PATRICK CHERRY

💌 pcherry [at] pm dot me | 📞 upon request | 🛍 Senior Scientist | Genomics | 🖫 Twist Bioscience | 🛍 San Francisco, California | 😚 pdcherry github.io | 🞧 github.com/pdcherry | in linkedin.com/in/p-cherry | 😇 United States Citizen | Updated on 2024-06-03

PhD scientist skilled in data visualization, statistical modeling, bioinformatics, next-generation sequencing (NGS), and toolbuilding. I've coded reproducible and rigorous pipelines for high-throughput experimental designs and multi-omic analyses for communication to technical and non-technical audiences. I've launched best-in-class oncology reference standards and analyzed NGS data from Illumina, MGI, and Element. Originally trained in Molecular Biology, I am passionate about advancing data science and bioinformatics to improve human health and understand biology.



EDUCATION

2019 2013

PhD

University of Colorado School of Medicine

Aurora/Denver. Colorado

- · Ph.D. in Molecular Biology. Advisor: Jay Hesselberth, PhD
- Thesis: RNA terminus chemistry impact decay events that target HAC1 mRNA during the Unfolded Protein Response

2013 2009

BA

Hendrix College

Conway, Arkansas

- Biochemistry and Molecular Biology, with Distinction. Advisor: Andres Caro, PhD
- · Senior Capstone Project showing key stress response gene expression changes to oxidative stress in liver cells
- · Minor in Mathematics; PI: Lars Seme; Project: Newton's method as a fractal chaotic dynamical system



INDUSTRY EXPERIENCE

2024 2021

Senior Scientist, Genomics

Twist Bioscience

South San Francisco, California

- Invented and introduced multiple new products to market yielding millions of dollars in new revenue as Tech Lead, including: Pan-cancer cfDNA (v1 & v2), CNV Controls, RNA Fusion Controls, Fragmentome Controls, and RNA-seq
- · Answered biological and business questions with DoE and data analysis using R and the libraries: dplyr, dbplyr, DBI, purrr, ggplot2, Bioconductor, DEseq2, seurat, tidymodels, glm, nls, lme4, AlgDesign, and more
- · Edited and maintained production QC pipelines with automated reporting using Python and the libraries: NumPy, pandas, polars, seaborn, statsmodels, biopython, pybedtools, pysam, vcfpy, scanpy, and others
- · Maintained production code (qit version control with code review) with CD (github actions); operated in highperformance compute environment aws s3 and Databricks using Unix shell / bash tools, like STAR-fusion
- · Authored internal R package "twistcolorpal" on Github with help files to help scientists style plots to Twist branding

2024 2021

Scientist, Genomics

Twist Bioscience

South San Francisco, California

- Tech Lead of Nov. 2021 launch of Twist Pan-Cancer Reference Standard, an ISO-13485 synthetic control with 458 variants among 84 cancer-associated genes at six QC'd VAFs, plus a WT control, earning \$1 million in revenue in year 1
- · Identified and optimized compatible ddPCR assays using web scraping in R with rvest for cfDNA quality control
- Used Python to author automated data / QC reports using Jinja2 (with CSS) and WeasyPrint
- · Managed data and ran bioinformatic analyses on Illumina RNA & DNA seq using bash tools like: awk, grep, scp, wget, Illumina BaseSpace CLI, ssh, bwa, bedtools, samtools, vcftools, UMI-tools/fgbio
- · Wrote original SQL queries for Snowflake-based database to answer production and business questions.

2021 2019

Scientist I, NGS & NPI-Build

Zymergen, Inc.

Emeryville, California

- · Boosted NGS Core genotyping success by 45% using DoE experimentation, data-driven decision-making, and teaching; Guided demanding and diverse internal customers on complex NGS experiments
- · Built and disseminated Rmarkdown notebook for autonomous NGS data exploration
- Coded build and QC experiments using Zymergen's Drawbridge alembic API Python library to LIMS
- · Rendered strain build and plasmid build reports from LIMS SQL database in MySQL Workbench

SELECTED INTELLECTUAL PROPERTY Libraries for mutational analysis 4/9/21 South San Francisco, California Twist Bioscience US Prov. Pat. Ref No 823.101 · Configuration and fabrication of synthetic DNA & RNA reference standards and synthetic variant sequences Method for counterselection in microorganisms 3/25/21 Emeryville, California Zymergen, Inc. · US 2021 0087586 A1 • Demonstration of novel counterselection mechanism in non-model Bacillus microbe for genetic modification SELECTED PUBLICATIONS Twist cfDNA Pan-Cancer Reference Standard v2 Technical Guidance 1/4/24 South San Francisco, California Twist Bioscience Product Sheet & FAQ · Patrick Cherry, Lydia Bonar, & Mike Bocek Characteristics and specificity of the wild-type / 0% VAF reference material 4/22/22 South San Francisco, California Twist Bioscience · Patrick Cherry & Mike Bocek Multiple decay events target HAC1 mRNA during splicing to regulate the unfolded protein response 3/19/19 Aurora/Denver, Colorado eLife · Cherry, P., Peach, S., & Hesselberth, J. Genetic bypass of essential RNA repair enzymes in budding yeast 12/6/17 Aurora/Denver, Colorado **RNA** · Cherry, P., White, L., York, K., & Hesselberth, J. SELECTED PRESENTATIONS & TALKS Twist pan-cancer reference standard V2: Enhanced precision and reduced errors in ctDNA analysis 2/6/24 Orlando, Florida Advances in Genome Biology and Technology Twist pan-cancer synthetic RNA fusion control for assay development 4/16/23 Orlando, Florida American Association for Cancer Researchers, Twist Bioscience Use of synthetic CNV fragments to mimic copy number alterations for ctDNA reference standards 2/7/23 Hollywood, Florida Advances in Genome Biology and Technology Twist pan-cancer synthetic reference materials for cell-free DNA (cfDNA) assay development 4/12/22 New Orleans, Louisiana American Association for Cancer Researchers R use at Zymergen 6/16/20 Emeryville, CA Z-Tech Talk Data-driven troubleshooting of NGS experiments 4/20/20 Data Science Talk RNA processing regulates the unfolded protein response 8/24/17 Ocld Spring Harbor, New York CSHL: mRNA Processing Meeting Talk