Identifying potential biomarkers through bivariate MALDI-MS data

Mariana R. Motta

Joint work with Nancy L. Garcia, Katia Roberta A. Belaz[b],

Alessandra Tata[b], Moana R. França[c], Mário Binelli[c],

Marcos N. Eberlin[b]

[a] Department of Statistics, (University of Campinas),

[b] ThoMSon Mass Spectrometry Laboratory, Institute of Chemistry, (University of Campinas),

[c] School of Veterinary Medicine and Animal Science (University of São Paulo)

Abstract

We investigate changes in the lipid composition of bovine uterus exposed to greater (LF-LCL group) or lower (SF-SCL group) concentrations of progesterone by matrix assisted laser desorption ionization-mass spectrometry (MALDI-MS). For each cow we consider two measurements after preprocessing of the data from which 76 m/z values were selected identifying specific ions in the spectra. There are 7 cows

1

in LF-LCL group and 10 cows in SF-SCL group, and due to the small sample size usual PCA methods could not identify biomarkers that discriminated between groups. Therefore we proposed a model-based approach and were able to classify the MALDI-MS data through a mixture of bivariate beta distributions to accommodate the large number of zero observations as well as the dependence present in the data.