldots, N$ in generation 0. Choose N of these descendants at random and remove the other ones.

Let $X_{i0} \leq \xi_i$ be the number of the remaining offspring of individual *i*.

-m runs through \mathbb{Z} .



N = 5

Assumptions:

 $-\xi \ge 1$ a.s. (for convenience)

 $- \mathbf{P}(\xi > k) \sim ck^{-\alpha}$ as $k \to \infty$ for some $\alpha > 2$ or $1 < \alpha < 2$.

Thus

 $1 < \mathrm{E}\xi < \infty$.

Choose $n \leq N$ individuals uniformly at random in generation 0 and label them from 1 to n.



n = 3, N = 5

The genealogy of these n individuals in generation 0:

For $t \geq 0$ and $1 \leq i, j \leq n$ set

 $i\sim_{t,N}j$

iff the individuals i,j have a common ancestor in the generations $m \leq -tc_N$,

where

$$c_N = \begin{cases} N & \text{for } \alpha > 2, \\ N^{\alpha - 1} & \text{for } 1 < \alpha < 2. \end{cases}$$

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Let $\Pi_{t,N}$ be the corresponding partition on $\{1, \ldots, n\}$.

 $(\prod_{t,N})_{t\geq 0}$ is a process with values in \mathcal{P}_n , the set of all partitions of $\{1, \ldots, n\}$.

Theorem (Schweinsberg 2003)

Fix $n \in \mathbb{N}$.

Then the processes $(\prod_{t,N})_{t\geq 0}$ converge in distribution to a limiting process $\Pi^{\alpha} = (\Pi^{\alpha}_t)_{t\geq 0}$,

$$(\Pi_{t,N})_{t>0} \stackrel{d}{\rightarrow} \Pi^{lpha} , \text{ as } N
ightarrow \infty .$$

For $\alpha > 2$ the limiting process is a *n*-Kingman coalescent, and for $1 < \alpha < 2$ a *n*-Beta $(2 - \alpha, \alpha)$ -coalescent.

The evolving Kingman *n*-coalescent (n = 5):



Moran's model with time $-\infty < t < \infty$: Links between pairs of lines appear at rate 1, independent between the different pairs. The evolving Kingman *n*-coalescent:



The genealogy of a sample of n = 5 individuals: Kingman's coalescent at time t_1 The evolving Kingman *n*-coalescent:



The coalescent tree evolves in time.

The evolving Lambda-coalescent:



Poisson Point Process on $[0,1] \times \mathbb{R}$ with intensity measure

$$\mu(dt, dx) = dt \cdot \frac{\Lambda(dx)}{x^2}$$

and a finite measure $\Lambda(dx)$ on [0, 1].

The rate, at which two specified individuals i, j (say i = 1, j = 2) are involved in a common coalescent event is

$$\int_0^1 x^2 \ \frac{\Lambda(dx)}{x^2} = \Lambda((0,1]) < \infty \ .$$

The evolving $Beta(2 - \alpha, \alpha)$ -coalescent:

Let

$$\Lambda(dx) = cx^{1-\alpha}(1-x)^{\alpha-1} dx$$

with $0 < \alpha < 2$.

- $\alpha \uparrow 2$: Kingman coalescent
- $\alpha = 1$: Bolthausen-Sznitman coalescent
- $\alpha \downarrow 0$: Star-shaped coalescent.

Why care about such kind of evolution?

One answer:

The diverse areas of the tree are differenly sensitive to time changes.

They vary at different rates, if the sample of the n individuals is taken at time t_2 instead of t_1 .

It is to be expected that the tree changes more quickly around the leaves and more slowly around the root. But what about some other, more global characteristics (of potential biological interest)?



total length total external length



n = 50

Here we focus on $1 \le \alpha \le 2$, between Bolthausen-Sznitman and Kingman case.

