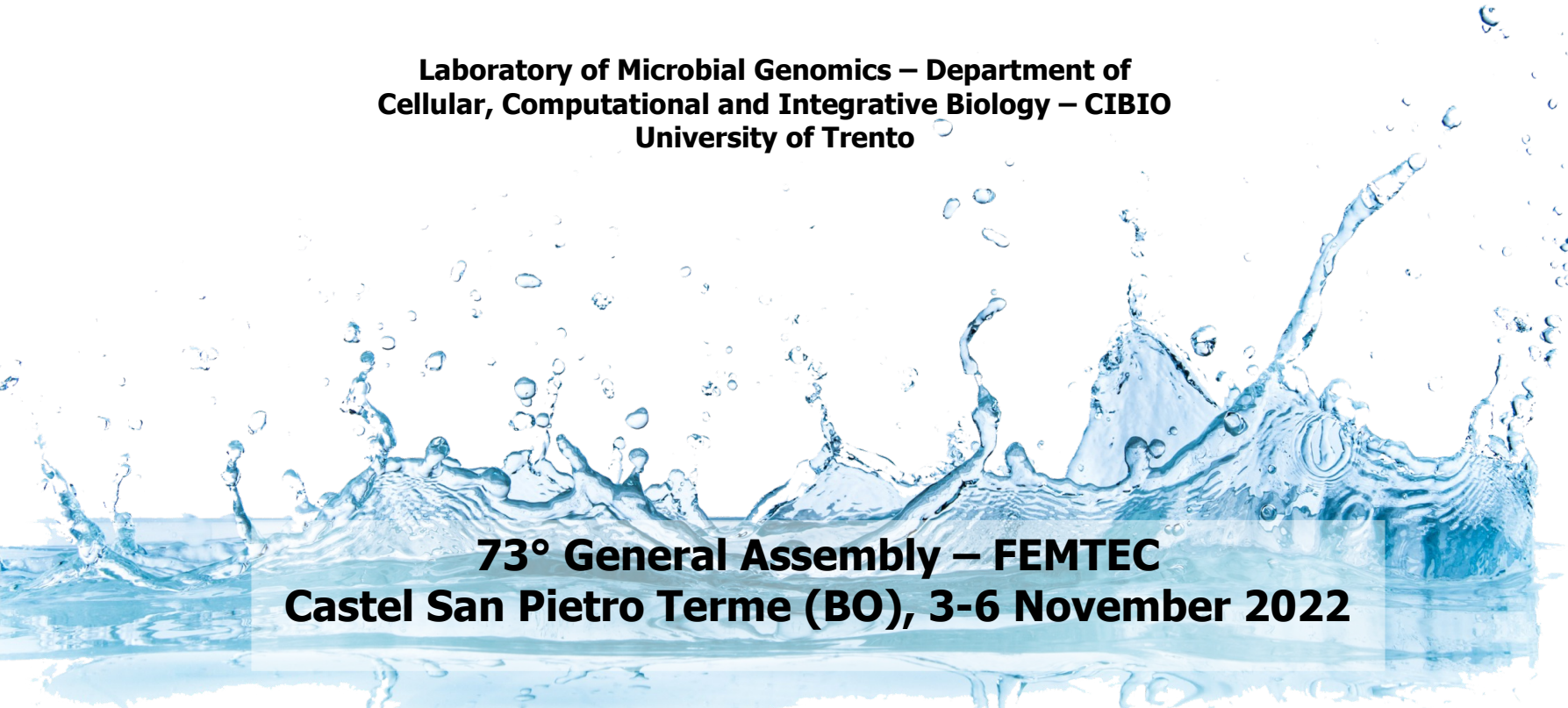




A longitudinal characterization of microbiome of alpine water springs used for human consumption

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Cellular, Computational and Integrative Biology – CIBIO
University of Trento**



**73° General Assembly – FEMTEC
Castel San Pietro Terme (BO), 3-6 November 2022**

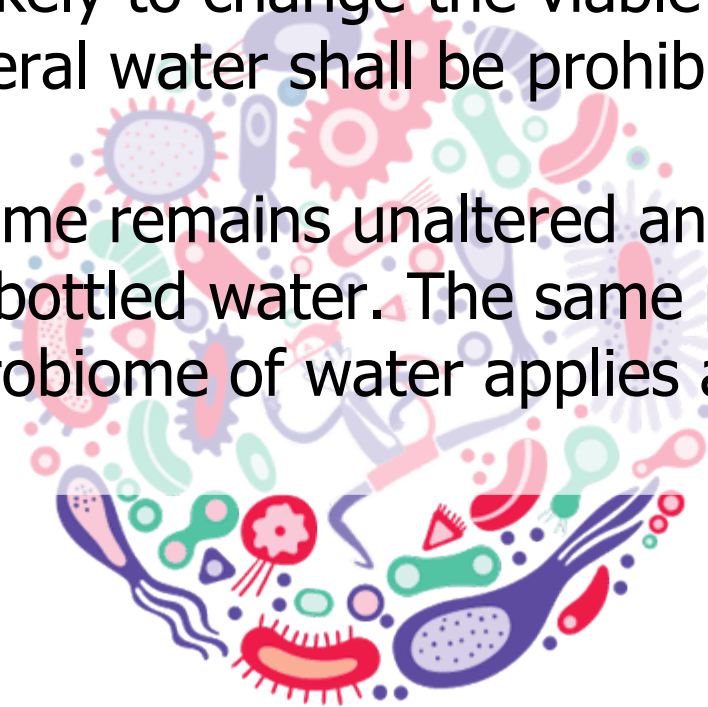
The groundwater microbiome

- Microbiome of **water springs** has been deeply explored by a large number of studies, but the majority of them focused on **extreme environments**
- The microbiome of **drinking water** has been explored mainly to describe spatial and temporal taxonomic compositional patterns, or to investigate the effects of distribution and purification plants on water quality and safety
- Springs that provide water destined for **human consumption** have been instead scarcely investigated
- The presence of bacteria in water sources used for human consumption is a **major concern for health authorities** and the management of microorganisms for water safety is strictly regulated, but it is focused only on total microbial load and on seeking for the presence of pathogenic species that represent a minor fraction of the microbiome diversity



The groundwater microbiome

- European Council Directive 80/777/EEC on the approximation of the laws of the Member States relating to the exploitation and marketing of natural mineral waters. The directive states that: "Any disinfection treatment ... and ... the addition of bacteriostatic elements or any other treatment likely to change the viable colony count of the natural mineral water shall be prohibited."
- Thus the spring microbiome remains unaltered and is consequently present in bottled water. The same principle of leaving intact the microbiome of water applies also to Spa and Medical Spa.



