Nicholas Attila Kovacs
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 collaborater 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 *Atlanta, GA*
Georgia Institute of Technology *Aug 2013 - Fall 2018 (expected)*

B.S. Biochemistry and Molecular Biology/Biotechnology *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**: Applied machine learning alogrithms to atomic structures of ribosomes comprised of over 50,000 residues, each with greater than 15 features to predict how proteins evolved over billions of years. Published 1 first-author paper. 2nd and 3rd first-author papers coming soon.
- **Collaboration**: Coauthored 2 research papers with experimental labmates. Coauthored 2 more research papers with computational labmates.
- **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 *Atlanta, GA*
Project for CS 7280 - Network Science *Fall 2017*
- Collaborated with a team member to apply course concepts and algorithms to 3 interaction networks of more than 100,000 non-covalent interactions (edges) between over 50,000 atoms (nodes).
- **Results**: Predicted RNA and protein folding domains by applying community detection algorithms.

Analysis and Interpretation of NGS Data from CDC *Atlanta, GA*
BIOL 7210 - Computational Genomics *Fall 2014 and 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 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