

## DANGEROUS CONNECTIONS : ON BINDING SITE MODELS OF INFECTIOUS DISEASE DYNAMICS

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### **ABSTRACT**

How to formulate models for the dynamics of a network and the superimposed transmission of an infectious disease ? The aim of the lecture is to describe a class of models that is amenable to analysis.

In the tradition of Physiologically Structured Population Models, the model formulation starts at the individual level by describing the dynamics of multiple (conditionally independent) binding sites. Influences from the 'outside world', in particular from partners of partners, are described by environmental variables.

Based on a 'mean field at distance one' assumption, these environmental variables are expressed in terms of population level averages. Next the system is closed via

-- a combinatorial relationship between binding site probabilities and individual probabilities.

-- identification of individual probabilities and population fractions in the large number limit.

The outcome is a rather low dimensional system of ODE for binding site probabilities, that nevertheless captures population level epidemiological quantities like  $R_0$  ,  $r$  , final size and endemic equilibrium.