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Transforming how we work with users

Mark Patterson
STM, May 2nd, 2012

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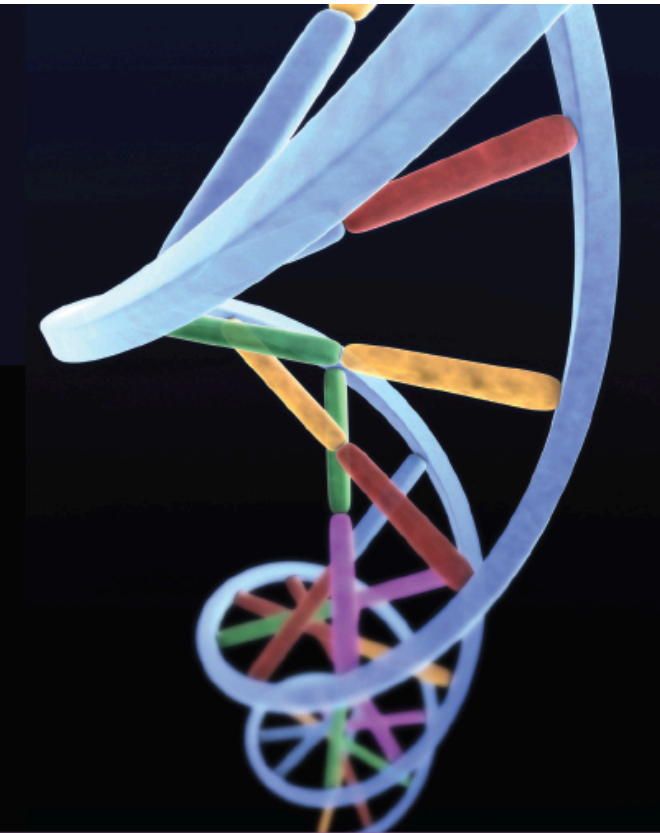
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What is eLife?

- A **collaboration** between funders and the research community to improve research communication
- A **researcher-led** digital publication for outstanding work across the life sciences
- A platform to **maximize the reach and influence** of new research and to **showcase new approaches** for the presentation and assessment of research

How is the user
interaction with content
being transformed?



Economic Impact of the Human Genome Project

How a \$3.8 billion investment drove \$796 billion in economic impact, created 310,000 jobs and launched the genomic revolution

Prepared by Battelle Technology Partnership Practice
May 2011



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Science 23 March 2001:
Vol. 291, no. 5512, pp. 2318 - 2319
DOI: 10.1126/science.1060273

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March 23rd, 2001

VIEWPOINTS

INFORMATION ACCESS:

Building A "GenBank" of the Published Literature

Richard J. Roberts,^{*} Harold E. Varmus, Michael Ashburner, Patrick O. Brown,[†] Michael B. Eisen, Chaitan Khosla, Marc Kirschner, Roel Nusse,[†] Matthew Scott,[†] Barbara Wold

To encourage community dialog about proposals that affect the scientific community, two viewpoints are presented regarding a controversial development in scientific publishing, the formation of a central archive of scientific literature. [Roberts et al.](#) believe that if journals make their scientific content freely available at PubMedCentral 6 months after publication researchers will be able to make the most effective use of the literature. The [Editors of Science](#) believe that there are other alternatives that may serve the scientific community as well or better without endangering scientific journals.

R. J. Roberts, New England Biolabs, Beverly, MA 01915, USA. H. E. Varmus, Memorial Sloan-Kettering Cancer Center, New York, NY 10021, USA. M. Ashburner, University of Cambridge, CB2 3EH, UK, and EMBL-European Bioinformatics Institute, Cambridge, CB10 1SD, UK. P. O. Brown, Stanford University School of Medicine, Stanford, CA 94305, USA. M. B. Eisen, Lawrence Berkeley National Laboratory, Berkeley, CA 94720, and University of California, Berkeley, CA 94720, USA. C. Khosla, Stanford University, Stanford, CA 94305, USA. M. Kirschner, Harvard Medical School, Boston, MA 02115, USA. R. Nusse and M. Scott, Stanford University School of Medicine, B. Wold, Biology Division, California Institute of Technology, Pasadena, CA 91125, USA.

