statistical details on Type I error control as well as correction for estimation bias for a general confirmatory basket design when different endpoints are used for pruning and pooling.

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› Implications of Different Methods of Borrowing Information in Basket Trials

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Basket trials are becoming extremely popular due to their ability to investigate a variety of histologic subgroups within a single trial. We consider Bayesian Borrowing of information, which models the individual baskets using a hierarchical model. The priors in the hierarchical model have an effect on the operating characteristics of the trial. In situations where there is a general trend, hierarchical modeling produces higher power and lower type I error. In mixed situations, power reductions and inflated type I error are possible. We will quantify these advantages and disadvantages for a variety of priors and suggest default choices that produce good operating characteristics. To address the potential disadvantages of hierarchical models while keeping the advantages, cluster based generalizations (via Dirichlet Process or other mixtures) have also been proposed. We will illustrate the operating characteristics and interpretability of cluster based methods, and again focus on default choices of priors with reasonable operating characteristics.

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33. ORAL POSTERS: Advances in Methods for Genetics and Genomics

33a. INVITED ORAL POSTER:

Integrative Genomic Analyses

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Advances in high-throughput technologies have led to the acquisition of various types of -omic data on the same biological samples. Each data type provides a snapshot of the molecular processes involved in a particular phenotype. While studies focused on one type of -omic data have led to significant results, an integrative -omic analysis can provide a better understanding of the complex biological mechanisms involved in the etiology or progression of a disease by combining the complementary information from each data type. We investigated flexible modeling approaches under different biological relationship scenarios between the various data sources and evaluated their effects on a clinical outcome using data from the Cancer Genome Atlas project. The integrative models led to improved model fit and predictive performance. However, a systematic integration that allows for all possible links between biological features is not necessarily the best approach.

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33b. INVITED ORAL POSTER:

Simplified Power Calculations for Aggregate-Level Association Tests Provide Insights and Challenges for Rare Variant Association Studies

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Genome-wide association studies are now shifting focus from analysis of common to uncommon and rare variants with an anticipation to explain additional heritability of complex traits. As power for association testing for individual rare variants may often be low, various aggregate level association tests have been proposed to detect genetic loci that may contain clusters of susceptibility variants. Typically, power calculations for such tests require specification of large number of parameters, including effect sizes and allele frequencies of individual markers, making them difficult to use in practice. In this report, we approximate power to varying degree of accuracy using a smaller number of key parameters, including the total genetic variance explained by a given locus. Using the simplified power calculation methods, we then develop an analytic framework to obtain bounds on genetic architecture of an underlying trait given results from a genome-wide study and observe important