# TBro - a transcriptome browser for *de novo* RNA-sequencing experiments

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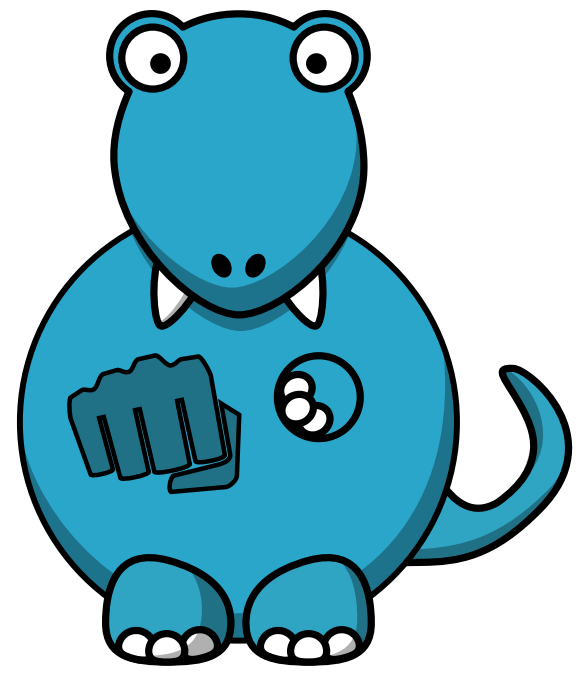
## Motivation
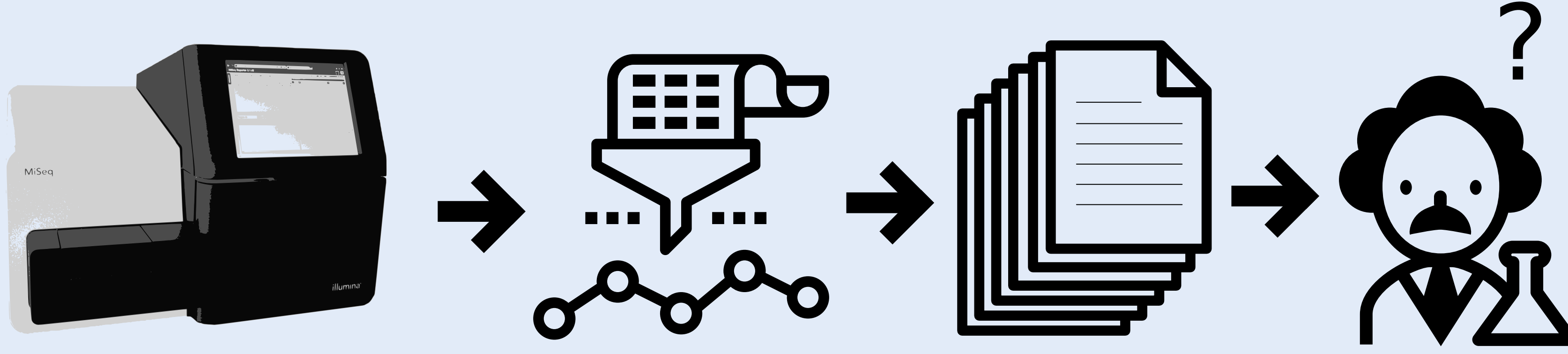


Identity of genes and their expression levels can be accessed by RNA-sequencing. Therefore, tools for de novo transcript assembly and quantification have been developed. Still, the problem remains, that the output is organized in huge text files which are difficult to handle and interpret especially for non-computational scientists. Here we present TBro which aggregates data from different sources, presents them in a user-friendly interface and features interactive data analysis.

## User-friendly Interface



The user accesses TBro through a web browser. There are multiple search features to explore the transcriptome. Custom data sets are displayed in a cart like fashion.

