Ron Yadin

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Experienced synthetic biologist turned computational engineer
helping R&D organizations accelerate research and extract valuable insights
by developing scientifically-informed software & FAIR data infrastructure

Experience

21ST.BIO | COMPUTATIONAL STRAIN ENGINEER | JAN 2024 – PRESENT

- Primary LIMS architect and administrator, helping craft R&D-wide data strategy & design an integrated informatics system
- Leading a requirements-based data model refresh project, to increase structured data capture & enable ML-ready dataset curation
- Building software tools & pipelines to support scientific workflows, bioinformatics tools, and data transformation & loading processes

SHIRU | LAB DATA ENGINEER | JUL 2023 – DEC 2023

- Led the design and implementation of Shiru's unified LIMS data model for a 7-stage biomaterial research pipeline
- Developed automated, scalable, and user-friendly solutions for complex challenges around structured data capture, transformation, and visualization
- Facilitated collaboration between computational team, laboratory researchers across multiple groups, and company leaders

SHIRU | SENIOR RESEARCH ASSOCIATE, HIGH-THROUGHPUT SCREENING | AUG 2021 – JUN 2023

- Transformed Shiru's screening capabilities from unstructured, low-throughput experiments into a robust, automated high-throughput platform
- Designed and executed combinatorial experiments for optimizing microbial cultivation parameters and functional protein assays
- Helped lead Shiru's values committee to synthesize updated company values

SESTINA BIO | RESEARCH ASSOCIATE III, BIOENGINEERING | JAN 2021 – AUG 2021

- Executed core strain engineering activities including ideation, DNA part design, and precision genome editing via CRISPR-Cas system
- Verified engineered strains using cPCR, Sanger Sequencing, and long-read next generation sequencing
- Translated high-level, large-scale exploratory experimental directives into concrete laboratory operations
- Force-multiplied design efforts through python tools development

AMYRIS | ASSOCIATE SCIENTIST I & II, AUTOMATED STRAIN ENGINEERING | MAY 2018 – JAN 2021

- Leveraged laboratory robotics and advanced data infrastructure to execute automated pipelines for high-throughput DNA assembly, multiplexed next generation sequencing, and strain genotype verification
- Worked at the interface of data architecture, software engineering, and laboratory automation to advance core strain engineering capabilities
- Established project-based learning groups to train new team members with an engaging and relevant learning program

Education

UC BERKELEY | COURSEWORK TOWARDS MOLECULAR SCIENCE AND SOFTWARE ENGINEERING MS | AUG 2020 – OCT 2021

- Inaugural cohort of new masters program covering software engineering for scientific computing, data science, and machine learning

UC BERKELEY | MOLECULAR AND CELLULAR BIOLOGY B.A. | JAN 2014 – DEC 2017

- **Core Coursework**: Molecular Immunology, Molecular Endocrinology, Molecular Physiology, Genetics & Genomics, Cell Biology, Biochemistry
- **Minors**: STEM education, Spanish linguistics
- **Honors**: Distinction in General Scholarship, 5 semesters with Dean's Honors— top 4% of the College of Letters and Sciences

Skills

PROGRAMMING & SOFTWARE ENGINEERING

- Python
    - Data pipeline building - file parsing, pandas, BioPython, REST APIs
    - Visualization - matplotlib, plotly, seaborn
    - Statistics & modeling - scipy, sklearn, pytorch
    - DevOps - version control (git), testing (pytest), CI/CD (CircleCI)
    - Deployment - Jupyterhub, Flask, Docker & docker-compose
- SQL
    - Skills: schema design, DDL & DML, advanced query building
    - Tools: MySQL, Postgres, SQLAlchemy, psycopg2, Snowflake
- Proficient in HTML & CSS, basic C++
- Scientific software
    - Benching R&D cloud LIMS application
        - Registry configuration, Insights queries, SDK & API automation
    - Superblocks full stack web application development platform
    - Public biological databases & tools
        - GenBank, BLAST, Alphafold, EMBL, UniProtKB, PDB
    - JMP & Spotfire
- Cloud Infrastructure
    - AWS: S3, EC2, ECS, Lambda, Batch, SSM, boto3 | IaC: Terraform
- Linux & command line interfaces

MOLECULAR BIOLOGY

- Microbial strain construction & verification
    - Genomic engineering - CRISPR-Cas & other systems
    - Nucleic acid purification, PCR design & visualization
    - DNA construct cloning, transformation, and sequencing
- Protein purification & characterization
    - HTP IMAC, ELISA, Thermal Shift Assay, Pierce660, Fluorescence assays
- Experience with a diverse array of lab instruments & liquid handlers

Data Engineering Project

- Bulk Primer Designer: Flask & MySQL web app with Dockerized multi-container architecture for automated PCR primer design
    - https://github.com/ron-yadin/bulk-primer-designer

Publications

- Ip, K., Yadin, R., & George, K. W. (2020). High-Throughput DNA Assembly Using Yeast Homologous Recombination. *Methods in molecular biology (Clifton, N.J.)*, *2205*, 79–89. https://doi.org/10.1007/978-1-0716-0908-8_5
- Christie, W., Yadin, R., Ip, K., & George, K. W. (2020). Highly Multiplexed, Semiautomated Nextera Next-Generation Sequencing (NGS) Library Preparation. *Methods in molecular biology (Clifton, N.J.)*, *2205*, 91–104. https://doi.org/10.1007/978-1-0716-0908-8_6

Volunteer Experience

SCIENCE AMBASSADOR | COMMUNITY RESOURCES FOR SCIENCE | NOV 2021 – FEB 2022

- Developed 4 virtual lessons & interactive activities on DNA and information encoding for a 4th grade class in Oakland Unified School District

APPRENTICE SCIENCE TEACHER | FIELDWORK IN BAY AREA PUBLIC SCHOOLS | JUN 2016 – DEC 2017

- Supported innovative STEM teachers in Berkeley and Oakland in science classes from biotechnology to computer science