Open Problems

for the Bath-Beijing-Paris Branching Structures Meeting

14th - 18th May 2018

Some problems on branching random walks

Pascal Maillard

May 8, 2018

I collect here some problems which I find interesting. I hope that they qualify as sufficiently deep/interesting to others and that there are no obvious solutions or previous work on them which I don't know about.

1 From branching Brownian motion to branching random walk

Consider one-dimensional branching Brownian motion with negative drift $-\mu$ and killed at the origin. There is a critical drift μ_c, such that this system dies out almost surely if and only if $\mu \geq \mu_c$. In the recent years, some very fine results have been obtained when the drift μ is equal or just below the critical drift μ_c, see for example [3, 2, 4, 5, 6]. For example, in [3], the authors show that as $\mu \uparrow \mu_c$, and with carefully chosen initial conditions, the number of particles in the system converges, after a suitable normalization, to a certain limiting process called *Neveu's continuous-state branching process*. The analysis adapts to critical drift and allows for example to obtain precise estimates on the probability of survival until a time t [6].

Adapting these and other results to branching random walk seems like a tough and interesting problem. The major hurdle seems to be to obtain precise estimates on random walks conditioned to stay in an interval $[a, b]$ or, more generally, between two curves. A typical result in this direction is Mogul'skii's estimate [13], which gives the first order in the (exponential) decay of such a probability. It seems that more refined estimates are needed and no general theory seems to be available up to now. See for example [10] for explicit calculations for random walks with steps distributed like $E - 1$, where $E \sim Exp(1)$.

2 Branching Brownian motion with time-varying variance

Consider a variant of branching Brownian motion, where the diffusion constant or variance of the particle motion changes over time. More precisely, let $\sigma : [0, 1] \to \mathbb{R}_+$. Then consider the generalization of branching Brownian motion where the infinitesimal variance of the particle motion at time $t \in [0, T]$ is given by $\sigma^2(t/T)$. So formally, we are considering a family of branching processes indexed by T. This is a continuous version of Derrida's *generalized random energy model* and similar to Bovier-Kurkova's *CREM* [7, 8].

The behavior of this model depends very much on the form of the function σ. I won't go into details here but rather refer to [7, 12] for a description of the various phases. One should also check out recent papers by Bovier and Hartung.

This model has been well studied, but fine limit theorems are still lacking. For example, the convergence of the point process formed by extremal points is only known in particular examples. There are inherent difficulties. For example, consider the law of the maximum M_T

at time T. With O. Zeitouni [11], we have studied the case where σ is strictly decreasing (and smooth). We have shown that there exists explicit constants v and w, such that the family of random variables $(M_T - m_T)_{T \geq 0}$ is tight, where

$$m_T = vT - wT^{1/3} - \sigma(1) \ln T.$$

An obvious next step is to prove convergence in distribution. The major difficulty here is that unlike in the time-homogeneous case, extremal particles at time T will, with positive probability, be extremal at some random intermediate time between ϵT and $(1 - \epsilon)T$ (this is related to the *full replica symmetry breaking* of the model in spin glass jargon). However, I believe that this can be handled as in BBM with absorption [3, 6], namely by showing convergence of a suitable statistic to Neveu's CSBP. This approach would then also allow to show convergence of the *extremal process*. It would also provide a way of studying the genealogy of the maximal particles.

Another interesting question is large deviation behavior of the maximum, i.e., what is the probability that the maximum is a constant times larger than its typical value and what does the process look like conditioned on this event? For the time-homogeneous case, this has been treated long ago by Chauvin and Rouault [9]. It is possible that their techniques (martingale change of measures) can be adapted to the time-inhomogeneous case.

3 N-branching random walk with heavy tails

In [1], we studied branching random walk with jumps of regularly varying tails and with selection of the N right-most particles at every step, $N \gg 1$ a parameter. We provided a quite precise limit theorem for the speed of this system, relying on a coupling with a certain limiting process, called the *stairs process* in our work.

A natural question and possibility for future research is to investigate what happens in between the two scenarios of light-tailed displacement distributions (satisfying an exponential moment assumption) and the polynomial tails considered in the present article. This seems to be a delicate and interesting question. Even the heuristic picture is not clear. For example, it is not clear to us whether for all subexponential displacement distributions the advance of the cloud of particles arises from jumps of single particles as is the case for the regularly varying tails considered here. One would expect this behavior from the large deviation behavior of general random walks with subexponential displacement distributions, but the interaction between the particles might cause other effects.

This question is related to the genealogy of the model. In the regularly varying case, we believe (but have not shown) the genealogy to be described by the star-shaped coalescent (i.e. the coalescent where all particles coagulate to a single block). Does this coalescent describe the genealogy of N-BRW for every subexponential displacement distribution?

References

[1] Jean Bérard and Pascal Maillard. The limiting process of N-particle branching random walk with polynomial tails. *Electronic Journal of Probability*, 19:no. 22, 1–17, 2014.

[2] Julien Berestycki, Nathanaël Berestycki, and Jason Schweinsberg. Survival of near-critical branching Brownian motion. *Journal of Statistical Physics*, 143(5):833–854, may 2011.

[3] Julien Berestycki, Nathanaël Berestycki, and Jason Schweinsberg. The genealogy of branching Brownian motion with absorption. *The Annals of Probability*, 41(2):527–618, mar 2013.

[4] Julien Berestycki, Nathanaël Berestycki, and Jason Schweinsberg. Critical branching Brownian motion with absorption: survival probability. *Probability Theory and Related Fields*, 160(3-4):489–520, 2014.

[5] Julien Berestycki, Nathanaël Berestycki, and Jason Schweinsberg. Critical branching Brownian motion with absorption: Particle configurations. *Annales de l'Institut Henri Poincaré, Probabilités et Statistiques*, 51(4):1215–1250, 2015.

[6] Julien Berestycki, Pascal Maillard, and Jason Schweinsberg. Yaglom-type limit theorems for branching Brownian motion with absorption. *in preparation*.

