Genomes and phenotypes

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Much of what we know about the workings of biological systems has been learned through genetics: either, identifying individuals in a population with remarkable phenotypes and mapping the causal genetic variant; or, systematically perturbing genes and gene products, and spotting the effects this might have. While traditionally the approaches were low-throughput and sometimes haphazard, automation of lab-work, computing and the availability of full genome sequences have enabled systematic, quantitative high-throughput approaches. In particular, I will give an overview over the use of genome-wide RNAi libraries for the mapping of the \textit{phenotypic landscape} of a cell population; and of large-scale combinatorial RNAi perturbation assays to dissect the underlying, “hidden” functional modules. This poses many exciting computational questions, including image analysis, machine learning and inference from high-dimensional data.

References


