

Protein Family Sorter

History of the Protein Family Sorter



AMERICAN
SOCIETY FOR
MICROBIOLOGY

Journal of
Bacteriology



[Advanced Search](#)

[Home](#)

[Articles](#)

[For Authors](#)

[About the Journal](#)

[Subscribe](#)

Computational Biology

Analysis of Ten *Brucella* Genomes Reveals Evidence for Horizontal Gene Transfer Despite a Preferred Intracellular Lifestyle

Alice R. Wattam, Kelly P. Williams, Eric E. Snyder, Nalvo F. Almeida Jr., Maulik Shukla, A. W. Dickerman, O. R. Crasta, R. Kenyon, J. Lu, J. M. Shallom, H. Yoo, T. A. Ficht, R. M. Tsolis, C. Munk, R. Tapia, C. S. Han, J. C. Detter, D. Bruce, T. S. Brettin, Bruno W. Sobral, Stephen M. Boyle, João C. Setubal

DOI: 10.1128/JB.01767-08

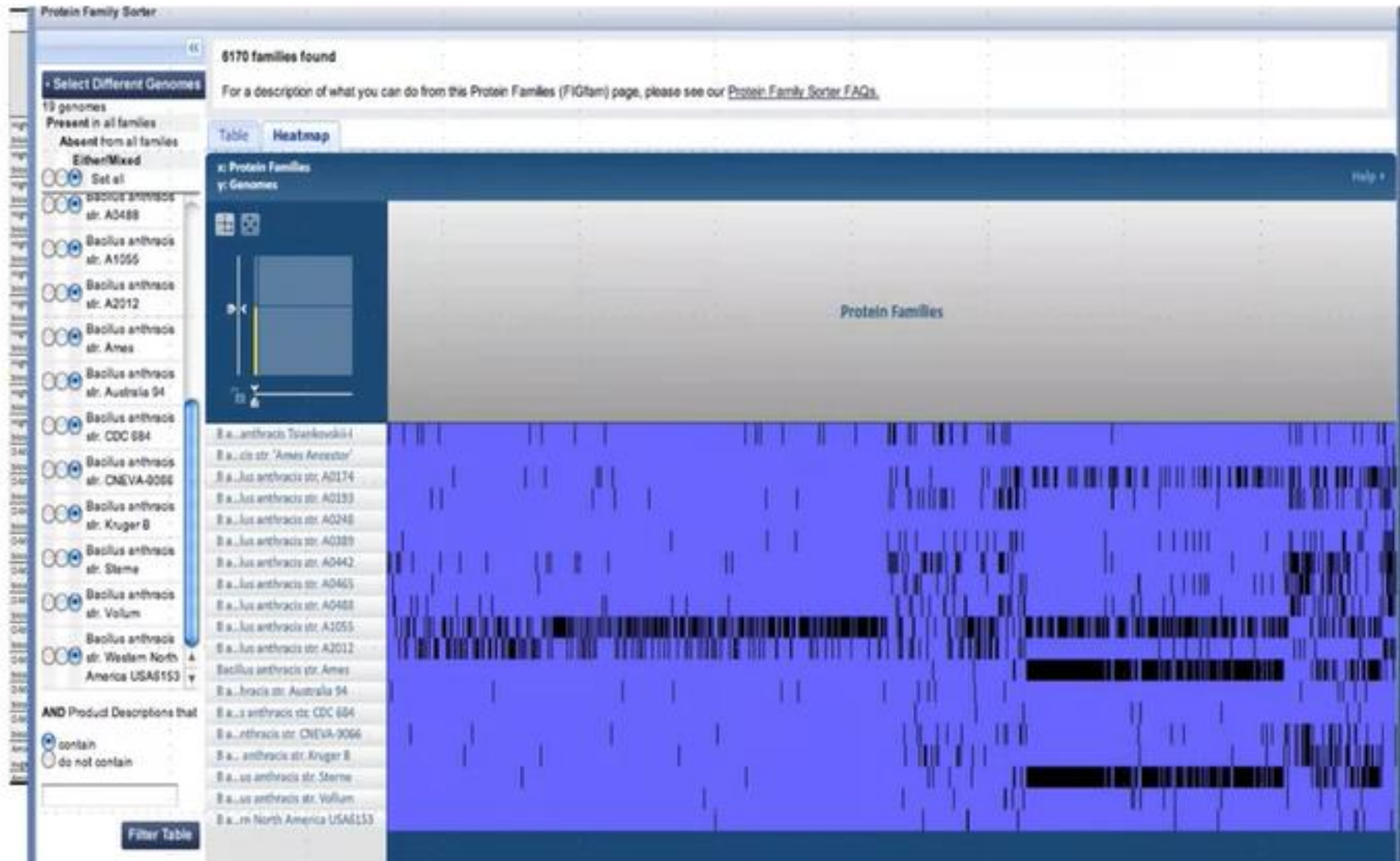
From excel to a dynamic analysis interface

The image displays a complex Gantt chart interface, likely from a project management software like Microsoft Project. The chart is organized into multiple columns representing time periods, with tasks listed on the left. The tasks are color-coded and include various status indicators (e.g., 'Not Started', 'In Progress', 'Completed'). The interface includes a top menu bar, a toolbar with various icons, and a bottom status bar. The chart shows a detailed timeline of project activities, with tasks like 'Project Start', 'Task 1', 'Task 2', etc., and their corresponding durations and dependencies.

