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To the editors of
Bioinformatics.

Manuscript “InCroMAP: Integrated analysis of Cross-platform MicroArray and Pathway data”, submitted to Bioinformatics

Dear Sir or Madam,

Attached, you can find the applications note about our latest software tool called ‘InCroMAP’, an acronym for ‘Integrated analysis of Cross-platform MicroArray and Pathway data’.

Today, not only messenger RNA microarrays, but also many other techniques, such as DNA methylation, microRNA and protein phosphorylation are available. Many biological conclusions have already been made, based on transcriptomic data. Especially in the field of tumor research, the transcriptomic changes are well-analyzed and published. However, biology includes several levels of gene regulation and expression. Therefore, novel important insights are possible by studying several layers in parallel. An example is a methylated microRNA promoter, which represses the expression of the corresponding microRNA, which in turn leads to a target’s mRNA increase. Such complex cascades can be identified with the InCroMAP application.

InCroMAP can read processed mRNA, microRNA, DNA methylation and protein modification datasets. Several methods for an individual, but especially for a joint analysis of those heterogeneous platforms are provided. On top of that, InCroMAP can analyze and jointly visualize all datasets within the context of metabolic and signaling pathways. There are no other tools that support a joint analysis of such diverse microarray datasets. Hence, InCroMAP substantially contributes to the microarray data analysis community.

The tool itself has been tested on several platforms (Windows, Linux and Mac OS X), can be downloaded separately or executed as Java Web Start, and comes with a comprehensive documentation and example files.

The manuscript has been seen and approved by all listed authors.

Sincerely Yours,

Clemens Wrzodek