[7] Anton Bovier and Irina Kurkova. Derrida's Generalized Random Energy models 2: models with continuous hierarchies. *Annales de l'Institut Henri Poincaré (B) Probabilités et Statistiques*, 40(4):481–495, aug 2004.

[8] Anton Bovier and Irina Kurkova. Much Ado about Derrida's GREM. In Erwin Bolthausen and Anton Bovier, editors, *Spin Glasses*, Lecture Notes in Mathematics, pages 81–115. Springer Berlin Heidelberg, jan 2007.

[9] Brigitte Chauvin and Alain Rouault. KPP equation and supercritical branching Brownian motion in the subcritical speed area. Application to spatial trees. *Probability Theory and Related Fields*, 80(2):299–314, dec 1988.

[10] Jian Ding, Nike Sun, and David B. Wilson. Supercritical minimum mean-weight cycles. *arXiv:1504.00918*, pages 1–28, 2015.

[11] Pascal Maillard and Ofer Zeitouni. Slowdown in branching Brownian motion with inhomogeneous variance. *Annales de l'Institut Henri Poincaré, Probabilités et Statistiques*, 52(3):1144–1160, 2016.

[12] Bastien Mallein. Maximal displacement of a branching random walk in time-inhomogeneous environment. *Stochastic Processes and their Applications*, 125(10):3958–4019, 2015.

[13] A. A. Mogul'skii. Fourier method for determining the asymptotic behavior of small deviations of a Wiener process. *Siberian Mathematical Journal*, 23(3):420–431, may 1982.

A Problem Associated With the Two-Parameter Dirichlet Process

Shui Feng

McMaster University

For any $0 \leq \alpha < 1$ and $\theta > -\alpha$, let $U_k, k = 1, 2, ...$, be a sequence of independent random variables such that U_k has $Beta(1 - \alpha, \theta + k\alpha)$ distribution. Set

$$V_1^{\alpha,\theta} = U_1, \ V_n^{\alpha,\theta} = (1 - U_1) \cdots (1 - U_{n-1})U_n, \ n \geq 2,$$

and let $\mathbf{P}(\alpha, \theta) = (\rho_1, \rho_2, ...)$ denote $(V_1^{\alpha,\theta}, V_2^{\alpha,\theta}, ...)$ in descending order. The distribution of $(V_1^{\alpha,\theta}, V_2^{\alpha,\theta}, \ldots)$ is called the two parameter GEM distribution. The law of $\mathbf{P}(\alpha, \theta)$ is called the two parameter Poisson-Dirichlet distribution, denoted by $PD(\alpha, \theta)$. For a locally compact, separable metric space S, and a sequence of i.i.d. S-valued random variables $\xi_k, k = 1, 2, ...$ with common diffusive distribution ν_0 on S, let

$$\Xi_{\alpha,\theta,\nu_0} = \sum_{k=1}^{\infty} \rho_k \delta_{\xi_k}. \tag{0.1}$$

The distribution of $\Xi_{\alpha,\theta,\nu_0}$, denoted by $Dirichlet(\theta, \alpha, \nu_0)$ is called the two-parameter Dirichlet process.

The Dirichlet process introduced by Ferguson corresponds to $\alpha = 0$. Let $C_b(S)$ be the set of bounded, continuous functions on a locally compact, separable metric space S, $\mathcal{M}_1(S)$ denote the space of all probability measures on S equipped with the usual weak topology. Define the operator A of the form

$$Af(x) = \frac{\theta}{2} \int (f(y) - f(x))\nu_0(dy), f \in C_b(S).$$

Define

$$\mathcal{D} = \{u : u(\mu) = f(\langle \phi, \mu \rangle), \ f \in C_b^{\infty}(\mathbf{R}), \phi \in C_b(S), \mu \in \mathcal{M}_1(S)\},$$

1

where $C_b^\infty(\mathbf{R})$ denotes the set of all bounded, infinitely differentiable functions on $\mathbf{R}$. Then the Fleming-Viot process with parent independent mutation is a pure atomic measure-valued Markov process with generator

$$Lu(\mu) = \langle A\nabla u(\mu)(\cdot), \mu \rangle + \frac{f''(\langle \phi, \mu \rangle)}{2}\langle \phi, \phi \rangle_\mu, u \in \mathcal{D},$$

where

$$\nabla u(\mu)(x) = \delta u(\mu)/\delta\mu(x) = \lim_{\varepsilon \to 0+} \varepsilon^{-1}\{u((1-\varepsilon)\mu + \varepsilon\delta_x) - u(\mu)\},$$
$$\langle \phi, \psi \rangle_\mu = \langle \phi\psi, \mu \rangle - \langle \phi, \mu \rangle\langle \psi, \mu \rangle,$$

and δ_x stands for the Dirac measure at $x \in S$. It is known that this Fleming-Viot process is reversible with Dirichlet process $Dirichlet(\theta, 0, \nu_0)$ as reversible measure.

Open Problem: Can one generalize the Fleming-Viot process to the two-parameter setting with $0 < \alpha < 1$ so that $Dirichlet(\theta, \alpha, \nu_0)$ is its reversible measure or stationary distribution?

Limits of multiplicative inhomogeneous random graphs and Lévy trees

T. DUQUESNE *Sorbone Université, Pierre and Marie Curie Sciences Faculty, France,*
E-mail: thomas.duquesne@upmc.fr
N. Broutin *Sorbone Université, Pierre and Marie Curie Sciences Faculty (Paris 6, Jussieu),*
E-mail: nicolas.broutin@upmc.fr
M. Wang *University of Bath, Probability Laboratory at Bath, United Kingdom*
Email: wangminmin03@gmail.com

Abstract:

We consider a model of inhomogeneous random graphs that extend Erdős–Rényi graphs and that shares a close connection with the multiplicative coalescence, as pointed out by Aldous [*Ann. Probab.*, vol. 25, pp. 812–854, 1997]. These models have been studied first by Aldous and Limic [*Electron. J. Probab.*, vol. 3, pp. 1–59, 1998] and their connected components evolve as a multiplicative coalescent: namely, let N be the number of vertices and let $w_1, \ldots, w_N$ be a set of positive weights; we independently put an edge between vertices i and j with probability $p_{i,j} = 1 - e^{-w_i w_j/s}$ (in our case, we consider, $s = w_1 + \ldots + w_N$).

