Naomi Yudanin, Ph.D.

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EXPERIENCE

Nanowear, New York, NY — *Chief Data Scientist*

JUNE 2021 - PRESENT

Set the technical vision and strategy for data product development, commercialization, and innovation

- Represent Nanowear interests as a member of **AdvaMed** and advisor to the **FDA** and **NIH** on AI/ML applications in digital health
- Oversee end-to-end data security restructuring and compliance with HIPAA and SOC2 standards
- Lead a fully remote software development team comprising in-house engineers and external contractors across mobile and web applications
- Manage infrastructure, budget allocation and hiring roadmap for the engineering and data teams

Fern Health, New York, NY — *Director of Data Science*

APRIL 2020 - JUNE 2021

Directed the development and implementation of enterprise-grade analytics and predictive modeling infrastructure that leverages multi-dimensional clinical data to enable digital delivery of high-quality, effective care for musculoskeletal pain.

- Managed a cross-functional team responsible for architecture, development and commercialization of the core data platform automating clinical stratification, personalization, and care customization provided by our mobile and web-based applications.
- Defined the corporate data strategy and managed the end-to-end data life cycle across the business, ensuring HIPAA compliance, governance and quality across datasets from disparate sources.

Envisagenics, New York, NY — *Senior Data Scientist*

JANUARY 2019 - APRIL 2020

Led the design, generation, and implementation of machine learning models that incorporate high-dimensional clinical data with whole-transcriptome sequencing to enable in-silico target discovery and prioritization by therapeutic modality for immuno-oncology drug development.

- Guided strategic development and construction of an immunology-focused IO platform, SpliceIO, that comprises the core algorithms used for antigenic splicing target discovery
- Co-authored 2 patents comprising the use of artificial intelligence to discover, prioritize and assess immunogenic potential of cancer-specific drug targets from DNA/RNAseq and scRNAseq
- Helped secure over **$2M** in NIH SBIR Phase I and Phase II grants to fund SpliceIO R&D
- Oversaw a team of data scientists and engineers in the development and implementation of novel algorithms as part of our SpliceCore discovery platform, and for clients to use in their drug development pipelines

Weill Cornell, New York, NY — *Postdoctoral Fellow*

JUNE 2015 - JANUARY 2019

Computationally interrogated the functional and transcriptional dynamics of adipose lymphocytes in human and murine progressive pathogenic obesity using single-cell and bulk RNAseq.

- Authored & co-authored 4 publications in top-tier journals, including **Cell & Science**

LANGUAGES

English (native)
Russian (fluent)
French (conversant)

SOFTWARE

Languages
R, SQL, Python, LookML, Javascript, HTML/CSS, Bash, Git

Databases & Platforms
Snowflake, PostgreSQL, MongoDB, Fivetran, DynamoDB, AWS, GCP, Azure

Data Visualization
R-shiny, D3.js, Looker, Tableau, Figma, Illustrator

SKILLS

Technical
Software engineering and production-grade development

Database architecture and pipeline development

Statistical inference and predictive modeling

Unsupervised and supervised machine learning; regression and time-series analysis

Data visualization and communication

Clinical analysis and interpretation

Management
Crafting corporate strategy, innovation, and monetization of data products

Talent recruitment & hiring

Agile / scrum software and product development

PATENTS

WO2020210537A1:
Cancer-specific molecules and methods of use thereof

US62/896,230:
Neoantigens, Methods of Detection and Use Thereof

PUBLICATIONS

Full list available here:
scholar.google.com/citations?hl=en&user=_P6dyDIAAAAJ

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- Successfully obtained and annually renewed independent NIH funding for over 3 years, totalling over **$4M** over 4 years.
- Built a full RNAseq alignment, read counting, and analysis pipeline from scratch, which is now the standard pipeline used by all Jill Roberts Institute members.
- Developed novel experimental and computational approaches to extract statistically rigorous and biologically meaningful information from longitudinal multi-dimensional datasets
- Oversaw the computational infrastructure for the Jill Roberts Institute that supported 80 users

Columbia University, New York, NY — *Graduate Research Fellow*

AUGUST 2010 - JUNE 2015

Quantitatively modeled and dissected molecular drivers of T cell distribution, maintenance, and retention in humans and mice over life. Received the Richard C. Parker Graduate Student Award for innovative and significant research contributions.

- Authored & co-authored 4 publications in top-tier journals, including **Cell & Nature Reviews Immunology**
- Co-authored numerous successful NIH grant applications, totaling over **$5.5M** over 5 years
- Developed novel experimental and computational approaches to extract statistically rigorous and clinically meaningful insights from human lymphocyte transcriptomes
- Built the first full RNAseq alignment, read counting, and differential expression analysis pipeline for use by researchers in the Columbia Center for Translational Immunology
- Oversaw training of 4 junior graduate students and 2 undergraduate students

EDUCATION

Columbia University, New York, NY — *Ph.D.*

Computational biology, Systems Immunology
Richard C. Parker award recipient for best graduate thesis

Carnegie Mellon University, Pittsburgh, PA — *B.Sc.*

Biochemistry, Molecular Biology
Graduated with research and academic honors

HONORS

NIH SBIR/STTR Chartered Review Group Member - Applied AI/ML

AdvaMed Executive Leadership Group Member

American Association of Immunologists Member

NIH Ruth L. Kirschstein National Service Award