IVENISE CARRERO GONZALEZ

Greater Boston Area, Massachusetts · 857-207-6996
ivenisec@gmail.com · https://www.linkedin.com/in/ivenise-carrero-ms-phd-99a4793a/
Residency status: US citizen

Relevant expertise, Precision Oncology

- CAP/CLIA certified environment
- Proficient use of genetic resources (JAX-CKB, oncoKB, cBioportal, Clinvar, Gnomad, Civic, amongst others)
- Ample knowledge of oncology targeted therapy
- Clinical trial matching based on mutation profile
- Somatic variant assessment and classification under the American College of Medical Genetics and Genomics guidelines.
- Ample knowledge in molecular oncology

EXPERIENCE

SEPTEMBER 2021 – PRESENT

INFORMATICS VARIANT SCIENTIST, FLORIDA CANCER SPECIALISTS AND RESEARCH INSTITUTE

Liaison between the Informatics Department (Precision Oncology area) and the Next Generation Sequencing Lab.

Implemented the variant classification pipeline and report process in our in-house NGS Laboratory.

Trained the Laboratory Director and Variant Scientists in variant interpretation, targeted therapy, and preparing reports.

Created knowledgebase documentation for our in-house NGS Laboratory, such as targeted therapy by disease and cancer type, educational material regarding cancer genetics, and a controlled language file with statements for different types of situations that we can encounter and need to be added in the report.

Provide guidance for the development of our in-house precision oncology knowledgebase.

Work side-by-side with FCS physicians, aiding in the interpretation of NGS reports and clinical therapeutic action based on the patients' mutation profile, optimizing patient care.

Work-side-by-side with clinical research coordinators, identifying targeted therapies, and enhancing clinical trial options.

Serve as a subject matter expert in the development of our in-house Precision Oncology Knowledgebase.

JANUARY 2021 – SEPTEMBER 2021

SOMATIC VARIANT SCIENTIST II, SEMA4 GENOMICS

Part of the founding group of curators working on whole-exome sequencing analysis (WES). This includes high throughput analysis of single nucleotide variants, assessment of copy number alterations, gene fusions, and germline variants.

Generate web-based applications and R functions for automatization of documents used in the reporting process.

Train the team members with no computational knowledge to use the R functions.

Analyze DNA and RNA sequencing variants of patient tumor samples to assess which variants are relevant to include in the report and discriminate which variants are pathogenic, benign, or sequencing artifacts.

Investigate the clinical significance of gene variants found in DNA and RNA sequencing by searching mutation databases (ClinVar, gnomAD, cBioportal, Jackson Laboratory, oncoKB, cancer hotspot, etc.) and published literature.

Prepare variant assessment summaries as part of the molecular genetic testing results.

Maintain an internal variant database for different disease areas for the curation of variants periodically.

Therapeutic options and clinical trial suggestions for pathogenic variants based on patients' profile.

Assist Directors in preparing reports.

MARCH 2019 – JANUARY 2021

SOMATIC VARIANT SCIENTIST I, SEMA4 GENOMICS

Analyzed DNA and RNA from the solid tumor panel to identify variants of patient tumor samples to assess which variants are relevant to include in the report and discriminate which variants are sequencing artifacts.

Investigated the clinical significance of gene variants found in DNA and RNA sequencing by searching mutation databases and published literature.

Prepared variant assessment summaries as part of the molecular genetic testing results.

Therapeutic options and clinical trial suggestions for pathogenic variants based on patients' profile.

Assisted Directors in preparing report.

EDUCATION

DECEMBER 2018

PH.D. MOLECULAR AND HUMAN GENETICS, BAYLOR COLLEGE OF MEDICINE, HOUSTON, TX

Graduate research assistant at Dr. Aleksandar Milosavljevic's laboratory. Involved in multiple projects:

- Histoepigenetic analysis of HPV- and tobacco-associated head and neck cancer to detect cell surface biomarkers.
- Pathogenicity calculator in Clingen consortium.
- Complexity and diversity of F8 genetic alterations in the 1000 Genomes.
- Allelic landscape of human epigenomes.

MAY 2011

M.S. BIOLOGY/GENETICS, UNIVERSIDAD DE PUERTO RICO-MAYAGUEZ CAMPUS

Graduate research assistant at Dr. Juan Carlos Martinez's laboratory

- Thesis project: Human population genetics, tracing human migrations through mtDNA.
- Teacher Assistant in Biology, Genetics, and Molecular Biology
- Lectured and trained other teaching assistants in the HHMI funded pilot genetics laboratory module: "The Study of Genetic Equilibrium in Drosophila Melanogaster", and the NSF funded pilot module: "Characterization of Puerto Rican Cassava".

