



## Evaluating of Genome-Scale Metabolic Models in Food Microbiology

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### DESCRIPTION

Food fermentation initially depended on uncontrolled process conditions and spontaneous fermentation by natural microbial consortia. The manufacturing became more regulated when self aggrandizing began and as microorganisms became more understood. At the industrial level, individuals are now studying, improving, and developing the fermentation process conditions and bacteria. Food safety and shelf life, particular biotransformations, and enhancing food with desired qualities are frequently the goals of food microbiology. To stop the formation of hazardous microorganisms, food preservation involves quick acidification. In addition to using substitute dairy products, biotransformations can involve preparing inedible food sources like coffee or cocoa. Food can be enhanced with flavorful substances, organoleptic qualities, higher nutritional value, or probiotic strains.

The methods for achieving these objectives have also improved. The systematic collecting and cataloguing of strains served as the foundation for advancements. The morphology, growth, or acidification qualities were the main topics of the phenotyping. The frequency and activity of strains in complex food matrices are now regularly tracked by multi-omics methods, and it now includes complete genome sequences. As technology and data have advanced, it has remained difficult to get beyond simple description to a more mechanical knowledge. Thus, Genome Scale Metabolic Models (GSMM), in particular, has a lot of potential for metabolic modelling. These GSMMs categorise an organism's metabolic processes into relationships between genes, proteins, and metabolic reactions. These models may therefore estimate metabolic capacities based on genomes and give a metabolic framework for the integration of genomics and cell physiology data.

### Safety and Food production

Acting microorganism metabolism is significantly responsible for the manufacture of goods that are secure, stable, and controlled with extended shelf life. To better comprehend metabolism and regulate fermentation processes, GSMMs have the potential to

be useful. These types of models have been created for a wide variety of food-related microorganisms, including baker's yeast, several lactic acid bacteria, and most recently acetobacteria. By mapping the entire metabolism, we may learn more about the relationships between different processes, such as how amino acid metabolism and redox balance are related or how the metabolism of arginine affects energy metabolism. Such models are less frequently utilised in food biotechnology than in chemical biotechnology, where they are strong tools for predicting and controlling cultivation and metabolic engineering tactics. Metabolic modelling is in fact made difficult by the numerous problems that occur in eating.

For one, foods are often solid, opaque, and turbid or exist as a multi-phase system. Complicated metabolite measurement in complex media, which is necessary to establish precise exchange boundaries in GSMMs, is a related challenge. Other readouts or accessible food-matrix models, like those recently created for milk, are required to monitor activities in such systems and collect data. Lactate is a crucial ingredient in food preservation products. Strangely, the primary modelling approach for GSMMs, classical Flux Balance Analysis (FBA), has problems forecasting it. As GSMMs only consider stoichiometry and exclude enzyme kinetics, they require uptake restrictions to limit the fluxes across the metabolic network. FBA optimises a goal, which in most situations equates to the maximum output of biomass constituents. FBA is an optimization challenge. FBA consequently forecasts the metabolic processes that result in high-yield methods that produce the maximum biomass from a finite amount of substrate. Even though inefficient overflow metabolism frequently happens under nutrient-rich circumstances in food, the FBA issue will always predict respiration over fermentation or acetate creation over lactate production in the absence of other limitations. The forecasting powers of GSMMs under situations relevant to food have been enhanced by recent improvements in modelling. It was demonstrated that lactate generation costs the least amount of protein per unit of ATP produced by considering resource allocation, or adding extra limitations to reflect the costs of executing a metabolic pathway.

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