

Gene autoregulation via intronic microRNAs and its functions

Bosia C^{1,2}, Osella M^{1,2}, El Baroudi M¹, Corà D³, Caselle M^{1,2}

Motivation

While many microRNAs are transcribed from their own genes, nearly half map within introns of "host" protein-coding genes. It may happen that these intronic microRNAs regulate the expression of their host genes, forming a microRNA-mediated self loop. A recent analysis of this phenomenon suggests that autoregulation mediated by intronic microRNAs may be under positive selective pressure but the functions of this regulatory circuit are currently unknown.

Methods

We studied the behaviour of this class of circuits using both stochastic and deterministic equations, validated via simulations (Gillespie algorithm and numerical integration of equations respectively).

Results

Our model suggests that microRNA-mediated self regulation, despite its simple topology, can perform different regulatory tasks. Firstly it can alter the response time of gene expression to upstream signals, secondly it can implement fold-change detection (a feature related to Weber's law) and finally it can confer robustness to noise. Moreover, we compare the features of this circuit with the analogous transcriptional self-regulation, which is an ubiquitous network motif in different species, to highlight in what situations a post-transcriptional self-regulation can be advantageous for the cell.

Contact e-mail

cbosia@to.infn.it

¹ Dipartimento di Fisica Teorica, Università degli Studi di Torino and I.N.F.N., Torino ² Center for Complex Systems in Molecular Biology and Medicine, Università degli Studi di Torino, Torino ³ Systems Biology Lab, Institute for Cancer Research and Treatment (IRCC), Università degli Studi di Torino, Torino