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## Trends in scholarly publishing - the impact of information technologies

Odile Hologne

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Submitted on 5 Jun 2020

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# Trends in scholarly publishing

The impact of information technologies

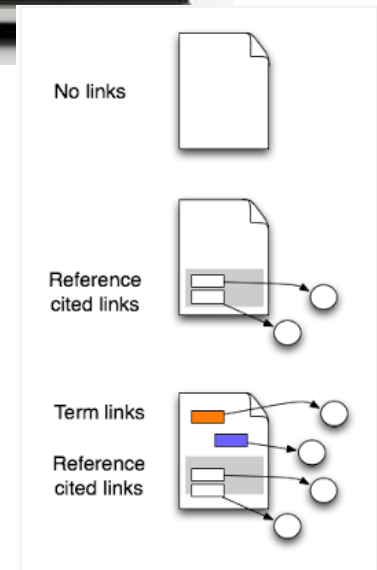
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# The end of Gutenberg era ...



<http://iphylo.blogspot.fr/2009/04/semantic-publishing-towards-real.html>

# A Quick Tour with in 6 questions

- ❖ What means « open » ?
- ❖ What is a journal ?
- ❖ What is an article ?
- ❖ What can we measure ?
- ❖ How to control text mining ?
- ❖ How to link data and articles ?
- ❖ Conclusion – What else ?



# Open access

But what means « open » ?

# Introduction

- ❖ What means « open »
  - ✓ put free PDF on line ?
  - ✓ Business models or APC
- ❖ We forget other aspects of openness
  - ✓ technical aspects
  - ✓ legal aspects

# Journals : How open is it ?

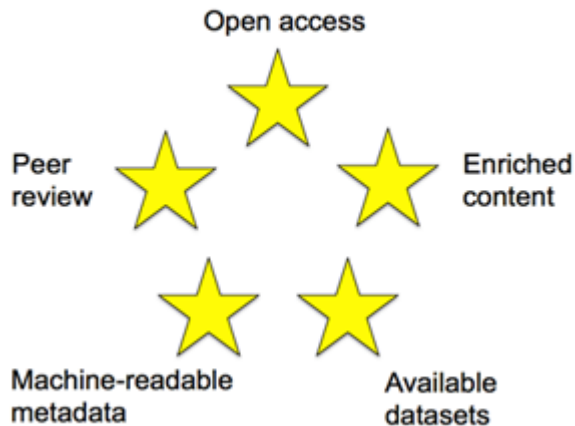
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[http://sparc.arl.org/sites/default/files/hoii\\_guide\\_rev4\\_web.pdf](http://sparc.arl.org/sites/default/files/hoii_guide_rev4_web.pdf) (2013)

# Articles : openness and quality

## The Five Stars of Online Journal Articles



The Five Stars of Online Journal Articles — a Framework for Article Evaluation  
David Shotton  
Department of Zoology, University of Oxford  
david.shotton@zoo.ox.ac.uk  
doi:10.1045/january2012-shotton

- ❖ **Peer review**  
Ensure your article is peer reviewed, to provide assurance of its scholarly value, quality and integrity.
- ❖ **Open access**  
Ensure others have cost-free open access both to read and to reuse your published article, to ensure its greatest possible readership and usefulness.
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Use the full potential of Web technologies and Web standards to provide interactivity and semantic enrichment to the content of your online article.
- ❖ **Available datasets**  
Ensure that all the data supporting the results you report are published under an open license, with sufficient metadata to enable their re-interpretation and reuse.
- ❖ **Machine-readable metadata**  
Publish machine-readable metadata describing both your article and your cited references, so that these descriptions can be discovered and reused automatically.
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- **Deposit** a machine-readable copy of the published version or final peer-reviewed manuscript accepted for publication in a repository of the researchers choice (possibly OpenAIRE compliant)
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- **Aim to deposit** at the same time **the research data needed to validate the results ("underlying data")**
- Ensure **OA to the bibliographic metadata** that identify the deposited publication, via the repository

Celina Ramjoue (Head of Sector "Open Access to scientific Publications and Data", EC DG CNECT)

Agenda

# Data publication

Linked Data ou  
publication  
Web de  
données

Données sur le Web, dans un format structuré et non propriétaire, données du fichier identifiées par des URIs et reliées à d'autres



Données sur le Web, dans un format structuré et non propriétaire, données du fichier identifiées par des URIs



Publication  
Web

Données sur le Web, identifié ou pas, dans un format structuré et non propriétaire



`http://data...`

Fichier sur le Web, identifié ou pas dans un format structuré



Fichier sur le Web, identifié ou pas, quel que soit le format



from <http://5stardata.info/>



# What is a journal ?

From a technical point of  
view

# From dissemination to data processing

## ❖ Old

- ✓ dissemination
- ✓ to be readable by human

## ❖ Now

- ✓ metadata processing
- ✓ data access and data processing
- ✓ to be readable by computers

# A platform – a software

5

BioMed Central  
The Open Access Publisher

Springer

# (GIGA)<sup>n</sup> SCIENCE

Journal, data-platform and database for large-scale data

华大基因  
BGI

in conjunction with

BioMed Central  
The Open Access Publisher

Open API to retrieve information from (GIGA)<sup>n</sup> DB

Open-Paper



DOI:10.1186/2047-217X-1-18

Highly accessed >11000 accesses

Linked to  
DOI

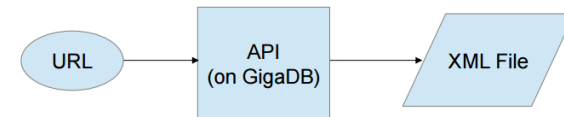
(GIGA)<sup>n</sup> DB  
Data sets

Open-Data  
DOI:10.5524/100038  
78GB CC0 data

Linked to  
DOI

(GIGA)<sup>n</sup> Galaxy  
by CBIIT  
Analyses

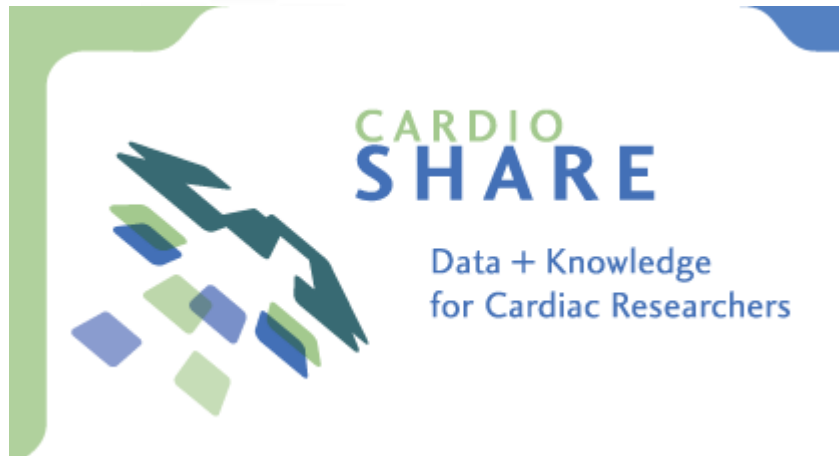
Open-Pipelines  
Open-Workflows  
DOI:10.5524/100044



