NATHANIEL D. OMANS

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ABOUT ME

I am a hybrid wet-dry biologist with experience developing single cell genomic assays. I am currently seeking opportunities to apply my hybrid expertise at innovative companies working in the scope of genomic technology development, synthetic biology, and regenerative medicine.

EXPERIENCE

PHD THESIS RESEARCH | *Laboratory of Dan Landau* **2018-*present***
Meyer Cancer Research Center and The New York Genome Center

- Invented a scalable method for lineage tracing in human tissues
- Designed novel computational methods to identify somatic microsatellite mutations in single cells
- Applied evolutionary modelling to study population dynamics in healthy and malignant human tissues

ROTATION STUDENT | *Laboratory of Yael David* **2018**
Memorial Sloan Kettering Cancer Center Chemical Biology Program

- Helped characterize a novel mechanism of histone maintenance by enzymatic deglycation *(Zhang et al.2019)*

ROTATION STUDENT | *Laboratory of Hagen Tilgner* **2017**
Feil Family Brain and Mind Institute, Cornell University

- Identified differential RNA splicing patterns in optogenetically activated neurons
- Developed single cell co-profiling of DNA and RNA with long read sequencing

LABORATORY MANAGER | *Laboratory of Dan Landau* **2017**
Meyer Cancer Center, Cornell University

- Purchased all equipment and setup new laboratory
- Oversaw growth of lab from 1 to over 20 employees
- Initiated clinical collaborations and managed IRB approvals
- Established best practices for isolation of cell-free DNA from blood

EDUCATION

PhD. Computational Biology and Medicine | New York, NY **2017–*present***

Cornell University, Weill Cornell Medical College

Thesis: Interrogating clonal hematopoiesis in healthy and early neoplastic tissues with novel single cell genomic methods

- Awarded NYSTEM Stem Cell Research Fellowship
- Selected as recipient of NIH T32 Training Fellowship

M.S. in Neuroscience | New York, NY **2014-2015**

Columbia University

B.S. in Ecology, Evolution and Behavioral Biology | Beloit, WI **2010-2014**

Beloit College

- Graduated with Honors in Biology
- Awarded Honors Term Scholar Award for scholarly contributions
- Awarded Sanger Research Scholarship to fund international field research

PUBLICATIONS

Gaiti, F., R. Chaligne, H. Gu, R. M. Brand, S. Kothen-Hill, R. C. Schulman, K. Grigorev, D. Risso, K.-T. Kim, A. Pastore, K. Y. Huang, A. Alonso, C. Sheridan, **Omans, N.D.**, et al. (2019). "Epigenetic evolution and lineage histories of chronic lymphocytic leukaemia". In: *Nature* 569.7757, pp. 576–580.

Kothen-Hill, S. T., A. Zviran, R. C. Schulman, S. Deochand, F. Gaiti, D. Maloney, K. Y. Huang, W. Liao, N. Robine, **Omans, N.D.**, et al. (2018). "Deep learning mutation prediction enables early stage lung cancer detection in liquid biopsy". In.

Lama, C., R. Chaligne, P. Chamely, A. Dueck, N. Dusaj, R. Hoffman, H. Kosiorek, A. Kubas-Meyer, D. Landau, E. Mimitou, S. Moein, A. Nam, **Omans, N.D.**, et al. (2022). "Deciphering the impact of type 1 interferon in human CALR-mutated and wildtype hematopoietic stem and progenitor cells in myeloproliferative neoplasms via single-cell multi-omics". In: *Experimental Hematology* 111, S104.

Lipsky, A., D. Luan, S. Chen, R. Chaligne, N. Dusaj, E. B. Bhavsar, C. Ang, A. S. Nam, F. Gaiti, P. Chamely, **Omans, N.D.**, et al. (2020). "Single-Cell Multi-Omics Reveals Distinct Paths to Survival of Admixed BTKC481 Mutant Vs. Wild-Type Cells in Clinically Progressing Chronic Lymphocytic Leukemia". In: *Blood* 136, pp. 40–42.

Nam, A. S., K.-T. Kim, R. Chaligne, F. Izzo, C. Ang, J. Taylor, R. M. Myers, G. Abu-Zeinah, R. Brand, **Omans, N.D.**, et al. (2019). "Somatic mutations and cell identity linked by Genotyping of Transcriptomes". In: *Nature* 571.7765, pp. 355–360.

Rosenberg, S., A. Kubas-Meyer, N. Parghi, **Omans, N.D.**, N. Dusaj, P. Chamely, E. Mimitou, A. C. Dueck, H. E. Kosiorek, R. S. Weinberg, et al. (2021). "Single-Cell Multi-Omics Reveals That Pegylated Interferon-Alfa Treatment Differentially Redirects Mutated and Wildtype Hematopoietic Cell Differentiation Trajectories in CALR-mutated Essential Thrombocythemia (ET) Patients". In: *Blood* 138, p. 57.

Zheng, Q., **Omans, N.D.**, R. Leicher, A. Osunsade, A. S. Agustinus, E. Finkin-Groner, H. D'Ambrosio, B. Liu, S. Chandarlapaty, S. Liu, et al. (2019). "Reversible histone glycation is associated with disease-related changes in chromatin architecture". In: *Nature communications* 10.1, pp. 1–12.

Zviran, A., R. C. Schulman, M. Shah, S. T. Hill, S. Deochand, C. C. Khamnei, D. Maloney, K. Patel, W. Liao, A. J. Widman, and P. Wong (2020). "Genome-wide cell-free DNA mutational integration enables ultra-sensitive cancer monitoring". In: *Nature medicine* 26.7, pp. 1114–1124.

CONFERENCES

BIOLOGY OF GENOMES, CSHL | Cold Spring Harbor, NY **2023**

Retrospective lineage tracing and phenotypic profiling in healthy human tissues by single cell microsatellite sequencing

HINDSIGHT 2020, ALLEN INSTITUTE | Seattle, WA **2020**

Genetic variations in RNA sequencing reads allow simultaneous readout of single cell lineage histories and transcriptional states

Note: poster session cancelled due to COVID-19

RECOMB-CCB, | Padova, Italy **2020**

Simultaneous readout of single cell lineage and transcriptional states in human samples

Note: conference cancelled due to COVID-19

SKILLS

●●● R, Bash, Nextflow

●●○ Python, Snakemake

●○○ Rust, LaTeX, d3.js, JavaScript