Multi-omic data integration enables discovery of hidden biological regularities (28/12/2018)

**Multi-omic data integration enables discovery of hidden biological regularities**

Rapid growth in size and complexity of biological data sets has led to the 'Big Data to Knowledge' challenge. We develop advanced data integration methods for multi-level analysis of genomic, transcriptomic, ribosomal profiling, proteomic and fluxomic data. First, we show that pairwise integration of primary omics data reveals regularities that tie cellular processes together in *Escherichia coli*: the number of protein molecules made per mRNA transcript and the number of ribosomes required per translated protein molecule. Second, we show that genome-scale models, based on genomic and bibliomic data, enable quantitative synchronization of disparate data types. Integrating omics data with models enabled the discovery of two novel regularities: condition invariant *in vivo* turnover rates of enzymes and the correlation of protein structural motifs and translational pausing. These regularities can be formally represented in a computable format allowing for coherent interpretation and prediction of fitness and selection that underlies cellular physiology.

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