BIBLIOGRAPHY

Books


Refereed Papers in Edited Books / Book Chapters


**Papers in Refereed Journals - Methodological**


**Papers in Refereed Journals - Applied**


**Scholarly Articles in Periodicals**


**Selected Conference Proceeding Papers (not published elsewhere)**


**SOFTWARE PACKAGES**

URL: http://www.stat.ohio-state.edu/~statgen/Software.html

1. MethylCap-Sig: Performs five statistical tests (t, MethMAGE, and three mean vector tests) to find regions that are differentially methylated using MethylCap-Seq data that have been processed by PrEMeR-CG.

2. GrammR (Graphical representation and modeling of metagenomic reads): To represent metagenomic samples on the Euclidean space to examine similarity amongst samples by studying clusters in the model. Given the matrix of metagenomic counts for samples, this package (1) quantifies dissimilarity between samples using Kendall’s tau-distance, (2) constructs multidimensional models of different dimension, and (3) plots the models for visualization and comparison.

3. SIMPLE (Sequential Imputation for MultiPoint Linkage Estimation): Calculates linkage statistics, such as LOD scores and NPL statistics by sequential imputation. (Joint work with Skrivanek, Z. and Irwin, M.)
4. START: Finds starting points for MCMC analysis performed on large, complex pedigrees and polymorphic markers. (Joint work with Luo, Y.)

5. MAXPROC: Calculates maximum likelihood estimates of linkage parameters under heterogeneity and their standard errors using EM and SEM algorithms. (Joint work with Biswas, S.)

6. CSI (Confidence Set Inference): Constructs confidence set of markers for a disease locus based on a nonparametric confidence set inference approach. (Joint work with Papachristou, C.)

7. DNC-MIX: Class discovery and classification of tumor samples by modeling the distribution of a gene expression profile as a mixture, with each component characterizing the expression levels in a class. (Joint work with Alexandridis, R. and Irwin, M.)

8. tagSNPFinder: Computes multilocus LD measures and selects tagging SNPs within haplotype blocks. (Joint work with Liu, Z.)

9. Pathway: Use methylation profiles and clinical variables to group tumor samples into clusters and then organize them into a tree to represent tumor progression pathways that conform to strict heritability. (Joint work with Wang, Z.)

10. DE-SAGE: Analyze SAGE library data using a Bayesian hierarchical and mixture modeling approach and RJMCMC computational algorithms. (Joint work with Wang, Z.)

11. miRComp: A filtering step of putative microRNA targets through aggregating the predictions by several algorithms using two composite statistics - composite ranks and composite "p-values". (Joint work with Zou, J., and Qiu, F.)

12. MC-PDT: Perform test of linkage disequilibrium in the presence of linkage using pedigree data based on Monte Carlo samples of complete data given observed data. (Joint work with Ding, J.)

13. TopKCEMC: A rank aggregation tool for integrating data from multiple sources based on ranks.

14. rGLM: Generalized linear modeling with regularization for Case-control association studies; suitable for both common disease/common variants and common disease/rare variance scenarios.

15. DIME: An ensemble of three mixture models (GNG, NUDGE, iNUDGE) for differential analysis. This package can be used for analyzing ChIP-seq, gene expression, and DNA methylation data.

16. LBL: Logistic Bayesian Lasso for finding association of SNP haplotypes with a trait in a case-control setting.