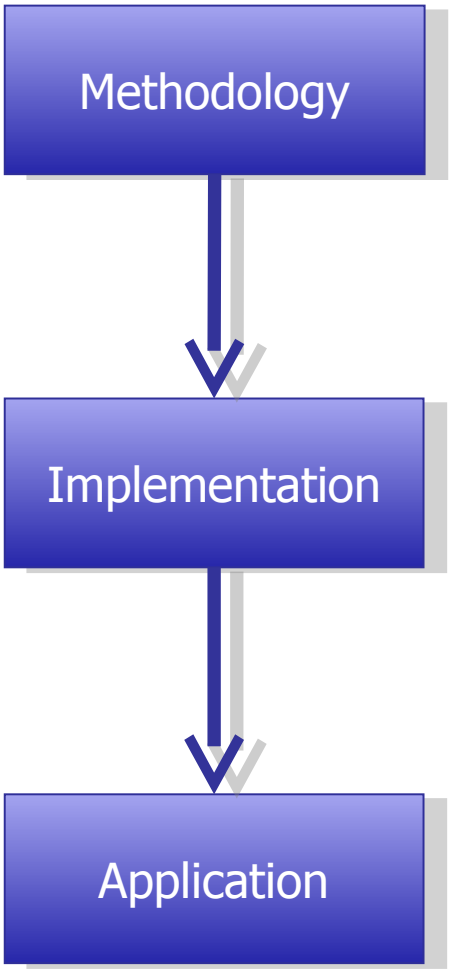
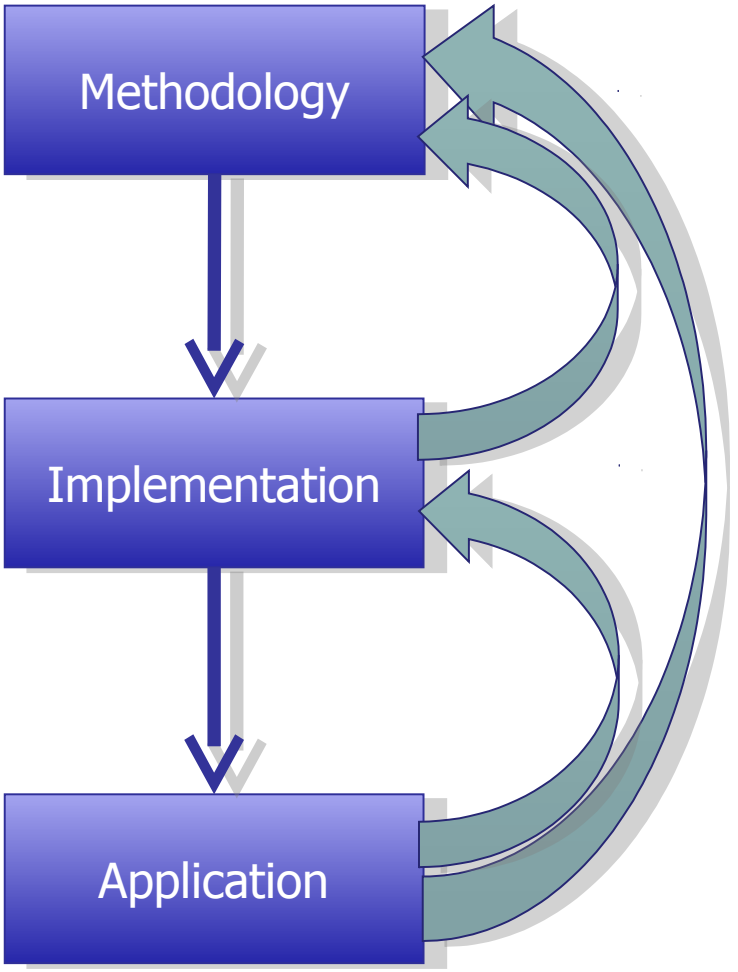
CC BY SA

GenABEL project: open methodology for statistical genomics

Agile methodology development



Agile methodology development



BIOINFORMATICS APPLICATIONS NOTE Vol. 23 no. 10 2007, pages 1294–1296
doi:10.1093/bioinformatics/btm108

Genetics and population analysis

GenABEL: an R library for genome-wide association analysis

Yurii S. Aulchenko[1,*], Stephan Ripke[2], Aaron Isaacs[1] and Cornelia M. van Duijn[1]

Copyright © 2007 by the Genetics Society of America
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

