NDnano Undergraduate Research Fellowship (NURF)
2015 Project Summary

1. **Student name**: Sushrut Ghonge

2. **Faculty mentor name**: Prof. Dervis Vural

3. **Project title**: Modelling aging in complex networks.

4. N**ew skills acquired during summer research**: This research project was a different experience because it involved thinking and solving problems on my own with very little time spent on reading research literature. This improved my problem-solving skills. Since this was a theoretical project and we got complicated equations, I also learned to use packages like MATLAB® for solving them.

5. **Practical application**: We attempt to determine how various components of an aging system depend on each other, or mathematically, determine the structure of a complex network from the diffusion data. This can be used to determine gene networks; in ecology to determine how various species depend on each other from sample death/extinction data; in social networks, to determine the network structure from data of spreading of opinions.

SUMMARY

We use complex networks to model aging. Aging can be modelled as a diffusion process on a complex network. Each node will represent a functional unit or a cell. Various cells/units depend on each other and death of many providers of a unit causes its death.

A complex network is a directed graph, i.e. it has nodes and directed edges. Complex networks are used to model various systems like power grids, neural networks, ecosystems, social networks and heart cells. Diffusion is a process on complex networks which is used to study spreading of epidemics, economic crises, opinions on social networks, deaths of species/cell types, and various other spreading processes.

We studied an irreversible Watts' model which resembles death, aging, spreading of opinion, extinction of species, etc. In this model, a node dies/gets activated either naturally with a small probability or when a certain specified fraction of its providers are dead/activated. It takes one time step for a node to get activated due to interactions.

The aim of the project is to determine the structure of the network, i.e. determine how every node depends on other nodes if we are given the time of activation of each node. For doing this we first need to study the process of diffusion. We derived equations governing the fraction of activated nodes in a network when such a process occurs.

$$P(t) = P(t-1) + \big(1 - P(t-1)\big)\gamma + \big(1 - P(t-1)\big)(1-\gamma) \sum_{k=0}^{n-1} \Gamma(k) \sum_{r=[fk]}^{k} \binom{k}{r} P(t-1)^r \big(1 - P(t-1)\big)^{k-r}$$
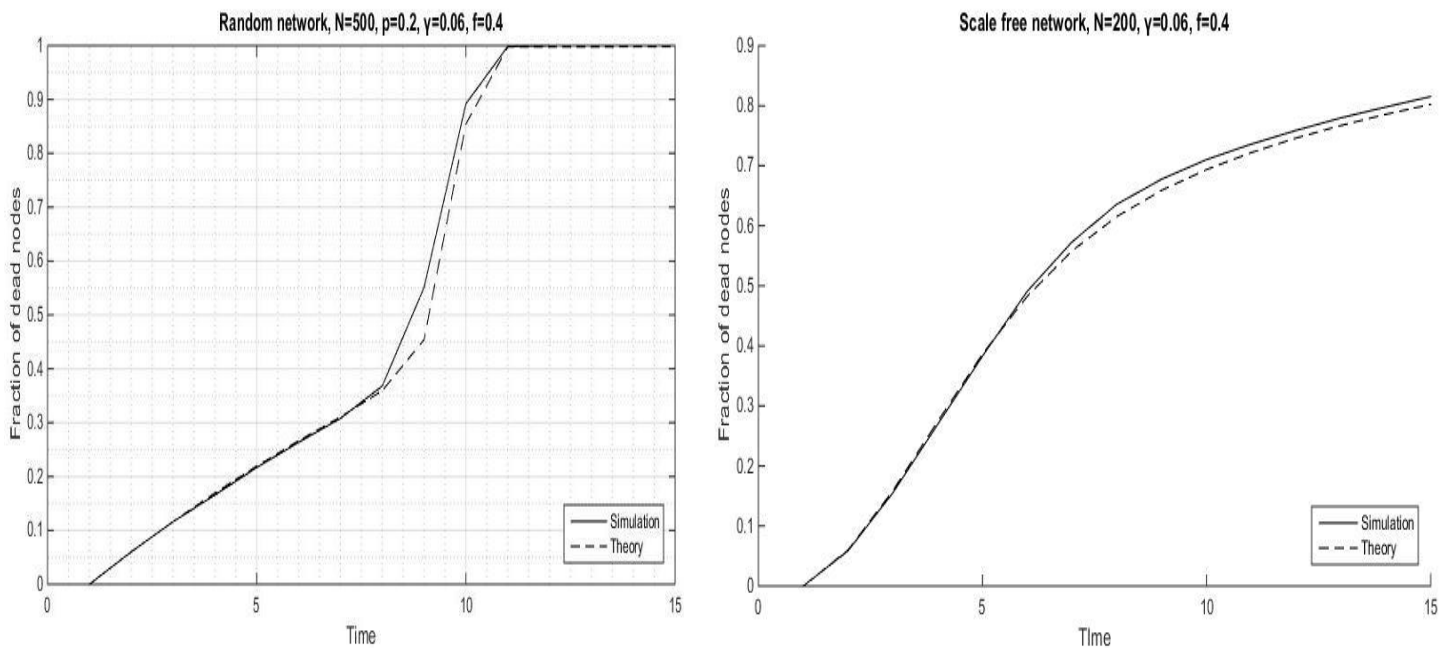
Here P(t) is the fraction of activated nodes at time t.

Given the data, there is a probability for every pair of nodes being connected. $P(i \rightarrow j \,|\, t(i), t(j))$. If a node provides to another, there is an increased chance of the provider dying just before it or shortly before it. Using the equation for P(t) above, we also derive the probability i→ j for all i,j in every experiment. We

want to combine the probabilities so that the data is scanned efficiently for correlations. Now that we know how an edge affects the times of death of two nodes, we use Bayesian inference to find the probability that a node provides to another.

Another way to combine the probabilities is to treat them like scores for edges, then choose the edges with highest scores (probabilities) to get the overall network.

RESULTS:

Above plots compare the fraction of dead nodes in simulations and as predicted by our formula. The plot on the left corresponds to a very densely connected network and the other to a very sparsely connected network.

Accuracy of inversion is about 60% for dense networks and about 80-85% for sparse networks.

Publications (papers/posters/presentations): I gave an oral presentation at the NDnano oral presentation session on 22$^{\text{nd}}$ July 2015.