

Scaling limits of multi-type Markov branching trees

Robin Stephenson
University of Oxford

Joint work with Bénédicte Haas.

Based on

- *Scaling limits of k -ary growing trees*. AIHP, 2015.
- *Bivariate Markov chains converging to Lamperti transform Markov Additive Processes*. SPA, 2018.
- *On the exponential functional of Markov Additive Processes, and applications to multi-type self-similar fragmentation processes and trees*. To appear in ALEA.
- *Scaling limits of multi-type Markov branching trees*. In preparation.

Scaling limits of k -ary growing trees

Construction

Fix an integer $k \geq 2$. We define a sequence $(T_n(k), n \geq 0)$ of random k -ary trees by the following recursion:

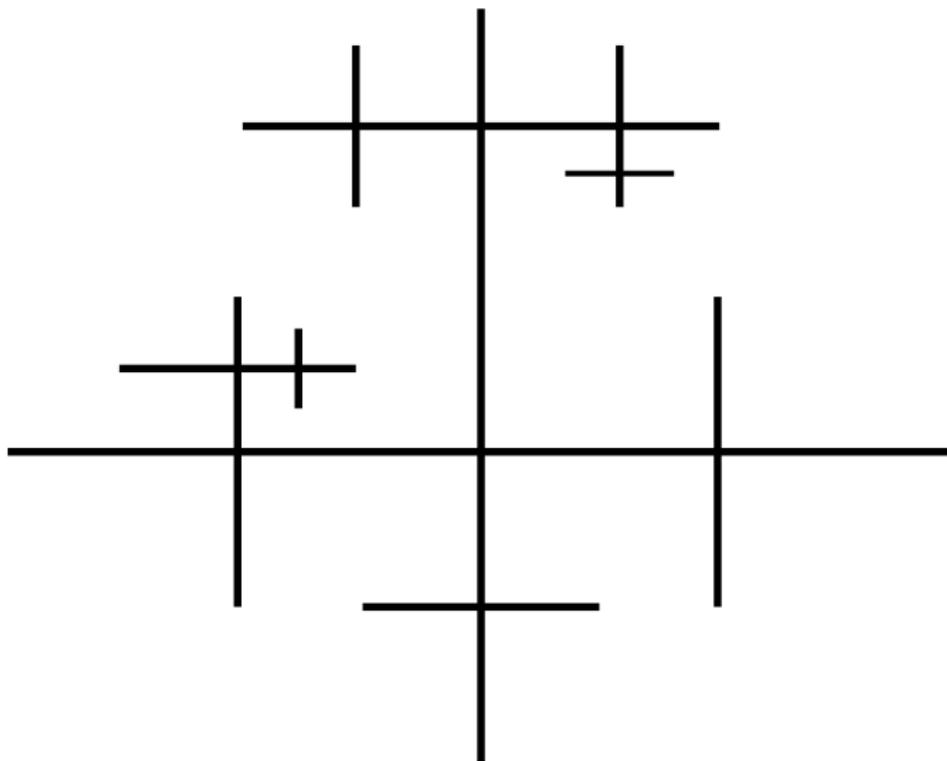
- $T_0(k)$ is the tree with a single edge and two vertices.

Construction

Fix an integer $k \geq 2$. We define a sequence $(T_n(k), n \geq 0)$ of random k -ary trees by the following recursion:

- $T_0(k)$ is the tree with a single edge and two vertices.
- given $T_n(k)$, to make $T_{n+1}(k)$, choose uniformly at random one of its edges, add a new vertex in the middle, thus splitting this edge in two, and then add $k - 1$ new edges starting from the new vertex.

After a few steps: $T_{10}(3)$



A few observations

- $T_n(k)$ has n internal nodes, $kn + 1$ edges and $(k - 1)n + 1$ leaves.

A few observations

- $T_n(k)$ has n internal nodes, $kn + 1$ edges and $(k - 1)n + 1$ leaves.
- $k = 2$: the algorithm constructs uniform binary trees (Rémy, 1985). It is then well-known (Aldous, 1991, 1993) that, when rescaled by \sqrt{n} , the tree $T_n(2)$ converges in distribution to a scalar multiple of Aldous' Brownian continuum random tree.

Scaling limit

Theorem (Haas-S.,2015)

We have the following convergence as n tends to infinity

$$\frac{1}{n^{1/k}} T_n(k) \xrightarrow{\mathbb{P}} \mathcal{T}_k.$$

This is a GHP convergence in probability to the measured continuum tree \mathcal{T}_k .

Scaling limit

Theorem (Haas-S.,2015)

We have the following convergence as n tends to infinity

$$\frac{1}{n^{1/k}} T_n(k) \xrightarrow{\mathbb{P}} \mathcal{T}_k.$$

This is a GHP convergence in probability to the measured continuum tree \mathcal{T}_k .

