

David Chelimo

Clinical Bioinformatics Scientist II – Labcorp

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Clinical bioinformatics scientist with nearly a decade of experience in cancer genomics and clinical NGS. Proficient in Python and SQL, comfortable with Bash, R, and Java. Deep experience in annotated genomic profiles, somatic variant review, and QA/QC in high-complexity regulated environments. Deeply interested in agentic coding workflows and AI coding assistants as tools for building more robust, reproducible bioinformatics pipelines.

EXPERIENCE

Clinical Bioinformatics Scientist II May 2026 – Present Labcorp · Remote (US)

- Visualize and assess genetic variants flagged for manual review, analyzing corresponding NGS and WGS data.
- Troubleshoot QC anomalies generated by automated pipelines to maintain data integrity.
- Analyze confirmatory assay results to support variant interpretation.
- Triage stuck samples, variants, and reports to sustain pipeline throughput.
- Support production operations including cross-team requests, on-call coverage, and program development.
- Collaborate with bioinformatics, automation, engineering, clinical genomics, and laboratory science teams.

NGS CLINICAL GENOMICS VARIANT REVIEW

Clinical Bioinformatics Analyst III Feb 2025 – Apr 2026 Foundation Medicine · Boston, MA

- Contributed and collaborated with lab, engineering, and clinical teams to improve dry lab operations and data workflows.
- Developed and implemented a Python/SQL script (with Git/GitHub) to automate failure communication with the lab, reducing manual entry errors and significantly decreasing team workload.
- Designed and deployed an automated sample comparison report generator (Python, SQL, HTML, CSS) to rapidly produce standardized PDF reports, streamlining data review processes.

PYTHON SQL AWS LAMBDA DOCKER JENKINS AUTOMATION

Clinical Bioinformatics Analyst II Aug 2019 – Feb 2025 Foundation Medicine · Cambridge, MA

- Led the migration of automation scripts from Python 2 to Python 3, improving code maintainability and enabling collaborative development.
- Built collaborative tools for data extraction, transformation, and reporting from Oracle SQL databases using Python, HTML, and CSS.
- Facilitated training sessions and contributed to the validation and launch of new genetic assays in partnership with cross-functional teams.
- Conducted manual review of NGS and assay data, ensuring high-quality variant calls and timely delivery of clinical results.

PYTHON ORACLE SQL NGS ASSAY VALIDATION

Clinical Bioinformatics Analyst I Sep 2017 – Aug 2019 Foundation Medicine · Cambridge, MA

- Developed annotated genomic profiles of somatic aberrations based on NGS data in cancer-patient samples.
- Reviewed genomic variant calls using proprietary and public tools (e.g., IGV) in collaboration with scientific teams.
- Delivered test results in compliance with SOPs, ensuring high quality within defined turnaround times.

SOMATIC VARIANTS IGV NGS SOPS

Quality Control Analyst I Jun 2017 – Sep 2017 Sanofi Genzyme · Boston, MA

- Executed rigorous quality control tests throughout manufacturing.
- Detected, quantified, and identified potential contaminants using advanced analytical techniques.
- Ensured strict compliance with CGMP guidelines.

CGMP QC REGULATED ENVIRONMENT

SKILLS

Programming

PYTHON SQL BASH JAVA R

Bioinformatics

CANCER GENOMICS NGS VARIANT ANALYSIS IGV

Data & Workflows

DATA ANALYSIS QC METRICS WORKFLOW DESIGN

AI & Agentic Coding

CLAUDE CODE AGENTIC WORKFLOWS PROMPT DESIGN

AI CODE VALIDATION

Collaboration

MENTORING TRAINING PRESENTATIONS

DOCUMENTATION

EDUCATION

B.A., Computational Biology

Minor: Mathematics

Colby College · Waterville, ME

2013 – 2017

- Capstone: Bioinformatic analysis of whole-genome sequence data from Diamond Blackfan Anemia patients to determine putative intronic mutations.

PUBLICATIONS

Whole-genome sequencing to detect small deletions in ribosomal protein genes in Diamond Blackfan Anemia patients.

Analyzed whole-genome data from DBA patients to determine putative intronic mutations. *Blood* (2019).

Measuring gene expression in bombarded barley aleurone layers with increased throughput.

Studied effects of TaABF1 serine phosphorylation on regulation of HVA1 and Amy32b. *JoVE* (2017).

Molecular Biology Lab Research Assistant

Feb 2014 - May 2017

Colby College · Waterville, ME

- › Investigated transcription factor regulation in cereal grains using advanced molecular biology techniques.
- › Analyzed gene expression and contributed to understanding stress response mechanisms in crops.

MOLECULAR BIOLOGY

GENE EXPRESSION

RESEARCH

Summer Research Intern

Jun 2016 - Sep 2016

National Human Genome Research Institute · Bethesda, MD

- › Analyzed whole genome sequences for DBA patients, identifying putative SNPs and CNVs that could be the drivers of the disorder.
- › Conducted GWAS and validated findings with research teams.

GENOMICS

GWAS

NHGRI