

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](https://www.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 tool-building. 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
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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
 - **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
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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 reproducible exploratory analysis using R and the libraries: dplyr, dbplyr, DBI, purrr, ggplot2, Bioconductor, DEseq2, seurat, tidymodels, glm, nls, lme4, 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 (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
 - **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.
 - **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



SELECTED INTELLECTUAL PROPERTY

4/9/21



Libraries for mutational analysis

Twist Bioscience

📍 South San Francisco, California

- US Prov. Pat. Ref No 823.101
- Configuration and fabrication of synthetic DNA & RNA reference standards and synthetic variant sequences

3/25/21



Method for counterselection in microorganisms

Zymergen, Inc.

📍 Emeryville, California

- US 2021_0087586 A1
- Demonstration of novel counterselection mechanism in non-model *Bacillus* microbe for genetic modification



SELECTED PUBLICATIONS

1/4/24



Twist cfDNA Pan-Cancer Reference Standard v2 Technical Guidance

Twist Bioscience [Product Sheet](#) & [FAQ](#)

📍 South San Francisco, California

- Patrick Cherry, Lydia Bonar, & Mike Bocek

4/22/22



Characteristics and specificity of the wild-type / 0% VAF reference material

Twist Bioscience

📍 South San Francisco, California

- Patrick Cherry & Mike Bocek

3/19/19



Multiple decay events target HAC1 mRNA during splicing to regulate the unfolded protein response

[eLife](#)

📍 Aurora/Denver, Colorado

- Cherry, P., Peach, S., & Hesselberth, J.

12/6/17



Genetic bypass of essential RNA repair enzymes in budding yeast

[RNA](#)

📍 Aurora/Denver, Colorado

- Cherry, P., White, L., York, K., & Hesselberth, J.



SELECTED PRESENTATIONS & TALKS

2/6/24



Twist pan-cancer reference standard V2: Enhanced precision and reduced errors in ctDNA analysis

[Advances in Genome Biology and Technology](#)

📍 Orlando, Florida

4/16/23



Twist pan-cancer synthetic RNA fusion control for assay development

[American Association for Cancer Researchers](#), [Twist Bioscience](#)

📍 Orlando, Florida

2/7/23



Use of synthetic CNV fragments to mimic copy number alterations for ctDNA reference standards

[Advances in Genome Biology and Technology](#)

📍 Hollywood, Florida

4/12/22



Twist pan-cancer synthetic reference materials for cell-free DNA (cfDNA) assay development

[American Association for Cancer Researchers](#)

📍 New Orleans, Louisiana

6/16/20



R use at Zymergen

Z-Tech Talk

📍 Emeryville, CA

4/20/20



Data-driven troubleshooting of NGS experiments

Data Science Talk

📍 Emeryville, CA

8/24/17



RNA processing regulates the unfolded protein response

CSHL: mRNA Processing Meeting Talk

📍 Cold Spring Harbor, New York