Online exploration of transcription profiles along B. subtilis and S. aureus

Sandra Derozier, Pierre Nicolas, Ulrike Mäder, Cyprien Guerin

HAL Id: hal-02904188
https://hal.inrae.fr/hal-02904188

Submitted on 21 Jul 2020

Online exploration of transcription profiles along *B. subtilis* and *S. aureus*

Dérozier S.[1,2], Nicolas P.[1], Mäder U.[3], Guérin C[1].

Summary: Genoscapist is a web-tool generating high-quality images for interactive visualization of hundreds of quantitative profiles along a reference genome together with various annotations. Relevance is demonstrated by deployment of two websites dedicated to large condition-dependent transcriptome data sets available for *Bacillus subtilis* and *Staphylococcus aureus*.

Websites and source code freely accessible at https://genoscapist.migale.inrae.fr.

Contact: sandra.derozier@inrae.fr, cyprien.guerin@inrae.fr.

[1] *Université Paris-Saclay, INRAE, MaIAGE, 78350, Jouy-en-Josas, France*
[2] *Université Paris-Saclay, INRAE, BioinfOmics, MIGALE bioinformatics facility, 78350, Jouy-en-Josas, France*
[3] *Interfaculty Institute for Genetics and Functional Genomics, University Medicine Greifswald, Greifswald, Germany*

Yet another genome browser?

Microbiologist collaborators needs on data visualization:

- non aggregated transcriptomic data on large datasets (allow non-canonical biological mechanisms discovery)
- navigation based on expression correlation between genes
- customizable views like sample selection and colouring
- easy online access

Static versions based on MuGeN used by the community of *B. subtilis*[1] and *S. aureus*[2].

Existing tools (JBrowse, IGV, ...) don't allow all those features in one browser.

Implementation:

- Java application (framework Google Web Toolkit)
- Graphical rendering follows the Scalable Vector Graphics (SVG) web standard
- Relational database (PostgreSQL)
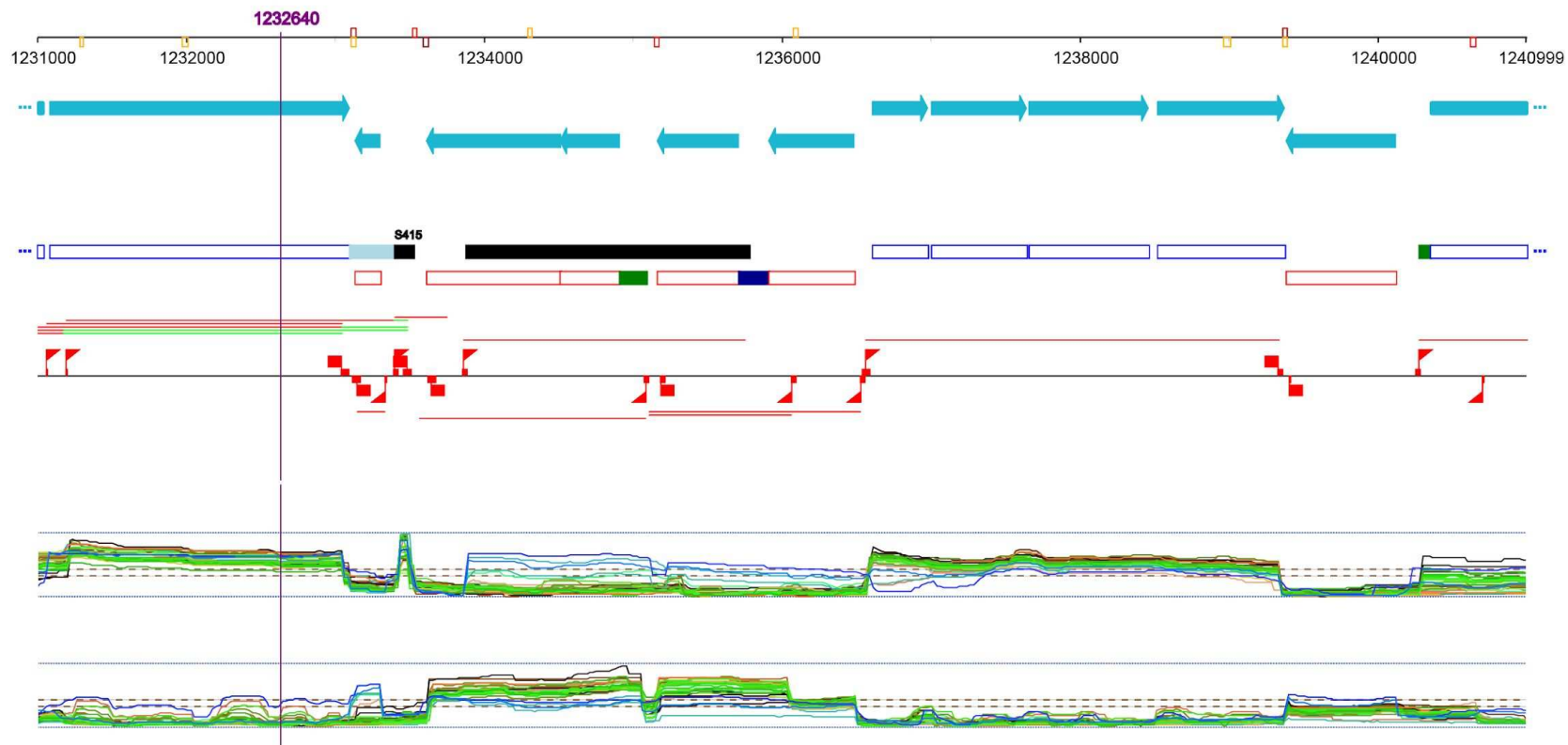- Source code available on Git repository (CeCILL-B licence)

