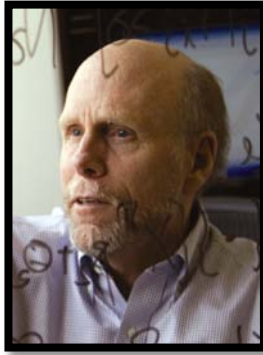# Raymond J. Carroll

YOUNG INVESTIGATOR AWARD CEREMONY

Monday, November 14, 2011
4:00 pm – 5:00 pm
Room 301, Rudder Tower

MARC A. SUCHARD
2011 RECIPIENT

Professor of Biostatistics
Professor of Biomathematics & Human Genetics
University of California, Los Angeles

Raymond J. Carroll, Distinguished Professor

The Raymond J. Carroll Young Investigator Award was established to honor Dr. Raymond J. Carroll, Distinguished Professor of Statistics, Nutrition and Toxicology, for his fundamental contributions in many areas of statistical methodology and practice, such as measurement error models, nonparametric and semiparametric regression, nutritional and genetic epidemiology. Carroll has been instrumental in mentoring and helping young researchers, including his own students and post-doctoral trainees, as well as others in the statistical community.

Dr. Carroll is highly regarded as one of the world's foremost experts on problems of measurement error, functional data analysis, semiparametric methods and more generally on statistical regression modeling. His work, characterized by a combination of deep theoretical effort, innovative methodological development and close contact with science, has impacted a broad variety of fields, including marine biology, laboratory assay methods, econometrics, epidemiology and molecular biology.

In 2005, Raymond Carroll became the first statistician ever to receive the prestigious National Cancer Institute Method to Extend Research in Time (MERIT) Award for his pioneering efforts in nutritional epidemiology and biology and the resulting advances in human health. Less than five percent of all National Institutes of Health-funded investigators merit selection for the highly selective award, which includes up to 10 years of grant support.

The Carroll Young Investigator Award is awarded bi-annually on odd numbered years to a statistician who has made important contributions to the area of statistics. Dr. S.C. Samuel Kou was named the Inaugural Recipient of the award in 2009. Dr. Marc A. Suchard, Professor of Biostatistics, Biomathematics and Human Genetics from the University of California, Los Angeles has been selected as the 2011 recipient of this prestigious award.

Marc A. Suchard
Professor of Biostatistics, Biomathematics & Human Genetics
University of California, Los Angeles

Marc Suchard received a bachelor's degree in biophysics from the University of California, Berkeley in 1995 and spent two years at Oxford University as a British Marshall Scholar, a scholarship designed to finance young Americans of high ability to study for a graduate degree in the United Kingdom. He then earned his Ph.D in biomathematics from the University of California, Los Angeles (UCLA) in 2002 and continued for a MD degree which he received in 2004, also from UCLA.

Prof. Suchard is currently a professor in the Departments of Biomathematics and of Human Genetics as well as the Department of Biostatistics at UCLA's David Geffen School of Medicine and School of Public Health, respectively. He is in the forefront of the new field of evolutionary medicine. Dr. Suchard is a leading Bayesian statistician who focuses on inference of stochastic processes in genomics and in the clinical application of statistical genetics. His training in both Medicine and Applied Probability help bridge the gap of understanding between statistical theory and clinical practicality.

He has been awarded several prestigious awards such as the 2003 Savage Award, the 2006 Mitchell Prize, as well as the 2007 Alfred P. Sloan Research Fellow in computational and molecular evolutionary biology. He was also awarded the 2008 Guggenheim Fellowship to promote Bayesian approaches in medicine and research gifts from both Microsoft Corporation and Google to further statistical computing.

Prof. Suchard was chosen to receive this award for his wide-ranging and influential contributions to computational statistics, Bayesian modeling and computing, evolutionary medicine and biology. For publications and more information on Prof. Marc Suchard, please visit www.biostat.ucla.edu/ and www.biomath.ucla.edu.

RIDICULOUSLY PARALLEL, SERIAL ALGORITHMS FOR STATISTICAL INFERENCE

Monday, November 14, 2011, 4:00 pm – 5:00 pm
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Intensive numerical computation plagues the statistical inference of massive data sets and high-dimensional models. I describe many-core computing algorithms that harness inexpensive graphics processing units (GPUs). This approach can achieve over 100-fold total run-time reduction on desktop computers across a rich variety of statistical problems. My first examples are Bayesian. One attacks the inference of partially observed stochastic processes, important in the study of the evolution of infectious diseases, and the other entertains fitting very large-scale mixture models to massive datasets, both via Markov chain Monte Carlo (MCMC). While MCMC is inherently serial, conditional data-independence and fine-scale parallelization within each step of the chain provide many exploitable advantages. Then, I undertake two high-dimensional numerical optimization problems. The first harnesses the Majorization/Minimization (MM) algorithm to reduce each step in the serial optimization to solving tens of thousands of simple, independent minimizations in parallel, with applications to low-rank matrix factorization and image analysis.

The final optimization capitalizes on fast GPU-based linear algebra and the lasso to fit generalized linear regressions to electronic health records from tens of millions of patients to monitor adverse drug events. I conclude with a discussion of the opportunities that massive parallelization offers non-parametric inference under Dirichlet processes and infinite hidden Markov models.

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