

## ABSTRACT

**Background:** Myocardial infarction is an important clinical problem because of its large contribution to mortality. Treatable risk factors of myocardial infarction are hypertension, hypercholesterolemia, diabetes mellitus and smoking. However, recent studies have shown the importance of genetic factors and the interaction between multiple genes and environmental factors in the susceptibility to the disease. Disease prevention is an important strategy for reducing the overall burden of myocardial infarction, with the identification of markers for disease risk being key for both risk prediction and for potential intervention to lower the chance of future events. The increasing availability and diversity of omics (proteomics and genomics) data in the post-genomic era and from various interaction studies offers new perspectives in most areas of biomedical research.

**Methodology:** In this study, I have aimed to identify the interactions between the various genes associated with myocardial infarction, using data retrieved from high-throughput experiments and literature available from databases such as HuGE Navigator, Online Mendelian Inheritance in Man Morbid Map, PubMed and GeneCards. Graph-based biological networks models capture the topology of the functional relationships between molecular entities such as gene, protein and small compounds and provide a suitable framework for integrating and analyzing these data. The development of software tools capable of integrating data from different sources and to provide flexible methods to reconstruct, represent and analyze topological networks is an active field of research in bioinformatics. The genes associated with myocardial infarction were identified from the databases and their interaction was visualized using, BisoGenet, one of the plugin of Cytoscape, an open-source software.

**Results:** The interaction network of the six most important genes (nodes with more connections) that were found to interact and affect the susceptibility of myocardial infarction was visualized using Cytoscape.

**Conclusion:** These interactions could provide a new insight into the multigenic architecture of myocardial infarction. Furthermore, it may be possible to prevent an individual from undergoing myocardial infarction by medical intervention based on his or her genotype for specific polymorphisms. BisoGenet, the tool that I have selected was able to build and visualize biological networks in a fast and user-friendly manner.