BIOGRAPHICAL SKETCH

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NAME: Enrique Israel Velazquez Villarreal

eRA COMMONS USER NAME (credential, e.g., agency login): VVILLARREAL2

POSITION TITLE: Assistant Professor of Research, Translational Genomics

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
School of Medicine, Nuevo Leon State University (UANL), Monterrey, Mexico	MD	11/2007	Medicine
Graduate School of Public Health, Multidisciplinary Master of Public Health Program, University of Pittsburgh	MPH	08/2011	Public Health
Graduate School of Public Health, Department of Epidemiology, University of Pittsburgh	MS	08/2011	Population Genomics
Graduate School of Public Health, Certificate in Global Health, University of Pittsburgh	CGH	08/2011	Global Health
Graduate School of Public Health, Department of Human Genetics, University of Pittsburgh	PhD	08/2015	Human Genetics/ Computational Genet
The Scripps Research Institute (TSRI), La Jolla, CA	Postdoc.	09/2016	Bioinformatics/ Functional Genomics
Rady Children Hospital San Diego (RCHSD), San Diego, CA	Postdoc.	09/2017	Bioinformatics/Data Management

A. Personal Statement

In my role as assistant professor focus on Bioinformatics, Machine Learning (ML), Artificial Intelligence (AI), Medicine, Genomics and Cancer Genomics, I dedicate my time to perform statistical and computational genomics analysis with emphasis in single cell DNA copy number variation. As bioinformatician and physician with experience in NGS analysis, I'm leader of the USC Bioinformatics, Statistical and Methodological Core U54 NIH-funded grant (http://grantome.com/grant/NIH/U54-CA233465-01-6675), and institutional grants. I have led research that are responsible for the applications of statistical and computational biology/bioinformatics analysis and potential planned ML/AI methods of the multidimensional data generated by the three proposed research projects: 1) Disparities in Mitochondrial Peptidomics and Transcriptomics in Prostate Cancer, 2) Enhancing Efficacy of Gemcitabine Nanoparticles in Pancreatic PDX Models, and 3) Contribution of Racial Disparity towards the Early Development of Pancreatic Cancer, as well as during other CaRE2 Center emerging studies. By providing developing and implementing the statistical and methodological environment necessary for heterogeneous data manipulation and analysis, seamless data workflow among the Center members, and dissemination of data to the research community the analyses will be focused on the following according with the three proposed research projects: 1) association of different peptides and prostate cancer risk in ethnic minorities through association analysis, compare prostate tissue expression levels via transcriptome analysis, and examine the contribution of mitochondrial DNA copy number variation using DNA sequencing copy number analysis. 2) genetic differences among Pancreatic Cancer tumors via exome sequencing analysis, identify new targets or candidate biomarkers using cellular pathway analysis, identify existing drugs which inhibit growth of racially diverse Pancreatic Cancer tumors through parametric tests, assess in vitro activity of nanoparticles using statistical modeling and cross-sectional analysis, and determine in vivo efficacy of tissue culture derived substances through pharmacokinetic modeling. 3) gene expression changes during acinar ductal metaplasia

(ADM), compare gene expression changes performing principal component analysis (PCA), identify specific genes that are unique to different racial groups through calculating fold changes and p values, examine the association between SNPs in genes associated with ADM and risk of PDAC via genetic association analysis, and study chromosomal patterns of DNA or histone modification by methyl groups of ADM driver genes using DNA methylation analysis. Overall, I have extensive experience in bioinformatics, statistical genomics and ML/AI methods, with experience in next generation sequencing (NGS) analysis, including transcriptome analysis, and databases management systems, SQL and NoSQL, as well as genomic and clinical data interpretation. This experience has been obtained through 17 years of training in several programs including PhD, MD, two Postdoctoral fellows, two master degrees, two adjunct assistant professor positions and a certificate in global health, most of these programs focused on statistical, ML / AI and computational genomics. This multidisciplinary training gave me the experience, capabilities, and existing validated pipelines that are needed to successfully manage, quality check, process, analyze, and share massive amounts of NGS data in a manner that is functional to clinicians, biologists, bioinformaticians, and statisticians.

As PI on single cell sequencing projects (i.e., “Multi-genomic single-cell characterization of endometrial cancer among different racial groups” - USC Keck School of Medicine Dean’s funding project), I has active collaborations leveraging new methods in single-cell copy number analysis and clonotype detection to uncover and characterize hidden sub-clones within standard cell-lines, single-cell gene expression data in renal cancer, and single-cell adapter-ligated DNA fragments profiling in cancer.

