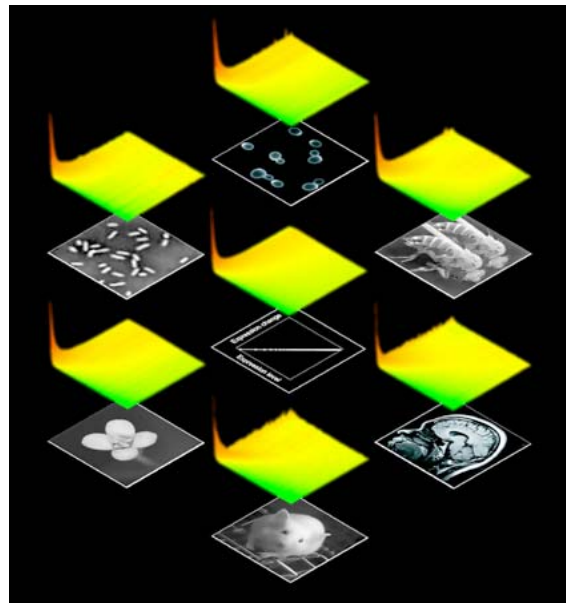


Rich genes travel more

March 1st, 2004 – In a study of changes in gene expression covering taxa from bacteria to human published in the PNAS Online Early Edition issue of the Proceedings of the National Academy of Sciences, Hiroki R. Ueda of the RIKEN Center for Developmental Biology (Kobe, Japan) and colleagues report their discovery of a fundamental governing principle to the dynamics capable of producing the heterogeneous distribution of gene expression.

Ueda, who heads the CDB Laboratory for Systems Biology, found that changes in gene expression scaled closely with initial expression levels in every organism studied; highly expressed genes tend to change in a highly dynamic way, while genes with lower expression levels are less likely to show such variability. Such proportionality governs many forms of expression changes, such as temporal oscillations, responses to environmental stimuli and developmentally determined or tissue-specific gene regulation, and underlies the heterogeneous distribution of gene expression. The distribution of gene expression can be described using what is known as a “power law” distribution. In such a system, it can be shown that the number of genes having expression level X is 100 times larger than that of the population having a tenfold greater expression level ($10X$).

The basic dynamics that underlie and produce this power-law distribution have yet to be worked out, but Ueda and colleagues now propose that the proportional dynamic operating in gene expression changes might be described as a “rich-travel-more” mechanism, a counter concept to the “rich-get-richer” metaphor that has been used to explain other power law-based distributions, such as the growth of network connections in the World Wide Web.



Transition probability representing gene expression dynamics in *E.coli* (left top), Budding yeast (center top), fruit fly (right top), *Arabidopsis* (left bottom), mouse (center bottom), human (right bottom) and theoretical model (center middle). Gene expression dynamics are evolutionary conserved from *E.coli* to human, and modeled as ‘proportional dynamics’ or ‘rich-travel-more mechanism’ (center middle) where gene expression changes are proportional to their expression levels.

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The PNAS study looked at gene expression dynamics in a broad range of model organisms familiar to life sciences researchers, including the intestinal bacteria *E. coli*, the yeast *S. cerevisiae*, *Arabidopsis thaliana* (thale cress), the fruit fly *Drosophila melanogaster*, mouse and human, by studying genome-wide RNA expression change using GeneChip microarrays. The team's analysis of distribution of gene expression in diverse species revealed that there is an apparently universal principle in expression dynamics, and showed that this principle can generate the observed heterogeneous power-law distribution of gene expression. These findings dovetail nicely with other ongoing studies that indicate a similar mechanism is at work in the evolution of metabolic networks, and point the way toward an improved understanding of the systems-level features capable of generating complex and dynamic biological network structures.