

April 21, 2006

Colorado-Wyoming Chapter

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(Updated 4/19/2006) This is the last announcement for the spring meeting. Its similar to the last announcement, with two differences. First, complete abstracts from Dennis Cox's ASA talk and Kathe Bjork are included. Second, I thought I might mention that NCAR's cafeteria only accepts cash - no credit cards.

As promised, the weather will be perfect Friday. For those not familiar with the Mesa lab, there are nice trails adjacent to the building for a lunchtime walk if you choose.

Friday Forecast: Mostly sunny, with a high around 71. Calm wind.

Thanks,
Matt

++ Spring Meeting - April 21st - Boulder Colorado
++ Dennis Cox at Colorado School of Mines, April 21st.

Spring Meeting

Colorado/Wyoming Chapter of the American Statistical Association
Friday April 21st - 9am - 5pm.
National Center for Atmospheric Research in Boulder, CO.

The agenda for next Friday's meeting follows. We have a broad range of topics that highlight topics being studied by the universities in our area. The meeting is being held at NCAR's Mesa Lab, overlooking Boulder Colorado. If you haven't visited the lab before, it is (I think) one of the most stunning locations anywhere. The weather should be perfect and there should be some time after lunch to take a walk outside. We will have refreshments before the meeting from 8:45 - 9:30 and then beer, wine and refreshments will be served at the end of the day. Advanced registration is not required and the event is free. Lunch is not free, but readily available in NCAR's cafeteria. Abstracts, information on the VisLab demonstration and direction are listed below.

Space in the VisLab is limited, so if you plan on coming to the demonstration, please rsvp.

There will be a sign-in sheet at the security desk for people attending the meeting.

Contact me with any questions.
-- Matt Pocernich pocernic@rap.ucar.edu
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Agenda

8:45 - 9:30 Registration - Coffee/ Donuts
9:00 - 9:30 **Tour of VisLab**
9:30 - 9:40 Welcome
9:40 - 10:20 **Steve Sain** - Models for Multivariate Spatial Lattice Data
10:20 - 10:40 **Kathe Bjork** University of Colorado - Health Sciences

10 minute break

10:50 - 11:00 **Anthony Hayter** - Introduction and overview of statistics
at University of Denver.
11:00 - 11:15 K-12 Outreach Efforts
11:15 - 12:00 **Dennis Cox** - P-CAP - Probability Calibration
Assessment Plots
Lunch - noon - 1:15.

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1:15 - 1:30 Chapter Elections and Maurice Davies Awards
1:30 - 2:10 **Katerina Kechris** - Statistical Methods in Bioinformatics
2:10 - 2:30 **Yu Yang** - Estimating parameters for continuous-time
autoregression models

10 minute break

2:40 - 3:00 **William Coar** - Smoothing through State-Space
Models for Stream Networks
3:00 - 3:40 **Thomas Lee** - Pattern Generation using Likelihood
Inference for Cellular Automata
3:40 - 4:00 **Caspar Ammann** - Perspectives on climate of the last millennium
4- 5pm refreshments.

****** Tour of NCAR's visualization lab***

Back by popular demand, a demonstration of NCAR's VisLab
The VisLab is a state-of-the-art scientific visualization environment,
providing an immersive environment for visualizing complex datasets in
stereo-3D and collaborating across sites via AccessGrid video
teleconferencing. From a statistical perspective, the VisLab allows
data to be illustrated with both motion and depth. before the main
meeting starts, a 30 minute demonstration will be held from 9 - 9:30.

More information on the VisLab can be found at

<http://www.vets.ucar.edu/Vislab/index.shtml>
<http://www.vets.ucar.edu/vg/index.shtml>

Directions to NCAR

<http://www.eo.ucar.edu/visit/>

(Basically, in Boulder head west on Table Mesa until the road ends ~
two miles west of Broadway)

ABSTRACTS FOR SPRING MEETING

William Coar

Colorado State University

Smoothing through State-Space Models for Stream Networks

Because of the natural flow of water in a stream network,
characteristics of a downstream reach may depend on characteristics of
upstream reaches. The flow of water from reach to reach provides a
natural time-like ordering throughout the stream network. By analogy
to structural time series models, we propose a local linear trend
model for a stream network and provide its expression in state-space
form. With this model, smoothed estimates generated from a variation
of the Kalman filter and smoother are the same as those obtained
through minimization of a standard penalized least squares criterion
used for spline smoothers in discrete time. That is, the state-space
formulation allows for the definition of spline smoothers on a stream
network. Estimation of the smoothing parameter is done through
maximum likelihood estimators of the variance components for the local
linear trend model.