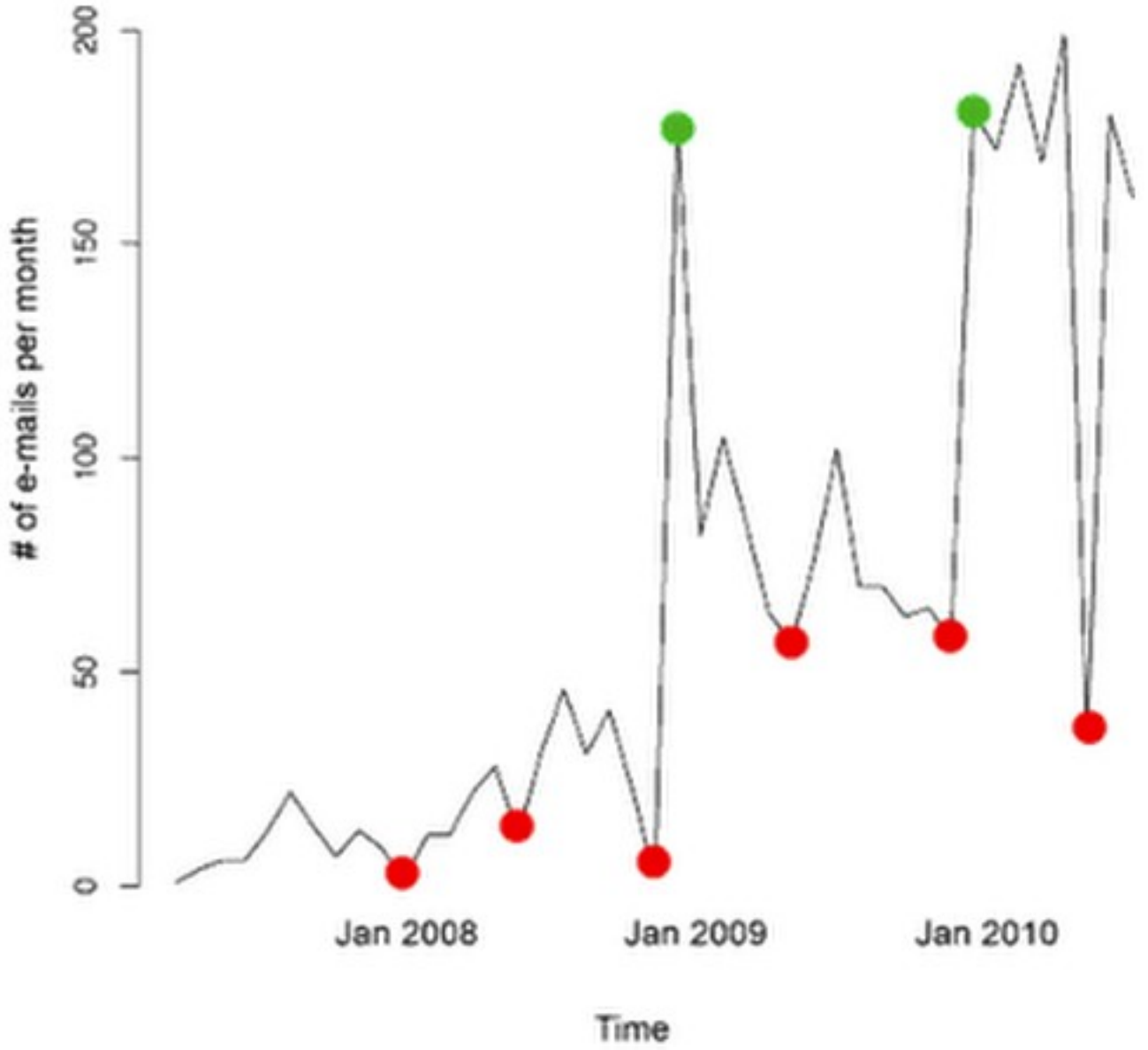
ProbABEL package for genome-wide association analysis of imputed data

