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Systems biology

# MINOMICS: visualizing prokaryote transcriptomics and proteomics data in a genomic context

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## ABSTRACT

**Summary:** We have developed MINOMICS, a tool that allows facile and in-depth visualization of prokaryotic transcriptomic and proteomic data in conjunction with genomics data. MINOMICS generates interactive linear genome maps in which multiple experimental datasets are displayed together with operon, regulatory motif, transcriptional promoter and transcriptional terminator information.

**Availability:** MINOMICS is freely accessible at <http://www.minomics.nl>

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**Supplementary information:** <http://bioinformatics.biol.rug.nl/supplementary/minomics/>

## 1 INTRODUCTION

Various web-based tools have been developed to generate visual representations of prokaryotic genomes, e.g. Conant and Wolfe (2008), Grant and Stothard (2008) and Kerkhoven *et al.* (2004). These tools allow visualizing one or a few experiments on a genome backbone together with genomic features, such as transcriptional terminators and functional annotations. However, to understand the biology underlying functional genomics experiments, the integration of multiple datasets from different 'omics platforms, e.g. transcriptomics and proteomics, with multiple operon predictions as well as other genomic features, such as transcriptional motifs, is a necessity.

For example, for a given organism, predicted operons are seldomly identical when using different operon prediction methods (Brouwer *et al.*, 2008). In addition, understanding the often complex regulatory interactions occurring in prokaryotes requires an overview of the gene expressions and/or protein abundances in multiple experiments. Therefore, visualization of 'omics data in context with multiple operon predictions and genomic features is required. This integration of data sources is lacking in current tools.

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To this end, MINOMICS was developed, a web-based tool that generates interactive linear genome-maps exclusively for prokaryotes incorporating large sets of experimental data, various genomic elements and functional annotations. MINOMICS enables the identification of differentially expressed genes, operons and the DNA motifs regulating their expression. Furthermore, this tool aids researchers identifying other experiments in which genes of interest are affected. Our Supplementary website lists these, and a number of other research questions, that could be answered by MINOMICS.

## 2 FEATURES

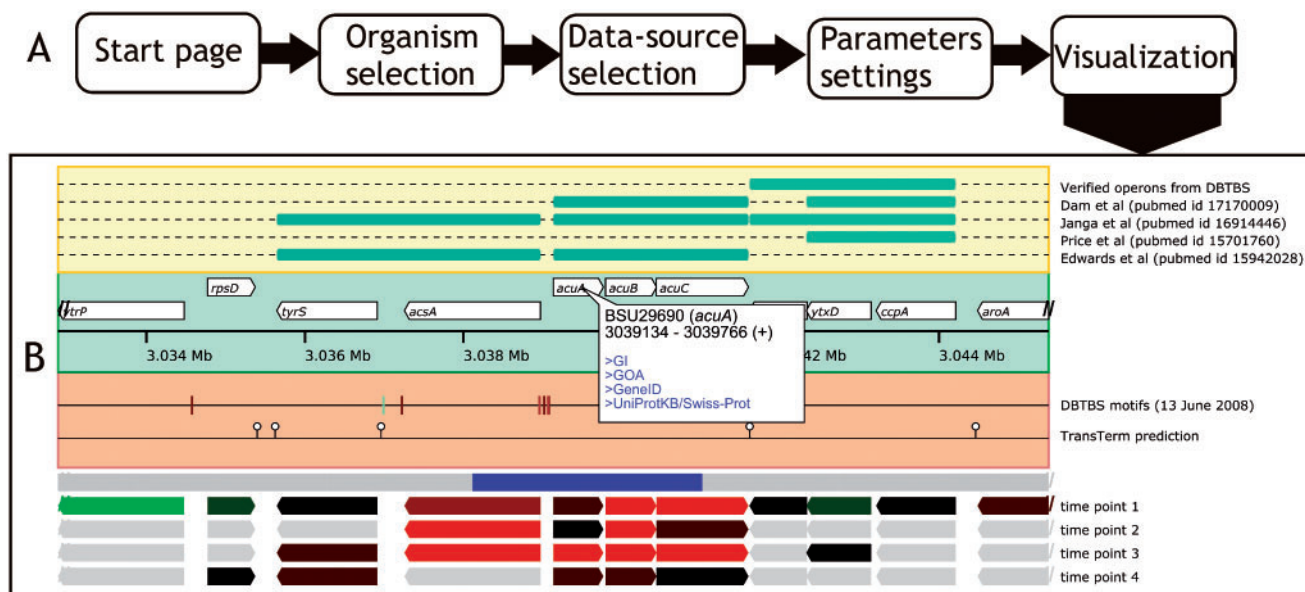
MINOMICS generates linear chromosome maps with proteomics data, transcriptomics data and various genomic elements: (i) operons, (ii) regulatory DNA motifs, (iii) transcriptional promoters and (iv) transcriptional terminators (Fig. 1). These interactive maps provide hyperlinks to relevant entries in external databases. Furthermore, displayed genome maps can be exported to publication grade images allowing researchers to share these views with colleagues.

MINOMICS has been designed as a web-based tool with a wizard-like web-interface (Fig. 1) implemented in the functional genomics web platform (FG-web; unpublished data). Processing and selection of the data sources is handled by this framework. Gene information is processed from Genbank files and transcriptional terminators are automatically predicted using TransTerm (Ermolaeva *et al.*, 2000). Experimental data, motif and operon annotations can be supplied by users in tab-delimited text formats.

## 3 IMPLEMENTATION

The MINOMICS web-interface is implemented in PHP 4 and is freely accessible. The software components generating the visualization are implemented in Perl 5.8 and designed to run on Unix-like operating systems.

The generated chromosome maps feature scalable vector graphics (SVG) and can be used in both the Opera and Firefox Internet browsers, which are available for all the major operating systems (Windows, Mac-OS and Linux). A detailed guide explains the use of the software and is available at the supplementary website.



**Fig. 1.** The MINOMICS web tool. (A) Schematic representation of the web wizard. (B) the genome map consists of five sections: (i) operon annotations (yellow panel), (ii) the genome ruler with genes (green panel), (iii) regulatory motifs annotated on the genome (brown panel), (iv) correlations between subsequent genes on the genome determined from experimental data (white panel; upper row) and (v) the experimental data (white panel; arrows). A four time-point DNA microarray time-course experiment is visualized in which labeled cDNA derived from wild-type *Bacillus subtilis* is compared with that of a *ccpA* deletion strain (Lulko et al., 2007). The measurements of the *acuABC* operon and the *acsA* gene are highly correlated (blue color in iv) indicating that these transcriptional units are co-regulated. Indeed, *cre* binding motifs for the CcpA protein (red vertical bars in iii) are present in their shared intergenic region.

#### 4 CONCLUSIONS

The linear chromosome maps created by MINOMICS provide researchers with a tool to comprehensively mine their experimental data. The tool facilitates documenting this procedure and sharing the results by allowing researchers to export currently displayed genome maps to publication grade images.

On the Supplementary website, several test cases are presented in which transcriptomics data are visualized for *Bacillus subtilis*. These cases provide potential users demonstrations on how to use MINOMICS and illustrate the need to integrate as much data as possible in order to understand the biology that underlies experiments.

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*Conflict of Interest:* none declared.

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