

**Wiener Biometrische Sektion  
der Internationalen Biometrischen Gesellschaft  
Region Österreich – Schweiz**

<http://www.akh-wien.ac.at/wbs/>

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Einladung zum

**Biometrischen Kolloquium**

am Donnerstag den 23.02.06 um 14:00 Uhr (pünktlich)

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

Es spricht Dr. Stefan Michiels (Institut Gustave Roussy in Villejuif  
und Institut National du Cancer in Paris) zum Thema:

**ISSUES IN THE PREDICTION OF CANCER  
OUTCOME WITH MICROARRAYS**

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

Karl Moder  
Präsident

Werner Brannath  
Sekretär

# ISSUES IN THE PREDICTION OF CANCER OUTCOME WITH MICROARRAYS

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Gene expression profiling is increasingly used to develop classifiers designed to predict the clinical outcome of cancer patients. Several experimental design questions need to be addressed before launching a study, such as the number of patients to be included. In addition, many approaches are available to classify patients based on the expression of thousands of genes. The objective of the present study was to compare error rates for different classification methods used in the microarray literature, applying a validation procedure with repeated random sampling.

The material consisted of 7 of the largest published microarray studies aiming at predicting a survival-related outcome in cancer patients (range: 60-240 patients). Three classification methods were considered: a simple nearest centroid classifier, a support vector machine with a linear kernel, and principal components regression, a method that takes into account correlation between genes.

On the whole, most of the data sets contained very little signal and the two more complicated algorithms did not outperform the nearest centroid classifier whose sensitivity and specificity was however poor. Validation procedures should be applied to larger data sets in order to study complex classifiers.