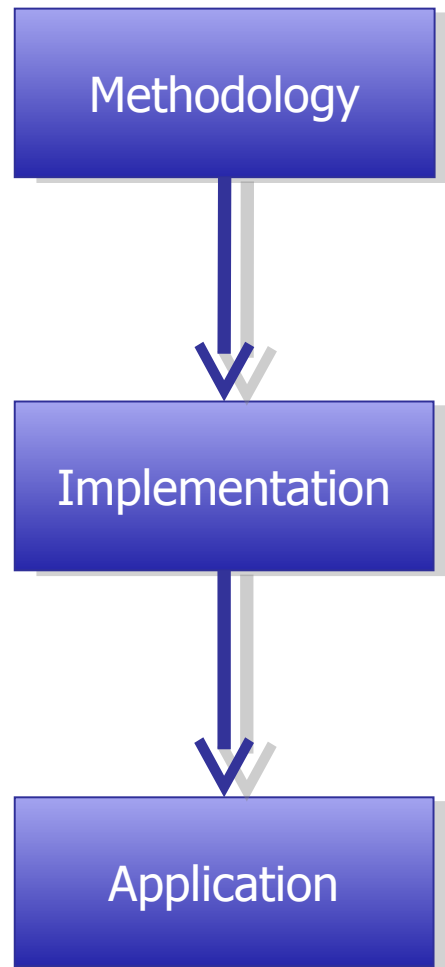


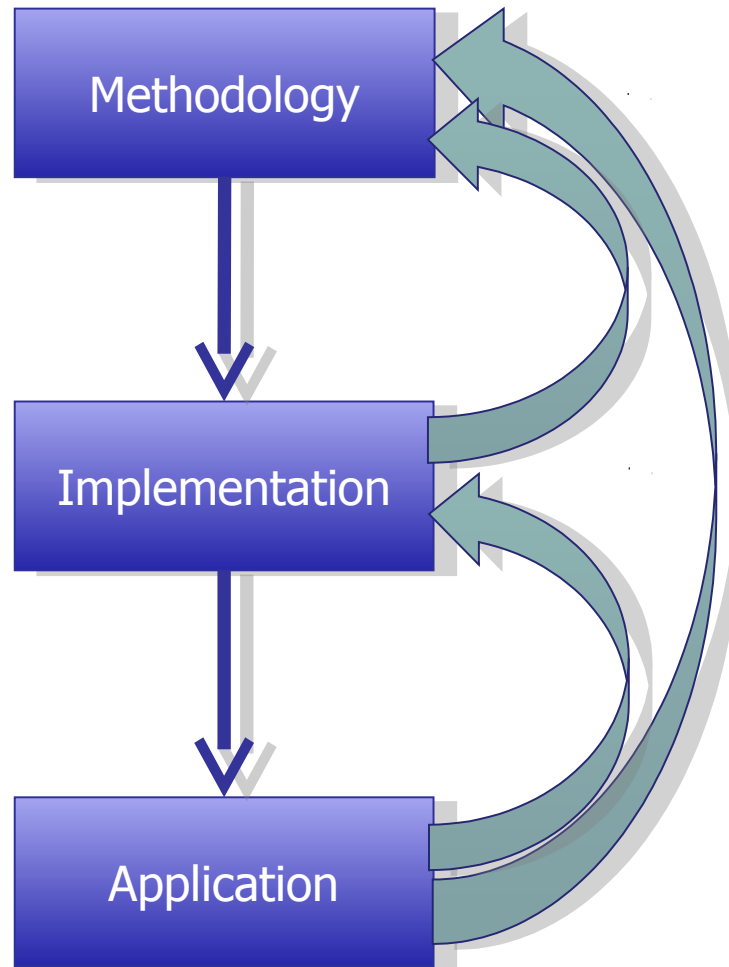


GenABEL project: open methodology for statistical genomics

Agile methodology development



Agile methodology development



Genetics and population analysis

GenABEL: an R library for genome-wide association analysis

Yurii S. Aulchenko^{1,*}, Stephan Ripke², Aaron Isaacs¹ and Cornelia M. van Duijn¹

