



**Donna J. Brogan, Ph.D.**  
**Emerita Professor**  
**Department of Biostatistics and Bioinformatics**  
**Rollins School of Public Health**

Donna J. Brogan received her Ph.D. in statistics from Iowa State University and was Assistant Professor of Biostatistics at UNC School of Public Health before joining Emory in 1971 as the first female faculty member in its Statistics/Biometry Department, later becoming only the fourth female full professor in its School of Medicine. In the Rollins School of Public Health, she was its first female full professor and its first female chair of the Department of Biostatistics. Dr. Brogan's research interests, reflected in her 150 publications, include design and analysis of complex sample surveys and collaboration with health scientists.

Dr. Brogan's honors include fellow of the American Statistical Association (ASA), Emory University's Thomas Jefferson Award, three distinguished alumni awards [Gettysburg College (BA), Purdue (MS), Iowa State (Ph.D.)], and the ASA's Elizabeth Scott Award for significant contributions to the advancement of women within the statistics discipline. Dr. Brogan's leadership talent in academic and government realms was applied to selected activism. Based on her experience in a male dominated discipline, she founded the Caucus for Women in Statistics in 1971. Dr. Brogan's experience as a breast cancer researcher and patient motivated her to help found the U.S. breast cancer advocacy movement in the 1990's.

Since her retirement in 2004, Professor Emerita Brogan continues to advise government agencies on design and analysis of complex sample surveys and teach continuing education courses on this topic. She is an avid participant in challenge level square dancing, a complicated activity that uses concepts from mathematics and geometry.

## ***DONNA J. BROGAN LECTURE IN BIOSTATISTICS***

### **“Statistics and Genetics Open a Window into Autism”**

**Presented by:**



**Kathryn Roeder, Ph.D.**  
**Department of Statistics and Lane Center for Computational Biology**  
**Carnegie Mellon University**

While studies have shown that autism is highly heritable, the nature of the genetic basis of this disorder has remained illusive. Recently, using a new study design, some progress has been achieved. Rare variants identified from DNA sequence, especially *de novo* loss of function mutations, have identified genes involved in risk for autism. We extract more information by using a statistical model (TADA) that integrates data from family and case-control studies to infer the likelihood a gene affects risk. Still, given limited sequence data, can we garner yet more information? Progress has been made to develop systems biological approaches to understanding autism pathophysiology. Using autism risk genes as foci, we hypothesize that genes expressed at the same developmental period and brain region, and with highly correlated co-expression, are functionally interrelated and more likely to affect risk. To find these genes we model two kinds of data: gene co-expression in specific brain regions and periods of development; and the TADA genetic scores. This analysis identifies  $\approx 100$  genes that plausibly affect risk, many novel and others implicated despite relatively weak genetic evidence. I will describe how these results can be used to expand our understanding of the genetics of autism.

## **DONNA J. BROGAN LECTURE IN BIOSTATISTICS**

### **“Statistics and Genetics Open a Window into Autism”**

**April 16, 2014  
4:00 PM**

**Lawrence P. & Ann Estes Klamon Room  
Rollins School of Public Health  
Claudia Nance Rollins Building, Rm. 8030  
1518 Clifton Road, N.E.**

Welcome: Amita Manatunga, Ph.D.  
Chair, Brogan Lecture Committee  
Department of Biostatistics and Bioinformatics

Introduction: Lance A. Waller, Ph.D.  
Rollins Professor and Chair  
Department of Biostatistics and Bioinformatics

Donna J. Brogan Lecturer:  
Kathryn Roeder, Ph.D.  
Department of Statistics & Computational Biology  
Carnegie Mellon University

#### **Reception immediately following the lecture**

*This lecture honors Donna J. Brogan, an outstanding former faculty member and chair in the Department of Biostatistics of the Rollins School of Public Health (RSPH), and is made possible in large part by the generous support of Donna, her colleagues and friends.*

## **Kathryn Roeder, Ph.D.**

Dr. Kathryn Roeder is Professor of Statistics and Computational Biology at Carnegie Mellon University. In her early work, she played a pivotal role developing the foundations of DNA forensic inference. Her current work focuses on statistical genomics, and the genetic basis of complex disease with an emphasis on autism. Dr. Roeder received her BS in Wildlife Resources from University of Idaho and Ph.D. in Statistics from Pennsylvania State University. Immediately securing an Assistant Professorship at Yale University, her career path then took her to Carnegie Mellon University in 1994. Dr. Roeder is an elected Member of the International Statistical Institute ('95), a Fellow of the Institute of Mathematical Statistics ('97), a Fellow of the American Statistical Association ('97). The Committee of Presidents of Statistical Societies (COPSS) has twice honored her with the Presidents' Award ('97) and the Snedecor Award ('97) for her outstanding work in statistical applications. In 2013, Dr. Roeder was also the recipient of the twelfth Annual Janet L. Norwood Award for Outstanding Achievement by a Woman in Statistical Sciences from the University of Alabama at Birmingham. Activities over her career include board positions with the Institute of Mathematical Statistics, advisor to both the FBI and NRC/NAS on DNA forensics and numerous editorial positions in prominent journals. She has served as an associate editor of JASA, Biometrics and American Journal of Human Genetics.

The primary goal of Dr. Roeder's research group is to develop statistical tools for finding associations between patterns of genetic variation and complex disease. Current data typically involves Next Generation Sequencing and gene expression, including RNAseq. Her methodological work is motivated by studies of schizophrenia, autism and other genetic disorders.