I have extensive experience in ML/AI, with training and expertise in both ML/AI applied in genomic and clinical data. I have made pioneering contributions to the development of Transplant genomics through the identification of biomarkers of kidney transplant rejection using ML/AI that have the clear ability to detect gene expression profiles for acute & subacute rejection and successful transplantation, and presented in recognized ML/AI conferences with experts in the field. (https://ml4health.github.io/2017/pages/speakers.html).

B. Positions and Honors

Positions and Employment

2000-2003	Medical Researcher, Medical Student Research Group of the School of Medicine, Nuevo Leon State University, Nuevo Leon, Monterrey, Mexico
2000-2006	Medical Fellowship, Department of Human Anatomy, School of Medicine, Nuevo Leon State University, Nuevo Leon, Monterrey, Mexico
2004	Medical Researcher, Vall D’Hebron University Hospital, Department of Neurosurgery, University of Barcelona, Barcelona, Spain
2005-2006	Medical Researcher, Neuroimaging Laboratory, National Institute of Neurology and Neurosurgery (INNNMVS), Mexico City, Mexico
2006	Medical Researcher at the Brigham and Women’s Hospital, Department of Surgery, Harvard Medical School, Harvard University, Boston, MA
2008-2009	Public Health Researcher at the Mexican Health Foundation, Mexico City
2009-2011	Public Health Researcher at the World Health Organization (WHO) Collaborating Centre, University of Pittsburgh, Pittsburgh, PA
2009-2015	Bioinformatics Analyst at the Center for Computational Genetics, University of Pittsburgh Pittsburgh, PA
2010-2011	Genetic Statistician at the Department of Psychiatry, Center of Neuroscience, University of Pittsburgh, Pittsburgh, PA
2010-2011	Global Health Researcher at the Center for Global Health, Graduate School of Public Health, University of Pittsburgh, Pittsburgh, PA
2011-2015	Bioinformatics Analyst at the Center for Simulation & Modeling, University of Pittsburgh, Pittsburgh, PA
2013-2015	Bioinformatics Analyst at the Bioinformatics Resource Center of the Institute for Personalized Medicine, University of Pittsburgh, Pittsburgh, PA
2014-2015	Bioinformatics Analyst at the Alzheimer’s Disease Lab in the Department of Human Genetics, University of Pittsburgh, Pittsburgh, PA
2015	Bioinformatics Analyst at Pittsburgh Supercomputing Center (PSC), University of Pittsburgh and Carnegie Mellon University, Pittsburgh, PA

2015-2016 Bioinformatics Analyst at Functional Genomics Laboratory, The Scripps Research Institute (TSRI), La Jolla, CA
2016-2017 Bioinformatics Analyst at Rady Children's Hospital San Diego (RCHSD), San Diego, CA
2017-2018 Adjunct Professor, National University, San Diego, CA
2017-present Adjunct Assistant Professor, San Diego State University (SDSU), San Diego, CA
2017-present Assistant Professor, University of Southern California (USC), Los Angeles, CA
2017-present Leader USC Bioinformatics, Statistical & Methodological Shared Resources (BSMSR) Core to the Cancer Research, Education & Engagement (CaRE2) Health Equity Center.

Honors

1999-2007 Graduated with Honors, Nuevo Leon State University (UANL), Nuevo Leon, Monterrey, Mexico
2007-2008 Graduated with Special Mention from medical social service training, National Institute of Neurology and Neurosurgery (INNNMVS), Mexico City, Mexico
2009-2015 Mexican National Scholarship

C. Contributions to Science

1. Since Oct 2017 as Assistant professor of research translational genomics at Keck School of Medicine, I have been exploring new single cell technologies in cancer genomics. In collaboration with Dr. David Craig, Dr. John Carpten and 10xGenomics Inc, I conducted studies on single cell DNA sequencing CNV in cancer genomics. For the first time we profiled a COLO829 cell line tumor using single cell 10x Genomics technology. This work was uploaded in Biorxiv.org and is now in the process of publication. In addition, I have working in studies using this this technology performing single cell sequencing analysis in melanoma, renal carcinoma and endometrial cancer, presenting them in different scientific annual meetings. Also, I have been exploring the benefits on big data and cancer genomics health disparities, presenting results to scientific communities, such as in the main campus at the National Institutes of Health, National Cancer Institute.

