

Abstract

Humans as of their nature, interact with the surroundings, hence forming a social system. These social systems interact with each other and form a complex social network, which has some -profound consequences along with it, be it good or bad. For instance there is a high chance that a person will be happy or get obese if his friend or even his friend of friend is happy¹ or obese², respectively. It is extremely important to understand these properties as they shape the health/behavior of the human beings. In this study, we try to study various kinds of networks present at IISER Mohali; and how the network attributes are related to one's personality and academic performance, thus allowing the scope for improving students' performance by tinkering their social interactions. Towards this, we had earlier acquired the network, personality and academic data of IISER-M students through an online survey. In the present project, we constructed various networks and performed statistical analysis. Our study suggested some degree of association between students' personality, network attributes and the academic performance, clearly suggesting the possible predictive power of our study. Among other observations, we saw homophilic mixing of personality traits among students, which was specific to Male-Female dyads only, highlighting the organizing principle of student's social network at IISER-Mohali.

Abstract 2: A complete genome is covered with ~5% coding region and ~95% non-coding region, which plays a vital role in the regulation of genes. Relative positioning of genes and non-coding regulatory elements can impact the transcriptional states of the genes. This effect is commonly known as the 'position effect'. This phenomenon is very important to study owing to its role in various diseases like cancer and developmental disorders. In this series of research, we hypothesize that the cis regulatory elements help in minimizing the gene expression noise of the proximal gene(s) by recruiting transcription factors stably. If a gene is being regulated by its neighboring conserved noncoding element (CNE), the expression of that particular gene would be expected to be relatively stable. If this linear proximity is somehow lost down the evolution, the noise in gene expression would increase due to infrequent or no access to its distant CNE. To test the hypothesis, we analyzed the single cell RNA-Seq data of 8 brain cortical cells of mouse and rat, and showed that the gene expression noise remains unchanged after the CNE-gene synteny was lost. We further propose that our observations can be explained by the 3D (spatial) proximity of the CNE and the gene after loss of this synteny