



SFB 680

Molecular Basis of Evolutionary Innovations

Molekulare Grundlagen evolutionärer Innovationen

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The mode of evolution of functional interactions among eukaryotic genes

Evolutionary biologists have long been fascinated by the mode of evolution, with arguments made in favour of either a gradual or a punctuational mode. We investigate the mode of evolution of interacting pairs of genes, using reliable data on craniofacial development in mouse. We evaluate the mode of evolution by the quality of predictions of functional interaction, assessed using these known data and present a whole-genome "correlated evolution network" for the mouse.

Functional interaction among gene products may be predicted bioinformatically, by testing for correlated gain and loss of genes from genomes over evolutionary time. Our comparative genomics approach assumes that, after a gene is lost from a genome, its interactors will have reduced importance for the survival of the organism. For each pair of genes in a genome, models of correlated gain/loss, and of uncorrelated gain/loss, on a phylogeny of several species may be fitted by maximum likelihood. The likelihood ratio indicates relative support for the hypothesis of correlated vs uncorrelated evolution. As with any single technique, the resulting interaction network is incomplete. However, it is reliable, in the sense of containing few false positive interactions. We may also test general hypotheses about evolution of pairs interacting genes, by assuming that more realistic models of evolution will lead to better predictions.

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3:15 p. m.

Institute for Genetics, Lecture Room, ground floor

Host: Johannes Berg

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