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DOI: 10.1534/genetics.107.075614

Genomewide Rapid Association Using Mixed Model and Regression: A Fast and Simple Method For Genomewide Pedigree-Based Quantitative Trait Loci Association Analysis

Yurii S. Aulchenko,^{*,†,1} Dirk-Jan de Koning[‡] and Chris Haley[‡]

Software

Highly accessed

Open Access

ProbABEL package for genome-wide association analysis of imputed data

Yurii S Aulchenko^{1,2*}, Maksim V Struchalin¹ and Cornelia M van Duijn¹

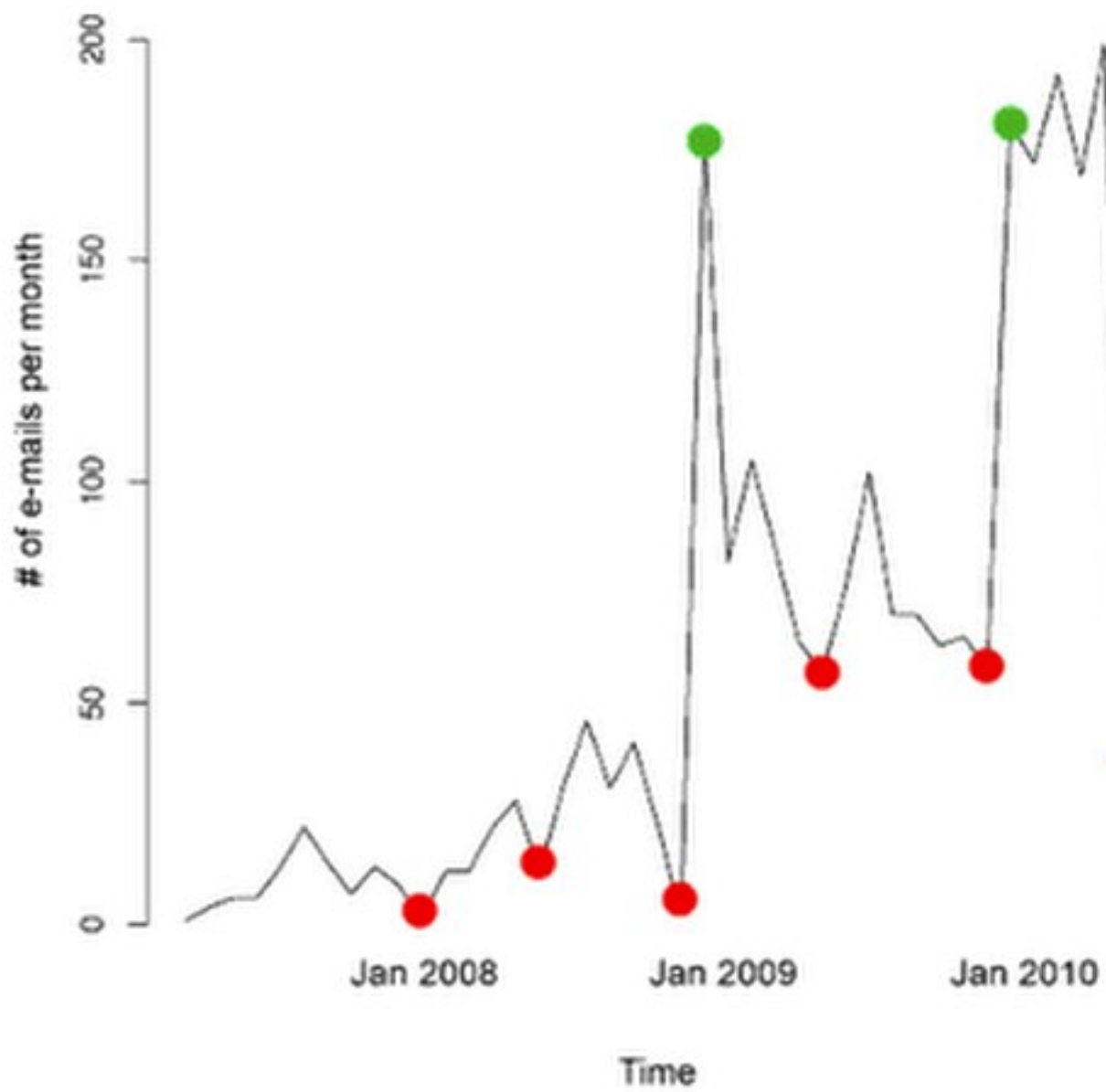
Methodology article

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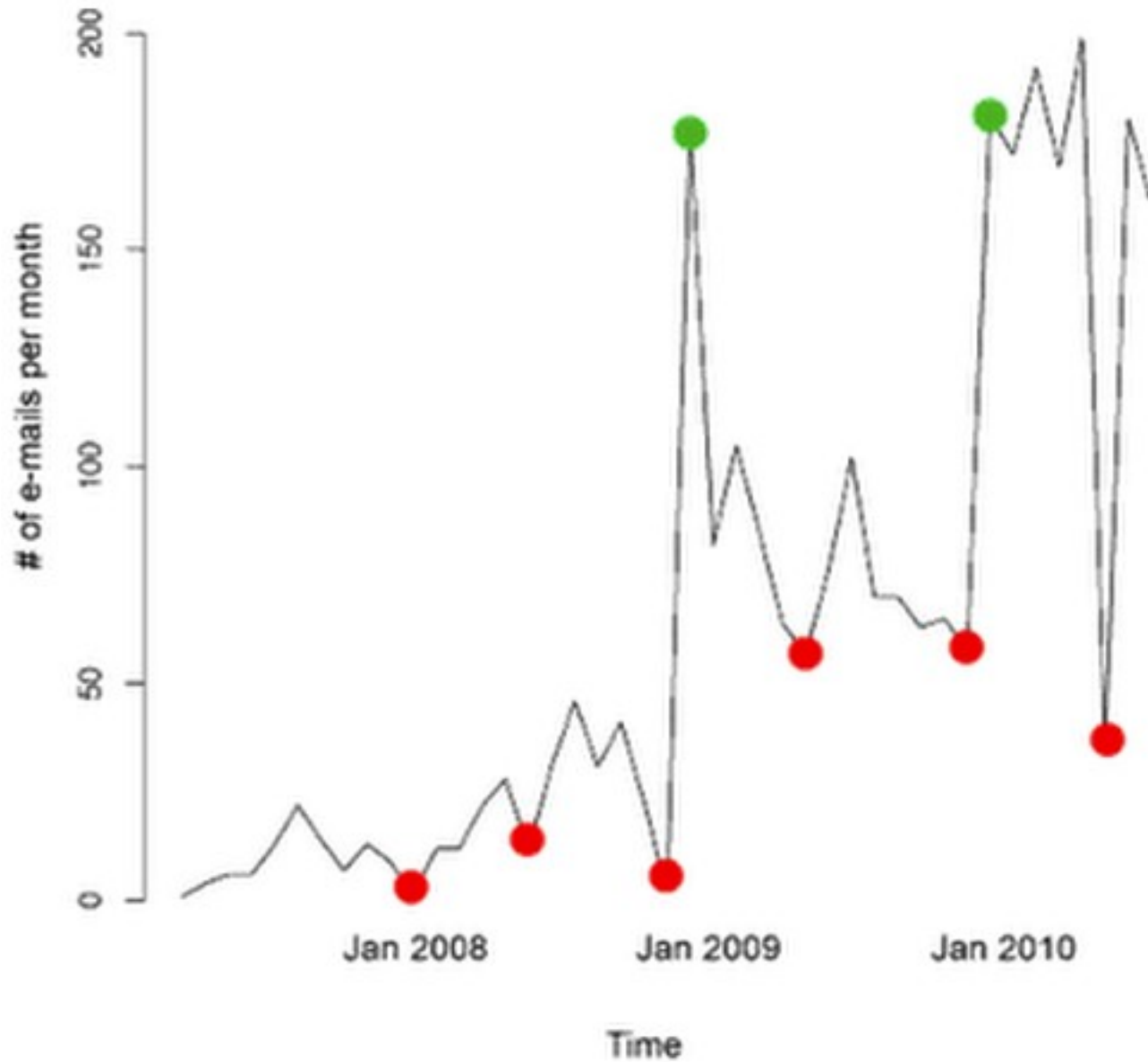
Open Access

