

Publishing genome-wide studies in the GSA journals: GENETICS and G3: Genes|Genomes|Genetics

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Take home message:
***Publishing is best when
community-driven***

COI

- Many journals and most have own purpose/scope
- Multiple hats:
 - Author
 - Referee
 - Editor
 - Colleague



Three types of papers

- Methods for genome-wide analysis
- GWAS Results
- Genomic Selection results

Genome-wide methods

- Proliferation of methods papers (QTL/GWAS/GS)
- Each method paper comes with its own simulations
- New method is always "*best*" on simulated data

Community initiatives

- QTL/MAS workshops (since 1996)
- Later GWAS/GS themed
- Shared sets of real and simulated data
- Contributed and summary papers

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Volume 3 Supplement 1

Proceedings of the 12th European workshop on QTL mapping and marker assisted selection

Proceedings
12th European workshop on QTL mapping and marker assisted selection
Uppsala, Sweden
15-16 May 2008
Publication of this supplement was supported by EADGENE (European Animal Disease Genomics Network of Excellence).

[Additional Information](#) | [Conference website](#)

Introduction [Open Access](#)
Comparative analysis of analyses of the QTLMAS XII common dataset. I. Genomic selection
Mogens Lund, Goutam Sahana, Dirk-Jan de Koning, Guosheng Su, Orjan Carlberg
BMC Proceedings 2009, 3(Suppl 1):51 (23 February 2009)
[Abstract](#) | [Full text](#) | [PDF](#) | [Published](#) | [Cited on BioMed Central](#)

Introduction [Open Access](#)
Comparative analysis of analyses of the QTLMAS XII common dataset. II. genome-wide association and fine mapping
Lucy Crooks, Goutam Sahana, Dirk-Jan de Koning, Mogens Lund, Orjan Carlberg
BMC Proceedings 2009, 3(Suppl 1):52 (23 February 2009)
[Abstract](#) | [Full text](#) | [PDF](#) | [Published](#) | [Cited on BioMed Central](#)

Proceedings [Open Access](#)
A strategy for QTL fine mapping using a dense SNP map
Joaquim Torres, François Guillaume, Sébastien Fren
BMC Proceedings 2009, 3(Suppl 1):53 (23 Feb
[Abstract](#) | [Full text](#) | [PDF](#) | [Published](#) | [Cited on](#)

Proceedings [Open Access](#)
A Bayesian QTL linkage analysis of the
Marco CAM Bink, Fred A van Eeuwijk
BMC Proceedings 2009, 3(Suppl 1):54 (23 Feb
[Abstract](#) | [Full text](#) | [PDF](#) | [Published](#) | [Cited on](#)

Proceedings [Open Access](#)
Evaluation of a genome-wide approach to
Matthew A Cleveland, Nader Ozdes
BMC Proceedings 2009, 3(Suppl 1):55 (23 Feb
[Abstract](#) | [Full text](#) | [PDF](#) | [Published](#) | [Cited on](#)

**A combined strategy for quantitative trait
Alex C Lam, Joseph Powell, Wen-Hua Wu, Gof
BMC Proceedings 2009, 3(Suppl 1):56 (23 Feb
[Abstract](#) | [Full text](#) | [PDF](#) | [Published](#) | [Cited on](#)**

Proceedings [Open Access](#)
Empowering the minimum recombinant
Jules Hernández-Sánchez, Sara Knott
BMC Proceedings 2009, 3(Suppl 1):57 (23 Feb
[Abstract](#) | [Full text](#) | [PDF](#) | [Published](#) | [Cited on](#)

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Volume 6 Supplement 2

Proceedings of the 15th European Workshop on QTL mapping and marker assisted selection (QTLMAS)

Proceedings
15th European workshop on QTL mapping and marker assisted selection (QTLMAS)
Rennes, France
19-20 May 2011
[Conference website](#)

Proceedings [Open Access](#)
20Yth QTLMAS: simulated dataset
Jean-Michel Elsen, Simon Teasdale, Olivier Flangi, Pascale Le Roy, Olivier Demiere
BMC Proceedings 2012, 6(Suppl 2):51 (21 May 2012)
[Abstract](#) | [Full text](#) | [PDF](#) | [Published](#) | [Cited on](#)

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Genomic Selection methods

- Again lots of methods and little structured comparison
- Incremental improvements
- => GSA journals started special collection in 2012

http://www.genetics.org/cgi/collection/genomic_selection



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Genomic Selection

In the April 2012 issues of *GENETICS* and *G3: Genes|Genomes|Genetics*, we launched a special focus on genomic selection. *GENETICS* features a loblolly pine data set and its corresponding analyses (Resende *et al.* 2012); *G3* presents a pig data set (Cleveland *et al.* 2012) and a compilation of 10 simulated data sets along with the software to simulate more (Hickey and Gorjanc 2012). The goal of these articles is to stimulate discussion in the community, and to provide data for the continuation of the discourse. We invite additional articles on this topic and encourage you to read the editorial for additional information.

