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Computational Biologist | Population Genetics | Genomic Epidemiologist
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Professional Summary

Genomic epidemiologist with over a decade of experience delivering pathogen-sequencing and analytic frameworks. Through the CDC Pathogen Genomics Center of Excellence (PGCoE), I lead genomic analytics supporting surveillance and modelling of respiratory-virus evolution and develop longitudinal genomic surveillance platforms that are used to inform decisions on immunisation and monoclonal-antibody (mAb) use by state public health and pharmaceutical partners.

Professional Experience

Yale School of Public Health   **2023–Present**
Lead —Genomic Surveillance & Pathogen Analytics (Associate Research Scientist)

- Lead design and delivery of genomic-epidemiologic sequencing assays and analytics for RSV, HMPV, and *Mycobacterium tuberculosis* within the CDC PGCoE.
- Developed pipelines integrating variant calling, phylodynamics and statistical inference to monitor local RSV/HMPV transmission dynamics and detect monoclonal-antibody escape mutations.
- Built reproducible workflows (Nextflow/WDL) for real-time variant surveillance and resistance prediction across state and national networks.
- Analytical outputs are being used to inform decisions on immunotherapy performance and deployment by both public health and pharmaceutical industry partners.

Queen Mary University of London   **2022–2023**
Faculty Lead — Computational Genomics & Population Genetics (Lecturer / Assistant Professor)

- Directed teaching and postgraduate supervision in infectious-disease, genomics, and data science.
- Applied population-structure/admixture analyses to inform vector-borne disease-control strategy; built analytical capability and reproducible practice across graduate programmes.

Monash University   **2019–2022**
Principal Investigator — Vector Genomics & Resistance Genetics (Senior Research Fellow)

- Led population- and functional-genomic analyses of arboviral vectors to identify adaptation and insecticide-resistance loci; translated findings into predictive models for control-strategy evaluation.
- Supervised interdisciplinary teams combining molecular, epidemiological and computational methods to connect genomic variation to intervention performance.

Broad Institute / Harvard School of Public Health   **2015–2019**
Computational Geneticist — Population & Evolutionary Genomics (Postdoctoral Associate)

- Performed large-scale genomic-epidemiology inference on malaria parasites and vectors to characterise transmission structure and evolutionary dynamics.
- Applied ML approaches to predict parasite origin and movement from high-volume genomic datasets.
- Developed variant-discovery and biomarker pipelines for translational applications.

Wellcome Sanger Institute   **2014–2015**

Senior Bioinformatician
- Optimized selective WGS of remnant parasitic samples for applied epidemiology; foundations later adapted for LMIC treatment/surveillance policies.

Imperial College London   **2006–2011**
Scientific Programmer
- Built and maintained population-genomic analysis pipelines linking genomic variation to transmission-relevant phenotypes.

Wellcome Sanger Institute   **2004–2006**
Senior Computational Biologist
- Delivered production-grade genomic-data infrastructure enabling large-cohort evolutionary inference.

Imperial College London   **2002–2004**
Bioinformatician
- Built laboratory and computational pipelines for functional-genomics screens supporting therapeutic-target discovery.

Education

Ph.D.	**Population Genetics** (*Tres hon.*)	**Institut Pasteur / Université de Paris**	**2011–2015**
M.Sc.	**Bioinformatics** *(Distinction)*	**University of Liverpool**	**2000–2001**
B.Sc.	**Biology** *(Hons)*	**University of Leeds**	**1996–2000**

CORE COMPETENCIES

Genomic epidemiology · Respiratory-virus evolution · Vax/mAb-escape monitoring · RWE integration
Phylodynamics · Selection inference · Translational analytics · Pathogen-genomics pipelines

Technical & Analytical Skills

Python · R · NumPy · PyTorch · Snakemake · Nextflow · WDL · Docker · HPC (LSF/SLURM/PBS)
Illumina & ONT pipelines · AWS · GCP · Terra · scikit-learn · GATK stack · BCFtools

Selected Translational Projects

- Developed tiled-amplicon sequencing protocols for *M. tuberculosis*, RSV and HMPV enabling variant-level inference from clinical specimens for modelling and intervention evaluation.
- Built population-genomic pipelines for malaria and arboviral vectors enabling resolution of transmission structure, movement and resistance-associated loci at scale.
- Established direct WGS of M. tuberculosis from clinical material enabling accelerated detection of resistance markers for integration into decision-support analytics.

Selected Competitive Funding / Awards

- Merck Investigator Studies Program (2025) - genomic surveillance of RSV/HMPV
- Ambrose Monell Foundation Award (2024) – Read-cloud assembly for biomarker discovery.
- Institut Pasteur International Ph.D. Fellowship – competitive award(2011).

Additional

Dual US/UK citizen · French (professional working proficiency)
Full publications: https://scholar.google.com/citations?user=Kty5i3wAAAAJ