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Title: What We Shouldn't Ignore When Studying Gene Regulation

Abstract: Until recently, the study of gene regulation has focused mostly on two major mechanisms: the regulation of transcription (typically described in terms of the binding to transcription factors to specific DNA sequence motifs) and on direct protein-protein interactions. A string of high-throughput experiments, however, has resulted in overwhelming evidence that several other layers of regulation are of comparable importance and cannot be neglected. Indeed, at least half of the diversity of the observable transcriptome is comprised by non-coding RNAs, and novel types and classes of ncRNAs keep being discovered. The oldest and best known, but as it seems by no means the only one of these RNA-mediated mechanism is post-transcriptional regulation through microRNAs. Anti-sense transcription is another one of the better-known effects.

In my presentation I will briefly review recent findings, both experimental and computational, that suggest that a substantial fraction of transcripts has regulatory function. Then I will focus on bioinformatics approaches to disentangle - at least partially - the various layers using two systems as examples: direct RNA-RNA and RNA-protein interactions. Because of their abundance (even though we understand very few specific systems in detail), we cannot ignore these multiple regulatory layers in attempts to reconstruct and eventually understand gene regulation networks.