(measure on $T_n(k)$ = uniform measure on the leaves)

k-ary trees

○○○○○●○○○○○

MT MB trees

○○○○

MT fragmentation trees

○○○

Scaling limits

○○○○○○○○○○

Branching structure

Branching structure

This sequence features a type of branching which we call the *Markov branching property*.

Branching structure

This sequence features a type of branching which we call the *Markov branching property*.

First, root the trees at one of the original vertices of $T_0(k)$.

Branching structure

This sequence features a type of branching which we call the *Markov branching property*.

First, root the trees at one of the original vertices of $T_0(k)$.

Let for $n \geq 1$:

- T_n^1, \dots, T_n^k be the k subtrees rooted at the first node of $T_n(k)$.
- X_n^1, \dots, X_n^k be their number of internal nodes. (sorted nonincreasingly)

Branching structure

This sequence features a type of branching which we call the *Markov branching property*.

First, root the trees at one of the original vertices of $T_0(k)$.

Let for $n \geq 1$:

- T_n^1, \dots, T_n^k be the k subtrees rooted at the first node of $T_n(k)$.
- X_n^1, \dots, X_n^k be their number of internal nodes. (sorted nonincreasingly)

Then, conditionally on X_n^1, \dots, X_n^k ,

Branching structure

This sequence features a type of branching which we call the *Markov branching property*.

First, root the trees at one of the original vertices of $T_0(k)$.

Let for $n \geq 1$:

- T_n^1, \dots, T_n^k be the k subtrees rooted at the first node of $T_n(k)$.
- X_n^1, \dots, X_n^k be their number of internal nodes. (sorted nonincreasingly)

Then, conditionally on X_n^1, \dots, X_n^k ,

- T_n^1, \dots, T_n^k are independent.

Branching structure

This sequence features a type of branching which we call the *Markov branching property*.

First, root the trees at one of the original vertices of $T_0(k)$.

Let for $n \geq 1$:

- T_n^1, \dots, T_n^k be the k subtrees rooted at the first node of $T_n(k)$.
- X_n^1, \dots, X_n^k be their number of internal nodes. (sorted nonincreasingly)

Then, conditionally on X_n^1, \dots, X_n^k ,

- T_n^1, \dots, T_n^k are independent.
- For all i , T_n^i has the same distribution as $T_{X_n^i}(k)$.

Proof of Markov Branching structure

Proof by induction on n . The base case $n = 1$ is immediate as everything is deterministic.

Proof of Markov Branching structure

Proof by induction on n . The base case $n = 1$ is immediate as everything is deterministic.

Induction step: let e be the selected edge of $T_{n-1}(k)$ by the algorithm.

- If $e \in T_{n-1}^i$ for some i then apply the induction hypothesis at rank $n - 1$ and take a step of the algorithm in T_{n-1}^i .

Proof of Markov Branching structure

Proof by induction on n . The base case $n = 1$ is immediate as everything is deterministic.

Induction step: let e be the selected edge of $T_{n-1}(k)$ by the algorithm.

- If $e \in T_{n-1}^i$ for some i then apply the induction hypothesis at rank $n - 1$ and take a step of the algorithm in T_{n-1}^i .
- If e is the "first" edge of $T_{n-1}(k)$ then $(T_n^1, \dots, T_n^k) = (T_{n-1}(k), T_0(k), \dots, T_0(k))$. They are independent since $T_0(k)$ is deterministic.

Proof of Markov Branching structure

Proof by induction on n . The base case $n = 1$ is immediate as everything is deterministic.

Induction step: let e be the selected edge of $T_{n-1}(k)$ by the algorithm.

- If $e \in T_{n-1}^i$ for some i then apply the induction hypothesis at rank $n - 1$ and take a step of the algorithm in T_{n-1}^i .
- If e is the "first" edge of $T_{n-1}(k)$ then $(T_n^1, \dots, T_n^k) = (T_{n-1}(k), T_0(k), \dots, T_0(k))$. They are independent since $T_0(k)$ is deterministic.

This essentially ends the proof.

Scaling limit

The distribution of $(T_n(k), n \geq 0)$ is then completely determined by the distribution of the sequences (X_n^1, \dots, X_n^k) .

Scaling limit

The distribution of $(T_n(k), n \geq 0)$ is then completely determined by the distribution of the sequences (X_n^1, \dots, X_n^k) . In fact, the scaling limit in distribution is also encoded in limiting properties of (X_n^1, \dots, X_n^k) .

Scaling limit

The distribution of $(T_n(k), n \geq 0)$ is then completely determined by the distribution of the sequences (X_n^1, \dots, X_n^k) . In fact, the scaling limit in distribution is also encoded in limiting properties of (X_n^1, \dots, X_n^k) .

