A branching-coalescence model of phylogenetic network

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Abstract. Phylogenies — that is, the evolutionary relationships between species — are traditionally represented by trees. Yet trees cannot be used to model phenomena such as horizontal gene transfers or hybridization. As a result, biologists are increasingly turning to networks to model phylogenies. However, to this days few models of random phylogenetic networks have been studied mathematically. In this talk, we will introduce a simple model of random phylogenetic network associated to a process where species can not only split ("branching"), but also merge ("coalescence"). We will see how branching process methods and stochastic geometry can be used to study this kind of model.