

Dr. Jacob. P. L. Brand

Address: 1665 Univ. Blvd. RPHB 327, Birmingham, AL 35294

JaapBrand@ms.soph.uab.edu

Tel: (205) 975-9172

Fax: (205) 975-2540

Statement of Research philosophy

Research interests:

My research interests are in the area of Statistical analysis of microarray data sets, Statistical Genetics, Bayesian Statistics, Markov Chain Monte Carlo methods, and statistical analysis of incomplete data.

My primary research goals are:

1. Development of more powerful algorithms for multiplicity control by taking full advantage of assumed and/or observed structures in the data
2. Assessing reliability and stability of clustering methods

More cost efficient multiplicity control

Finding differentially expressed genes, linkage studies, proteomics and biochemical system theory are situations in High Dimensional Biology involving statistical testing of many – often thousands – null-hypotheses. Because each true null-hypothesis has a small probability to be falsely rejected, a large number of false positive results will occur if the results are not corrected for multiplicity. Standard procedures for multiplicity control, such as Bonferroni's procedure for controlling the Family Wise Error Rate (FWER) and the method proposed in (Benjamini and Hochberg 1995), are not optimal because independence of statistical tests is assumed and observed and/or assumed structures in the data are not taken into account. The specific aim is to develop algorithms for multiplicity control with a higher statistical power by taking full advantages of these structures. I have developed an alpha spending algorithm for controlling the FWER for finding differentially expressed genes in microarray data sets. In this algorithm alpha spending weights w_1, \dots, w_g satisfying

$\sum_{i=1}^g w_i = 1$ are assigned to each of the g genes being studied. Each weight w_i is computed on the

basis of predictive information from surrounding genes and specifies for each gene the individual type 1 error allowed in declaring this gene significant. If a highly differentially expressed gene is strongly correlated to many non-differentially expressed genes, than this gene is acting "out of order" and it is likely that this gene is falsely declared differentially expressed. The alpha spending algorithm corrects for this by assigning to this gene a relatively low alpha spending weight w_i . Because the FWER is too strong I propose to develop an alpha spending algorithm for controlling the FDR.

Assessing reliability and stability of clustering methods

Clustering algorithms are commonly applied to microarray data sets in order to find groups of co-expressed genes to be investigated in future studies. Up until now, little work has been done in assessing the reliability and stability of clustering methods. By reliability I mean the correspondence of the structures in the data found by clustering methods to the underlying true structures in the data. Stability means that if exactly the same experiment is repeated under exactly the same experimental conditions, then similar clusters in the data will be found. I will investigate both stability and reliability by extensive simulation studies where data sets with known structures are generated. I will also develop diagnostic statistics for assessing reliability and stability of clustering's found in data sets.

Statement of Teaching Philosophy

I enjoy both classroom instruction as well as one-to-one mentoring. I would enjoy teaching classes in Statistics, Mathematics and Microarrays Data Analysis. The simple and real life examples are essential in teaching such classes. There is no one best teaching style, but there are fundamentals that must be followed in order to excel. These teaching fundamentals include a solid knowledge and preparation of the material, enthusiasm and passion in the delivery process, communication of the relevance of the material and a demonstrated willingness to help each student. A very effective way of teaching is to encourage students to solve problems in small groups using the things they have learned.