- Only journal where data and source code behind article + article can be mined through open API
- Only journal offering a home for complex image data (like fMRIs, eg) right next to article

Amye Kenall [http://www.gfii.fr/uploads/docs/GFII\\_Springer.pdf](http://www.gfii.fr/uploads/docs/GFII_Springer.pdf)

# Be able to do queries on articles and data



*What proteins is Pubmed article 9207092 written about? What organisms do these proteins belong to?*

```
PREFIX sad: <http://sadiframework.org/ontologies/properties.owl#>
PREFIX ss: <http://semanticscience.org/resource/>
PREFIX pubmed: <http://lsrn.org/PMID:>
SELECT ?protein ?organismName
WHERE {
    pubmed:9207092 ss:SIO_000252 ?protein .
    ?protein sad:fromOrganism ?organism .
    ?organism sad:hasName ?name .
    ?name ss:SIO_000300 ?organismName .
}
```

# Journal and data processing

## An Analysis of the Viola-Jones Face Detection Algorithm

Yi-Qing Wang

article demo archive

published reference • 2014-06-26 -- BibTeX  
• Yi-Qing WANG, *An Analysis of the Viola-Jones Face Detection Algorithm*, Image Processing On Line, 4 (2014), pp. 128–148.  
<http://dx.doi.org/10.5201/ipol.2014.104>

Communicated by Jose-Luis Lisani  
Demo edited by Yi-Qing Wang

### Abstract

In this article, we decipher the Viola-Jones algorithm, the first ever real-time face detection system. There are three ingredients working in concert to enable a fast and accurate detection: the integral image for feature computation, AdaBoost for feature selection and an attentional cascade for efficient computational resource allocation. Here we propose a complete algorithmic description, a learning code and a learned face detector that can be applied to any color image. Since the Viola-Jones algorithm typically gives multiple detections, a post-processing step is also proposed to reduce detection redundancy using a robustness argument.

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- source code: TAR/GZ

### Preview

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LOW RESOLUTION PDF: Images may show compression artifacts. A full resolution PDF is available at [www.ipol.im](http://www.ipol.im).



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Submitted on 2013-08-31, accepted on 2014-05-09.  
ISSN 2105-1232 © 2014 IPOL & the authors CC-BY-NC-SA  
This article is available online with supplementary materials,  
software, datasets and online demo at  
<http://dx.doi.org/10.5201/ipol.2014.104>

## An Analysis of the Viola-Jones Face Detection Algorithm

Yi-Qing Wang

CMLA, ENS Cachan, France ([yiqing.wang@cmla.ens-cachan.fr](mailto:yiqing.wang@cmla.ens-cachan.fr))

## An Analysis of the Viola-Jones Face Detection Algorithm

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### Select Data

Click on an image to use it as the algorithm input.



image credits

### Upload Data

Upload your own image files to use as the algorithm input.

input image  Aucun fichier choisi

<http://www.ipol.im/>



# What is an article



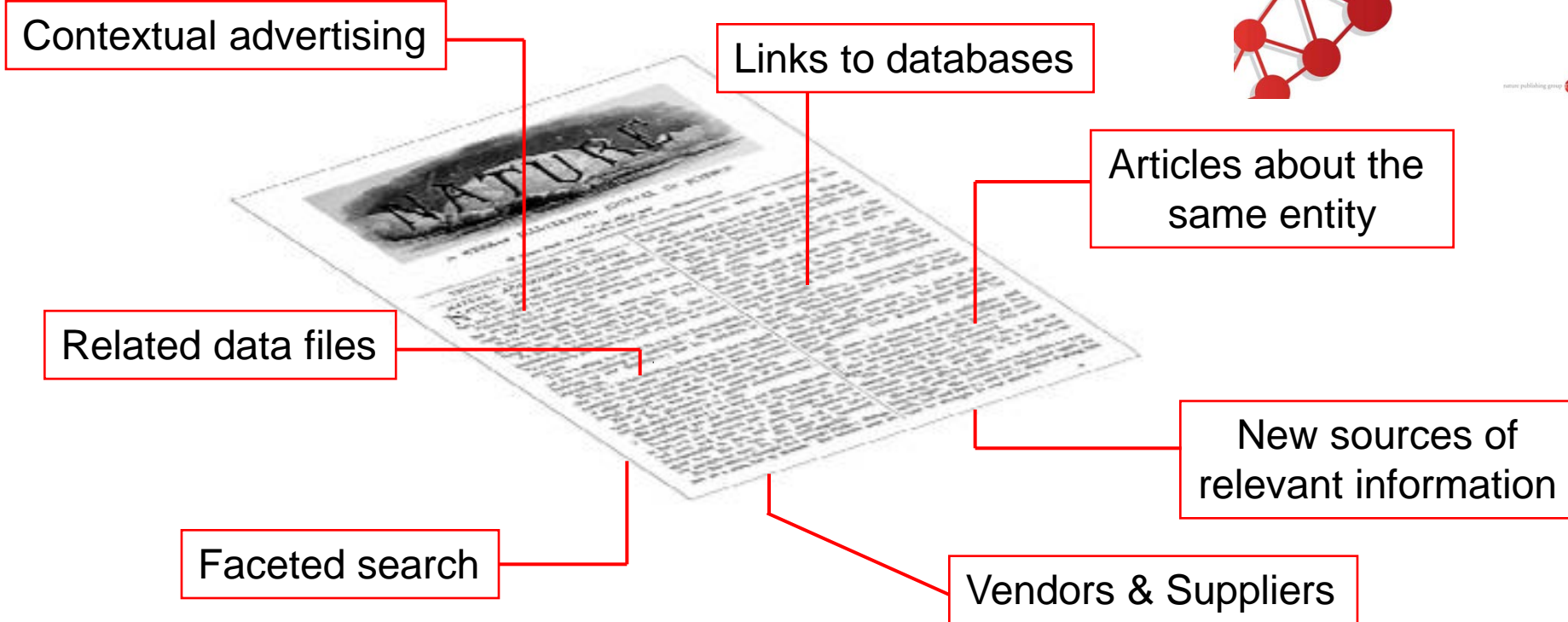
# Evolution of scientific publishing

From articles to particles:  
How Nature's semantically-enriched content  
boosts scientific discovery

Dr Jason Wilde  
Director, Business Development  
Nature Publishing Group  
30<sup>th</sup> November 2011



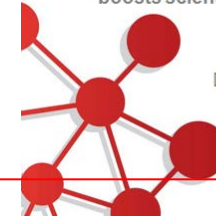
nature publishing group



Articles need to move from being 2D into a 3D entity in the information space.