## Interactive Analysis

### MA-Plot
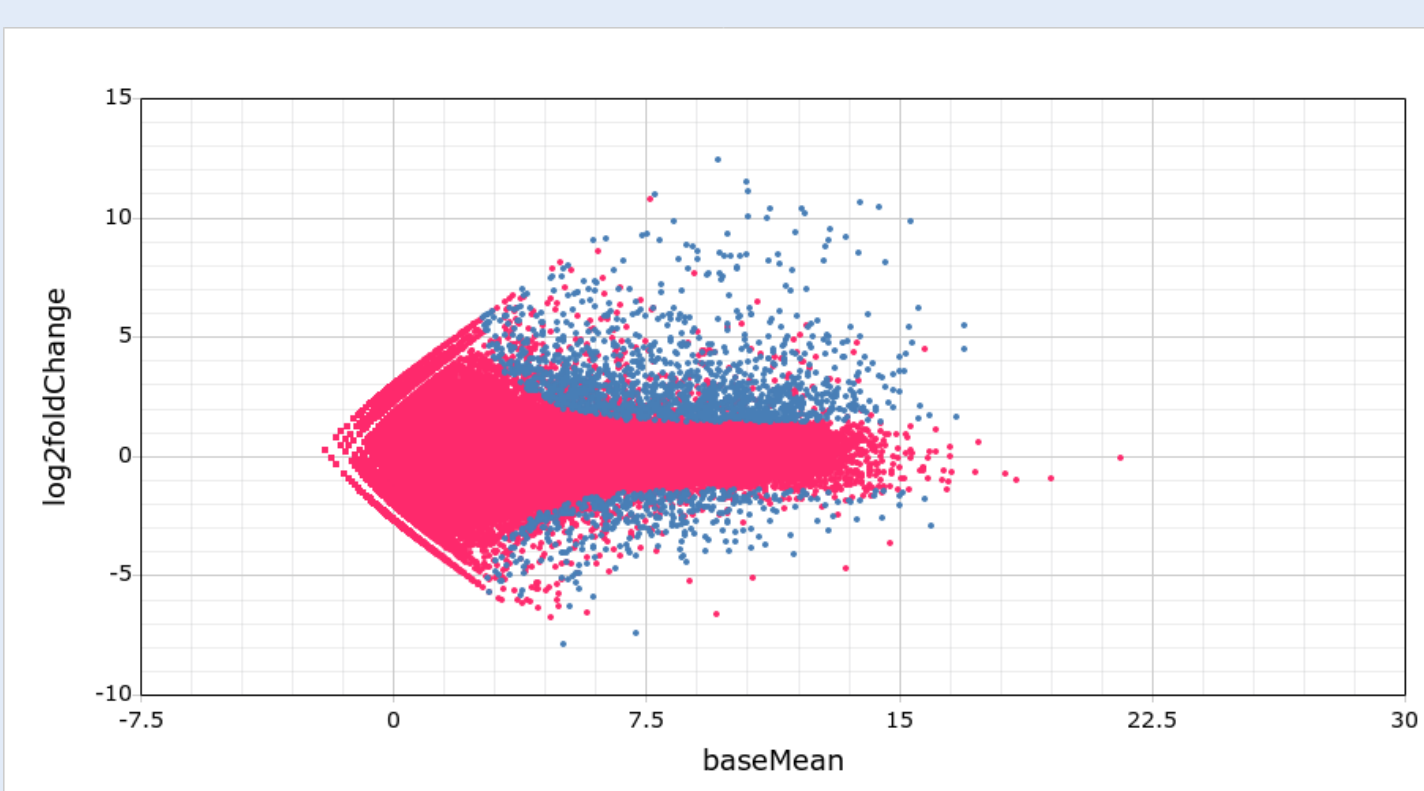
### Pairwise Differential Expression
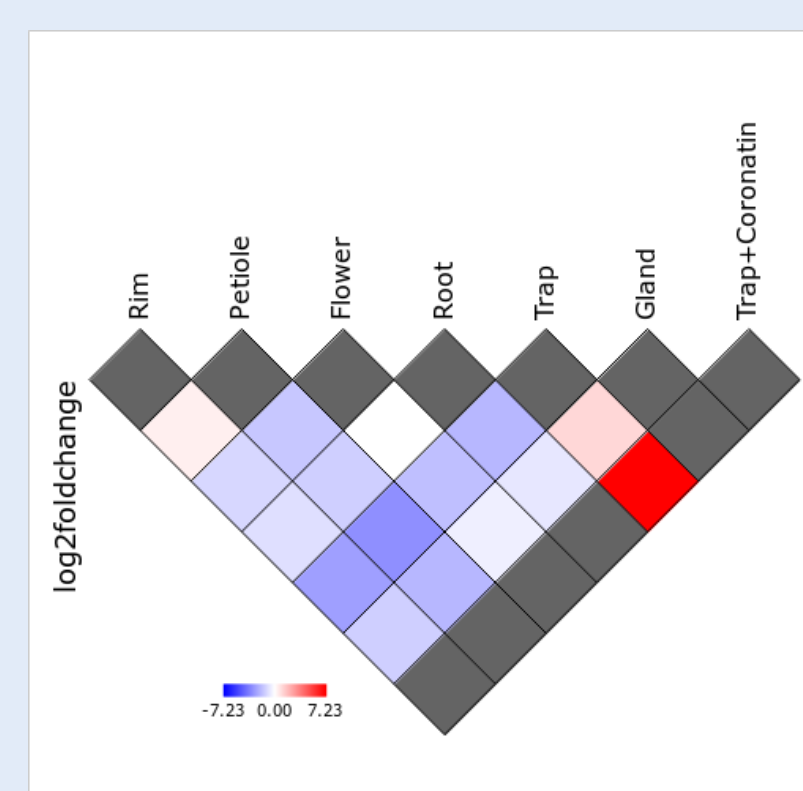
### Expression Heatmap
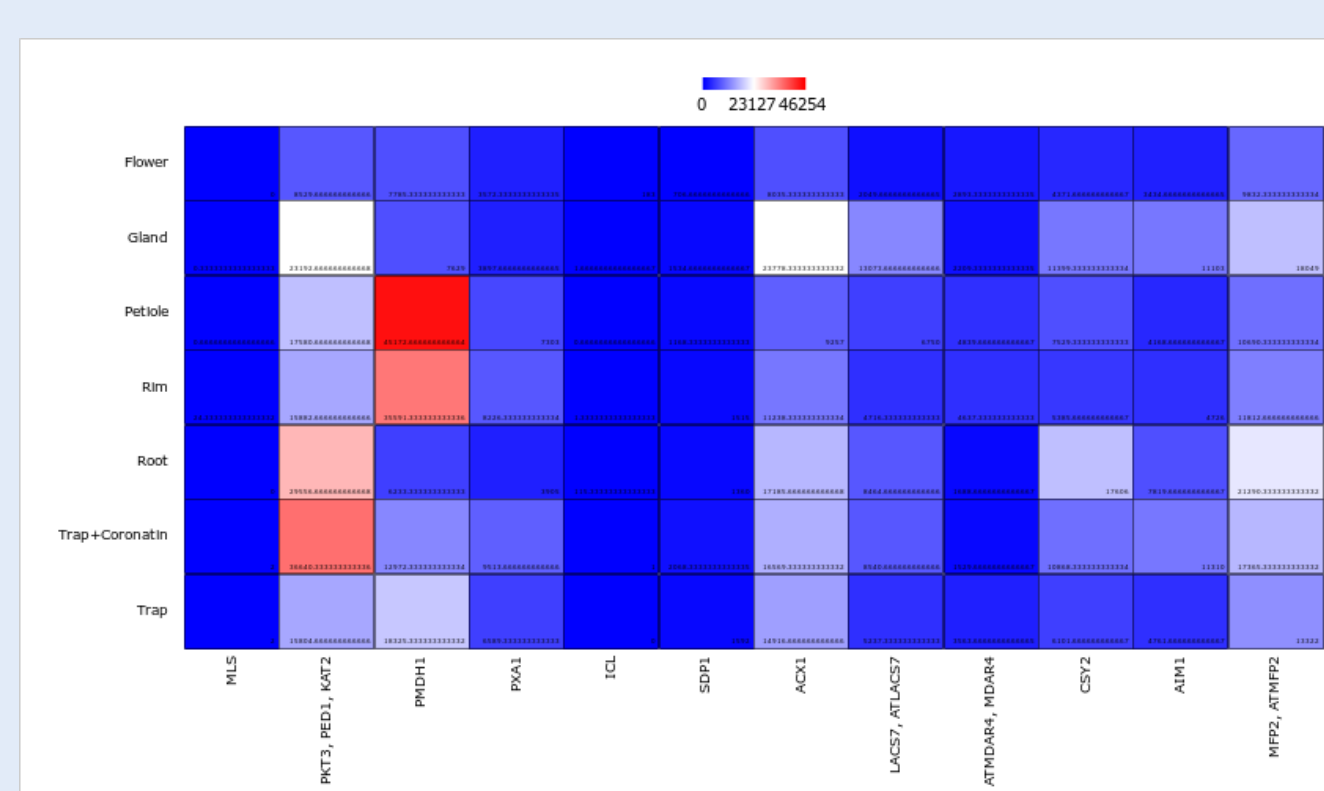


