

Stochasticity in biological systems: signals in the ‘noise’

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To most biologists, variation in biological measurements is simply noise and the role of the biostatistician or bioinformatician is to extract the signal as cleanly as possible. This is enshrined in the ‘classical’ population-genetics model that ascribes phenotypic variation to the combined effects of genes plus environment. Typically, any variance unexplained by this model is attributed to unspecified biological error. For some time it has been clear that such thinking flies in the face of the known intrinsic error rates in biological information processing, which is such that key mechanisms in the synthesis and processing of macromolecules operate with low but nevertheless important levels of intrinsic inaccuracy. The consequences of such inaccuracies are seen particularly in the accumulation of intrinsic errors that are thought to underlie the ageing process. The general importance of intrinsic stochastic variation in the development, maintenance and ageing of biological systems will be considered, with particular reference to recent work on the systems biology of ageing.