MODELING AND OPTIMIZATION OF PROBIOTIC BACTERIA – GUT MICROBIOTA INTERACTION PROCESSES

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Modern probiotic biotechnology views the gut microbiota as a dynamic ecosystem where the efficacy of probiotic strains is determined by their ability to integrate and modulate the functional state of the microbial community. Mathematical modeling serves as a key tool for analyzing these processes, enabling the prediction of microbial population dynamics and optimization of therapeutic strategies. Among the most promising approaches are metabolic network models (e.g., Flux Balance Analysis), which reveal competitive and synergistic interactions between probiotics and resident bacteria [1]. Studies demonstrate that integrating metagenomic data with metabolic models allows for predicting how Lactobacillus or Bifidobacterium influence short-chain fatty acid (SCFA) production under varying environmental conditions. Accurate simulation of real-world conditions requires accounting for intestinal spatial heterogeneity, achieved through agent-based modeling. These models reproduce microbial distribution in the mucosal layer and gut lumen, predicting behavior based on localization. Optimizing probiotic formulations necessitates analyzing bacterial survival factors in vivo, including bile acid resistance and competition with autochthonous microbiota. Machine learning methods (e.g., Random Forest, neural networks) enable identification of key colonization parameters and optimal dosing, as evidenced by metatranscriptomic studies [2]. Personalized probiotic therapy relies on integrating multi-omics data (metagenomics, metabolomics) with artificial intelligence. For instance, in silico modeling of synthetic microbiomes allows testing probiotic effects in patients with dysbiosis or obesity. A promising direction involves microbiome-on-a-chip systems, where response surface methodology (RSM) algorithms optimize conditions mimicking gut physiology [1]. Key challenges remain, including limited data on intercellular communication and host influence. To address these, hybrid models combining systems biology with physiological parameters (e.g., gut motility, immune factors) are being developed. Blockchain technology implementation for clinical data analysis could enhance personalized prediction accuracy.

In conclusion, modeling probiotic-microbiota interactions enables a shift from empirical approaches to precision biotechnological solutions. Further progress will require interdisciplinary collaboration to develop integrated platforms capable of predicting individualized therapeutic efficacy.

References:

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