Our previous work



TERME DI COMANO



G ITAL DERMATOL VENEREOL 2000;135

Valutazione dell'efficacia dell'acqua della fonte termale

Comano's (Trentino) thermal water interferes with tumour necrosis factor- α expression and interleukin-8 production and secretion by cultured human psoriatic anti-psi

International Journal of Molecular Medicine

Balneotherapy for atopic dermatitis in children at Comano spa in Trentino, Italy

Journal of Dermatological Treatments

Authors: Ilar...
Zanoni, Ubaldo

Stefania Farina, Paolo Gisondi ✉, Mauro Zanoni, Manuela Pace, Laura Rizzoli, Ermanno Baldo & Giampiero Girolomoni

Page 366-371 | Received 22 Apr 2010, Accepted 08 Jul 2010, Published online: 22 Jan 2011

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<https://doi.org/10.1186/s40168-019-0625-6>


Microbiome

RESEARCH

Open Access

Genomic and metagenomic insights into the microbial community of a thermal spring



Renato Pedron^{1†}, Alfonso Esposito^{1†}, Irene Bianconi¹, Edoardo Pasolli¹, Adrian Tett¹, Francesco Asnicar¹, Mario Cristofolini², Nicola Segata¹ and Olivier Jousson^{1*} 

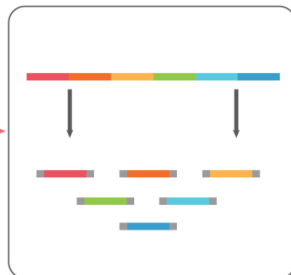
Next Generation Sequencing Workflow



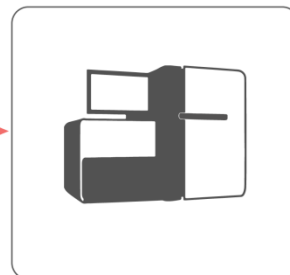
Whole Genome Sequencing (WGS)



