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## Evolutionary genomics to improve functional prediction of parasite genes and proteins

The availability of genomic data provides an opportunity to understand parasite biology and to identify new drug candidates against neglected diseases affecting millions of people worldwide. Functional annotation of genomes, transcriptomes and predicted proteomes is one of the major challenges in sequencing projects. We address this challenge by applying an evolutionary framework to the interpretation of sequence data. Our research projects have been focused on the analyses of distinct protein families in helminths (*Schistosoma* and others) and protozoans (*Leishmania, Trypanosoma*, and *Plasmodium*), which cause a broad range of diseases. These protein families include mainly protein kinases, protein deacetylases, and proteases. Potential homologues in the predicted proteomes of selected taxa are identified by using hidden Markov model profiles. Evolutionary relationships of protein sequences are reconstructed by two character-based methods (Bayesian inference and maximum likelihood). Evolutionary trees are annotated with taxonomic and experimental information based on the scientific literature. Our work improves functional annotation of genes and proteins of diverse parasites and their homologues in humans. Furthermore, our work potentially identifies molecular biomarkers with various applications.

## **Biography**

Laila Alves Nahum completed her PhD at the University of São Paulo, Brazil and Postdoctoral studies from the Marine Biological Laboratory and Louisiana State University, USA. She is a Researcher at Fiocruz Minas and a Teacher at Promove College of Technology. Her research is focused on the Phylogenomics (Phylogenetics + Genomics) of a broad range of organisms including human pathogens and their vectors. She has published research papers in reputed journals and book chapters.

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