

Meili Vanegas Hernández  
(m.vanegas10@uniandes.edu.co)

Fabio Andrés López Corredor  
(fa.lopez10@uniandes.edu.co)

John Alexis Guerra Gómez  
(ja.guerrag@uniandes.edu.co)  
Advisor

# BioCicle

A visual analytics tool for summarize  
and compare biological sequence  
alignments

## The goal

BioCicle intends to provide a visualizing tool designed to facilitate understanding and further analysis of taxonomic reports as results of protein sequence comparisons

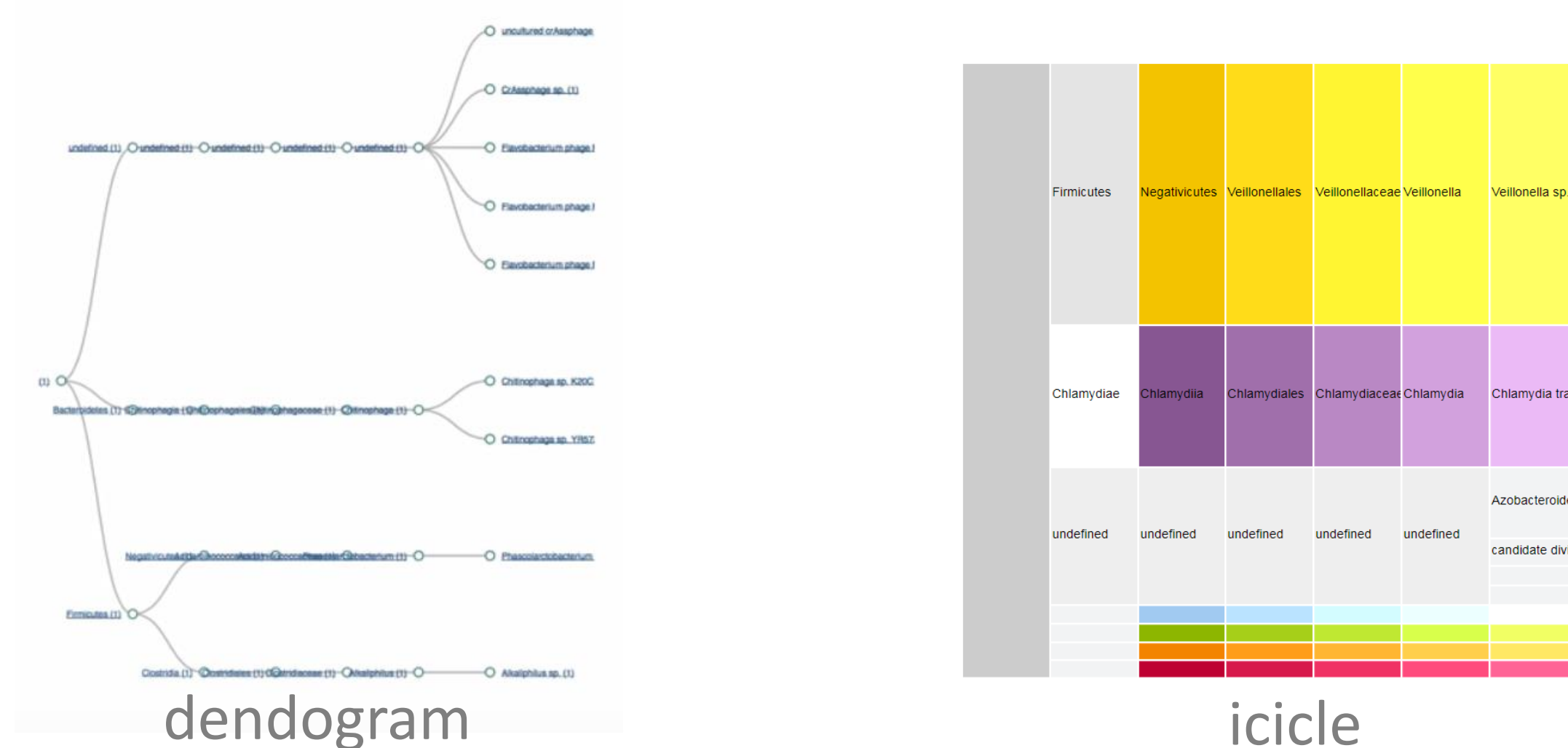
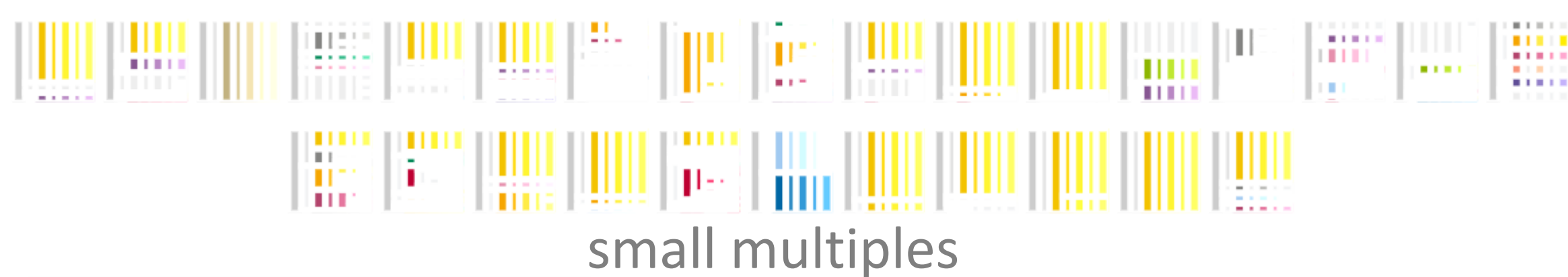
## The Tool

BioCicle receives the resulting XML Output including the resulting matching organisms after executing BLASTp on the NCBI Web page.

### Analysis Tasks



For each match, BioCicle displays an **icicle** containing its taxonomy. A **dendrogram** shows a summary of the ranks found among all the queried sequences



The analyst is now able to filter and obtain details for each sequence, and explore through the different levels of the taxonomy tree to keep track of common ranks

## Improvements

- Usage focused on NCBI's BLAST XML format
- Option to locally run the platform, updating to the latest or desired database
- Details from each resulting hit are shown as a table

## Results

The web version was tested by computational biology students and teachers.

They found the tool useful inside their projects of interest, validating its findings with their knowledge

As main users, they are contributing to the capacity of BioCicle to provide further insights in the area of bioinformatics

## Conclusions and future work

- Bioinformaticians save the work of parsing XML manually by filtering visually the most relevant ranks
- We'll perform experiments to measure BioCicle and comparing it to alternative approaches on taxonomy visualization.
- Along with the visual aid, users need a concrete, numeric summary of the nature from the common hits

Demo available at  
<http://biocicle.johnguerra.co>