An R package "VariABEL" for genome-wide searching of potentially interacting loci by testing genotypic variance heterogeneity

Maksim V Struchalin¹, Najaf Amin¹, Paul HC Eilers², Cornelia M van Duijn¹ and Yurii S Aulchenko^{1,3*}



Get him out of the way!



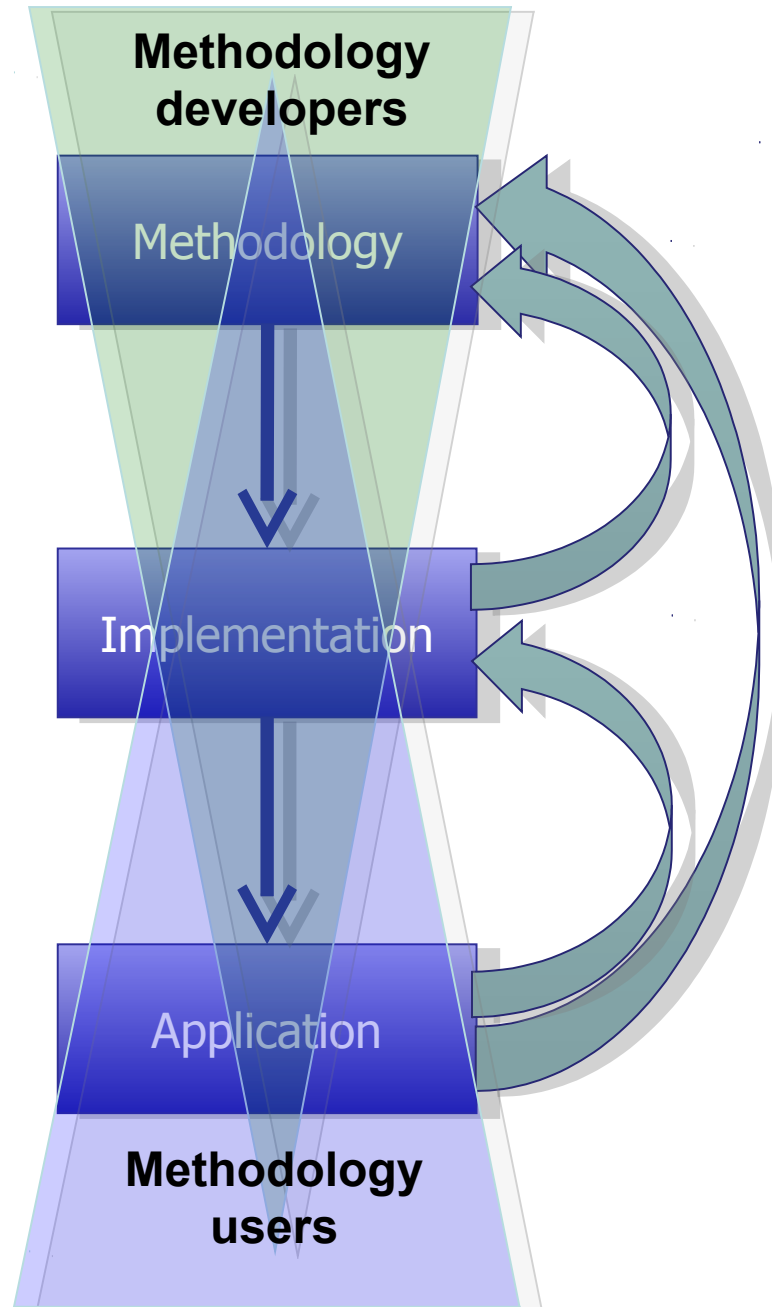


Aim of GenABEL project

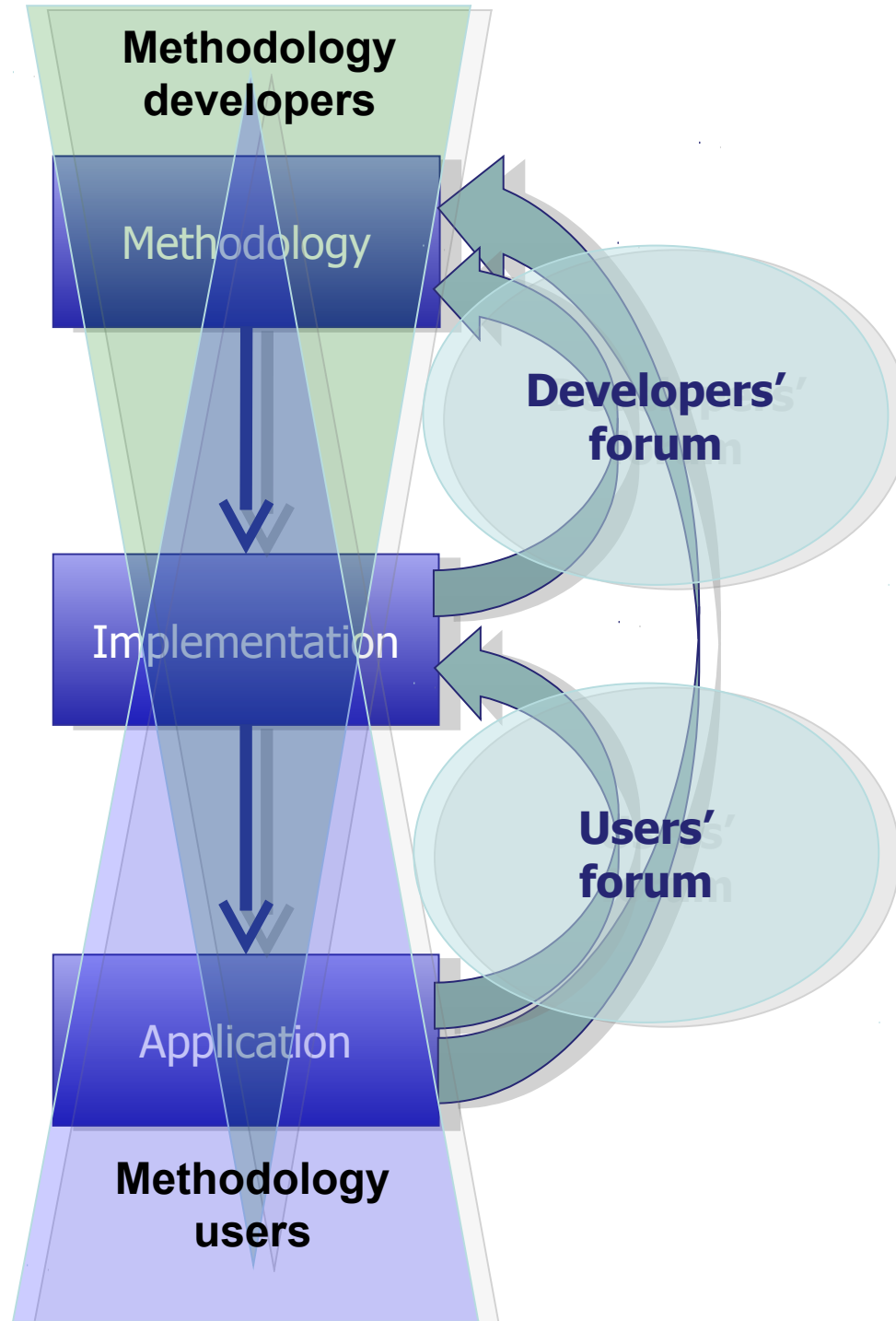
To create a framework for robust development, implementation and application of novel statistical genomics methodology

