

Title: Bayesian hierarchical modeling to investigate genes associated with frequently comorbid autoimmune diseases

Mentors: Nusrat Jahan and Elizabeth Ward

Necessary student background: Calculus-based statistics course, an applied statistics class (Regression analysis), familiarity with R.

Project description:

Autoimmune disease is a self-destructive disease that causes people's immune system to mistakenly attack their own tissues. Approximately 5% of the population suffers from one or more types of immune system disorders (Kochi, 2016). Some of the commonly known autoimmune diseases are Type I diabetes, rheumatoid arthritis, inflammatory bowel disease, psoriatic arthritis, celiac, multiple sclerosis, Vitiligo, and Hashimoto's thyroiditis. Patients with one autoimmune disease are more likely to develop another; about 25% of patients suffering from one autoimmune disease develop additional autoimmune diseases (Cojocaru, 2010, Steinman et al., 2011, Gill et al., 2016). The comorbidity or co-occurring of several autoimmune diseases is suggested to be a consequence of shared genetic factors (Kochi, 2016). Identifying a set of genes linked with autoimmune comorbidities may lead to better understanding of the mechanisms of action and targets for treatments.

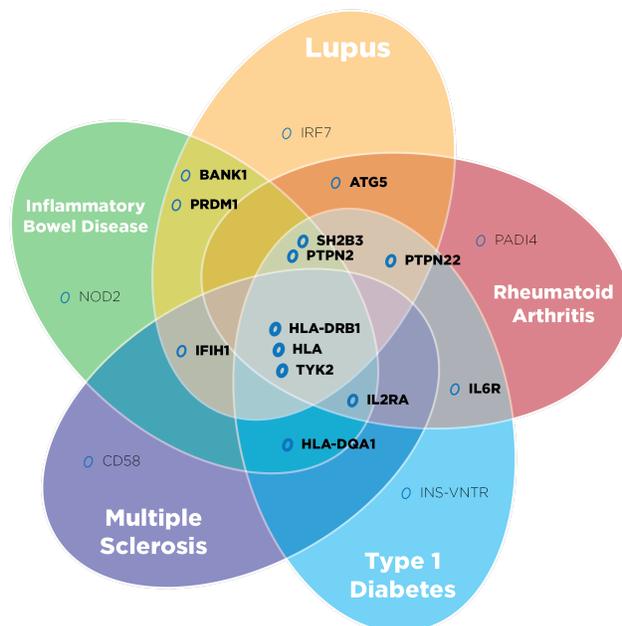


Figure 1: Genes implicated in multiple autoimmune diseases. <https://www.benaroyaresearch.org/blog/post/mystery-multiple-autoimmune-diseases>

We propose a Bayesian hierarchical model to simultaneously model associations between a gene and multiple diseases. Modeling multiple diseases at once can improve

power, reduce type 1 error, and help to identify biological pathways important in disease development.

In this project, students will retrieve gene expression studies related to multiple autoimmune diseases from the publicly available GEO website. They will have hands-on experience in genomic data preprocessing and analysis using the software R. In the first step, students will analyze each of the individual autoimmune data set. In the second step, they will combine the findings from the individual data sets using hierarchical Bayesian modeling in OpenBUGS, an open source application for doing Bayesian data analysis.

References:

Kochi, Y. (2016). Genetics of autoimmune diseases: perspectives from genome-wide association studies. *International Immunology*, Vol. 28, No. 4, pp. 155–161.

<https://doi.org/10.1093/intimm/dxw002>

Cojocar, M., Cojocar, IM., and Silosi I. (2010). Multiple autoimmune syndrome. *Maedica (Buchar)*. Vol. 5(2), pp. 132–134.

Berkovich, R., Subhani, D., and Steinman, L. (2011). Autoimmune comorbid conditions in multiple sclerosis. *US Neurology*, Vol. 7(2), pp. 132–138.

DOI: <http://doi.org/10.17925/USN.2011.07.02.132>

Gill, L., Zarbo, A., Isedeh, P., Jacobsen, G., Lim, and Hamzavi, I. (2016). Comorbid autoimmune diseases in patients with vitiligo: A cross-sectional study. *Journal of American Academy of Dermatology*, Vol. 74, Issue 2, pp. 295–302.

DOI: <https://doi.org/10.1016/j.jaad.2015.08.063>