

GenABEL'ing genome-wide association analysis (and more)

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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 for hundreds of thousands to millions of single nucleotide polymorphisms (SNPs), and then the trait values of these individuals are tested for association with typed SNPs. During last 5 years, hundreds of loci for dozens of human common disease and many other complex traits were identified using GWA analyzes.

We have developed **GenABEL** package (Aulchenko et al., 2007) to facilitate genome-wide association (GWA) analyzes. Specific, semi-independent types of GWA analysis were arranged as separate R packages, such as **MetABEL** package for meta-analysis of the results of GWA scans. Given large amounts (from Giga- to Terabytes) of data used in current GWA scans, and amount of computations (millions to billions of tests), we have also developed a number of supporting R packages. Among these, a package facilitating access to and management of very large amounts of data in out-of-RAM mode, **DatABEL**, and a package facilitating high-performance parallel analysis of GWA data. The packages are distributed under GPL or LGPL and are available at *ABEL home page <http://mga.bionet.nsc.ru/~yurii/ABEL/>.

Our *ABEL suite for R makes GWA analysis of millions of SNPs typed or imputed in thousands of individuals feasible using wide range of hardware – from a NetBook to a powerful computational cluster.

References

- Aulchenko et al. (2007). GenABEL: an R library for genome-wide association analysis. *Bioinformatics*, 23, 1294–1296.