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Title: Applications of a Griffiths-type generator representation

Abstract: *Random genetic drift* is the unbiased (miss)fortune inherent in the respro-ductive mechanism of any species. Two ways of modelling it in population genetics are the *Fisher-Wright diffusion* with generator

$$\mathcal{A}_{\mathrm{FW}} f(x) = \frac{1}{2} x(1-x) \frac{\partial^2}{\partial x^2} f(x)$$

(for $f \in \mathcal{C}^2([0,1])$) and the *two-type* Λ*-Fleming-Viot process*, a piecewise deterministic process whose generator has a representation in terms similar to $\mathcal{A}_{\mathrm{FW}}$ of the form

$$\mathcal{A}_{\Lambda} f(x) = \frac{1}{2} x(1-x) \mathbb{E}\left[\frac{\partial^2}{\partial x^2} f(x(1-W) + WV)\right]$$

for V uniform on $[0,1]$ and $W = UY$, where U has density $u \mapsto 2u$ on $[0,1]$ and $Y \sim \Lambda$, for a distribution Λ on $[0,1]$, and V, U and Y are independent, as was uncovered in [Gri14]. In a suitable sense, the former describes *independent* behavior, whereas the latter is induced by added *correlation*, driven by a Poisson Point process. We obtain an analogous result when we include the modeling of *selection* ([GCSWB19]) or a *seed bank* ([BKGCWB19]) and consider their correlated analoga (selection in random environment and the seed bank with simultaneous migration). We present how this respresentation can then be used to study the long-term behaviour of the jump-diffusions, but also their *moment duals*, uncovering a critical parameter determining the ergodicity of the resulting *branching coalescing process* in the model for selection and a precise description of *coming down from infinity* in the seed bank case.

References

[GCSWB19] A. González Casanova, D. Spanò and M. Wilke-Berenguer. The effective strength of selection in random environment. *arXiv:1903.12121*, 2019.

[Gri14] R. C. Griffiths. The Λ-Fleming-Viot process and a connection with Wright-Fisher diffusion. *Adv. in Appl. Probab.*, 46(4):1009–1035, 2014.

[BKGCWB19] J. Blath, A. González Casanova, N. Kurt, and M. Wilke-Berenguer. The seed bank coalescent with simultaneous switching. *arXiv:1812.03783*, 2019.

Fernando Cordero

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Titulo: General selection models: Bernstein duality and (minimal) ancestral structures.

Abstract:

The Lambda-Wright–Fisher process describes the type-frequency evolution of an infinite population. We model frequency-dependent selection pressure with a general polynomial drift vanishing at the boundary. In a first step, we construct a sequence of Moran-type models converging under suitable conditions to the solution of the associated SDE. The genealogical structure inherent to these finite population models leads in the large population limit to a generalization of the ancestral selection graph of Krone and Neuhauser. Next, we introduce an ancestral process that keeps track of the sampling distribution along the ancestral structures and that satisfies a duality relation with the type-frequency process. We refer to it as Bernstein coefficient process and to the relation as Bernstein duality. As an application, we derive criteria for the accessibility of the boundary and determine the time to absorption. An intriguing feature in our construction is that multiple ancestral processes can be associated to the same forward dynamics. If there is enough time, I will explain how to characterize the set of optimal ancestral structures and provide a recipe to construct them from the drift.

Based on joint work with E. Schertzer and S. Hummel.

Jason Schweinsberg

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Title: Branching Brownian motion and populations undergoing selection

Abstract: Certain populations undergoing selection can be modeled using branching Brownian motion. In this setting, the particles represent individuals in a population, branching events correspond to births, and the position of a particle represents the fitness of the individual. One way to model selection is to set the branching rate of each particle to be the same, but to kill particles when they hit the origin, meaning that individuals die when their fitness drops below a threshold. An alternative is to set the death rate of each particle to be the same but to allow the branching rate of a particle to be an increasing function of the position, so that fitter individuals are more likely to produce offspring. We will show how some results for branching Brownian motion can be used to obtain insights into the behavior of populations undergoing selection.

Nested Coalescents and transport-coagulation PDE

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Consider the following transport-coagulation equation
\begin{equation}
\forall t>0, \forall x\geq0, \ \ \partial_t n (t,x) \ = \ \partial_x (x^\gamma n)(t,x) \ + \ \frac{1}{2} \int_{0}^x n(t,x-y) n(t,y) dy \ - \   n(t,x) \int_{0}^\infty n(t,y) dy.
\end{equation}
If we think of $n(t,x) dx$ as the ``number'' of clusters carrying a mass in an interval of size dx around x at time t, then
the previous equation can be interpreted as the following dynamics: clusters coalesce at rate 1, and the mass of each cluster is depleted
at a rate proportional to $\mbox{mass}^\gamma$.

Our main motivation for studying the latter PDE is the nested coalescent model in which gene lineages are constrained by a phylogeny, i.e., ancestral lineages can only coalesce if they belong to the same species. In particular, when $\gamma=2$, we show that the latter PDE can be recovered the nested Kingman coalescent (where gene and species lineages are both described by a standard Kingman coalescent) at small time scales. In particular, we show that the existence of a self-similar solution for the PDE relates to the speed of coming down from infinity in the nested Kingman coalescent. I will also address some open problems related to the previous results.

This is joint work with A. Lambert