

# BT5240: Computational Systems Biology

## Inverse Comorbidities – A Networks Based Analysis

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### Project Idea

To identify disease pairs of inverse comorbidity using network analysis of disease-gene networks and disease function networks.

### Inverse Comorbidities

Comorbidities are a common phenomenon in many diseases. It refers to the presence of multiple diseases or medical conditions in a patient, often leading to a worse state of disease. However, it has been observed that inverse comorbidities also exist. This condition – when an unexpectedly low probability of a disease occurring in people with another disease is observed – is intriguing, as it may help us gain insight into the pathogenesis of certain diseases and allow us to understand the underlying mechanisms of certain unknown disease pathways.

### Network Analysis Methodology

This project aims to find various such inverse comorbidity relations that are conferred due to the onset of a few diseases. We are planning to approach this problem by analyzing disease-gene and disease-function networks. The approach will involve perturbations to the aforementioned bipartite networks, followed by the analysis of the network using centrality measures and deduction of which sets of diseases show inverse comorbidity.

### Future Goals

This project may be extended to finding the diseases that have been evolutionarily selected in such cases of inverse comorbidity. A common example is sickle cell anemia and malaria, where sickle cell patients have a lesser than expected probability of acquiring the malarial parasite due to faulty hemoglobin in the red blood cells. Discovering the root evolutionary causes of such diseases may help identify other pathogenic pathways and increase our understanding of pathogenesis.