MONTH YEAR

B.A./BIOLOGY, UNIVERSIDAD DE PUERTO RICO-MAYAGUEZ CAMPUS

- Biology major, minors in Genetics and Psychology

SKILLS

· Molecular biology
· Cancer genetics
· Precision oncology
· Variant analysis
· Variant visualization tools: IGV, Alamut
· Variant interpretation
· Targeted therapies
· Clinical trial matching
· Programing skills: R studio, Linux environment

PROJECTS AND PUBLICATIONS

EPIGENOMIC DECONVOLUTION OF HEAD AND NECK SQUAMOUS CELL CARCINOMA

Baylor College of Medicine

- Applied the *in silico* tool, EDec, to predict the cell-type composition and the cell-type specific gene expression profiles in head and neck cancer. Using this method, we were able to identify cell surface proteins specifically overexpressed in cancer cells and overexpressed genes in immune cells associated with immunotherapy response.
  Analyses: Survival analysis, Cox regression analysis, pathway enrichment analysis, differential methylation and gene expression analysis, machine learning, as well as **deep understanding of cancer biology and immunology, epigenomics, and transcriptomics.**

- Programming in R.
- **Publication**: Ivenise Carrero, Hsuan-Chen Liu, Andrew G. Sikora, Aleksandar Milosavljevic. "Epigenomic deconvolution of HPV- and tobacco-associated head and neck squamous cell carcinoma identifies both subtype-specific and common therapeutic targets despite divergent etiology and tumor microenvironments." *Oncogene,* 2019.

ALLELIC LANDSCAPE OF HUMAN EPIGENOMES
Baylor College of Medicine

- Multi-institutional collaboration in the analysis of genetic and epigenetic variation within the NIH Roadmap Epigenomics Project dataset. Provided insights into the effect of genetic mutations on the epigenome. Improved identification of non-coding genetic variants that are likely to have effects on human phenotypes and diseases. Performed integration of large-scale databases such as 1000 Genomes and ExAC for variant annotation. Combined **GTEx dataset, GWAS dataset**, and ***in silico* predictor tools for better risk variant prioritization**.
- Programming in R and Ruby. Database querying.
- Poster presentation in Epigenomics 2016 meeting.
- Oral presentation in the Baylor College of Medicine Genetics Retreat.
- **Publication**: Vitor Onuchic†, Eugene Lurie†, Ivenise Carrero, Piotr Pawliczek, Ronak Y. Patel, Joel Rozowsky, Timur Galeev, Zhuoyi Huang, Robert C. Altshuler, Zhizhuo Zhang, R. Alan Harris, Cristian Coarfa, Lillian Ashmore, Jessica W. Bertol, Walid D. Fakhouri, Fuli Yu, Manolis Kellis, Mark Gerstein, Aleksandar Milosavljevic, on behalf of the NIH Roadmap Epigenomics project. "Allele-specific epigenome maps reveal sequence-dependent stochastic switching at regulatory loci". *Science*. 2018

PATHOGENICITY CALCULATOR IN CLINGEN CONSORTIUM
Baylor College of Medicine

- Populated the database with evidence tags for pathogenicity: population databases from **ExAC**, **1000 Genomes** and **ClinVar**, and functional prediction tools like **CADD, Polyphen2, SIFT, and GERP++2** for the Pathogenicity Calculator as part of the Clingen Consortium.
- **Sequence variant classification made under the American College of Medical Genetics and Genomics guidelines.**

COMPLEXITY AND DIVERSITY OF F8 GENETIC VARIATIONS IN THE 1000 GENOMES
Baylor College of Medicine

- Performed genetic analysis of F8 gene to find new variants predisposing to Hemophilia A using the **1000 Genomes dataset**.
- **Functional prioritization of variants using SIFT, PolyPhen-2, and GERP++**.
- Population genetics analysis: Fst, linkage disequilibrium, haploview for linkage disequilibrium visualization.
- **Publication**: J. N. Li, I. G. Carrero, J. F. Dong and F. L. Yu. Complexity and diversity of F8 genetic variations in the 1000genomes. *Journal of thrombosis and hemostasis*. 2015

TRACING MATERNAL AMERINDIAN ANCESTRY IN THE ARUBAN POPULATION THROUGH mtDNA SEQUENCING
University of Puerto Rico, Mayaguez

- Performed DNA extraction, PCR amplification, and sequencing of hypervariable regions of mitochondrial DNA.
- DNA sequencing analysis to classify the Aruban population into mitochondrial haplogroups (European, Amerindian, African).
- Population genetics analyses for Amerindian haplogroups to trace their migration route.

Network analysis, Tajima's test, diversity analysis, and heterozygosity analysis.

- I discovered that the most predominant Amerindian haplogroup in Aruba is haplogroup D. However, it does not represent the native Amerindian population in Aruba. The expansion of this haplogroup in Aruba was a result of the slave trade between territories, especially from Venezuela.
- Poster presentation in "Congreso de Antropologia Biologica", 2010.