^{*}To whom correspondence should be addressed. E-mail: roberts@neb.com

[†][Howard Hughes Medical Institute investigator.](#)

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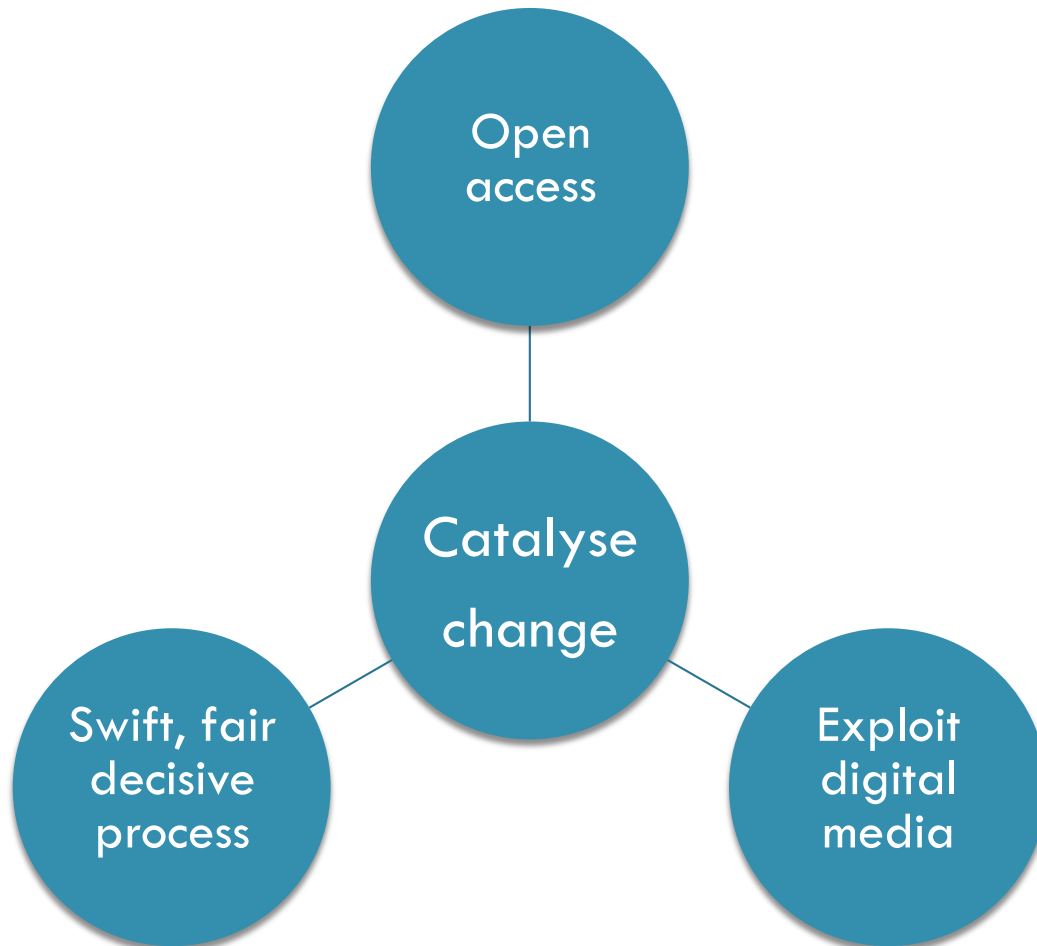


Our Planet
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Chicago
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Cost of publishing is one
of the costs of research

