# Genealogies of Interacting Particle Systems

## An Afternoon of Activities on Wednesday, 16 August 2017

***2.00pm - 3.00pm***

**Colloquium Lecture**
**Anton Wakolbinger, Goethe-Universität Frankfurt**

***Mathematical population genetics meets experimental evolution: A stochastic model of Lenski's long term experiment***

---

***3.20pm - 4.20pm***

**Young Mathematician Lecture**
**Matthias Hammer, Technische Universität Berlin**

***From the symbiotic branching model to annihilating Brownian motions***

---

***4.30pm - 5.30pm***

**Seminar**
**Adrian Roellin, NUS**

***Dirichlet approximation of equilibrium distributions in Cannings Models with mutation***

---

*Venue:* *Department of Mathematics, NUS*
*Seminar Room 1 , Block S17, Level 4*
*10, Lower Kent Ridge Road, Singapore 119076*

Jointly Organised by

NUS National University of Singapore | IMS Institute for Mathematical Sciences

NUS National University of Singapore | Department of Mathematics Faculty of Science

# Mathematical population genetics meets experimental evolution: A stochastic model of Lenski's long term experiment

Anton Wakolbinger

*Goethe-Universität Frankfurt, Germany*

ABSTRACT

The fascinating new field of experimental evolution lends itself to an application of ideas from mathematical population genetics. We will start by explaining some of these ideas in our talk, and will then describe a parsimonious stochastic model (and its rigorous analysis) which leads to a power law in the increase of the relative fitness as observed and described ([1]) in Lenski's long term evolution experiment on E. coli. The talk is based on joint work [2] with Adrian Gonzáles Casanova, Noemi Kurt and Linglong Yuan.

# References

[1] M. J. Wiser, N. Ribeck, and R. E. Lenski, *Long-term dynamics of adaptation in asexual sopulations.* Science 342 (2013), 1364-1367.

[2] A. González Casanova, N. Kurt, A. Wakolbinger, and L.Yuan, *An individual-based model for the Lenski experiment, and the deceleration of the relative fitness.* Stoch. Processes Appl. 126 (2016), 2211-2252.

# From the symbiotic branching model to annihilating Brownian motions

Matthias Hammer

*Technische Universität Berlin, Germany*

ABSTRACT

The continuous-space symbiotic branching model describes two interacting spatial populations on the real line whose evolution is given by a system of SPDEs with correlated driving noises. It includes as special cases the well-known stepping stone model from mathematical population genetics and the mutually catalytic branching model of Dawson and Perkins.

We give a survey on recent results showing that for negative correlations, the system converges under diffusive rescaling, which corresponds to an infinite branching rate. We will discuss some properties of this limit and make a connection to the corresponding discrete-space model introduced by Klenke and Mytnik. In particular, we report on a new moment duality, which for perfectly anticorrelated noises (including the stepping stone case) gives a fully explicit description of the limit in terms of a countable system of annihilating Brownian motions with drift. This also allows us to provide a full classification of entrance laws for annihilating Brownian motions. We will also discuss some open problems.

Based on joint work with Jochen Blath (TU Berlin) and Marcel Ortgiese and Florian Völlering (both University of Bath).

# Dirichlet approximation of equilibrium distributions in Cannings Models with mutation

Adrian Roellin

*National University of Singapore*

ABSTRACT

Consider a haploid population of fixed finite size with a finite number of allele types and having Cannings exchangeable genealogy with neutral mutation. The stationary distribution of the Markov chain of allele counts in each generation has no tractable description in general. We provide upper bounds on the distributional distance between the Dirichlet distribution and this finite population stationary distribution for the Wright-Fisher genealogy with general mutation structure and the Cannings exchangeable genealogy with parent independent mutation structure.