The GenABEL suite for genome-wide association analyses

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Genome-wide association (GWA) analysis is a widely recognized technique for identification of genomic regions (loci) in which changes in DNA sequence lead to changes in complex phenotype. In GWA scans, genomes of thousands of individuals are assessed by use of single nucleotide polymorphisms (SNP) arrays or whole-genome resequencing to gather information on hundreds of thousands to millions of genetic variants. The trait values of genotyped individuals are then tested for association with this genetic variation. During the last eight years, hundreds of loci for dozens of human common diseases and other complex traits were identified using GWA scans.

The GenABEL project aims to provide a free framework for collaborative, robust, transparent, open-source based development of statistical genomics methodology. In the framework of this project we have developed a suite of packages facilitating different semi-independent types of GWA analyses. The suite currently includes nine packages, of which seven are R libraries, such as the GenABEL for generic GWA quality control and analyzes, MetABEL for meta-analysis, DatABEL for large data sets management, VariABEL for identification of potentially interacting variants, and others. The packages are distributed under GPL or LGPL and are available at the GenABEL project home page, http://www.genabel.org.

Here, I will describe the GenABEL project in general and will also introduce some of the packages of the suite.