Genomic DNA



Tagmentation
of Genomic DNA

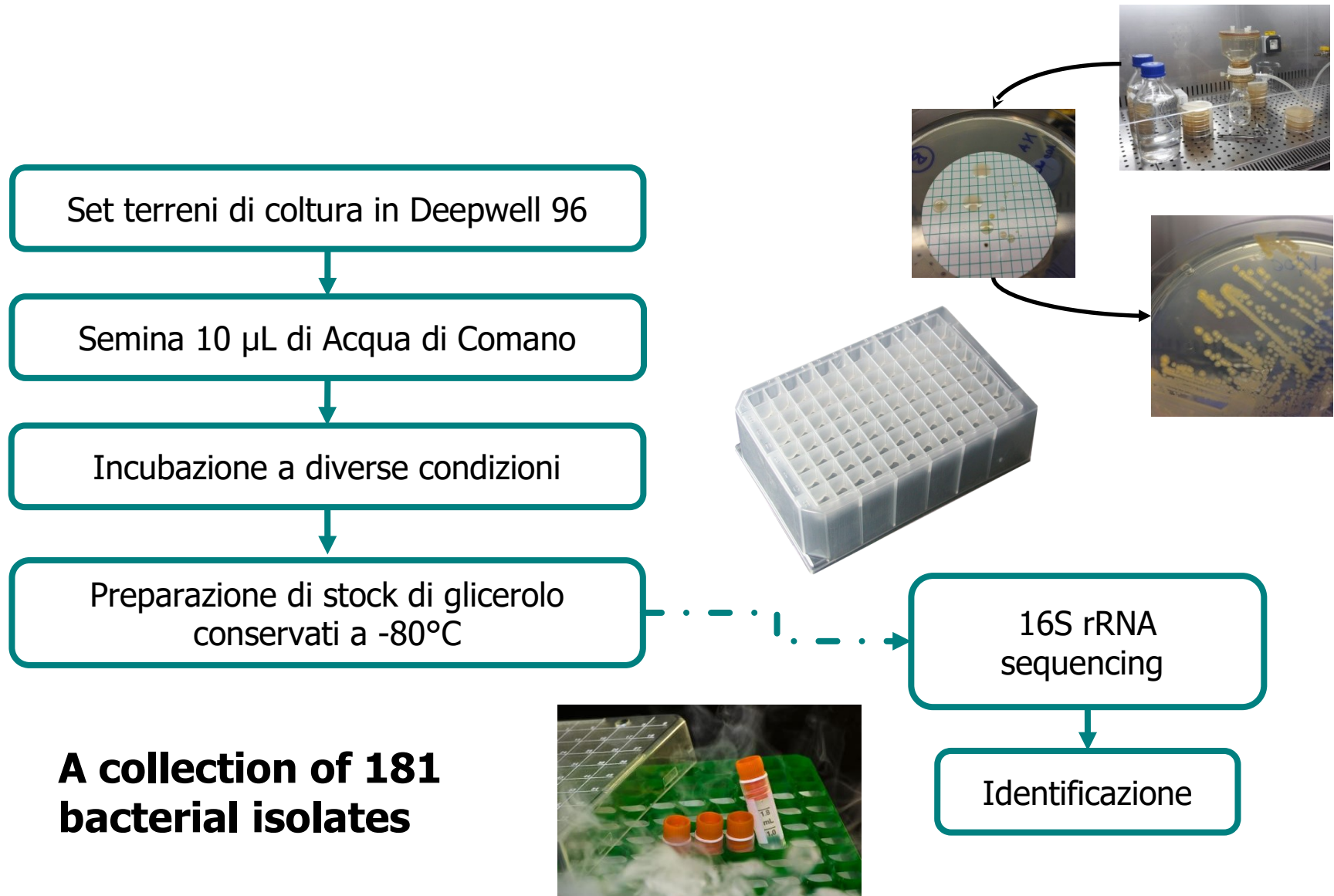


Sequencing



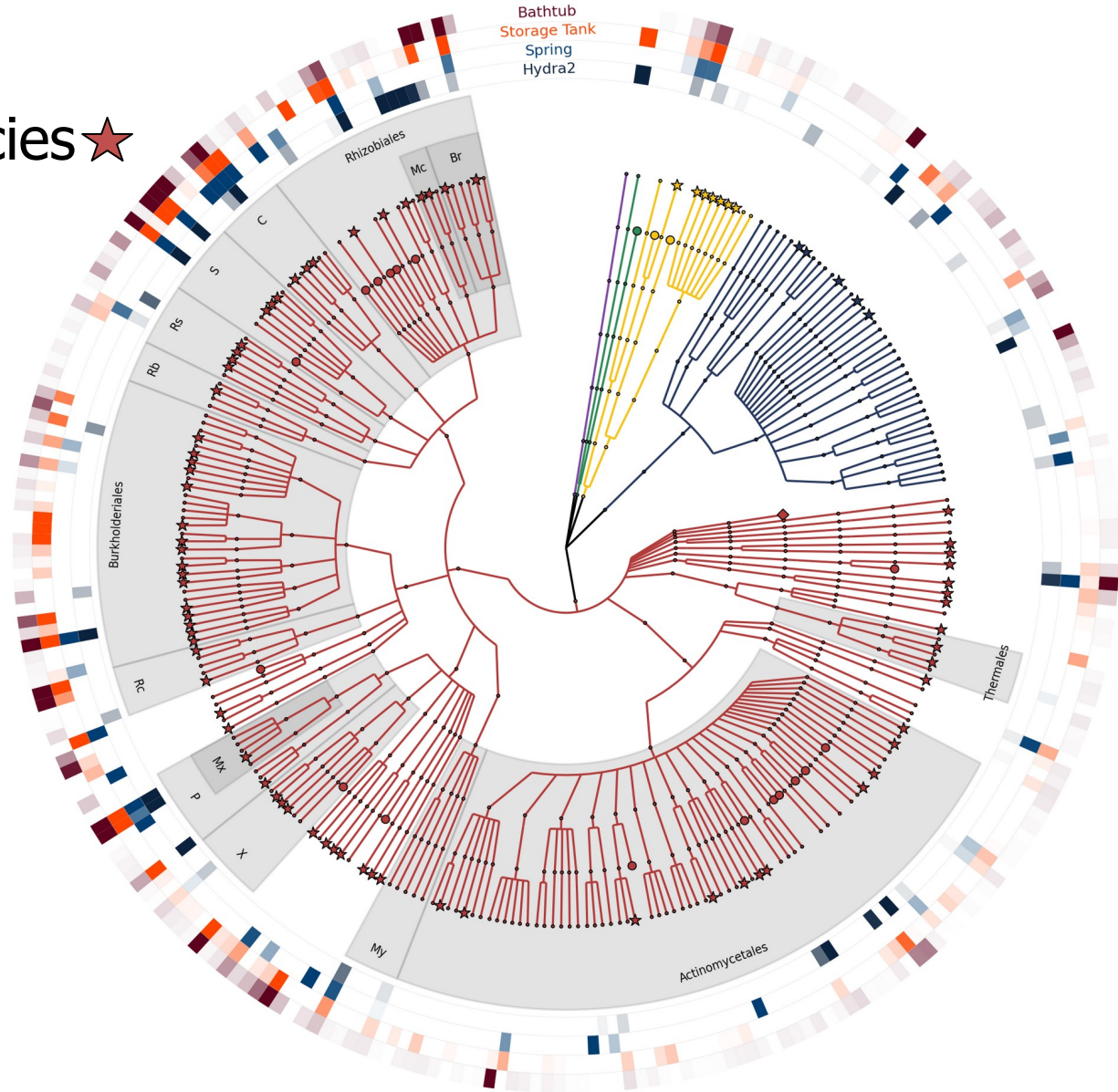
Data Analysis and
Report Generation

Strain isolation workflow

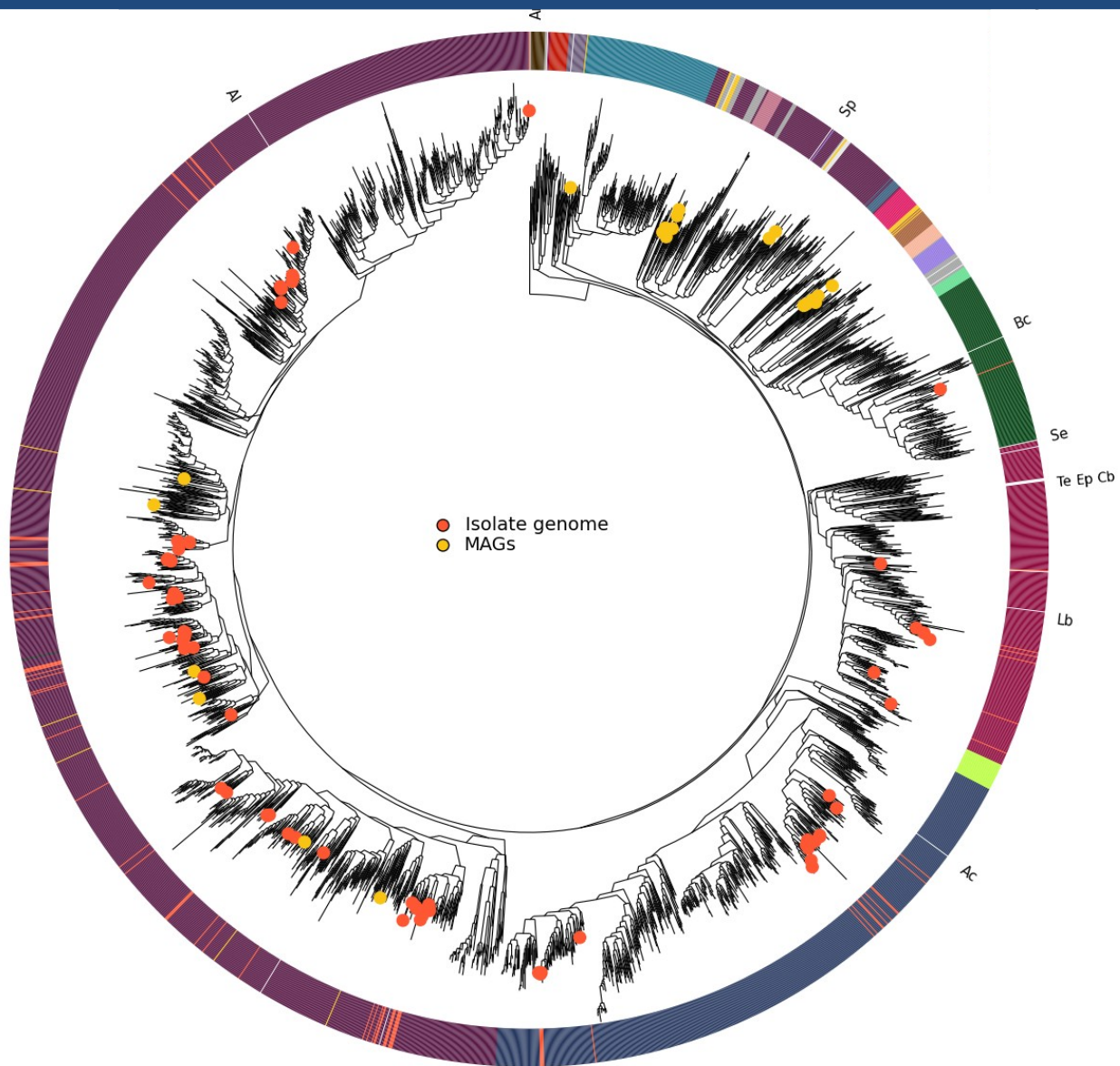


Comano Terme Microbiome

About 40% of
unknown species ★

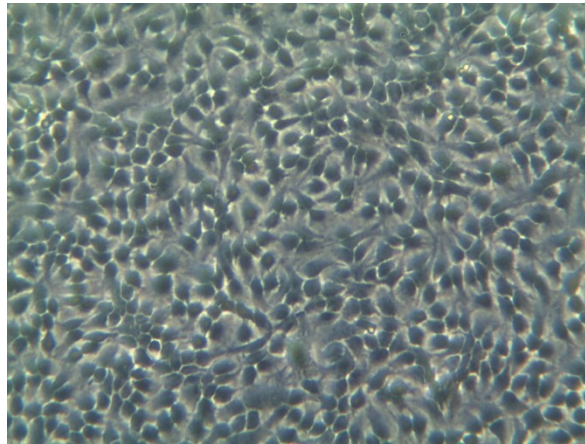
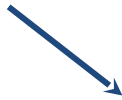


Isolate Genomes vs Metagenome-Assembled Genomes



Characterization of the strain collection: seeking for immunomodulatory properties

Inflammation:
IL-17A e IFN- γ 100 ng/ml



Co-treatment:
5mg lysate
bacterial
sterile



Human immortalized keratinocytes
(HaCat cells)



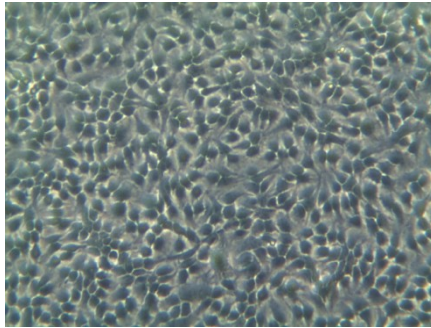
Visual evaluation:
growth and morphology



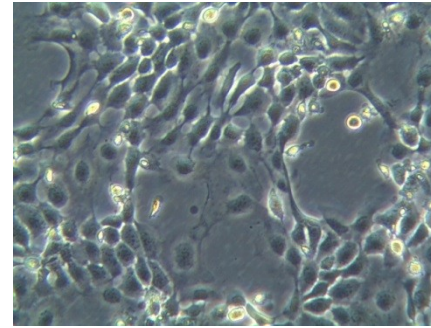
Transcriptional analysis:
IL-6 mRNA level

