

# A Unified Publication Platform for Systems Biology Standards

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# Problem

- Standard specifications are often difficult to cite
- Former platform (Nature Preceedings) no longer available
- Best case: there is a paper (e.g. Bioinformatics, Nat. Biotech.) briefly describing the standard (and other papers cite this one)
- Worst case: there is only an url to cite

# Proposal

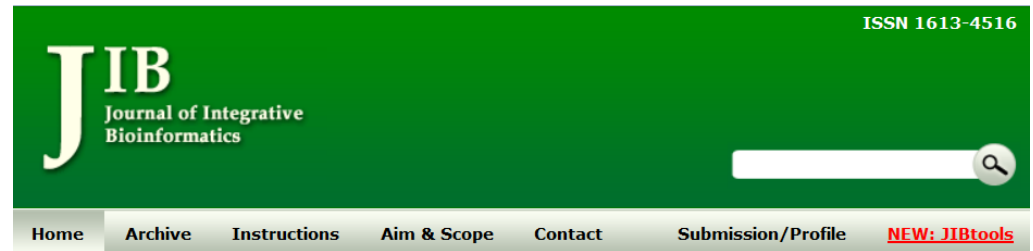
- A yearly special issue of a journal containing the current version of the standard
  - For many/all COMBINE standards
  - Also current version of extensions / packages
- Advantages
  - All specifications available in one place (special issue)
  - Easy to cite
  - Additional value for standard developers (journal publication)

# Proposal

- Special issue in „Journal of Integrative Bioinformatics“
- <http://journal.imbio.de/>

- Since 2004
- Free (for both authors and readers)
- Non-exclusive
- Creative Commons license
- PubMed and DBLP listed
- To do: Title page + abstract according to journal style

- Editors of standards
  - Discuss it within community
  - Let me know by end of October ([schreibe@ipk-gatersleben.de](mailto:schreibe@ipk-gatersleben.de))



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## Journal of Integrative Bioinformatics (JIB)

JIB is an open access journal publishing original peer-reviewed research articles in all aspects of integrative bioinformatics. JIB (ISSN 1613-4516) is indexed/tracked/covered by [PubMed](#) (since 2008), [DBLP Computer Science Bibliography](#) and [Google Scholar](#).

### Topics

- Molecular Databases, Information Systems and Data Warehouses
- Integration of Data, Methods and Tools
- Metabolic and Regulatory Network Modeling and Simulation
- Signal Pathways and Cell Control
- Network Analysis
- Applications in Medical Informatics, Biomedicine and Biotechnology
- Integrative Approaches for Drug Design
- Integrative Data and Text Mining Approaches



### Recent articles

[Discovery of miR-mRNA interactions via simultaneous Bayesian inference of gene networks and clusters using sequence-based predictions and expression data](#)

Brian Godsey  
2013-07-10. Research Article

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## **A Graphical Notation to Describe the Logical Interactions of Biological Pathways**

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### **Summary**

The modelling of biological intra-cellular pathways requires the systematic capture and representation of interactions between components that are biologically correct and computationally rigorous. The challenge is two fold, to verify and extend our understanding of such pathways by comparing *in silico* models to experiments; and to ensure that such models are understandable by biologists and for checking biological validity. In this report we present a graphical notation, the Edinburgh Pathway Notation (EPN), which satisfies the central biologically driven requirements while providing a strict formal framework for analysis. The EPN emphasises the use of a logical representation of pathways, which is particularly suited to pathways where some mechanisms are not known in detail.