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BMS

Judging Dept.

**Ajish George**

Student

BMS

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Scott Tenenbaum

Dept or Program Years in program

Mentor

## Cinema: Correlation-interaction Networks Of Expression In Microarrays

Author (s)

**Ajish George**

Array experiments measure expression levels of transcribed gene sequences. Integrating this expression data with networks of known pathway, transcription factor, or protein interactions allows us to see regulatory networks driving expression changes and to find their important control points (ex: dominant transcription factors) or their isolated subcomponents (where treatments can be effected with the fewest side-effects). We have developed a tool that uses transcription factor interactions from TRANSFAC and protein-protein interaction networks from BIND and integrates correlation information from array data to highlight interactions of interest and their behaviour in the experiment. Using this in a study of p38 mediated tumor-dormancy we have found many well-characterized transcriptional interactions and a few novel ones that may prove the missing links in our understanding of the system.