**Presentation title:** Trees, networks, communities: mapping genetic transmission in the microbial biosphere

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**Abstract:**
The year 1995 marked the beginning of the era of prokaryotic genomics, with publication of the complete sequence of *Haemophilus influenzae* ; today more than 2500 prokaryotic genomes are publicly available. Two discoveries so far have been particularly surprising: the extent to which genomes of even closely related strains can differ in gene content, and the extent to which genetic material has been transmitted laterally among genomes. Not only close relatives, but distantly related genomes too, can share genetic material at appreciable frequencies, driving physiological and metabolic innovation including the colonisation of new environments and hosts. Whereas eukaryotes have diversified *via* a treelike process of speciation and descent-with-modification, evolutionary relationships among prokaryotes take the form of a network – the Network of (Microbial) Life.

This presentation begins with a reflection on the early, problematic application of phylogenetic methods to prokaryotes, and the expectation that phylogenomics (genome-scale molecular phylogenetics) would eventually clarify microbial relationships. I will introduce phylogenomic workflows for vertical and lateral genetic transmission (LGT), construction of a reference topology, and a second-generation workflow that takes into account fragmentary as well as whole-gene LGT. I will present new results on the physical units of lateral transfer, and how laterally introduced genetic material integrates into cellular networks of genetic regulation and biomolecular interaction. Finally, I will describe the state-of-the-art in mapping genetic transmission not only among genomes but also across vectors, hosts and environments; present a graph-based definition of genetic exchange communities; and outline a scalable third-generation workflow that frees us from the need to pretend that genes are the units of transfer and recombination. Our goal is no longer (just) a cell-centric tree or network, but rather a map of genetic exchange communities that illuminates the processes, connectivity and dynamics of genetic flow across all of living Nature.