

Clemente Aguilar

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Education	<p>Ph.D. in Computational Science (Concentration in Computational Biology), The University of Texas at El Paso (UTEP), <i>El Paso, TX, USA</i>. 5/2013</p> <p><i>Advisors:</i> Professor Ming-Ying Leung and Professor Igor C. Almeida</p> <p><i>Research Interests:</i> Analysis of mass spectrometry experiments including computational proteomics and glycolipidomics; Statistical methods for molecular biology; Algorithm design for molecular biology; Application of Machine Learning Algorithms.</p> <p><i>Dissertation:</i> Automatic annotation of GPI structures using grid computing.</p>
	<p>M.S. in Computational Science (Concentration in Computational Biology), UTEP. 2011</p> <p><i>Thesis:</i> Computational tool for automated large-scale GPIomic analysis.</p>
	<p>M.S. in Bioinformatics, UTEP. 2008</p>
	<p>D.V.M Universidad Autonoma de Ciudad Juarez (UACJ), Ciudad Juarez, Chihuahua, Mexico. 2005</p> <p><i>Thesis:</i> Effect of supplementation on a basal diet of wheat straw on voluntary intake and in vivo digestibility of the diet components in sheep.</p>

Employment	<p>Postdoctoral Researcher, NIMBioS. 7/13 - Present</p> <ul style="list-style-type: none">• My interest is in the area of immunoinformatics. Currently I am developing algorithms and computational tools for in silico epitope mapping.
	<p>Bioinformatician, Border Biomedical Research Center (UTEP). 1/09 –</p>

- Research in computational molecular biology, developing a computational tool to aid in the identification of glycolipids using mass spectrometry data. 6/13
 - Analysis of mass spectrometry-based proteomic experiments including label-free quantitative proteomics.
- UPBiT** coordinator, *Department of Mathematics, UTEP* 1/12 – 6/13
- The Undergraduate Participation in Bioinformatics Training (UPBiT) is a NSF-funded interdisciplinary training program for undergraduates in biological and mathematical sciences to better prepare them to pursue graduate studies and careers in the integration of these fields. I prepared lectures, workshops and different activities to accomplish the goals of the program. Also, mentored students.
- Research Assistant**, *Department of Mathematics, UTEP* 1/07 – 12/08
- My research was focused on developing a computational and statistical tool to predict RNA secondary structures.
- Intern**, *Dow AgroSciences, Indianapolis, IN.* 5/08 – 08/08
- Wrote wrappers for command line programs using: Object Oriented Perl, Linux, SQL and EMBOSS.
- Research Assistant**, *Department of Biology, UACJ* 11/04 – 12/05
- Research assistant in Genomics Lab, conducting experiments to find chromosomal nucleolar organizer region (NOR) in dogs with silver staining reaction.
- Technical Support**, *Toro Company, Ciudad Juarez, Chihuahua, Mexico* 1999 - 2004
- While Studying Veterinary Medicine worked in the area of Technical Support at Toro Company.
Responsibilities: Install, maintain, test and repair computer desktop PCs (Windows NT, XP, Office). Keep manuals and records for the equipment. Provide customer support and troubleshooting.

- Technical Skills**
- Algorithm Design, data visualization, scientific computing.
 - Experience applying machine learning approaches to complex problems.
 - Computing platforms: UNIX/LINUX, Windows; some Macintosh.
 - High Throughput Computing (HTC) with HTCondor
 - Programming languages: Extensive experience with Perl, R, SAS and Matlab; moderate experience with C/C++, SQL and Python.
 - Mass spectrometry data analysis software: Proteome Discoverer, Sorcerer, Scaffold, X! tandem and Bioworks.
 - Experience with major public databases and tools: NCBI, Uniprot, Kegg, Blast2GO
 - Protein modeling software: PDB viewer, RASMOL.
 - Trained in protein purification and HPLC-MS

