

January 31, 2014

GATP Selection Committee  
UCLA Department of Human Genetics  
6506 Gonda (Goldschmied) Research Center  
Los Angeles, CA 90095-7088

Dear GATP Selection Committee,

From the moment I decided to return to school in 2008, I knew for the first time in my life what I wanted to commit my life to. Coming from a scientific and mathematical background, I had had great difficulty in figuring out what I wanted to do with my life. Everything seemed interesting: medicine, physics, math, biology, engineering, computer science. So when I realized I could quite literally work in all those fields, while keeping my studies focused, I was thrilled.

After my undergraduate career at UCLA was over (I majored in Pure Mathematics and Computational and Systems Biology), I was hired by one of my former professors, Dr. Matteo Pellegrini, to do research in his lab. Little did I know how little I knew. I was completely floored by how immense and complex the field of bioinformatics was. But, I hunkered down and I learned. And learned. I developed new methods of solving known problems, I collaborated with stem cell research labs, studied methylation and epigenomics, and ended up as co-author on multiple papers. Most of my work was in RNA Seq, a rather well-studied subfield in bioinformatics. Because it is a relatively new field, scientists are still trying to figure out how to tackle the more difficult problems in it. While I saw many of the shortcomings of the current approaches, whenever I tried to solve the problems myself, I would inevitably hit a wall, as I simply did not have the knowledge to get past a certain point.

So I decided to learn more, and applied to the Bioinformatics Ph.D. program here at UCLA. As is custom for first year students, each quarter I am rotating with a different PI, in part to decide which laboratory to do my thesis in, and in part to get a more rounded understanding of the huge field. Last quarter was my first. Working with Dr. Bogdan Pasaniuc in population genetics has given me a view of genomics that I had never seen: looking at the genetics of thousands of individuals to detect patterns of inheritance and structure in populations. In my classes, I learned what I call “the black arts” of mathematics – algorithms and methods so ingenious and powerful that they’re used in essentially all of bioinformatics sub-disciplines. This quarter, I’m rotating with Dr. Eleazar Eskin, in the department of Computer Science. I’m studying more complex methods (such as linear mixed models) and multivariate statistics in order to detect very small signals in very noisy data.

Next quarter, I’m planning on rotating with a relatively new faculty, Dr. Jason Ernst. I will be working with Dr. Ernst and another Bioinformatics Ph.D. student on non-coding RNA, which fascinates me. Although much of the genome (99%) does not code for

proteins, a large portion is used to modulate and control transcription signals. Coming from my undergraduate major of Systems Biology, this is particularly interesting to me; the vast network suppression and enhancement is possibly a greater influence on what makes us than our actual genome.

Because Dr. Ernst's lab focuses mostly on method development, to come up with better methods I will need to take more classes: advanced algorithms, machine learning, and stochastic methods. If I am awarded this grant, I will be fulfilling my greatest aspirations in life: working on interesting mathematical problems and applying it to biology to ultimately help save lives.

Thank you very much for your consideration.

Sincerely,

Artur Jaroszewicz  
Ph.D. candidate