

Abstracts

Estimating soil moisture depletion from multiple data sources

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With increasing limitations on water for irrigation, agriculture managers need better estimates of soil moisture depletion to minimize crop stress and maximize yield. Several estimates of soil moisture depletion are available, though they can be inadequate for various reasons-spatial and temporal heterogeneity of soil moisture and field capacity, as well as differential evapotranspiration rates complicate the picture. In this talk, I describe these estimates and the measurements from which they are obtained. I outline a Bayesian approach for combining information from various sources, including field-specific experimental information about soil moisture, to obtain a comprehensive estimate for soil moisture depletion at a field. Using hypothetical data, I illustrate the model and describe several potential uses of model outputs.

Advancing Bayesian methods in hydrologic modeling: A study of recently developed MCMC techniques

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Bayesian methods, and particularly Markov chain Monte Carlo (MCMC) techniques, are extremely useful in uncertainty assessment and parameter estimation of hydrologic models. However, MCMC algorithms can be difficult to implement successfully due to the sensitivity of an algorithm to model initialization and complexity of the parameter space. Many hydrologic studies, even relatively simple conceptualizations, are hindered by complex parameter interactions where typical uncertainty methods are harder to apply. Comparisons between three recently introduced MCMC approaches, the Adaptive Metropolis (AM), the Delayed Rejection Adaptive Metropolis (DRAM) and the Differential Evolution Markov Chain (DE-MC) algorithms are presented via two case studies: (1) a synthetic Gaussian mixture with five parameters and two modes and (2) a real-world hydrologic modeling scenario where each algorithm will serve as the uncertainty and parameter estimation framework for a conceptual precipitation-runoff model.

An investigation of spatial statistical models for landscape genetics

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Genetic variation across a landscape can be used to make inferences about the underlying patterns of gene flow. By combining genetic and spatial information on an individual, in the form of an individual's location and genotype, we can make inference about its population of origin. One goal of landscape genetics, the study of genetic variation over space, is to locate genetic discontinuities between populations on the landscape using individual multilocus genotype data (Manel et. al. 2003). Spatially explicit clustering methods are available for quantitative, univariate data, but the multivariate and categorical nature of genetic data necessitates a new set of spatial statistical tools. Guillot et al. (2005, 2007) recently proposed and extended a spatial statistical model that holds promise as a unified approach for addressing the multiple problems defined by the field of landscape genetics. The model proposed by Guillot et al. (2005) uses Bayesian methods to estimate the number of populations, degree of divergence among populations, and spatial organization of populations over the landscape. The model relies exclusively on individual locations and genotypes. The spatial component is based on Voronoi tessellation coupled with a Poisson point process whose intensity reflects the degree of spatial dependence. The spatial structure can be paired with a variety of different gene flow models to investigate how populations are genetically separated (or mixed) over the landscape. We explore two gene flow models within Guillot et al.'s spatial context using their R package Geneland. The first assumes two completely independent populations are present on the landscape, while the second assumes two populations arose from the same ancestral population, but diverged via separate Markov processes (Falush et. al. 2003). We compare the ability of the two models to estimate the number of populations, and to correctly assign individuals to those populations in three hypothetical biological scenarios: one with a clear spatial barrier separating the two genetic populations, one with a less-clearly demarcated barrier, and one with two completely spatially mixed genetic populations.

Three Q's about Simpson's Paradox: A Logic-Based Account

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There are three distinct questions associated with Simpson's paradox. (i) Why or in what sense is Simpson's paradox a paradox? (ii) What is the proper analysis of the paradox? (iii) How should one proceed when confronted with a typical case of the paradox? We propose a "formal" answer to the first two questions which contrasts sharply with Pearl's causal (and questionable) account of them. We argue that the third question does not have a unique response, and comment briefly on the so-called "sure thing principle"

Teaching Statistics Online

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Taking classes online is becoming increasingly popular in the academic world because of tremendous opportunities they offer, such as flexibility, convenience, more individual attention. This presentation will outline the presenter's journey through the planning, development, and implementation of an online statistics course.

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