## Großes Physikalisches Kolloquium an der Universität zu Köln

## Prof. Dr. Arne Traulsen

Max Planck Institute for Evolutionary Biology, Plön

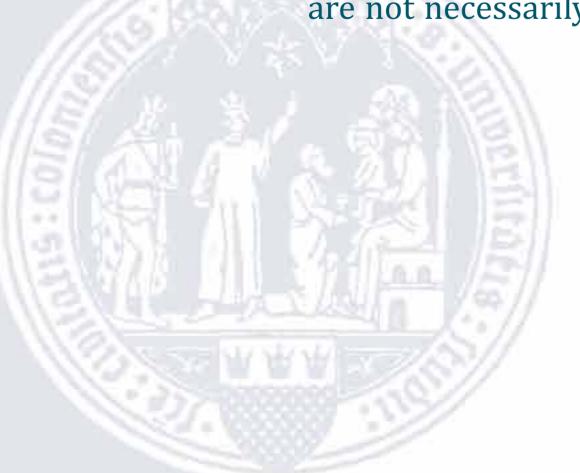


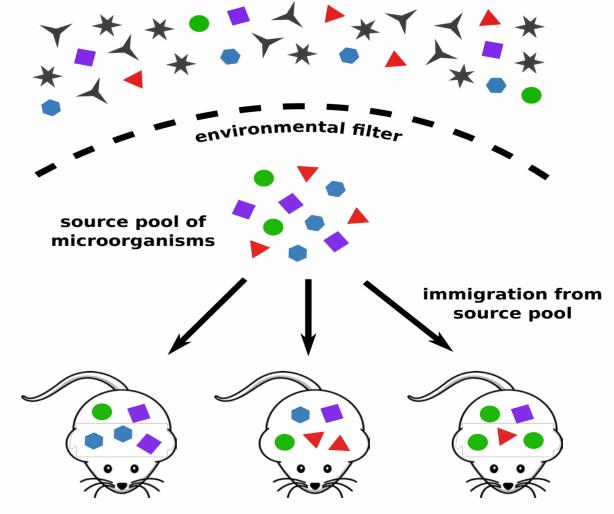
**20.11.2018** 16<sup>45</sup> Uhr / HS III

## Stochastic and deterministic models of microbiomes



All animals and plants are associated to a huge number of microbes that live together with them or even within them. These microbes often have fundamental roles in the functioning of their hosts, from metabolic functions to defense against diseases. In many cases, a disease microbiome seems distinct from a healthy one. This multi-stability of microbiomes can be understood in terms of game theoretical models that describe the interactions between microbes, but it is challenging to assess the associated parameters from experimental data. On the other hand, many microbes will randomly vary in their abundance, such that stochastic models are more appropriate to describe them. In the most extreme case of neutral models, it is assumed that all microbes are identical. Such neutral models are widely used in theoretical ecology and they can be directly applied to the microbiomes of a wide variety of host organisms. Neutral models allow to identify key microbial types, which! are not necessarily those that are found in particularly high abundance.





local communities of microorganisms