# Behind the scenes - interface



## Sequence-specific regulator Prdm14 safeguards mouse ESCs from entering extraembryonic endoderm

Prdm14 is a PR-domain and zinc-finger protein whose expression is restricted to the pluripotent cells of the early embryo, embryonic stem cells (ESCs) and germ cells. Here, we show that Prdm14 safeguards mouse ESC (mESC) maintenance by preventing induction of extraembryonic endoderm (ExEn) fates. Conversely, Prdm14 occupies and represses genomic loci encoding ExEn differentiation factors, while also binding to and promoting expression of genes essential for ESC self-renewal. Prdm14-associated genomic regions substantially overlap those occupied by Nanog and Oct4, are enriched in a chromatin signature associated with pluripotency, and contain a unique DNA-sequence motif recognized by Prdm14 *in vitro*. Our work identifies a new member of the mESC transcriptional network, Prdm14, which plays a dual role as a context-dependent transcriptional repressor or activator.

In the mammalian embryo, each cell of the inner cell mass (ICM) of the blastocyst is destined to choose between two prospective fates: that of the epiblast, which gives rise to all tissues of the embryo proper, and that of the primitive endoderm, which develops into the visceral and parietal extraembryonic endoderm, providing nutrient exchange and inductive signals for the embryo.

Segregation of the epiblast and the primitive endoderm begins in the early ICM, where Nanog and Gata6, master regulators of pluripotency and endoderm formation, respectively, are expressed in a progressively mutually exclusive manner. Indeed, within the early ICM, two cell subpopulations with distinct expression profiles exist: one characterized by the upregulation of certain primitive endoderm genes (for example, Gata4 and Gata6) and the other characterized by expression of certain early epiblast genes (for example, Nanog and Fgf4). The FGF-Grb2-MAPK signaling pathway is important for breaking of the expression symmetry by upregulation of Gata6 and downregulation of Nanog, although even after the initial establishment of this asymmetry, cells of the ICM retain the ability to switch their lineage choice. Eventually, however, Nanog-positive cells form the epiblast, whereas Gata6-positive cells commit to the primitive endoderm fate, induce transcription of specific adhesion molecules such as Lamb1 and Dab2, and migrate to the ICM surface, where they later diversify into parietal and visceral extraembryonic endoderm lineages.

Because of its biochemical, genomic and genetic tractability, the mESC model provides a useful tool for studies of molecular mechanisms governing early cell fate transitions and can be used to investigate the fate choice between the pluripotent epiblast and ExEn. Similar to its function in the transcription factors Gata4, Gata6, Sox7 or Sox17 is sufficient to induce mESC differentiation into

In search of new regulators of mESC self-renewal and repression of the ExEn differentiation program, we characterized by the presence of tandem zinc fingers and a PR (PRDI-BF1 and RIZ) domain. This repressor and a potent regulator of cell fate decisions in various tissues. Moreover, the critical factor beginning to emerge. Among the 16 PRDM proteins present in mammalian genomes, Prdm14 is the only one characterized by the presence of a PR domain. Prdm14 is a member of the PRDM protein family of putative transcriptional regulators, which is characterized by the presence of a PR domain. Prdm14 is a sequence-dependent transcriptional repressor and a potent regulator of cell fate decisions in various tissues. Moreover, the critical factor beginning to emerge. Among the 16 PRDM proteins present in mammalian genomes, Prdm14 is the only one characterized by the presence of a PR domain. Prdm14 is a member of the PRDM protein family of putative transcriptional regulators, which is characterized by the presence of a PR domain. Prdm14 is a sequence-dependent transcriptional repressor and a potent regulator of cell fate decisions in various tissues. Moreover, the critical factor beginning to emerge. Among the 16 PRDM proteins present in mammalian genomes, Prdm14 is the only one characterized by the presence of a PR domain.

Here, we demonstrate that Prdm14 is a sequence-dependent transcriptional regulator that protects mESCs from entering ExEn fates. Using a combination of cell biology, genomic and biochemical approaches, we identified Prdm14-regulated genes, Prdm14's genomic binding patterns and its unique DNA-sequence specificity.

## Results

### Differentiation to ExEn fates upon Prdm14 knockdown

To examine whether Prdm14 contributes to the maintenance of the mESC state, we treated mESCs with Prdm14-targeting short interfering RNA (siRNA), leading to a partial Prdm14 mRNA and protein depletion (Supplementary Fig. 1a), and cultured cells under conditions compatible with self-renewal. Within 3 d of transfection, Prdm14 siRNA-treated cells were morphologically indistinguishable from cells transfected with control nontargeting siRNA or from untreated, wild-type (WT) mESCs (not shown). However, 5–7 d after initial treatment and specifically in the Prdm14 siRNA-transfected samples, we noted the appearance of dispersed refractive cells, which morphologically resembled previously described ExEn cells (Fig. 1a) and which lost alkaline phosphatase and Nanog expression (Fig. 1b,c). Consistent with ExEn differentiation, the vast majority—if not all—of these dispersed cells stained positively for ExEn markers, such as the transcription factor Gata4 and surface molecules Lamb1 and Dab2 (Fig. 1c; Supplementary Fig. 1b). The described knockdown phenotype was recapitulated with an independent, non-overlapping Prdm14 siRNA (Supplementary Fig. 2). In contrast, control siRNA-treated cells did not exhibit differentiated morphology or ExEn marker staining (Fig. 1a–c; Supplementary Fig. 1b; Supplementary Fig. 2). Of note, a substantial subpopulation of cells treated with Prdm14 siRNA retained ESC morphology and Nanog expression and stained negatively for Gata4, Lamb1 and Dab2 (Fig. 1 and Supplementary Fig. 2). This suggests that a partial knockdown of Prdm14 is insufficient to abrogate self-renewal in some cells and/or a cell subset that retains ESC characteristics corresponds to the cells that remained untransfected. Although, given those caveats, we could not determine whether Prdm14 is absolutely required for self-renewal, our data suggest that Prdm14 protects mESCs from spontaneous differentiation to ExEn fates.

