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

DJ de Koning, SLU, Deputy EIC G3 and associate editor Genetics
Tracey DePellegrin, GSA, executive editor Genetics and G3
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
Volume 8 Supplement 5
Proceedings of the 16th European Workshop on QTL Mapping and Marker Assisted Selection (QTL-MAS)

Proceedings
16th QTL-MAS Workshop
4-5 March 2012

Edited by: Antoinette Carle, Sara Casas, Xavier Castella, Jordi P. M. P. Nasr, and Manos Konstantinides

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Proceedings
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Articles

Proceedings
Full issue
BMC Proceedings publishes selected collections of research articles, conference proceedings, reviews and reports as supplements, which are free to access online. All articles published in supplements are subject to peer review, meeting standards and criteria set by the Supplement Editors.

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

Volume 6 Supplement 2
Proceedings of the 15th European workshop on QTL mapping and marker assisted selection (QTLMAS)

Articles

Proceedings
Full issue
BMC Proceedings publishes selected collections of research articles, conference proceedings, reviews and reports as supplements, which are free to access online. All articles published in supplements are subject to peer review, meeting standards and criteria set by the Supplement Editors.
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
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 (Rosario et al. 2012), G3 presents a pig data set (Clayland 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

Selection on Optimal Haploid Value Increases Genetic Gain and Preserves More Genetic Diversity Relative to Genomic Selection
Hans D. Daelwyler, Matthew J. Haydon, 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
n3 2015 5:1419-1428; doi:10.1534/n3.115.018838
At the core of the collection

• Review

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

Gustavo de los Campos,*† 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

A Common Dataset for Genomic Analysis of Livestock Populations

Matthew A. Cleveland,*,1 John M. Hickey,* and Selma Forni*

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

M. F. R. Resende, Jr.,*,1 P. Muñoz,*,1 M. D. V. Resende,1,2 M. B. Garrick,1,2 D. J. Garrick,1,2 R. L. Fernando,1,2 J. M. Davis,*,1 E. J. Jokela,1 T. A. Martin,1 G. F. Peter,1,2 and M. Kirst1,2

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Volume 2 | 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
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
PLEASE WELCOME THE NEWEST MEMBER OF OUR EDITORIAL BOARD, WHO BRINGS TO THE TABLE A WEALTH OF EXPERIENCE IN TWEETING.