Stochastic **P**rocesses **I**n **E**vo**L**ution and **E**cology

Bath - Berlin - Frankfurt - Mainz - Warwick

Genetic composition of supercritical branching populations under rare mutation rates

Better understanding the genetic diversity within tumors is of key interest for clinicians to propose adaptive strategies. I will present a probabilistic model of tumorogenesis to provide quantitative results over time on the genetic diversity.

The trait space is modelled using a finite oriented graph. The population of cells follows a continuous time branching process. The biological phenomenon taken into account are cell death and cell division. During each division event each daughter cell mutates, independently from each other, to another trait (using the edges of the graph) with a certain probability.

The classical regime of « large population and rare mutation » is considered. It means that a parameter $n \in \mathbb{N}$ is used to quantify both the decrease of the mutation probabilities, as negative powers of n, and also the typical size of the population, depending on n as positive power of n, at which we are interested in understanding the genetic composition. The results are on the asymptotic sizes of the subpopulations of cells. Notably, the behaviour of mutant cells will depend on whether the mutation is deleterious, neutral or selective.

Speaker: Dr. Vianney Brouard from ENS de Lyon
Time: Monday, 03.07.23, 4 P.M. CET

The lecture will be held online. Interested? Link available from Cornelia Pokalyuk
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