### Prdm14 depletion leads to the induction of ExEn genes

Gene expression profiling by RNA-seq identified 480 upregulated and 173 downregulated genes in the Prdm14 knockdown sample, as compared to the control siRNA-treated sample (at 1.4-fold change cutoff and criteria representing statistical significance, false discovery rate (FDR) < 0.0001; genes listed in Supplementary Data 1). Examination of upregulated genes showed a striking

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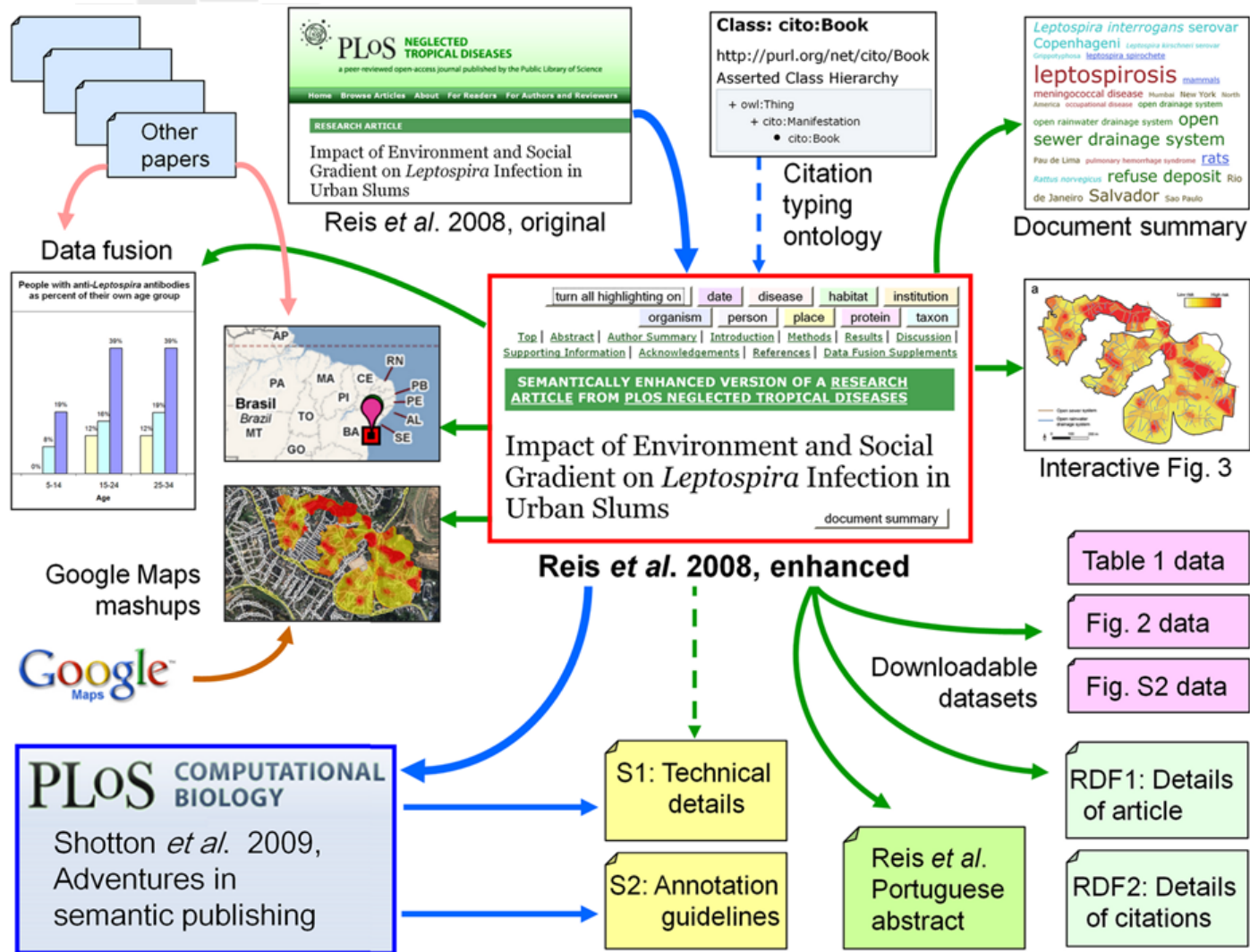
Identified as a  
Biological entity  
and editable

Name	UniProtID	EntrezGeneID	Gene Symbol
Nanog			

Search: Mus musculus | Wikipedia | Google | DBGET | SGD

Results for name: Nanog


<b>UniProt (20)</b> <a href="#">See all</a>	<b>EntrezGene (5)</b> <a href="#">See all</a>	<a href="#">Compare</a>
<b>Protein Name</b> Homeobox protein NANOG		
<b>UniProt ID</b> <a href="#">Q80Z64</a>		
<b>Reviewed</b> Yes		
<b>Mnemonic</b> NANOG_MOUSE		
<b>Organism</b> Mus musculus		
<b>Genes</b> <a href="#">Nanog</a> , <a href="#">Ecat4</a> , <a href="#">Enk</a>		
<b>Synonyms</b> Homeobox protein NANOG, ES cell-associated protein 4, Early embryo (4 synonyms)...		
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<b>Reviewed</b> Yes		
<b>Mnemonic</b> NANOG_MUSMIM		
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<b>UniProt ID</b> <a href="#">E7ZN41</a>		
<b>Reviewed</b> No		
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<b>Synonyms</b> Nanog protein (1 synonym)...		
<a href="#">Choose Entity for selected</a> <a href="#">hide</a>		
<b>Protein Name</b> MCG132219		
<b>UniProt ID</b> <a href="#">A2RS90</a>		
<b>Reviewed</b> No		
<b>Mnemonic</b> A2RS90_MOUSE		
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<b>Synonyms</b> MCG132219, Nanog homeobox (2 synonyms)...		
<a href="#">Choose Entity for selected</a> <a href="#">hide</a>		



<http://iphylo.blogspot.fr/2009/04/semantic-publishing-towards-real.html>

# Negative results

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### Aims & scope


*Journal of Negative Results in BioMedicine* is an open access, peer-reviewed, online journal that provides a platform for the publication and discussion of unexpected, controversial, provocative and/or negative results in the context of current tenets.

*Journal of Negative Results in BioMedicine* aims to encourage scientists and physicians of all fields to publish results that challenge current models, tenets or dogmas. The journal invites scientists and physicians to submit work that illustrates how commonly used methods and techniques are unsuitable for studying a particular phenomenon. *Journal of Negative Results in BioMedicine* strongly promotes and invites the publication of clinical trials that fall short of demonstrating an improvement over current treatments. The aim of the journal is to provide scientists and physicians with responsible and balanced information in order to improve experimental designs and clinical decisions.