eLife – goals



eLife – scope

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- **SELECTIVE**

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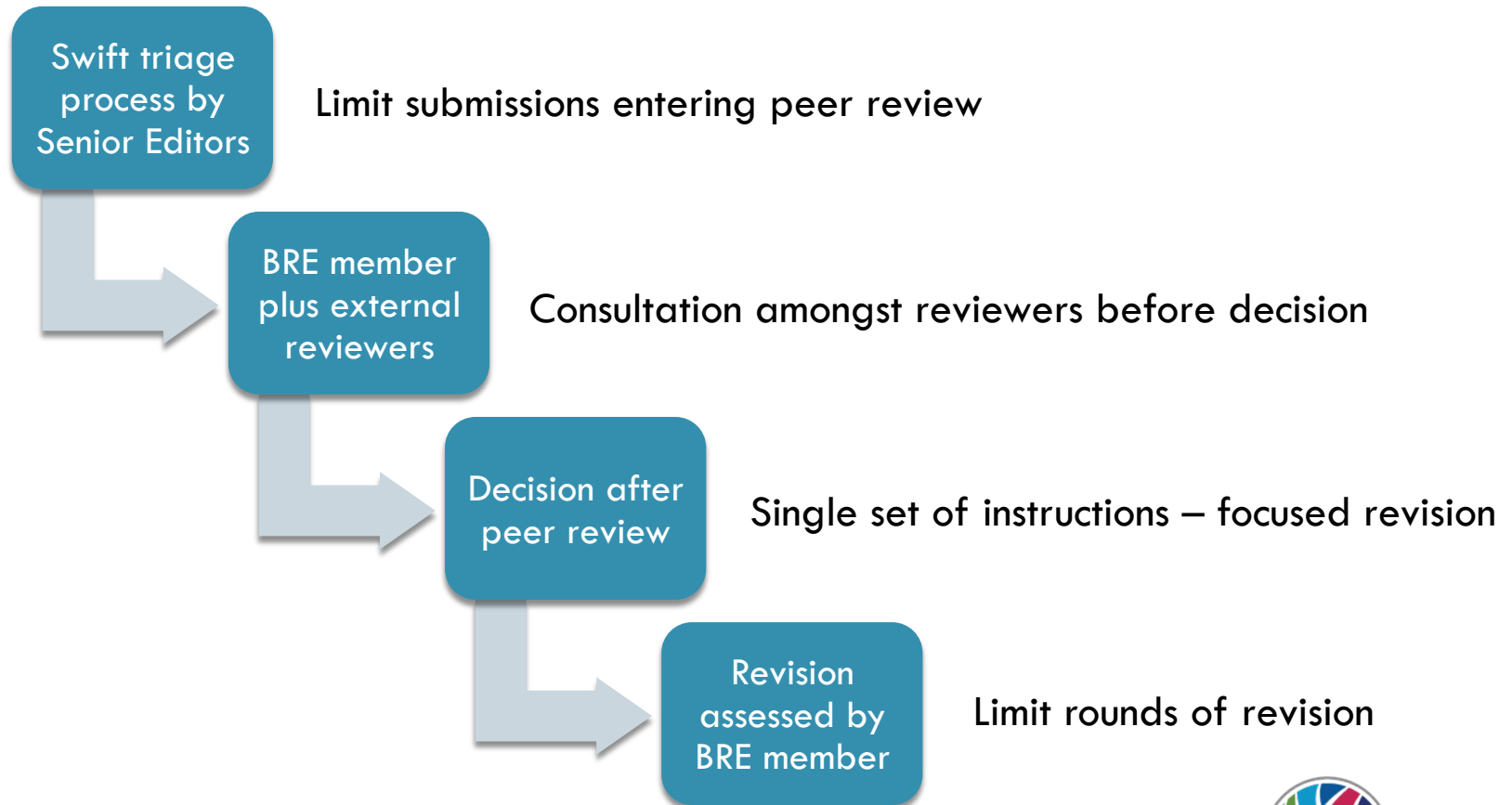
Tony Hunter

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Martin Raff, Alexander Johnson
- and Peter Walter

"The stress associated with publishing experimental results... can drain much of the joy from practicing science."

