New software and developments in the GenABEL project

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The GenABEL project for statistical genomics

Our mission:

- Provide a free and open framework for development of statistical genomics methodology.
- Develop and maintain free and opensource implementations of these methodologies: the GenABEL suite.



New additions and updates

Recent improvements to the GenABEL suite and project:

• **OmicABEL**: extremely fast mixed-model based GWAS analysis of many phenotypes (e.g. metabolomics, glycomics)



- **Dissemination** of these methods and software.
- Foster collaboration between methodology developers, software developers and end users.

Packages in the GenABEL suite

- GenABEL^[3] core (2007), ProbABEL^[4] (2009) and MixABEL (2010); for flexible analysis of genome-wide association studies (GWAS)
- MetABEL (2009), for meta-analysis of GWAS results
- VariABEL^[5] (2011), genome-wide search of interacting loci
- **PredictABEL**^[6] (2011) facilitates evaluation of genomic prediction models
- **ParallABEL**^[7] (2010), for parallelization of GWA analyses
- **DatABEL** (2010), a library for management of very large files
- **OmicABEL** (2013), extremely fast analysis of omics traits (omics GWAS), see Figure

Web site statistics		
Percentage of visits in Feb. 2014	Web site views in Feb	national institutes of health -

MAX 📥 GWFGLS 🖶 FaST-LMM 🔶 OmicABEL

- Papers published: Tsepilov 2013^[1] and Belonogova 2013^[2]
- ProbABEL packaged for:
 - **Debian** (.deb), included in "testing" and "unstable".
- Ubuntu (.deb), using a Personal Package Archive (PPA).
- More packages will follow, as well as .rpm packages.



2014: 2295

- Web site views since Jan 1st, 2011: **69 464**
- Total nr. of forum users since Jan 1st, 2011: **479**
- Total nr. of forum posts since Jan 1st, 2011: **1213**
- Number of downloads of the ProbABEL package from the Ubuntu PPA: **110**



- Improved software development: Use the Jenkins Continuous Integration server to monitor stability and quality of the code.
- The GenABEL tutorial has been made fully open source.
- New package releases in 2014:
 - **ProbABEL:** v0.4.3
 - GenABEL: v1.8-0
 - MetABEL: v0.2-0
 - VariABEL: v0.9-2

How to contribute?

We welcome all sorts of contributions:

- Answer questions on the forum
- Add/correct the documentation
- Graphics and/or web design
- Report and/or fix bugs

Plans for the near future

• OmicABEL:

- Improved user-friendliness
- More efficient storage of output data
- Release of a non-mixed-model version of OmicABEL

• **ProbABEL**:

References

- [1] Y. A. Tsepilov et al. Development and application of genomic control methods for genome-wide association studies using non-additive models. PLoS One, 8: e81431, 2013.
- [2] N. M. Belonogova et al. Region-based association analysis of human quantitative traits in related individuals. PLoS One, 8: e65395, 2013.

- Creating .deb or .rpm packages
- Help maintaining packages
- Write new packages
- Financial support/feature on request
- Speed up of analyses
- Support for *p*-values in output
- Support for reading and writing zipped files

URLs

• Home page:

http://www.genabel.org

- Support forum:
 - http://forum.genabel.org
- **Development:** GenABEL @ http://r-forge.r-project.org

Financial support

- Erasmus MC, Rotterdam, NL
- YuriiA Consulting, Groningen, NL
- MIMOmics (EU FP7 project)
- New sponsors needed since we have no dedicated funding!

- [3] Y. S. Aulchenko et al. GenABEL: an R library for genome-wide association analysis. Bioinformatics, 23: 1294-1296, 2007.
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- [5] M. V. Struchalin et al. Variance heterogeneity analysis for detection of potentially interacting genetic loci: method and its limitations. BMC Genet, **11**: 92, 2010.
- [6] S. Kundu et al. PredictABEL: an R package for the assessment of risk prediction models. Eur J Epidemiol, 2011.
- [7] U. Sangket et al. ParallABEL: an R library for generalized parallelization of genome-wide association studies. BMC Bioinformatics, **11**: 217, 2010.