Effect of bacterial lysates on Hacat cells

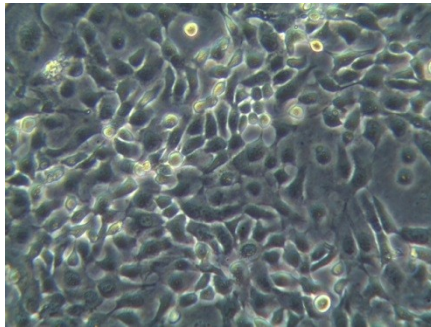
Cellule non trattate



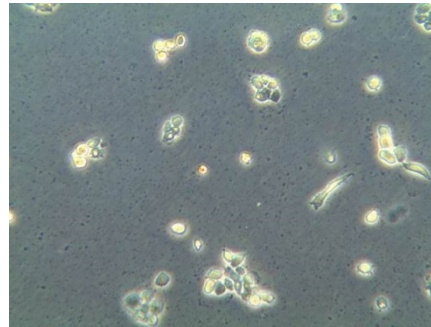
**Cellule infiammate:
IL-17A + IFN- γ**



IL-17A + IFN- γ + Lisato batterico

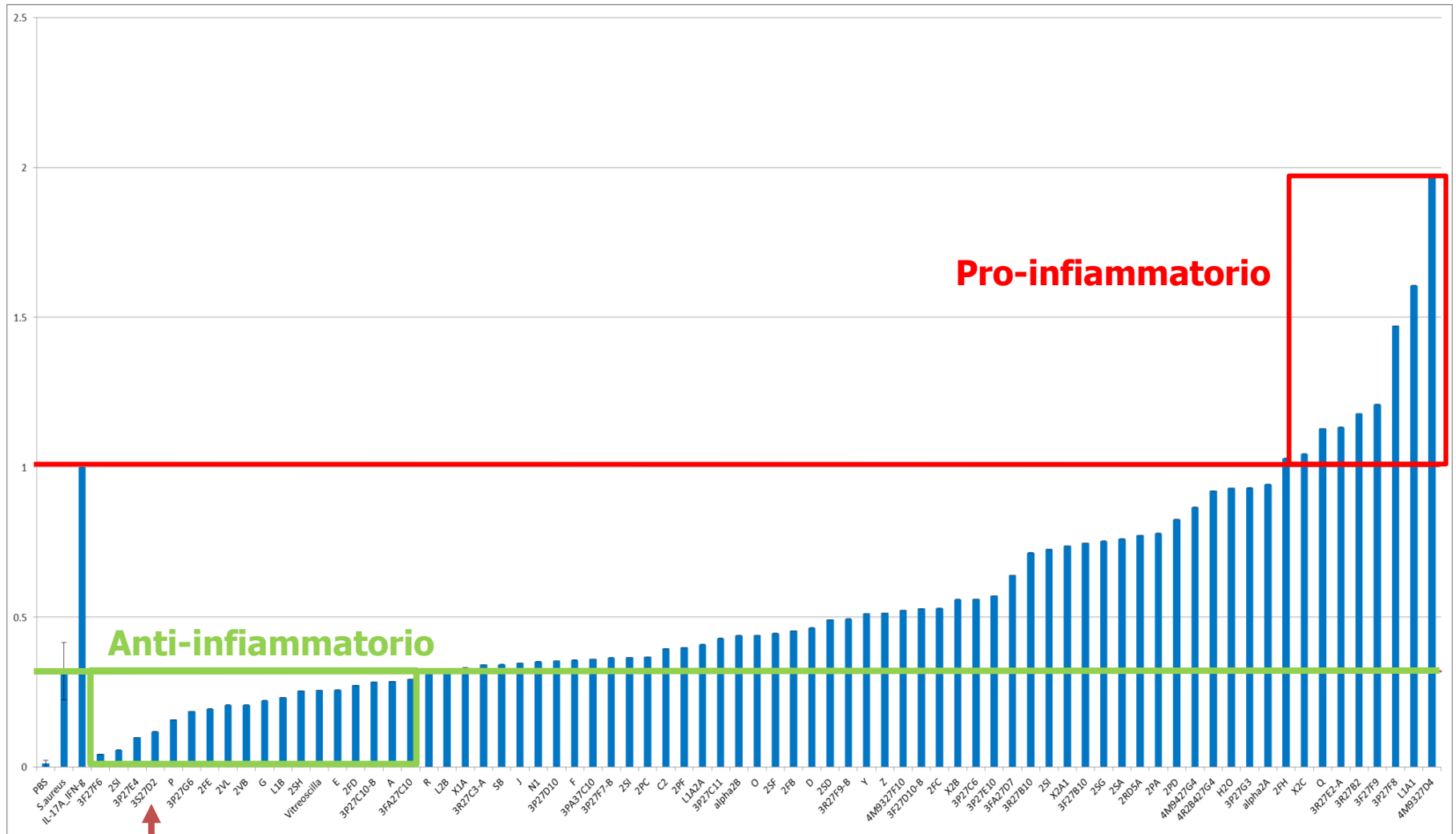


**Effetto positivo:
incremento crescita**



**Effetto negativo:
morte cellulare**

Screening output



Mesorhizobium comanense sp. nov.

Mesorhizobium comanense sp. nov., isolated from groundwater

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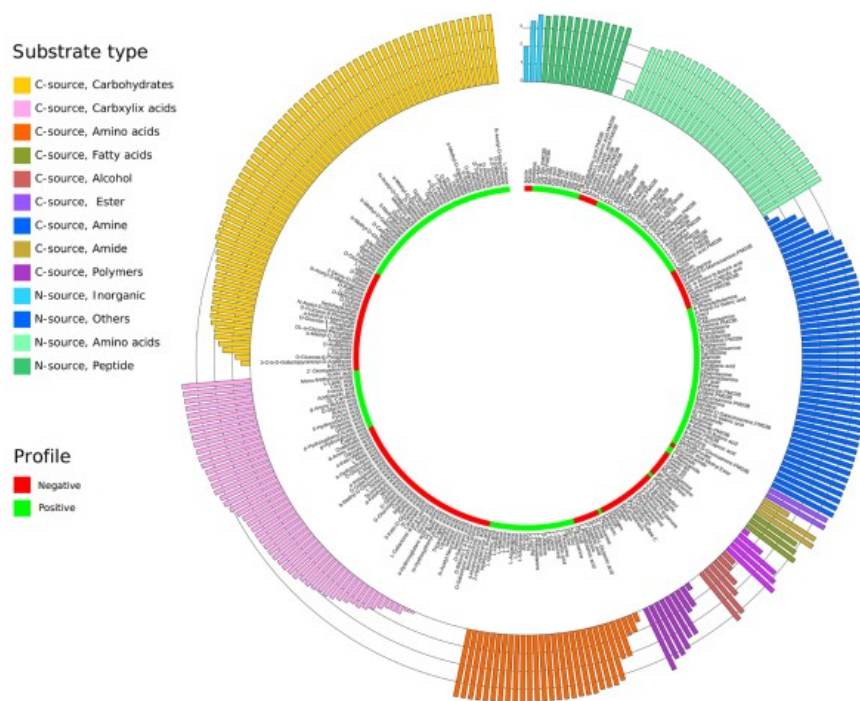
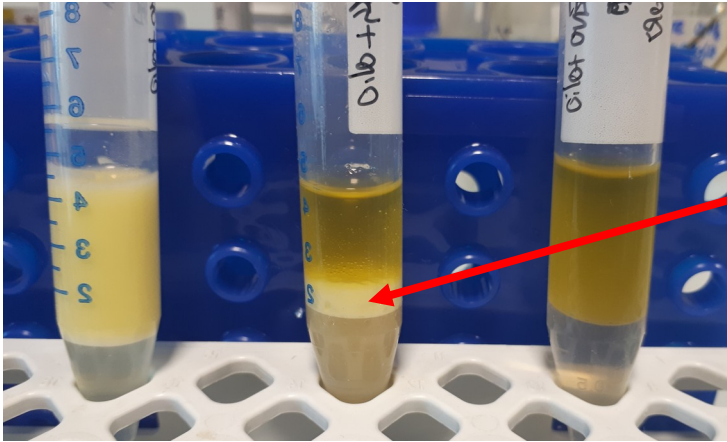
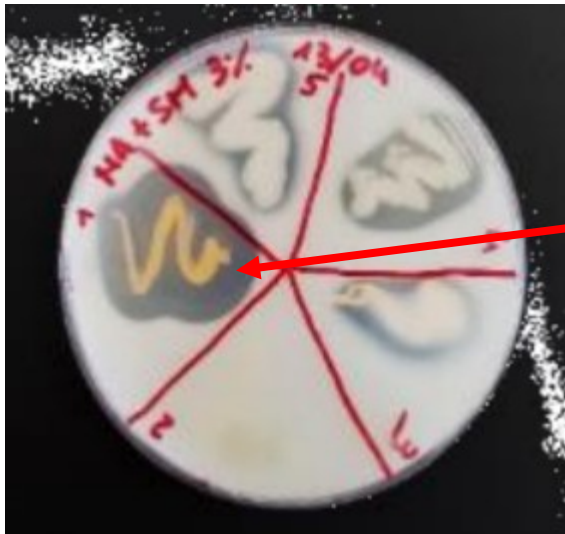


