



Decoherence in yeast cell populations and its implications for genome-wide expression noise

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ABSTRACT. Gene expression “noise” is commonly defined as the stochastic variation of gene expression levels in different cells of the same population under identical growth conditions. Here, we tested whether this “noise” is amplified with time, as a consequence of decoherence in global gene expression profiles (genome-wide microarrays) of synchronized cells. The stochastic component of transcription causes fluctuations that tend to be amplified as time progresses, leading to a decay of correlations of expression profiles, in perfect analogy with elementary relaxation processes. Measuring decoherence, defined here as a decay in the auto-correlation function of yeast genome-wide expression profiles, we found a slowdown in the decay of correlations, opposite to what would be expected if, as in mixing systems, correlations decay exponentially as the equilibrium state is reached. Our results indicate that the populational variation in gene expression (noise) is a consequence of temporal decoherence, in which the slow decay of correlations is a signature of strong interdependence of the transcription dynamics of different genes.

Key words: Decoherence; Gene expression noise; Transcription; Cell biology; Biophysics; Mathematical biology