Yurii S Aulchenko[1,2]*, Maksim V Struchalin[1] and **Cornelia M van Duijn[1]**

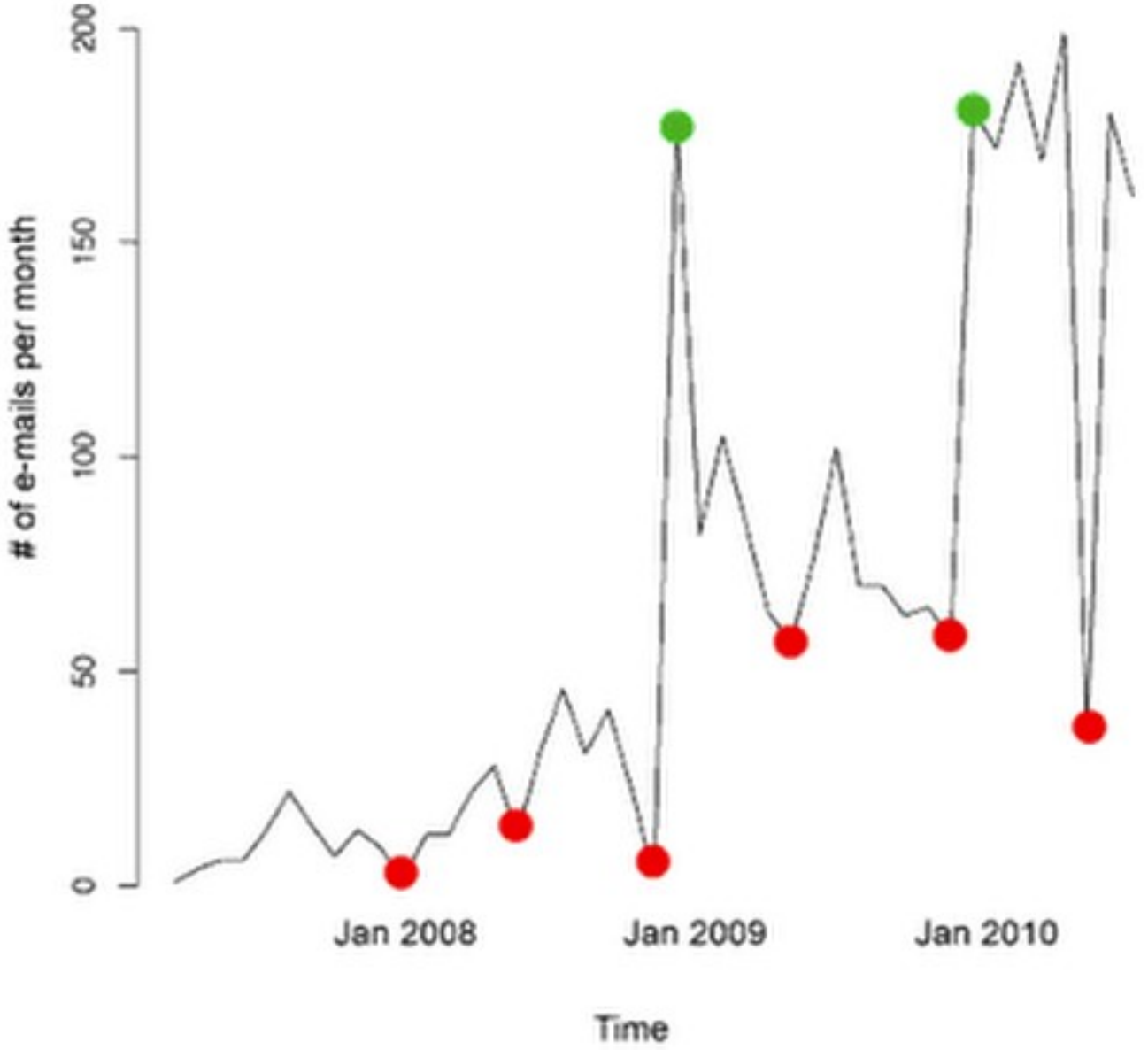
Methodology article Highly accessed Open Access

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

Maksim V Struchalin[1], Najaf Amin[1], Paul HC Eilers[2], Cornelia M van Duijn[1] and **Yurii S Aulchenko[1,3]***


# of e-mails per month
0
50
100
150
200
Jan 2008
Jan 2009
Jan 2010
Time

Get him out of the way!



