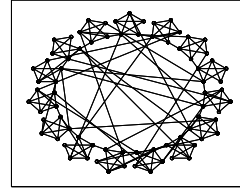# A Network Model of Alcoholism and Alcohol Policy

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Data are available from random surveys of populations regarding alcohol abuse. This information is relatively reliable compared to many types of hard drug abuse. Data are available in relatively small geographic areas such as zip codes. Can these data be used to evaluate the ecology of the population and to help make effective policy decisions? We will using real data from recent surveys of the Delaware population [1]. With that data, we wish to construct a social network consistent with those statistics and study the epidemiology of alcoholism with some known population structures [2, 3, 4, 5, 6, 7].

The key idea is to study the effect of previously-studied social structures on alcohol-related problems within, say, zip codes of Delaware. We would like to begin to answer the question "What is the effect, if any, of different social structures on the spread and persistence of alcohol-related problems and what policy conclusions can be drawn from understanding this effect?" We would like to build on the pioneering work of Watts [3, 4] and Newman [6], who addressed similar questions in the case of infectious disease. We note that while alcoholism is a disease, the epidemiology is distinctly different from that of *infectious* disease. We do not intend to solve the riddle of what causes alcoholism; we aim to merge data available for alcohol-related problems with the science of networks to provide ideas and tools for estimating policy costs.

As a beginning, we propose studying some very basic models. One possibility is to study the evolution of fraction of a population on a network via a continuum model as discussed below. Another possibility is to study the evolution of a population consistent with available survey data and simulate its evolution on different realizations of social networks.

In a simulation approach, we could begin in the following way. A detailed survey data file is available on a sample of 2627 people with differing degrees of alcohol-related problems which can all be easily read into Matlab and subsets of the results can be easily extracted and used. A good beginning would be to try some beginning problems where some subset of the survey population is embedded into a larger population (consistent with survey and general population), connect them with social interactions of a small world or power law form. Links would be created if the two people knew each other well enough to eat or drink together (perhaps the latter should be emphasized). Then, using rules for changing people (vertices) from sick to healthy or vice verse, we can see what if any difference it makes in the population with different network realizations and rule changes. (Example rule: If a person has a majority of friends who are "sick", that person bcomes sick; if a sick person has a majority of friends who are healthy, then the sick person is healed. If the person had an alcoholic parent, then perhaps only two "sick" friends are needed to make healthy turn to sick, etc.) The social network must be hypothesized and sensitivity to it evaluated. If the participants are ambitious and can code rapidly, then we could also try adding a demographic model to change the age distribution of the population and then to modify the network as well (e.g., [8]); this is essentially a simulation that ages the population as it progresses. This last option is complicated, but it is a valuable ingredient in the eyes of the policy evaluators.

To begin in a continuum approach, we could study the fraction of the population which is alcohol dependent, $\rho(t)$, with a single ordinary differential equation as in [5] used for an SIS model; in this approach, the structure of the network affects the dynamics of the spread of an epidemic. We will modify the ODE to reflect the dynamics of alcoholism as opposed to an infectious epidemic. In the infectious case, the fraction of the population that is infected decays linearly, but for alcoholism, we could hypothesize either decay or growth.

After understanding the most basic single equation case, we can add in the effect of treatment. This can be accomplished by modifying the single equation, or by generalizing to a system where the infected population is divided into different categories. For example, we could have fractions of the infected population that are treated or untreated; we could also add mortality to the model. Policy decisions that impact initial or ongoing values of the proportion of treated individuals could be evaluated from the behavior of the models; it may then be possible to use the results to make policy decisions.

References

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