Fig. 3. Phenotypic profile of strain 3P27G6^T. The tested compounds are grouped by substrate family and displayed as bar charts in the outer ring of the figure. The represented value is the log₁₀ normalized mean of three biological replicates of the area under the curve calculated using non-parametrical free spline methods. The inner ring marks the compounds for which the strain tested positive (green) or negative (red).

Other bioactivities of potential medical and industrial interest

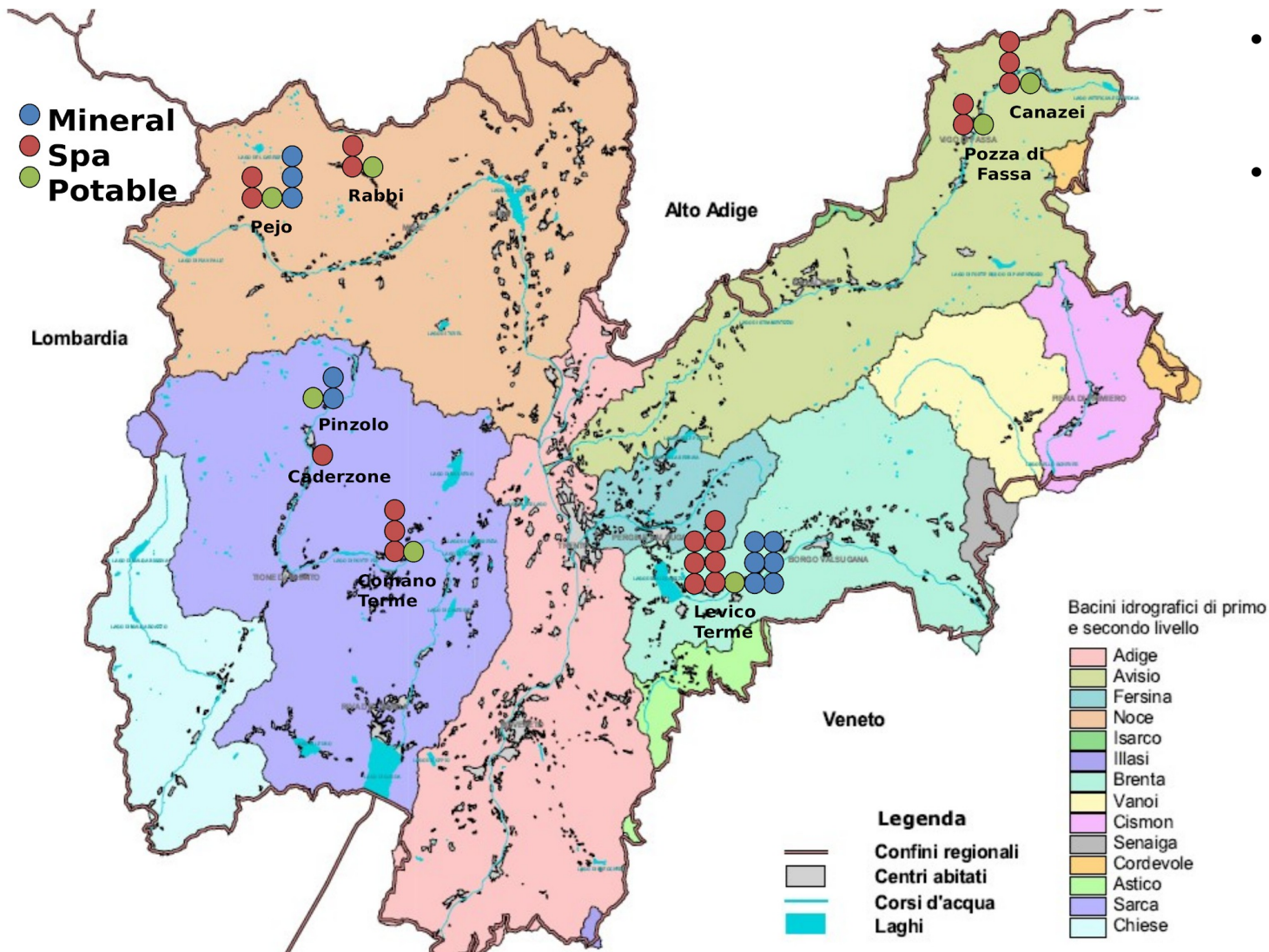


Biosurfattanti



Biodegradazione (di
proteine, lipidi, zuccheri)

