El Departamento de Estadística del ITAM

anuncia la siguiente sesión de

EL SEMINARIO ALEATORIO

que con el título

RECENT MONTE CARLO METHODS FOR COMPLEX STOCHASTIC SYSTEMS

será impartida por el

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RESUMEN

Stochastic models of real-world systems which exhibit great complexity can be built by combining simple local relations through conditional independence assumptions. Such complex models have been applied in areas as diverse as genetics, medical monitoring, financial forecasting, archaeology and signal processing, to name just a few. Inferences from these models, whether in a Bayesian or classical framework, rarely admit a closed analytical form, and therefore requiere use of simulation methods such as importance samplig (IS) and Markov chain Monte Carlo (MCMC) sampling. In these approaches to inference, samples are drawn from a target distribution, , and then used to estimate the quatities of interest. For example, in a Bayesian framework, will be a posterior or predictive distribution for some unknown quantity θ of interest. Use of sophisticated sampling methods as IS and MCMC is motivated by the fact that π will generally be a very complicated distribution, given up to an unknown normalizing constant. Combined use of IS and MCMC has revolutionized statistical practice, particularly in the Bayesian area, by allowing increasingly realistic models of real-world systems to be applied to data.

Most of the real-world applications of IS.MCMC so far involved *statistic* problems, where there is a single (and usually small) data set and a single target distributtion. However, many complex problems have a natural *dynamic* aspect to them, whether due to the fact that the modelled systems evolves with time, or because the data set itself evolving with time, for example when the data become available sequentially and we need to update the inferences of interest in real time every time a new data item arrives. Problems of this type include financial forecasting and tracking of military targets. Also relevant are problems involving such a huge search space that the only way to tackle them is by a sequential approach that gradually incorporates the data through incremental changes of the distributions of interest. Problems of this kind arise in the study of biological (DNA or protein) sequences, or analysis of long signal sequences in speech recognition. The talk will illustrate the applicability of advanced simulation methods to problems of the above kind, with the aid of examples in the study of polypetide sequences and in the tracking of moving targets based on noisy observations.

Fecha: Viernes 3 de marzo
Hora: 11:00
Lugar: Salón G1

El Seminario Aleatorio está destinado tanto a profesores como a estudiantes, por lo que el Departamento de Estadística agradece a los profesores que colaboren invitando a sus alumnos a estas sesiones.