Michael Dacre

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Research Experience

Research Professional, Stanford University

Stanford, CA — January, 2012 – Present

My research at Hunter Fraser's lab has focused on investigating the intersection between changes in various aspects of gene expression and pathological states.

Fine Mapping of Causal Variants

A big problem in molecular biology is the identification of single causal variants associated with a phenotype. The reason for this is that vertebrates inherit alleles from their two parents in blocks (known as linkage disequilibrium); the result is that even with excellent power, it is impossible to resolve associations down to the single variant level. We are addressing that problem by sequencing 1000 cell lines in 10 different human populations using the ATAC-seq protocol (to identify chromatin accessibility). We can then use the differences in linkage disequilibrium between populations to attempt to identify causal variants. I am currently working on a statistical framework to successfully identify those variants.

Major Depressive Disorder

Very little is known about the pathophysiology of major depressive disorder (MDD), or how it is inherited, despite increasing evidence that it is more than just a psychological phenomenon. I have been re-analyzing RNA-sequencing data from the work by Battle *et al.* (2014) to ascertain if the major depressive disorder can be partially explained by variation in the abundance of alternate splice-forms of genes, particularly those in relevant biochemical pathways, or by changes in allele-specific gene expression.

Evolution of Mitochondrial Abundance

I am working on a method to infer mitochondrial DNA abundance directly from a meta-analysis of GWAS data from 125,000 individuals in an effort to use this information to shed light on the mechanisms controlling mitochondrial abundance. These mechanisms are not well understood and low or high relative levels of mitochondria have been implicated in many diseases.

Other work

In addition to this work, I built a 22 machine (160 core) compute cluster, with 768GB of RAM and more than 200TB of hard drive space. I also obtained a grant giving us access to the San Diego Supercomputer Center, valued at $48,989.882, and designed and purchased an $85,000 computer cluster for our group to use on campus. I provide extensive computational support to the lab.

Research Assistant, Salk Institute

San Diego, CA — 2008 – 2012

I worked with Gerard Manning's group investigating the evolution of the kinases in eukaryotes. Due to the deep conservation of kinases they are an excellent model for the study of evolution in distantly related species. My particular interest lay in the evolution of multicellularity at the base of the metazoan lineage. My work in this lab resulted in several publications and earned me an award.

In addition to this research, I helped to create a pipeline that used conserved intron-exon boundaries to improve upon gene models in divergent non-human eukaryotic species. These improved models then allowed us to infer evolutionary rate, and ask questions about selection that would have otherwise been impossible. I used this data to contribute extensively to the annotation of the kinase compliments of all of the eukaryotic species mentioned above, 12 species in total, including Human.

Volunteer Experience

President, StEMS

Stanford, CA — May, 2016 – Present

As president of Stanford EMS I am working to grow our organization in several different ways. In just two months I have overhauled our training system and implemented a transparent online CME program for the unit. I have also radically altered the member acceptance and promotion procedure, to increase medical accountability, and completely overhauled our documentation. I am currently working on a greater integration with the Palo Alto Fire Department, to provide an avenue for our members to greatly improve their skills and to provide medical coverage in more situations on campus.

Crew Chief, StEMS

Stanford, CA — May, 2016 – Present

After working for two years with StEMS and volunteering many hours, I was promoted to Crew Chief, allowing me to actually lead teams in the field and work as medical command for campus events.

Volunteer EMT, StEMS

Stanford, CA — May, 2014 – May, 2016

I worked as a volunteer EMT-B with Stanford EMS (StEMS) providing emergency medical coverage to the Stanford community at all large on-campus events.

Member, Bay Area Mountain Rescue Unit

San Mateo, CA — May, 2013 – Present

I am a wilderness EMT with the Bay Area Mountain Rescue Unit (BAMRU), an organization that specializes in expert search and rescue anywhere, any-time, and in any environment. I am additionally a prominent member of the BAMRU medical committee, where I have been working to improve our medical readiness. We regularly train in advanced mountain rescue techniques and in all aspects of wilderness and rescue medicine.

Emergency Department Volunteer, SCOPE

Stanford, CA — February, 2014 – Present

With SCOPE, I shadow physicians at the Santa Clara Valley Medical Center. For more information on the program, see http://beagooddoctor.org/scope/why-scope.

Teaching Experience

Wilderness Medicine Instructor, Stanford University

Stanford, CA — February, 2014 – July, 2015

I teach wilderness first aid (WFA) with the Stanford Outdoor Education center. This is an intensive 16-hour weekend class with lots of hands on drills and simulations.

Publications

- Suga, H., **Dacre, M.**, de Mendoza, A., Shalchian-Tabrizi, K., Manning, G., & Ruiz-Trillo, I. (2012). Genomic survey of premetazoans shows deep conservation of cytoplasmic tyrosine kinases and multiple radiations of receptor tyrosine kinases.
  Science Signaling, 5(222)

- Manning, G., Reiner, D. S., Lauwaet, T., **Dacre, M.**, Smith, A., Zhai, Y., … Gillin, F. D. (2011). The minimal kinome of *Giardia lamblia* illuminates early kinase evolution and unique parasite biology.
  Genome Biology, 12(7)

- Banks, J. A., et al. (2011). The *Selaginella* genome identifies genetic changes associated with the evolution of vascular plants.
  Science, 332(6032)

- Srivastava, M., et al. (2010). The *Amphimedon queenslandica* genome and the evolution of animal complexity.
  Nature, 466(7307)

Talks

- 6th Annual Cell Cycle Meeting, The Salk Institute (2009)
  Title: The Evolution of Metazoan Cell Cycle and Growth Control

Posters

- Symposium on Biological Complexity, UC Berkeley (2010)
  Title: The Evolution of Kinase Signaling

- Protein Phosphorylation Meeting, The Salk Institute (2010)
  Title: An Explosion of Kinase Signaling at the Origin of Multicellularity

- Plant and Animal Genome Conference, San Diego (2010)
  Title: Exploring the Evolution of the Genome through the Kinome

- Mechanisms and Models of Cancer Meeting, The Salk Institute (2009)
  Title: The Emergence of Kinase Tumor Pathways

- JGI User Meeting, Walnut Creek (2009)
  Title: Protein Kinase Evolution in Plants

Awards Received

- Biochemical Journal Young Scientist Award (2010)

Education

Post-Bacc Medical Education, UC Berkeley Extension

2014 – 2016

To prepare myself for medical school in the USA, I have taken a number of undergraduate level science courses through UC Berkeley. These include Physics, Chemistry, Organic Chemistry, and Biochemistry including all available labs. I have achieved and A or A+ in every one of these courses, including 100% or greater in Organic Chemistry and Biochemistry.

BSc. (Hons) Forensic Science, University of Central Lancashire

2003 – 2006

Concentrations in molecular biology and anthropology.
Thesis title: The use of the auricular surface of the ilium in estimating adult age at death.

Certifications

- Wilderness Upgrade for Medical Professionals (2015)
- NREMT EMT-B (2014)
- Wilderness First Responder (2013)