Specifically, letting $Y_n^i = \frac{X_n^i}{n}$, we have

$$n^{1/k} \mathbb{E}[(1 - Y_n^1) f(Y_n^1, \dots, Y_n^k)] \rightarrow \int_{\mathcal{S}_k} (1 - x_1) f(x_1, \dots, x_k) d\nu_k(\mathbf{x})$$

where \mathcal{S}_k is the $k - 1$ -dimensional simplex and

Scaling limit

The distribution of $(T_n(k), n \geq 0)$ is then completely determined by the distribution of the sequences (X_n^1, \dots, X_n^k) . In fact, the scaling limit in distribution is also encoded in limiting properties of (X_n^1, \dots, X_n^k) .

Specifically, letting $Y_n^i = \frac{X_n^i}{n}$, we have

$$n^{1/k} \mathbb{E}[(1 - Y_n^1) f(Y_n^1, \dots, Y_n^k)] \rightarrow \int_{\mathcal{S}_k} (1 - x_1) f(x_1, \dots, x_k) d\nu_k(\mathbf{x})$$

where \mathcal{S}_k is the $k - 1$ -dimensional simplex and

$$d\nu_k(\mathbf{x}) = \frac{(k-1)!}{k(\Gamma(\frac{1}{k}))^{(k-1)}} \prod_{i=1}^k x_i^{1/k-1} \left(\sum_{i=1}^k \frac{1}{1-s_i} \right) \mathbf{1}_{\{x_1 \geq x_2 \geq \dots \geq x_k\}} d\mathbf{x}$$

Scaling limit

By a theorem of Haas and Miermont ('12), this implies the convergence in distribution of $n^{-1/k}T_n(k)$ to \mathcal{T}_k , where \mathcal{T}_k is the *self-similar fragmentation tree with self-similarity index $-1/k$ and dislocation measure ν_k* .

Scaling limit

By a theorem of Haas and Miermont ('12), this implies the convergence in distribution of $n^{-1/k}T_n(k)$ to \mathcal{T}_k , where \mathcal{T}_k is the *self-similar fragmentation tree with self-similarity index $-1/k$ and dislocation measure ν_k* .

Informally, \mathcal{T}_k is the family tree of a branching population model where:

- individuals are characterised by their mass $x \in (0, 1]$
- for $\mathbf{s} \in \mathcal{S}_k$ and $x > 0$, an individual with mass x splits into k individuals with masses xs_1, \dots, xs_k at rate $x^{-1/k}d\nu_k(\mathbf{s})$.

Generalising the recursive construction

How can we make the *k*-ary construction more general?

- make *k* random.

Generalising the recursive construction

How can we make the k -ary construction more general?

- make k random. Can say some things, but not explicit and difficult.

Generalising the recursive construction

How can we make the k -ary construction more general?

- make k random. Can say some things, but not explicit and difficult.
- instead of adding a “star” at each step, add a more complex figure.

Generalising the recursive construction

How can we make the k -ary construction more general?

- make k random. Can say some things, but not explicit and difficult.

- instead of adding a “star” at each step, add a more complex figure. This is interesting!

Generalised growth model

Let τ be a fixed rooted tree. Consider the following algorithm for building random trees $(T_n(\tau), n \geq 0)$:

Generalised growth model

Let τ be a fixed rooted tree. Consider the following algorithm for building random trees $(T_n(\tau), n \geq 0)$:

- T_0 is the tree with a single edge and two vertices, a root and a leaf.

Generalised growth model

Let τ be a fixed rooted tree. Consider the following algorithm for building random trees $(T_n(\tau), n \geq 0)$:

- T_0 is the tree with a single edge and two vertices, a root and a leaf.
- given $T_n(\tau)$, to make $T_{n+1}(\tau)$, choose uniformly at random one of its edges, add a new vertex in the middle, thus splitting this edge in two, and then graft a copy of τ at the new vertex.

Generalised growth model

Let τ be a fixed rooted tree. Consider the following algorithm for building random trees $(T_n(\tau), n \geq 0)$:

- T_0 is the tree with a single edge and two vertices, a root and a leaf.
- given $T_n(\tau)$, to make $T_{n+1}(\tau)$, choose uniformly at random one of its edges, add a new vertex in the middle, thus splitting this edge in two, and then graft a copy of τ at the new vertex.

If τ is a star with $k - 1$ vertices, we get the previous construction.

Problem... ?

This sequence $(T_n, n \in \mathbb{N})$ is not really Markov branching in the previous sense. Some vertices seem to have different roles from others.

Problem... ?

This sequence $(T_n, n \in \mathbb{N})$ is not really Markov branching in the previous sense. Some vertices seem to have different roles from others.

But it is Markov branching if we take more information into account and enter the *multi-type* world.

Multi-type Markov branching trees

Definition

Definition

Consider a discrete branching population model where:

- Individuals are characterised by their *size* $n \in \mathbb{N}$, and their *type* $i \in \{1, \dots, K\}$.
- The sum of the sizes of the offspring of one individual with size $n \in \mathbb{N}$ is at most n .

Definition

Consider a discrete branching population model where:

- Individuals are characterised by their *size* $n \in \mathbb{N}$, and their *type* $i \in \{1, \dots, K\}$.
- The sum of the sizes of the offspring of one individual with size $n \in \mathbb{N}$ is at most n .

