BIOGRAPHICAL SKETCH

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NAME: Jesus Gerardo Galaz Montoya

eRA COMMONS USER NAME (credential, e.g., agency login): jgalaz

POSITION TITLE: Basic Life Research Scientist

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
Universidad de Sonora, Hermosillo, SON, Mexico	B.Sc.	05/2007	Physics
University of British Columbia, Vancouver, BC, Canada	1 yr exchange	12/2005	Physics, Biology & German
Baylor College of Medicine, Houston, TX, USA	Ph.D.	02/2014	Biochemistry and Molecular Biology

A. Personal Statement

I am a Basic Life Research Scientist in the Department of Bioengineering at Stanford University with expertise in the development, testing, and application of computational tools for analyses of cryo electron microscopy and tomography (cryoEM/ET) datasets, with a focus on "subtomogram averaging" (STA) and various other processing techniques for 3D images of biological specimens related to human disease. I also participate in the design of experiments, writing of scientific papers and grant applications, and one-on-one training in data analysis for rotation students, interns, and colleagues. The datasets I routinely analyze include cryoET images of macromolecular complexes and pathogens, such as viruses, bacteria, molecular chaperones, ribosomes, toxic protein aggregates, and other molecular nanomachines both *in vitro* and within cells. By imaging individual instances of macromolecular complexes in 3D, STA is well-suited to study conformationally and compositionally heterogeneous specimens, including chaperonins and other cellular factors interacting with their substrates. In addition, computational annotation and quantitative analyses of organelles and pleomorphic structures such as protein aggregates in cellular cryoET data can reveal structural hallmarks of disease and uncover some of the mechanisms underlying pathogeny directly in patient-derived cells. In addition to algorithmic development using Python, the main diseases of interest my computational analyses have focused on have been viral infection of human cells and protein aggregation in Huntington disease. Recent work concerning the visualization of protein aggregates *in situ* is of particular relevance to this proposal:

Wu GH*, Mitchell PG*, Galaz-Montoya JG*, Hecksel CW, Sontag EM, Gangadharan V, Marshman J, Mankus D, Bisher ME, Lytton-Jean AKR, Frydman J, Czymmek K, Chiu W. Multi-scale 3D Cryo-Correlative Microscopy for Vitrified Cells. Structure. 2020 Aug 15:S0969-2126(20)30281-1. doi: 10.1016/j.str.2020.07.017. Epub ahead of print. PMID: 32814034. *Equal contribution.* (Selected for Journal Cover).

B. Positions and Honors

<u>Positions/Employment</u>
03/2019 – *present*   Basic Life Research Scientist, Stanford University, Stanford, CA, USA.
07/2017 – 02/2019   Postdoctoral Associate, Stanford University, Stanford, CA, USA.
02/2015 – 06/2017   Postdoctoral Fellow, Baylor College of Medicine, Houston, TX, USA.
03/2014 – 02/2015   Postdoctoral Associate, Baylor College of Medicine, Houston, TX, USA.
07/2007 – 02/2014   Graduate Research Assistant, Baylor College of Medicine, Houston, TX.

<u>Memberships</u>
2008 – present   Microscopy Society of America
2008 – present   Biophysical Society
2013 – present   International Society for Computational Biology

<u>Honors</u>
2007 – 2018   Several fellowships and travel grants to attend and present talks and posters at national and international conferences
01/2015 – 01/2016   Fellowship from the Gulf Coast Consortia's Computational Cancer Biology Training Program; Houston, TX
08/2010 – 05/2012   Elected mentor for Science and Education Leadership Fellows (SELF), Baylor College of Medicine; Houston, TX
06/2011 – 08/2011   Elected mentor for Houston Community College's Summer Science Intern Program
06/2010 – 08/2010   Mentor for Baylor College of Medicine's SMART (Summer Medical and Research Training) program; Houston, TX, USA.
08/2006 – 05/2007   Research assistantship grant, UNISON, Mexico
01/2006 – 12/2007   Academic achievement scholarship by STAUS, UNISON, Mexico
01/2005 – 12/2005   Full board exchange scholarship, Department of Student Exchange, UNISON, Mexico
2005   Hugh M Brock Education Abroad Scholarship, University of British Columbia, Vancouver, Canada
2002   1st place ITESM national poetry contest, 1st place ITESM national short story contest, Mexico

<u>Other Experience</u>
2005   Spanish tutor (Vancouver, BC, Canada)
2006   Chemistry, physics and English tutor (Hermosillo, SON, Mexico)
2007 – 2014   Math, physics and Spanish tutor (Houston, TX, USA)
2010 – 2014   Spanish/English, English/Spanish scientific translator (USA)
2016 – present.   Scientific writer, editor, and reviewer.

