

Cologne Evolution Colloquium

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Scanning Genomes for Single-Cell Probabilistic Trait Loci

We are exploring a novel angle of genetics by studying how genotypes shape the statistical properties of single-cell phenotypic traits. Using yeast as an experimental model system, we found that natural genetic backgrounds confer different statistical properties of single-cell molecular and cellular traits. For example, some wild yeast strains display elevated cell-cell trait variability as compared to other strains. We identified genomic loci causing probabilistic changes and we propose to call them single-cell Probabilistic Trait Loci. Identifying such loci extends the usual QTL or GWAS genome scans by providing a probabilistic framework where cellular individualities are considered. For example, one locus we identified is a *cis*-eQTL (variant in one gene affecting its own expression) that also acts non-deterministically in *trans* by modulating the expression 'noise' of another gene. We recently developed a novel statistical method to scan genomes for such loci with no prior assumption of their mode of action. The method identified a yeast locus affecting gene expression noise, and simulations showed that it can also detect loci affecting other properties than mean and variance of single-cell traits. Our approach bridges single-cell biology with quantitative genetics, which may be particularly relevant when studying the hidden roots of incomplete penetrance and disease predisposition.

Wednesday, May 20, 2015, 17:00
University of Cologne, Institute for Genetics
Seminar Room 0.46

Hosted by Andreas Beyer