

# Using GenABEL suite for genetic analysis

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Genome-wide association (GWA) analysis is a modern, but already widely recognized technique for identification of genomic regions (loci) in which changes in DNA sequence lead to changes in complex phenotype. In GWA scans, thousands of individuals are typed using 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 typed genetic variation. During last 6 years, hundreds of loci for dozens of human common disease and many other complex traits were identified using GWA analyzes.

We have developed **GenABEL** suite of libraries for *R* to facilitate different aspects of GWA analyzes in polymorphic populations. Specific, semi-independent types of GWA analysis were arranged as separate *R* packages, such as **GenABEL** for GWA analyzes, **MetABEL** for meta-analysis, **DatABEL** for large data sets management, **VariABEL** for identification of potentially interacting variants, etc. The packages are distributed under GPL or LGPL and are available at **GenABEL** home page <http://www.genabel.org>.

The **GenABEL** is more than a collection of packages as it also is a project aiming to provide a free framework for collaborative, robust, transparent, open-source based development of statistical genomics methodology. The infrastructure facilitating this consist of the developers' mailing list and source code repository hosted at R-Forge and the **GenABEL** user forum.

In this tutorial, I will outline main features and uses of the **GenABEL** suite, and will give practical examples of its use.

## References

GenABEL project, <http://www.genabel.org/>.