THE UNIVERSITY   **OF HONG KONG**

Department of Mathematics

Numerical Mathematics and Applied Analysis Group Seminar (NMAA)

A study on some missing value estimation algorithm for DNA microarray data

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on Wednesday, February 14, 2007 at 2:00p.m.
in Room 309, Run Run Shaw Building, HKU

Abstract

Normalized Root Mean Squared Error (NRMSE) is popular used for measuring performance of missing value estimation algorithms for DNA microarray data. In this talk, I will propose a new performance criterion which allows more detailed comparisons among different algorithms. The characteristics of different selecting neighboring genes methods arising from this new criterion will be discussed. I will give a new gene-selection strategy by making uses of the strengths of different nearest genes selection methods. Numerical examples will also be given to demonstrate the performance of the proposed methods.

All are welcome