

# Spatial Location of Genes within Cells in Gene Interaction Networks

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## ABSTRACT

Text mining techniques have become a popular method for discovering relationships between genes based on searching the biomedical literature. The co-occurrence of gene names within individual documents is used to produce hypothetical interaction networks, which are used to explore hypotheses regarding gene interaction. However, the incorporation of the spatial interaction between gene products, although highly informative to the biologists, has largely been ignored.

Although the use of interaction networks has some promise, there are additional sources of information within literature that is not normally exploited. In particular, gene interaction is a significantly spatial activity, with genes being expressed in different ways depending on where they are located within a cell. Biomedical literature uses a set of keywords that describe an abstract set of locations or compartments within a cell, and these are often used in conjunction with the description of gene activity.

The incorporation of spatial relationships between network elements within the cell is likely to increase the interpretation and value of these hypothetical networks. For example, the cells physical space can be shown when producing a visualization of the gene network. The topological relationship between abstract cell sites can be used to verify and isolate gene interactions according to their spatial location within the cell.

This talk will present a methodology for incorporating spatial location of genes into gene interaction networks and the challenges that are likely to be faced when applying this approach.

**Keywords and phrases:** physical space, gene networks, visualisation, gene location.