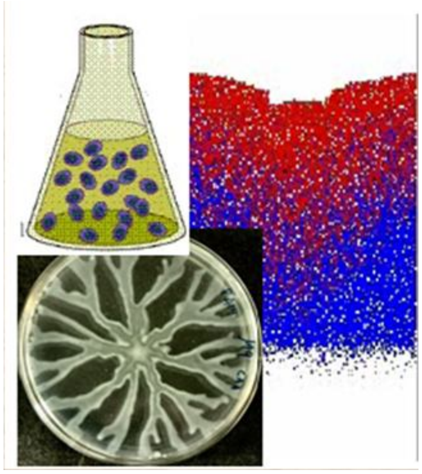
Bioinformatics of microbial communities



.Microbial communities play fundamental roles in health and disease as well as the stability of the ecosystem. A better understanding of these systems may provide insights into the mechanisms of infections, epidemics as well as environmental and social processes. Multispecies bacterial communities are a major form of life, examples range from giant underwater microbial mats of the oceans to the rich bacterial flora of the human body and to the microbial communities of the rhizosphere. Communities can add up the skills and the metabolic repertoire of the constituent species so they are able to solve problems that a single cell or a single species can not. Recent research shows that human, animal and plant diseases are polymicrobial i.e. they are caused by a team of microbial species in which pathogens and otherwise harmless symbionts collaborate in exploiting the host.

Our group uses use bioinformatics tools to map the chromosomal location and the local topology of the genes responsible for communication and cooperation, and maintain a repository of the participating genes in over one thousand microbial genomes. We also use agent based models to simulate bacterial communities, and to establish how sharing of signals and/or public goods contributes to colonization and infection. We showed that sharing public goods allows several bacteria species to cross barriers that the single species can not.

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