

Bioinformatics Analyst / Data Scientist

Analytical and results-driven professional with over 10 years of data analytics experience and skilled at using statistical analysis and data visualization to uncover valuable insights and drive informed decision-making.

Stellar record of conducting data analysis and visualization through projects, including developing RShiny infrastructure for UC patient data, identifying response biomarkers in lung and UC datasets, and investigating composite biomarkers for Merkel Cell Carcinoma. Demonstrated expertise in machine learning with a proven track record of developing and applying advanced computational techniques to solve complex biological problems. Extensive knowledge of scientific techniques including preparation, characterization, testing, evaluation, data analysis, and collection. Well-versed in leading and coaching teams and the ability to establish professional development programs to improve staff performance. Proven experience in analyzing bulk and single-cell RNA-seq, functional enrichment, and deconvolution. Competency in utilizing cloud computing, high-performance computing, and Linux/Ubuntu operating systems.

Areas of Expertise

- Bioinformatics / Machine Learning
- Biomarker Discovery / Validation
- Data Analysis / Interpretation
- Project / Program Management
- Continuous Improvement / Innovation
- Report Writing / Presentation
- Quality Control / Assurance
- Gene Expression Profiling
- Team Development / Leadership
- Statistical Analysis / Data Mining
- Problem Solver / Decision Maker
- Research / Development

Career Experience

Bioinformatics Contractor | EMD Serono R&D Institute, Billerica, MA (Remote)

2021 – 2022

Utilized RShiny to extract, process, and load RNAseq data and full exome sequencing profiles from four phase I-III UC trials, including TCGA. Identified loss-of-function mutations to validate the mutation status of one gene as a biomarker for resistance of the avelumab maintenance in the internal UC cohort.

- Conducted research, analyzed, and disproved the avelumab combination hypothesis for two major DNA damage response genes.

Key Projects

RShiny infrastructure for visualizing & analyzing clinical data & molecular profiles for Urothelial carcinoma patients.

- Extracted, processed, and imported RNAseq data and whole exome sequencing (WES) profiles of four multiple phase I-III UC trials into RShiny integrated analysis app, including TCGA.
- Created and implemented configuration for R6 classes to import clinical information, genomic data, and efficacy association information.

Identifying response biomarkers & combination rationale to overcome avelumab resistance in Lung & UC datasets.

- Verified mutation status of gene as a biomarker for avelumab maintenance resistance in internal UC cohort by defining loss-of-function mutations in personal-generated mutation calling output from tumour-only sequencing.
- Aided in creating a synthetic comparator for a combination trial by assessing existing phase III monotherapy datasets and real-world evidence data from TEMPUS.

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- Utilized Kaplan-Meier and forest plots to validate the patient stratification hypothesis through the development of univariate and multivariate survival models.
- Rejected the avelumab combination hypothesis for two significant DNA damage response (DDR) genes

Understanding biomarkers of response & resistance to Merkel Cell Carcinoma for patients treated with avelumab in 1L and 2L

- Integrated omics data such as PD-L1/CD8 status from manual & digital pathology, gene expression, gene signatures, somatic mutations, mutational signatures, and tumour mutation burden to study composite biomarkers.
- Verified a treatment resistance hypothesis by utilizing a publicly accessible scRNAseq dataset for tSNE clustering and immune cell type annotation

Quality Manager | MadTree Brewing, Cincinnati, OH

2014 – 2021

Managed a cross-functional team to develop, execute, and maintain quality management systems/processes. Drove initiatives for continuous improvement to maximize effectiveness and guarantee reliable product output. Chaired and organized regular team meetings to inform and update staff regarding progress, challenges, and opportunities. Conducted research and presented outcomes at various conferences, including delivering presentations, organizing and moderating panel discussions, and participating in roundtable discussions. Acted as a chair of the American Society of Brewing Chemists (ASBC) Technical Committee and Craft Beer Subcommittee while leading Committee meetings and the development and launch of the ASBC Sampling Plans.

