EXAMPLES OF THE USE OF HAPLOTYPING IN CLINICAL TRIALS

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As the current era of genomics advances, the amount of available genetic information is rapidly expanding. This information can be utilized in various ways within clinical trials. For example, prior to initiating a trial, one can identify subgroups of patients that may respond well or poorly to a drug by using information on variants of genes that code for drug metabolizing enzymes or receptors. Although the use of genetic information has the potential to reduce sample sizes and clinical trial duration, sorting through the massive amount of variation in the human genome to identify the genetic variation that may be relevant to the endpoint under study is challenging. One approach that is commonly used to "make sense" of the variation is haplotyping. Haplotyping takes advantage of the correlation, which exists within the human genome to identify patterns consisting of a smaller amount of the variation, which reflects enough of the total variation to be useful. Presented here are examples of the use of haplotyping within the clinical trial setting, and a discussion of issues related to effectively applying haplotyping.