

# Co-expression structure and network analysis for deciphering disease mechanism

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## Abstract

Gene expressions change due to the stress experienced by the cells. The changes are not necessarily significant but the relays of such form co-expression networks implicating the underlying molecular interactions and signaling cascades for adapting the stress.

This study aims to identify the difference in co-expression distributions between normal and neoplastic states and explain such structural difference through the scatter plot of co-expression levels in the two states on both genomic scale and specific functional gene sets.

The distributions and the corresponding scatter plot are called co-expression structures and galaxy in this project. Structural analysis will be applied to determine the difference in distributions and the optimal co-expression threshold for partitioning the co-expression galaxy into nine regions. The central region contains weakly co-expressed gene pairs. The surrounding eight regions contain normal-specific, neoplasm-specific, conforming and opposing strongly co-expressed gene pairs. This study also aims to explore how the regional difference in gene pair counts determines the structural difference between the two states on genomic scale.