Our results are the following: we first generate such graphs by an exploration that reduces to a LIFO queue. This point of view allows to code an appropriate spanning tree of the graph thanks to a contour process (and a modified Lukasiewicz path) and to get a simple control on the surplus edges. The spanning tree encompasses most of the metric structure. This construction also allows to embed such graphs into Galton-Watson trees.

This embedding transfers asymptotically into an embedding of the limit objects into a forest of Lévy trees, which allows us to rpove a limit theorem and an explicit construction of the limit objects from the excursions of a Lévy-type process. As a consequence of our construction, we give a transparent and explicit condition for the compactness of the limit objects and determine their fractal dimensions. These results extend and complement several previous results that had obtained via model- or regime-specific proofs, for instance: the case of Erdos-Renyi random graphs obtained by Addario-Berry, Goldschmidt and B. [*Probab. Theory Rel. Fields*, vol. 153, pp. 367–406, 2012], the *asymptotic homogeneous* case as studied by Bhamidi, Sen and Wang [*Probab Theory Rel. Fields*, vol. 169, pp. 565–641, 2017], or the *power-law* case as considered by Bhamidi, Sen and van der Hofstad [*Probab. Theory Rel. Fields*, vol. 170, pp. 387–474, 2018].

Open problems:

The questions are in close connections with the talk and I refer to the preprint available on arXiv:

$$\text{https://arxiv.org/abs/1804.05871}$$

for precise definitions and notation.

Problem 1. The law of a continuous multiplicative graph is characterised by an increasing function $\psi : (0, \infty) \to (0, \infty)$. We have proved that if $\int_1^\infty d\lambda/\psi(\lambda) < \infty$, then the limiting graph is compact. *Question:* Is this condition sharp ?

Problem 2. Is it possible to recover in a measurable way the blue process (and red process) from the Markovian process X ? Even in the purely Brownian case (that corresponds to the limit of Erdős–Rényi graphs), this question does not seem clear.

In this case, it can be rewritten independently of the paper as follows: let $(B_t^{\mathtt{b}})_{t \in [0, \infty)}$ and $(B_t^{\mathtt{r}})_{t \in [0, \infty)}$ be two independent one-dimensional Brownian motions with initial value 0; we set

$$\theta_t^{\mathtt{b}} = t + \inf \left\{ s \in [0, \infty) : B_s^{\mathtt{r}} < -\tfrac{1}{2} t^2 \right\}, \quad \Lambda_t^{\mathtt{b}} = \inf \left\{ s \in [0, \infty) : \theta_s^{\mathtt{b}} > t \right\} \quad \Lambda_t^{\mathtt{r}} = t - \Lambda_t^{\mathtt{b}} \quad \text{and} \quad B_t = B^{\mathtt{b}}(\Lambda_t^{\mathtt{b}}) + B^{\mathtt{r}}(\Lambda_t^{\mathtt{r}}) \,.$$

It turns out that B is a one-dimensional Brownian motion with initial value 0. *Question*: Is it possible to derive $B^{\mathtt{b}}$ and $B^{\mathtt{r}}$ from B in a measurable way ?

Spatial limit theorems for superprocesses and branvhing Markov processes without the discrete spectrum assumption

Renming SONG *University of Illinois at Urbana-Champaign, USA*, E-mail: rsong@illinois.edu

Recently, many "spatial" limit theorems, such as law of large numbers, $L \log L$ criterion and central limit theorems, have been established for superprocesses and branching Markov processes under the assumption that the mean semigroup has discrete spectrum (plus some other conditions), see [1]–[12]. This excludes the case of super Brownian motions. It is natural to ask for versions of these spatial limit theorems without this discrete spectrum assumption. The paper [13] of S. Watanabe might be useful.

References

[1] R. Adamczak and P. Milos (2015). CLT for Ornstein-Uhlenbeck branching particle system *Electron. J. Probab.* **20**, no. 42, 35 pp.

[2] Z.-Q. Chen, Y.-X. Ren and T. Yang (2017). Skeleton decomposition and law of large numbers for supercritical superprocesses, arXiv:1709:00847

[3] Z.-Q. Chen, Y.-X. Ren, R. Song and R. Zhang (2015). Strong law of large numbers for supercritical superprocesses under second moment condition, *Front. Math. China* **10** (2015), 807–838.

[4] P. Milos (2018). Spatial central limit theorem for supercritical superprocesses, *J. Theoret. Probab.* **31**, 1–40.

[5] Y.-X. Ren, R. Song and R. Zhang (2014). Central limit theorems for super Ornstein-Uhlenbeck processes, *Acta Appl. Math.* **130** , 9–49.

[6] Y.-X. Ren, R. Song and R. Zhang (2014). Central limit theorems for supercritical branching Markov processes, *J. Funct. Anal.* **266**, 1716–1756.

[7] Y.-X. Ren, R. Song and R. Zhang (2015). Central limit theorems for supercritical superprocesses, *Stochastic Process. Appl.* **125**, 428–457.

[8] Y.-X. Ren, R. Song and R. Zhang (2015). Limit theorems for some critical superprocesses, *Illinois J. Math.* **59**, 235–276.

[9] Y.-X. Ren, R. Song and R. Zhang (2017). Functional central limit theorems for supercritical superprocesses, *Acta Appl. Math.* **147**, 137–175.

[10] Y.-X. Ren, R. Song and R. Zhang (2017). Central limit theorems for supercritical branching nonsymmetric Markov processes *Ann. Probab.* **45**, 564–623.