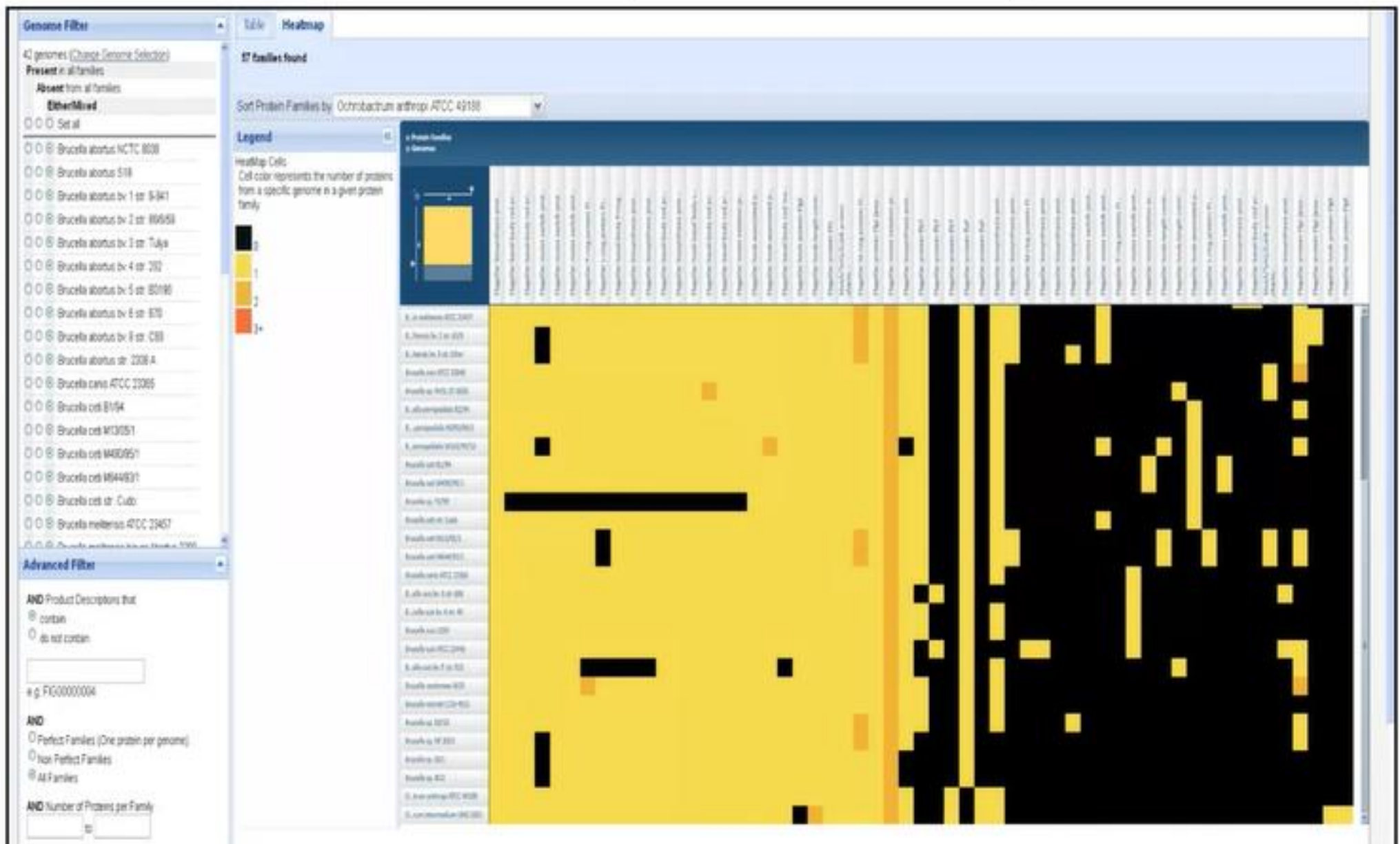
From excel to a dynamic analysis interface

[illegible]

From excel to a dynamic analysis interface



From excel to a dynamic analysis interface



Protein Family Sorter uses Protein Families



[Front Microbiol.](#) 2016; 7: 118.

Published online 2016 Feb 8. doi: [10.3389/fmicb.2016.00118](https://doi.org/10.3389/fmicb.2016.00118)

PMCID: PMC4744870

PMID: [26903996](#)

PATtyFams: Protein Families for the Microbial Genomes in the PATRIC Database

[James J. Davis](#),^{1,2,*} [Svetlana Gerdes](#),^{2,3} [Gary J. Olsen](#),⁴ [Robert Olson](#),^{1,5} [Gordon D. Pusch](#),^{2,3} [Maulik Shukla](#),^{1,2}
[Veronika Vonstein](#),^{2,3} [Alice R. Wattam](#),⁶ and [Hyunseung Yoo](#)^{1,2}

Exercises for the Protein Family Sorter

- Use the genomes assembled in the Comprehensive Genome Analysis section using the hybrid reads
 - Unicycler assembly strategy
 - Canu assembly strategy
 - Variations in Racon iterations
 - Variation in Pilon iterations
- Examine patterns in these genomes to determine the strengths and weaknesses of the different strategies