

Hans Vasquez-Gross

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Education

2005 – 2010

University of California, Davis

Bachelors of Science in Genetics

- Minor : Quantitative Biology and Bioinformatics

Skills Summary:

- **Life Science skills**

- Skilled in statistics: basic probability, densities, distributions, sampling distributions, mean, variance, and covariance
- Dynamic Modeling: matrix models, differential equations, complex dynamics – understanding models, assumptions, and implications
- DNASEquence assembly and error correction: Phred, Phrap, Consed, Chromas, staden package (Pregap, Gap, Spin), Illumina Genome Analyzer Pipeline, MAQ, Bowtie/cufflinks suite, Trinity, velvet, and BWA. Quality trimming through sickle & scythe
- Nucleotide and protein sequence alignment analysis and annotation (coding regions, transposable elements, splice junctions, etc): T-Coffee, Dotter, RepeatMasker, BLAST and its derivatives BLASTX, BLASTP, etc.
- Understand the principles behind maximum likelihood estimation of phylogeny, Bayesian inference, hidden Markov models, bootstrapping, and model selection, adequacy, and averaging. Skilled in using the following for phylogenetic analysis: BayesTraits, Mega 4, DNASP, Tassel, Mapmaker, DOLLOP, and QTL Cartographer.

- **Computer Technical skills**

- MS Office Suite: Word, Excel, Access, PowerPoint, Visio
- Proficient in configuring many types of network infrastructures to include Unix, Windows, and Mac
- Proficient with Perl, Python, Java, SQL, and Shell programming and skilled with C, C++, VBS, and R languages

- **Project Management & Communication Skills**

- Experienced in overseeing resources, time, and budget
- Experienced in delegating tasks to other colleagues
- Effective verbal communication and Strong written skills

Publications and Meetings

Publications:

- I.M. Henry, U. Nagalakshmi, M.C. Lieberman, K.J. Ngo, K.V. Krasileva, **H.A. Vasquez-Gross**, A. Akunova, E. Akhunov, J. Dubcovsky, T.H. Tai and L. Comai. “Efficient genome-wide detection and cataloging of EMS-induced mutations using next-generation sequencing and exome capture”. *Plant Cell*. In Press.
- D.B. Neale, J.L. Wegrzyn, K.A. Stevens, A. Zimin, D. Puiu, M. Crepeau, C. Cardeno, M. Koriabine, A.E. Holtz-Morris, J.D. Liechty, P.J. Martínez-García, **H.A. Vasquez-Gross**, B.Y. Lin, J.J. Zieve, W.M. Dougherty, S. Fuentes-Soriano, L. Wu, D. Gilbert, G. Marçais, M. Roberts, C. Holt, M. Yandell, J.M. Davis, K. Smith, J.F.D. Dean, W.W. Lorenz, R.W. Whetten R. Sederoff, N. Wheeler, P.E. McGuire, D. Main, C.A. Loopstra, K. Mockaitis, P.J. deJong, J.A. Yorke, S.L. Salzberg, and C.H. Langley. “Decoding the massive genome of loblolly pine using haploid DNA and novel assembly strategies”. *Genome Biology*. March 2014; 3:15.
- J.L. Wegrzyn, J.D. Liechty, K.A. Stevens, L. Wu, C.A. Loopstra, **H.A. Vasquez-Gross**, W.M. Dougherty, B.Y. Lin, J.J. Zieve, P.J. Martínez-García, C. Holt, M. Yandell, A. Zimin, J.A. Yorke, M. Crepeau, D. Puiu, S.L. Salzberg, P. de Jong, K. Mockaitis, D. Main, C.H. Langley, and D.B. Neale. “Unique Features of the Loblolly Pine (*Pinus taeda* L.) Megagenome Revealed Through Sequence Annotation”. *Genetics*. March 2014; 196: 891-909.

- **H.A. Vasquez-Gross**, J.J. Yu, B. Figueroa, D.D.G. Gessler, D.B. Neale, and J.L. Wegrzyn. “CartograTree: connecting tree genomes, phenotypes, and environment”. *Molecular Ecology Resources*. May 2013;13(3) 528-537.

