Nicholas Attila Kovacs

Structural Bioinformaticist

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Expertise

- Exceptional communication skills and outgoing personality
  - 5 oral and 2 poster presentations at international and domestic scientific conferences
  - Two 1st author publications. 3rd in preparation
  - Independently wrote and awarded NSF grant to conduct summer research in Taiwan
- Enjoys working in multidisciplinary teams and teaching others
  - Coauthored 6 scientific publications with computational and experimental scientists
  - Applied and awarded materials and travel money for mentoring an undergraduate student
  - Managed 8 senior undergraduates per semester as a teaching assistant for biophysical chemistry lab

Education

Ph.D. Bioinformatics GPA: 3.47 — *Atlanta, GA*
Georgia Institute of Technology — *Aug 2013 - Fall 2018 (expected)*

B.S. Biochemistry and Molecular Biology/Biotechnology GPA: 3.23 — *East Lansing, MI*
Michigan State University — *Aug 2008 - May 2012*

Experience

Graduate Research Assistant
Atlanta, GA
Georgia Institute of Technology — *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**: Two 1st author research articles published. 3rd in preparation.
- **Collaboration**: Coauthored 2 experimental and 4 computational research articles.
- **Communication**: Independently wrote NSF and awarded grant to support summer research in Taiwan. Oral and poster presentations at 7 domestic and international scientific conferences.
- **Mentoring**: Awarded conference and travel funding for mentoring undergraduate student.

Atomic Interaction Network Analysis of the Ribosome
Atlanta, GA
Course Project for CS 7280 - Network Science — *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 amino acid residues (nodes).
- **Results**: Predicted RNA and protein folding domains within the ribosome by applying community detection algorithms.

Analysis and Interpretation of NGS Data from CDC
Atlanta, GA
Course Project for BIOL 7210 - Computational Genomics — *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*, *Haempophilus influenza*, and *Haemophuilus haemolyticus* generated from GAII 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
Atlanta, GA
Georgia Institute of Technology — *9 Semesters*

- **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.

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, 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, Amazon Web Services, Microsoft Office, Adobe Illustrator, Git, Cytoscape