This model needs a set of *offspring distributions* which give, for all $n \in \mathbb{N}$ and $i \in \{1, \dots, K\}$, give the distribution of the sizes and types of the children of a (n, i) individual.

Example I: The growth model $T_n(\tau)$

Example I: The growth model $T_n(\tau)$

- Let K be the number of non-root vertices of τ , and write these vertices as $(v_i, 1 \leq i \leq K)$.

Example I: The growth model $T_n(\tau)$

- Let K be the number of non-root vertices of τ , and write these vertices as $(v_i, 1 \leq i \leq K)$.
- For all i , let T_0^i be the subtree of τ rooted at v_i , with an extra edge behind v_i .

Example I: The growth model $T_n(\tau)$

- Let K be the number of non-root vertices of τ , and write these vertices as $(v_i, 1 \leq i \leq K)$.
- For all i , let T_0^i be the subtree of τ rooted at v_i , with an extra edge behind v_i .
- $T_{n+1}^{(i)}$ is obtained by taking a step of the algorithm in $T_n^{(i)}$.

Example I: The growth model $T_n(\tau)$

- Let K be the number of non-root vertices of τ , and write these vertices as $(v_i, 1 \leq i \leq K)$.
- For all i , let T_0^i be the subtree of τ rooted at v_i , with an extra edge behind v_i .
- $T_{n+1}^{(i)}$ is obtained by taking a step of the algorithm in $T_n^{(i)}$.
- When an edge $u \rightarrow v$ is broken in two, the type of the new vertex is v , and we mark it as "red".
- The size of any vertex is its number of red descendants, including itself.

Example I: The growth model $T_n(\tau)$

- Let K be the number of non-root vertices of τ , and write these vertices as $(v_i, 1 \leq i \leq K)$.
- For all i , let T_0^i be the subtree of τ rooted at v_i , with an extra edge behind v_i .
- $T_{n+1}^{(i)}$ is obtained by taking a step of the algorithm in $T_n^{(i)}$.
- When an edge $u \rightarrow v$ is broken in two, the type of the new vertex is v , and we mark it as "red".
- The size of any vertex is its number of red descendants, including itself.

Under this notation, the sequence $T_n^{(i)}$ is (planted) Markov branching.

Example II: Conditioned multi-type Galton-Watson trees

Consider a K -type Galton-Watson population. We will condition it on its number of individuals with a specific type, say 1.

- Let $T_n^{(i)}$ be the family tree when we start with an ancestor of type i , and conditioned on having n vertices of type 1.

Example II: Conditioned multi-type Galton-Watson trees

Consider a K -type Galton-Watson population. We will condition it on its number of individuals with a specific type, say 1.

- Let $T_n^{(i)}$ be the family tree when we start with an ancestor of type i , and conditioned on having n vertices of type 1.
- Give to each vertex a size equal to its number of descendants of type 1 (including itself).

Example II: Conditioned multi-type Galton-Watson trees

Consider a K -type Galton-Watson population. We will condition it on its number of individuals with a specific type, say 1.

- Let $T_n^{(i)}$ be the family tree when we start with an ancestor of type i , and conditioned on having n vertices of type 1.
- Give to each vertex a size equal to its number of descendants of type 1 (including itself).

This then forms a Markov Branching sequence.

The scaling limit candidates: multi-type fragmentation trees

Definition

The limit candidates are the *multi-type self-similar fragmentation trees*.

Definition

The limit candidates are the *multi-type self-similar fragmentation trees*.

A multi-type fragmentation tree is the family tree of a branching population model where individuals are characterised by

- their mass $x \in (0, 1]$.
- their type $i \in \{1, \dots, K\}$.

Definition

The limit candidates are the *multi-type self-similar fragmentation trees*.

A multi-type fragmentation tree is the family tree of a branching population model where individuals are characterised by

- their mass $x \in (0, 1]$.
- their type $i \in \{1, \dots, K\}$.

An individual with mass x and type i splits into a set of individuals with masses $(xs_n, n \in \mathbb{N})$ and types $(i_n, n \in \mathbb{N})$ at rate $x^\alpha d\nu_i(\mathbf{s}, \mathbf{i})$.

Definition

The limit candidates are the *multi-type self-similar fragmentation trees*.

A multi-type fragmentation tree is the family tree of a branching population model where individuals are characterised by

- their mass $x \in (0, 1]$.
- their type $i \in \{1, \dots, K\}$.

An individual with mass x and type i splits into a set of individuals with masses $(xs_n, n \in \mathbb{N})$ and types $(i_n, n \in \mathbb{N})$ at rate $x^\alpha d\nu_i(\mathbf{s}, \mathbf{i})$.

The distribution of such a process is characterised by the *index of self-similarity* $\alpha < 0$ and the *dislocation measures* $\nu_i, i \in \{1, \dots, K\}$.