Expression counts as well as differential expression results can be interactively explored for the full data set, individual transcripts or custom subsets using canvasXpress [3].
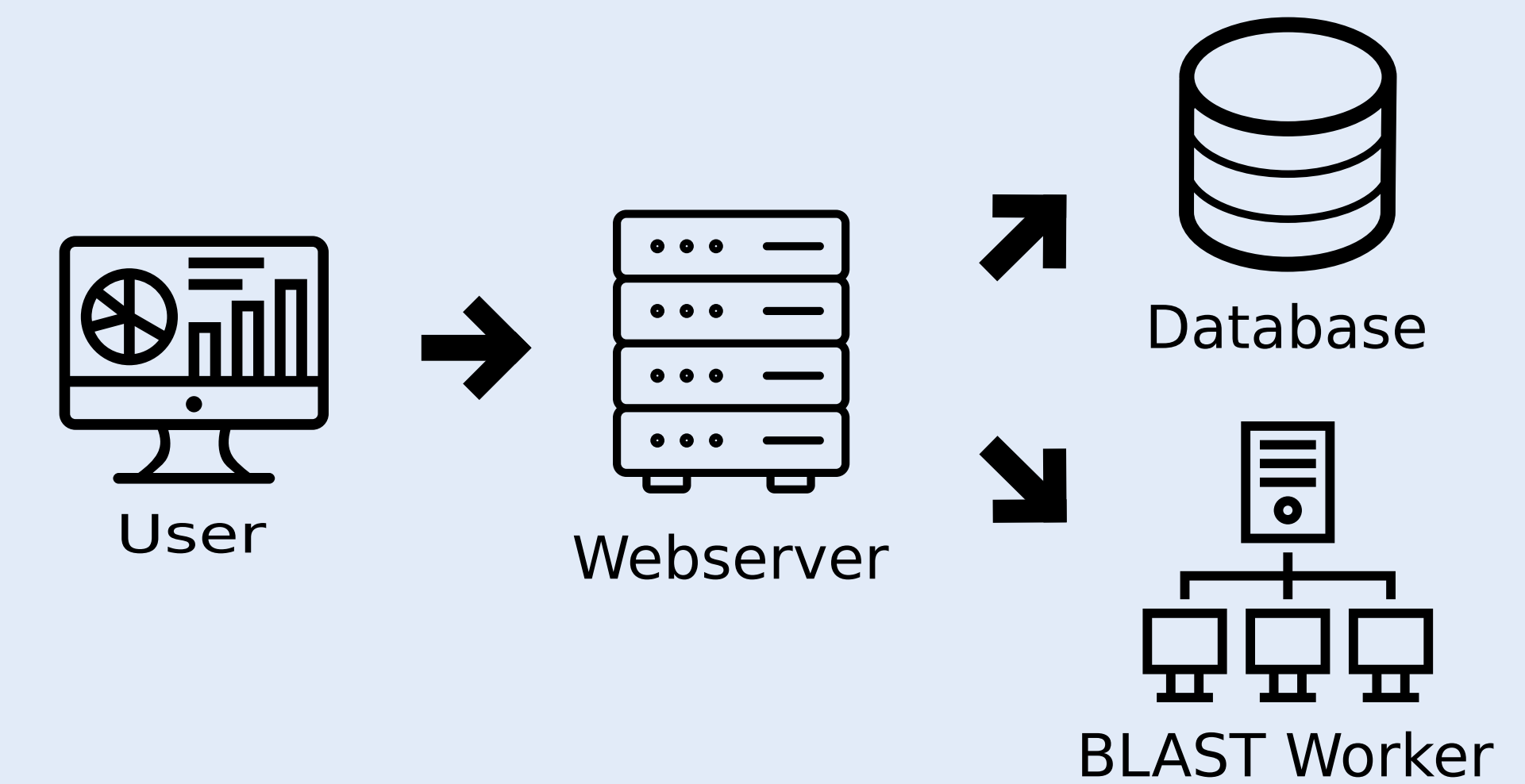
## Data Aggregation



