# 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 2024-05-22

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 quesitons with reproducible exploratory analysis using R and the libraries: dplyr, dbplyr, DBI, purrr, ggplot2, Bioconductor, DEseq2, seurat, tidymodels, glm, nls, lme4, and more
- · Edited and mainteined production QC pipelines with automated reporting using Python and the libraries: numpy, pandas, polars, seaborn, statsmodels, biopython, pybedtools, pysam, vcfpy, scanpy, and others
- · Mintained production code (git version control with code review) and operated in high-performance compute environment aws s3 & ec2 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

- As Tech Lead, launched the Twist Pan-Cancer Reference Standard, an ISO-13485 synthetic positive control with 458 unique variants among 84 cancer-associated genes at six QC'd VAFs, plus a WT control; Launched in Nov of 2021, and earned \$1 million in new revenue in first year
- · 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 awk, grep, scp, wget, 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 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

