

Felipe da Veiga Leprevost

Ann Arbor – Michigan – USA

+1 734 436-1805 • felipe@leprevost.com.br

www.leprevost.com.br • github.com/prvst

Education

University of Michigan <i>Research Fellow, Computational Proteomics</i>	Ann Arbor, USA <i>2015-present</i>
Carlos Chagas Institute - Fiocruz <i>Postdoc, Computational Proteomics</i>	Curitiba, Brazil <i>2014</i>
Carlos Chagas Institute - Fiocruz <i>Doctorate, Bioinformatics & Computational Biology</i>	Curitiba, Brazil <i>2010–2014</i>
Positivo University <i>BTech, Systems Analysis & Development</i>	Curitiba, Brazil <i>2010–2013</i>
Oswaldo Cruz Instituto - Fiocruz <i>Masters, Molecular & Cellular Biology</i>	Rio de Janeiro, Brazil <i>2006–2009</i>
Positivo University <i>BSc, Biological Sciences</i> considered the best Biology course in Parana State	Curitiba, Brazil <i>2003–2006</i>

PhD thesis

title: *Validation and Protein Inference Based on Peptides Analyzed by de novo Sequence*

supervisors: Dr. Paulo Costa Carvalho

description: We combined sequence alignment techniques with artificial intelligence to develop a software designed to filter and process shotgun proteomics data after being generated by *de novo* sequencing.

Master thesis

title: *Characterization of Genes with Unknown Function and with Higher Expression in the Infective Forms of Trypanosoma cruzi*

supervisors: Dr. Marco Aurélio Krieger

description: A small set of genes was selected by microarray analysis and characterized using modern molecular biology techniques (*wetlab*).

Professional

Hexabio <i>CEO & co-founder, Company dedicated to Proteomics data analysis.</i>	Brazil <i>2013-present</i>
---	--------------------------------------

Experience

Biological skills.....

- Advanced Cell Biology Techniques
- Advanced Molecular Biology Techniques
- Light & Fluorescent Microscopy
- DNA & RNA Characterization
- Protein Characterization
- Antibody Induction

Computational Skills.....

- Advanced GNU-Linux
- General programming
- Database management
- Cloud computing
- Computational Proteomics
- Proteomics Data Analysis

Programming Languages

Perl: expert

Go: high

R: high

C++: intermediate

Java: intermediate

C#: intermediate

Languages

Brazilian Portuguese: High

Native

English: High

Fluent

Spanish: Low

French: Low

Interests

- 1: Bioinformatics & Computational Biology
- 2: Genomics & Proteomics
- 3: Proteomics Data Analysis
- 4: Protein Functional Annotation
- 5: Systems Biology

References

Dr. Alexey I. Nesvizhskii: Proteome Bioinformatics - University of Michigan nesvi@umich.edu

Dr. Paulo Costa Carvalho: Computational Mass Spectrometry - Fiocruz paulo@pcarvalho.com

Dr. Samuel Goldenberg: Director, Fiocruz Parana sgoldenb@fiocruz.br

Projects

Software Development for Proteomics

Computational Proteomics is a challenging area that is still growing accordingly to new technologies and methodologies. This project aims to develop and promote open-source software for proteomics data analysis. Making tools for both broader audiences and for bioinformatics will help creating a better environment for data analysis.

BioContainers

BioContainers is an open source and community-driven framework which provides system-agnostic executable environments for bioinformatics software. The BioContainers framework provide specification and standards for creating bioinformatics containers. Also, it allows software to be installed and executed under an isolated and controllable environment by distributing pre-configured images.

Software Development in Bioinformatics

Bioinformatics is now one of the major research areas in biological sciences, and yet the formal training of new professionals, the availability of good services for data deposition, and the development of new standards and software coding rules are still major concerns. This project aims to propagate and stimulate the use of good practices of software development in bioinformatics.

