

Alper Kucukural, PhD

DATA SCIENCE · AI ENGINEERING · LIFE SCIENCES PLATFORMS

Senior technology executive with 10+ years building enterprise AI and multi-omics platforms for biomedical and biopharma research, from strategy and governance through production delivery at scale.

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● AT A GLANCE

CURRENT ROLE

Co-founder & CTO, Via Scientific

ACADEMIC APPOINTMENT

Associate Professor, UMass Chan Medical School

EXPERIENCE

10+ years data & AI leadership

CITATIONS

13,500+ · h-index 26 · i10-index 33

LOCATION

Cambridge, MA, USA

● CORE COMPETENCIES

- Enterprise Data & AI Strategy and Governance
- Data Science / AI Engineering Leadership
- Platform & Product Architecture
- MLOps & AI Lifecycle Management
- Data Engineering & Reproducible Analytics
- Scientific Software Productization
- Third-party AI Evaluation & Vendor Management
- Cross-functional Delivery in Matrix Orgs
- Regulatory Alignment & Ethical AI
- Team Building, Mentoring, Capability Development

● TECHNICAL STACK

- **AI / LLMs:** Claude, Claude Code, GPT, Gemini, Vertex, Llama; Generative AI; Agentic workflows
- **ML frameworks:** PyTorch, scikit-learn, MLflow, Hugging Face, LangChain
- **Developer tooling:** CLI, SDK, MCP server development, VSCode extension, Claude Code plugin development
- **Languages & data:** Python, Perl, R, Shiny, SQL, TypeScript, Node.js, Pandas, Nextflow, Snakemake, PostgreSQL, MongoDB, Zarr, TileDB
- **Infrastructure:** Linux, AWS, Azure OpenAI, Databricks, Docker, Kubernetes, Apache, Nginx
- **Delivery:** Agile / SDLC, JIRA, Confluence, GitHub, CI/CD

● EDUCATION

PhD, Biological Sciences & Bioengineering

Sabancı University, Istanbul
2004 to 2009

MS, Systems Analysis (Engineering Management)

Istanbul Technical University
2000 to 2004

BS, Mathematics Engineering

Istanbul Technical University
1995 to 2000

Postdoctoral Fellow, Computational Structural Biology

University of Kansas · Yang Zhang Lab
2008 to 2009

● RECOGNITION

- Founder of venture-backed Via Scientific, commercialized from UMass Chan
- Co-author · *Nature Protocols* (I-TASSER) · 7,800+ citations
- Published in Nature, Cell, Science, Nature Methods, Nature Communications
- Invited speaker: Nextflow Camp; OSU Center for RNA Biology; ABRF

● EXECUTIVE PROFILE

Data Science, AI, and computational biology leader with a decade of progressively senior impact across **venture-backed biotech and academic medicine**. Track record of **setting technical strategy, building and mentoring multidisciplinary teams**, and **shipping AI and analytics products** from feasibility through production. As Co-founder and CTO of Via Scientific, I build reproducible, regulatory-aware platforms used in biopharma R&D. Backed by a 35-publication, 13,500-citation research record and a Cambridge advisory bench that includes a former Moderna CSO and a former DataRobot EVP Engineering.

● QUANTIFIED IMPACT

13.5K+

scholar citations

35+

peer-reviewed publications

80+

labs & 240+ scientists supported

1000s

global users of tools I built

● LEADERSHIP VALUE PROPOSITION

- **Strategy.** Set and evolve the AI platform strategy; establish the standards and reference architectures other teams can build on.
- **Full AI product lifecycle.** Ownership of the path from feasibility to MVP, production, scaling, and operations, with clear KPIs, stakeholder reporting, and drift monitoring after deployment.
- **Third-party solution evaluation.** Build-vs-buy discipline; technical, regulatory, security, and ethical assessment of external AI tools.
- **Matrix leadership.** Collaboration with science, product, engineering, legal, data privacy, quality, security, and business operations.
- **Regulated-environment fluency.** A decade of reproducibility, versioning, and auditability in biomedical research. Familiar with GxP, 21 CFR Part 11, and the EU AI Act.
- **Team and capability building.** Hired, mentored, and retained data scientists, AI engineers, data engineers, and computational biologists across Via Scientific and the UMass Chan Bioinformatics Core.

- **Executive communication.** Comfortable translating between science, AI, and business, with investors, clinicians, regulators, and engineers in the same room.

● PROFESSIONAL EXPERIENCE

Co-founder & Chief Technology Officer

2023 to Present

Via Scientific, Inc., Cambridge, MA

Lead technology strategy, architecture, and engineering for Via Foundry, an enterprise multi-omics and AI analytics platform licensed from UMass Chan and used by biotech and pharma research teams. Venture-backed; advisors include Melissa J. Moore (former CSO, Moderna), Rob Hickey (former EVP Engineering, DataRobot), and Shah Nawaz (former VP Digital Transformation, Regeneron).

