



WORKSHOP

30/10 – Sala 102 do Prédio B do IME – Campus do Vale

PROBABILIDADE

ESTATÍSTICA

APLICAÇÕES

14h–15h

Bivariate Version of the Law of Uniform Seniority

Nikolai Kolev
IME - USP

15h–16h

Efficient Closed-Form MAP Estimators for embedded Systems

Francisco Louzada Neto
ICMC - USP

16h–16h30

Coffee Break

16h30–17h30

Evaluation of genome similarities: a wavelet-domain approach

Thelma Safadi
DES - UFLA

Bivariate Version of the Law of Uniform Seniority

The law of uniform seniority applies to mortality tables and can be identified as follows. The chance of two or more lives (following the same law of the table) surviving a given term is always equal to the chance of one life, older than either, surviving a term of the same length, see Greville (1956). We will define and characterize a bivariate version of the law of uniform seniority. Its relations with non-aging concepts will be established.

Evaluation of Genome Similarities: a Wavelet-domain Approach

The wavelet transform is a technique of seeing and represents a signal which is decomposed at different levels of resolution, where each level brings a detailing. Mathematically, it is represented by a function oscillating in time or space. As a feature, it has sliding windows that expand or compress to capture low and high frequency signals, respectively. One of the characteristics of wavelet analysis into genomic data is the extraction of features that are hidden. We applied the discrete non-decimated wavelet transform, NDWT, to the GC-content sequences of the Mycobacterium tuberculosis (MTB) genome strains. The GC-content is an important parameter of bacterial genomes used to scan the basic composition of the genome as well as to understand the evolution of the coded sequence. We propose a clustering method to similarities of genomes based on the energy and elastic net method. The energy (variance) obtained at each level provides a new set of information that can be used to search similarities between sequences. The elastic net simultaneous does automatic variable selection and continuous shrinkage, and it can select groups of correlated variables. The proposed methodology is applied to MTB sequences, being 4 Drug Resistant, 4 Drug Susceptible, 1 Multi Drug Resistant and 1 Extensively Drug Resistant, obtained from NCBI (2017).

Efficient Closed-Form MAP Estimators for Embedded Systems

Embedded systems are commonly used in communication engineering. Particularly, they can consist of an electronic system inside a microcontroller, which can be programmed to maintain communication between a transmitting antenna and mobile antennas, which are operating at the same frequency. In this context, from the statistical point of view, closed-form estimators are needed, since they are embedded in mobile devices and need to be sequentially recalculated at real time. In this talk, we discuss the proposition a maximum a posteriori (MAP) estimator, which has a simple closed-form expression. In principle, we focus on the Nakagami distribution, which plays an essential role in communication engineering problems, particularly to model fading of radio signals. In a second phase of the presentation, we show that the obtained results can be extended to other survival probability distributions, such as the gamma and generalized gamma ones. Numerical results reveal that the MAP estimator outperforms the existing estimators and produces almost unbiased estimates even for small sample sizes. This work is co-authored by Pedro Luiz Ramos, Eduardo Ramos, and Dipak Dey.