[11] Y.-X. Ren, R. Song and R. Zhang (2017). Supercritical Superprocesses: Proper Normalization and Non-degenerate Strong Limit. arXiv:1708:04422

[12] Y.-X. Ren, R. Song and Z. Sun (2017). Spine decompositions and limit theorems for a class of critical superprocesses, arXiv:1711.09188

[13] S. Watanabe (1967). *Limit theorem for a class of branching processes*, in: Chover J. (Ed.), Markov Processes and Potential Theory, Wiley, New York, 1967, pp. 205–232

Ellen Powell: Questions

Generalising the construction of the Gaussian free field from a nested CLE_4, the authors in ([5]) define a family of "CLE_κ nesting fields", for $\kappa \in (8/3, 8)$, in the following way. Let μ be a probability measure on $\mathbf{R}$ with finite second moment and let Γ be a nested CLE_κ in a simply connected domain D. Let $(\xi_L)_{L \in \Gamma}$ be i.i.d random variables, one for each loop $L \in \Gamma$, with distribution μ. Finally for $\varepsilon > 0$ and $z \in D$ define

$$S_z(\varepsilon) = \sum_{\substack{L \in \Gamma \\ B_x(\varepsilon) \subset int(L)}} \xi_L \quad ; \quad h_\varepsilon(z) = S_z(\varepsilon) - \mathbf{E}[S_z(\varepsilon)].$$

It is shown in ([5]) that for any $\delta > 0$ the field h_ε converges almost surely in $H^{-2-\delta}(D)$ (as $\varepsilon \to 0$ along any given geometric sequence), to a limiting field h. The Gaussian free field corresponds to the case when $\kappa = 4$ and $\mu(\{\lambda\}) = \mu(\{-\lambda\}) = 1/2$, where λ is a fixed constant depending on the normalisation of the free field ([3],[4]).

1. Using the procedure in ([1]) it is possible to construct a family of measures (indexed by some parameter β) associated with a nested CLE_κ. Can the same measures be obtained as exponential/chaos measures (in some suitable sense) of the nesting field h defined using the same CLE_κ and with $\mu(\{1\}) = 1$? Are they deterministic given the field h (i.e. if you just know the field and not the loops used to build it)? Is the field a deterministic function of the family of measures?

2. Now suppose that you assign i.i.d centered ± 1 weights to a nested CLE_κ. Using the same method as in ([2]), can you construct a family of measures from the loops and weights?

3. Keeping the set up above, one can also define a new loop ensemble as follows:
    - Sample the first level CLE_κ and the weights for each of the loops.
    - Keep all the loops having weight $+1$ and inside the other loops repeat the procedure, adding the new weights to the previous one. Keep any loops with total weight $+1$, and then iterate the procedure inside all of the others.
    - Continue until all the loops have total weight $+1$.

    Does this loop ensemble satisfy the conditions of ([1])? If so, do the measures you get using ([1]) correspond to those constructed in point 2?

4. If the answers to all the above are yes, do these measures correspond (in some suitable sense) to exponential/chaos measures of the nesting field h with $\kappa \neq 4$ and $\mu(\{1\}) = \mu(\{-1\}) = 1/2$? Are they deterministic given the field h?

5. Conversely, is the field h deterministic given the family of measures?

6. When the Gaussian free field is constructed as a nesting field with $\kappa = 4$, it is known that the loops used to build it are deterministic given the field. Is this true for other values of κ and laws μ?

7. What can one say about the extremal process of the CLE_κ nesting field?

References

[1] E. Aïdekon (2015). The extremal process in nested conformal loops, *Preprint available on the webpage of the author.*

[2] J. Aru & E. Powell & A. Sepúlveda (2017). Approximating Liouville measure using local sets of the Gaussian free field, *Preprint arXiv:1701.05872.*

[3] J. Aru & A. Sepúlveda & W. Werner (2017). On bounded-type thin local sets (BTLS) of the two-dimensional Gaussian free field, *Journal of the Institute of Mathematics of Jussieu.*

[4] J. Miller, S. Sheffield (2014). The GFF and CLE_4, *Slides and private communications.*

[5] J. Miller, S. Watson and D. Wilson (2015). The conformal loop ensemble nesting field, *Probability Theory and Related Fields.*

Éric Brunet: An asymptotic expansion for the velocity of the BBM

In a branching Brownian motion, the median position of the rightmost particle is [Bramson],

$$\mu_t = 2t - \frac{3}{2}\log t + a + o(1), \qquad \text{as } t \to \infty, \tag{1}$$

where a is some constant. (I assumed the diffusivity constant of the Brownians is $\sqrt{2}$, you need to divide everything by $\sqrt{2}$ if you choose a diffusivity 1)

From the point of view of PDE, call h the solution to the F-KPP equation

$$\partial_t h = \partial_x^2 h + h - h^2, \qquad h(x,0) = \mathbb{1}_{x<0}; \tag{2}$$

it turns out that $h(x,t) = \mathbb{P}\big[R(t) \geq x\big]$ and thus μ_t satisfies $h(\mu_t, t) = 1/2$. The solution to the F-KPP equation develops into a front, and we say that μ_t is the position of the front.

There seems to be no result for an asymptotic expansion for the instantaneous velocity $\partial_t \mu_t$ of the front. However (ask any physicist), it is certain that

$$\partial_t \mu_t = 2 - \frac{3}{2t} + o(t^{-1}), \qquad \text{as } t \to \infty. \tag{3}$$

Can one prove it ?

Bonus:

- There are various ways one could define the position of the front μ_t and still have the expansion (1) hold (for a different value of a). Examples of valid choices are the expected position of the rightmost particle $\mu_t^{(1)} = \mathbb{E}[R(t)] = -\int \mathrm{d}x\, x \partial_x h(x,t)$, or its most likely position $\mu_t^{(2)}$, solution to $\partial_x^2 h(\mu_t^{(2)}, t) = 0$. Then can one prove that (3) also hold for these positions?

- What about different initial conditions ? If $h(x,0)$ decays fast enough, then (1) still holds (with a different value for a...) So should (3), but can one prove it ?

