PhD, Amhed Missael Vargas Velazquez

avargas0lcg@gmail.com
amhedvargas.github.io

Summary Statement

I am a person who has a knack for solving problems but has no interest in creating them. I have worked for more than 10 years on multidisciplinary research projects where I acquired skills ranging from molecular biology to bioinformatics analysis and, more recently, scientific workflows and software development on the web. I seek an organization where I can continue honing my skills, contribute my scientific experience, and share my values of responsibility, honesty, and independence.

Work experience

Post-doctoral fellow - Froekjaer-Jensen lab, KAUST, Saudi Arabia	08/2019 - Present
Research consultant - Froekjaer-Jensen lab, KAUST, Saudi Arabia	01/2019 - 06/2019

Education

Philosophy Doctorate in Molecular genetics – ENS /UPMC, France	09/2014 - 12/2018
Interdisciplinary Master in Life sciences – ENS, France	09/2013 – 09/2014
Bachelor of Genomic Sciences – UNAM, Mexico	08/2008 – 05/2012
Chemical Laboratory Technician – IPN, Mexico	08/2005 - 06/2008

Skills

Molecular biology

- Molecular cloning techniques such as **Gibson assembly** or Restriction site based-methods
- Single-molecule Fluorescence In-situ Hybridization (**smFISH**)
- Genomic editing techniques via **CRISPR** or random mutagenesis
- Handling of nematodes such as ***C. elegans*** culture, microinjection, and phenotypic characterization
- Microscopy imaging via bright-field, and **fluorescence microscopy**
- Standard molecular biology methods such as **PCR**, **bacterial transformation**, and **DNA extraction**

Bioinformatics and DevOps

- Vast knowledge of computational algorithms and programming proficiency in **C++**, **Javascript**, **Matlab**, **Perl**, **Python**, and **R**
- Application of numerical simulations and mathematical modelling with **Simulink** (Matlab), **Kappa**, **GINSIM**, and **L-py**
- **Macro** developer on software belonging to **Microsoft Office** suite and **ImageJ** (Microscopy image analysis)
- Repository and code handling though **Github**, **gitlab** and **IBM Watson environment**
- Documentation and report creation in **Markdown** language and **Jupyter notebooks**
- Extensive use of **Linux** based systems (e.g., **Ubuntu**), code and library compilation in **bash (shell/.sh)**, and command one-liners on programs like **awk**, **sed,** and **perl**
- Pipeline development for evolutionary and ancestry analysis, **GWAS** studies, and **NGS** treatment for multiple analysis like **Genome assembly and mapping**, **RNA-Seq** and **Chip-Seq** analysis with tools such as **samtools**, **bwa**, **GATK**, **vcftools**, **plink**, **admixture**, **StarSeq**, **MACS2** and **bedtools** among many others
- Software development for cloud app deployment on **R-shiny** and J**avascript** and within virtual environments such as **Docker containers** or **Nginx** / **Apache** based cloud servers
- Creation and query implementation of databases with **MySQL** and **MariaDB** on **php** and **html**
- Knowledge and basic implementation of Machine Learning packages like CUDA software and **tensorflow**, and libraries like **keras** and **py-torch**

Interpersonal skills

- Mentoring skills
- Conflict management through emotional intelligence
- Language proficiency in: **English**, **French,** and **Spanish**

Additional Training

Visit my LinkedIn profile to verify the authenticity of the following online courses (among others):

- Problem Solving and Critical Thinking Skills
- Negotation skills: Negotiate and resolve conflict
- Storytelling and influencing: Communicate with impact
- Neuronal networks and Deep Learning
- Linear algebra with Python programming
- Tools for Data Science

Interdisciplinary School in Animal and Plant Morphogenesis, SFDB	26/02/2014 – 04/03/2017
Modelling Approaches towards epigenetics workshop, University of Cambridge	14/06/2014 - 18/06/2014
Models, epigenetics and evolution course, EpiGenesys	30/05/2014 - 11/06/2014
Summer School on Mathematical Modeling of Biological Systems, CIMAT	18/06/2012 – 22/06/2012
12º Autumn School on Biological Mathematics and Complex Systems, UAEH	10/10/2012 – 15/10/2010
Basis for medical genomics, INMEGEN	26/07/2010 – 06/08/2010
2º School of computational and biology theory, UAEM	06/07/2010 – 09/07/2010
XLI Annual Theoretical-Practical course of Human Genetics, UNAM	22/06/2009 – 26/06/2009
Programming in Java, UNAM	01/02/2009 – 01/06/2009

Undergrad research projects

Modelling the interplay between transcriptional regulation chromatin remodeling during cell differentiation
Dennis Thieffry lab, ENS – France 15/03/2014 – 01/08/2014
Analysis of DNA dynamics under different transcriptional levels
Xavier Darzacq lab, ENS – France 01/11/2013 – 01/03/2014
Bioinformatics analyzes of ancient DNA and modern human population structures
Ludovic Orlando group and Tom GIlbert group, GeoGenetics - Denmark 05/06/2011 – 06/07/2013
Quality assessment of short read sequences and bioinformatics
Moret lab, IBT and Winter Genomics - Mexico 15/01/2011 – 06/06/2011
Modelling engineered genetic networks on WiFiColi project (iGEM)
CCG/UNAM – Mexico, MIT - USA 07/01/2010 – 10/11/2010
Recollection, amplification and analyses of DNA samples through forensic methodologies
Palacios lab, CCG/UNAM - Mexico 25/07/2009 – 09/08/2009

