Jean-Paul Courneya, MS

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SUMMARY

Bioinformatics lead with 20 years in life-science research, from translational wet-lab studies and a genomics core to building research computing services. I run GPU and HPC infrastructure for multi-lab genomics teams, maintain a self-hosted language model and retrieval stack, and study genome language models. Carpentries instructor and Nextflow Ambassador who teaches everything from 10-person hands-on sessions to talks for 100+ researchers. Earlier experience in technical sales and as a small-business founder.

TECHNICAL SKILLS

AI and GPU: NVIDIA BioNeMo and Nemotron models, containerized GPU workflows, CUDA-accelerated ML libraries, AlphaFold, self-hosted LLMs, RAG, MCP servers, GPU jobs on SLURM (V100, H100)

Genomics: variant calling, amplicon sequencing, population genetics, single-cell and spatial transcriptomics (Seurat, Visium HD), RNA-seq

Workflows and infrastructure: Nextflow/nf-core, Docker, Apptainer, Git and CI/CD, Linux administration (Ubuntu, RHEL), AWS, Azure, Google Cloud, Jetstream

Languages: Python, R, Bash, Rust, SAS, JavaScript, Java; Shiny, Quarto, Jupyter. Fluent Spanish.

EXPERIENCE

Lead Bioinformatics Analyst Feb 2023 – present

Center for Vaccine Development and Global Health, University of Maryland School of Medicine

- Lead genomic and multi-omic analysis for CVD research teams from study design through publication, across malaria, mosquito vector, vaccine, and transplant immunology projects.
- Administer the center's multi-user Linux bioinformatics server (about 25 users); set the group's standards for data QC, storage, pipeline reproducibility, and secure sharing; review team code and pipelines.
- Run GPU workloads on SLURM clusters, including V100 nodes on the Institute for Genome Sciences cluster and H100s through the national ACES allocation.
- Built and maintain a self-hosted LLM, RAG, and MCP stack for the group, including an MCP server that searches public SRA/GEO metadata (OmicIDX) alongside the lab's own dataset catalog.
- Predict parasite and host protein interactions on GPUs with AlphaFold to study *P. falciparum* binding partners.
- Evaluated NVIDIA BioNeMo and Nemotron models in containerized GPU workflows on the group's cluster allocations.
- Genotyped *P. falciparum* and *P. vivax* for Bhutan's malaria elimination program; analyzed *Anopheles gambiae* population structure and *Aedes aegypti* amplicon panel variants; delivered single-cell and spatial transcriptomics for yellow fever vaccine and lung transplant studies.
- Designed and taught a custom Nextflow course for collaborators in Mali built on the snp_call_nf pipeline; led an internal Hello Nextflow workshop for CVD staff.

Senior Health Services Research Programmer Sep 2022 – Feb 2023

Pharmaceutical Research Computing, University of Maryland, Baltimore

- Analyzed and validated clinical and public health datasets in R and SAS for manuscripts and regulatory reports; built study databases, wrote SOPs, and taught R and SAS workshops.

Data Scientist and Bioinformatics Information Specialist Jan 2016 – Sep 2022

Health Sciences and Human Services Library, University of Maryland, Baltimore

- Built the library's bioinformatics program from inception: consultations, biological databases, data management planning, and research computing.

- Stood up and administered a campus high-performance computing service (Ubuntu) and deployed bioinformatics environments on Jetstream national cloud; published the service model in JMLA.
- Co-founded the Center for Data and Bioinformation, extending services campus-wide with a research data catalog and data management training.
- Analyzed sequencing data with UMB research groups, leading to co-authorship on pulmonary fibrosis and astrocyte biology papers.
- Taught R, Python, SAS, command line, cloud computing, and NCBI APIs in workshops from 10-person hands-on sessions to 100+ attendee talks; built R Shiny apps for research teams.

Earlier research and industry roles, 2006 – 2016

Senior Research Specialist, *Golding Lab*, *Rheumatology*, *UM School of Medicine* 2012 – 2016
Human immunology with flow and imaging flow cytometry and PBMC culture; co-developed two published assay methods; mentored graduate students.

Senior Research Specialist, *Lowe Family Genomics Core*, *Johns Hopkins Bayview* 2011 – 2012
Set up RNA-seq library prep and microarray workflows; handled data delivery, billing, and outreach.

Senior Research Specialist, *Saini Lab*, *Johns Hopkins Asthma and Allergy Center* 2010 – 2012
Basophil assays in omalizumab clinical studies; consented participants and managed data for a phase 3 study.

Liquid Handling Specialist, *Eppendorf North America* 2009 – 2010
One of six national specialists for the liquid handling portfolio, with accounts including NIH intramural labs.

Senior Research Specialist, *Schon Orthobiologics Lab*, *MedStar Union Memorial Hospital* 2006 – 2009
Collected OR specimens and consented patients; ran primary tenocyte culture and gene expression studies; first-author paper.

Founder and Operator, *Ra Superfood, LLC (Outlier Snacks)* 2015 – 2020
Ran a food production business: production, food safety compliance, finances, sales, and two employees.

TEACHING, COMMUNITY, AND SOFTWARE

- The Carpentries certified instructor; Nextflow Ambassador.
- nih-dmsp (GitHub): open-source tool for drafting NIH Data Management and Sharing Plans.

SELECTED PUBLICATIONS

19 peer-reviewed papers and 2 preprints; full list on Google Scholar.

- Taheri M, Mei Z, …, **Courneya JP**, et al. Activation of donor-derived eosinophils during static storage contributes to primary graft dysfunction after lung transplantation. Am J Transplant. 2026.
- Mei Z, Khalil MA, …, **Courneya JP**, et al. Eosinophils restrain humoral alloimmunity after lung transplantation. JCI Insight. 2024.
- McCann RS, **Courneya JP**, et al. Variation in spatial population structure in the *Anopheles gambiae* species complex. bioRxiv. 2024.
- **Courneya JP**, Mayo A. High-performance computing service for bioinformatics and data science. J Med Libr Assoc. 2018.
- Anekalla KR, **Courneya JP**, Fiorini N, Lever J, Muchow M, Busby B. PubRunner: a light-weight framework for updating text mining results. F1000Res. 2017.
- **Courneya JP**, Luzina IG, …, Schon LC, Atamas SP. Interleukins 4 and 13 modulate gene expression and promote proliferation of primary human tenocytes. Fibrogenesis Tissue Repair. 2010.

EDUCATION

MS, Biology, Towson University, 2008
BS, Molecular Biology, Biochemistry and Bioinformatics, cum laude, Towson University, 2006
Data Science Specialization (10 courses), Johns Hopkins University via Coursera, 2018