PATRICK CHERRY

PhD scientist skilled in data visualization, statistical modeling, bioinformatics, biological data science, next-generation sequencing (NGS), and tool-building. I've coded reproducible and rigorous pipelines for high-throughput experimental designs and multiomic 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

- Tech Lead of multiple NPIs and custom OEMs; invented and launched products to yield millions of dollars in new revenue, 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 on new product introductions, increasing revenue. Delivered quality science on deadline by managing research assistants
- · Original research and presentations unveiled novel products and underwrote multiple patents for product configuration and biochemical approaches. Gained new customers in RNA standards space with the design and implementation of high-throughput RNA synthesis and pooling
- · Analyzed public databases and feedback from alpha testers to optimize design of multiple products; routinely craft custom data analysis pipelines in R and Python; documented analyses using Rmarkdown, Quarto, and Jupyter; maintain git repo of dockerized bioinformatic QC packages for Pan-cancer cfDNA product line
- · Generated actionable data for new technology evaluations of a new NGS platform with custom experiments and bioinformatic analyses in Python, R, and SQL to enable faster gene QC in Production. Launched a time-saving gene synthesis change into production, supported by original experimental data. Boosted colleagues in publication-ready plots by coding and distributing on company GitHub the internal package twistcolorpal, which automatically styles plots and sets up database connectors to SOL / 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

CONTACT

- pcherry [[at]] pm [[dot]] me
- upon request
- Senior Scientist | Genomics
- Twist Bioscience
- III San Francisco, California
- opdcherry.github.io
- github.com/pdcherry
- in linkedin.com/in/p-cherry
- 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

- Tech Lead of 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
- 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
- Made extensive use of UMI sequencing and created 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 a genetic edit 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 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 microbe improvement KPIs 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
- Expressed, purified, and used wild-type and mutant recombinant protein in *E. coli* to carry out an RNA modification enzymatic assay
- 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

11/12/21

Expansion of cfDNA for Libraries

Twist Bioscience

South San Francisco, California

• US Prov. Pat. Ref No 823.102

Working at Twist and Zymergen on new product research requires confidentiality, but public evidence of accomplishments often comes in patent applications. The Legal teams know me well for being a helpful expert in the process.

Libraries for mutational analysis 4/9/21 South San Francisco, California Twist Bioscience US Prov. Pat. Ref No 823.101 Method for counterselection in microorganisms 3/25/21 ♥ Emeryville, California Zymergen, Inc. · US 2021_0087586 A1 SELECTED PUBLICATIONS Twist Pan-cancer synthetic reference materials technical guide 12/21/21 South San Francisco, California Twist Bioscience · Patrick Cherry & Mike Bocek I communicate my results clearly, Multiple decay events target HAC1 mRNA during splicing to regulate the both in writing and in live 2019 unfolded protein response presentations. I enjoy writing research papers, but my career has eLife required more tech notes and app · Cherry, P., Peach, S., & Hesselberth, J. notes recently. Genetic bypass of essential RNA repair enzymes in budding yeast 2018 **RNA** · Cherry, P., White, L., York, K., & Hesselberth, J. ♣ SELECTED PRESENTATIONS & TALKS Twist pan-cancer reference standard V2: Enhanced precision and reduced 2/6/24 errors in ctDNA analysis Orlando, Florida Advances in Genome Biology and Technology I give audience-centered Twist pan-cancer synthetic RNA fusion control for assay development 4/16/23 presentations by adapting on the fly Orlando, Florida American Association for Cancer Researchers and over time to the venue and occasion. I like to transfer knowledge by giving methods/best practices Use of synthetic CNV fragments to mimic copy number alterations for 2/7/23 talks whose slides can also serve as ctDNA reference standards documentation. ♣ Hollywood, Florida Advances in Genome Biology and Technology Twist pan-cancer synthetic reference materials for cell-free DNA (cfDNA) 4/12/22 assay development New Orleans, Louisiana American Association for Cancer Researchers Molecular Methods Meet the Standards: Or how I learned to stop worrying 7/13/21 and love UV-quantification South San Francisco, CA Twist R&D Meeting R use at Zymergen 6/16/20 P Emeryville, CA Z-Tech Talk Data-driven troubleshooting of NGS experiments 4/20/20 P Emeryville, CA Data Science Talk