Through infrastructure connecting the people developing and applying statistical genomics methodology

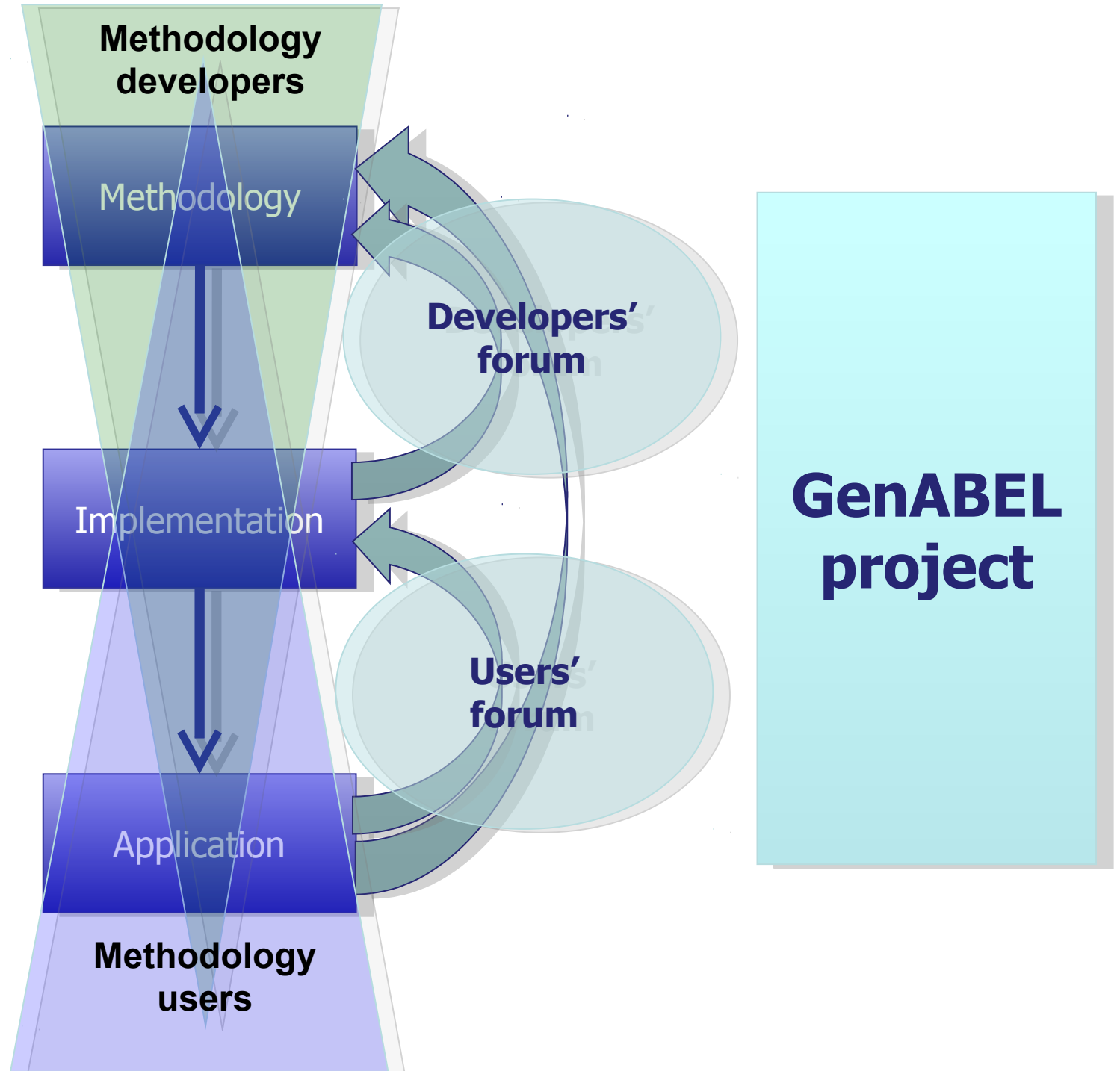
