

# Searching for differential expression in microarray analysis: comparison of two nonparametric approaches

Israel Ortega<sup>1</sup>, M.C. Ruiz de Villa<sup>2</sup>,  
and Antonio Miñarro<sup>2</sup>

<sup>1</sup>*Fundació Institut de Recerca del Hospital Universitario Vall d'Hebron,  
Barcelona, Spain*

<sup>2</sup>*University of Barcelona, Spain*

## Abstract

This work studies the performance of a nonparametric density estimation based method to detect differentially expressed genes in microarray experiments.

The method makes use of a density estimation by orthogonal polynomials and an stepwise algorithm to select terms based on likelihood increments. Density estimations obtained trough this methodology allow us to define a natural distance between genes.

Given the expression of a set of genes from two experimental conditions we obtain density estimates of a Student-type test statistics ( $f$ ) and the corresponding density under the null hypothesis of non differential expression ( $f_0$ ).

Deciding whether a gene is differentially expressed is taken based on the distance between that gene and a "representative gene" of those non differentially expressed.

In order to evaluate the performance of this method we have simulate data under several conditions and we have compared the results obtained, in term of power and false discovery rate, with those obtained using the normal mixture model of Wei Pan.

Results show that this method performs well in a wide set of conditions.

## Keywords

Density estimation, Microarray analysis, Differential expression.

## References

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