The Microbiome of Trentino springs



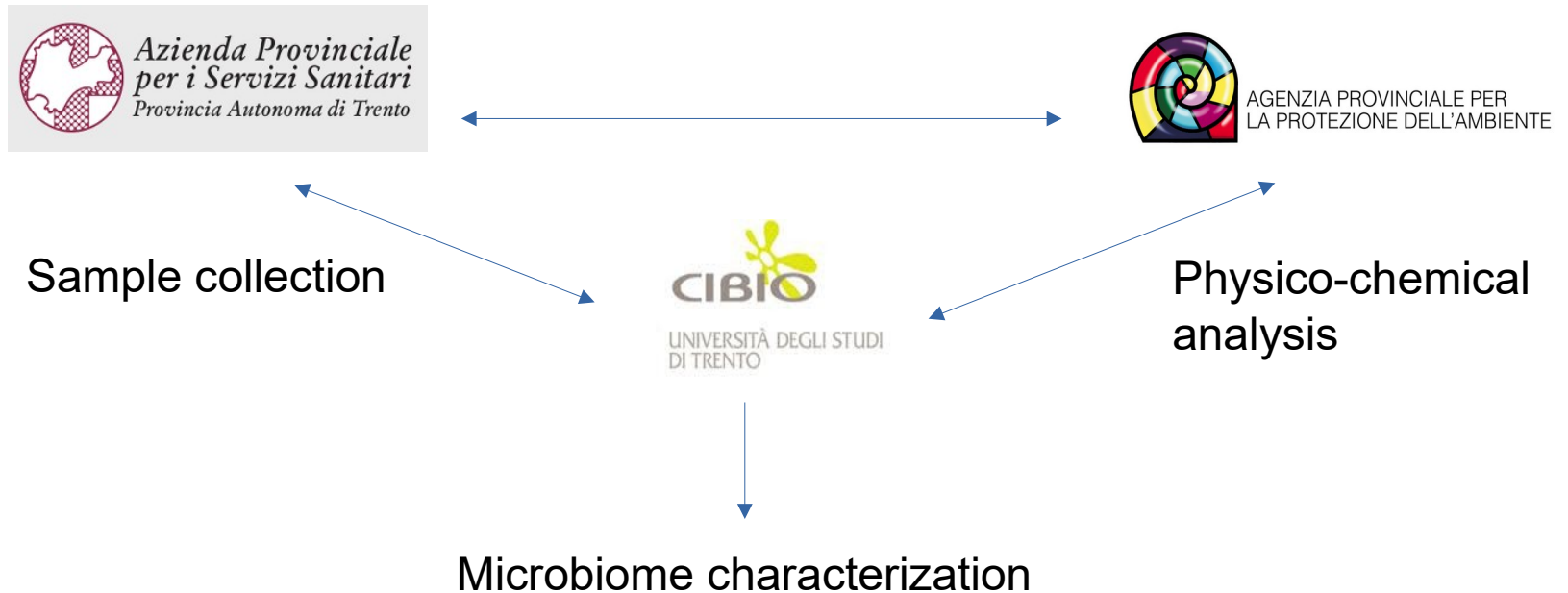
- 38 springs in Trentino
- 8 time points over a two-year period

Microbiome characterization of alpine water springs for human consumption reveals site- and usage-specific microbial signatures

Renato Pedron^{1†}, Alfonso Esposito^{2†}, William Cozza¹,
Massimo Paolazzi³, Mario Cristofolini⁴, Nicola Segata¹ and
Olivier Jousson^{1*}

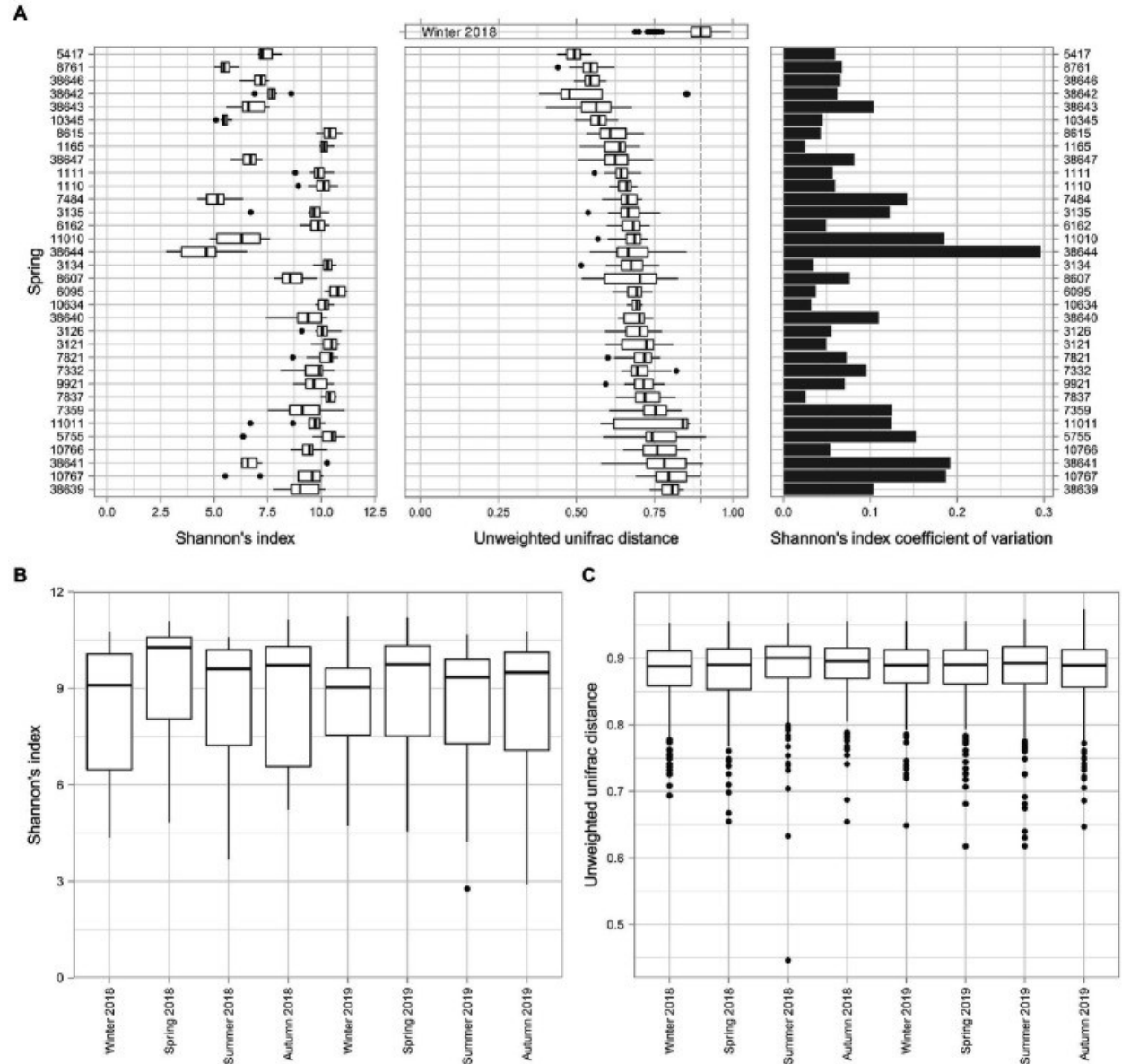
¹Department of Cellular, Computational and Integrative Biology – CIBIO, University of Trento, Trento, Italy, ²International Centre for Genetic Engineering and Biotechnology – ICGEB, Trieste, Italy, ³Agenzia provinciale per la protezione dell'ambiente – APPA, Trento, Italy, ⁴Istituto G.B. Mattei, Stenico, Italy

