

Abstract Submitted
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Biophysical constraints on the computational capacity of biochemical signaling networks¹ CHING-HAO WANG, PANKAJ MEHTA, Physics Department, Boston University — Biophysics fundamentally constrains the computations that cells can carry out. Here, we derive fundamental bounds on the computational capacity of biochemical signaling networks that utilize post-translational modifications (e.g. phosphorylation). To do so, we combine ideas from the statistical physics of disordered systems and the observation by Tony Pawson and others that the biochemistry underlying protein-protein interaction networks is combinatorial and modular. Our results indicate that the computational capacity of signaling networks is severely limited by the energetics of binding and the need to achieve specificity. We relate our results to one of the theoretical pillars of statistical learning theory, Cover's theorem, which places bounds on the computational capacity of perceptrons.

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