Meetings:

- Vasquez-Gross, H. et al. “ Case Study: Enabling Forest Tree Genomics through Association Studies with the use of SSWAP”. PAG XXII – Workshop. January 14, 2014.
- Vasquez-Gross, H. et al. “ Use of CartograTree to Explore Forest Tree Genomes, Phenotypes, and Environment”. PAG XXI – Computer Demo. January 13-18, 2013.
- Vasquez-Gross, H. et al. “ CartograTree: Connecting Forest Tree Genomes, Phenotypes, and Environment”. PAG XXI – Poster. January 13-18, 2013.
- Vasquez-Gross, H. et al. “ Case Study: TreeGenes uses SSWAP to Serve Semantic Data to Existing Web Applications, New Web Applications, and Semantic Pipelines”. PAG XXI – Workshop. January 13-18, 2013.

Work Experience

Programmer III – Bioinformatics Programmer

July 2013 – Present

UC Davis – Plant Sciences – Dubcovsky Lab

- Analysis & interface design for the 1000 Wheat TILLING lines project
- Maintenance of the server
- Bioinformatics support for the lab

Consultant –Administrator & Programmer

February 2014 – Present

University of Connecticut – Plant Sciences – Wegrzyn Lab

- Systems administrator on multiple servers including: webserver, database server, and application server
- Developing new and maintaining existing of pages on the TreeGenes Database website:
<https://dendrome.ucdavis.edu/>
- Assisting in Genomic analysis in projects through bioinformatics

Programmer II – iPlant Developer

June 2011 – January 2014

UC Davis – Plant Sciences – Neale Lab

- Primary developer on CartograTree: a web-based application
- Development of Web Services for use with the iplantcollaborative.org
- Systems administrator on multiple servers including: webserver, database server, and application server
Developing new and maintaing existing of pages on the TreeGenes Database website:
<https://dendrome.ucdavis.edu/>
- Aided in various bioinformatics analysis using PERL and python scripts
- Performed Protein Family analysis using Tribe-MCL and custom scripts
- Implemented a GIT version control system for our in house scripts

Computer Resource Specialist September 2010 – January 2011

UC Davis ETOX Department

- Desktop computer installation and maintenance (patching/updating, virus scans, etc)
- Server installation and maintenance for windows and linux systems
- Implemented an OpenBSD Firewall for security purposes
- Implemented a calendaring system for faculty and staff to reserve common rooms and presentation laptops for their use

Student Bioinformatics Programmer January 2009 – April 2010

UC Davis Genome Center – Bioinformatics Core

- Wrote PERL scripts for data analysis on a variety of flat file formats (data mining)
- Used a variety of software packages to analyze large datasets with our SGE computing cluster
- Provided extracted data from MySQL databases which other software generated to lead scientists
- Helped create automated PERL scripts for pipelines with parallel processing
- Taught a portion of a summer week long bioinformatics course to graduate students, post-docs, faculty and industry professionals (Next Generation Sequencing Course – coordinated through the UC Davis Biotechnology Program).

- Performed weekly presentations and instructional training to co-workers
- Effective communication skills and worked well with customers and co-workers

Student Computer Technical Assistant

October 2006 – June 2009

UC Davis College of Biological Sciences – Dean's Office

- Supported College Of Biological Sciences Dean's Office and Neurobiology, Physiology, & Behavior department with technical problems on Hardware and Software issues
- Problem-solving skills with hardware, software, and network issues on Mac OSX, Windows XP/Vista/7, and Unix (mainly Ubuntu, FreeBSD, and OpenBSD)
- Completed product comparisons to find the optimal solution and purchased with PO forms
- Used effective verbal and written skills in communicating with colleagues

Bioinformatics Programmer Research Assistant

June 2008 – January 2009

UC Davis Plant Biology Department

- Programmed PERL scripts for large data queries to NCBI
- Integrated published software within the PERL scripts to analyze data
- Provided synthesized results in a MS Excel document