Agile methodology development



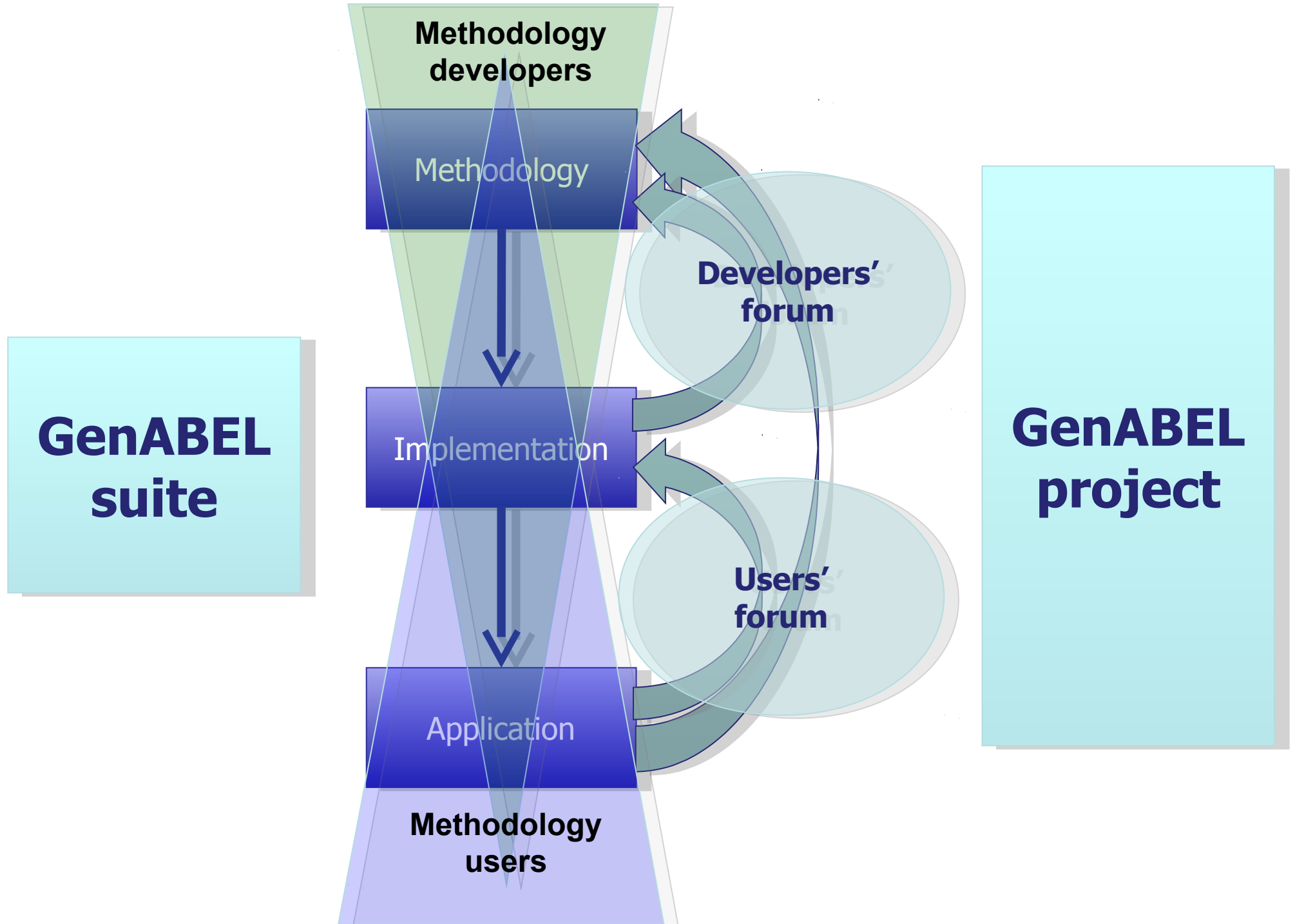
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Infrastructure for the GenABEL project

