

Title: Laws of prokaryotic genome evolution

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Abstract: Since the publication of the first whole prokaryotic genome in 1995, a number of quantitative 'laws' of large-scale genome structure and evolution have been uncovered. These quantitative laws concern features including the distribution of evolutionary rates and gene family sizes, the distribution of genes across different functional categories, and large-scale properties of transcription regulatory networks. In this talk I will discuss some of these quantitative laws and their implications for our understanding of the process and mechanisms of genome evolution in prokaryotes. In particular, I will try to argue that, taken together, these quantitative laws provide enough constraints so as to make whole genome evolution in prokaryotes an attractive area for developing rigorous quantitative models. In this context I will discuss some recent work from my group including analysis of scaling laws in gene-content across different prokaryotic clades, analysis of the evolution of intergenic regions and large-scale regulatory network structure, and a general quantitative model for the evolution of protein domain-content.