- **Set the AI strategy** across data ingestion, feature engineering, model training, deployment, and drift monitoring, along with the standards and reference architectures that hold up under scrutiny.
- **Led cross-functional delivery** across AI/ML engineers, software engineers, computational scientists, and customer-facing teams; set the hiring bar, the delivery cadence, and the engineering culture.
- **Evaluated and integrated third-party AI** (LLM providers, vector stores, agent frameworks, cloud AI services) against in-house builds on technical, regulatory, and security merit.
- **Owned reliability, reproducibility, and security** for a platform supporting regulated biomedical workflows; versioned, auditable pipelines by design.
- **Partnered with business leaders and advisors** (ex-Moderna, ex-DataRobot, ex-Regeneron) to turn scientific and customer needs into prioritized roadmaps.

Associate Professor, Program in Molecular Medicine

2020 to Present

UMass Chan Medical School, Worcester, MA

Faculty appointment in the Program in Molecular Medicine and the Department of Genomics and Computational Biology. Research spans AI for multi-omics, RNA therapeutics, and reproducible analytics at institutional scale.

- **Co-directed the UMass Chan Bioinformatics Core** supporting **80+ labs and 240+ scientists**; established standards for reproducibility, usability, and reliability of computational workflows.
- **Delivered institution-scale platforms**, including DolphinNext, DEBrowser, GUIDeSeq, and the scRNA-Seq browser, that became shared infrastructure and were later productized as Via Foundry.
- **Led training programs and bootcamps** in NGS and bioinformatics analysis that scaled institutional capability; mentored trainees, staff scientists, and collaborators.
- **Represented the institution** as invited speaker, session chair, and editorial reviewer; active in ABRF's Genomic Bioinformatics Research Group.

Assistant Professor & Bioinformatics Core Lead

Feb 2015 to 2020

UMass Chan Medical School · Worcester, MA

Promoted into the faculty track to lead the scale-up of the Bioinformatics Core. Designed and built the NGS analytics stack that ultimately became Via Foundry; standardized RNA-Seq, scRNA-Seq, CHIP-Seq, ATAC-Seq, and GATK variant-calling pipelines; delivered the training program that scaled bioinformatics literacy across the institution.

Bioinformatician III

Jun 2013 to Jan 2015

UMass Chan Medical School · Bioinformatics Core · Worcester, MA

Senior engineer on the Bioinformatics Core, building the reusable pipeline platform and training programs that matured into the subsequent faculty appointment.

- **Designed and productionized reusable, robust bioinformatics pipelines** (NGS, microarray, genomics, proteomics, chemogenomics) supporting hundreds of concurrent users on HPC clusters.
- **Installed and maintained institutional analysis platforms** (Galaxy, GenePattern, Genome Space) and built custom databases, web portals, and visualization applications where off-the-shelf tools fell short.
- **Partnered directly with PIs** to scope, deliver, and document bioinformatics solutions for manuscripts and grants; ran project reviews and stakeholder presentations.
- **Led institution-facing training workshops** and coordinated with biostatisticians, IT, and interdepartmental project teams.

Bioinformatician

Aug 2009 to Jun 2013

UMass Chan Medical School · Moore and Zamore Labs · Worcester, MA

Worked in the labs of Prof. Melissa J. Moore and Prof. Phillip D. Zamore on post-transcriptional gene regulation via RNA mechanisms. Built the next-generation sequencing software and algorithmic foundations that later became DolphinNext, DEBrowser, and ASPeak.

- **Developed bioinformatics software and visualizations** for SOLEXA and SOLiD NGS platforms used across both labs.
- **Built peak-calling and noise-reduction algorithms** accounting for experimental bias and genome-mapability artifacts; foundational work that informed ASPeak (*Bioinformatics*, 2013).
- **Engineered custom scientist-facing interfaces** so researchers could reach, summarize, analyze, and visualize data with different algorithmic approaches.
- **Developed pattern-search algorithms** using machine-learning methods; installed and maintained UCSC Genome Browser mirrors and data-conversion pipelines for UCSC and Galaxy formats.

Postdoctoral Fellow, Computational Structural Biology

2008 to 2009

University of Kansas · Yang Zhang Lab · Lawrence, KS

Co-developed I-TASSER, the unified platform for automated protein structure and function prediction. Co-author on the *Nature Protocols* (2010) method paper, now cited **7,800+ times** and still a reference tool in computational structural biology and early drug-design workflows.