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Modelling the Emergent Dynamics of Microbial Communities in the Human Colon

Modelling microbial ecosystem dynamics in the human colon is challenging due to large variations between individuals and limited amounts of data. In an attempt to overcome these issues we take a complex adaptive systems (CAS) approach to the problem. Thus a model is developed in which the dominant bacterial strains are not defined a priori but are allowed to 'emerge' from a stochastically generated bacterial population. To do this we begin by assuming that every bacterial strain falls into one of ten bacterial functional groups (BFGs) which are distinguished by their metabolic pathways and their preferred pH ranges. The metabolic pathways form a network which determines the dietary substrates each BFG grows on and which metabolites it may consume or produce. The parameters controlling the exact rates of transfer along these pathways, and the preferred pH ranges are then generated stochastically, within appropriate limits, for a population of 300 bacterial strains. The rates of change of mass of each strain, resource and metabolite are computed by solving a system of ordinary differential equations. Due to competition for resources, and interactions within the metabolic network, some strains will flourish and some will disappear, such that over time a viable community for the given environment emerges. In this work, the equations governing the model are described and the model results are compared to data from a fermentor study which examines the effects of pH on the microbial community. We then demonstrate how this CAS modelling approach allows the system to adapt to its environment through species succession and investigate different mechanisms for avoiding competitive exclusion within the BFGs.