Bayesian inference of interaction rates in a metabolite-bacteria network using time-series counts

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The human gut hosts a vast and diverse set of microbes that indirectly interact with each other through consuming and producing compounds, called metabolites. Disruptions in this network between gut microbes and their human host can contribute to the onset and progression of various disorders, including obesity, inflammatory bowel syndrome and Parkinson's disease. Understanding the intricate and dynamic interactions between microbes, metabolites and the host is essential for developing microbiota-targeted interventions to improve human health. To this end a precise mathematical framework is crucial to capturing the complex dynamics of the system.

Here, we develop a dynamic network model of coupled ordinary differential equations and present a computational workflow that integrates computer algebra with Bayesian inference for model identification. Our approach infers interaction rates—quantifying metabolite consumption and production—from experimental time-series count data within a Bayesian framework, incorporating prior knowledge and uncertainty quantification. This workflow enables in silico predictions of system behaviour under perturbations and offers a robust method to integrate high-dimensional biological data with mechanistic models. By refining our understanding of gut microbial dynamics, this framework facilitates the assessment of microbiota-targeted therapeutic interventions.

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