Data from lots of different sources is stored in the database and aggregated by TBro on individual unigene and isoform pages. This way all annotations are accessible in one place. The page also provides the user with the capability of adding notes, directly BLAST [2] the sequence, store it in a custom subset and explore expression

## Implementation



TBro consists of an Apache web server with PHP. Data is stored in a Postgresql database with a CHADO schema [1] managed by the admin using the TBro command line interface. BLAST [2] jobs are delegated to one or more worker machines. All elements of TBro are available as docker images.

## Availability

https://github.com/TBroTeam/TBro

https://hub.docker.com/r/tbroteam

http://tbro-tutorial.readthedocs.io

http://tbro.carnivorom.com [4]

[1] Mungall, Christopher J., David B. Emmert, and The FlyBase Consortium. "A Chado Case Study: An Ontology-Based Modular Schema for Representing Genome-Associated Biological Information." Bioinformatics 23, no. 13 (July 2007): i337–46. doi:10.1093/bioinformatics/btm189.
[2] Altschul, S. F., W. Gish, W. Miller, E. W. Myers, and D. J. Lipman. "Basic Local Alignment Search Tool." Journal of Molecular Biology 215, no. 3 (October 1990): 403–10. doi:10.1016/S0022-2836(05)80360-2.
[3] Neuhaus, I. CanvasXpress http://canvasxpress.org (accessed Mar 29, 2016).
[4] Bemm, Felix, Dirk Becker, Christina Larisch, Ines Kreuzer, Maria Escalante-Perez, Waltraud X. Schulze, Markus Ankenbrand, et al. "Venus Flytrap Carnivorous Lifestyle Builds on Herbivore Defense Strategies." Genome Research, May 4, 2016. doi:10.1101/gr.202200.115.

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