SOFTWARE DEVELOPER · ALGORITHM DEVELOPER · DATA SCIENTIST · COMPUTATIONAL BIOLOGIST

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References available upon request

"The science of today is the technology of tomorrow." – Edward Teller

Highlights & Qualifications

- Innovative domain expert in proteomics (structure, global expression, integrative -omics)
- Ten years in computational biology, data-science and high-throughput computing
- Five years supporting biologists as a domain expert in mass spectrometry data analysis
- Experience preparing lectures in computational mass-spectrometry, data-science and machine learning
- Enthusiastic to join a software team and facilitate the next generation of analytical proteomics with your software

Education

University Of Toronto

Toronto, ON, Canada

2012 - 2017 (October)

PHD IN MEDICAL BIOPHYSICS (PROTEOGENOMICS)

- To inform decision makers on key issues in a multi-disciplinary setting, outlined key problems and ranked solutions delivered by succinct 2-line written communications and maximally 15-minute presentations; key decision makers were informed on issues arising in the project and timely achieved project milestones.
- To deliver computational expertise to a cancer biomarker discovery lab specialized in clinical proteomics, acquired mass spectrometry techniques and data analysis mastery, developed a novel analytical pipeline that that identifies cancercausing mutations; customer has adopted use of the pipeline in analyzing all clinical samples.
- Business: Finalist in a pitch competition for \$50,000 in startup funding, participant in 2 case study competitions.
- Skills: Project management, pipeline development, critical thinking, data analysis, oral and written communication
- Languages: Perl, R, PostgreSQL

Dalhousie University

Halifax, NS, Canada

MASTERS IN BIOCHEMISTRY (BIOINFORMATICS)

September 2009 - 2012

- Understanding the contraints imposed by protein structure on protein evolution is of critical importance to protein engineering. Working closely with a statistician and a biologist, I developed and implemented a mathematical model of protein evolution that integrated protein structure. My model significantly out-performed standard models that neglect protein structure.
- Skills: Math/Stats, algorithm development, pipeline development, data analysis, writing and presentation
- · Languages: Python, R, C/C++

University of Victoria

Victoria, BC, Canada

DOUBLE MAJOR BIOCHEMISTRY (HONOURS,) AND COMPUTER SCIENCE

2003 - 2008

- The ABO blood group enzyme plays a critical role in graft vs host disease and understanding how this enzyme recognizes its substrate was badly needed. I analyzed the diffraction data obtained from eighty crystallography experiments. Results supported an international collaborative research effort that clarified important behavioral intricacies of the ABO blood group enzymes.
- Excellent understanding of biochemistry, from genomics to proteomics. Computer Science degree supports adaptive quantitative biology.
- Languages: Java, R, C, Python

Experience_

Department of Computer Science, University of Victoria

Victoria, BC Canada

DATA SCIENTIST

2008-2008

To gain insights into glycosyltransferase enzyme family mechanisms. I employed a machine learning approach to intelligently distinguish between two classes of enzymes with unknown mechanism from crystal structures.

Dept. Biochemistry, University of Victoria

Victoria, BC, Canada

BIOCHEMIST AND DATA ANALYST

2005-2009

• To develop strategies for Sample preparation of As a technician and student, I purified proteins for crystallization and analyzed the results of x-ray crystallography experiments.

Victoria, BC, Canada

HOME CARE AIDE 2007-200

• Assisted ten head injured patients at a residence home with their personal needs. Ensured their timely medication and overall wellness. Improved, overall resident lifestyle by engaging in after-work social activities.

• To help a visually impaired resident connect with family, developed a program in Python that read contact information aloud and dialed the number of the selected contact; resident used the program frequently resulting in reduced feelings of isolation and greater social independence

Pacific Forestry Center

Victoria, BC, Canada

FOREST ECOLOGY RESEARCHER

2003-2003

• Understanding and modelling insect infestations plays an important role in predicting outbreaks. Worked in a two man team for four months in a remote region of British Columbia collecting data on an insect infestation. Careful planning, dedication and long hours ensured that a very high quality dataset was collected.