Science



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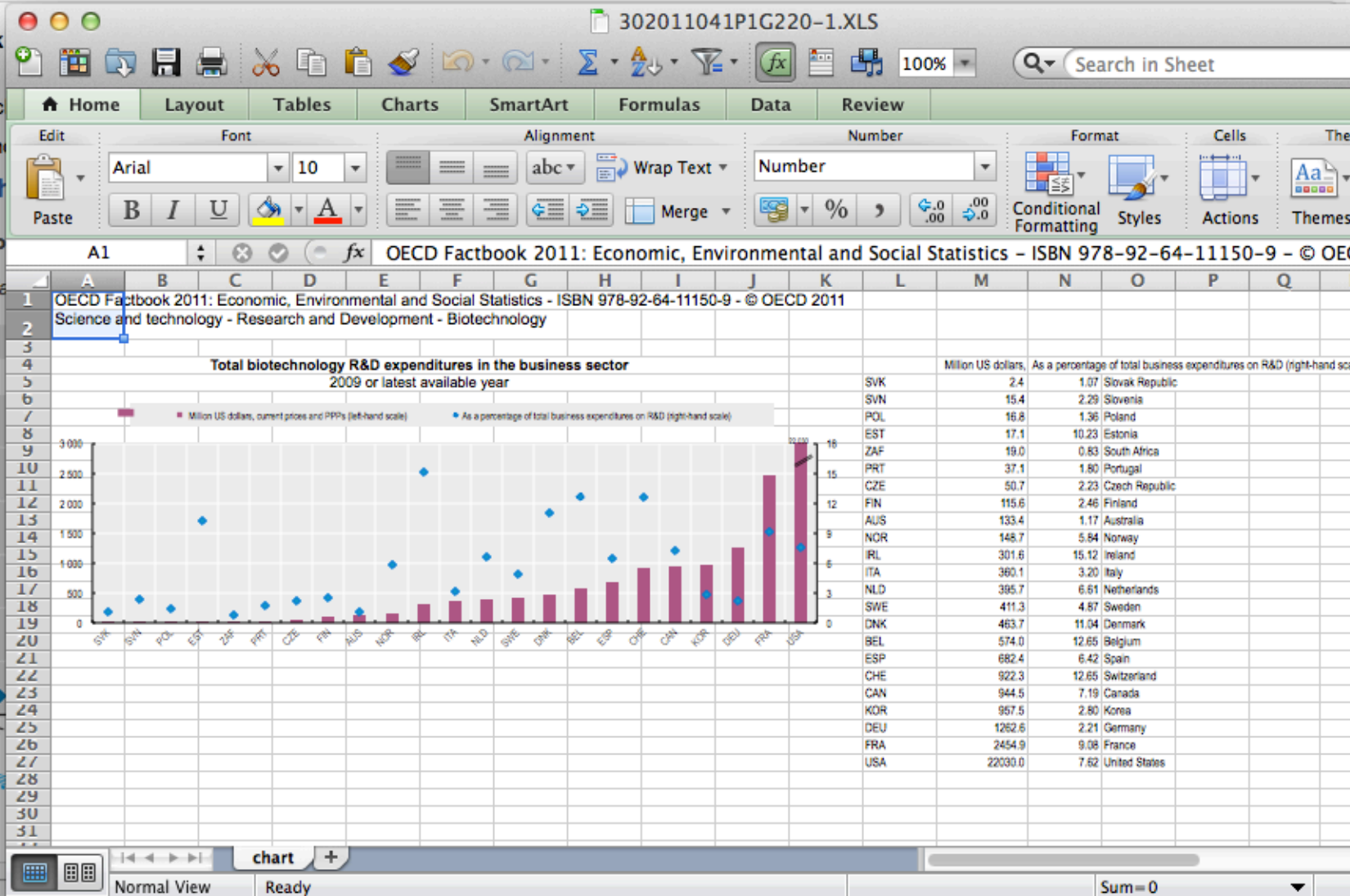
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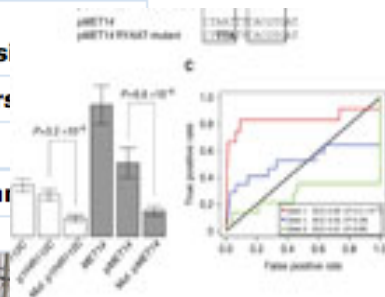


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RYAAT motif is critical to promoter activity and specification of Class I regulon genes. (A) Schematic of wild-type and mutant versions of the composite Met4 recruitment sites from *YHR112C* and *MET14* gene promoters (*pYHR112C* and *pMET14*) cloned upstream of *LYS2* reporter gene. (B) Expression fold change, under switch to low-sulfur growth conditions, for endogenous genes (*YHR112C* and *MET14*) and the *LYS2* reporter gene driven by wild-type (*pYHR112C* and *pMET14*) and RYAAT mutant (Mut. *pYHR112C* and Mut. *pMET14*) gene promoters. (C) ROC analysis for the prediction (identification) of the Met4 regulon genes using the Met4 recruitment 'strength' of the 673 Cbf1 sites used in our genome-wide affinity analysis. Met4 recruitment strength is the ratio of PBM fluorescence intensities shown in [Figure 3G](#) (i.e., ratio of PBM fluorescence intensities for the Met4/Met28/Cbf1 and Met4/Cbf1 PBM experiments). ROC analysis was performed using 500 top-scoring non-regulon genes as false positives. Wilcoxon–Mann–Whitney *U*-test was applied to each regulon gene set to calculate significance of the AUC value. Source data is available for this figure in the Supplementary Information.

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[Source data for figure 6B \(36K\)](#)

S. cerevisiae is governed by recruitment of the transcriptional co-activator Met4. We developed genome-scale approaches to measure transcription factor (TF) DNA-binding affinities and cofactor recruitment to >1300 genomic binding site sequences. We report that genes responding to the TF Cbf1 and cofactor Met28 contain a novel recruitment motif (RYAAT)

