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NOISE ABATEMENT AND GENOME EVOLUTION

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Noise in gene expression is inevitable, but is it selectively important? Here I approach the issue by asking whether genomes adapt to modify expression in noise. In particular I will show how clustering of essential genes in yeast into domains of open chromatin and co-linearity of metabolic genes in bacterial operons both are expected as noise abatement mechanisms. Both models have striking predictive ability. The operon model uniquely explains why co-linearity is strongest for lowly expressed operons and the essential gene noise minimization model correctly predicts the dearth of sub-telomeric essential genes and that noise levels should be predicted by the local density of essential genes. If selection to modify noise can determine gene order, noise must itself be selectively important.