Protein Family Sorter

History of the Protein Family Sorter

search

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
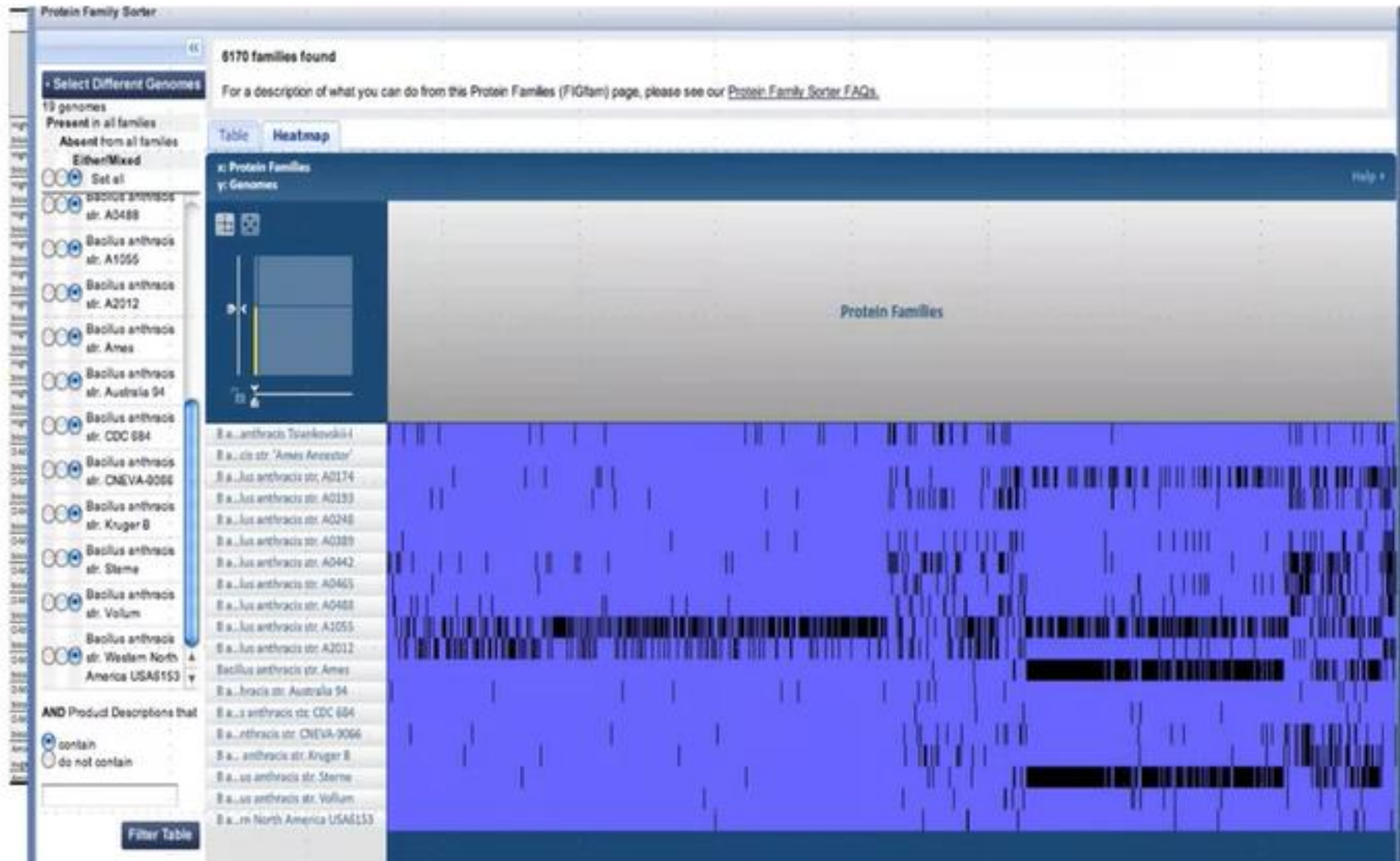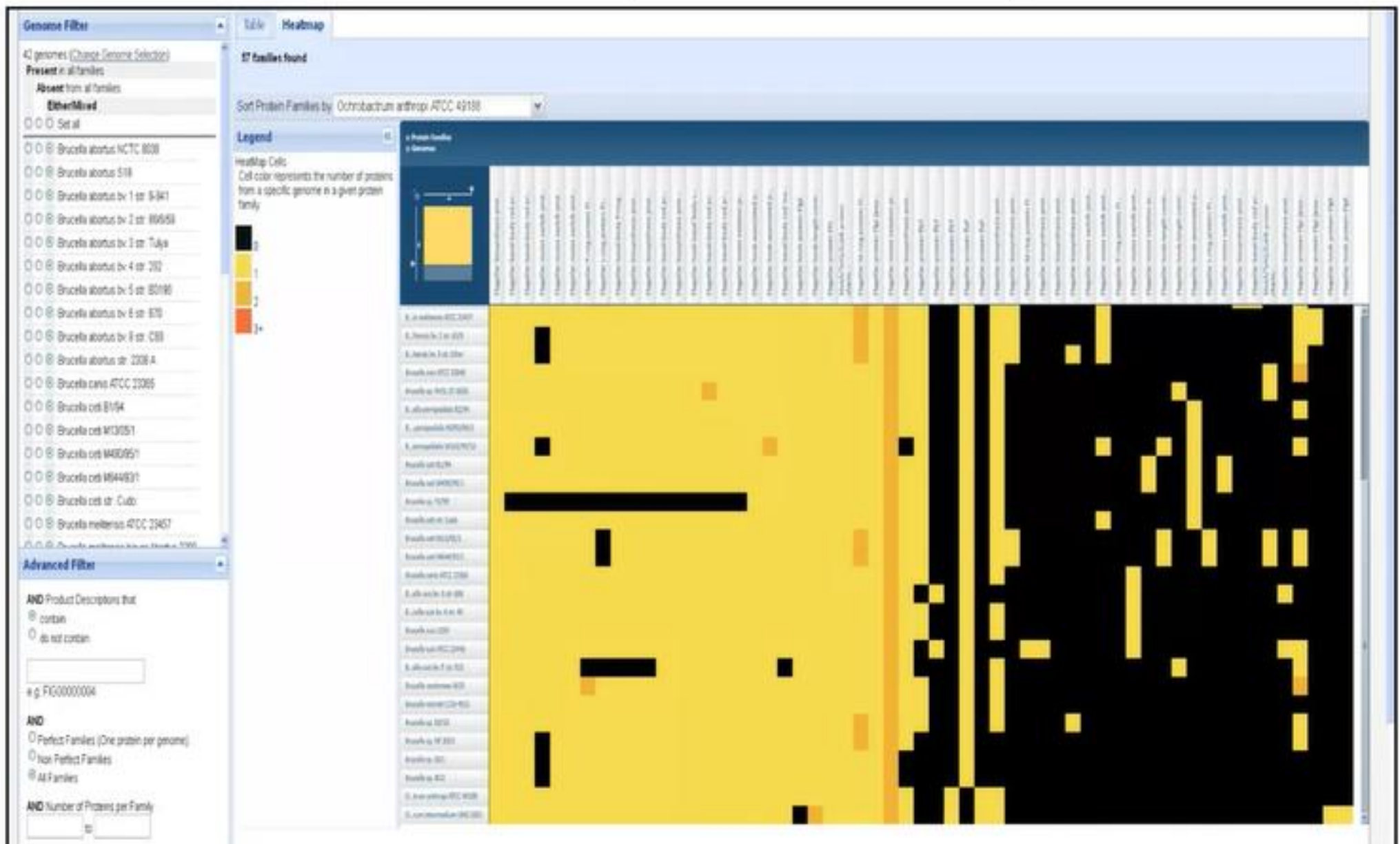
From excel to a dynamic analysis interface

From excel to a dynamic analysis interface

From excel to a dynamic analysis interface

From excel to a dynamic analysis interface

Protein Family Sorter uses Protein Families

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