

Alejandro D. Meruelo

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Birth

January 25th, 1984 (New York, NY)

Education

Ph.D., Biology, Caltech or UCLA (Expected)

M.D., Medicine, UCLA (Expected)

B.S., Physics (Cumulative GPA: 4.0; Physics GPA: 4.1), Caltech, 2006

Honors and Awards

NIH Medical Scientist Training Program Fellowship, UCLA-Caltech, 2006-2014

President's Scholar (full tuition scholarship), Caltech, 2002-2006

Award of Excellence, Caltech, 2005-2006, 2004-2005, 2003-2004

Mellon Mays Undergraduate Fellowship, Caltech, 2004-2006

Holt Ashley Summer Undergraduate Research Fellowship, Caltech, 2004

Summer Undergraduate Research Fellowship, Caltech, 2003

Caltech/Irvine Foundation Scholar, Caltech, 2002

Valedictorian, Hackley School, 2002

Cum Laude Society Member, Hackley School, 2002

The Class of 1921 Scholastic Achievement Cup - To the senior with the highest achievement in his or her final year, Hackley School, 2002

The Stanley Pennock Prize in Science, Hackley School, 2002

Mrs. Frederick W. Sherman Book Prize in Mathematics, Hackley School, 2002

Mrs. Frederick W. Sherman Book Prize in Modern Languages, Hackley School, 2002

Departmental Honors in Mathematics, Modern Languages, and Science, Hackley School, 2002

National AP Scholar, Hackley School, 2002

New York State Education Department Scholarship for Academic Excellence, Hackley School, 2002

Certificate for Scholarship from the Lower Hudson Council of School Superintendents, Hackley School, 2002

Hackley School Commendation of Service Award - For Extraordinary Commitment to Community Service, Hackley School, 2002

Harvard Book Award - To the junior with the highest academic average in the junior year, Hackley School, 2001

Yale Book Award - Awarded to the junior who exhibits outstanding personal character and intellectual promise, Hackley School, 2001

National Hispanic Scholar, Hackley School, 2001

Middle School Computer Science Award, Hackley School, 1998

Research Experience

Researcher

Summer 2007

James U. Bowie

University of California Los Angeles, LA, CA

SAM (sterile alpha motif) domains are a common motif in the protein-protein interaction universe and are characterized by a diversity of functions. I developed a computational method combining homology and comparative genomic techniques to discriminate homopolymeric SAM domains from other classes on the genome-wide scale. Polymeric prediction true positive rate was 100% while false positive rate was 8%. This method may be more widely applicable to prediction of homopolymers in other protein domains. The 8-week work resulted in a manuscript to be submitted for publication.

Researcher

Winter 2006

John M. Allman

California Institute of Technology, Pasadena, CA

I examined the differences between humans and chimpanzees by surveying available literature of microarray, northern blot, RT quantitative PCR, in-situ hybridization, and MRI work done. Specifically, I learned about the great deal of evidence explaining that while the genomic sequences of humans and chimps are very similar, we differ dramatically in terms of gene expression and this likely accounts for the qualities that make us uniquely human and susceptible to a different array of diseases.

Researcher

Summer 2005 - Spring 2006

Hideo Mabuchi

California Institute of Technology, Pasadena, CA

I studied the determination of function from sequence of DNA and RNA through their secondary structure kinetics. Specifically, I applied an approach from control theory that used the Kalman decomposition and balanced truncation algorithms to approximate the kinetics of large systems. The most immediate result of this work was a MATLAB program for accurately computing effective transition rates between initial and final states of large systems. I then studied the kinetics of 3- and 4-state systems using transition-rate matrices and Jordan forms to understand macroscopic structure. Finally, I studied the topology of large systems to learn more about their underlying microscopic structure. Thus a better understanding of the relationship between macroscopic and microscopic structure was gained and a foundation laid to understand the secondary-structure kinetics theory of real biological systems.

Researcher

Summer 2004

Paul W. Sternberg

California Institute of Technology, Pasadena, CA

I extended the work of the prior summer by expanding and refining the program developed in order to perform three-way parallel genome-wide searches under a friendly graphical user interface with the ability to explore relationships in both sequence having and lacking annotation (using the BLAST search algorithm), thus providing the end user with additional flexibility and power. Experimental work of the prior summer was continued in addition to pursuing new findings resulting from the extension of the program to an additional genome. Thus growth of *E. coli* cultures, worm injection and care, PCR purification, gel extraction, DNA purification, and fast-GFP fusion primer design were practiced once again, in addition to GFP expression analysis.

Researcher

Summer 2003

Paul W. Sternberg

California Institute of Technology, Pasadena, CA

I designed an open-source bioinformatics tool to perform parallel genome-wide searches for different configurations of clusters of sequence elements and to filter and enrich the dataset on the basis of orthologous relationships and gene function information shared between the genomes searched. I gained experience with growth of *E. coli* cultures, worm injection and care, PCR purification, gel extraction, DNA purification, and fast-GFP fusion primer design while working on the project to test resulting matches from the program.