B. subtilis Expression Data Browser

Genomic View

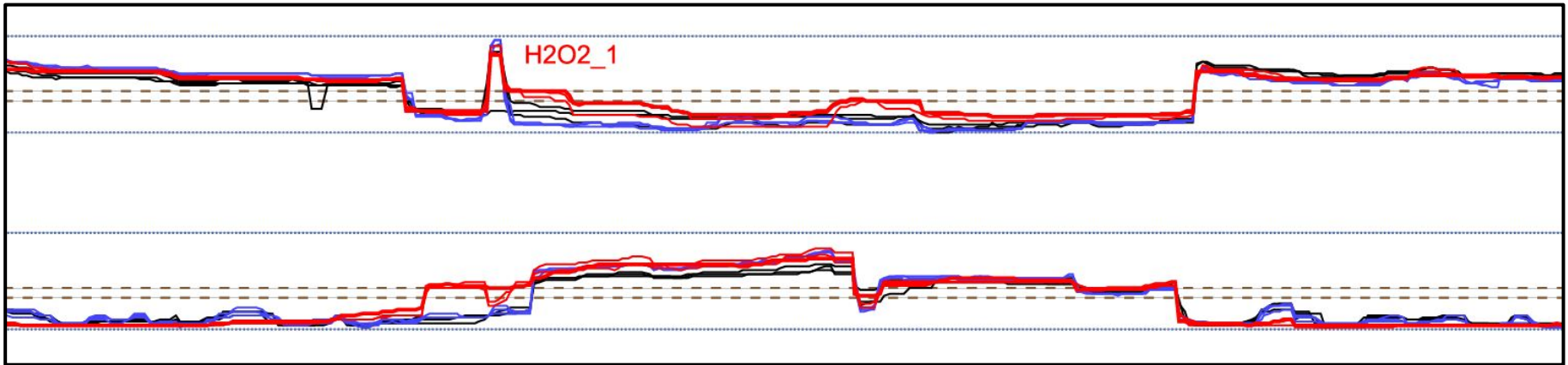Sample selection | Switch to Median normalisation | Add Rho samples track | Add Feature Names
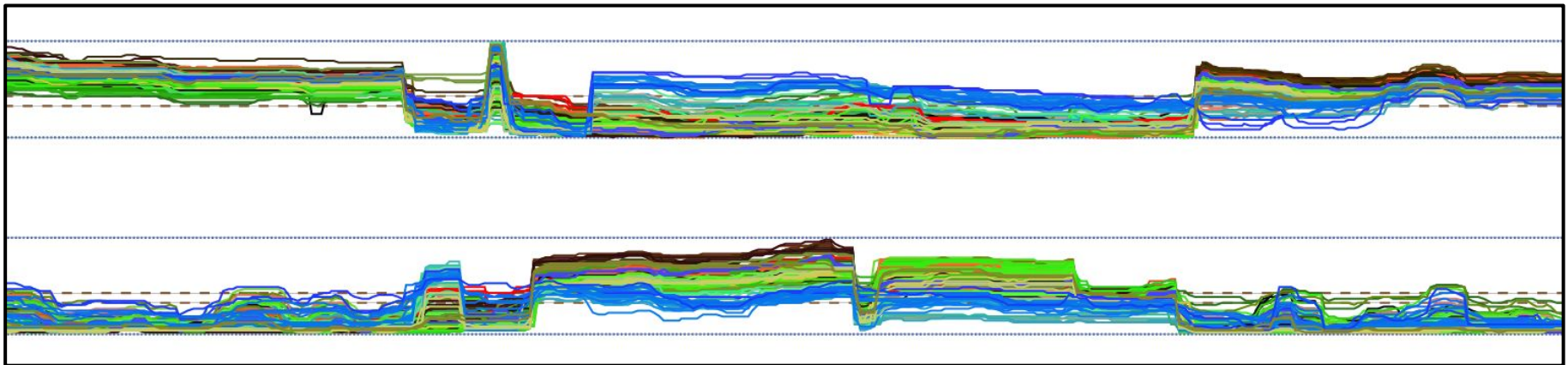
SVG | legend

1232640

1231000 | 1232000 | 1234000 | 1236000 | 1238000 | 1240000 | 1240999

S415

Graphical representation of transcription profiles

User customized view allowing specific colourization and *B. subtilis* sample selection.

All the 269 *B. subtilis* samples profiles on both strands with default colours.

Conclusion

Relevance is demonstrated by deployment of websites dedicated to condition-dependent transcriptomes of two important bacteria:

- *Staphylococcus aureus*
- *Bacillus subtilis*

Interactive visualization of hundreds of quantitative profiles along a reference genome together with various annotations.

Alternative navigation between genes based on transcriptomic correlation.

Images saved in SVG format can directly be processed by vector graphics editors to assemble high-quality figures for scientific communication.

Share or save customized view using direct generated links.

Genoscapist can handle multi-chromosome reference genomes and can be extended to display any type of quantitative profiles along genomes.