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Interplay of Noisy Gene Expression and Dynamics Explains Patterns of Bacterial Operon Organization¹
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Bacterial chromosomes are organized into operons – sets of genes co-transcribed into polycistronic messenger RNA. Hypotheses explaining the emergence and maintenance of operons include proportional co-regulation, horizontal transfer of intact “selfish” operons, emergence via gene duplication, and co-production of physically interacting proteins to speed their association. We hypothesized an alternative: operons can reduce or increase intrinsic gene expression noise in a manner dependent on the post-translational interactions, thereby resulting in selection for or against operons in depending on the network architecture. We devised five classes of two-gene network modules and show that the effects of operons on intrinsic noise depend on class membership. Two classes exhibit decreased noise with co-transcription, two others reveal increased noise, and the remaining one does not show a significant difference. To test our modeling predictions we employed bioinformatic analysis to determine the relationship gene expression noise and operon organization. The results confirm the overrepresentation of noise-minimizing operon architectures and provide evidence against other hypotheses. Our results thereby suggest a central role for gene expression noise in selecting for or maintaining operons in bacterial chromosomes. This demonstrates how post-translational network dynamics may provide selective pressure for organizing bacterial chromosomes, and has practical consequences for designing synthetic gene networks.

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