

# Nicholas Attila Kovacs

BIOINFORMATICIST & DATA SCIENTIST

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## Expertise

- Computational biologist aspiring to be a biopharmaceutical consultant and scientific diplomat
  - Presented research as oral and poster presentations at conferences in Tokyo, Central Vietnam, and US
  - Independently wrote and awarded NSF grant to conduct summer research in Taipei, Taiwan
  - Two 1<sup>st</sup>-author scientific publications with 3<sup>rd</sup> in preparation
  - Coauthor of 7 scientific publications
  - Managed 8 senior undergraduates per semester for 6 semesters as a teaching assistant for a biophysical chemistry lab course

## Education

**Ph.D. Bioinformatics** GPA: 3.5

GEORGIA INSTITUTE OF TECHNOLOGY

Aug 2013 - Dec 2018

Atlanta, GA

**B.S. Biochemistry and Molecular Biology/Biotechnology** GPA: 3.3

MICHIGAN STATE UNIVERSITY

Aug 2008 - May 2012

East Lansing, MI

## Experience

**Graduate Research Assistant**

GEORGIA INSTITUTE OF TECHNOLOGY

Aug 2013 - Current

Atlanta, GA

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

- **Summary:** Applied structural bioinformatics and machine learning algorithms to atomic coordinate datasets from over 100 biomolecules composed of 150,000-200,000 atoms to unravel the interrelatedness and diversification of life.
- **Results:** Two 1<sup>st</sup>-author research articles published. 3<sup>rd</sup> in preparation.
- **Collaboration:** Coauthored 2 experimental and 4 computational research articles.
- **Communication:** Independently wrote and awarded \$7,000 NSF grant to support summer research in Taiwan. Oral and poster presentations at 7 domestic and international scientific conferences.
- **Mentoring:** Awarded \$2,500 conference and travel funding for mentoring undergraduate student.
- **Courses:** 9 courses in biochemistry, computational biology, statistics, and computer science. Concept-to-Market business short-course completed.

**Atomic Interaction Network Analysis of the Ribosome**

COURSE PROJECT FOR CS 7280 - NETWORK SCIENCE

Fall 2017

Atlanta, GA

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

**Graduate Teaching Assistant**

GEORGIA INSTITUTE OF TECHNOLOGY

Aug 2013 - Dec 2016

Atlanta, GA

- **Biophysical Chemistry Lab(CHEM 4582)** - 6 semesters - Instructed ~8 undergraduate students on experimental and computational protocols.
- **Macromolecular Structure(CHEM 6572)** - 2 semesters - Directed ~25 graduate students on the use of computational modelling programs.
- **Survey of Biochemistry(CHEM 3511)** - 1 semester - Guided ~40 undergraduate students to solve homework problems in weekly recitation.

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

COURSE PROJECT FOR BIOL 8803B - PROGRAMMING FOR BIOINFORMATICS AND BIOL 7210 - COMPUTATIONAL GENOMICS

Aug 2014 - May 2015

Atlanta, GA

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

## Skills

### Programming

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

### Python Packages

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

### Machine Learning

Linear Regression, Logistic 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 Software

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