

**C**omputation and **I**nformatics in **B**iology and **M**edicine  
Training Program

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Michael Waddell

CIBM Predoctoral Fellow  
Department of Computer Sciences  
Laboratory of Prof. David Page  
University of Wisconsin-Madison

**Toward the Development of Diagnostic Models  
Capable of Distinguishing Multiple Myeloma, MGUS,  
and Normal Plasma Cells Using  
Global Gene Expression Profiles**

**Abstract:**

Standard laboratory classification of the plasma cell dyscrasia monoclonal gammopathy of undetermined significance (MGUS) and the overt plasma cell neoplasm multiple myeloma (MM) is quite accurate, yet, for the most part, prognostically uninformative. Most, if not all, cancers are caused by inherited or acquired genetic mutations that manifest themselves in altered gene expression patterns in the clonally related cancer cells. Microarray technology allows for qualitative and quantitative measurements of the expression levels of thousands of genes simultaneously, and it has now been used both to classify cancers that are morphologically indistinguishable and to predict response to therapy. However, standard data analysis techniques are not trivial to employ on these large data sets. We report on the application of a panel of statistical and data mining methodologies to classify groups of samples based on expression of 12,000 genes derived from a high density oligonucleotide microarray analysis of highly purified plasma cells from newly diagnosed MM, MGUS, and normal healthy donors and the prediction errors for each of the models and each of the methods. Additionally, we report ROC curves for the comparisons of MM versus MGUS and results on predicting MGUS from a model that distinguishes MM samples from normal samples.

**Tuesday, February 11th  
4:00 p.m.**

Room 1221  
Computer Sciences / Statistics Building  
1210 West Dayton Street