Summary of Goals. the kinds of research in which you would like to be engaged during your graduate study or in the longer term; specific research questions that interest you and how you became interested in them; how your research might be of interest to the Department of Defense (DoD); and your long-term goals and how the science fits into your life as an individual, especially your future career.

It's important to me to pursue something not just because it's interesting, but because it matters. I first learned of bioinformatics upon the success of the Human Genome Project, and was excited by the potential of personalized medicine. Armed with the genome sequence, researchers used bioinformatics to help create drugs to target specific disease-causing mutations, but also realized most conditions cannot be described by a single gene. I am electrified by this complexity and am thrilled to use bioinformatics to solve current and future biological problems.

My three goals for my future career are to (1) learn, (2) teach, and (3) collaborate.

(1) In my graduate work, I will continue to study biology by studying how differences in single-cell RNA regulation affects disease. Single-cell research is critical because current methods to study a complex disease such as cancer use homogeneous cell lines to model tumors, which in reality are a chaotic mix of different, interacting cell types. Thus, while the majority of a tumor may respond to treatment, a subpopulation may be resistant and cause future relapse. We need to study these subpopulations to understand how the interactions within the mosaic of individual cells help the larger cancer survive, and Prof Gene Yeo at UCSD has a prototype of a single-cell sorting device that I will use for my graduate work.

To study cancer survival, I need access to tools for studying alternative splicing because every disease in humans has a known mutation in a non-coding region such as a splice site. Yeo's lab is at the forefront of alternative splicing research and is the best place for me to research alternative splicing in cancer at the single cell level. After graduation, I want to become a professor at a top research institution, where I will be surrounded by incredibly intelligent people who will question, support, and challenge my research. I hope to be constantly humbled by my colleagues.

(2) Training the next generation of scientists is critical for the United States' future success. I taught bioinformatics modules to high school and undergraduate students, and a key component of my teaching style is mirroring authentic research. I want learners to relish the struggle through a problem because it leads to marvelous moments of insight.

(3) The quote, "None of us is as smart as all of us," is increasingly true in integrative fields such as bioinformatics. We cannot do bioinformatics as hermits; we need experimentalists, clinicians, and biotechnologists to drive forward our understanding of biology. As a professor, I will forge connections with experts in other disciplines to create new fields of research. With my colleagues, I want to create a collaborative research institute which partners with biotechnology companies to transform research advancements into realized pharmaceuticals as quickly as possible. This way, the discoveries aren't locked away in an ivory tower, but used to improve public health.

==Leadership Experiences==
Bioinformatics in AP Bio (2012): Kevin Karplus █████████████████
Co-chair, Intelligent Systems for Molecular Biology Student Council Symposium 2012:
Alex Goncearenco ████████████
DanceTroupe; Choreographer, Publicity Chair: Valerie Chia ████████████
Baker House Social Chair (2008): Jonathan Nolan ███████████████████
Gordon-MIT Engineering Leadership (2009): Leo McGonagle ██████████████

==Teamwork Experiences==
Taught stem cells to underrepresented minorities (June 2012) Beth Walker
walker@ucolick.org
Co-chair, Intelligent Systems for Molecular Biology Student Council Symposium 2012 -
Alex Goncearenco ████████████
Biological Engineering Design final project (Spring 2010) – John Essigmann
████████████

MIT Lightweight Men's Crew; Coxswain (Fall 2006 – Spring 2007) – Seth Davis
█████████████████

==Memberships and Certifications==
Co-Chaired Intelligent Systems for Molecular Biology Student Council Symposium
(2012)
Member, International Society of Computational Biology (since November 2010)
Member, Society of Women Engineers (since May 2011)
Certified Russian-English Medical Interpreter (since August 2011)

==Community and Volunteer Work==
Taught stem cells to underrepresented minorities 3h/w 02/12-06/12 Beth Walker
█████████████

We Teach Science Foundn 8th grade Algebra Tutor 2h/w 10/11–05/2012 Camille Stone
████████████████

Science Club for Girls 2nd grade Mentor 4h/w 1/11-5/11 Rosalind Gould
████████████████

Mission Hill Middle Sch, Math tutor 2h/w 2/09–5/11 Ann Ruggerio
███████████████

==Research experiences== (400 char max each)
Mesirov Lab
At the Broad Institute of Harvard and MIT, I helped develop REVEALER, an algorithm
that finds associations between continuous phenotypic output such as gene expression, or
response to RNA-interference (RNAi), and discovers additional putative activators or
repressors. We are currently preparing a publication. I also worked on single-sample Gene
Set Enrichment Analysis, resulting in 3 publications.

