
Lunes 5 11:30, 0.09 - Aula de proyectos 2

Bioestadística

Moderador/a: Víctor Manuel Casero Alonso

FANOVA models, with correlated error term, in the statistical analysis of fMRI data. J. Álvarez Liébana, M. D. Ruiz Medina

Ponente: *Javier Álvarez Liébana, javialvalviebana@ugr.es*

The statistical analysis of functional magnetic resonance neuroimaging (fMRI) data has led to a substantial improvement in the field of neurology. The investigation of the temporal evolution of the neuronal response to a stimulus usually requires the analysis of fMRI data correlated in space and time. Functional Analysis of Variance (FANOVA) is then considered here, from a correlated sequence of functional data with rectangular support (i.e., from a temporal correlated sample of functional MRI data). Specifically, a multivariate Hilbert-valued fixed effect model, with correlated functional error term, is fitted, considering the RKHS quadratic loss function. The optimality of the projection methodology adopted is analyzed, regarding the dimension reduction problem. The results obtained are compared with those ones derived by applying the FMRISTAT software, available at <http://www.math.mcgill.ca/keith/fmristat/>.

Palabras clave: Functional analysis of variance, Hilbert-valued multivariate fixed effect model, Hemodynamic response function, MRI and fMRI applications.

nsROC: análisis no-standard de curvas ROC. S. Pérez Fernandez, N. Corral Blanco, P. Martínez-Camblor

Ponente: *Sonia Pérez Fernandez, perezsonia@uniovi.es*

La curva ROC es un método frecuentemente utilizado para el estudio y comparación de la capacidad diagnóstica de un marcador. Por supuesto, la mayoría de paquetes estadísticos comerciales incluyen procedimientos para su cálculo. También existen varios paquetes de R que implementan gran parte de los análisis estándar relativos a la curva ROC: estimaciones paramétricas y no paramétricas, incluyendo la estimación suavizada, la comparación de la capacidad diagnóstica general, estimación de curvas ROC tiempo-dependientes o el cálculo de puntos de corte son algunos ejemplos. En este trabajo se presenta un paquete de R que implementa algunos métodos no usuales: la comparación general de curvas ROC procedentes de muestras dependientes e independientes, el cálculo de bandas de confianza, estimación no paramétrica de la curva ROC generalizada son algunos de los métodos nuevos que se implementan en esta función.

Palabras clave: curvas ROC, paquete de R, comparación no-parametrica.

Evaluation of microarray normalization strategies to detect cyclic circadian genes. Y. Larriba González, C. Rueda Sabater, M. A. Fernández Temprano

Ponente: *Yolanda Larriba González, yolanda.larriba@uva.com*

Microarrays are a widely used research tool in gene expression analysis. A large variety of preprocessing methods for raw intensity measures is available to establish

gene expression values. Normalization is the key stage in preprocessing methods, since it removes systematic variations in microarray data. Then, the subsequent analyses may be highly dependent on normalization strategy employed. Our research focuses on detecting rhythmic signals in measured circadian gene expressions. We have observed that rhythmicity detection depends not only upon the rhythmicity detection algorithm but also upon the normalization strategy employed. We analyze the effects of well-known normalization strategies in literature within three different rhythmicity detection algorithms; JTK, RAIN and our recently proposal ORI, a novel statistical methodology based on Order Restricted Inference. The results obtained are compared using artificial microarray data and publicly available circadian data bases.

Palabras clave: Order Restricted Inference, Microarray Normalization Strategies, Rhythmic Circadian Gene Detection.

A novel approach to project dynamic life tables. A. Benchimol, I. Albarrán, J. M. Marín, P. Alonso-González

Ponente: *Andres Benchimol*, abenchim@est-econ.uc3m.es

Some groups of countries are connected not only economically, but also socially and even demographically. This last fact can be exploited when trying to forecast the death rates of their populations. In this paper we propose a hierarchical specification of the Lee-Carter model and we assume that there is a common latent mortality factor for all of them. We introduce an estimation procedure for this kind of structures by means of a data cloning methodology. To our knowledge, this is the first time that this methodology is used in the actuarial field. It allows approximating the maximum likelihood estimates, which are not affected by the prior distributions assumed for the calculus. Finally, we apply the methodology to France, Italy, Portugal and Spain data. The forecasts obtained using this methodology can be considered as very satisfactory.

Palabras clave: Lee-Carter model, data cloning, longevity risk.