

Title of proposed idea: Completing and connecting interaction maps

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What is the major obstacle/challenge in the field? What is needed to overcome this obstacle/challenge?

Interaction maps have great promise for revealing how a cell works. Major obstacles limit their full use, however. Maps are largely incomplete. Different maps, such as metabolic networks, protein interaction networks, and gene regulatory networks, do not communicate. Understanding how a network remodels or activates under specific conditions is also a challenge.

What emerging scientific opportunity is ripe for investment by a Trans-NIH program (e.g. the NIH Common Fund)?

Given technology advances, for example the use of next-gen sequence as a readout for two-hybrid screens, there is an opportunity to generate complete interaction maps for model organisms. Ample access to data presents a growing need for methods that can combine information about proteins with information about gene regulation, metabolic state, and cell fate.

What are the potential Trans-NIH investments that could accelerate scientific progress in this field?

Investments in completing interaction maps for model organisms, or for the set of proteins expressed in relevant human cell types.

Methods for joint analysis of multiple data types.

If a Trans-NIH program on this topic achieved its objectives, what would be the impact?

Predictive models of the cell.