- Why stop at the first derivative ? Do we have

$$\partial_t^n \mu_t = (-1)^n \frac{3(n-1)!}{2t^n} + o(t^{-n}), \qquad t \to \infty, n \geq 2? \tag{4}$$

- Bramson's expansion can be refined. With different levels of proof, one has

$$\mu_t = 2t - \frac{3}{2}\log t + a - \frac{3\sqrt{\pi}}{\sqrt{t}} + \frac{8}{9}(5 - 6\log 2)\frac{\log t + b}{t} + \mathcal{O}\Big(\frac{\log t}{t^{3/2}}\Big), \tag{5}$$

where b is another constant depending on the precise definition of μ_t and on the initial condition. Then one should have

$$\partial_t \mu_t = 2 - \frac{3}{2t} + \frac{3\sqrt{\pi}}{2t^{3/2}} - \frac{8}{9}(5 - 6\log 2)\frac{\log t + b - 1}{t^2} + \mathcal{O}\Big(\frac{\log t}{t^{5/2}}\Big), \tag{6}$$

but a proof might be needed.

Open problems on branching Brownian motion with decay of mass

Sarah Penington [*]

May 8, 2018

Branching Brownian motion with decay of mass is a model of competition for resources in a spatially structured population, introduced in [?]. The model is based on a one-dimensional branching Brownian motion (BBM). We assign a mass to each particle in the BBM; the mass of a particle decays at rate proportional to the total mass of particles in a window of radius μ centred at the location of the particle, for some fixed $\mu > 0$. More precisely, we let $N(t)$ denote the number of particles in the BBM at time t and let $(X_i(t), i \leq N(t))$ denote the locations of the particles. For $t \geq 0$, $x \in \mathbb{R}$, let

$$\zeta(t, x) = \frac{1}{2\mu} \sum_{\{i : |X_i(t) - x| \in (0, \mu)\}} M_i(t).$$

Then for $i \leq N(t)$, let

$$M_i(t) = \exp\left(-\int_0^t \zeta(s, X_{i,t}(s)) ds \right),$$

where $X_{i,t}(s)$ is the location of the ancestor of $X_i(t)$ at time s.

In joint work with Louigi Addario-Berry [?], we showed that in a weak sense, there are arbitrarily large times t at which the front location in this model is $\Theta(t^{1/3})$ behind the location of the rightmost particle in the BBM. For $m > 0$, we let $d(t, m) = \inf\{x > 0 : \zeta(t, x) < m\}$ and $D(t, m) = \sup\{x : \zeta(t, x) > m\}$. Then using results on consistent maximal displacement for BBM [?, ?], we showed in [?] that for $m \in (0, 1)$, almost surely,

$$\limsup_{t \to \infty} \frac{\sqrt{2}t - d(t, m)}{t^{1/3}} \geq c^* \quad \text{and} \quad \liminf_{t \to \infty} \frac{\sqrt{2}t - D(t, m)}{t^{1/3}} \leq c^*,$$

where $c^* = 3^{4/3}\pi^{2/3}/2^{7/6}$. In recent joint work with Louigi Addario-Berry and Julien Berestycki [?], we showed that there exists $m^* = m^*(\mu) > 0$ such that for $m \in (0, m^*]$, there exist $R < \infty$ and a random time $T < \infty$ almost surely such that for $t \geq T$,

$$\inf_{s \geq 0} d(t + R \log t + s, m) \geq D(t, m).$$

---

[*]penington@maths.ox.ac.uk, Mathematical Institute, University of Oxford

It follows that for $m \in (0, m^*]$, almost surely

$$\limsup_{t \to \infty} \frac{\sqrt{2}t - D(t, m)}{t^{1/3}} \geq c^* \quad \text{and} \quad \liminf_{t \to \infty} \frac{\sqrt{2}t - d(t, m)}{t^{1/3}} \leq c^*.$$

Question 1: Do we have that for $m \in (0, 1)$, almost surely

$$\lim_{t \to \infty} \frac{\sqrt{2}t - D(t, m)}{t^{1/3}} = c^* \quad \text{and} \quad \lim_{t \to \infty} \frac{\sqrt{2}t - d(t, m)}{t^{1/3}} = c^* \ ?$$

Even showing that there exist $0 < a < \frac{1}{3} < b < 1$ such that almost surely

$$\liminf_{t \to \infty} \frac{\sqrt{2}t - d(t, m)}{t^a} = \infty \quad \text{and} \quad \limsup_{t \to \infty} \frac{\sqrt{2}t - D(t, m)}{t^b} = 0$$

would be a new result.

Question 2: In [**?**], we proved the following upper bound on the largest particle mass: for any $\alpha < 1$ and $n \in \mathbb{N}$, for t sufficiently large,

$$\mathbb{P}\left(\max_{i \leq N(t)} M_i(t) \geq t^{-\alpha}\right) \leq t^{-n}.$$

We believe that in fact the largest particle mass decays much more quickly - can we improve on this upper bound? An improved bound on the largest particle mass would help us make progress in Question 1.

References

[1] L. Addario-Berry, S. Penington. *The front location in branching Brownian motion with decay of mass*, Annals of Probability **45(6A)** (2017), 3752–3794.

[2] L. Addario-Berry, J. Berestycki, S. Penington. *Branching Brownian motion with decay of mass and the non-local Fisher-KPP equation*, arXiv preprint arXiv:1712.08098 (2017).

[3] B. Jaffuel. *The critical barrier for the survival of branching random walk with absorption*, Annales de l'Institut Henri Poincaré, Probabilités et Statistiques **48(4)** (2012), 989–1009.

[4] M. Roberts. *Fine asymptotics for the consistent maximal displacement of branching Brownian motion*, Electronic Journal of Probability **20(28)** (2015), 1–26.

Some open problems related to the talk:
Modelling Darwinian evolution as interacting particle systems

G. Berzunza,* A. Sturm †   and   A. Winter‡

Abstract

In this note, we provide a very rough "introduction" to a particular individual-based model for adaptive dynamics of interacting populations. The goal is to present some open problems in this field.

1 Introduction

The study of interactions between organisms and their environment which influences their reproductive success, and contribute to genotype and phenotype variation is one of the main questions in evolutionary ecology and population genetics. In this note, we are interested in modelling the dynamics of populations by emphasizing the ecological interactions, namely the competition between individuals for limited resources, where each individual is characterized by a quantitative trait which remains constant during the individual's life and which is passed on to offspring unless a mutation occurs. Motivated by the work of Bolker-Pacala [2] and Dieckmann-Law [6], several models have been rigorously developed in this context. For example, Fournier and Méléard [9], Champagnat, et al. [4], Jourdain, et al. [10], Méléard and Viet Chi [13], Méléard and Viet Chi [12] and the work in preparation [1].

