

Nicholas Attila Kovacs

BIOINFORMATICIST & DATA SCIENTIST

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Application for Research Scientist Comp/Informatics

Dear Hiring Staff at the Microbial and Environmental Genomics group at JCVI West,

About Me

Transitioning from an experimental, bench-top biochemist in undergrad to a computational biologist in graduate school is a transition I am very proud of because I became the go-to guy in my lab and department to analyze data which led to my involvement in a diverse range of projects spanning drug development, nanoparticles, and the origin and diversification of life. I chose my PhD project because I wanted to work on answering the question that inspired me to pursue a career in science, “how did life originate and evolve?”. My published research articles include first-author publications on the evolution of protein folding, as well as coauthored publications concerning the evolution of ribosomal RNA, the development of anti-fungal therapeutics, and molecular simulations of DNA repair enzymes. In my 3rd, 1st-author publication of my PhD, I compare more than 400 ribosomal structures that are available on the Protein Data Bank to reveal the evolution of protein-protein interactions.

My favorite courses I have taken are “Programming for Bioinformatics” and “Computational Genomics”. In programming for bioinformatics, I completed assignments in bash and perl that taught me good practices and familiarized me with basic bioinformatics software such as Bioperl and BLAST. In computational genomics, I worked in teams to assemble genomes and identify the species and strains from which they were isolated from via Hi-Seq NGS reads provided by the CDC. I also really enjoyed two computer science graduate courses which I completed in my preferred programming language, Python; in Computing for Bioinformatics, I learned data structures and how to design efficient algorithms, and in Network Science I identified network motifs in protein-protein interaction data and did a pandemic analysis on epidemiology data. I was awarded an “A” in all 4 of these courses.

Why the position Research Scientist Comp/Informatics?

The Microbial & Environmental Genomics group at the J. Craig Venter Institute provides an excellent environment for a postdoc to continue answering fundamental biological questions that will have a big impact on our understanding of biology. As a Research Scientist Comp/Informatics, I would undertake evolutionary and ecological analyses of various genomic and transcriptomic datasets in the area of microbial oceanography and biotechnology to evaluate the metabolism and patterns of genome evolution and adaptation in various environments. I would elucidate the links between molecular evolution, cellular metabolism, and ecosystem biogeochemistry by applying comparative genomics tools related to the informatics analysis of protein structure and associated within and between lineage domain recombinations. This would be an incredibly exciting project that would increase my skills and interests in bioinformatics, microbial ecology, and evolution.

Why Me?

I am a productive and interdisciplinary scientist that works well in multidisciplinary teams and has a strong desire to continue answering fundamental biological questions. I like to stay up to date with new technologies, adhere to reproducibility and version control, and love teaching others. Having recently been awarded a PhD in bioinformatics with a minor in biochemistry, I am eager to apply my expertise to new problems, while improving my foundational skills and learning new methodologies. The position of Research Scientist Comp/Informatics at the JCVI fits very well with what I want to do as an early-career scientist and my skills and interests are more than sufficient for the required and preferred qualifications. My desired start date is approximately February 1, 2019.

Sincerely,

Nicholas Attila Kovacs