Publications

- Priyadarshini M, Ni JZ, **Vargas-Velazquez AM**, Gu SG, Frøkjær-Jensen C. Reprogramming the piRNA pathway for multiplexed and transgenerational gene silencing in *C. elegans*. **Nat Methods**. doi: 10.1038/s41592-021-01369-z (2022)
- Aljohani M.D.*, El-Mouridi S.*, Priyadarshini M.*, **Vargas-Velazquez AM*** and Frøkjær-Jensen C. Engineering rules that minimize germline silencing of transgenes in simple extrachromosomal arrays in *C. elegans*. **Nature Communications.** doi: 10.1038/s41467-020-19898-0 **(**2020)
- **Vargas-Velazquez AM,** Besnard F, and Félix MA**.** Necessity and contingency in developmental genetic screens: EGF, Wnt, and semaphorin pathways in vulval induction of the nematode *Oscheius tipulae*. **Genetics** doi: 10.1534/genetics.119.301970 (2019)
- Grimbert S, **Vargas-Velazquez AM**, and Braendle C. Physiological Starvation Promotes *Caenorhabditis elegans* Vulval Induction. **G3: Genes, Genomes, Genetics** doi: 10.1534/g3.118.200449 (2018)
- Barkoulas M*****, **Vargas-Velazquez AM***, Peluffo A, and Félix MA**.** Evolution of New *cis*-Regulatory Motifs Required for Cell-Specific Gene Expression in *Caenorhabditis*. **PLOS Genetics** 12(9): e1006278 (2016)
- Fernández R, Schubert M, **Vargas-Velázquez AM**, Brownlow A, Víkingsson GA, Siebert U, Jensen LF, Øien N, Wall D, Rogan E, Mikkelsen B, Dabin W, Alfarhan AH, Alquraishi SA, Al-Rasheid KAS, Gilles G, Orlando L. A genome wide catalogue of single nucleotide polymorphisms in white-beaked and Atlantic white-sided dolphins. **Molecular Ecology Resources.** doi: 10.1111/1755-0998 (2015)

- Zhang G [and 136 others, including **Vargas-Velazquez AM**]. Comparative genomics reveals insight in avian genome evolution and adaptation. **Science** 346:1311-1320 (2014)
- Jarvis ED [and 103 others, including **Vargas-Velazquez AM**]. Whole-genome analyses resolve early branches in the tree of life of modern birds. **Science** 346:1320-1331 (2014)
- Schubert [and 33 others, including **Vargas-Velazquez AM**]. Prehistoric genomes reveal the genetic foundation and cost of horse domestication. **PNAS** (2014)
- Pedersen JS, Valen E, **Vargas Velazquez AM**, Parker BJ, Rasmussen M, Lindgreen S, Lilje B, Tobin DJ, Kelly TK, Vang S, Andersson R, Jones PA, Hoover C, Tikhonov A, Prokhortchouk E, Rubin EM, Sandelin A, Gilbert MTP, Krogh A, Willerslev E, Orlando L**.** Genome-wide nucleosome map and cytosine methylation levels of an ancient human genome. **Genome Research** 24: 454-466 (2014)
- Orlando L [and 54 others, including **Vargas-Velazquez AM**]. Recalibrating Equus evolution using the genome sequence of an Early Middle Pleistocene horse. Nature letters. **Nature** 499, 74- 78 (2013)
- Sánchez-Quinto F, Schroeder H, Ramirez O, Avila-Arcos MC, Pybus M, Olalde I, **Velazquez AM**, Marcos ME, Encinas JM, Bertranpetit J, Orlando L, Gilbert MT, Lalueza-Fox C**.** Genomic Affinities of Two 7,000-Year-Old Iberian Hunter- Gatherers. **Current biology**. Vol. 22 issue 16 pp.1494 – 1499 (2012)

Awards and recognitions

- Recipient of MemoLife Labex scholarship
- 1° Poster place winner on the Geogenetics Meeting 2012
- Recipient of UNAM Carlos Slim scholarship
- iGEM 2010 gold medal for the project “WiFiColi: A communicolight system”
- Been called a computer whiz in a scientific journal

Invited speaker at:

- Vers-midi conference, Marseille France 2018
- Mexico’s first national workshop of synthetic biology, LANGEBIO, México 2010

Speaker at:

- European conference in *C. elegans*, Barcelona Spain 2018
- Young Reseachers in Life Sciences conference, Paris France 2017

Expositor at:

- *C. elegans* International Meeting, UCLA, LA USA 2019
- 18th International Congress of Developmental Biology, NUS, Singapore 2017

Teacher at:

- Master in Genetics course, IMALIS, ENS, France 2014-2016
- Teaching course of tools for mathematical modelling of biological systems, UNAM LCG, Mexico 2012
- Talks on bioremediation and taboos on science a perspective into genomics, PREPA28-CBT, Mexico 2012

Attendee at:

- Evolutionary Systems Biology Meeting, Welcome Genome Campus, Cambridge UK 2016
- EMBO Conference: Genetic Control of Development and Evolution, Institute Pasteur, Paris France 2015
- *C. elegans* International Meeting, UCLA, LA USA 2015
- VerMidi meeting, IJM, Paris France 2015
- 10th Epigenetic Course 2014, Curie Institute, Paris France 2014
- 12th International Conference on Systems Biology, Heidelberg Germany 2011
- International Symposium in Nutrigenomics, NESTLE México 2009

Interests and hobbies

Latino dancing, sports, cooking, DIY projects and technology (among many others)