The plan of the rest of this note is as follows. Section 2 is devoted to the introduction of a simple the individual-based model studied by Champagnat, et al. [4]. In Section 3, we state the main convergence result obtained in [4] based on a large population limit. In the talk, we are going to see a more general model that yields to a different convergence result. Finally, in Section 4, we present some open questions

---

*Institut für Mathematische Stochastik, Georg-August-Universität Göttingen. Goldschmidtstrasse 7, 37077 Göttingen, Germany. E-mail: gabriel.berzunza-ojeda@uni-goettingen.de

†Institut für Mathematische Stochastik, Georg-August-Universität Göttingen. Goldschmidtstrasse 7, 37077 Göttingen, Germany. E-mail: asturm@math.uni-goettingen.de

‡Fakultät für Mathematik, Universität Duisburg-Essen. Thea-Leymann-Strasse 9, 45127 Essen, Germany. E-mail: anita.winter@uni-due.de

related to the limiting process obtained in Theorem 1. It is important to point out that similar questions can be made about the model we are going to discuss in the conference. In this note, we keep things simple for an easier presentation of the topic.

In the present note we use the following notation. Given two topological spaces V and W, we denote by $B(V,W)$ the set of bounded measurable functions from V to W. Let $B(V,\mathbb{R})$ be furnished with the supremum norm (i.e. for $f \in B(V,\mathbb{R})$, we rite $\| f \|_\infty = \sup_{x \in V} |f(x)|$) and $B(V,\mathbb{R}_+)$ denote the subset of $B(V,\mathbb{R})$ of positive elements. Let $T > 0$ and $\mathbb{D}([0,T],V)$ (resp. $\mathbb{D}([0,\infty),V)$) denote the space of càdlàg paths from $[0,T]$ (resp. from $[0,\infty)$) to V furnished with the Skorokhod topology. We use $C_b(V,\mathbb{R})$ (resp. $C_b(V,\mathbb{R}_+)$) to denote the set of bounded continuous functions from V to $\mathbb{R}$ (resp. from V to $\mathbb{R}_+$). For any integers $d,n \geq 1$, let $C_b^n(\mathbb{R}^d,\mathbb{R})$ (resp. $C_b^n(\mathbb{R}^d,\mathbb{R}_+)$, $C_b^n(\mathbb{R}_+^d,\mathbb{R}_+)$) be the subset of $C_b(\mathbb{R}^d,\mathbb{R})$ (resp. $C_b(\mathbb{R}^d,\mathbb{R}_+)$, $C_b^n(\mathbb{R}_+^d,\mathbb{R}_+)$) of functions with bounded continuous derivatives up to the n-th order. We use the superscript "+" to denote the subsets of non-negative elements bounded away from zero e.g., $B(V,\mathbb{R}_+)^+$, $C_b(V,\mathbb{R}_+)^+$, etc. That is, for $f \in B(V,\mathbb{R}_+)^+$ (or $C_b(V,\mathbb{R}_+)^+$) there exists a $\varepsilon > 0$ such that $f(x) \geq \varepsilon$ for all $x \in V$.

2 The individual-based model

In this section, we formally introduce our interacting particle Markov process for Darwinian evolution in an asexual population with non-constant population size in which each individual is characterized by hereditary types. Our model's construction starts with a microscopic description of a population in which the adaptive traits influence the birth rate, the mutation process, the death rate, and how the individuals interact with each other and their external environment. More precisely, we assume that the phenotype of each individual is described by a quantitative trait. Throughout the paper, we will assume that

$$\text{the trait (or type) space } \mathcal{X} = \mathbb{R}^d, \text{ for some } d \geq 1.$$

We consider a parameter $K \in \mathbb{N}$ that scales the resources or area available. It is called the "system size" by Metz et al. [14]. It will become apparent later that this parameter is linked to the size of the population: large K means a large population (provided that the initial condition is proportional to K). We have the following definition of the stochastic interacting individual system where individuals behave independently:

1. **Birth and mutation:** An individual of trait $x \in \mathcal{X}$ gives birth to a single individual at rate $Kr(x) + b(x)$. We assume that $r \in B(\mathcal{X},\mathbb{R}_+)^+$ and $b \in B(\mathcal{X},\mathbb{R}_+)$. The new individual is a clone (has the same type) of his parent with with probability $1 - p(x)$, where $p(x) \in [0,1]$ is the mutation probability of an individual with trait $x \in \mathcal{X}$. Otherwise, it produces a mutant of type h with probability $p(x)m_K(x,z)\mathrm{d}z$, where $m_K(x,z)\mathrm{d}z$ is a probability measure on $\mathcal{X}$ called the

mutation kernel or mutation step law. We assume that there is a density function $\bar{m}$ on $\mathcal{X}$ such that $m_K(x, z) \leq C_K \bar{m}_K(x - z)$, for some constant $C_K > 0$.

2. **Natural death:** An individual of type $x \in \mathcal{X}$ dies naturally at rate $Kr(x) + d(x)$, where $d \in B(\mathcal{X}, \mathbb{R}_+)$.

3. **Competition:** We let $c(x, y) \in B(\mathcal{X} \times \mathcal{X}, \mathbb{R}_+)$ be the competition kernel which models the competition pressure felt by an individual with trait $x \in \mathcal{X}$ from an individual with type $y \in \mathcal{X}$. We then add extra death due to competition. Specifically, each individual of type y points independent exponential clocks of parameter $\frac{1}{K}c(x, y)$ on each individual of type x. Then, the death of an individual of type x occurs as soon as a clock pointed at this individual rings.