Articles published in traditional journals frequently provide insufficient evidence regarding negative data. They hardly allow a rigorous evaluation of the quality of these results. In addition, controversial results that refute a current model or simply negative results within a current dogma, frequently meet considerable resistance before they are acknowledged. This is particularly the case if current techniques and technologies are too crude to shed further light on the findings. As more sophisticated techniques become available such findings may turn out to have been groundbreaking only decades later.

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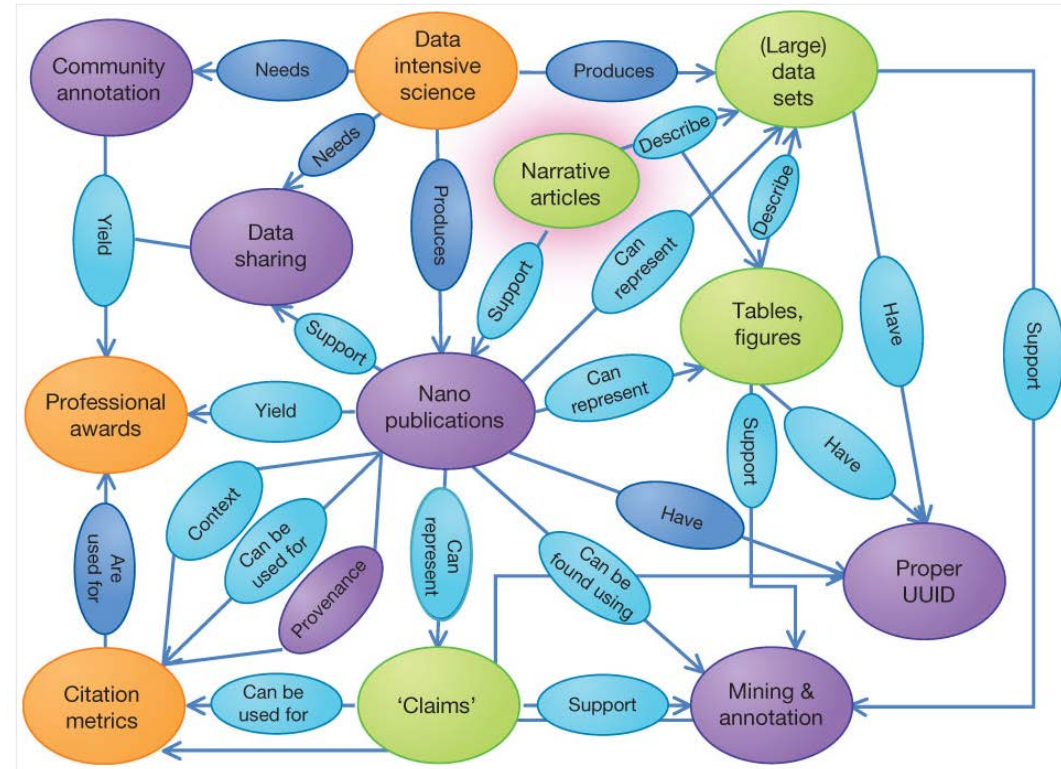


# Why do we need literature ? Nanopublication



Figure 2: A proposal for the future of scholarly communication.

From  
 The value of data  
 Barend Mons, Herman van Haagen, Christine Chichester, Peter-Bram 't Hoen, Johan T den Dunnen, Gertjan van Ommen, Erik van Mulligen, Bharat Singh, Rob Hoof, Marco Roos, Joel Hammond, Bruce Kiesel, Belinda Giardine, Jan Velterop, Paul Groth & Erik Schultes  
*Nature Genetics* 43, 281–283 (2011) | doi:10.1038/ng0411-281  
 Published online 29 March 2011



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NATURE GENETICS | COMMENTARY

The value of data

Barend Mons, Herman van Haagen, Christine Chichester, Peter-Bram 't Hoen, Johan T den Dunnen, Gertjan van Ommen, Erik van Mulligen, Bharat Singh, Rob Hoof, Marco Roos, Joel Hammond, Bruce Kiesel, Belinda Giardine, Jan Velterop, Paul Groth & Erik Schultes

Affiliations | Contributions | Corresponding author

*Nature Genetics* 43, 281–283 (2011) | doi:10.1038/ng0411-281  
 Published online 29 March 2011

<http://dx.doi.org/10.1038/ng0411-281>



# What can we measure ?

## Metrics

# What does DORA say?

DORA makes one general and 17 specific recommendations.

## General recommendation:

Do not use journal-based metrics, such as Journal Impact Factors (JIFs), as surrogate measures of the quality of individual research articles, to assess an individual scientist's contributions, or in hiring, promotion, or funding decisions.

### For Organizations That Supply Metrics

- Be transparent
- Provide access to data
- Discourage data manipulation
- Provide different metrics for primary literature and reviews

### For Publishers

- Cease to promote journals by Impact Factor; provide an array of metrics
- Focus on article-level metrics
- Identify different author contributions
- Open the bibliographic citation data
- Encourage primary literature citations

### For Research Institutions

- When hiring and promoting, state that scientific content of a paper, not the JIF of the journal where it was published, is what matters
- Consider value from all outputs and outcomes generated by research

### For Funding Agencies

- State that scientific content of a paper, not the JIF of the journal where it was published, is what matters
- Consider value from all outputs and outcomes generated by research

### For Researchers

- Focus on content
- Cite primary literature
- Use a range of metrics to show the impact of your work
- Change the culture!

San Francisco  
**DORA**  
Declaration on Research Assessment



# Evaluation

What kind of new metrics ?



