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Adaptive sorting: a new mechanism for ligand recognition

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Many biological networks have to filter out useful information from a vast excess of spurious interactions. We use computational evolution to predict design features of networks processing ligand categorization. The important problem of early immune response is considered as a case-study. Rounds of evolution with different constraints uncover elaborations of the same network motif that we name “adaptive sorting”. An instance of this module is present in mammalian T-cell biochemical networks. Analytical study of this motif unifies several puzzling properties of immune recognition, such as ligand antagonism and non-monotonic response time of immune response as a function of ligand concentration. It also predicts counter-intuitive loss of response at high ligand concentrations of foreign ligands for some parameter regime, which is checked experimentally.

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