

# Margherita Carletti

Department SUAN, University of Urbino "C. Bo", Italy  
margherita.carletti@uniurb.it

## Modelling intrinsic noise in biology

Physical systems described by deterministic differential equations represent idealised situations as they ignore stochastic effects. Stochastic models arise if we assume that such systems operate in noisy environments or if we want to model noisy behaviour in the systems themselves, for example the intrinsic variability of interaction between individuals of two or more competing species. In the context of *biomathematical modelling* we distinguish between *environmental* or *external* noise and *demographic* or *internal* noise, for which it is assumed that the variation over time is due to demographic variation of two or more interacting populations (birth, death, immigration and emigration). In this talk we investigate how intrinsic, i.e. internal, noise can be modelled in biology. In particular, we consider the methods developed in the field of computational biology, for example in Genetic Regulatory Networks (GRNs), and apply them to epidemic models when we are interested in understanding the effects of intrinsic noise on an ODE system. We provide a general framework for the modelling in different regimes - discrete stochastic, continuous stochastic and continuous deterministic - that is when the number of individuals (molecules, in GRNs) is small, when the numbers of individuals is small but also continuity arguments hold, and when the number of individuals is large. We also show how this approach can be used in DDEs models when demographic fluctuations are of interest. (M. Carletti, *Stochastic modelling of biological processes*, PhD Thesis, The University of Queensland, Australia, 2008).

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