Remark 1. *A classical choice of the competition function is $c \equiv 1$ which corresponds to density dependence involving the total population size known as the "mean field case" or the "logistic case". See also [4, Equation (2.7) in Section 2.2] where an example of asymmetrical competition is discussed.*

Let $\mathcal{M}(\mathcal{X})$ denote the set of finite Borel measures on $\mathcal{X}$ equipped with the weak topology, and define the subset $\mathcal{M}^K(\mathcal{X})$ of $\mathcal{M}(\mathcal{X})$ by

$$\mathcal{M}^K(\mathcal{X}) = \left\{ \frac{1}{K} \sum_{i=1}^n \delta_{x_i} : n \geq 0, \ x_1, \ldots, x_n \in \mathcal{X} \right\},$$

where δ_x is the Dirac measure at x. For any $\mu \in \mathcal{M}(\mathcal{X})$ and any measurable function f on $\mathcal{X}$, we set $\langle \mu, f \rangle = \int_{\mathcal{X}} f \, \mathrm{d}\mu$.

At any time $t \geq 0$, we let N_t be the finite number of individuals alive, each of which is assigned a trait type in $\mathcal{X}$. Let us denote by $x_1, \ldots, x_{N_t}$ the trait types of these individuals. The state of the population at time $t \geq 0$, rescaled by K, can be described by the finite point measure ν_t^K on $\mathcal{X}$ defined by

$$\nu_t^K = \frac{1}{K} \sum_{i=1}^{N_t} \delta_{x_i}.$$

We let $\mathbb{1}_A$ be the indicator function of a set $A \subset \mathcal{X}$. For simplicity, we denote by $\mathbf{1} := \mathbb{1}_{\mathcal{X}}$ the indicator function on the whole space. We observe that $\langle \nu_t^K, \mathbf{1} \rangle = N_t K^{-1}$. For any $x \in \mathcal{X}$, the positive number $\langle \nu_t^K, \mathbb{1}_{\{x\}} \rangle$ is called the density of the trait x at time t.

Champagnat, et al. [4] (see also [9]) have shown that the population process $(\nu_t^K, t \geq 0)$ is a (unique in law) càdlàg $\mathcal{M}^K(\mathcal{X})$-valued Markov process with infinitesimal generator, $\mathscr{L}^K$, defined for any bounded

3

measurable function f from $\mathcal{M}^K(\mathcal{X})$ to $\mathbb{R}$ and for all $\mu^K \in \mathcal{M}^K(\mathcal{X})$ by

$$
\begin{aligned}
\mathscr{L}^K f(\mu^K) = K \int_{\mathcal{X}} (Kr(x) + b(x))(1 - p(x)) \left(f\left(\mu^K + \frac{\delta_x}{K}\right) - f(\mu^K) \right) \mu^K(\mathrm{d}x) \\
+ K \int_{\mathcal{X}} (Kr(x) + b(x))p(x) \int_{\mathcal{X}} \left(f\left(\mu^K + \frac{\delta_z}{K}\right) - f(\mu^K) \right) m_K(x,z)\mathrm{d}z\mu^K(\mathrm{d}x) \\
+ K \int_{\mathcal{X}} \left(Kr(x) + d(x) + \int_{\mathcal{X}} c(x,y)\mu^K(\mathrm{d}y) \right) \left(f\left(\mu^K - \frac{\delta_x}{K}\right) - f(\mu^K) \right) \mu^K(\mathrm{d}x). \quad (1)
\end{aligned}
$$

Remark 2. *In the related talk, we are going to discuss a more general setting where multiple offspring can occur at the birth event. Moreover, we consider that the offspring distribution may depend on the parent individual's trait as well as on the phenotypic variation of the offspring due to mutation. As a consequence, we are going to obtain a more general convergence result that the one presented in this note. Loosely speaking, the presence of multiple offspring is going to allow us to get a random measure-valued process with jumps.*

3   The superprocess limit

In this section, we investigate the limit when the system size K increases to $+\infty$ of the interactive particle system described in Section 2, which leads to a random measure-valued process. In an obvious way, we regard the previous interactive particle system as a process with state space $\mathcal{M}^K(\mathcal{X}) \subset \mathcal{M}(\mathcal{X})$.

We consider the following hypothesis.

Assumption 1. *The mutation kernel $m_K(x,z)$ is the density of a random variable with mean $x \in \mathcal{X}$ and variance-covariance matrix $\Sigma(x)/K = (\Sigma_{ij}(x)/K, 1 \leq i, j \leq l)$. The function Σ is bounded and the third moment of $m_K(x,z)$ is of order $1/K^{1+\varepsilon}$ uniformly on $x \in \mathcal{X}$ with $\varepsilon > 0$.*

Remark 3. *We notice that as $K \to \infty$, mutant traits become more concentrated around their progenitors. For instance,*

$$
m_K(x,h)\mathrm{d}h = \left(\frac{K}{2\pi\sigma^2(x)} \right)^{d/2} \exp\left(-\frac{K|h-x|^2}{2\sigma^2(x)} \right) \mathbb{1}_{\{h \in \mathbb{R}^d\}} \, \mathrm{d}h,
$$

where $\sigma^2(x)$ positive and bounded on $\mathcal{X}$.

Let us now state our main convergence result due to Champagnat, et al. [4, Theorem 4.5].

Theorem 1. *Suppose that Assumption 1 is fulfilled. Assume also that there exists $\mu \in \mathcal{M}(\mathcal{X})$ (possibly random) such that*

$$
\lim_{K \to \infty} \nu_0^K = \mu
$$

4

in law for the weak topology on $\mathcal{M}(\mathcal{X})$ and that

$$\sup_{K} \mathbf{E}[\langle \nu_0^K, \mathbf{1} \rangle^3] < \infty. \tag{2}$$

Then, for each $0 < T < +\infty$, The sequence of processes $(\nu^K)_K$, converges in law in $\mathbb{D}([0,T], \mathcal{M}(\mathcal{X}))$ to the unique (in law) continuous super-process $\nu \in \mathbb{D}([0,T], \mathcal{M}(\mathcal{X}))$, defined by the following conditions

1. *We have that*

$$\sup_{t \in [0,T]} \mathbf{E}[\langle \nu_t, \mathbf{1} \rangle^3] < +\infty.$$