Recent Publications

Discovering and linking public omics data sets using the Omics Discovery Index: *Perez-Riverol Y, Bai M, Leprevost FV, Squizzato S, Park YM, Haug K, Carroll AJ, Spalding D, Paschall J, Wang M, del-Toro N, Ternent T, Zhang P, Buso N, Bandeira N, Deutsch EW, Campbell DS, Beavis RC, Salek RM, Sarkans U, Petryszak R, Keays M, Fahy E, Sud M, Subramaniam S, Barbera A, Jiménez RC, Nesvizhskii AI, Sansone S, Steinbeck C, Lopez R, Vizcaíno JA, Ping P, Hermjakob H* Nature Biotechnology. 2017

MSFragger: ultrafast and comprehensive peptide identification in mass spectrometry-based proteomics: *Kong AT, Leprevost FV, Avtonomov DM, Mellacheruvu D, Nesvizhskii AI* Nature Methods. 2017

BioContainers: An open-source and community-driven framework for software standardization: *Leprevost FV, Grüning BA, Aflitos SA, Röst HL, Uszkoreit J, Barsnes H, Vaudel M, Moreno P, Gatto L, Weber J, Bai M, Jimenez RC, Sachsenberg T, Pfeuffer J, Alvarez RV, Griss J, Nesvizhskii AI, Perez-Riverol Y* Bioinformatics. 2017

Quantitative proteomic analysis of the *Saccharomyces cerevisiae* industrial strains CAT-1 and PE-2: *Santos RM, Nogueira FCS, Brasila AA, Carvalho PC, Leprevost FV, Domont GB, Eleutherio ECA.* Journal of Proteomics. 2016

Ten Simple Rules for Taking Advantage of git and GitHub: *Perez-Riverol Y, Gatto L, Wang R, Sachsenberg T, Uszkoreit J, Leprevost FV, Fufezan C, Ternent T, Eglén SJ, Katz DSS, Pollard TJ, Konovalov A, Flight RM, Blin K, Vizcaíno JA.*

PLOS Computational Biology & bioRxiv). 2016

Venomous extract protein profile of Brazilian tarantula *Grammostola iheringi*: searching for potential biotechnological applications: *Borges MH, Figueiredo SG, Leprevost FV, De Lima ME, Cordeiro MN, Diniz MRV, Moresco J, Carvalho PC, Yates III JR.*

Journal of Proteomics. 2016

Integrated analysis of shotgun proteomic data with PatternLab for proteomics 4.0: *Carvalho PC, Lima DB, Leprevost FV, Santos MDM, Fischer JSG, Aquino PF, Moresco, Yates III JR, Barbosa VC.*

Nature Protocols. 2016

Using PepExplorer to Filter and Organize De Novo Peptide Sequencing Results: *Leprevost FV, Carvalho PC, Barbosa VC.*

Current Protocols in Bioinformatics. 2015

Reevaluating the *Trypanosoma cruzi* proteomic map: the shotgun description of blood-stream trypomastigotes: *Brunoro GVF, Caminha MA, Ferreira AT da Silva F, Leprevost FV, Carvalho PC, Perales J, Valente RH, Menna-Barreto FRS.*

Journal of Proteomics. 2014

On best practices in the development of bioinformatics software: *Leprevost FV, Barbosa VC, Francisco EL, Perez-Riverol Y, Carvalho PC.*

Frontiers in Genetics. 2014

PepExplorer: a similarity-driven tool for analyzing de novo sequencing results: *Leprevost FV, Valente RH, Borges DL, Perales J, Melani R, Yates III JR, Barbosa VC, Junqueira M, Carvalho PC.*

Molecular & Cellular Proteomics. 2014

Bio::DB::NextProt: A Perl Module for neXtProt Database Information Retrieval: *Leprevost FV.*

PeerJ. 2014

Proteome Analysis of Formalin-Fixed Paraffin-Embedded Tissues from a Primary Gastric Melanoma and its Meningeal Metastasis: A Case Report: *Fischer JSG, Canedo NHS, Gonçalves KMS, Chimelli MC, França M, Leprevost FV, Aquino PF, Carvalho PC, Carvalho MGC.*

Current Topics in Medicinal Chemistry. 2014

Pinpointing differentially expressed domains in complex protein mixtures with the cloud service of PatternLab for Proteomics: *Leprevost FV, Borges D, Crestani J, Perez-Riverol Y, Zanchin N, Barbosa VC, Carvalho PC.*

Journal of Proteomics. 2013

Effectively addressing complex proteomic search spaces with peptide spectrum matching: *Lima DB, Perez-Riverol Y, Nogueira FCS, Domont GB, Noda J, Leprevost FV, Besada V, Franca*

FMG, Barbosa VC, Sanchez A, Carvalho PC.

Bioinformatics. 2013

Computational Proteomics Pitfalls and Challenges: HavanaBioinfo 2012 Workshop Report:

Perez-Riverol Y, Hermjabok H, Kohlbacher O, Martens L, Creasy D, Cox J, Leprevost, FV, Shan BP, Cabrera G, Padron G, Gonzales LJ, Besada V.

Journal of Proteomics. 2013