Six Sigma project: Kolsch Yeast Counts: Improving Reliability of Representative Samples to improve beer consistency

- Improved random sampling and counting of yeast to provide a more accurate pitch of yeast into the wort.
- Utilized Six Sigma methodology and design of experiments (DOE), resulting in enhancing brewhouse efficiency for the house IPA brand by 4%.
- Improved data gathering processes and optimized team performance by designing and introducing 14 inductive automation ignition data input dashboards.
- Minimized the number of test batches for new brands by 50% through the execution of mixture experiments for recipe development.
- Conceptualized and established a professional development program for staff, resulting in the promotion of four team members to supervisory positions within the organization.

Additional Experience

Graduate Student, Teaching & Research Assistant | University of Cincinnati, Cincinnati, OH, 2011 – 2014

Education

MS, Biological Sciences | University of Cincinnati, Cincinnati, OH, 2013

BS, Aerospace Engineering | Saint Louis University, St. Louis, MO, 2006

Licenses & Certifications

Data Science Certificate – Springboard (Online), 2021

Six Sigma Black Belt Certification – Xavier Leadership Center, Cincinnati, OH

Publications & Presentations

- **Genetic, transcriptional, and immunological biomarker analyses** to investigate the biology of metastatic Merkel cell carcinoma and outcomes with avelumab treatment in the phase 2 JAVELIN Merkel 200 trial." D'Angelo S.P et al. (In preparation)
- "De novo assembly and annotation of the transcriptome of the agricultural weed *Ipomoea purpurea* uncovers gene expression changes associated with herbicide resistance." Leslie, Trent, and Regina S. Baucom. G3: Genes, Genomes, Genetics 4.10 (2014): 2035-2047. http://bit.ly/TL_Publication.
- **You Can't Always Get What You Want - Use of Design of Experiments (DOE) to Optimize Dry Hop Mixtures for Aroma and Flavor**, ASBC Virtual Presentation (co-author) 2021; https://bit.ly/ASBC_Talk2.
- **But Sometimes You Get What You Need - Using R to Optimize Dry Hop Mixtures for Aroma and Flavor**, American Society of Brewing Chemists (ASBC) Virtual Presentation 2021; https://bit.ly/ASBC_Talk3.
- **Standardized Data Collection with ASBC Sampling Plan**, ASBC Webinar 2021; http://bit.ly/ASBC_Webinar3.
- **Data Collection, Organization, and Integration**, ASBC Webinar 2020; http://bit.ly/ASBC_Webinar2.
- **Exploration of the flavor space - Using design of experiments (DOE) to model the sensory impact of post-fermentation additions**, ASBC Presentation (co-author) 2019; http://bit.ly/ASBC_Talk1.
- **From Bytes to BeeR - Leveraging the Statistical Programming Language R in Brewing Data Science**, ASBC Conference Workshop 2019; http://bit.ly/ASBC_Workshop1.
- **Five Critical Quality Checks for Small Breweries**, ASBC Webinar 2017; https://bit.ly/ASBC_Webinar1.

Technical Proficiencies

Data Analysis:	Bulk & single cell RNASeq whole-exome DNA sequencing functional enrichment (Gene Ontology, GSEA, CAMERA) deconvolution (xCell, Cibersort) de-novo transcriptome assembly (SOAPdenovo-Trans) trichromatic Bowtie2 BLAST samtools Primer3 H&E and PD-L1/CD8 IHC output from PathAI & Definiens
Languages:	R & Bioconductor (DESeq2 edgeR, survival Seurat tidyverse fGSEA limma shiny markdown) Python (Jupyter Pandas NumPy Scikit-Learn PySpark Keras Tensorflow) SQL (PostgreSQL)
Data Visualization:	ggplot2 plotly survminer ComplexHeatmap Cytoscape Matplotlib Seaborn RShiny
Statistics & ML:	Design of Experiments (DOE) Statistical Process Control Hypothesis Testing Regression Classification kNN Random Forest K-Means Clustering Neural Networks
Other Skills:	Cloud computing (AWS) High-performance computing (PBS Cluster Computing Environment) Operating system (Linux/Ubuntu, Windows) Version control (GitHub/GitLab)