
Context-based functional synthesis

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Abstract

Technological progress has dramatically changed Biology over the last 3-4 decades. High-throughput sequencing made transcriptomics accessible, and whole genome sequencing affordable. Miniaturization made proteomics amenable to normal cells. Flow cytometry with increasing numbers of fluorescent probes, mass spectrometry and single-cell sequencing permitted and revolutionized the study of individual cells. One is now confronted with an exponential wealth of information. Ascribing a function to biological objects has been a task of Biologists since ever; it is more than ever necessary. The problem, however, has changed. Instead of dissecting organisms into systems, systems into organs, organs into cells, cells into organelles, organelles into smaller parts and, ultimately of giving molecules a function in the context of organisms, one must assemble innumerable molecules with no known function into a biologically coherent whole. Functional analysis cannot anymore be applied as proposed by Wimsatt and Cummins in the 1970s. I propose instead a functional synthesis aiming at understanding how function emerges from interactions of proteins with other proteins in a given context. I will use the example of antibodies and show how they can be protective and pathogenic, generate antagonistic signals when engaging different receptors, both induce and inhibit cellular responses and select biological responses within the potential functional repertoire of cells. Finally, I will argue that the concept of "structure-function relationship" is inaccurate because, like antibodies, molecules have no function but properties, and that the function(s) they exert depend(s) primarily on the context in which their properties operate when they interact with other molecules.

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