Pourmand lab
In Prof. Nader Pourmand's laboratory at Univ. Calif.-Santa Cruz (UCSC), I developed an
open-source RNA-Seq differential expression pipeline to study breast cancer drug
resistance at the single-cell level. We studied individual cells escape chemotherapy,

specifically paclitaxel which inhibits microtubule elongation, preventing proper mitotic spindle formation and subsequently cells from dividing.

Stuart lab
Ovarian cancer patients have very limited options, but if we can show that basal breast cancer (as opposed to lumenal breast cancer) is a similar disease, we can borrow basal breast cancer treatment strategies to help cure ovarian cancer patients. I used statistical methods to show similarity between ovarian cancer and basal breast cancer.

Ideker lab
Transcriptional networks are radically different between different species, and yet organisms still perform the same high-level biological functions such as cell cycling. I studied 13 cell cycle transcription factors in S. pombe and compared to all transcription factors in S. cerevisiae (last common ancestor of these yeasts: 400 million years ago, same as humans to cerevisiae).

Publications
REVEALER paper
I wrote the code for the REVEALER algorithm which uses a mutual information metric coupled with iterative removal to discover novel associations between binary features such as mutations or copy number status, and continuous features such as expression data or RNAi resistance. We used REVEALER to verify a hunch Dr. William Kim had, and we have since worked together to use both algorithmic and experimental approaches to understanding cancer genomics.

ssGSEA paper
I wrote the code for single-sample Gene Set Enrichment Analysis (GSEA), and Chet Birger has since optimized the underlying mutual information algorithm.

SCS8 paper
I co-chaired the International Society for Computational Biology's (ISCB) Student Council Symposium, which is held the day before Intelligent Systems for Molecular Biology (ISMB), the largest computational biology conference in the world. This publication is a summary of the day's events.

Galili et al
I wrote the code for single-sample Gene Set Enrichment Analysis (GSEA), which was used in this paper to analyze microRNAs and pathways involved in resistance to ezatiostat.

Wood et al.
I wrote the code for single-sample Gene Set Enrichment Analysis, which was used in this publication to compare expression in several melanoma samples.

Berger t al.
I performed molecular biology experiments on protein-binding DNA microarrays to find binding motifs of homeodomain transcription factors.

ISMB 2012
This is a summary of my work during my master's at University of California, Santa Cruz, where I created an RNA-Sequencing differential expression pipeline to analyze resistance to the chemotherapy taxol (paclitaxel) in triple-negative (no mutations in known "druggable" markers) breast cancer.

ISMB 2011
This was the initial presentation of the REVEALER algorithm, which uses a mutual information metric in conjunction with a novel iterative method to uncover previously unknown associations between pathways and mutations in cancer.

Awards and Honors

Gordon-MIT Engineering Leadership Scholar (September 2008)
The Bernard M. Gordon-MIT Engineering Leadership Program is committed to developing next-generation technical leaders who are equipped to understand and address significant engineering problems in real-world situations.
Prof. Edward Crawley engineeringleaders@mit.edu ██████████

First person to finish 2-year M.S. in 9 months at UCSC (June 2012)
University of California, Santa Cruz (UCSC) has a 2-year master's program in Bioinformatics which I completed in 9 months (requirements: http://www.bme.ucsc.edu/graduate/requirements). I was able to do this because I had completed one of the courses (Computational Systems Biology) in undergrad, got credit at UCSC and TA'd the course, thus taking care of both credit and a TA requirement at once. I also took an extra class each quarter, more than any of my peers. Both the extra classes and the previous credit contributed to my quick completion of the program.
Kevin Karplus ██████████████ ███████████

National Science Foundation Graduate Research Fellowship Honorable Mention (March 2012)
Awarded to top 20% of applicants.
NSF GRFP   info@nsfgrfp.org   ███████████

Howard Hughes Medical Institute Janelia Farm Research Campus Summer Scholar (March 2008)
Chosen as one of 14 students from 700 applicants to work at the prestigious Howard Hughes Medical Institute Janelia Farm Research Campus, I worked with Sean Eddy to study protein sequence homology null models.
Janelia Farm Summer Scholars Program   ████████████████████████
████

University of California Regents' Fellowship (September 2011)
Students with outstanding academic records and personal achievement are considered for
Regents Scholarships, UC's most prestigious scholarship award.
University of California   ucinfo@applyucsupport.net   ██████████