DARIYA SYDYKOVA

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QUALIFICATIONS
- Four years experience analyzing models of molecular evolution to gain insights into the behavior and limitations of the models widely popular in the field
- Strong quantitative skills with an emphasis on bioinformatics, statistics, and mathematics
- Proficient in Python, R, and Unix with an ability to develop and conceptualize pipelines
- Strong written and communication skills with a passion for explaining complex topics to a non-expert
- Active in promoting STEM and recruiting underrepresented groups and women for STEM
- Fluent in Russian

EDUCATION
The University of Texas at Austin
Doctor of Philosophy, May 2019, Cell and Molecular Biology, advised by Dr. Claus O. Wilke
Graduate Portfolio Program in Applied Statistical Modeling, May 2019, Department of Statistics and Data Science
Bachelor of Science, May 2014, Computational Biology

SKILLS
Statistical methods: Continuous-time Markov chain models ● maximum likelihood inference ● principal component analysis ● linear regression ● logistic regression
Programming languages: Python ● Python packages: NumPy, SciPy, SymPy, keras, and Biopython ● R ● R packages: tidyverse, ggplot2 ● Unix command line ● some exposure to SAS, Matlab, Mathematica, and C.
Selected coursework: Graduate: Statistical Methods, Regression Analysis, Systems Biology and Bioinformatics ● Undergraduate: Biostatistics, Elements of Software Design, Elements of Computers/Programming, Probability, Intro to Mathematical Statistics, Scientific and Technical Computing, Computational Biology and Bioinformatics ● Workshops: Introduction to Deep Learning in R

RECENT EXPERIENCE AND PROJECTS
Graduate Research Assistant ● The University of Texas at Austin ● Austin, TX
Object detection for single-cell virology
- Trained a neural network in Python using keras to detect individual human cells in microscopy images
- Developed a pipeline in R that implemented the trained model to study Poliovirus replication and host interaction at single-cell resolution (the pipeline will be released as an R package) - *This approach improves on current methods in single-cell image analysis that use image segmentation to detect cells*

Analysis of models of molecular evolution
- Developed a theory and simulated the evolution of amino acid sequence in Python to determine how model choice affects maximum likelihood inference of site-specific rate of evolution (in press, *bioRxiv*) - *This theory explains previously unknown physical quantities that are measured by the rate of evolution*
- Conceptualized a pipeline to measure rates of evolution in protein-coding genes and to compare these rates with structural features of the expressed protein (published 2018, *F1000Research*) - *This pipeline laid out proper procedural and conceptual steps for analyzing protein evolution*
- Simulated sequence evolution in Python to establish the relationship between amino acid models and codon models of evolution (published 2017, *PeerJ*) - *This approach established a previously unknown relationship between amino acid and codon models of sequence evolution*

Undergraduate Research Assistant ● The University of Texas at Austin ● Austin, TX
Gene expression analysis
● Developed a pipeline to analyze differences in gene expression levels of *E.coli* grown in different conditions (published 2015 and 2017, *PLOS Computational Biology* and *Scientific Reports*) - *This pipeline was used as the backbone for gene expression analyses in a 6-year project sponsored by the US Department of Defense*

TEACHING EXPERIENCE
Department of Statistics and Data Science, The University of Texas at Austin
Teaching Assistant, Spring 2017, Spring 2018 and Spring 2019, Computational Biology and Bioinformatics course
Topics covered: data wrangling and visualization with tidyverse, logistic regression, cross validation, principal component analysis, k-means clustering, regular expressions, sequence alignment, python objects/classes
Half of the course is taught in R and half in Python
● Led discussion sessions as a teaching assistant to reinforce concepts learned in class
● Taught several main lectures when the lead professor was absent
● Assisted with in-class programming exercises during lectures

ACADEMIC HONORS AND AWARDS
● Summer 2018: Graduate School Summer 2018 Fellowship, The University of Texas at Austin
● Fall 2016: McNair Intellectual Entrepreneurship Internship, The University of Texas at Austin
● Fall 2015: McNair Intellectual Entrepreneurship Internship, The University of Texas at Austin
● Spring 2015: Honorable mention, National Science Foundation (GRFP)
● Spring 2014: Honorable mention, National Science Foundation (GRFP)

COMMUNITY OUTREACH
● Fall 2017: Mentor and research advisor for Crockett High School Internship Program
● Fall 2016: Mentor and graduate student panelist for McNair Scholars Program at St. Edward's University
● Spring 2015: Peer-led Biocomputing course teaching assistant and lecturer at The University of Texas at Austin
● Fall 2015: Mentor and graduate student panelist for McNair Scholars Program at St. Edward's University
● March 2015: Graduate student panelist for South Central Regional Conference organized by the Society of Asian Scientists and Engineers
● January 2014 - May 2015: Open coding hour volunteer for The Center of Computational Biology and Bioinformatics at The University of Texas at Austin
● October 2014: Graduate student panelist for Women in Science at The University of Texas at Austin
● Spring 2014: Peer-led Biocomputing course teaching assistant and lecturer at The University of Texas at Austin
● Summer 2012: ESL teaching assistant and youth academic support volunteer at El Buen Samaritano, Austin, TX