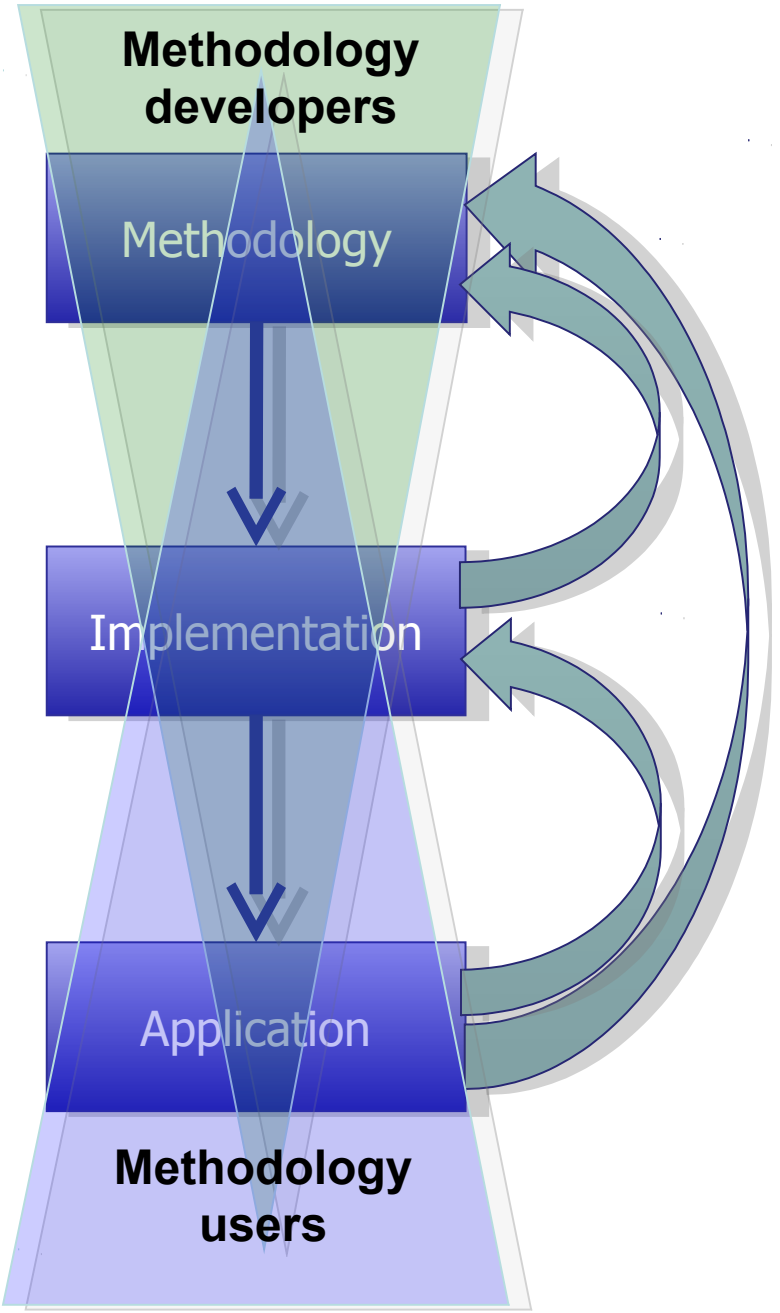
CC BY SA

Aim of GenABEL project

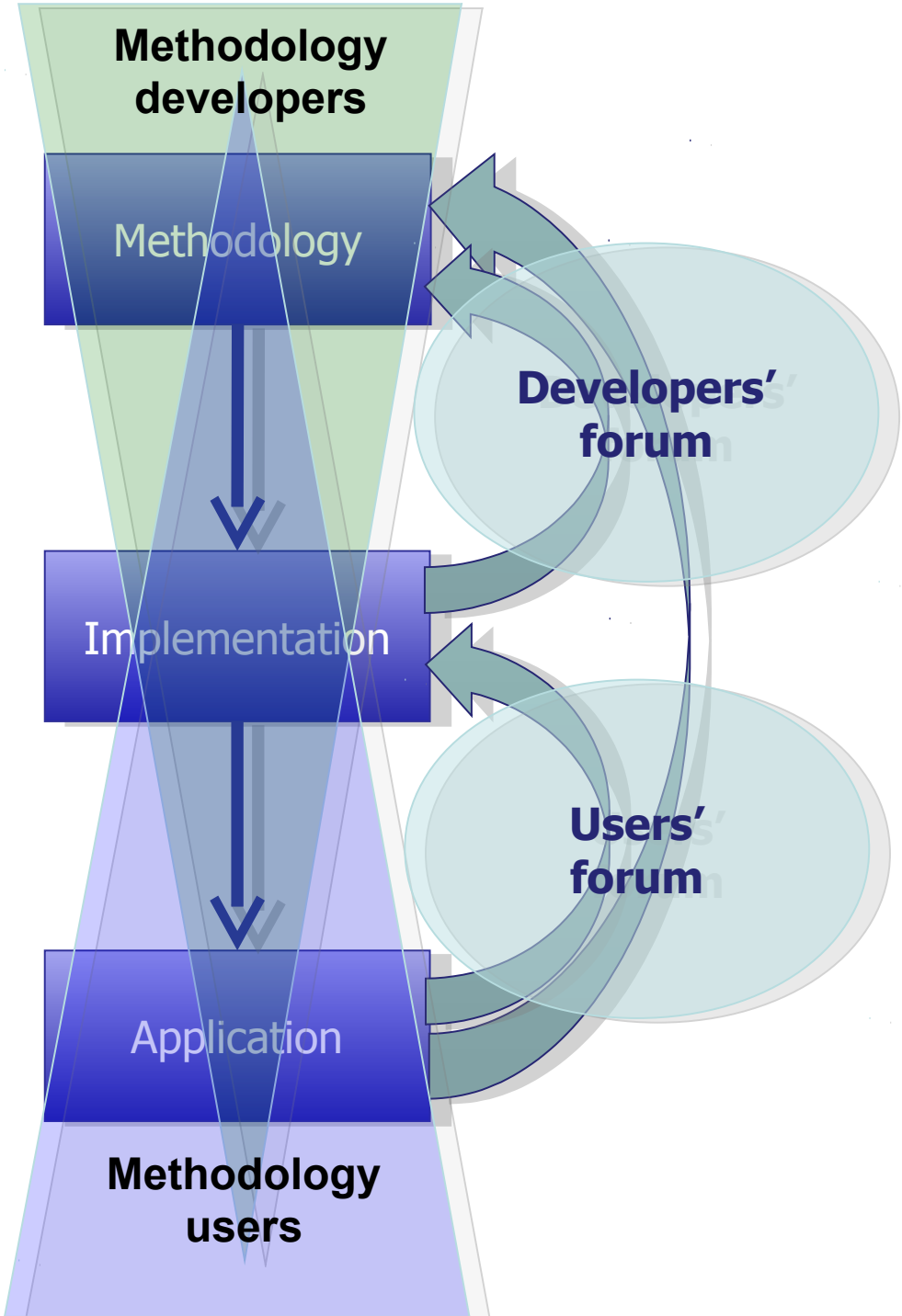
To create a framework for robust development, implementation and application of novel statistical genomics methodology

