Lung infections are one of the most severe health concerns and the leading cause of death for cystic fibrosis (CF) patients. Cystic fibrosis is caused by a genetic mutation that inhibits ion transport across cell membranes, resulting in dehydrated mucus in the lung airways. The dehydrated mucus is highly viscous, promoting the colonization of a pathogenic microbial community, which persists throughout the lifetime of CF patients. The composition of the microbial community is critical for CF patients’ health and treatment decisions. In this study, we develop novel mathematical models to study the composition of two bacterial communities (aerobic and anaerobic) in the lungs of CF patients and the role of oxygen availability to alter the composition. We implemented two approaches: an ordinary differential equation-based model to gain basic insights into the community dynamics, and agent-based models to explore the impact of spatial heterogeneity. Our models are consistent with the data from a patient undergoing interrupted treatment for a CF-caused lung infection. We analyzed our models to determine conditions that minimize growth of the pathogenic anaerobic community and discuss optimal treatment strategies for CF lung infections. Finally, we investigate how the inclusion of spatial dependence affects our model predictions of the community health of the ecosystem.

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