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TITLE:

Integrative Analysis to Select Genes Regulated by Methylation in a Cancer Colon Stud

PRESENTATION TYPE: Oral

CURRENT METHODOLOGICAL TOPIC AREA: Statistical Topics | Application Areas

CURRENT APP. AREAS/STATISTICAL TOPICS: Microarrays and omics data | Bioinformatics

ABSTRACT BODY:

Abstract Body:

Methylation of CpG dinucleotides in the promoter of genes involved in the oncogenic process is considered a key process contributing to tumor initiation and/or progression. Methylation often acts by inhibiting the expression of the gene, that is the more methylated is the gene the less it is expressed, but if methylation is absent or low then any values of expression can be found. This suggests that a way to select genes regulated by methylation might be looking for patterns in the relation between gene expression and methylation consistent with this form of regulation, such as L-shapes. This work aims at comparing several methods to select genes regulated by methylation and at testing them on an ongoing study on colon cancer.

We consider two methods to select patterns of regulation that could be attributable to methylation: (i) Rely on conditional Mutual Information (Liu and Qiu, 2012) and (ii) Perform a clustering based on Splines Regression (Hastie and Tibshirani, 2009). Both methods are compared against a naive approach consisting of selecting genes whose expression is negatively correlated with methylation.

Applying the methods to a study of drug sensitivity in colon cancer shows that all methods are able to select biologically relevant genes, clustering of splines regression returns similar findings as the naive approach whereas the mutual information based approach seems to provide more relevant results.

References

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