Through infrastructure connecting the people developing and applying statistical genomics methodology

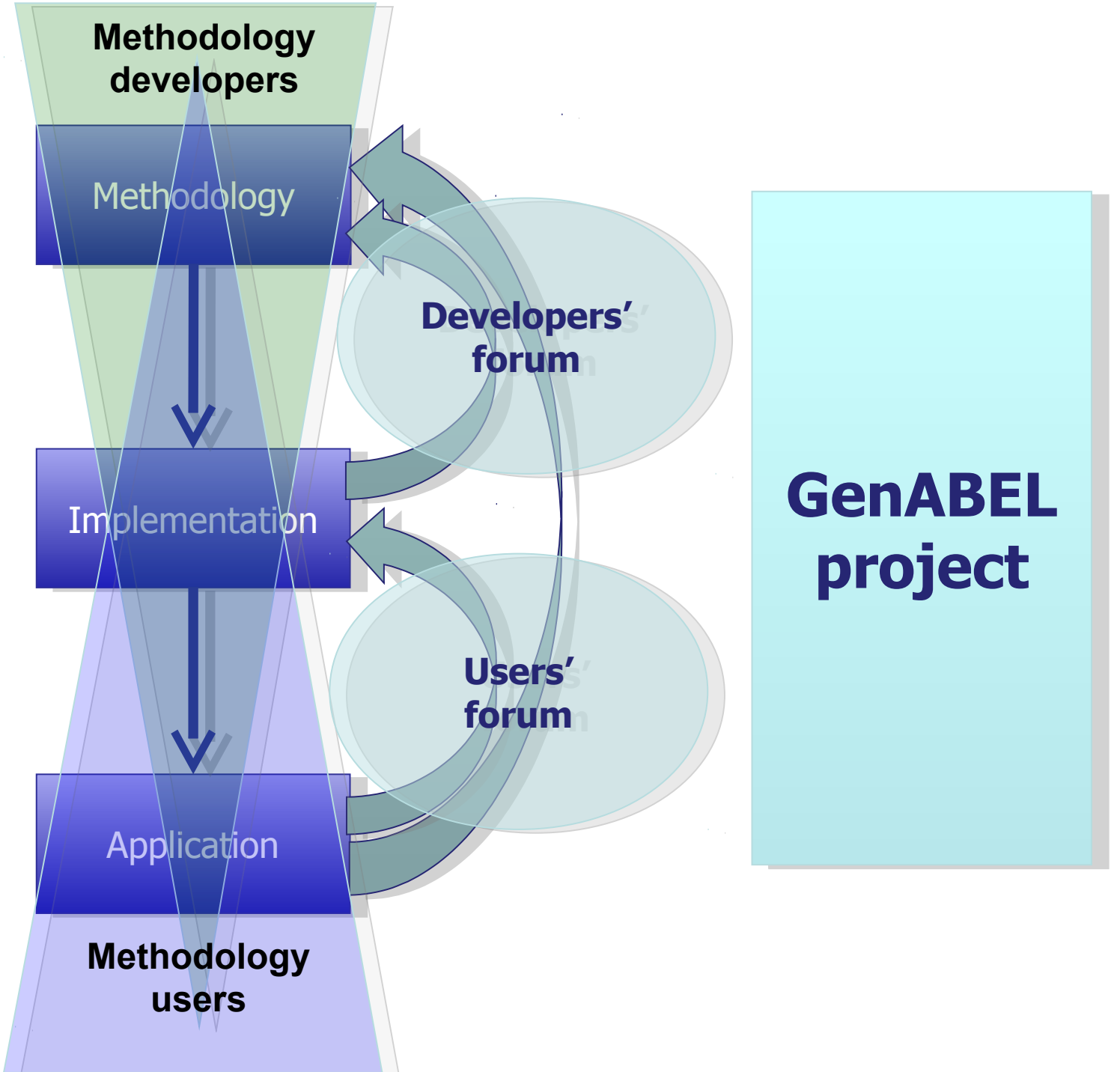
Agile methodology development



