**Assignment 1**

**Part 1 - Plagiarism Review**

The paraphrased version written in step 2 clearly appears to be plagiarized. Each line in the text is identical to that of the original source text, with the only difference being that a few words were modified. For example, words such as ‘rise’, ‘expansion’, ‘great developments’ were replaced with words like ‘increase’, ‘growth’ and ‘large factors’, when viewing the first line. Furthermore, no credit has been given to the original author by writing it in quotes and citing this article. It should also be noted that when words are being replaced or modified, the overall meaning of the text should not change. An act of plagiarism is committed when the original work has been used as someone else’s without giving credit to the source. Therefore, in this context it is clearly a sign of plagiarism since it is not summarized/paraphrased, and no attribution is given to the author.

*The original text can be paraphrased as,*

Significant developments were seen with the growth of industry and the expansion of population during the late 19th century of the American history. With the introduction of steam powered factories, jobs were provided to the increasing number of immigrants living in America, by converting farm workers to factory laborers [1]. Places such as Fall River, Massachusetts, the home of the Borden family, have grown into large cities and became centers of production, trade and commerce.

[1] Lizzie Borden: A Case Book of Family and Crime in the 1890s by Joyce Williams et al.

**Part 2 – Summary on Network Biology**

The intercellular web of interactions contributing to its structure and functions have been explained in this paper. Emphasis is placed on the complex molecular structure when the cell is isolated and surrounded by other cells. These interactions can be explained by tools such as 'Protein chips' or semi-automated 'Yeast two hybrid screens.’ The origin, biological details, patterns and functionality must be explored in order to understand the cell’s network and interactions. Interactions can be either directed or undirected. When it comes to the network architecture, most cellular networks adopt a scale free topology as compared to a random network topology. This scale free topology is a characteristic attribute of the modules containing a collection of molecules or nodes responsible for cell function. The cell network is highly clustered, i.e., locally 'sprinkled,' resulting in isolated modules. The subgraphs have the ability to capture certain interconnection patterns at the local level that characterizes of a network. Large motifs become difficult to understand when these subgraph’s grow exponentially with the nodes present in it. As a result, from the topology of the graph, highly interconnected modules are considered instead and are corelated with their possible functions. When it comes to the topological robustness, the scale free networks are more robust compared to the random topology since it does not possess a threshold for disintegration and work well in times of accidental failures thereby maintaining a route to the nodes forming a compact cluster. Some important findings have shown that, a. robustness and adaptability is a feature of a network and does not depend on fine tuning the component attributes, b. When components are disrupted, the networks can collapse, c. The modules ability to evolve can limit or improve robustness. For future work, more data needs to be acquired and tools to be developed in order to understand the interactions of the molecules both in space and time. A framework needs to be designed for clinical data that can identify pathologically altered molecules for a disease and eventually bring changes in the practice of medicine.

[2] Barabasi, A. L., & Oltvai, Z. N. (2004). Network biology: understanding the cell's functional organization. *Nature reviews genetics*, *5*(2), 101-113.