

Title: A maximisation model for genetic organisation in bacterial DNA

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Abstract:

A model for capturing the disposition of genes throughout bacterial genomes will be presented. The model comprises a pair of independent Markovian processes, each of which represents an arrangement of "candidate" genes along a strand of DNA. An optimisation procedure selects a subset of the gene candidates on both strands so as to maximise the total space utilised by genes in the DNA sequence while ensuring that no two genes overlap. The set of "final" genes selected in this way is then taken to represent the actual organisation of genes in the DNA sequence.

I will discuss the model, Some theoretical results, various upper and lower bounds on the space occupied by gene arrangements it produces and some numerical results from the application of the model to the escherichia coli genome.