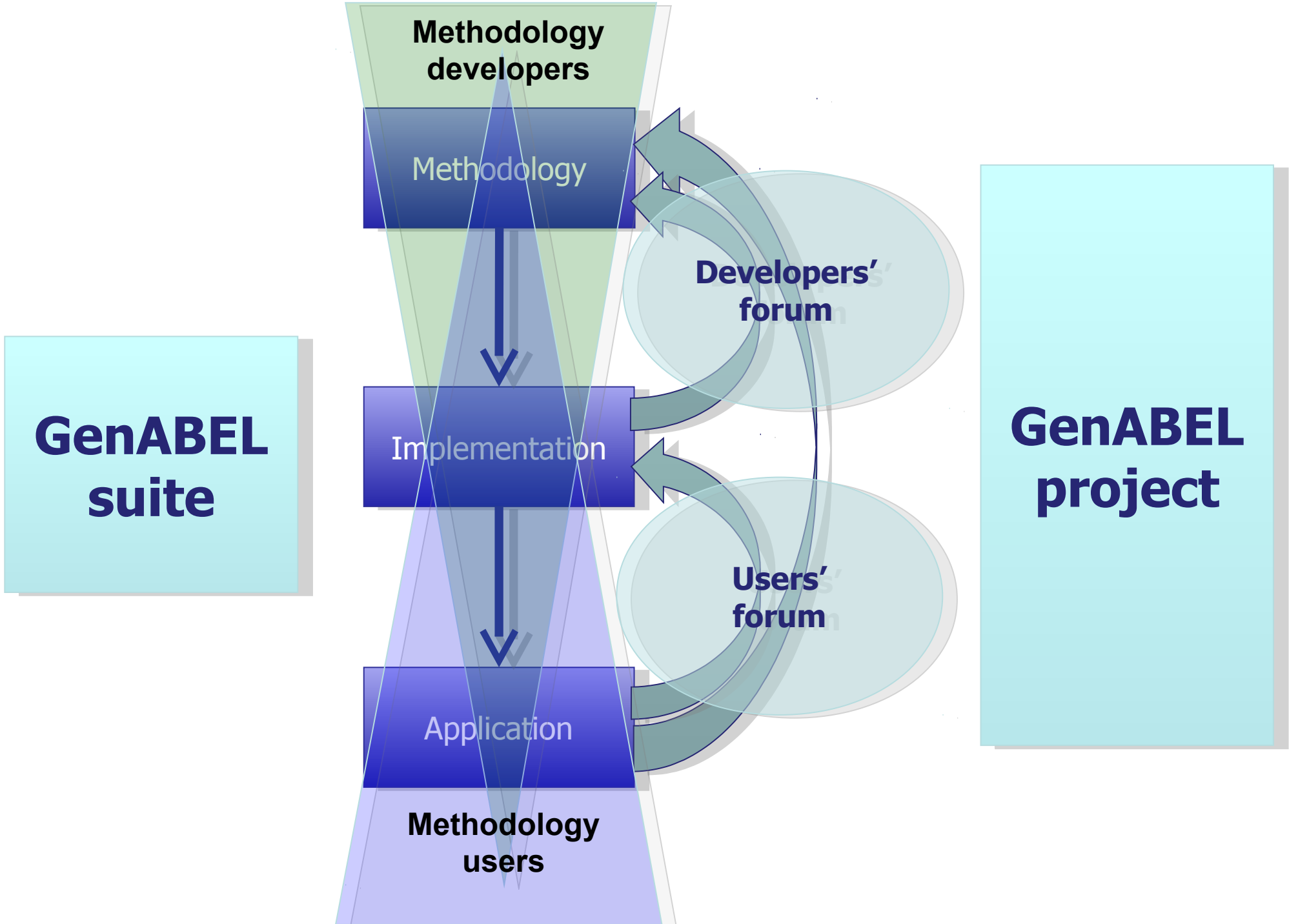
GenABEL project



GenABEL project

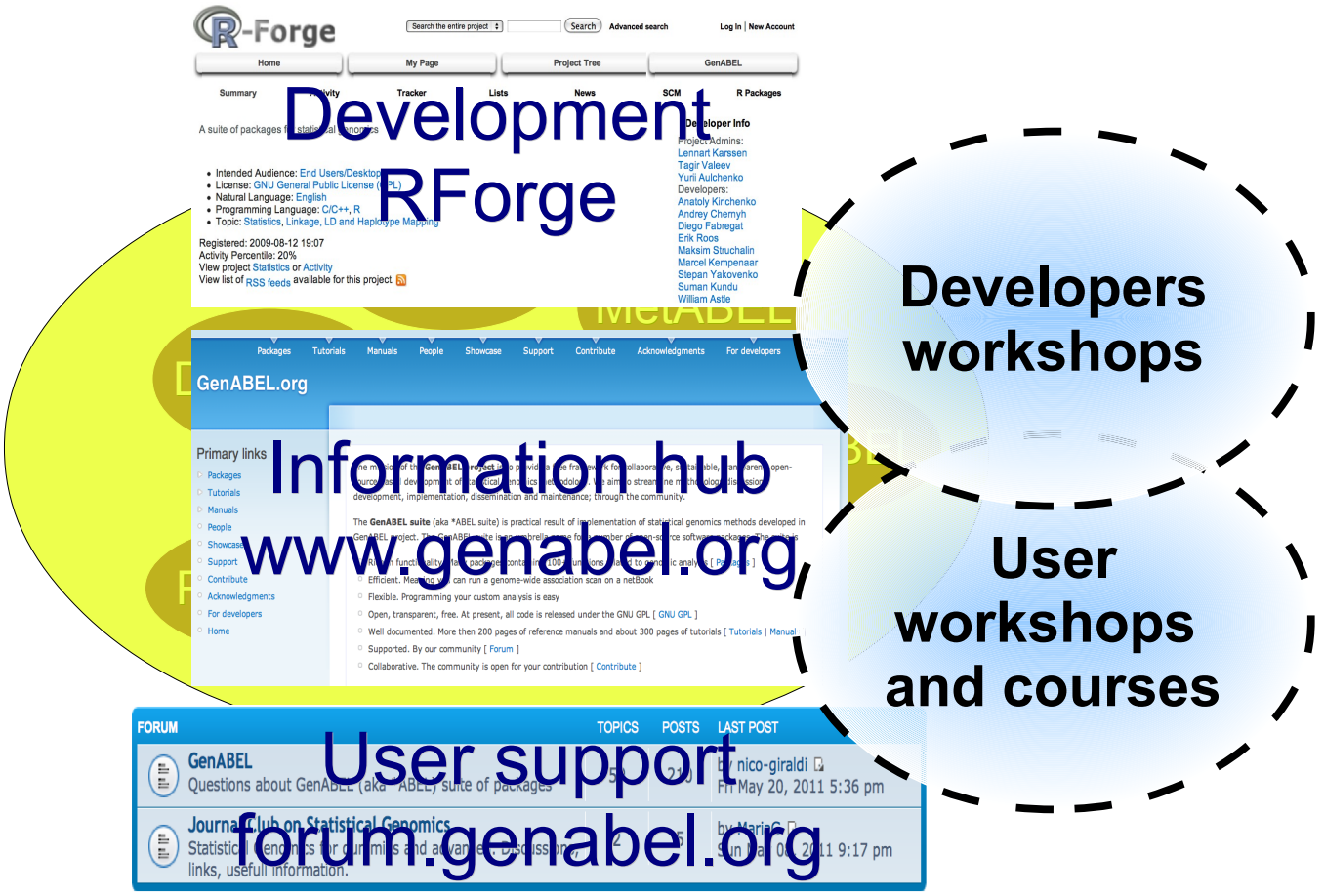


GenABEL project

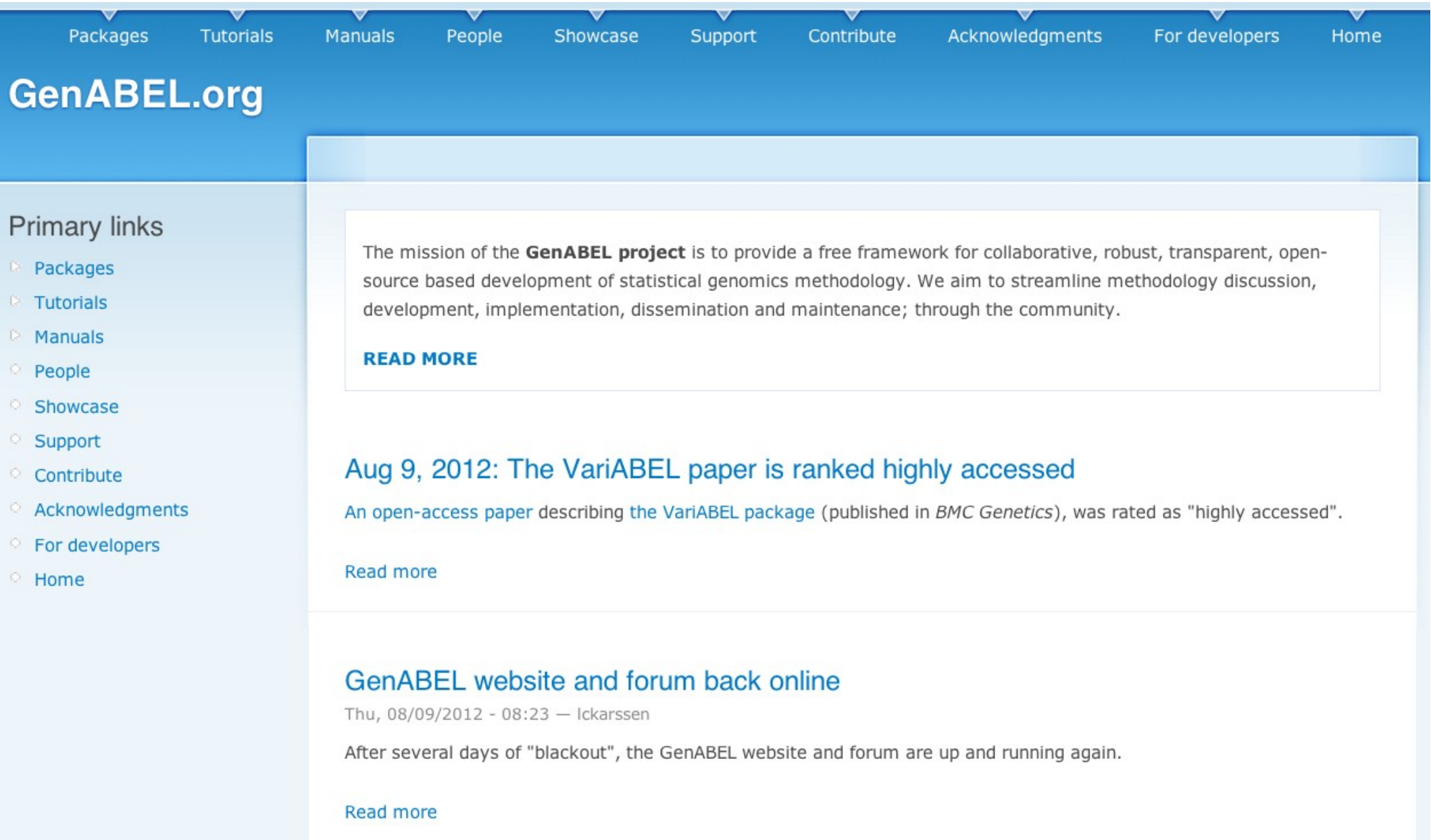


