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

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

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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>.

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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)



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Genoscapist - <https://genoscapist.migale.inrae.fr/>

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¹ Nicolas, P. et al. (2012). DOI: [10.1126/sciences.1206848](https://doi.org/10.1126/sciences.1206848)

² Mäder, U. et al. (2016). DOI: [10.1371/journal.pgen.1005962](https://doi.org/10.1371/journal.pgen.1005962)

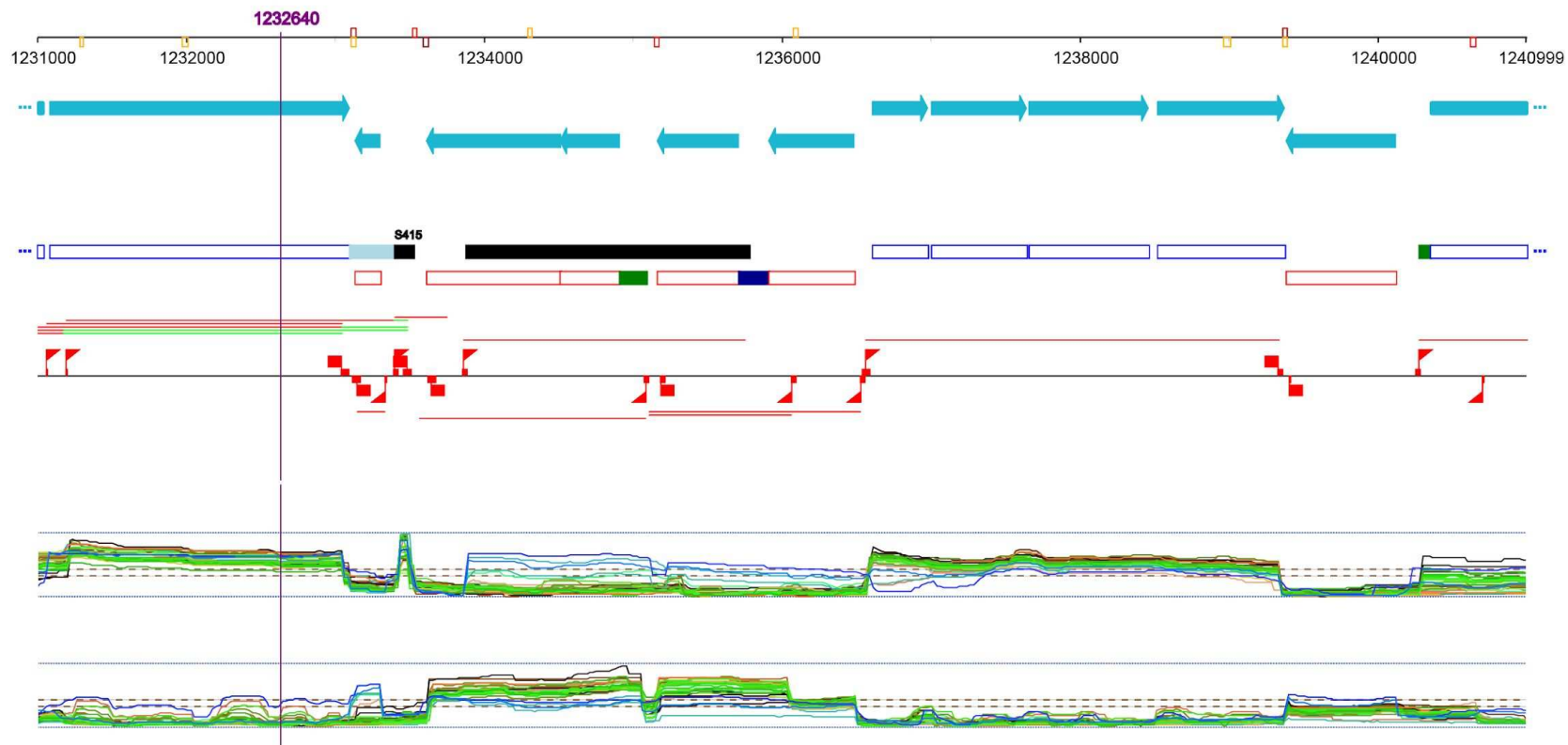


B. subtilis Expression Data Browser



Genomic View

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

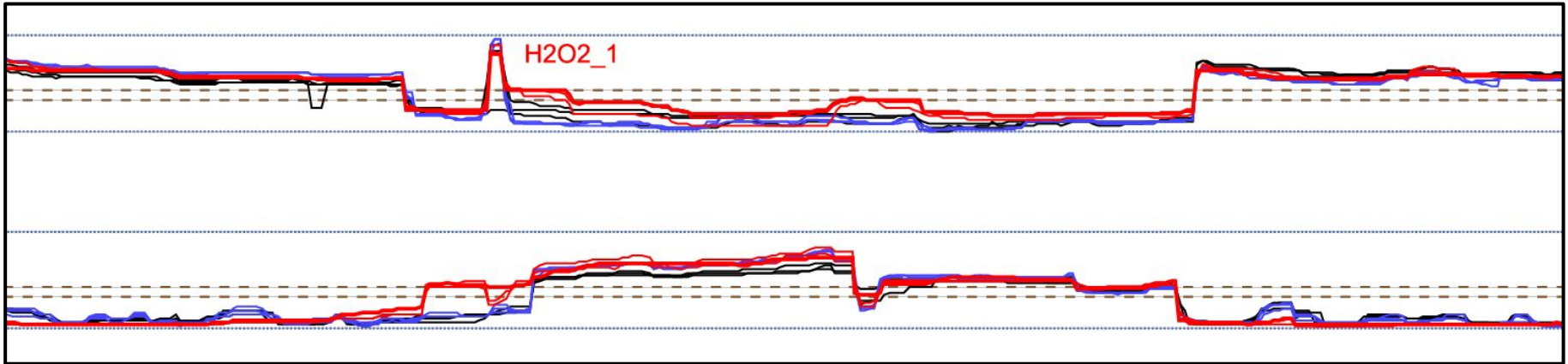


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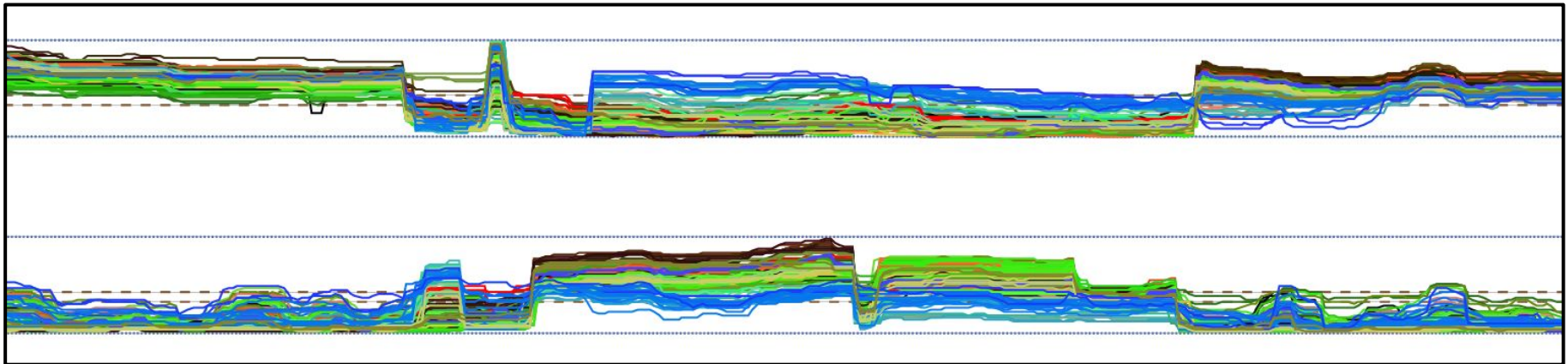
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Graphical representation of transcription profiles

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



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



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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.

