

Title:

The specificity of bacterial protein-protein interactions & the inverse Potts problem

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Abstract:

The inverse Potts model has been used to identify structural details of interacting proteins in prokaryotic two-component signaling systems. The involved proteins show strong structural and sequence conservation across hundreds of bacterial species, but they are also characterized by high interaction specificity, to avoid crosstalk between different signaling pathways. Here we show that the inverse Potts approach can be extended toward a quantitative understanding of interaction specificity. Our analysis of the natural sequence variability in families of homologous proteins inside and between species leads to robust high-quality predictions in identifying interacting protein pairs. Extensions toward predicting the influence of single mutations on the interaction specificity are also discussed.