Technical Skills

Bioinformatics Integrative -omics, computational mass-spectrometry, computational molecular evolution, pathway analysis

Analytical Machine learning, computational methods, mathematics and statistics

Programming Perl, Python, C/C++, JAVA, R, LaTeX **Visualization** lattice, ggplot, plotting.general, d3.js

Environments Sun Grid engine (cluster computing), Windows, Unix, Mac OS

Languages English, Spanish

Publications

1. **Alfaro JA**, Ignatchenko A, Ignachenko V, Sinha A, Boutros C and Kislinger T. Detecting protein variants by mass-spectrometry: A comprehensive study in cancer cell-lines. (Submitted) Genome Medicine.

- 2. Sinha A, **Alfaro JA**, and Kislinger T. 2017. Characterization of Protein Content Present in Exosomes Isolated from Conditioned Media and Urine. Current Protocols in Protein Science, 24-9.
- 3. **Alfaro JA**, Sinha A, Kislinger T, Boutros PC. Onco-proteogenomics: cancer proteomics joins forces with genomics. 2014. Nat Methods. 11(11):1107-13.
- 4. Weinreb I, Piscuoglio S, Martelotto LG, Waggott D, Ng CK, Perez-Ordonez B, Harding NJ, **Alfaro JA**, *et al.* Hotspot activating PRKD1 somatic mutations in polymorphous low-grade adenocarcinomas of the salivary glands. 2014. Nat Genet. 46(11):1166-9.
- 5. Planello AC, Ji J, Sharma V, Singhania R, Mbabaali F, Müller F, **Alfaro JA**, Bock C, De Carvalho DD, Batada NN. Aberrant DNA methylation reprogramming during induced pluripotent stem cell generation is dependent on the choice of reprogramming factors. 2014. Cell Regen. 3(1). 1.
- 6. Johal AR, Blackler RJ, **Alfaro JA**, Schuman B, Borisova S, Evans SV. Glycobiology. pH-induced conformational changes in human ABO(H) blood group glycosyltransferases confirm the importance of electrostatic interactions in the formation of the semi-closed state. 2014. 24(3):237-46.
- 7. Johal AR, Schuman B, **Alfaro JA**, Borisova S, Seto NOL and Evans SV. Sequence-dependent effects of cryoprotectants on the active sites of the human ABO(H) blood group A and B glycosyltransferases. 2012. Acta Cryst. D68, 268–276.
- 8. **Alfaro JA**, Zheng RB, Persson M, Letts JA, Polakowski R, Bai Y, Borisova SN, Seto NO, Lowary TL, Palcic MM, Evans SV. ABO(H) Blood Group A and B Glycosyltransferases Recognize Substrate via Specific Conformational Changes. 2008. J Biol Chem. 283(15):10097-10108.

Posters, Presentations & Lectures _____

- 1. **Conference Poster:** Detecting protein variants by mass-spectrometry: A comprehensive study in cancer cell-lines. (2017). Toronto.
- 2. **Lecturer:** Machine learning applied to cancer biology. (2016). São Paulo.
- 3. **Conference Poster:** Onco-proteogenomics: Exploring the Complexity of the Cancer Genome at the Proteome Level Canadian Cancer Research Conference. (2015). Montreal.
- 4. **Wright Keynote talk:** A site-independent structurally constrained phylogenetic model of protein evolution. Mechanisms of Protein Evolution. (2011) Denver.
- 5. **Conference Poster 3DSIG:** Applications of structurally constrained models of protein evolution to problems in structural bioinformatics. (2010) Boston.

Honors & Awards_

2013-2016 \$105,000, Alexander Graham Bell Canada Graduate Scholarships-Doctoral Program.

2011-2012 \$16,824, Nova Scotia Health research award recipient.

2016-2017 \$9,134, Medical Biophysics Excellence UTF scholarship.

2012-2013 \$9,134, Medical Biophysics Excellence UTF scholarship.

Internal

Departmental Committees

2017-2017 Senior student representative, Committee for improved student experience

2016-2017 **Social Committee Member**, Medical biophysics graduate student association

2016-2017 Departmental Retreat organizer, Geneva park departmental retreat organizer