

# Anastasiia Kazovskaia

Current location: Hong Kong SAR

Email: [akazovskaia@connect.ust.hk](mailto:akazovskaia@connect.ust.hk)

Telegram: [@Chickypicky](https://www.instagram.com/Chickypicky)

Skype: [kazovskayan13](https://www.skype.com/people/kazovskayan13)

Phone number: +852 6844 8483

GitHub: [Chicky-Picky](https://github.com/Chicky-Picky)

## Research interests

- Time Series, Mathematical Statistics
- Machine Learning, Deep Learning
- Bioinformatics

## Education

<b>St Petersburg Governor's Physics and Mathematics Lyceum No. 30</b> <i>Computer graphics support group</i>	St Petersburg, Russia 2016 – 2018
<b>St Petersburg State University, Bachelor's degree</b> <i>Faculty of Mathematics and Computer Science, Data Science</i>	St Petersburg, Russia 2018 – 2022
<b>Bioinformatics Institute, one-year program</b> <i>Program «Algorithmic Bioinformatics»</i>	St Petersburg, Russia 2022 – 2023
<b>St Petersburg State University, MPhil degree</b> <i>Faculty of Mathematics and Computer Science, SDDS</i>	St Petersburg, Russia 2022 – 2024
<b>Hong Kong University of Science and Technology, PhD degree</b> <i>Department of Mathematics</i>	Hong Kong SAR 2023 – current

## Research activities

- [Winning the research competition](#):  
«Multidimensional analogues of Poisson service systems»: *a generalisation of the Poisson service system model for the case of «multidimensional» time is presented and the characteristics of the obtained generalised model are calculated*
- Bachelor's graduation research (Supervisor: [Mikhail Lifshits](#)):  
«Multidimensional stable telecom process and related limit theorem»: *a generalisation of the stable telecom process and the associated limit theorem for the case of «multidimensional time» is presented*
- MPhil graduation research project at [Biomolecular NMR Laboratory \(St Petersburg State University\)](#) (Supervisor: [Nikolai Skrynnikov](#)):  
[Prediction of protein-protein binding affinity](#): *transfer learning approach with GNN and ESM embeddings for dissociation constant prediction*

## Software activities

- [XXVI Russian scientific conference of students «Intellectual revival»](#):  
«Design and implementation of a system for visualizing three-dimensional scenes in real time»
- Android application:  
[«Vectorization of raster images of elementary shapes»](#)
- Software project:  
[«CBS Basics and enhancements. Conflict-Based Search Algorithms for Multi-Agent Pathfinding problem»](#)

## Achievements

- School:
  - Certificate of distinction graduation: GPA is 5.0 / 5.0
- Bachelor's degree:
  - «Yandex» scholarship for the entire period of study
  - Diploma with distinction: GPA is 4.75 / 5.0
- Bioinformatics Institute:
  - Diploma: GPA is 5.0 / 5.0
  - Certificate for the best academic results among all students
- Master's degree:
  - «VKontakte» scholarship
  - Diploma with distinction: GPA is 3.9 / 4.0
- PhD:
  - [Hong Kong PhD Fellowship Scheme](#) awardee
  - 2023-2024 MATH Best Teaching Assistant

## Employment

- Tutor:
  - For high school students (2019 – 2023): *Mathematics, Physics, Computer Science, Programming*
  - For UG students (2021 – 2023): *Mathematics, Computer Science, Programming*
  - For graduates (2021 – 2023): *English*
- JetBrains Academy (2020 – 2021): *Author of educational articles, tasks, and projects on Mathematics*
- Teaching Assistant:
  - MATH4425 Introductory Time Series: *Spring 2023-24, Spring 2024-25*
  - MATH4423 Nonparametric Statistics: *Fall 2024-25*

## Skills

- **Languages:** Russian (native), English (C1)
- **Software:**
  - Python, R, C/C++, Kotlin
  - PostgreSQL, SAS
  - git, bash
  - $\text{\LaTeX}$
  - HTML, CSS, JavaScript
  - OpenGL, GLSL

- **Subjects:**

- Time Series, Mathematical Statistics, Stochastic Processes, Probability Theory
- Machine Learning, Deep Learning, Smart Video Systems, Natural Language Processing
- Computer Science, Heuristic Search
- Bioinformatics
- Computer Algebra, Computational Geometry
- Web-technologies

## Publications

- [PCANN Program for Structure-Based Prediction of Protein–Protein Binding Affinity: Comparison With Other Neural-Network Predictors](#): *a new structure-based affinity predictor for protein–protein complexes*