

# Nicholas Attila Kovacs

STRUCTURAL BIOINFORMATICIST & DATA SCIENTIST

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## Summary

- Adaptive computational scientist with an experimental background that enjoys learning and mastering new skills and technologies.
- Excellent team player and collaborator in computational and experimental research which have resulted in 6 peer-reviewed publications.
- Effective and confident science communicator, both oral and written, making scientific concepts accessible to audiences of diverse backgrounds.

## Education

**Ph.D. Bioinformatics** GPA: 3.47

GEORGIA INSTITUTE OF TECHNOLOGY

Atlanta, GA

Aug 2013 - Fall 2018 (expected)

**B.S. Biochemistry and Molecular Biology/Biotechnology** GPA: 3.23

MICHIGAN STATE UNIVERSITY

East Lansing, MI

Aug 2008 - May 2012

## Experience

**Graduate Research Assistant**

GEORGIA INSTITUTE OF TECHNOLOGY

Atlanta, GA

Aug 2013 - Current

**Dissertation:** *Data Mining the Atomic Structure of the Ribosome to Unravel the History of Protein Folding*

- **Summary:** Analyzed atomic structures of ribosomes comprised of over 400,000 atoms, using structural bioinformatics and machine learning.
- **Results:** 1<sup>st</sup> first-author research article published, 2<sup>nd</sup> is submitted, and 3<sup>rd</sup> in preparation.
- **Collaboration:** Coauthored 2 experimental and 3 computational research articles. 3<sup>rd</sup> computational coauthored research article under review.
- **Communication:** Independently wrote NSF grant to support summer research at National Taiwan University, including RT flights and housing. Presented research as oral and poster presentations at 7 scientific conferences domestically and internationally.
- **Mentoring:** Awarded conference and travel funding for mentoring undergraduate student.

**Atomic Interaction Network Analysis of the Ribosome**

COURSE PROJECT FOR CS 7280 - NETWORK SCIENCE

Atlanta, GA

Fall 2017

- Collaborated with a team member to apply course concepts and algorithms to 3 interaction networks of the ribosome, each composed of more than 100,000 non-covalent interactions (edges) between approx. 50,000 atoms (nodes).
- **Results:** Predicted RNA and protein folding domains within the ribosome by applying community detection algorithms.

**Analysis and Interpretation of NGS Data from CDC**

COURSE PROJECT FOR BIOL 7210 - COMPUTATIONAL GENOMICS

Atlanta, GA

Spring 2015

- Worked in multidisciplinary teams of biologists and computer scientists to analyze NGS reads provided by the CDC.
- Analyzed 97 genomic single-end and paired-end reads of *Neisseria meningitidis*, *Haemophilus influenza*, and *Haemophilus haemolyticus* generated from GAI or Illumina HiSeq/MiSeq instruments.
- **Results:** Developed a typing-tool that identifies the organism and its serotype/serogroup from fasta file inputs and constructed a genome browser of 53 annotated genomes.

**Graduate Teaching Assistant**

GEORGIA INSTITUTE OF TECHNOLOGY

Atlanta, GA

9 Semesters

- **Biophysical Chemistry Lab(CHEM 4582)** - 6 semesters - Instructed 8 undergraduate students per semester on experimental and computational biophysical chemistry protocols.
- **Macromolecular Structure(CHEM 6572)** - 2 semesters - Directed a graduate class of approx. 25 students on the use of computational modelling programs. Graded assignments.
- **Survey Biochemistry(CHEM 3511)** - 1 semester - Guided a class of approx. 40 undergraduate students on the solution to assignment problems in weekly recitation. Graded homework and exams.

## Skills

### Programming

Python, Perl, Bash, SQL, R, Javascript, MATLAB, HTML, CSS

### Python Packages

Numpy, Pandas, Scipy, SK-Learn, Matplotlib, Seaborn, Plotly, NetworkX, igraph, Biopython

### Machine Learning

Linear Regression, SVM, Decision Trees, Random Forest, KNN, K-Means, PCA, Community Detection

### Structural Bioinformatics

PyMOL, Maestro, PyRosetta, VMD, NAMD, AutoDock, MODELLER

### Computational Genomics

de Novo Genome Assembly, SAMtools, BCFtools, VCFtools, bwa, GATK, JBrowse

### OS and Programs

Ubuntu, RHEL, Windows, Amazon Web Services, Microsoft Office, Adobe Illustrator, Git, Cytoscape