CC BY SA

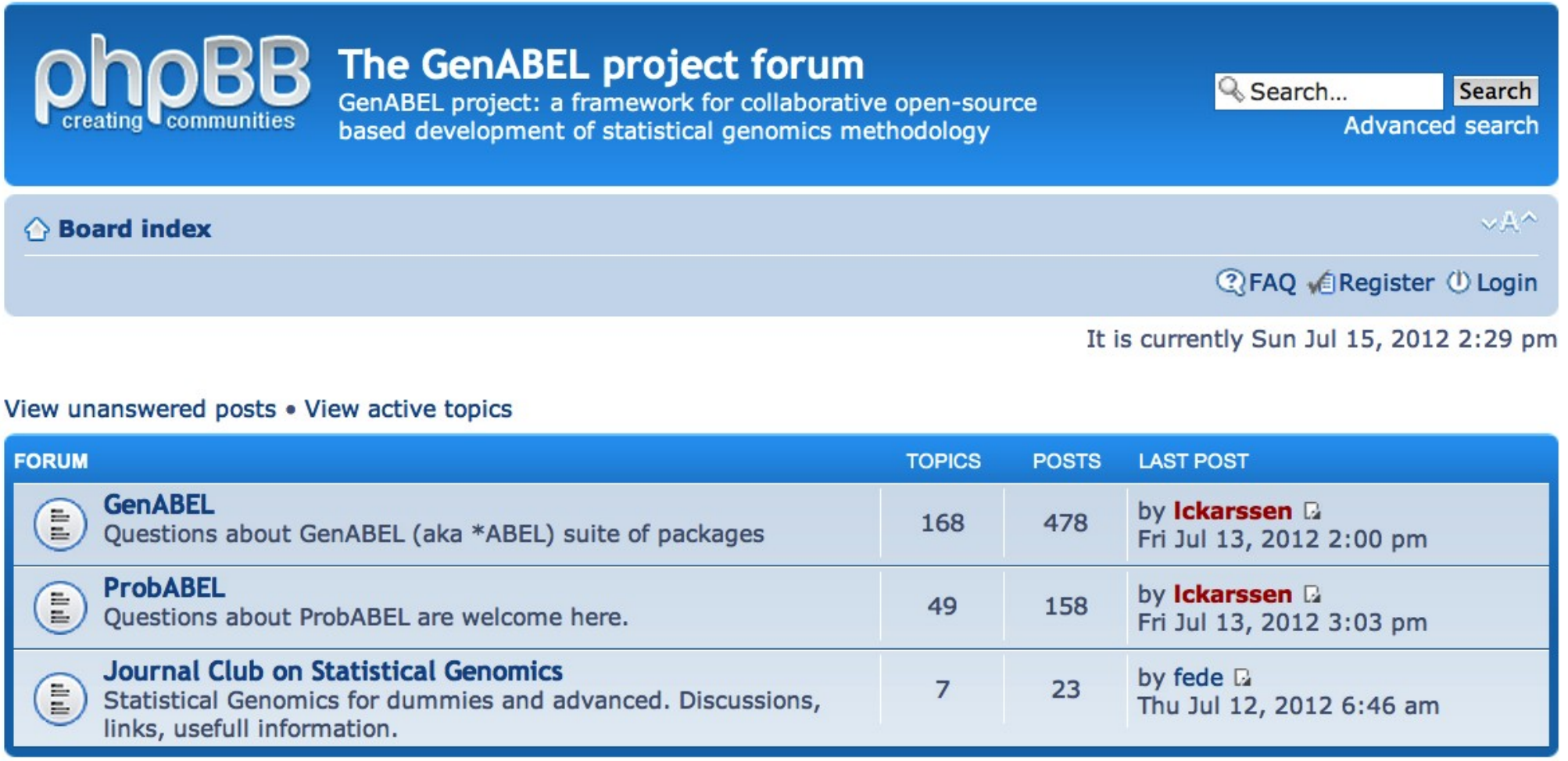
Infrastructure for the GenABEL project



www.GenABEL.org



forum.GenABEL.org



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 then 200 pages of reference manuals and about 300 pages of tutorials
- Supported – by the community
- Collaborative – and **open for for your contribution**