## Métriques

Journal : Ecography (2013)

Facteur d'impact à 2 ans : 4,207

Facteur d'impact à 5 ans : 5,776

Notoriété à 2 ans : Excellente (biodivers.conserv. ; ecology)

### Article

Nb de consultations de cette notice : 80

Web of Science® Times Cited : 181

Altmetric 6

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429 readers on Mendeley  
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# Next step : over the audience

## ❖ Need to qualify the citation

Citation Function	Description
Based_on <sup>+</sup>	A work is based on the cited work
Corroboration <sup>+</sup>	Two works corroborate each other
Discover <sup>+</sup>	Acknowledge the invention of a technique
Positive <sup>+</sup>	The cited work is successful
Practical <sup>+</sup>	The cited work has a practical use
Significant <sup>+</sup>	The cited work is important
Standard <sup>+</sup>	The cited work is a standard
Supply <sup>+</sup>	Acknowledge the supplier of a material
Contrast <sup>=</sup>	Compares two works in a neutral way
Co-citation <sup>=</sup>	Citations that appear closely
Neutral <sup>=</sup>	The cited work not belonging to other functions
Negative <sup>-</sup>	The weakness of the cited work is discussed

Table 1: Annotation Scheme for Citation Function: <sup>+</sup> represents POSITIVE sentiment, <sup>=</sup> represents NEUTRAL sentiment, and <sup>-</sup> represents negative sentiment

<http://www.aclweb.org/anthology/R13-1052>





# How to change peer reviewing ?

# Peer reviewing

Debats on research integrity,  
transparence

- ❖ Review Post publication
- ❖ The end of anonymous PR?
- ❖ Review citable
- ❖ New Players

**Peerage of Science**

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### How it works

Overview  
Process Flow  
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Abstract  
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Competing Interests  
Publishing Notes

Version 1 - Current

Reviews 1

Article statistics

Average rating: ★★★★★  
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Intersubject information mapping: revealing canonical representations of complex natural stimuli

Authors: Nikolaus Kriegeskorte<sup>1,\*</sup>  
Publication date: 26 March 2015  
Journal: ScienceOpen Research – Section: SOR-SOCSCI  
Publisher: ScienceOpen

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DOI: 10.14293/S2199-1006.1.SOR-SOCSCIAPDXF.v1  
Keywords: Social & Behavioral Sciences, Intersubject information mapping, Canonical correlation analysis, Complex natural stimuli, Intersubject correlation mapping

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Review

JUSSI TOHKA evaluated the article as: ★★★★★

Very interesting proposal for data analysis of fMRI acquired using naturalistic stimuli

Publication date: 18 June 2015  
DOI: 10.14293/S2199-1006.1.SOR-SOCSCIAPDXF.v1.RXSXYL

Level of importance: ★★★★★  
Level of validity: ★★★★★☆  
Level of completeness: ★★★★★☆  
Level of comprehensibility: ★★★★★

Competing interests: None  
Recommend this review: +1

Comments

PubPeer > Genet. Mol. Res.

## "Screening relevant genes of tolerance to low phosphorus in maize using cDNA-amplified fragment length polymorphism"

H.Y. Jiang, Z. Li, J. Zhao, Q. Ma, B.J. Cheng, S.W. Zhu, Genet. Mol. Res. (2015)

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“ *The scientists who get credit for peer review* ”

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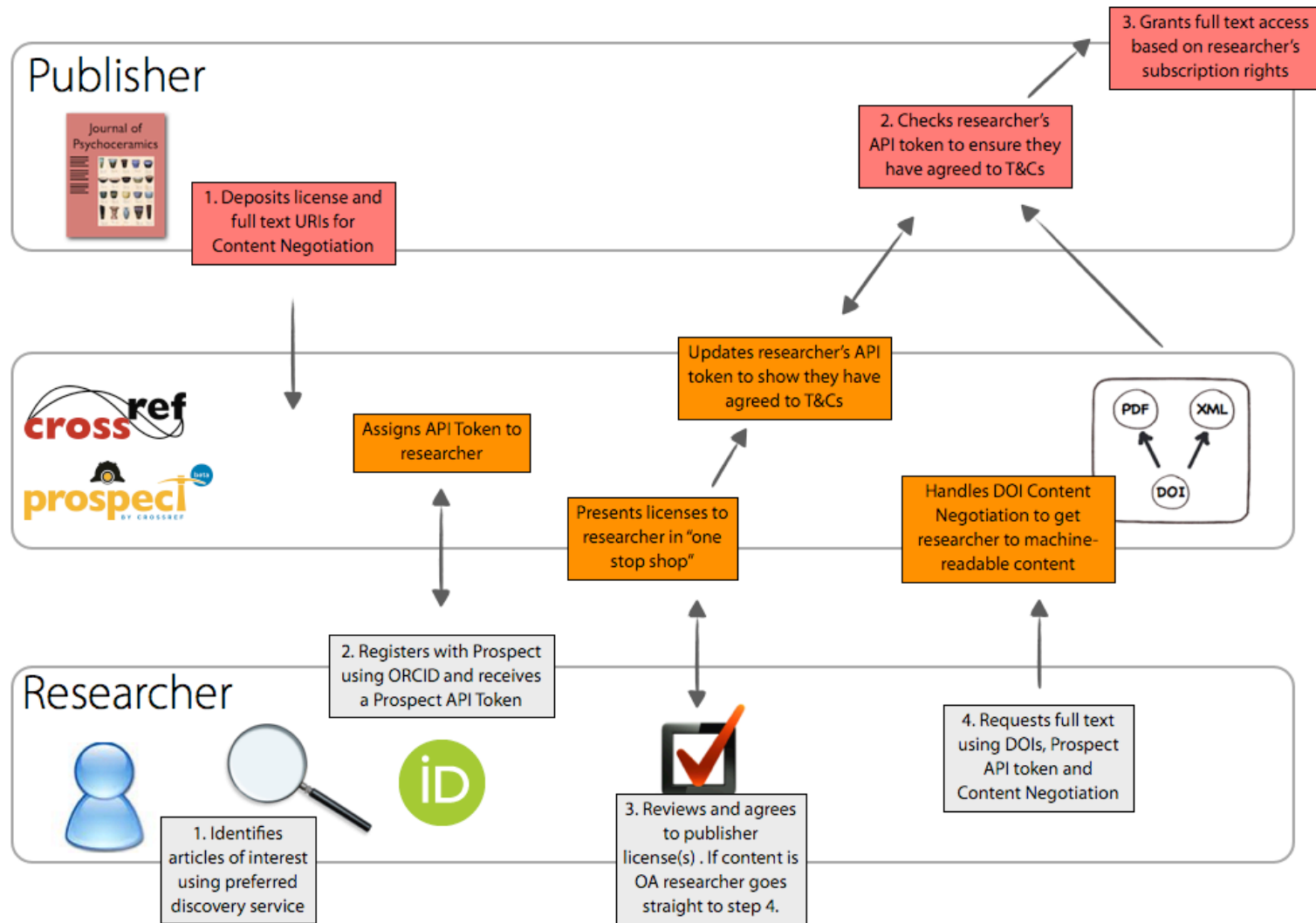
# Text mining

## How to control it

# Challenges

- ❖ The need : Textual big data : we can't read everything
- ❖ To extract information from unstructured text
- ❖ Without having nothing more to pay to the publishers
  - ✓ a « natural right » to do it
  - ✓ download without restriction

