JOHANNA JAKOBSDOTTIR
Department of Biostatistics, Graduate School of Public Health
University of Pittsburgh

Interpreting Genetic Association Studies in Terms of the Value of Genetic Variants in Personalized Medicine

MONDAY, January 26, 2009 at 12:00 NOON
110 Eckhart Hall, 5734 S. University Avenue

ABSTRACT

Recent successes in the discoveries of potentially causal SNPs for complex diseases hold great promise and commercialization of genomics in personalized medicine has already begun. The hope is that genetic testing will benefit patients and their families and encourage positive life-style changes and guide clinical decisions. However, for many complex diseases, such as age-related maculopathy (ARM), it is arguable whether the era of genomics in personalized medicine is here yet. We discuss and explore some of the issues geneticists and physicians face when presenting the 'individual-level risk calculations. Our focus will be the clinical validity and utility of genetic testing with additional emphasis on two popular statistical methods for evaluating markers. The majority of genetic association studies are etiological studies aimed at finding variants strongly correlated with disease risk. We then hope to use these variants in individual-level risk estimation, classification, and clinical decision-making.

Using our ARM data, we examine the validity of the three strongest risk SNPs discovered so far. For example by using an additive model of the CFH, LOC387715, and C2 variants, with odds ratios (ORs) 2.9, 3.4, 0.4 and P-values $10^{-13}$, $10^{-13}$, $10^{-3}$, respectively, the area under the receiver operating characteristic curve is 0.79 but the positive predictive values (PPVs) assuming prevalence of 15%, 5.5%, and 1.5% (which are realistic for age groups 80 yr, 65 yr, and 40 yr and older, respectively) are only 30%, 12%, and 3%. PPV is the probability of disease given genotypes and therefore a more relevant risk estimator than the OR.