2. *The measure-valued process $\nu \in \mathbb{D}([0,T], \mathcal{M}(\mathcal{X}))$ solves the following martingale problem: For any $\phi \in C_b^2(\mathcal{X}, \mathbb{R}_+)$, the process $M(\phi) = (M_t(\phi), t \in [0,T])$ given by*

$$M_t(\phi) = \langle \nu_t, \phi \rangle - \langle \nu_0, \phi \rangle - \frac{1}{2} \int_0^t \int_{\mathcal{X}} p(x) r(x) \sum_{i \leq i, j \leq d} \Sigma_{ij}(x) \partial_{ij}^2 \phi(x) \nu_s(\mathrm{d}x) \mathrm{d}s$$

$$- \int_0^t \int_{\mathcal{X}} \phi(x) \left(b(x) - d(x) - \int_{\mathcal{X}} c(x,y) \nu_s(\mathrm{d}y) \right) \nu_s(\mathrm{d}x) \mathrm{d}s \tag{M}$$

is a continuous martingale with quadratic variation

$$2 \int_0^t \int_{\mathcal{X}} r(x) \phi^2(x) \nu_s(\mathrm{d}x) \mathrm{d}s,$$

Remark 4. *Jourdain, et al. [10] obtained a similar result by considering that the mutation kernel belongs to the domain of attraction of a stable law. The limiting-measure valued process in Theorem 1 can be seem as an extension of the one of Etheridge [7] by taking $c(x,y) = h(|x - y|)$ for $x, y \in \mathcal{X}$ with a nonnegative decreasing function h on $\mathbb{R}_+$ that satisfies $\int_0^\infty h(r) r^{d-1} \mathrm{d}r < \infty$. As we are going to see in the related talk, we can assume even a more general mutation kernel and obtain a different limiting process.*

4 Open Problems

In this section, we present some open problems related to the models introduced in Section 2 and Theorem 1. Similar questions can be made for the most general framework that it is going to be presented at the conference.

Problem 1. *Is there a density for the limiting measure-valued process ν in Theorem 1? One could expect*

a positive answer when $d = 1$, as for the Super-Brownian motion; see for example [8] and reference there for general background.

Natural questions that one can expect to answer about the individual-based model in Section 2 and the limiting measure-valued process ν in Theorem 1:

Problem 2. *What can we say about the extinction (or survival) probability and the distribution of the extinction time of the different sub-populations or the global population?. We refer to [7], where this question has been answered in a very particular framework.*

Problem 3. *What can we say about the quasi-stationary distributions (assuming that the population will be extinct almost surely) ?. See for instance [3] [5] where some particular cases are considered.*

A significant interest in evolutionary biology is devoted to reconstructing phylogenies based on available data on the extant species (of molecular or another type). The assumption is that in the distant past there was a common ancestor from which the extant species evolved according to some (stochastic) evolutionary model. One then tries to find the ancestral history (genealogy) of the extant species which optimizes some "best fit" criterion. Using shapes of such phylogenetic trees one then hopes to make some inference on the diversification properties of the evolutionary process. Therefore, we have the following problem:

Problem 4. *Is it possible to provide a description of the genealogies in the proposed (microscopic) individual-based model in Section 2, and the limiting (macroscopic) model in Theorem 1? see [11].*

References

[1] Berzunza, G., Sturm, A., and Winter, A. Stochastic particle systems with competition and multiple branching. *In preparation*, 2018.

[2] Bolker, B. and Pacala, S. W. Using moment equations to understand stochastically driven spatial pattern formation in ecological systems. *Theoretical population biology*, 52(3):179–197, 1997.

[3] Cattiaux, P. and Méléard, S. Competitive or weak cooperative stochastic Lotka-Volterra systems conditioned on non-extinction. *J. Math. Biol.*, 60(6):797–829, 2010.

[4] Champagnat, N., Ferrière, R., and Méléard, S. From individual stochastic processes to macroscopic models in adaptive evolution. *Stoch. Models*, 24(suppl. 1):2–44, 2008.

[5] Collet, P., Martí nez, S., Méléard, S., and San Martí n, J. Quasi-stationary distributions for structured birth and death processes with mutations. *Probab. Theory Related Fields*, 151(1-2):191–231, 2011.

[6] Dieckmann, U. and Law, R. *Relaxation projections and the method of moments.* Pages 412-455 in The Geometry of Ecological Interactions: Symplifying Spatial Complexity (U Dieckmann, R. Law, J.A.J. Metz, editors). Cambridge University Press, Cambridge, 2000.

[7] Etheridge, A. M. Survival and extinction in a locally regulated population. *Ann. Appl. Probab.*, 14(1):188–214, 2004.

[8] Etheridge, A. M. *An introduction to superprocesses*, volume 20 of *University Lecture Series.* American Mathematical Society, Providence, RI, 2000.

[9] Fournier, N. and Méléard, S. A microscopic probabilistic description of a locally regulated population and macroscopic approximations. *Ann. Appl. Probab.*, 14(4):1880–1919, 2004.

[10] Jourdain, B., Méléard, S., and Woyczynski, W. A. Lévy flights in evolutionary ecology. *J. Math. Biol.*, 65(4):677–707, 2012.

[11] Kliem, S. and Winter, A. Evolving phylogenies of trait-dependent branching with mutation and competition. part i: Existence. *arXiv preprint arXiv:1705.03277*, 2017.

[12] Méléard, S. and Tran, V. C. Nonlinear historical superprocess approximations for population models with past dependence. *Electron. J. Probab.*, 17:no. 47, 32, 2012.

[13] Méléard, S. and Tran, V. C. Slow and fast scales for superprocess limits of age-structured populations. *Stochastic Process. Appl.*, 122(1):250–276, 2012.

[14] Metz, J. A. J., Geritz, S. A. H., Meszéna, G., Jacobs, F. J. A., and van Heerwaarden, J. S. Adaptive dynamics, a geometrical study of the consequences of nearly faithful reproduction. In *Stochastic and spatial structures of dynamical systems (Amsterdam, 1995)*, volume 45 of *Konink. Nederl. Akad. Wetensch. Verh. Afd. Natuurk. Eerste Reeks*, pages 183–231. North-Holland, Amsterdam, 1996.