Dislocation measures

Dislocation measures

The dislocation measures are measures on the simplex-like space $\overline{\mathcal{S}}^\downarrow$ which is the space of sequences $(\mathbf{s}, \mathbf{i}) = ((s_n, i_n), n \in \mathbb{N})$ such that

- $\sum_n s_n = 1$ and for all n , $s_n \geq 0$
- for all n , i_n is a type given to the n -th fragment
- the pairs are sorted in lexicographically decreasing order.

Dislocation measures

The dislocation measures are measures on the simplex-like space $\overline{\mathcal{S}}^\downarrow$ which is the space of sequences $(\mathbf{s}, \mathbf{i}) = ((s_n, i_n), n \in \mathbb{N})$ such that

- $\sum_n s_n = 1$ and for all n , $s_n \geq 0$
- for all n , i_n is a type given to the n -th fragment
- the pairs are sorted in lexicographically decreasing order.

The measures are allowed to have infinite total mass, however they must satisfy

$$\int_{\mathcal{S}} (1 - s_1 \mathbf{1}_{i_1=i}) d\nu_i(\mathbf{s}, \mathbf{i}) < \infty.$$

Dislocation measures

The dislocation measures are measures on the simplex-like space $\overline{\mathcal{S}}^\downarrow$ which is the space of sequences $(\mathbf{s}, \mathbf{i}) = ((s_n, i_n), n \in \mathbb{N})$ such that

- $\sum_n s_n = 1$ and for all n , $s_n \geq 0$
- for all n , i_n is a type given to the n -th fragment
- the pairs are sorted in lexicographically decreasing order.

The measures are allowed to have infinite total mass, however they must satisfy

$$\int_{\mathcal{S}} (1 - s_1 \mathbf{1}_{i_1=i}) d\nu_i(\mathbf{s}, \mathbf{i}) < \infty.$$

We call $\mathcal{T}_{\alpha, \nu}^{(i)}$ the tree with self-similarity index α and set of dislocation measures (ν_j) , when starting with an ancestor with characteristics $(1, i)$.

Our scaling limit results

The general principle

Let $(T_n^{(i)})$ be a K -type family of Markov branching trees,
 $(X_n^{(i)}, J_n^{(i)}) =$ size and type of the largest individual in the first
 generation of $T_n^{(i)}$.

The general principle

Let $(T_n^{(i)})$ be a K -type family of Markov branching trees,
 $(X_n^{(i)}, J_n^{(i)})$ = size and type of the largest individual in the first
 generation of $T_n^{(i)}$.

Assume that, for some $\gamma > 0$ and $\beta \geq 0$,

$$\mathbb{P}[X_n^{(i)} \leq (1 - \varepsilon)n] \underset{n \rightarrow \infty}{\sim} c_\varepsilon^{(i)} n^{-\gamma},$$

The general principle

Let $(T_n^{(i)})$ be a K -type family of Markov branching trees,
 $(X_n^{(i)}, J_n^{(i)})$ = size and type of the largest individual in the first
 generation of $T_n^{(i)}$.

Assume that, for some $\gamma > 0$ and $\beta \geq 0$,

$$\mathbb{P}[X_n^{(i)} \leq (1 - \varepsilon)n] \underset{n \rightarrow \infty}{\sim} c_\varepsilon^{(i)} n^{-\gamma},$$

and

$$\forall j \neq i, \mathbb{P}[J_n^{(i)} = j] \underset{n \rightarrow \infty}{\sim} p_{i,j} n^{-\beta}.$$

The general principle

Let $(T_n^{(i)})$ be a K -type family of Markov branching trees,
 $(X_n^{(i)}, J_n^{(i)}) =$ size and type of the largest individual in the first
generation of $T_n^{(i)}$.

Assume that, for some $\gamma > 0$ and $\beta \geq 0$,

$$\mathbb{P}[X_n^{(i)} \leq (1 - \varepsilon)n] \underset{n \rightarrow \infty}{\sim} c_\varepsilon^{(i)} n^{-\gamma},$$

and

$$\forall j \neq i, \mathbb{P}[J_n^{(i)} = j] \underset{n \rightarrow \infty}{\sim} p_{i,j} n^{-\beta}.$$

Then

$$\frac{1}{n^\gamma} T_n^{(i)} \xrightarrow[n \rightarrow \infty]{(d)} \mathcal{T}^{(i)}$$

where $\mathcal{T}^{(i)}$ is a fragmentation tree with index of self-similarity $-\gamma$
and which is:

- K -type if $\beta = \gamma$
- monotype if $\beta < \gamma$.

Scaling limits I: to a K -type fragmentation tree

Theorem (Haas-S., 18+)

Let $(X_n^{(i)}(k), J_n^{(i)}(k))$ be the sizes and types of the first generation in $T_n^{(i)}$, sorted in decreasing lexicographical ordering. Let also

$$Y_n^{(i)}(k) = \frac{X_n^{(i)}(k)}{n}.$$

Scaling limits I: to a K -type fragmentation tree

Theorem (Haas-S.,18+)

Let $(X_n^{(i)}(k), J_n^{(i)}(k))$ be the sizes and types of the first generation in $T_n^{(i)}$, sorted in decreasing lexicographical ordering. Let also $Y_n^{(i)}(k) = \frac{X_n^{(i)}(k)}{n}$.

