Daniel A Cuevas, PhD

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BIOINFORMATICS AND DATA SCIENTIST

Analysis and software product development life cycle experience from early conception to clinical validation. Involved in model development, data analysis, data management, pipeline development, and software management. Software development experience ranges from quick prototyping to late-stage, ISO standardized software design and testing. Data analysis for biomarker discovery, identifying data features, establishing QC methods, and experiment reports.

RELEVANT SKILLS

- Proficient languages: Python, R, Perl, bash, PHP, SQL
- Intermediate languages: Java, C++, MATLAB
- Sequencing: QC, alignment, bisulfite sequencing
- Microbiome: 16S, metagenomics, annotation
- Automated analysis pipeline reports
- Multivariate statistical analysis, regression, classification
- Model parameter optimization, data exploration
- Supervised/unsupervised machine learning techniques
- Cluster computing, AWS
- Prototyping and ad-hoc analysis

PROFESSIONAL EXPERIENCE

Bioinformatics Scientist II   *March 2018 – Present*
Progenity, Inc.

- Led development and design of single-molecule detection assay analytical software, processing daily experiments as an integral piece for rapid results during early stage product development

- Performed genome wide discovery for differentially methylated DNA loci as potential biomarkers for NASH liver disease in acquired clinically diagnosed NASH samples

- Developed probabilistic classifier to distinguish between levels of NASH liver disease severity and fibrosis measures in bisulfite sequence samples using methylation biomarkers, achieving proof-of-concept performance targets

- Led development and design of paired-end shallow whole genome sequencing NIPT analytical software (aneuploidies, microdeletions, and fetal fraction prediction); optimized algorithm parameters achieving MVP and TPP targets

- Implemented key pre-processing and QC components for the protein biomarker-based Preeclampsia diagnostic rule-out test analytical software, achieving software performance validation at each product milestone

- Established the in-house microbiome 16S analysis pipeline as lead bioinformatics scientist for microbiome analyses

- Created and managed R&D automated pipelines across several projects (NASH, Preeclampsia, NIPT, single-molecule detection platform), ensuring daily experiments underwent quality control, pre-processing, and primary analysis within 1-day turnaround times

Graduate Bioinformatics Research Assistant   *July 2012 – March 2018*
Robert Edwards Bioinformatics Lab, San Diego State University

- Led production of PyFBA, a genome-scale metabolic model builder using a wide range of bacterial growth assays to identify novel metabolic pathways and transporters within bacterial genomes

- Participated in design and development of a full NGS metagenome and metatranscriptome computational pipeline used for emergency Cystic Fibrosis patient sputum sequencing data

EDUCATION

Doctor of Philosophy (PhD), Computational Biology and Bioinformatics   *February 2018*
San Diego State University with Claremont Graduate University

Bachelor of Science (BS), Computer Science   *May 2011*
San Diego State University