# But ... They organize the control ...





# How to link articles and data ?

# Data and journals

❖ Data linked to articles in « old journals »

❖ Data journals

The screenshot shows a journal article page from *Chemical Geology*, Volume 273, Issues 3-4, 15 May 2010, Pages 151-167. The article title is "An ancient metasomatic source for the Walvis Ridge basalts" by Vincent J.M. Salters and A.S. Sach-Kocher. The abstract discusses the proposed origins for the Enriched Mantle 1 (EM1) component, suggesting an ancient character for the EM1 component. It mentions that the data is consistent with the EM1 composition being formed by the addition of a melt to a mantle with bulk Earth-like composition, followed by melt extraction of a low degree melt. The article also notes that the Walvis Ridge data shows two distinct two component mixing trends, one formed by the less enriched Site S27 and Site S28 basalts and one formed by the Site S26A basalts. The two trends have the EM1 endmember in common. The less depleted end of the Site S27-Site S28 basalts is FOZO-like and can be explained by the addition of a recycled component (basaltic oceanic crust plus sediment). This recycled component was altered during subduction. The sense and magnitude of the chemical fractionation resulting from the subduction alteration are in agreement with dehydration experiments on basalts and sediment. Compared to other EM1 like basalts the Walvis Ridge basalts have flatter REE patterns and show less fractionation between large ion lithophile and heavy REE elements. Using the isotopic compositions as constraints for the parent-daughter ratios we were able to model the trace element patterns of the basalts as

## Data journals, data articles

A growing list:

<http://proj.bank.ac.uk/prepare/blog/DataJournalsList>

A data paper describes a dataset, giving details of its collection, processing, software, file formats etc, without the requirement of novel analyses or ground breaking conclusions. It allows the reader to understand the when, how and why data was collected and what the data-product is

The infographic is titled "Data journals, data articles" and features a central image of a journal cover. To the right, a quote reads: "Science is a combination of gathering facts and making theories; neither can progress on its own. In the history of science, the laborious accumulation of facts is the dominant mode, not a novelty." - Peter Norvig. Below this, three circular icons represent key benefits:

- Making "small" data big:**
  - No lower/upper limit of manuscript size
  - Publish all kinds of biodiversity related data
  - Reduced page charges affordable to all
- More than just data journals!**
  - Integrated text and data publishing
  - Complete online reviews and editing
  - Community ownership of data
  - Free of charge in launch phase
- Community peer-review:**
  - 7 weeks from submission to decision
  - 3 days from acceptance to publication
  - Public peer-review on author's choice

At the bottom, the INRA logo is displayed along with the text: "O. Hologne / Les données : data / Microsysteme data publications - Biokey - novembre 2014".

❖ Data must be in data repositories (avoid supplementary materials)



# But which one ?

- ❖ Only one (linked with the publication workflow)
  - ✓ linked to the journal (ex : Giga Science)
  - ✓ Outside the journal
- ❖ Many ?
  - ✓ Is there any quality standards ?

# How to assess a data repository ?

SCIENTIFIC DATA

To assist our authors, *Scientific Data* maintains a list of repositories that are compatible with our [data deposition policies](#)<sup>1</sup>. Please provide the following information to help us evaluate the suitability of your repository for inclusion in this list<sup>2</sup>:

## Basic details

1. Repository Name:
2. Repository URL:
3. If indexed by BioSharing<sup>3</sup> provide the ID or the URL for your database record:
4. If indexed by re3data<sup>4</sup> provide the ID or the URL for your database record:
5. How large is your current user base?
6. How many datasets are currently hosted by the repository?
7. How long has your resource been available to the community?
8. Do you accept data submissions from the entire scientific community? If data submission is restricted to certain groups, please describe who may deposit data.

## File limitations

9. What type of experimental data can be hosted by the repository? If the repository only accepts specific file formats please state what these are.
10. What is the maximum file size that can be handled by the repository?
11. Are there any limitations to the amount of data that an individual is able to upload?

## Licensing

12. Are there any terms of use or registration processes that data users must agree to, prior to gaining access to the data? Under what licence is data access provided? If you do not provide free and open access to the data hosted, please state the reason for this.
13. Can data depositors choose which licence they wish to use for their particular dataset?

## Data persistency and stability of access

14. What type of identifier is assigned to hosted datasets? N.B. We strongly encourage new repositories to mint DataCite DOIs.
15. Are researchers able to modify or remove datasets after publication?
16. Is there a versioning system in place?
17. Do you guarantee persistent access to datasets, and for how long?

## Costs

18. What is the cost to researchers wishing to host their research data?
19. What are the current and long-term cost recovery (sustainability) plans?

Questionnaire to assist with Scientific Data repository evaluation  
Document Last Updated: April 2015

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SCIENTIFIC DATA

20. If any proportion of the running costs are currently met by an academic grant, what is the plan for maintaining access to hosted data should funding be withdrawn in the future?

## Peer review

21. Are you able to facilitate confidential peer review of hosted datasets by the scientific peer reviewers invited to review the data by *Scientific Data*? N.B. *Scientific Data* peer reviewers must be able to access datasets in a manner in which they remain anonymous to repository managers, as well as repository users.
22. If possible please provide examples of currently hosted research datasets, with associated peer-reviewed publications

## Curation and metadata

23. Is there any curation support for researchers uploading their datasets?
24. Do you capture any metadata about hosted datasets in a standardised form?

## Notes

<sup>1</sup>This list is not intended to be a comprehensive list of research data resources, and should not be considered as a substitute for other data repository accreditation efforts.

<sup>2</sup>The aim of this evaluation process is to identify those repositories which are able to serve the wider community, and so are appropriate for *Scientific Data* to recommend to authors. We are glad to consider descriptions of data stored in project-specific or community-specific repositories on a case-by-case basis, even if the host repository is not selected for listing on our recommended repository list. Therefore please be aware that a decision not to list a repository as recommended should not be interpreted as a comment on the quality and utility of a repository for the immediate community it serves.

<sup>3</sup>BioSharing (<http://www.biosharing.org>) is a repository indexing service for life science, environmental and biomedical databases, whilst re3data (<http://www.re3data.org>) indexes data repositories in all other fields.

