Potential gene linking transmission of chemical synapses to plaques and tangles using BiNGO statistically significant genes

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Introduction
Alzheimer's disease is 6th leading cause of death in the United States, and the number of people living with this condition is growing every year. Alzheimer's is believed to be caused by 2 abnormal structures known as plaques and tangles. Scientists are still searching for direct correlation between plaques and tangles and the known effects of Alzheimer's. One such effect is the lack of transmission across chemical synapses. Recent studies on mice have proved that gene therapy is an effective way of reversing the loss of memory. While scientist have looked into gene therapy to assist with memory loss, the direct application of gene therapy to transmission of synapses has been overlooked. Exploring the potential of gene therapy in reinitiating communication between synapses will assist in prevention of Alzheimer's for future generations through adjusted treatment.

Methods
The data set originally used was reference series GSE28146, downloaded from NCBI (National Center for Biotechnology Information). The data obtained was derived from a study that analyzed laser-captured hippocampal CA1 gray matter from FFPE hippocampal sections of subjects at varying stages (incipient, moderate, severe) of Alzheimer's disease. Two sample sets were compared; one of a group of seven patients with severe Alzheimer's and a control group of eight patients with no Alzheimer's. Genes that were expressed differently between the two groups were calculated using a student T-test with a p-value of less than 0.01 through R. The list of upregulated genes produces from the test were run through the BiNGO plugin for Cytoscape, This process determines which biological processes are statistically overrepresented in the common biomarkers. If relevant pathways are overrepresented, it confirms conclusions about relatedness. After specific genes relating to the effects of Alzheimer's were found, further research was done using gene cards databases and published papers from other researchers to confirm hypothesized connections.

Results
31 genes were identified as BiNGO statistically significant genes. 13 biomarkers fell under the biological process of response to hormone stimulus. After researching these genes carefully, HCN2 was identified as the gene most directly correlated to the effect of lack of transmission of chemical synapses.

Conclusion
The BiNGO plugin for Cytoscape identified HCN2 as an upregulated gene related to the response to hormone stimulus biological process. According to the GeneCards database, HCN2 is associated with the Neuronal system pathway. Further research must be done to confirm the connection between the effects of Alzheimer's and this pathway, but there is a strong possibility of relation between the two.
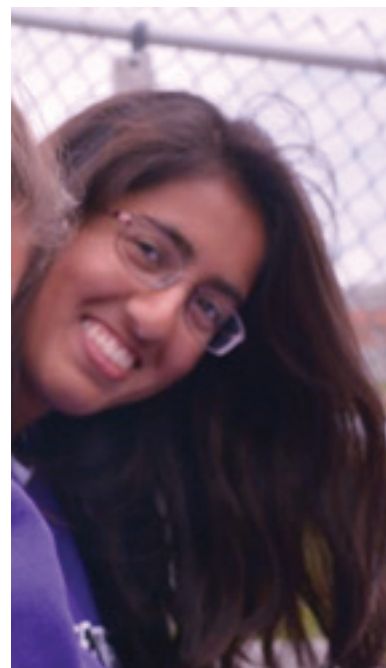
Hi, I'm Sanika Kulkarni and I'm a member of the miRcore volunteer group as well as the Pioneer High School GIDAS club. I joined the miRcore program in December 2012 after attending a one-day camp organized by Dr. Inhan Lee, the founder and mentor to our volunteer group. The ideas of changing gene expression to solve many medical puzzles of today intrigued me. In addition, I had never been exposed to computational research, and was fascinated by its huge potential in applications. I did not know what I was doing at first, but my fellow miRcore members and Dr. Lee patiently guided in each programming session. More importantly, however, they helped me understand what I was attempting to achieve through this research, and this deeper understanding of the science has kept me coming back to each meeting again and again. Outside of Saturday miRcore meetings, I enjoy playing the flute and am a member of my school's tennis team. Next year will be my senior year of high school, which I'm looking forward to!

I have always had an interest in biology, which led me to miRcore and GIDAS originally. I hope to go into medicine in the future, and apply the research that we are learning right now to whichever field I end up in.