Assume that, for continuous f on $\overline{\mathcal{S}}^\downarrow$,

$$n^\gamma \mathbb{E} \left[(1 - Y_n^{(i)}(1) \mathbf{1}_{J_n^{(i)}(1)=i}) f(\mathbf{Y}_n^{(i)}, \mathbf{J}_n^{(i)}) \right] \\ \xrightarrow{n \rightarrow \infty} \int_{\mathcal{S}^\downarrow} (1 - s_1 \mathbf{1}_{i_1=i}) f(\mathbf{s}, \mathbf{i}) d\nu_i(\mathbf{s}, \mathbf{i}).$$

Scaling limits I: to a K -type fragmentation tree

Theorem (Haas-S.,18+)

Let $(X_n^{(i)}(k), J_n^{(i)}(k))$ be the sizes and types of the first generation in $T_n^{(i)}$, sorted in decreasing lexicographical ordering. Let also $Y_n^{(i)}(k) = \frac{X_n^{(i)}(k)}{n}$.

Assume that, for continuous f on \overline{S}^\downarrow ,

$$n^\gamma \mathbb{E} \left[(1 - Y_n^{(i)}(1) \mathbf{1}_{J_n^{(i)}(1)=i}) f(\mathbf{Y}_n^{(i)}, \mathbf{J}_n^{(i)}) \right] \\ \xrightarrow{n \rightarrow \infty} \int_{\overline{S}^\downarrow} (1 - s_1 \mathbf{1}_{i_1=i}) f(\mathbf{s}, \mathbf{i}) d\nu_i(\mathbf{s}, \mathbf{i}).$$

Then

$$\frac{1}{n^\gamma} T_n^{(i)} \xrightarrow[n \rightarrow \infty]{(d)} \mathcal{T}_{-\gamma, \nu}^{(i)}.$$

Application I: the growth model

The convergence of the k -ary model $T_n(k)$ can be generalised to that of $T_n(\tau)$.

Application I: the growth model

The convergence of the k -ary model $T_n(k)$ can be generalised to that of $T_n(\tau)$.

Theorem

Let $k = 1 + \#\tau$, then

$$\frac{1}{n^{1/k}} T_n(\tau) \xrightarrow[n \rightarrow \infty]{(d)} \mathcal{T}_\tau$$

where \mathcal{T}_τ is a multi-type fragmentation tree with index of self-similarity $-1/k$.

Application I: the growth model

The convergence of the k -ary model $T_n(k)$ can be generalised to that of $T_n(\tau)$.

Theorem

Let $k = 1 + \#\tau$, then

$$\frac{1}{n^{1/k}} T_n(\tau) \xrightarrow[n \rightarrow \infty]{(d)} \mathcal{T}_\tau$$

where \mathcal{T}_τ is a multi-type fragmentation tree with index of self-similarity $-1/k$.

The dislocation measures are explicit, and involve modifications of Dirichlet laws again.

Application I: the growth model

The convergence of the k -ary model $T_n(k)$ can be generalised to that of $T_n(\tau)$.

Theorem

Let $k = 1 + \#\tau$, then

$$\frac{1}{n^{1/k}} T_n(\tau) \xrightarrow[n \rightarrow \infty]{(d)} \mathcal{T}_\tau$$

where \mathcal{T}_τ is a multi-type fragmentation tree with index of self-similarity $-1/k$.

The dislocation measures are explicit, and involve modifications of Dirichlet laws again.

Actually the convergence is a.s. - see upcoming work by Sénizergues.

Scaling limits II: the mixing case

Scaling limits II: the mixing case

Theorem (Haas-S., 18+)

Assume this time that, if we ignore the types,

$$n^\gamma \mathbb{E} \left[(1 - Y_n^{(i)}(1)) f(\mathbf{Y}_n^{(i)}) \right] \xrightarrow{n \rightarrow \infty} \int_{\mathcal{S}^\downarrow} (1 - s_1) f(\mathbf{s}) d\nu_i(\mathbf{s}).$$

Scaling limits II: the mixing case

Theorem (Haas-S.,18+)

Assume this time that, if we ignore the types,

$$n^\gamma \mathbb{E} \left[(1 - Y_n^{(i)}(1)) f(\mathbf{Y}_n^{(i)}) \right] \xrightarrow{n \rightarrow \infty} \int_{\mathcal{S}^\downarrow} (1 - s_1) f(\mathbf{s}) d\nu_i(\mathbf{s}).$$

and that, for $j \neq i$,

$$n^\beta P(J_n^{(i)}(1) = j) \xrightarrow{n \rightarrow \infty} q_{i,j}$$

where $Q = (q_{i,j})$ is the transition rate matrix of an irreducible continuous time Markov chain.

