

# 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



 San Francisco, California

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 United States Citizen

Last updated on 2024-05-14.

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 express 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 team

- 11/12/21 • **Expansion of cfDNA for Libraries**  
Twist Bioscience • US Prov. Pat. Ref No 823.102  
📍 South San Francisco, California
- 4/9/21 • **Libraries for mutational analysis**  
Twist Bioscience • US Prov. Pat. Ref No 823.101  
📍 South San Francisco, California
- 3/25/21 • **Method for counterselection in microorganisms**  
Zymergen, Inc. • US 2021\_0087586 A1  
📍 Emeryville, California



## SELECTED PUBLICATIONS

- 12/21/21 • **Twist Pan-cancer synthetic reference materials technical guide**  
[Twist Bioscience](#) • Patrick Cherry & Mike Bocek  
📍 South San Francisco, California
- 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.



## 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 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.

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.