For the *n*-coalescent let at time $-\infty < t < \infty$

 $\ell_n(t) := total external length$

Theorem: (K., Schweinsberg, Wakolbinger, EJP 2014)

Let $1 < \alpha < 2$ and $c := (\alpha - 1)\Gamma(\alpha)/(2 - \alpha)$. Then

$$\left(\frac{\ell_n(n^{1-\alpha}t) - cn^{2-\alpha}}{n^{\frac{1}{\alpha}+1-\alpha}}\right)_{t \in \mathbb{R}} \xrightarrow{f.d.d.} Lévy-driven MA$$

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$$1 < \alpha < \frac{1}{2}(1+\sqrt{5}) \text{ and } c' = c/(2-\alpha), \text{ then}$$

$$\begin{pmatrix} \frac{\mathcal{L}_n(n^{1-\alpha}t) - c'n^{2-\alpha}}{n^{\frac{1}{\alpha}+1-\alpha}} \end{pmatrix}_{t \in \mathbb{R}} \xrightarrow{f.d.d.} \quad \text{other Lévy-driven MA}$$

(For $\alpha = 1$ see Schweinsberg, 2011)

If

In entire contrast:

Theorem: (Pfaffelhuber, Wakolbinger, Weisshaupt, PTRF 2011)

For the evolving Kingman n-coalescent in Skorohod space

 $(\mathcal{L}_n(t) - 2\log n)_{t \in \mathbb{R}} \stackrel{d}{\rightarrow} (\text{pure}) \text{ jump process }.$

In entire contrast:

Theorem: (Pfaffelhuber, Wakolbinger, Weisshaupt 2011)

For the evolving Kingman *n*-coalescent in Skorohod space $\begin{pmatrix} \mathcal{L}_n(t) - 2\log n \end{pmatrix}_{t \in \mathbb{R}} \stackrel{d}{\to} \quad \text{(pure) jump process }.$

Theorem: (Dahmer, K. 2014)

For the evolving Kingman n-coalescent

 $\left(\sqrt{\frac{n}{4\log n}} \left(\ell_n(\frac{t}{n}) - 2\right)\right)_{t \in \mathbb{R}} \stackrel{f.d.d.}{\longrightarrow} \text{ cont. gaussian process },$ with covariance function $c(s,t) = (1 + |t-s|)^{-2}$.

Note the different time scales:

- the evolutionary scale t

(each pair of lines involved at rate 1 in a coalescence)

- the generation scale $\frac{t}{n}$ (each individuum involved at rate 1) Note the different time scales:

- the *evolutionary* scale t(each pair of lines involved at rate 1 in a coalescence)
- the generation scale $\frac{t}{n}$ (each individuum involved at rate 1)

The scale $n^{1-\alpha}t$ for the Beta $(\alpha, 2-\alpha)$ -*n*-coalescent is generation scale!

The sources and order of noise



order $O\left(n^{\frac{1}{\alpha}+1-\alpha}\right)$ source: 'topology' of the tree affects \mathcal{L}_n and ℓ_n

order O(1)source: waiting times affects only \mathcal{L}_n The evolution of the external length in Kingman's coalescent:



The evolution of the external length in Kingman's coalescent:



 $Cov(\ell_t, \ell_{t+h}) = (1 + |h|)^{-2} =$

probability that in a critical branching process there is exactly 1 individual after time \boldsymbol{h}

Let for $r \geq 1$

 $\mathcal{L}_n^r = \text{total length of order } r$

 $\mathcal{L}_n^1 = \ell_n$ is the total external length.

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Theorem. (Iulia Dahmer, K., AAP 2015)

For $s \in \mathbb{N}$

$$\sqrt{\frac{n}{4\log n}} \left(\mathcal{L}_n^1 - \mu_1, \dots, \mathcal{L}_n^s - \mu_s \right) \quad \stackrel{d}{\to} \quad \mathcal{N}(0, Id_s)$$

as $n \to \infty$, with

$$\mu_r = E(\mathcal{L}_n^r) = \frac{2}{r} \; .$$

1000 realisations of $(\mathcal{L}_n^1, \mathcal{L}_n^2)$ with n = 100:



Branch numbers V_2, \ldots, V_n and W_2, \ldots, W_n .



