

# Dynamic Regulation of Gene Expression

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## Motivation

One key point in the analysis of gene expression dynamics is that mRNA abundance is determined by two regulated processes: transcription and degradation, both specifically affecting transcript levels. It is becoming progressively more evident that mRNA degradation and its regulation is an important factor in determining the expression pattern of many genes. When trying to infer the global phenotypes of cells from large-scale mRNA expression profiling data, it would be important to consider both transcriptional and post-transcriptional level of gene regulation.

## Methods

Here we model gene expression in order to capture the specific part of mRNA expression dynamically changing in response to regulatory signals affecting transcription, mRNA stability or both. To this end, we introduced the net mRNA expression, i.e. the mRNA expression normalized to basal transcription and degradation rates, computed by the NEMES (NEt MRNA ExpreSsion) algorithm.

## Results

Evaluating net-mRNA expression using genome wide cell cycle time series data and decay the method strikingly identifies regulatory switching points, thus revealing the underlying dynamic link between gene expression and regulatory programs. As global decay data can be easily obtained by means of microarray experiments, we anticipate that net-mRNA expression will prove to be a powerful tool to fully understand the dynamics of gene regulation in single and multicellular organisms.

**Availability:** <http://www.dis.uniroma1.it/~farina/NEMES/>

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