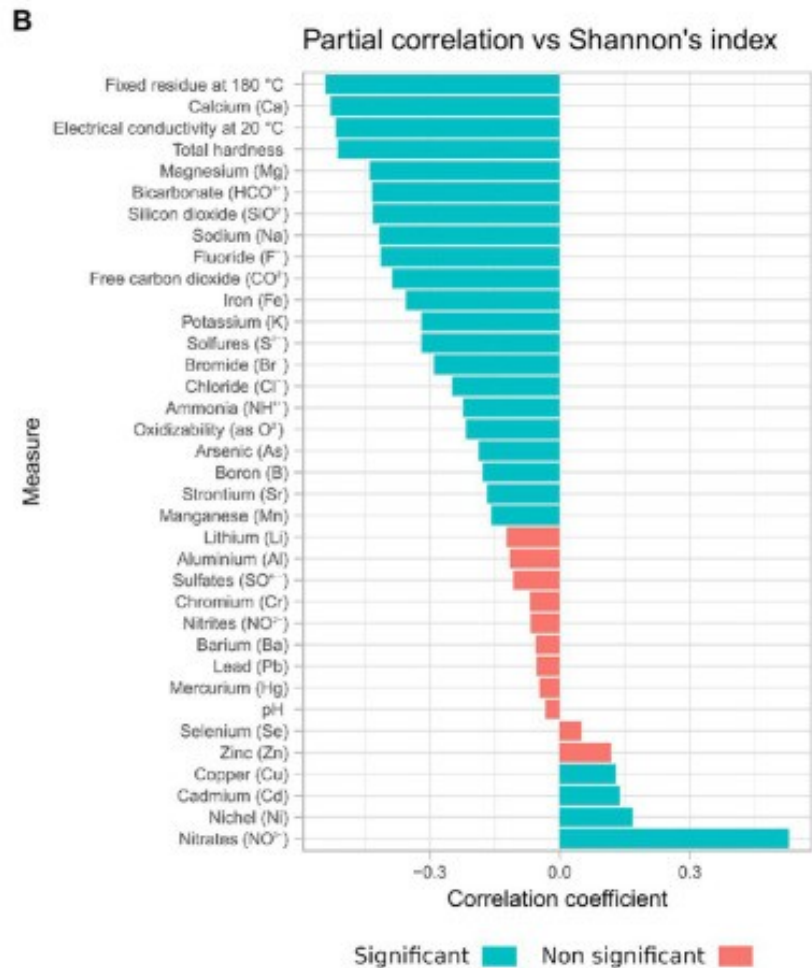
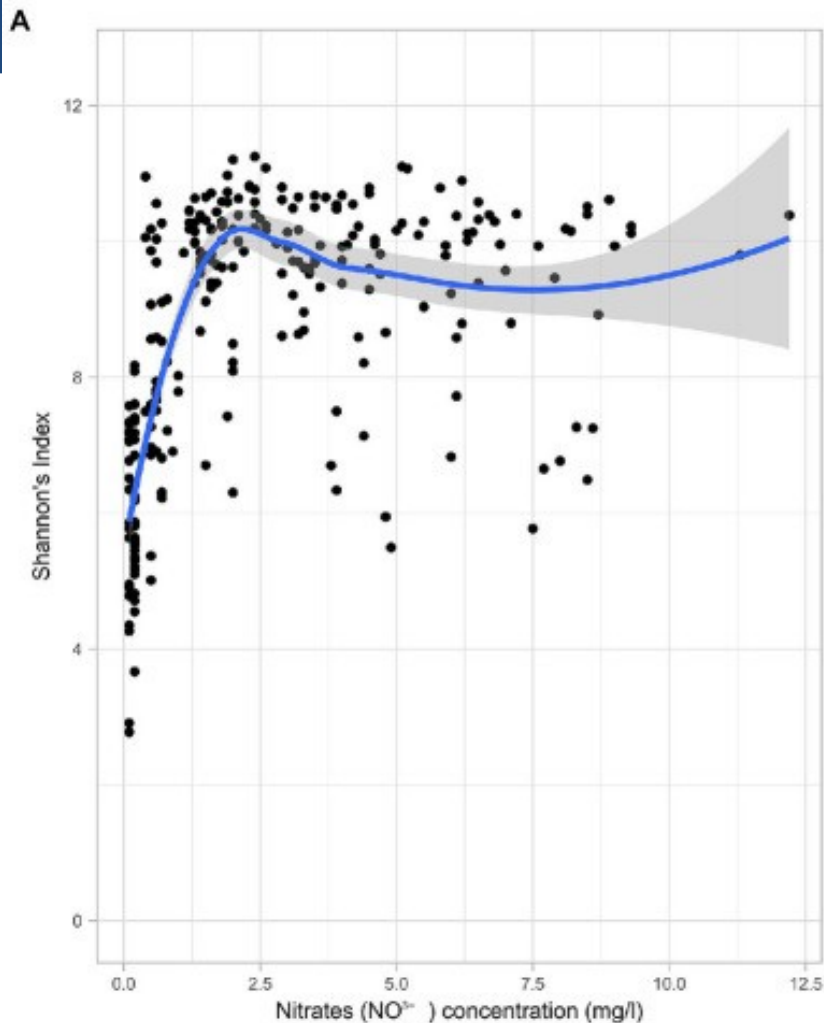
Integration of microbial community composition with physico-chemical metadata



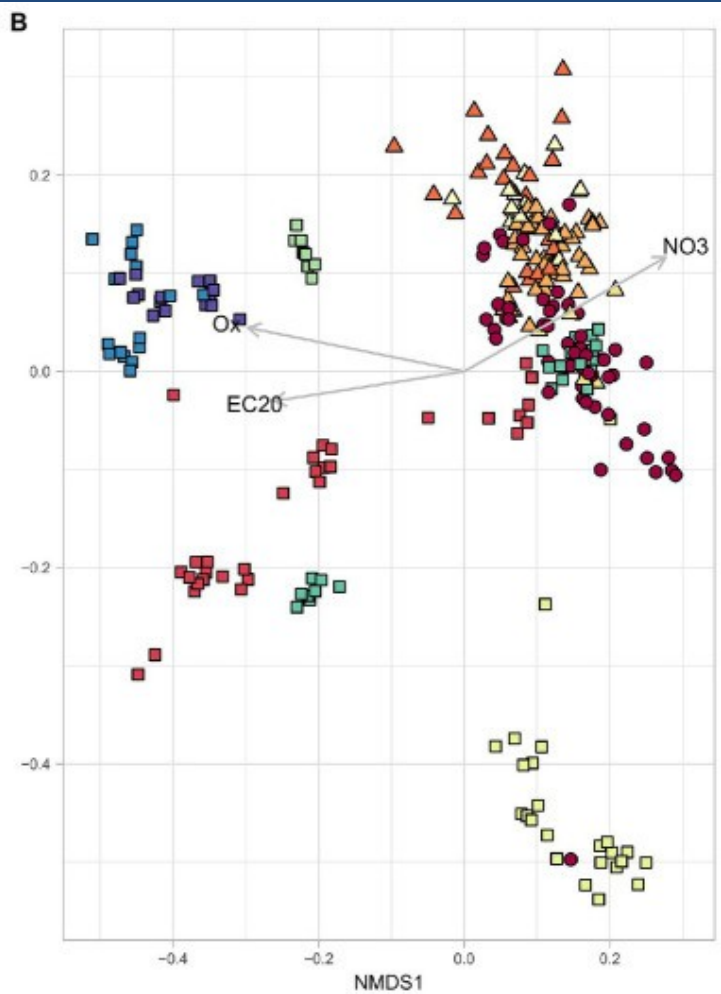
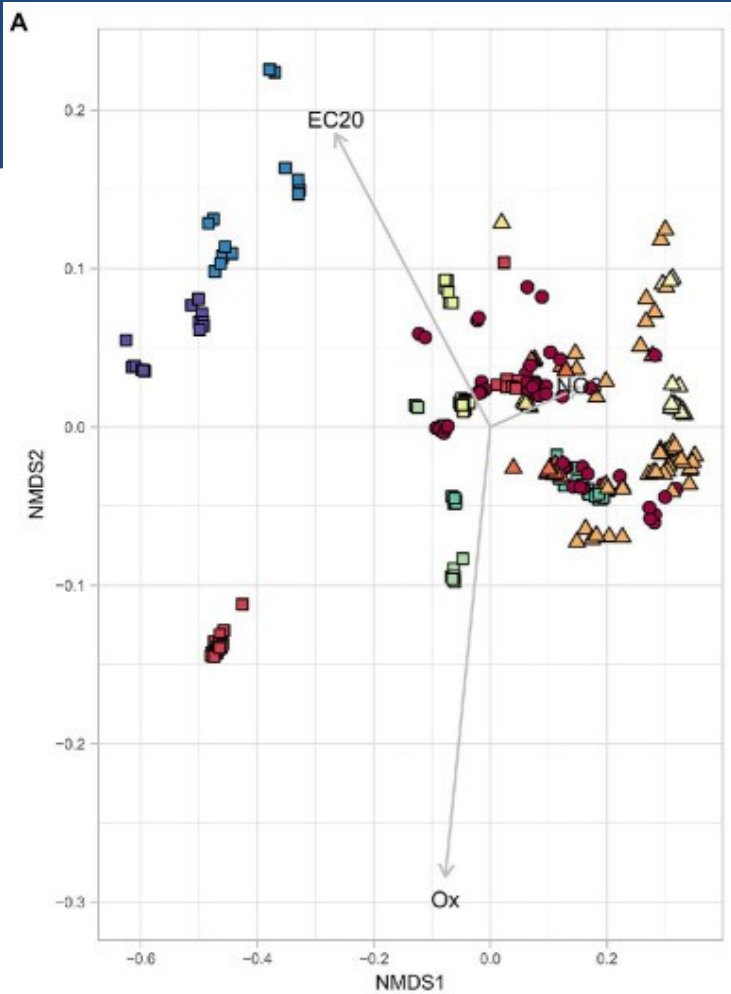
Evaluation of the microbiome stability of the springs