Editorial - Setting the Standard: A Special Focus on Genomic Selection in *GENETICS* and *G3*

[Next Results »](#)

Selection on Optimal Haploid Value Increases Genetic Gain and Preserves More Genetic Diversity Relative to Genomic Selection

Hans D. Daetwyler, Matthew J. Hayden, German C. Spangenberg, and Ben J. Hayes

Genetics 2015 200:1341-1348; doi:10.1534/genetics.115.178038

[» Abstract](#) [» Full Text](#) [» Full Text \(PDF\)](#) [» Supporting Information](#)

Using the Animal Model to Accelerate Response to Selection in a Self-Pollinating Crop

Wallace A. Cowling, Katia T. Stefanova, Cameron P. Beeck, Matthew N. Nelson, Bonnie L. W. Hargreaves, Olaf Sass, Arthur R. Gilmour, and Kadambot H. M. Siddique

G3 2015 5:1419-1428; doi:10.1534/g3.115.018838

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This Month's Issue



August 2015,
200 (4)

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At the core of the collection

- **Review**

Whole-Genome Regression and Prediction Methods Applied to Plant and Animal Breeding

Gustavo de los Campos,^{*,1} John M. Hickey,[†] Ricardo Pong-Wong,[‡] Hans D. Daetwyler,[§] and Mario P. L. Calus^{**}

Genetics, Vol. 193, 327–345 February 2013

At the core of the collection

- **Benchmark data sets**

Simulated Data for Genomic Selection and Genome-Wide Association Studies Using a Combination of Coalescent and Gene Drop Methods

John M. Hickey^{*1} and Gregor Gorjanc[†]

 G3 Genes | Genomes | Genetics

Volume 2 | April 2012

A Common Dataset for Genomic Analysis of Livestock Populations

Matthew A. Cleveland,^{*1} John M. Hickey,[†] and Selma Forni^{*}

 G3 Genes | Genomes | Genetics

Volume 2 | April 2012

Accuracy of Genomic Selection Methods in a Standard Data Set of Loblolly Pine (*Pinus taeda* L.)

M. F. R. Resende, Jr.,^{*1,1} P. Muñoz,^{†,1,1} M. D. V. Resende,^{§,2,2} D. J. Garrick,^{††} R. L. Fernando,^{††}
J. M. Davis,^{†††} E. J. Jokela,[†] T. A. Martin,[†] G. F. Peter,^{†,††} and M. Kirst^{†,††,2}

Genetics, Vol. 190, 1503–1510 April 2012

At the core of the collection

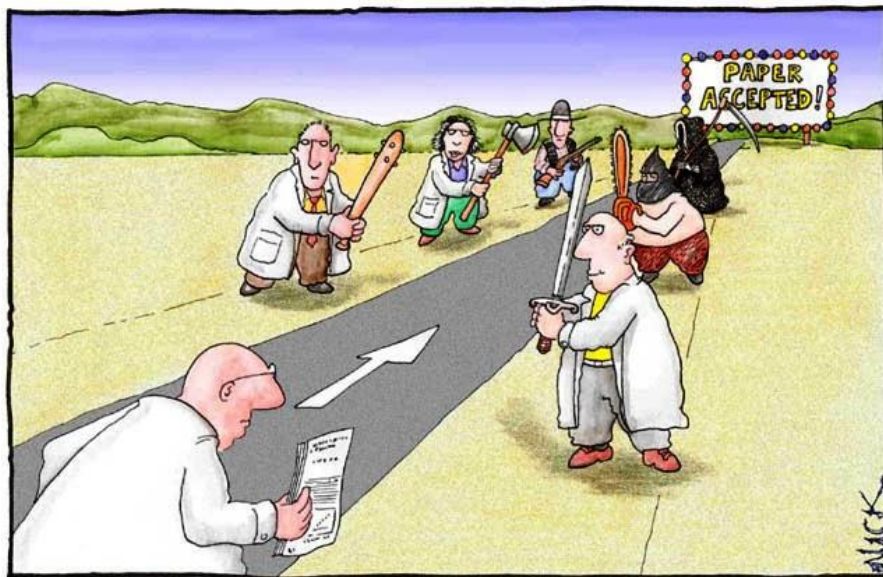
- Reporting guidelines + analysis of benchmark data

Genomic Prediction in Animals and Plants: Simulation of Data, Validation, Reporting, and Benchmarking

Hans D. Daetwyler,^{*,1} Mario P. L. Calus,[†] Ricardo Pong-Wong,[‡]
Gustavo de los Campos,[§] and John M. Hickey^{**,**}

Genetics, Vol. 193, 347–365 February 2013

So you want to publish a GS method?



Option 1) Use public data

- Already analysed
- Only need to add results for your new method
- Include code/software/tool to replicate analysis

Option 2) Use Own data

- Include the data and/or simulation code
- Apply benchmarked methods for comparison
- Include code/software/tool to replicate analysis

GSA Journals Collection on Genomic Selection

- Continues to grow
- Important resource for
 - Data
 - Tools
 - Reference Material

Some pointers for publishing genome-wide studies

Guiding principle

Provide the reader with enough detail, data, and tools to replicate your study – it's good for your work, and for science

What should I provide?

- Experimental design
- Quality Control
- Model of analysis
- Tool(s) for analysis
- Details of post-analyses (scripts)

DATA

- The GSA journals have a strict data policy, established ~2009
- More journals are following suit
- Can be challenging when working with private sector/companies



PUBLICATIONS AND DATA

Community-driven journals

- E.g. Those ran by a scholarly Society
- G3, Genetics, Heredity, JDS, JAS, GSE, Animal Genetics, etc.
- Peer-editing: editors are your scientific peers, colleagues, who can interpret reviews and make decisions on your papers

Peer-editing at the GSA journals

- EIC, Senior Editors, Associate editors
- Senior Editors are responsible for a broad area
- Associate Editors handle the review of individual manuscripts
- Each manuscript evaluated by at least two editors

Take home message:
Publishing is best when community-driven

This means a partnership between scientific communities, editors, journals, scholarly societies – to reflect your real world, the desired impacts of your work, and the needs of our constituents



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