



Swiss Institute of
Bioinformatics



UNIL | Université de Lausanne

**Monday Oct. 4, 14:00, Auditorium A,
Genopode**

**Protein complexes are essential in the
monochromatic genetic landscape of the yeast cell**

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Abstract:

If perturbing two genes together has a stronger effect than expected they are said to genetically interact. Genetic interactions are important because they help map gene function - functionally related genes have similar patterns of genetic interactions. Mapping quantitative (positive and negative) interactions on a global scale has recently become possible. Clustering this data clearly shows groupings of genes with similar positive or negative interactions, termed monochromatic groups. Based on this, the established model holds that monochromatic patterns identify pathways and complexes. We systematically studied the monochromatic nature of biological processes using the most comprehensive quantitative genetic interaction dataset available, including 5.4 million gene pair measurements made in normal growth conditions in the yeast *Saccharomyces cerevisiae*. We find that only 10% of biological processes, as defined by Gene Ontology annotations, and less than 1% of inter-process connections are monochromatic. Further, we show that protein complexes are responsible for a surprisingly large fraction of this pattern. These results lead to development of a new model of the monochromatic landscape of the yeast cell.

Host: Dr. David Gfeller, SIB Molecular Modelling Group