Scaling limits II: the mixing case

Theorem (Haas-S., 18+)

Assume this time that, if we ignore the types,

$$n^\gamma \mathbb{E} \left[(1 - Y_n^{(i)}(1)) f(\mathbf{Y}_n^{(i)}) \right] \xrightarrow{n \rightarrow \infty} \int_{\mathcal{S}^\downarrow} (1 - s_1) f(\mathbf{s}) d\nu_i(\mathbf{s}).$$

and that, for $j \neq i$,

$$n^\beta P(J_n^{(i)}(1) = j) \xrightarrow{n \rightarrow \infty} q_{i,j}$$

where $Q = (q_{i,j})$ is the transition rate matrix of an irreducible continuous time Markov chain. Then

$$\frac{1}{n^\gamma} T_n^{(i)} \xrightarrow[n \rightarrow \infty]{(d)} \mathcal{T}_{-\gamma, \nu}.$$

where $\mathcal{T}_{-\gamma, \nu}$ is a monotype fragmentation tree.

Scaling limits II: the mixing case

The dislocation measure ν is given by a mixing of the ν_i :

$$\nu = \sum_i \chi_i \nu_i$$

where χ is the invariant measure of the matrix Q .

Application II: Galton-Watson trees

Let $(\xi_i, i \in \{1, \dots, K\})$ be the offspring distributions of a critical K -type Galton-Watson process *which has finite second moments*.

Application II: Galton-Watson trees

Let $(\xi_i, i \in \{1, \dots, K\})$ be the offspring distributions of a critical K -type Galton-Watson process *which has finite second moments*.

Let $T_n^{(i)}$ be a Galton-Watson tree with offspring distributions (ξ_j) , with root of type i , and conditioned to have n vertices of type 1.

Application II: Galton-Watson trees

Let $(\xi_i, i \in \{1, \dots, K\})$ be the offspring distributions of a critical K -type Galton-Watson process *which has finite second moments*.

Let $T_n^{(i)}$ be a Galton-Watson tree with offspring distributions (ξ_j) , with root of type i , and conditioned to have n vertices of type 1.

Theorem (Haas-S., 2018+)

There exists $C > 0$ (which does not depend on i) such that

$$\frac{1}{\sqrt{n}} T_n^{(i)} \xrightarrow{(d)} C \mathcal{T}_{\text{Br}}$$

where \mathcal{T}_{Br} is the Brownian continuum random tree.

Application II: Galton-Watson trees

Let $(\xi_i, i \in \{1, \dots, K\})$ be the offspring distributions of a critical K -type Galton-Watson process *which has finite second moments*.

Let $T_n^{(i)}$ be a Galton-Watson tree with offspring distributions (ξ_j) , with root of type i , and conditioned to have n vertices of type 1.

Theorem (Haas-S., 2018+)

There exists $C > 0$ (which does not depend on i) such that

$$\frac{1}{\sqrt{n}} T_n^{(i)} \xrightarrow{(d)} C \mathcal{T}_{\text{Br}}$$

where \mathcal{T}_{Br} is the Brownian continuum random tree.

This is an improvement of a result of Miermont ('08), which gives the same convergence under exponential moments.

Thank you!

Growth model: the limiting dislocation measures

Let

- $N_i =$ number of descendants of v_i in τ

Growth model: the limiting dislocation measures

Let

- $N_i =$ number of descendants of v_i in τ
- $((N_{i,1}, j_{i,1}), \dots, (N_{i,p_i}, j_{i,p_i})) =$ number of descendants and types of the children of v_i .

Growth model: the limiting dislocation measures

Let

- $N_i =$ number of descendants of v_i in τ
- $((N_{i,1}, j_{i,1}), \dots, (N_{i,p_i}, j_{i,p_i})) =$ number of descendants and types of the children of v_i .
- $((N_1, j_1), \dots, (N_p, j_p)) =$ same for the children of the root of τ .

Growth model: the limiting dislocation measures

Let

- N_i = number of descendants of v_i in τ
- $((N_{i,1}, j_{i,1}), \dots, (N_{i,p_i}, j_{i,p_i}))$ = number of descendants and types of the children of v_i .
- $((N_1, j_1), \dots, (N_p, j_p))$ = same for the children of the root of τ .
- S_1 follow $\text{Dir}(\frac{N_{i,1}}{k}, \dots, \frac{N_{i,p_i}}{k})$ and $I_1 = (j_{i,1}, \dots, j_{i,p_i})$
- S_2 follow $\text{Dir}(\frac{N_i}{k}, \frac{N_1}{k}, \dots, \frac{N_p}{k})$ and $I_2 = (j_1, \dots, j_p)$

