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**On the control of gene expression in small RNA post-transcriptional regulation pathway: role of conserved weak targets<sup>1</sup>**  
DANIEL JOST, ANDRZEJ NOWOJEWSKI, EREL LEVINE, Department of Physics and FAS Center for Systems Biology - Harvard University — Small RNA molecules play critical regulatory roles in organisms across all kingdoms of life. Many small RNA families achieve target-specificity via base-pairing of a very short (6-8 nucleotides) “seed” region with the targeted mRNA, and consequently many genes carry a matching seed in their sequence. Evidence in bacteria and animals suggest that a single small RNA may regulate the gene expression of many different targets, although most of them very weakly. On the other hand, in all cases we are aware of where the functionality of a small RNA has been carefully studied, only a small number of target genes were identified as being phenotypically relevant. Here, we present a Langevin formalism which describes the dynamics of the different interacting entities (small RNA and targets), including the stochasticity of the underlying biochemical reactions and the effect of transport. Using analytical or numerical computations, we study the influence of (many) weak targets on the mean and noise properties of (few) principal targets. In particular, we argue that the role of these weak targets is to confer robustness to the regulation of the principal targets without significantly affecting their temporal responses to changing environments.

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