Microbiome diversity is affected by seasonal cycle



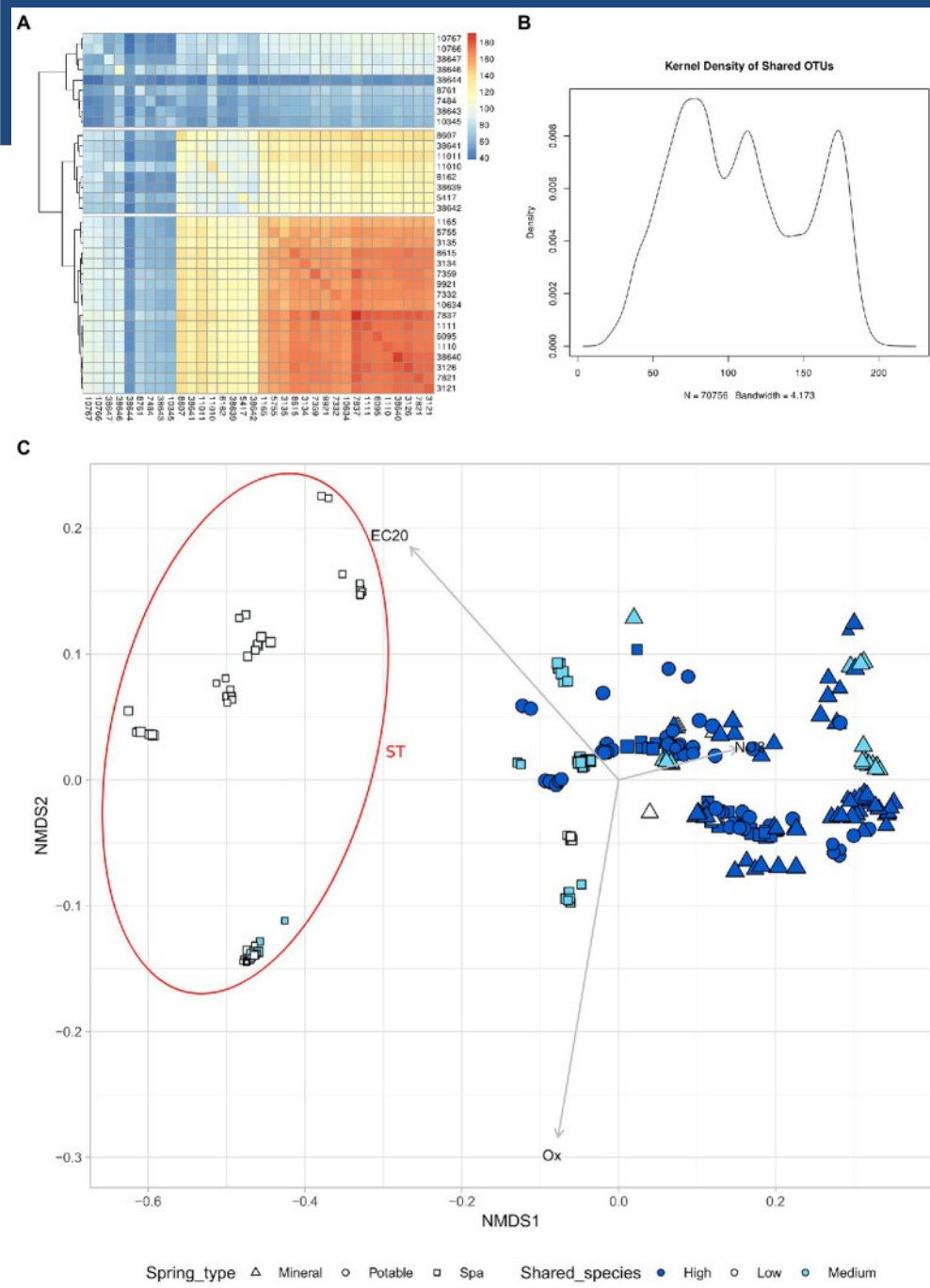


Nitrate concentration influences the microbiome diversity. Correlation of chemical data with alpha diversity. **(A)** Scatterplot of Shannon alpha diversity index of all samples in the study vs. Nitrate concentration. **(B)** Spearman partial correlations, given Nitrates, of all measured chemical parameters.



- Spring type Δ Mineral \circ Potable \square Spa
- Comune ● Levico acque minerali ● Terme Comano ● Terme di Pejo
- Structure ● Fassa Terme ● Rizzi minerali ● Terme di Caderzone ● Terme di Rabbi
- Idropejo ● Surgiva ● Terme di Levico

The physico-chemical parameters and the sequencing data present similar behavior



High nitrates concentration leads to a higher alpha diversity and **more shared species**.

(A) Heatmap of the number of shared species between different springs (mean of all timepoints)

(B) Kernel density of shared ASV

(C) NMDS of all samples based on chemical parameters

The samples can be divided in 3 groups based on the number of shared species with other springs. **High** number of shared species (**High**), **Medium** number of shared species (**Medium**), low number of shared species (**Low**).

Conclusions and future perspectives

- Diversity of spring microbiome is affected by seasonal cycle
- Environmental parameters are partially correlated with microbial community composition
- The analysis of the number of shared species reveals three distinct groups of springs
- Our results sum up to the recent literature in support of the use of microbial communities as bioindicators for groundwater quality assessment
- The present study constitutes an example for standard water spring monitoring integrated with microbial community composition on a regional scale, and provides information which could be useful in the design and application of future water management policies

Acknowledgements



ISTITUTO
G.B. MATTEI
RICERCA IN IDROLOGIA MEDICA
E MEDICINA TERMALE



TERME DI COMANO



FONDAZIONE
CASSA DI RISPARMIO
DI TRENTO E ROVERETO



PROVINCIA
AUTONOMA DI TRENTO

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- Nicola Segata (CIBIO)
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