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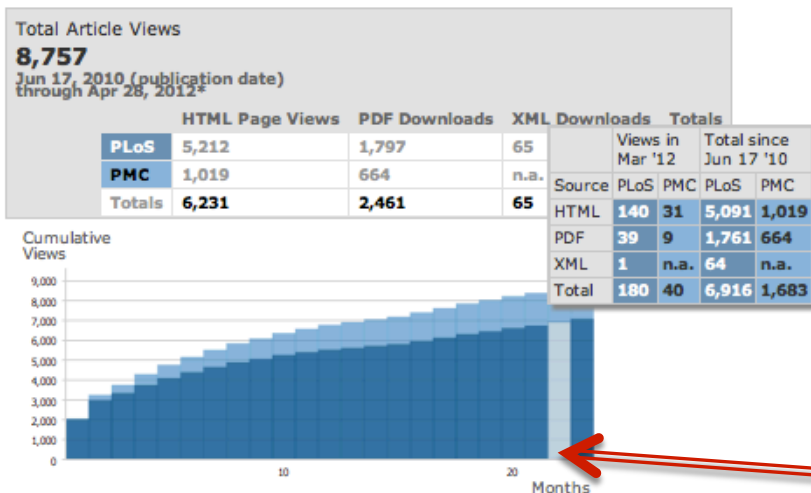
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Altmetrics in the wild: Using social media to explore scholarly impact

Jason Priem, Heather A. Piwowar, Bradley M. Hemminger

(Submitted on 20 Mar 2012)

In growing numbers, scholars are integrating social media tools like blogs, Twitter, and Mendeley into their professional communications. The online, public nature of these tools exposes and reifies scholarly processes once hidden and ephemeral. Metrics based on this activities could inform broader, faster measures of impact, complementing traditional citation metrics. This study explores the properties of these social media-based metrics or "altmetrics", sampling 24,331 articles published by the Public Library of Science. We find that that different indicators vary greatly in activity. Around 5% of sampled articles are cited in Wikipedia, while close to 80% have been included in at least one Mendeley library. There is, however, an encouraging diversity; a quarter of articles have nonzero data from five or more different sources. Correlation and factor analysis suggest citation and altmetrics indicators track related but distinct impacts, with neither able to describe the complete picture of scholarly use alone. There are moderate correlations between Mendeley and Web of Science citation, but many altmetric indicators seem to measure impact mostly orthogonal to citation. Articles cluster in ways that suggest five different impact "flavors", capturing impacts of different types on different audiences; for instance, some articles may be heavily read and saved by scholars but seldom cited. Together, these findings encourage more research into altmetrics as complements to traditional citation measures.

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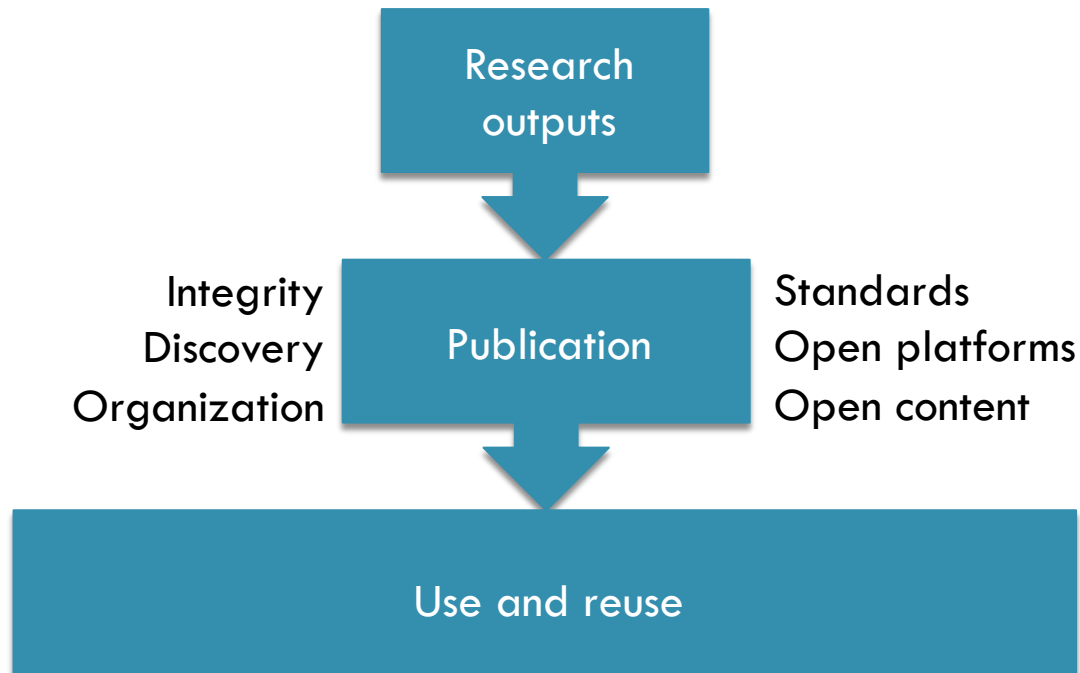
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