Combining Text Mining and Microarray Analysis

Christoph M. Friedrich[1,*] and Michaela Gündel[1]

1. Fraunhofer Institute for Algorithms and Scientific Computing (SCAI); Department of Bioinformatics; Schloss Birlinghoven; D-53754 Sankt Augustin; Germany

* Contact author: friedrich@scai.fraunhofer.de

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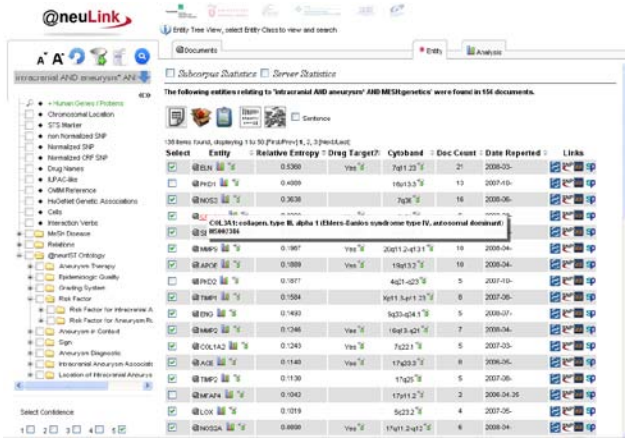

Microarrays are well established experimental tools to measure gene expression in biological samples. The Bioconductor project [1] provides a wealth of R packages to analyse the resulting gene expression data. In [2] a semi-automatic microarray analysis workflow with limma [3] as the main analysis engine has been developed. This workflow is part of @neuLink [4], a biomedical Knowledge Discovery application suite. Another module of this application suite allows for Knowledge Discovery in biomedical text sources, namely Medline. Combining prior published knowledge with experimental data allows for example the identification of co-mentioned diseases or drugs in similar published gene expression data.

The microarray analysis workflow will be presented in detail as well as "lessons learnt" during the development and use. Additionally it will be shown how text mining is combined with microarray analysis in this Knowledge Environment [5].

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