

Networks and Information: Explanatory Arguments in Contemporary Biology

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Network representations of biological function invoking genes, RNA, proteins, signalling molecules and metabolites, have introduced an articulation of dynamical complexity in the description of fundamental biological systems. Earlier characterisations of the “central dogma” in molecular biology – that information flows from the gene to the protein, nucleus to cytoplasm – have often been extended to provide gene-determined explanations. The contemporary articulation of causal influences of components “downstream” of the gene in this traditional view have opened up the notion of information flow, and a varied toolbox of quantitative methods are now being invoked to pose questions of biological systems and models. This paper will look at some of the explanatory roles that properties of network based characterisations are being made to fulfill, and explore the conceptual traces these techniques carry from the more theoretical-mathematical practices that engineering and physical sciences where they have been traditionally used.