**Phylogenetic methods for computationally correlating genotypes and phenotypes** FARHAT HABIB, The Ohio State University, DANIEL JANIES, The ohio State University, RALF BUNDSCHUH, The Ohio State University — Single nucleotide polymorphisms or SNPs are DNA sequence variations among genomes of a population or other closely related group. While many SNPs have no effect on cell functions other SNPs predispose an organism to disease and or influence its response to a drug. Thus, SNPs are important for biomedical, biophysical, and pharmaceutical research. Given that SNP databases now have millions of SNPS it is imperative to develop automated methods of finding SNPs that are correlated with a phenotype of interest. We demonstrate a method of correlating phenotypes with genotypes with the aid of phylogenetic trees. Phylogenetic trees serve as hierarchical summaries of evolutionary change between ancestors and descendants. Our method maps phenotype data on the phylogenetic tree based on SNPs to look for associations with a chosen phenotype. The patterns in variation in SNPs and phenotypes are assessed using the Maddison's concentrated changes test (CCT). Some exemplary results from large SNP datasets from many strains of inbred mice will be presented.

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Date submitted: 23 Sep 2005                    Electronic form version 1.4