Headline	**Watching how viruses friend social network**		
Date	**04 Sep 2011**	Language	**English**
MediaTitle	**Borneo Post (Kuching)**	Page No	**a10**
Section	**World**	Article Size	**182 cm²**
Journalist	**N/A**	Color	**Black/white**
Frequency	**Daily**	ADValue	**1,048**
Circ / Read	**88,150 / 166,173**	PRValue	**3,144**

Watching how viruses 'friend' social network

TEL AVIV: A new application through Facebook, developed in a Tel Aviv University lab, is poised to serve as a better indicator of how infections spread among populations.

Dr Gal Almogy and Professor Nir Ben-Tal of the Department of Biochemistry and Molecular Biology have developed a Facebook application called PiggyDemic, which allows users to "infect" their friends with a simulated virus or become infected themselves.

The resulting patterns will allow researchers to gather information on how a virus mutates, spreads through human interaction, and the number of people it infects.

Currently, scientists use mathematical algorithms to determine which virus will spread and how, but this method has some flaws.

It assumes that a virus has equal distribution across populations, but that is simply not the case, the researchers say.

Patterns of social interaction must also be taken into account. "HIV is concentrated in Africa; certain types of flu are widespread in North America and Asia," explains Dr Almogy. "Adding the element of human interaction, and looking at the social networks we belong to, is critical for investigating viral interaction."

Facebook, notes Dr Almogy, is an ideal tool for such an undertaking. The social networking site's digital interactions simulate in-person interactions.

Once added to a user's Facebook account, PiggyDemic follows the user's newsfeed to determine the people they interact with. Users are deemed "susceptible," "immune" or "infected" with various simulated viruses, and can pass them on to their online contacts. Researchers then follow these interactions using network visualisation software, and watch the links between users as the "viruses" are passed on.

According to Dr Almogy, accurate modelling of viral dynamics is critical for developing public health policy. Issues such as the use of vaccinations, medications, quarantine and anti-viral procedures will be better informed if we are able to predict more accurately the course of infection.

"People who have this software can report if they are actually ill," says Dr Almogy. "If we know who their friends are and the sequence of the infecting virus, we can figure out which virus they have and how it passes from one person to another."