Researcher

Summer 2002

Stephen R. Quake

California Institute of Technology, Pasadena, CA

I worked with a colleague to produce a four-dimensional phase-space mapping of the valve closing pressure versus channel dimensions and spin speeds for Sylgard PDMS microfluidic chips and contributed to the theory describing these chips' behavior. In doing so I became familiar with the microfabrication process, learning to design and manufacture the chips using wafer molds and by working in a 1000 ppm clean room.

Work Experience

Film and DVD Editor

February 2006

UCLA School of Medicine, Los Angeles, CA

During block 3, I filmed the DGSOM Class of 2010 Talent Show and produced a 2 DVD set that netted over \$700 as a class fundraiser.

Network and Hardware Technical Assistant

2000-2002

Hackley School, Tarrytown, NY

During my junior and senior years of high-school I expanded the Hackley Macintosh Laboratory with upgrades and new technology through different projects that focused on everything from wireless networking to videoconferencing. In one project, I deployed and managed a campus-wide Airport network for the school. I also managed and worked to resolve problems with the campus-wide network.

Assistant to Network Administrator

Summer 1999

NYU School of Medicine, New York, NY

I supported the network administrator and interphased with users to resolve a variety of problems as they arose.

Programmer

Summer 1998

NYU School of Medicine, New York, NY

I wrote the program for a hand-held device that physicians use at the patient's bedside to enter clinical histories and access some of the school's databases to improve the clinical care they provide.

Clinical Experience

Medical Student

2006-2007

UCLA School of Medicine, Los Angeles, CA

I have shadowed in several areas including doing chaplain rounds on the wards of UCLA's main hospital, observed a schizophrenic patient at the VA in LA, and have seen a couple of patients in neurology (multiple sclerosis, spinal shock). I also have participated in workshops in pediatrics and geriatrics. My most valuable experience thus far has been working at a family practice office (UCLA Medical Center in Santa Monica) for this past year where I conducted 15 minute patient interviews with appropriate physical exam maneuvers, wrote up and orally reported on cases, and explored possible differential diagnoses.

Technical Experience

Programming

Perl/CGI & Objective Perl

C, C++, Objective C

Java

Cocoa

NewtonScript

LaTeX

HTML

Systems

Mac OS

Windows

UNIX

Linux

Applications

Scientific

Mathematica

MATLAB

Maple

Design

Bryce

Carrara

Dreamweaver

Director

FormZ

ElectricImage

Final Cut Pro

Flash

GoLive

Illustrator

InDesign

Photoshop

Premiere

Other Skills

Black Belt in Taekwondo (including Two Gold Medals at the NY State Governor's Cup)

Beginning German (1 year in college)

Intermediate Spanish (6 years in high-school, including AP Language, Literature)

Publications

Meruelo AD and Bowie JU. A computational approach to identifying polymer SAM domains. Manuscript in preparation.

Hwang BJ, Meruelo AD, and Sternberg PW. *C. elegans* EVI1 proto-oncogene, EGL-43, is necessary for Notch-mediated cell fate specification and regulates cell invasion. *Development*. 2007;134:669-79.

Alejandro D. Meruelo

Abstracts

Meruelo AD, Hwang BJ, and Sternberg PW. A bioinformatical technique for the identification and exploration of gene interactions using *C. elegans*, *C. briggsae*, and *C. remanei*. Presented at SURF Summer Seminar Day, Pasadena, CA, August, 2004.

Meruelo AD, Hwang BJ, and Sternberg PW. A bioinformatical approach to genome-wide identification of lin-3 regulatory sites across *C. elegans* and *C. briggsae*. Presented at SURF Summer Seminar Day, Pasadena, CA, August, 2003.

Talks

“A bioinformatical technique for the identification and exploration of gene interactions using *C. elegans*, *C. briggsae*, and *C. remanei*.” Presented at SURF Summer Seminar Day, Pasadena, CA, August, 2004.

“A bioinformatical approach to genome-wide identification of lin-3 regulatory sites across *C. elegans* and *C. briggsae*.” Presented at SURF Summer Seminar Day, Pasadena, CA, August, 2003.

Goals and Objectives

My goal is to become an expert in systems biology, especially in bioinformatics. I plan to combine broad training in several areas (biology and/or chemistry, medicine, bioinformatics, and physics) to achieve novel insights at the interface between some of these fields (e.g., structural genomics, chemical informatics). I envision combining both experimental and computational approaches to understand human disease and help develop therapies and drugs to reverse the mechanisms of disease. In the future, I would like to be running a laboratory doing cutting-edge research at a thriving medical center or at the NIH. I see myself as holding a significant leadership role, both in mentoring budding scientists and breaking ground in my area of expertise.