# PATRICK CHERRY

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 invented new molecular methods for DNA and microbe manipulation. Originally trained in Molecular Biology, I am passionate about advancing data science and bioinformatics to improve human health.

## 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 affects the 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

Current | 2022

**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
- Built positive team culture; mentored and promoted a report from Senior Research Associate to Scientist; Coached reports who served as Tech Leads; Delivered quality science on deadline by managing research assistants; Guided cross-functional teams through product launch and beyond
- Original research and presentations to non-experts and outside stakeholders unveiled novel products and underwrote multiple patents; Gained new customers in RNA standards space with the design and launch of HTP RNA synthesis
- Analyzed public databases and alpha feedback to optimize design of multiple products; Routinely crafted custom NGS data analysis pipelines in R, Python, and UNIX command line / shell tools; documented analyses using `Rmarkdown`, `Quarto`, and `Jupyter`; Maintained git / *Github* repo of *Dockerized* bioinformatic QC packages for *Pan-cancer cfDNA* product line; Communicated results to technical audience using high-performance compute environments on *Databricks*, `aws`, and *Snowflake* SQL
- Generated actionable data for new technology evaluations of a new NGS platform (*MGI* / *Complete Genomics*, *Element*, *Illumina*), with to enable faster gene QC; Launched a time-saving gene synthesis change, supported by original experimental data; Boosted colleagues with publication-ready data viz. by coding and distributing the internal package *`twistcolorpal`* (sets up database connectors to `SQL` / Snowflake for parameterized `dbplyr` querying); Regularly use R, tidyverse, Python, Polars, AWS `s3`, `Spark`/`PySpark`, and `Sparklyr`, locally and on *Databricks*; Regularly implements and runs automated code tests; Practices good data hygiene

## CONTACT


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upon request

Senior Scientist | Genomics

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United States Citizen


*Last updated on 2024-03-27.*

*Data-driven résumé made in R using pagedown.*

I currently split my time between wet lab and computational activities. I have worked in a variety of roles ranging from HTP strain onboarding to genomics scientist. I like collaborative environments where I can learn from my peers and in turn teach others.

Current | 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
- Invented, validated, and deployed to production multiple widely-used primer removal methods for DNA standards and high-complexity synthetic dsDNA pools
- Devised and validated precise high-throughput DNA quantification process for accurate pooling; On-boarded droplet digital PCR (ddPCR) system into production; Designed and validated custom ddPCR assays for use in production
- Led multiple iterations of custom NGS analysis; refined the QC approach and thresholds for ensuring a contamination-free production process; extensively used data visualization to communicate complex data to cross-functional teams and non-experts
- Made extensive use of UMI sequencing and invented novel method to rigorously quantify library conversion efficiency to evaluate products and reference materials

2021 | 2019

**Scientist I, NGS & NPI-Build**

Zymergen, Inc. — Emeryville, California

- Achieved a 95% success rate for obtaining genetic edits by designing and implementing multiple automated high-throughput methods for a non-model microbe: transformation, counterselection, and NGS genotyping
- Determined best methods for genetic manipulation, propagation, and archiving of a non-model microbe through design & execution of complex experiments (DoE) on lab automation, with and without LIMS sample tracking
- Boosted *NGS Core* genotyping success by 45% using data-driven decision-making and teaching; Guided demanding and diverse internal customers on complex NGS experiments
- Applied statistical methods to screen and optimize a genetic engineering protocol for newly-on-boarded microbe; delivered robust process while working on New Product Introduction team
- Delivered on KPIs for microbe improvement by designing and building hundreds of plasmids using modern molecular techniques like *Gibson* and *Golden Gate*

## RESEARCH EXPERIENCE

2019 | 2014

**Doctoral Research**

University of Colorado School of Medicine — Aurora/Denver, Colorado

- Wrote, revised, & published two academic papers on RNA repair & yeast genetics
- Engineered and characterized *genetic bypass of essential genes* in budding yeast; on-boarded CRISPR/*Cas9* for efficient and precise gene knock-in and scarless knock-out
- Cultured large batches of wild-type and mutant *E. coli* to expressed and purified recombinant proteins, which enabled carrying out RNA library prep and RNA modification enzymatic assays
- Optimized custom RNA-seq library protocol; independently planned, executed, troubleshooted RNA modification detection
- Routinely conducted northern blotting, targeted depletion, primer extension, splinted ligation, and other esoteric DNA and RNA experiments

I worked on a few projects during my PhD, and the RNA repair project led me to custom 5'-OH RNA-seq libraries, which inspired my fascination with transcriptomics and bioinformatics.

## INTELLECTUAL PROPERTY

3/7/23

**Methylation-mediated adapter removal on nucleic acid sequences**

Twist Bioscience — South San Francisco, California

- US 63/317,466

Working at Twist and Zymergen on new product research requires confidentiality, but public evidence of accomplishments often comes in patent applications. The Legal teams

11/12/21

**Expansion of cfDNA for Libraries**
Twist Bioscience — South San Francisco, California
• US Prov. Pat. Ref No 823.102

4/9/21

**Libraries for mutational analysis**
Twist Bioscience — South San Francisco, California
• US Prov. Pat. Ref No 823.101

3/25/21

**Method for counterselection in microorganisms**
Zymergen, Inc. — Emeryville, California
• US 2021_0087586 A1

## SELECTED PUBLICATIONS

12/21/21

**Twist Pan-cancer synthetic reference materials technical guide**
Twist Bioscience — South San Francisco, California
• Patrick Cherry & Mike Bocek

2019

**Multiple decay events target HAC1 mRNA during splicing to regulate the unfolded protein response**
eLife
• Cherry, P., Peach, S., & Hesselberth, J.

2018

**Genetic bypass of essential RNA repair enzymes in budding yeast**
RNA
• Cherry, P., White, L., York, K., & Hesselberth, J.

I communicate my results clearly, both in writing and in live presentations. I enjoy writing research papers, but my career has required more tech notes and app notes recently.

## 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 — 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

7/13/21

**Molecular Methods Meet the Standards: Or how I learned to stop worrying and love UV-quantification**
Twist R&D Meeting — South San Francisco, CA

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

I give audience-centered presentations by adapting on the fly and over time to the venue and occasion. I like to *transfer knowledge* by giving methods/best practices talks whose slides can also serve as documentation.