    a. Enrique I. Velazquez-Villarreal, Shamoni Maheshwari, et al. Resolving sub-clonal heterogeneity within cell-line growths by single cell sequencing genomic DNA. doi: https://doi.org/10.1101/757211
    b. Enrique I. Velazquez-Villarreal. Benefit from using Big Data to Enhance Genomic and Cancer Health Disparities Research. [accessed on Oct 24, 2019. Available at: http://www.cancermeetings.org/PDW2019/Presentations/Velazquez%20Villarreal_PDW2019.pdf]
    c. Enrique I. Velazquez Villarreal et al. Leveraging new methods in single-cell copy number analysis and clonotype detection to uncover and characterize hidden subclones within standard cell lines. DOI: 10.1158/1538-7445.AM2018-437 Published July 2018. [accessed on Oct 24, 2019. Available at: https://cancerres.aacrjournals.org/content/78/13_Supplement/437]
    d. Enrique I. Velazquez Villarreal et al. Understanding cancer heterogeneity in relation to minor sub-clones at single cell profiling level in renal cell carcinoma. DOI: 10.1158/1538-7445.AM2019-2530 Published July 2019] [Accessed on Oct 24, 2019. Available at: https://cancerres.aacrjournals.org/content/79/13_Supplement/2530.article-info]

2. Since September 2018 as Leader USC Bioinformatics, Statistical & Methodological Shared Resources (BSMSR) Core to the Cancer Research, Education & Engagement (CaRE2) Health Equity Center. Here, I have been leading statistical and computational bioinformatics analysis to several projects focused on cancer health disparities. These studies are related with Disparities in Mitochondrial Peptidomics and Transcriptomics in Prostate Cancer (PC), Enhancing Efficacy of Gemcitabine Nanoparticles in Pancreatic PDX Models, and Contribution of Racial Disparity towards the Early Development of Pancreatic Cancer. In addition, I have been working on establishing protocols to develop and maintain a central data and resources and sample management systems that enables interface between multiple disciplines including genomics, basic sciences, and clinical medicine. Also,

I'm providing bioinformatics, statistical and methodological support and educational opportunities to the Cancer Research, Education & Engagement (CaRE2) Health Equity Center

a. Enrique I. Velazquez Villarreal. Bioinformatics, Statistical and Methodological Core (http://grantome.com/grant/NIH/U54-CA233465-01-6675 , https://care2bioinformatics.org).
b. USC Cancer Research, Education & Engagement (CaRE2) Health Equity Center [Accessed on Oct 24, 2019. Available at: https://care2usc.org)
c. Enrique I. Velazquez Villarreal et al. Single cell cancer heterogeneity: Clonotype detection in renal cell carcinoma. American Society of Human Genetics (ASHG) Annual Meeting 2019 (Abstract Control Number: 1921950) [Accessed on Oct 24, 2019. Available at: https://eventpilotadmin.com/web/page.php?page=IntHtml&project=ASHG19&id=1921950]
d. Enrique I. Velazquez Villarreal et al. Introducing single cell sequencing genomic DNA copy number analysis to study cancer heterogeneity in renal cell carcinoma and its potential benefits in cancer health disparities research. American Association for Cancer Research (AACR) Health Disparities Conference 2019 (Abstract Number: A004). [Accessed on Oct 24, 2019. Available at: https://www.aacr.org/Documents/CHD19_Poster%20Session%20A.pdf]

3. From August 2015 to September 2016 as Bioinformatics analyst in the Functional Genomics Laboratory at The Scripps Research Institute, I conducted a study named "Multi-dimensional "shotgun" epigenetics of CD4 memory T cell immunity in kidney transplant patients with clinical and biopsy-proven sub-clinical acute and chronic rejection" using big computational resources and Artificial Intelligence / Machine Learning Analyses with Dr. Daniel Salomon. This project focused on identifying biomarkers that predict clinical acute rejection after human kidney transplantation.

    a. Kurian, S.M., Velazquez, E., Thompson, R., Whisenant, T., Rose, S., Riley, N., Harrison, F., Gelbart, T., Friedewald, J.J., Charette, J., Brietigam, S., Peysakhovich, J., First, M.R., Abecassis, M.M. & Salomon, D.R. (2017). Orthogonal comparison of molecular signatures of kidney transplants with subclinical and clinical acute rejection: equivalent performance is agnostic to both technology and platform. Am J Transplant, 17(8), 2103-2116. PMCID: PMC5519433