Questionnaire to assist with Scientific Data repository evaluation  
Document Last Updated: April 2015

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<http://www.nature.com/sdata/data-policies#repo-suggest>

# The list approved by Scientific data

The screenshot shows a Figshare article page. At the top, the Figshare logo is on the left, and a search bar with the text 'search figshare (titles, tags, authors, etc.)' is in the center. To the right of the search bar are 'Browse' and 'Upload' buttons, and further right are 'Sign up' and 'Login' buttons. The main content area has a title 'Scientific Data recommended repositories\_June 2015'. Below the title is a table with 9 rows and 2 columns. The first column is numbered 1-9, and the second column is labeled 'A' and contains repository names. To the right of the table are statistics: '464 views', '3 shares', and a 'Cites coming soon' badge. Below these are the publication date 'Published on 03 Jun 2015 - 12:35 (GMT)' and file size 'Filesize is 10.58 KB'. Further down are sections for 'Categories' (Science Policy), 'Authors' (Scientific Data), 'Tags' (data repositories, data sharing), 'License' (CC-BY), and 'Export' (Export to RefWorks, Export to BibTeX). At the bottom of the article content are 'Enlarge' and 'Download' buttons, and a 'Share this:' section with social media icons for Facebook (0), Twitter (3), and Google+ (0), along with an 'Embed\*' button. Below the social media icons is a 'Cite this:' section with the following text: 'Data, Scientific (2015): Scientific Data recommended repositories\_June 2015. figshare. http://dx.doi.org/10.6084/m9.figshare.1434640 Retrieved 16:27, Jul 01, 2015 (GMT)'. At the very bottom of the article content is a small note: '\*The embed functionality can only be used for non commercial purposes... more'.

	A
1	Repository Name
2	DNA DataBank of Japan
3	EMBL Nucleotide Sequence Database
4	GenBank
5	dbSNP
6	European Variation Archive
7	dbVar
8	Database of Genomic Variants Archive
9	FBI Metagenomics

SciData repos list\_June 2015

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Cite this: Data, Scientific (2015): Scientific Data recommended repositories\_June 2015. figshare. <http://dx.doi.org/10.6084/m9.figshare.1434640> Retrieved 16:27, Jul 01, 2015 (GMT)

\*The embed functionality can only be used for non commercial purposes... more

<http://www.nature.com/sdata/data-policies/repositories>

[http://figshare.com/articles/Scientific Data recommended repositories June 2015/1434640](http://figshare.com/articles/Scientific_Data_recommended_repositories_June_2015/1434640)



# Conclusion

Or some perspectives

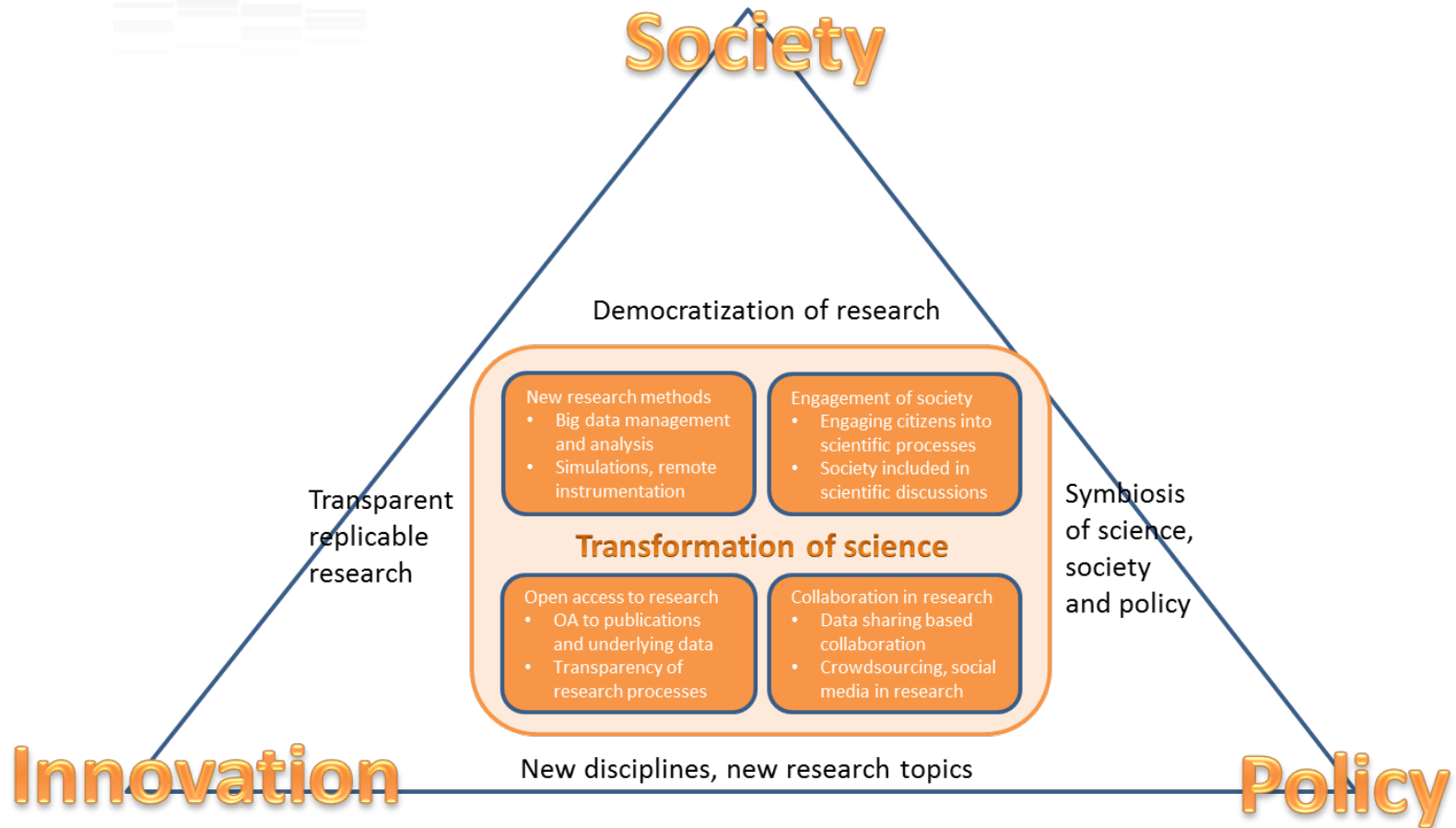
# New tools for the scientific process

## Typical workflow examples



<https://101innovations.wordpress.com/>

# How journals can tackle this challenges ?



<https://ec.europa.eu/digital-agenda/en/open-science>



- ❖ Rethink the scientific publishing process :
  - ✓ less and less frontiers between e-labnotebooks and results dissemination and treatment
- ❖ What are you waiting from your publisher :
  - ✓ only to put PDF on line
  - ✓ what else ?
- ❖ What is the publisher of the future ?