

# Comparative Biology: Network Evolution

Objective: To give a presentation of about 60 minutes at the end of the week covering the key aspects of the finding regulatory signals in genomes by computational means.

Comparative Biology has recently experienced a major boom in the form of comparative genomics, where the interpretation of a genome is strongly augmented by the comparison with other genomes. This trend is now moving into networks, but comparison is ubiquitous in biology and as data and models accumulate at higher biological levels and structures, the application of evolutionary modelling will expand accordingly. There are key classes of networks in biology: Metabolic, Regulatory, Signalling and Protein Interaction Networks. The concept of network is so general (set of objects with pairwise relationships – or higher degree relationships in case of hypergraphs) that it will appear everywhere in science. The different kinds of network in biology describe different kinds of dynamics and the reasonable model of evolution will vary from class to class.

The questions and contents below are meant as motivators and need not be followed.

## The Big Questions Are:

- What are the key classes of networks?
- Are there hidden assumptions in network representations?
- How do networks evolve?
- How well are networks known?
- How does networks of different types interact?

## Maximal Contents of Presentation

Basic Types of Biological Networks

Network Inference

  Data available

  Methods available

Network Dynamics

Network Inference

Network Evolution

Network Integration, Inference and Evolution

## Recommended literature

Babu et al. (2005) "Structure and Evolution of Transcriptional Regulatory Networks" *Curr.Opin.* 14,283-91

Giannoulatou's DTC report on <http://mathgen.stats.ox.ac.uk/bioinformatics/projects/>

P.J. Ingram, M.P.H. Stumpf, J. Stark, *Network motifs: structure does not determine function*, *BMC Genomics* 7, 108 (2006).

S. A. Kauffman (1969) Metabolic stability and epigenesis in randomly constructed genetic nets *J. Theoretical Biology, Volume 22, Issue 3.437-467*

Koskinen, J. (2004) Bayesian Inference for Longitudinal Social Networks. Research Report, number 2004:4, Stockholm University, Department of Statistics.

Koskinen, J. and Snijders, T. (2007) Bayesian inference for dynamic social network data, *Journal of Statistical Planning and Inference*, 137, 3930–3938.

Lynch, M. (2007) "The Evolution of Genetic Networks by Non-Adaptive Processes" *Nature Genetics* 8,803-

R. Sharan, T. Ideker, *Modeling cellular machinery through biological network comparison*, *Nature Biotechnology*, 24, 427 (2006).

I. Miklos, G.A. Lunter and I. Holmes (2004) A "long indel" model for evolutionary sequence alignment. *Mol. Biol. Evol.* 21(3):529-540. Appendix A

Quayle and Bullock (2006) "Modelling the evolution of genetic regulatory networks" *J.Theor.Biol.* 238.737-753.

R. Sharan, T. Ideker, *Modeling cellular machinery through biological network comparison*, *Nature Biotechnology*, 24, 427 (2006).

□T. Shlomi et al. (2007) [A genome scale computational study of the interplay between transcriptional regulation and metabolism](#). □ *Molecular Systems Biology (MSB)*.

Torsten Reil: Dynamics of Gene Expression in an Artificial Genome - Implications for Biological and Artificial Ontogeny. *ECAL* 1999: 457-466

Snijders, T. (2001) "Statistical evaluation of social networks dynamics" in *Sociological Methodology* By Michael Sobel

Snijders, T. et al. (2008) "Maximum Likelihood Evaluation for Social Network Dynamics" In press

R.Somogyi & CA Sniegowski (1996) Modelling the Complexity of Genetic Networks *Complexity* 1.6.45-64.

Soyer, Pfeiffer and Bonhoeffer (2006) "Simulating the Evolution of Signal Transduction Networks" *J. Theor. Biol.* 241.223-232.

Tanaka, Ikeo and Gojobori (2006) "Evolution of metabolic networks by gain and loss of enzymatic reaction eukaryotes" *Gene* 365.88-94.

C. Wiuf, M. Brameier, O. Hagberg, M.P.H. Stumpf, (2006) *A likelihood approach to analysis of network data*, *PNAS*, 103.20.7566-70

Chen-Hsiang Yeang and Martin Vingron, "A joint model of regulatory and metabolic networks" (2006). *BMC Bioinformatics*. 7, pp. 332-33.