Michelle Buyanova
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Curriculum Vitae
Michelle Buyanova

Personal Details

Date of Birth: 1997/07/25

Citizenship: Russian Federation

Gender: Female

Scientific Interests

machine learning approach in context of structural bioinformatics; RNA/protein interactions; molecular modelling; algorithm design

Education

2015/09 – present

Faculty of Bioengineering and Bioinformatics, Lomonosov Moscow State University, Specialist degree (3rd year of combined BSc+MSc program in progress).

Research Experience

06/2018 – present

Intern at Insilico Medicine, Inc.

09/2017 – present

Virtual Structural Biology group (Golovin A. V., PhD, Doctor of Chemical Sciences; Zalevsky A. O., MSc, PhD student), Faculty of Bioengineering and Bioinformatics, Lomonosov Moscow State University
"In silico design of aptamer binding loops"

09/2016 – 04/2017

Virtual Structural Biology group (Golovin A. V., PhD, Doctor of Chemical Sciences; Zalevsky A. O., MSc, PhD student), Faculty of Bioengineering and Bioinformatics, Lomonosov Moscow State University
"Novel approach for structure-based prediction of zinc binding sites in biomolecules"

Awards

2017

Diploma for the best report in the section "Bioengineering and Bioinformatics" at the International Conference for Students and Young Scientists "Lomonosov"

Extracurricular Activity

09/2018

Interdisciplinary School and Conference ITaS (Information technologies and systems) 2018, poster session report
"Novel approach for structure-based prediction of zinc binding sites in biomolecules"

07/2017 – 08/2017

Kaggle contest participant, "Personalized Medicine: Redefining Cancer Treatment"

05/2017
Seminar at the "Voronovo" HSE Study Center, "Machine learning for bioinformatic data analysis"

Skills

Programming skills
Python, R, bash scripts

Python packages
numpy, pandas, scipy, scikit-learn, prody, biopython, matplotlib, seaborn, jupyter notebook

Bioinformatics skills
basic knowledge of bioinformatics algorithms and common databases; structural bioinformatics (PyMol, Jmol, 3DNA package, NUCPLOT); programms for sequence analysis and alignment (MEME suite, Jalview, BLAST, EMBOSS package, HMMER package), gene prediction, read mapping and genome assembly (bwa, velvet), phylogeny analysis (MEGA)

Machine learning skills
basic knowledge of theory and machine learning algorithms; experience with Python packages: scikit-learn, keras, xgboost, CatBoost

Other skills
HTML/CSS, LaTeX, git basics

Languages
Russian (native), English (fluent)