Sala PC3 de la FME (Campus Sud)

Content: Rehearsals of the oral presentations for the IBC congress:

- Lore Zumeta. A multi-state model for the prognosis of non-mild acute pancreatitis

Acute pancreatitis (AP) is an inflammatory condition of the pancreas with low mortality in its mild forms. Nevertheless, the most severe forms, and consequently patients with AP admitted to Intensive Care Units (ICU), showed high mortality. In addition, prediction of AP mortality is not straightforward due to the low incidence of the most severe forms and because its fluctuating clinical course. Although several prediction score systems had been developed, all of them are complex and cumbersome to achieve and, moreover, present a high rate of false positive results. It is, consequently, of paramount importance to determine risk factors for AP so that an adequate prognosis of the disease can be established.

Motivated by data from an observational, prospective study of 286 patients with non-mild AP who entered the ICU of the Donostia University Hospital between 2001 and mid-2017, we propose a multi-state modeling approach to describe the evolution of patients with AP and at least one organ failure or local complications. The so-called illness-death model is used allowing to take into account the disease-related events of interest, that is, entry to ICU, discharge from ICU and death due to AP.

The main goal of this joint project between the Donostia University Hospital and the Universitat Politècnica de Catalunya is the subject-specific management of the patients according to the observed progression of the disease. To this end the purposes of the present study are to describe the course of AP patients, to evaluate the relationship between surgery and mortality, and to develop a predictive process that allows the risk of a patient to be updated whenever new information of his or her evolution is available.

- J. Ocaña. Integrative analysis of gene lists based on equivalence testing on functional profiles

The analysis of features lists (genes, proteins, etc..) has been a very active field since the beginning of omics data analysis [1]. One topic that has received little attention is their comparison from the point of view of their biological meaning. This seems a very relevant problem in the post-genomics age, where multiple datasets are available for study. This can be used for example to decide if some datasets may be merged or in a meta-analysis context where several studies can be compared through the lists they have produced. Although a few comparison methods have been developed, the goProfiles approach [2] is, to our knowledge, one of the few that are being used for that purpose. It consists of projecting lists of genes into predefined levels or more generally slices of the Gene Ontology (www.geneontology.org), in such a way that a multinomial model can be used for estimation and testing. Our main interest here is establishing the similarity between two lists, instead of proving differences between them i.e. rejecting the null hypothesis of equality. With this aim, we derived an equivalence method which uses a distance-based approach and the confidence interval inclusion principle. Equivalence is declared if a one-sided confidence interval for the distance between two profiles is below a pre-established equivalence limit. We show how this method is extended to establish the equivalence of any number of gene lists. A graphical visualization of equivalences is obtained by an iterative approach that combines a bottom-up approach to determine the most to least equivalent gene lists while adjusting for multiple testing. The applicability of the method will be demonstrated on two typical situations for this approach. By one side it will be applied to the comparison of two groups of gene lists, one made by Cancer-related gene lists (http://www.bushmanlab.org/links/genelists) and the other by pathogenesis-based transcripts sets (http://atagc.med.ualberta.ca/Research/GeneLists/Pages/default.aspx). The methods developed are available in the last version of the goProfiles package (http://bioconductor.org/packages/goProfiles).

References:
