Wiener Biometrische Sektion der Internationalen Biometrischen Gesellschaft Region Österreich – Schweiz

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Einladung zum

Biometrischen Kolloquium

am Freitag, dem 11.01.08, um 15:00 Uhr (s.t.)

in der Bibliothek (Ebene 3, gegenüber Lift) der Besonderen Einrichtung für Medizinische Statistik und Informatik (MSI) der Medizinischen Universität Wien Spitalgasse 23, 1090 Wien

Es spricht Frau Dr. Lara Lusa, Department of Experimental Oncology, Fondazione IRCCS Istituto Nazionale dei Tumori, Milano, and Molecular Genetics of Cancer Group, Fondazione Istituto FIRC di Oncologia Molecolare (IFOM), Milano, Italy

Filtering Enhanced Feature Selection: A Multiple Testing Strategy for the Identification of Differentially Expressed Features in High-Dimensional Data Sets

Wir ersuchen um zahlreichen Besuch für diesen sehr interessanten und aktuellen Vortrag.

Werner Brannath Präsident Thomas Lang Sekretär

Filtering Enhanced Feature Selection: A Multiple Testing Strategy for the Identification of Differentially Expressed Features in High-Dimensional Data Sets

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High-throughput molecular analysis technologies can produce thousands of measurements for each of the assayed samples. The statistical cost of trying to identify which features are differentially expressed between pre-specified classes in highdimensional data sets is related to the risk of identifying many features that truly are not differentially expressed and many different multiple testing strategies are being used to control for this problem. An approach that is often used in practice with high-throughput data is to reduce the multiple comparisons problem lessening the number of comparisons being performed by filtering out features that are considered non-informative before the analysis. However, deciding which and how many features should be filtered out can be highly arbitrary and different filtering strategies can result in different features being identified as differentially expressed. We propose the filtering enhanced feature selection (FEFS) method, a new multiple testing strategy based on a multivariate permutation procedure. This method identifies differentially expressed features by combining the results obtained using a variety of filtering methods. We prove that the FEFS method probabilistically controls the number of false discoveries, and we show with a set of simulations and with an example from the literature that FEFS can be useful for gaining sensitivity in the detection of truly differentially expressed features.

This is a joint work with Edward L. Korn and Lisa M. McShane from Biometric Research Branch of the National Cancer Institute (NIH).