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Development RForge

A suite of packages for statistical genomics

- Intended Audience: End Users/Desktop
- License: GNU General Public License (GPL)
- Natural Language: English
- Programming Language: C/C++, R
- Topic: Statistics, Linkage, LD and Haplotype Mapping

Registered: 2009-08-12 19:07
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Developer Info
Project Admins:
Lennart Karlsen
Tagir Valeev
Yuri Aulchenko
Developers:
Anatoly Kirichenko
Andrey Chernykh
Diego Fabregat
Erik Riise
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Marcel Kempenaar
Sergey Yakovenko
Suman Kundu
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The GenABEL suite (aka "ABEL suite") is practical result of implementation of statistical genomics methods developed in GenABEL project. The GenABEL suite (currently consisting of a number of open-source software packages) includes the following functions: efficient, open-source tools for collaborative, reproducible, open-source development, implementation, dissemination and maintenance; through the community.

The GenABEL suite (aka "ABEL suite") is practical result of implementation of statistical genomics methods developed in GenABEL project. The GenABEL suite (currently consisting of a number of open-source software packages) includes the following functions: efficient, open-source tools for collaborative, reproducible, open-source development, implementation, dissemination and maintenance; through the community.

- Efficient. Memoscan can run a genome-wide association scan on a netBook
- Flexible. Programming your custom analysis is easy
- Open, transparent, free. At present, all code is released under the GNU GPL [GNU GPL]
- Well documented. More than 200 pages of reference manuals and about 300 pages of tutorials [Tutorials | Manual]
- Supported. By our community [Forum]
- Collaborative. The community is open for your contribution [Contribute]

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GenABEL Questions about GenABEL (aka "ABEL") suite of packages	5	74	by nico-giraldi Fri May 20, 2011 5:36 pm
Journal Club on Statistical Genomics Statistical genomics for dummies and advanced. Discussion, links, useful information.	4	5	by Maria C. P. Sun Feb 06, 2011 9:17 pm

User support forum.genabel.org

Developers workshops

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The mission of the **GenABEL project** is to provide a free framework for collaborative, robust, transparent, open-source based development of statistical genomics methodology. We aim to streamline methodology discussion, development, implementation, dissemination and maintenance; through the community.

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Aug 9, 2012: The VariABEL paper is ranked highly accessed

An open-access paper describing the [VariABEL package](#) (published in *BMC Genetics*), was rated as "highly accessed".

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GenABEL website and forum back online

Thu, 08/09/2012 - 08:23 — Ickarssen

After several days of "blackout", the GenABEL website and forum are up and running again.

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The GenABEL project forum

GenABEL project: a framework for collaborative open-source based development of statistical genomics methodology

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 ProbABEL Questions about ProbABEL are welcome here.	49	158	by Ickarsen  Fri Jul 13, 2012 3:03 pm
 Journal Club on Statistical Genomics Statistical Genomics for dummies and advanced. Discussions, links, usefull information.	7	23	by fede  Thu Jul 12, 2012 6:46 am

GenABEL suite

- Open, transparent, free
- Rich in functionality. Now 7 packages containing ~150 functions related to genomic analysis
- Efficient. We aim that you can run a genome-wide association scan on a netBook
- Flexible. Programming your custom analysis is easy
- Well documented. More than 200 pages of reference manuals and about 300 pages of tutorials
- Supported – by the community
- Collaborative – and **open for for your contribution**