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The case s = 1:

$$\mathcal{L}_n^1 = \sum_{i=2}^n V_i (T_{i-1} - T_i)$$
$$= \sum_{k=1}^{n-1} T_k (V_{k+1} - V_k) + T_1 V_2$$
$$\approx \sum_{k=1}^{n-1} \frac{2}{k} \Delta V_k$$

 ΔV_k is easy to analyse for k close to n. However:

The big fluctuations arise at k close to 1.

The key:

For the (total) internal numbers $U_1 = 1 - V_1, \dots, U_n = n - V_n$ we have reversibility:

Theorem: (S. Janson, K. 2011)
$$(U_1, \dots, U_{n-1}) \stackrel{d}{=} (U_{n-1}, \dots, U_1)$$
.

Theorem: (S. Janson, K. 2011)

$$\sqrt{rac{n}{4\log n}}(\ell_n-2) \ extstyle \mathcal{N}(0,1) \ .$$

The representation of the (total) internal numbers U_1, \ldots, U_n as diminishing urn:

- Take urn with *blue* balls, altogether n balls.
- Remove them stepwise:
 Successively remove a random pair of balls and replace it by one *orange* ball.
- If i balls are left,
 - let U_i the number of orange balls among them and V_i the number of blue balls.

The case $s \geq 2$.

Recall

Note:

 V_n, \ldots, V_2 external branch numbers W_n, \ldots, W_2 internal order 2 branch numbers

 $V_n, V_{n-1}, \ldots, V_2$ is a *Markov chain* (inhomogeneous in time). $(V_n, W_n), (V_{n-1}, W_{n-1}), \cdots, (V_2, W_2)$ is a Markov chain, or W_n, \ldots, W_2 is a Markov chain, given the *random environment* V_n, \ldots, V_2 . The transition probabilities:

$$P_{v,w}^{k}(v',w') = \mathbf{P}(V_{k-1} = v', W_{k-1} = w' \mid V_{k} = v, W_{k} = w)$$

$$P_{v,w}^k(v,w) = \frac{\binom{k-v-w}{2}}{\binom{k}{2}} \qquad P_{v,w}^k(v-1,w-1) = \frac{vw}{\binom{k}{2}}$$

$$P_{v,w}^{k}(v-1,w) = \frac{v(k-v-w)}{\binom{k}{2}} \qquad P_{v,w}^{k}(v,w-1) = \frac{w(k-v-w)}{\binom{k}{2}}$$

$$P_{v,w}^{k}(v-2,w+1) = \frac{\binom{v}{2}}{\binom{k}{2}} \qquad P_{v,w}^{k}(v,w-2) = \frac{\binom{w}{2}}{\binom{k}{2}}$$

The transition probabilities:

For k close to 1:

$$P_{v,w}^{k}(v,w) = 1 - 2\frac{v+w}{k} + o(\frac{v+w}{k}) \qquad P_{v,w}^{k}(v-1,w-1) = o(\frac{v+w}{k})$$
$$P_{v,w}^{k}(v-1,w) = \frac{2v}{k} + o(\frac{v+w}{k}) \qquad P_{v,w}^{k}(v,w-1) = \frac{2w}{k} + o(\frac{v+w}{k})$$
$$P_{v,w}^{k}(v-2,w+1) = o(\frac{v+w}{k}) \qquad P_{v,w}^{k}(v,w-2) = o(\frac{v+w}{k})$$

Idea of proof:

Reversing time is no longer practical for $s \geq 2$.

We couple the Markov chain

 $(V_n, W_n), \ldots, (V_2, W_2)$

with two independent urns, i.e. with

 $(V_n, \tilde{V}_n), \ldots, (V_2, \tilde{V}_2)$,

where $(\tilde{V}_n, \ldots, \tilde{V}_2)$ is an independent copy of (V_n, \ldots, V_2) .

Now the urns can be reversed.