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April 30, 2010

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Re: Letter of Intent for R21 “Social Network Analysis and Health” PAR – 10 – 146 (r21)

Dear [redacted] –

I am writing to let you know that I intend to submit an R21 application under the “Social Network analysis and Health” RFP tentatively titled “Simulation Models for Diffusion over Multirelational Dynamic Networks.” The research team will consist of [redacted] (PI) and two advanced network graduate students.

Our understanding of the network effects on health tend to model networks as simple network systems, with people connected or not (sometimes treated as weighted edges, but often not) and transmission dependent on fairly deterministic models of how “susceptible” nodes are linked to “infected” nodes.

However, we know that in reality, diffusion is conditioned by the joint properties of the type(s) of relations connecting pairs and the types of diffusion determining health. Thus, disease diffusion will vary by the type of contact (fluid exchange vs. physical contact, for example) while diffusion of information or behavior norms (affecting health behavior and risk, such as with recent models on smoking or obesity) depend crucially on the social content of the relation (coworker, friend, family, etc.) and substantive rules for how information is transferred and incorporated into actors’ worldviews. Moreover, in all diffusion cases, we expect the network structure to change over time, and often in response to the health-relevant diffusion.

Thus, our goal is to build a unified simulation system for articulating the features relevant for network diffusion across multiplex networks. The system will allow one to model diffusion in general, with network structures ranging from simplest-case networks (single binary relations over stable networks) to complex (multiple dynamic relations with recursive rules linking diffusion and network change). The innovative new strategy we intend to employ is three-fold. First we will identify a reasonable range of multiplex network evolution models from available empirical data. We will then construct formal algebraic models for multiplex network formation. Finally, we will use the compositional rules identified in these models to construct dynamic network simulations for exploring diffusion potential.

The result will be a set of models, linked to shared software, that can be used by health and social scientists to explore the range of potential diffusion regimes in realistic settings.

Thanks for your consideration of this proposal, please let us know if there is anything we can provide to help in the review process.

Sincerely,

[redacted]