C. Contributions to Science

<u>1. Computational algorithms and methods development:</u> As one of the main components of my PhD dissertation work, I spearheaded the development of algorithms for automated subtomogram averaging (STA) in EMAN2, one of the most widely used software packages for electron microscopy analysis, at a time when the community relied almost entirely on *ad hoc* manual tools.

   a. Galaz-Montoya, J. G., Flanagan, J., Schmid, M. F., & Ludtke, S. J. (2015). *Single particle tomography in EMAN2.* Journal of Structural Biology 190(3):279-290. Doi: 10.1016/J.Jsb.2015.04.016

   b. Jesús G. Galaz-Montoya[*], Corey W. Hecksel[*], Steven J. Ludtke[*], Philip R. Baldwin, Eryu Wang, Scott C. Weaver, Michael F. Schmid[1] and Wah Chiu. (2016) *Alignment Algorithms and Per-Particle CTF Correction for Single Particle Cryo Electron Tomography.* Journal of structural biology, 194(3), 383-394. *Equal contribution.*

   c. Corey W. Hecksel[*], Michele C. Darrow[*], Wei Dai, Jesús G. Galaz-Montoya, Jessica A. Chin, Patrick G. Mitchell, Shurui Chen, Jemba Jakana, Michael F. Schmid & Wah Chiu. (2016). *Quantifying Variability of Manual Annotation in Cryo-Electron Tomograms.* Microscopy and microanalysis, 1-10. *Equal contribution.*

2. Neurobiology: Working with collaborators, we uncovered structural mechanisms by which the TRiC chaperonin and a related, synthetic CCT5 ring complex powerfully inhibit the aggregation of the exon 1 cleave product of the mutant huntingtin protein that causes Huntington disease, a neurodegenerative disease among the polyglutamine aggregation disorders. Recently, my colleagues and I visualized protein aggregates inside yeast cells and found that they consist of dense, globular pockets that cluster together.

    a. Shahmoradian, S.H.*, Galaz-Montoya, J.G.*, Schmid, M.F., Cong, Y., Ma, B., Spiess, C., Frydman, J., Ludtke, S.J. and Chiu, W., 2013. TRiC's tricks inhibit huntingtin aggregation. Elife, 2, p.e00710..*Equal contribution

    b. Darrow, M. C., Sergeeva, O. A., Isas, J. M., Galaz-Montoya, J., King, J. A., Langen, R., ... & Chiu, W. (2015). *Structural Mechanisms of Mutant Huntingtin Aggregation Suppression by Synthetic Chaperonin-like CCT5 Complex Explained by Cryo-electron Tomography.* Journal of Biological Chemistry, jbc-M115.

    c. Wu GH*, Mitchell PG*, Galaz-Montoya JG*, Hecksel CW, Sontag EM, Gangadharan V, Marshman J, Mankus D, Bisher ME, Lytton-Jean AKR, Frydman J, Czymmek K, Chiu W. Multi-scale 3D Cryo-Correlative Microscopy for Vitrified Cells. Structure. 2020 Aug 15:S0969-2126(20)30281-1. doi: 10.1016/j.str.2020.07.017. Epub ahead of print. PMID: 32814034. *Equal contribution.* (Selected for Journal Cover).

3. Viral infection: I participated in collaborative projects to visualize infection of bacteria by phages, as well as to understand the mechanisms by which antibodies are able to inhibit the replication of Chikungunya virus inside human cells.

    a. Murata, K., Zhang, Q., Galaz-Montoya, J.G., Fu, C., Coleman, M.L., Osburne, M.S., Schmid, M.F., Sullivan, M.B., Chisholm, S.W. and Chiu, W., (2017). *Visualizing Adsorption of Cyanophage P-SSP7 onto Marine Prochlorococcus.* Scientific Reports, 7.

    b. Jin, J.*, Galaz-Montoya, J.G.*, Sherman, M.B., Sun, S.Y., Goldsmith, C.S., O'Toole, E.T., Ackerman, L., Carlson, L.A., Weaver, S.C., Chiu, W. and Simmons, G., (2018). *Neutralizing antibodies inhibit chikungunya virus budding at the plasma membrane*. Cell host & microbe, 24(3), pp.417-428. *Equal contribution.* (Selected for Journal Cover).

Complete List of Published Work in MyBibliography
    https://www.ncbi.nlm.nih.gov/myncbi/jesus.montoya.1/bibliography/public/

D. Additional Information: Research Support and/or Scholastic Performance
Past Research Support
01/2015 – 01/2016   Fellowship from the Gulf Coast Consortia's Computational Cancer Biology Training Program; Houston, TX

Scholastic Performance
08/2007 – 02/2014   Ph.D. Biochemistry and Molecular Biology, GPA 3.37/4.0; Baylor College of Medicine, Houston, TX, USA.
01/2005 – 12/2005   Exchange student (Physics, Biology and German courses), GPA 3.29/4.0; University of British Columbia, Vancouver, BC, Canada, 01/2005 – 12/2005
08/2002 – 05/2007   B.Sc. Physics, summa cum laude, GPA 96.74/100.00; UNISON, Mexico
08/1999 – 05/2002   High school diploma, summa cum laude, GPA 98.64/100.00; ITESM-CSN, Mexico