Growth model: the limiting dislocation measures

Let

- N_i = number of descendants of v_i in τ
- $((N_{i,1}, j_{i,1}), \dots, (N_{i,p_i}, j_{i,p_i}))$ = number of descendants and types of the children of v_i .
- $((N_1, j_1), \dots, (N_p, j_p))$ = same for the children of the root of τ .
- S_1 follow $\text{Dir}(\frac{N_{i,1}}{k}, \dots, \frac{N_{i,p_i}}{k})$ and $I_1 = (j_{i,1}, \dots, j_{i,p_i})$
- S_2 follow $\text{Dir}(\frac{N_i}{k}, \frac{N_1}{k}, \dots, \frac{N_p}{k})$ and $I_2 = (j_1, \dots, j_p)$
-

$$\int f(\mathbf{s}, \mathbf{i}) d\nu^{(i)} = \frac{\Gamma(\frac{N_i}{k})}{\Gamma(\frac{N_i-1}{k})} \mathbb{E}[f(S_1, I_1)] + \frac{\Gamma(\frac{N_i}{k})}{k\Gamma(\frac{N_i+k-1}{k})} \mathbb{E}\left[\frac{1}{1 - \max S_2} f(S_2, I_2)\right]$$

Growth model: the limiting dislocation measures

Let

- N_i = number of descendants of v_i in τ
- $((N_{i,1}, j_{i,1}), \dots, (N_{i,p_i}, j_{i,p_i}))$ = number of descendants and types of the children of v_i .
- $((N_1, j_1), \dots, (N_p, j_p))$ = same for the children of the root of τ .
- S_1 follow $\text{Dir}(\frac{N_{i,1}}{k}, \dots, \frac{N_{i,p_i}}{k})$ and $I_1 = (j_{i,1}, \dots, j_{i,p_i})$
- S_2 follow $\text{Dir}(\frac{N_i}{k}, \frac{N_1}{k}, \dots, \frac{N_p}{k})$ and $I_2 = (j_1, \dots, j_p)$
-

$$\int f(\mathbf{s}, \mathbf{i}) d\nu^{(i)} = \frac{\Gamma(\frac{N_i}{k})}{\Gamma(\frac{N_i-1}{k})} \mathbb{E}[f(S_1, I_1)] + \frac{\Gamma(\frac{N_i}{k})}{k\Gamma(\frac{N_i+k-1}{k})} \mathbb{E}\left[\frac{1}{1 - \max S_2} f(S_2, I_2)\right]$$

And take the push-forward of $\nu^{(i)}$ by reordering.

GW technical setup

Let $m_{i,j} = \sum_{\mathbf{z} \in (\mathbb{Z}_+)^K} \zeta^{(i)}(\mathbf{z}) z_j$ be the average number of children of type j among the progeny of an individual of type i . Let

$$M = (m_{i,j})$$

be the *mean matrix*, which we assume irreducible in the Perron-Frobenius sense, and has largest eigenvalue 1 (= criticality).

GW technical setup

Let $m_{i,j} = \sum_{\mathbf{z} \in (\mathbb{Z}_+)^K} \zeta^{(i)}(\mathbf{z}) z_j$ be the average number of children of type j among the progeny of an individual of type i . Let

$$M = (m_{i,j})$$

be the *mean matrix*, which we assume irreducible in the Perron-Frobenius sense, and has largest eigenvalue 1 (= criticality).

Let \mathbf{a} and \mathbf{b} be the left and right positive eigenvectors for the eigenvalue 1, normalised such that

$$\mathbf{a} \cdot \mathbf{1} = \mathbf{a} \cdot \mathbf{b} = 1$$

GW: the normalising constant

Define the following quantities:

$$Q_{j,k}^{(i)} = \sum_{\mathbf{z} \in (\mathbb{Z}_+)^K} \zeta^{(i)}(\mathbf{z}) z_j z_k, \quad i, j, k \in [K], j \neq k,$$

$$Q_{j,j}^{(i)} = \sum_{\mathbf{z} \in (\mathbb{Z}_+)^K} \zeta^{(i)}(\mathbf{z}) z_j (z_j - 1), \quad i, j \in [K],$$

$$\sigma^2 = \sum_{i,j,k} a_i b_j b_k Q_{j,k}^{(i)}.$$

GW: the normalising constant

Define the following quantities:

$$Q_{j,k}^{(i)} = \sum_{\mathbf{z} \in (\mathbb{Z}_+)^K} \zeta^{(i)}(\mathbf{z}) z_j z_k, \quad i, j, k \in [K], j \neq k,$$

$$Q_{j,j}^{(i)} = \sum_{\mathbf{z} \in (\mathbb{Z}_+)^K} \zeta^{(i)}(\mathbf{z}) z_j (z_j - 1), \quad i, j \in [K],$$

$$\sigma^2 = \sum_{i,j,k} a_i b_j b_k Q_{j,k}^{(i)}.$$

Then

$$\frac{1}{\sqrt{n}} T_n^{(i)} \xrightarrow{(d)} \frac{2}{\sigma \sqrt{a_1}} \mathcal{T}_{\text{Br}}$$