

ANGELINA VOLKOVA

PhD Candidate, New York University Langone Medical Center
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EDUCATION

NYU Sackler Institute of Graduate Biomedical Sciences, New York, NY

Master of Science in Basic Medical Sciences September 2018
Cumulative GPA 3.57

Hunter College, CUNY, New York, NY

Bachelor of Arts in Chemistry with Bioinformatics Concentration, Minor in Computer Science, Minor in Mathematics June 2016
Cumulative GPA 3.60

Kingsborough Community College, CUNY, New York, NY

Associate of Science in Biology with Pharmacy Concentration June 2013
Cumulative GPA 3.88

SKILLS

- Ability work on a high-performance computing cluster
- Strong background in machine learning and deep learning fields
- Comprehensive knowledge of Natural Language Processing algorithms
- Excellent knowledge of bioinformatics 'omics data processing tools
- Sound familiarity with Bash, Python, R, SQL and MATLAB
- Ability to handle large data such as next-generation sequencing and imaging data
- Profound knowledge of biomedical databases
- Excellent statistical and analytical background
- Excellent communication, writing, presentation and collaborative skills
- Fluent in English and Russian

PROFESSIONAL EXPERIENCE

Consultant, Netrias LLC, Cambridge, MA

Summer 2019

- Identified publicly available data sets to augment in-house data
- Performed data concatenation and integration of biological assays and PATRIC database
- Built machine learning ensemble models to predict pathogenic bacteria based on phenotypic assays
- Applied NLP approaches to select relative entries from PATRIC database

PhD Candidate, Ruggles Lab, NYU Langone Medical Center, New York, NY

- Processed microbiome next-generation sequencing data 2016-current
- Performed statistical analysis and data visualization
- Built predictive models for microbial data
- Applied natural language processing techniques to raw metagenomics data
- Performed RNA-seq and microarray array data analysis

Research Assistant, Kawamura Lab, Hunter College, CUNY, New York, NY

- Assembled bacterial genome using Velvet algorithm 2014-2016
- Analyzed gene clusters using antiSMASH and NCBI BLAST

- Modified scripts in Perl and Python
- Built bioinformatics tools pipelines on Galaxy project website and in Unix
- Executed DNA metagenomic analysis using QIIME
- Performed DNA extraction and purification, NanoDrop, PCR, gel electrophoresis

Research Assistant, Kanwisher Lab, MIT, Cambridge, MA Summer 2015

- Analyzed fMRI data using Freesurfer, SamSurfer, AFNI, SPM and MATLAB
- Worked with fMRI scanner
- Implemented scripts in MATLAB and bash

TEACHING ACTIVITIES

- Teaching Assistant, NYU Langone Medical Center, New York, NY 2018-current
Graduate courses:
Advanced Topics in Bioinformatics (BMSC-GA 4456)
Introduction to Health Informatics (BMSC-GA 4455)
Next-Generation Sequencing Informatics (BMSC-GA 4452)
- MATLAB Tutor, NYU Langone Medical Center, New York, NY Spring 2018
- Volunteer Math Teacher, New York Cares, New York, NY Fall 2015

ORAL AND POSTER PRESENTATIONS

- **June 2019** *Predictive Metagenomic Analysis of Autoimmune Disease*. Oral and poster presentations at ASM Microbe 2019 conference, San Francisco, CA
- **April 2019** *Advances in the Human Microbiome Field*. Lecture at NYU Medical Center, New York, NY
- **December 2018** *Predictive Metagenomic Analysis of Autoimmune Disease*. Poster presentation at RSGDREAM 2018 conference, New York, NY
- **June 2017** *Impact of Short-Term Lifestyle Change on the Human Microbiome*. Poster presentation at American Society for Microbiology Microbe 2017 conference, New Orleans, LA
- **November 2015** *Comparison Between Population Receptive Field Sizes in Autistic Individuals and Neurotypical Controls*. Poster presentation at Annual Biomedical Research Conference for Minority Students 2015, Seattle, WA
- **August 2015** *Comparison Between Population Receptive Field Sizes in Autistic Individuals and Neurotypical Controls*. Poster presentation at MIT Summer Program in Biology and Neuroscience poster session, Cambridge, MA
- **August 2015** *Comparison Between Population Receptive Field Sizes in Autistic Individuals and Neurotypical Controls*. Poster presentation at MIT Center for Brains, Minds and Machines poster session, Cambridge, MA
- **March 2015** *From Chemotype to Genotype: 17-Hydroxycycloactatin*. Oral presentation at Undergraduate Research Conference, Hunter College, CUNY, New York, NY

RELEVANT GRADUATE LEVEL COURSEWORK

- Natural Language Processing with Representation Learning (DS-GA 1011)
- Deep Learning in Medicine (BMSC-GA 4493)
- Scientific Computing (CSCI-GA 2112)
- Machine Learning (BMSC-GA 4439)

PUBLICATIONS

- Kelly V. Ruggles, Jincheng Wang*, **Angelina Volkova***, Monica Contreras, Oscar Noya-Alarcon, Orlana Lander, Hortensia Caballero, Maria G. Dominguez-Bello. Changes in the Gut Microbiota of Urban Subjects during an Immersion in the Traditional Diet and Lifestyle of a Rainforest Village. *mSphere*, 2018; 3 (4).
- **Angelina Volkova**, Kelly V. Ruggles. Predictive Metagenomic Analysis of Autoimmune Disease. *In submission*.

AWARDS

- National Science Foundation Graduate Research Fellowship, March 2016
- ABRCMS Travel Fellowship, November 2015
- MIT Summer Research Fellowship, June 2015