Publications

- **Aguilar-Bonavides C**, Sanchez-Arias R, Lanzas C. Accurate prediction of major histocompatibility complex class II epitopes by sparse representation via ℓ_1 -minimization. *In review*.
 - **Aguilar-Bonavides C**, Cruz-Cano R, Lanzas C. Prediction and rule extraction of major histocompatibility complex class II epitopes by logic minimization. Proceedings of the 14th International Conference on Bioinformatics and Computational Biology BIOCOMP'14. 2014 Jul: 167-173.
 - **Aguilar-Bonavides C**, Cardenas Gerardo A, Nakayasu ES, Gazos-Lopes F, Almeida IC, Leung M-Y. Automatic Annotation of GPI Structures Using Grid Computing Technology. Proceedings of the 5th International Conference on Bioinformatics and Computational Biology - BICoB2013.
 - Bayer-Santos E, **Aguilar-Bonavides C**, Rodrigues SP, Cordero EM, Marques AF, Varela-Ramirez A, Choi H, Yoshida N, da Silveira JF, Almeida IC. Proteomic analysis of Trypanosoma cruzi secretome: characterization of two populations of extracellular vesicles and soluble proteins. J Proteome Res. 2012 Dec 8.
 - **Aguilar-Bonavides C**, Leung, M-Y, Nakayasu, ES, Felipe Gazos-Lopes, Almeida, IC Computational Tool for Large-Scale GPIomic analysis. Proceedings of the ACM International Conference on Bioinformatics and Computational Biology. Oct 2012.
 - Rodrigues SP, Ventura JA, **Aguilar C**, Nakayasu ES, Choi H, Sobreira TJ, Nohara LL, Wermelinger LS, Almeida IC, Zingali RB, Fernandes PM. Label-free quantitative proteomics reveals differentially regulated proteins in the latex of sticky diseased Carica papaya L. plants. J Proteomics. 2012 Jun 18;75(11):3191-8. Epub 2012 Mar 24.
 - Bayona JC, Nakayasu ES, Laverrière M, **Aguilar C**, Sobreira TJ, Choi H, Nesvizhskii AI, Almeida IC, Cazzulo JJ, Alvarez VE. SUMOylation pathway in Trypanosoma cruzi: functional characterization and proteomic analysis of target proteins. Mol Cell Proteomics. 2011 Dec;10(12):M110.007369. Epub 2011 Aug 10. PubMed PMID: 21832256.
 - Rodrigues SP, Ventura JA, **Aguilar C**, Nakayasu ES, Almeida IC, Fernandes PM, Zingali RB. Proteomic analysis of papaya (Carica papaya L.) displaying typical sticky disease symptoms. Proteomics. 2011 Jul;11(13):2592-602. doi: 10.1002/pmic.201000757. Epub 2011 Jun 1.
 - Yichoy M, Nakayasu ES, Shpak M, **Aguilar C**, Aley SB, Almeida IC, Das S. Lipidomic analysis reveals that phosphatidylglycerol and phosphatidylethanolamine are newly generated phospholipids in an early-divergent protozoan, Giardia lamblia. Mol Biochem Parasitol. 2009
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Posters & Talks

- The 14th International Conference on Bioinformatics and Computational Biology BIOCOMP'14. Las Vegas, NV. July 21 – 24, 2014.
Talk: Prediction and rule extraction of major histocompatibility complex class II epitopes by logic minimization.
 - NIMBioS seminar **talk:** Computational characterization of GPI-anchored proteins in *Trypanosoma cruzi* and their potential use as vaccine candidates.
 - Invited speaker at the Department of Mathematics seminar series at Howard University, November 8, 2013.
Talk: Using Computational Tools for Accelerating the Development of Vaccines for Chagas Disease.
 - BICoB 2013. International Conference on Bioinformatics and Computational Biology. Honolulu, Hawaii. March 4 – 6 2013.
Talk: Automatic annotation of GPI structures using grid computing.
 - Rio Grande Branch ASM Meeting. Albuquerque, NM. March 4-5, 2011.
Poster: Computational Tool for the Identification of GPI Structures Using Mass Spectrometry Data.
 - RECOMB-CP 2010. Research in Computational Molecular Biology - Computational Proteomics. San Diego, California. March 27-28, 2010.
Poster: Developing a Computational Tool for the Automated Large-Scale GPIomic Analysis.
 - ABRCMS - Annual Biomedical Research Conference for Minority Students. Phoenix, Arizona. November 4 -7, 2009.
Talk: Computational Tool for Estimating the Association of RNA Secondary Structures with Inversion Concentration.
 - SACNAS National Conference – Salt Lake City, Utah. October 8 – 12, 2008.
Talk: Distribution of inverted repeats occurring among different types of Papillomavirus.
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References

Available upon request
