

Javier A. Alfaro

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

PHD IN MEDICAL BIOPHYSICS (PROTEOGENOMICS)

2012 - 2017 (October)

- Developed an analytical pipeline to improve the characterization of the cancer proteome from MS-datasets.
- Worked closely with a clinical proteomics group from within a large computational biology lab.
- **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

- Developed and implemented a mathematical model of protein evolution that integrated 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

- Analyst in protein structural biology lab studying the ABO blood group enzymes.
- Excellent understanding of biochemistry, from genomics to proteomics. Computer Science degree supports adaptive quantitative biology.
- **Skills:** Software development, pipeline development, data analysis, writing and presentation
- **Languages:** Java, R, C, Python

Experience

Department of Computer Science, University of Victoria

Victoria, BC Canada

DATA SCIENTIST

2008-2008

- Applied Bayesian statistics and artificial intelligence techniques to develop an algorithm that could 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

- Responsible for the analysis of diffraction data obtained from crystallography experiments. Results supported an international collaborative research effort that clarified important behavioral intricacies of the ABO blood group enzymes.

Cridge Brain injury Centre

Victoria, BC, Canada

HOME CARE AIDE

2007-2008

- Responsible for the care of ten patients at a residence home, including their timely medication and safety

Pacific Forestry Center

Victoria, BC, Canada

FOREST ECOLOGY RESEARCHER

2003-2003

- Worked as part of a team for four months in the field collecting data on an insect infestation

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-Ordóñez 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, Singhanian 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 NO 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.	External
2011-2012 \$16,824 , Nova Scotia Health research award recipient.	External
2016-2017 \$9,134 , Medical Biophysics Excellence UTF scholarship.	Internal
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