Kathe Bjork - UCHSC

Oligonucleotide microarrays manufactured for structural and
functional genomic analyses present numerous statistical challenges, including
selection of the expression value in the low-level analysis, computations with
massive datasets, adjustment for false positives and significant background
noise, and the presence of influential and outlying gene expressions. Numerous
statistical approaches for functional genomic analyses have been published in
the biostatistical literature and some have been implemented in software
available to researchers. The investigations in this study focus on the
outcomes of mean-based and robust statistical algorithms in differential gene
expression between two tissue types, a common type of study design for
exploring the role of genetics in diseases such as cancer and heart disease.
Data for these investigations were MAS5.0 signal value (SV) and robust
multichip average (RMA) expressions derived from publicly available Affymetrix
GeneChip .CEL files, and simulations designed to represent SV and RMA

expressions. The algorithms proceed stepwise through the two types of expression value computation, filtering for significant genes via Student's and biweight t-tests, singular value decomposition and median polish dimension reduction, cluster analyses, and robust sample discrimination. Results showed that outcomes and genes detected as differentially expressed varied according to branches followed within the algorithms, and these different outcomes could easily be visualized. By following the steps in the complete algorithm, investigators can distinguish genes likely to be most informative among different tissues, and can use those genes to determine discriminating capability by tissue type.

Dennis Cox - Rice University, Texas

Probability Calibration -- How statisticians can assess if the probability forecasts are correct ("P-CAP - Probability Calibration Assessment Plots").

Based on an interpretation of the randomized probability integral transform, we propose a distribution that can be used assess the calibration of a probability model for one dimensional numerical or ordinal data. The Probability Calibration Assessment Distribution can be used with purely discrete models (e.g., assessing goodness of fit for a logistic regression model) or mixed discrete/continuous models (e.g., a model for daily rainfall, where there is a positive probability of zero and a continuous distribution for positive values). Several examples from a variety of applications will be presented to indicate how the results can be interpreted. It will be shown how to implement a goodness of fit test in certain situations. A few results and open problems on the asymptotics of the associated empirical process will be discussed.

Note, Dennis Cox will also be speaking in the afternoon at the School of Mines in Golden)

[\[Cowystats\] Last Notice - ASA Spring Meeting - a few new details](#)

Katerina Kechris

Department of Preventive Medicine and Biometrics
University of Colorado at Denver and Health Sciences Center

"Statistical Methods in Bioinformatics"

In the last few decades, new experimental technology in the life sciences has created an exponentially growing quantity of biological data. The challenge for the statistics community is to organize this increasing amount of knowledge to help answer questions about biological systems and processes. In this talk, I will give an overview of statistical methods in several areas of bioinformatics research.

Thomas Lee

Colorado State University
Pattern Generation using Likelihood Inference for Cellular Automata

Abstract:

Cellular automata (CA) is a dynamical system that evolves on a discrete lattice. In this talk CA is applied to model and generate various binary image textures. The idea is to, given an observed binary texture image, estimate the unknown CA "rule" that generated the image. As to be demonstrated in this talk, this estimation problem can be posed as a statistical model selection problem, and the minimum description length principle is adopted to provide a solution.

Steve Sain

University of Colorado - Denver

Models for Multivariate Spatial Lattice Data

Many spatial problems, particularly those concerning environmental investigations, are inherently multivariate, in that more than one variable is typically measured at each spatial location. Focusing on spatial lattice data, this talk will cover the details of a multivariate Markov random field model (also referred to as a conditional autoregressive or CAR model). Attention will be given to the spatial covariance structure, in particular to the potential asymmetry in the spatial cross-covariances. Incorporating these multivariate Markov random

field models into a hierarchical framework, the models will be demonstrated on examples including combining climate model output for assessing climate change and analyzing the racial distribution of traffic and pedestrian stops by police in the city of Denver.

Yu Yang

Colorado State University

Estimating parameters for continuous-time autoregression models

In this talk, we consider the problem of estimating the parameters of a continuous-time autoregression (linear and non-linear), based on a closely and regularly spaced time series. Our method consists of two parts. We first calculate the exact maximum likelihood estimators of the autoregressive coefficients, conditional on the initial observations and assuming the process is observed continuously. There is a close form expression for these estimators. Then we approximate the exact solution using the observations which are sampled at discrete times. This procedure can be carried out for both linear and non-linear autoregressions. And our simulation results demonstrate the good performance of it.

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Dennis Cox at Colorado School of Mines

Chauvenet Hall 143 3:00-4:00 pm.

Convergence of Gibbs Measures Associated with Simulated Annealing

Dr. Cox's visit to Colorado is sponsored by the School of Mines. While this gives us the opportunity to have Dennis speak at the chapter meeting in the morning, it creates a conflict in the afternoon. On the bright side of things, there is no reason not to see a interesting statistical talk on the 21st.

The motivating application for this research concerns modeling the equilibrium properties of functional materials including shape memory alloys. This leads one to seek solutions of differential inclusions: find a function satisfying given boundary conditions whose derivative is allowed to take on values from a set of allowed values corresponding to allowable crystalline configurations of the material. There are corresponding variational problems, but the practical solution of these has proven notoriously difficult. One promising approach is Simulated Annealing, a stochastic optimization algorithm, but computational experience suggests that it has major problems. We present here an analysis of the probability measures of the simulated annealing algorithm that shows they can converge to an incorrect result.