

# Nicholas Attila Kovacs

## BIOINFORMATICIST & DATA SCIENTIST

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## Profile

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I am a computational biologist graduating from Georgia Tech in December 2018 that is applying for the position Research Scientist Comp/Informatics at the J. Craig Venter Institute so that I can continue diving deeper into computational genomics and structural bioinformatics while elucidating the links between molecular evolution, cellular metabolism, and ecosystem biogeochemistry. In addition to my hard skills gained as a PhD candidate which included my dissertation that answered fundamental biological questions using the scipy stack, and coursework in genomics and computer science, I developed the following soft skills: team leading experience gained as a laboratory-course teaching assistant, mentoring experience through a graduate-undergraduate mentoring scholarship program, public speaking experience from presentations at international and domestic conferences, project management skills via providing computational analyses for five coworkers' projects during PhD candidacy, and written communication skills sharpened through academic journal article and grant writing.

## Education

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### Ph.D. Bioinformatics – GPA: 3.47

GEORGIA INSTITUTE OF TECHNOLOGY

- Awarded 2017 NSF East Asia and Pacific Summer Institutes Scholarship for Research in Taipei, Taiwan

Aug 2013 - Dec 2018

Atlanta, GA

### B.S. Biochemistry and Molecular Biology/Biotechnology – GPA: 3.22

MICHIGAN STATE UNIVERSITY

Aug 2008 - May 2012

East Lansing, MI

## Experience

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### Graduate Research Assistant

GEORGIA INSTITUTE OF TECHNOLOGY - ADVISOR: DR. LOREN WILLIAMS

Aug 2013 - Current

Atlanta, GA

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

- Summary:** The origin of life is found within the structure of the ribosome, the archaeal ribosome is found within the eukaryotic ribosome, and species across life's 3 domains contain a ribosomal common core composed of RNA and protein.
- Results:** Two, 1<sup>st</sup>-author research articles published, third 1<sup>st</sup>-author research article in preparation.
- Funding:** NASA Astrobiology Institute
- Collaboration:** Computational analysis for coworkers' projects resulted in coauthor of 2 experimental and 3 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:** 4 Biochemistry, 3 Biology, 3 Computer Science, 3 Korean, and 1 Math courses taken or audited. 1 certification for Business course.

### Atomic Interaction Network Analysis of the Ribosome

COURSE PROJECT FOR CS 7280 - NETWORK SCIENCE

Aug 2017 - Dec 2017

Atlanta, GA

- Collaborated with a team member to apply course concepts and algorithms to PhD project data consisting of 3 atomic interaction networks of 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 GAI 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.

## Publications

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- (9) **Kovacs, N. A.**, Penev, P. I., Chivukula, V., Petrov, A. S., Williams, L. D. “Ribosomal Protein Structure: Deep Evolution”, In preparation
- (8) **Kovacs, N. A.**, Penev, P. I., Venapally, A., Petrov, A. S., Williams, L. D. “Circular Permutation Obscures the Universality of a Ribosomal Protein”, *J. Mol. Evol.* 86, pgs 581-592 (2018)
- (7) Bernier, C.R., Petrov, A. S., **Kovacs, N. A.**, Penev, P. I., Williams, L. D. “Translation: The Universal Structural Core of Life”, *Mol. Biol. Evol.* 35, pgs 2065-2076 (2018)
- (6) Gómez Ramos, L. M., Degtyareva, N. N., **Kovacs, N. A.**, Holguin, S. Y., Jiang, L., Petrov, A. S., Biesiada M., Hu, M. Y., Purzycka, K. J., Arya, D. P., Williams, L. D. “Eukaryotic Ribosomal Expansion Segments as Antimicrobial Targets”, *Biochemistry* 56, pgs 5288-5299 (2017)
- (5) **Kovacs, N.A.**, Petrov, A.S., Lanier, K.A., and Williams, L.D. “Frozen in Time: The History of Proteins”, *Mol. Biol. Evol.* 34, pgs 1252-1260 (2017)
- (4) Gómez Ramos, L.M., Smeekens, J.M., **Kovacs, N.A.**, Bowman, J.C., Wartell, R.M., Wu, R., and Williams, L.D. “Yeast rRNA Expansion Segments: Folding and Function”, *J. Mol. Biol.* 428, pgs 4048-4059 (2016)
- (3) Petrov, A.S., Gulen, B., Norris, A.M., **Kovacs, N.A.**, Bernier, C.R., Lanier, K.A., Fox, G.E., Harvey, S.C., Wartell, R.M., Hud, N.V., and Williams, L.D. “History of the Ribosome and the Origin of Translation”, *Proc. Natl. Acad. Sci. U.S.A.* 112, pgs 15396-15401 (2015)
- (2) Petrov, A.S., Bernier, C.R., Hsiao, C., Norris, A.M., **Kovacs, N.A.**, Waterbury, C.C., Stepanov, V.G., Harvey, S.C., Fox, G.E., Wartell, R.M., Hud, N.V., and Williams, L.D. “Evolution of the Ribosome at Atomic Resolution”, *Proc. Natl. Acad. Sci. U.S.A.* 111, pgs 10251-10256 (2014)
- (1) Sharma, M., Predeus, A.V., **Kovacs, N.A.**, and Feig, M. “Differential Recognition Specificities of Eukaryotic MutS $\alpha$  and MutS $\beta$ ”, *Biophys. J.* 106, pgs 2483-2492 (2014)

## Skills & Interests

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<b>Clubs</b>	GaTech PhD2Consulting Club, Bioengineering & Bioscience Unified Grad Students, Data Science for Scientists
<b>Computational Acumen</b>	Python, R, SQL, Bash, Perl, MATLAB, Javascript, Git, PySpark, Tableau, Adobe
<b>Computational Sciences</b>	Structural Bioinformatics, Next-Generation Sequencing, Molecular Dynamics, Drug Docking
<b>Data Science</b>	Machine Learning, Network Science, Statistics, Software Engineering
<b>Experimental Sciences</b>	Molecular Biology, Biochemistry, Organic Chemistry, Analytical Chemistry
<b>Personal Interests</b>	Bodyweight Fitness, Yoga, Nutrition, Snowboarding, Guitar, Bachata Dance, Korean Culture