Consistency of gene expression profiles with metabolic flux predictions

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Understanding the interplay between metabolism and gene regulation is one of the major challenges of systems biology. *Within* each level of cellular organization we recently studied the consistency between high-throughput data and the network architecture of the respective cellular system.

Together with Georgi Muskhelishvili (Bremen) we studied systematic interplay between two types of control in gene expression profiles in *E. coli*, one network-mediated and the other mediated by DNA topology (Marr et al. 2008).

Together with Wolfram Weckwerth (Vienna) we analyzed metabolomics data from a network perspective (Müller-Linow et al., 2007).

Here we address the interrelation between the two systemic levels by quantifying the consistency between gene expression profiles and metabolic pathways and show that this is a very informative starting point for elucidating the interplay between gene regulation and metabolism.

In particular we find that the consistency of the expression pattern with metabolic demands changes systematically under variation of DNA supercoiling energy and when going from wildtype E. coli to mutants in structural proteins.

We observe a significantly higher metabolic control for the wildtype expression data compared to the mutants. This effect is even more pronounced, when we compute a wildtype metabolic flux distribution with flux balance analysis and restrict our analysis to active reactions.

Marr, C., Geertz, M., Hütt, M.-Th. and Muskhelishvili, G. (2008) Dissecting the logical types of network control in gene expression profiles, BMC Systems Biology 2, 18.

Müller-Linow, M., Weckwerth, W. and Hütt, M.-Th. (2007) Consistency analysis of metabolic correlation networks, BMC Systems Biology 1, 44.