4. From September 2009 to August 2015 as Bioinformatics analyst at the Center for Computational Genetics, University of Pittsburgh, I conducted several projects in cancer genomics, precision medicine and public health. I worked with with Dr. Michael M. Barmada on projects related to precision medicine informatics, specifically on the integration of genomic data into Electronic Health Records (EHRs) and proposing innovative and transformative informatics systems that provides data extensibility, replication, liquidity, scalability and flexibility to make cross-disciplinary and systems-level analysis more achievably by automating integration. In this period of time, I was conducting a study as Bioinformatics analyst at Pittsburgh Supercomputer Center (PSC), University of Pittsburgh and Carnegie Mellon University, I conducted my dissertation project using computer clusters that support databases with Dr. Michael M. Barmada, Eleonor Feingold, Ph.D., Harry Hochheiser, Ph.D., Alexandros Labrinidis, Ph.D., and Ryan Minster, Ph.D. Also in collaboration with Drs. Nick Nistrom, Philip Blood and Bryon Gill. My project focused on finding NoSQL alternatives to relational database in precision medicine for big data storage. From January 2010 to August 2011 as Genetic Statistician at the Department of Psychiatry, Center of Neuroscience, University of Pittsburgh, I conducted my master thesis project in Dr. Etienne Sibille's Lab to gain knowledge and experience in genetics of aging. The project focused on performing association analysis of a genetic variant and three functional markers of brain health that were applicable tests to measure cognitive function, motor function and depressed mood using aging population from the Health ABC longitudinal cohort study database. From September 2009 to August 2011 as Public Health Researcher at the World Health Organization (WHO) Collaborating Centre, University of Pittsburgh, I conducted a research with Dr. Ronald E. Laporte to gain knowledge and experience in public and global health informatics. The project focused on collecting and managing data related to public health schools, medical schools and public health leaders from around the world to build a useful database for future telecommunication research purposes.

    a. Dr. Enrique I. Velazquez Villarreal. Alternatives to relational databases in precision medicine: comparison of nosql approaches for big data storage using supercomputers. [accessed on Oct

24, 2019. Available at: http://d-scholarship.pitt.edu/25614/1/velazquezvillarrealei_etdPitt_2015.pdf]

b. Dr. Enrique I. Velazquez Villarreal. Association between a sirtuin 5 snp (rs sirt5 snp, rs9382222) and three functional markers of brain health. [accessed on Oct 24, 2019. Available at: http://d-scholarship.pitt.edu/8575/1/VelazquezEI.pdf]

c. Supercourse, Epidemiology, the Interntet and Global Health [accessed on Oct 24, 2019. Available at: http://www.pitt.edu/~super1/]

5. From September 2008 to May 2009 as Public Health Researcher at the Mexican Health Foundation, I collaborated in a research project related with breast cancer in the Mexican population. The project focused on publishing a paper named “the health care cost of breast cancer in the Mexican social security institute” in a peer review journal.

    a. Knaul FM1, Arreola-Ornelas H, Velázquez E, et al. The health care costs of breast cancer: the case of the Mexican Social Security Institute. Salud Publica Mex. 2009;51 Suppl 2:s286-95. (https://www.ncbi.nlm.nih.gov/pubmed/19967284)

Complete List of Published Work in MyBibliography:
https://www.ncbi.nlm.nih.gov/sites/myncbi/1LCq53tG7dks/bibliography/40053944/public/?sort=date&direction=ascending

D. Additional Information: Research Support

Ongoing Research Support

U54 CA233465 Carpten (Multi-PI) 09/19/18-08/31/23
3/3 Florida-California Cancer Research, Education and Engagement (CaRE2) Health Equity Center. Bioinformatics, Statistical and Methodological (BSM) Core
The goal of the BSM Core at the Florida-California Cancer Research, Education & Engagement (CaRE2) Health Equity Center is to provide the data management, data cleaning, data storage, and data release to public databases for all information generated by our CaRE2 center.
Role: PI/Project Leader of the Bioinformatics Core.

Completed Research Support

U19 AI063603 Salomon (PI) 09/01/04-08/31/17
Genomics for Transplantation: Discovery and Biomarkers
The goal of this project was taking cutting edge technologies for genomics, proteomics and genetics and applying these tools rigorously and critically to the major challenges of transplantation immunology and biology.
Role: Postdoctoral Fellow

R34 MH111491 Baker (PI) 02/15/17-12/31/19
High School Success: Vocational Soft Skills Program for Transition-age ASD Youth
The goal of this project is focused on developing and testing an integrated intervention to increase neurocognitive and social cognitive skills to improve functioning and postsecondary outcomes for transition-age students with autism spectrum disorders (ASD).
Role: Postdoctoral Fellow