

Open Access Journal policies and operations

Matthew Cockerill
Managing Director, BioMed Central

Summary

- ◆ What is different about the open access model?
- ◆ How is BioMed Central putting open access into practice?
- ◆ How important is the recent growth in mobile platforms to publishers?
- ◆ How can publishers support open data?

Digital technology enables new business models



What is different about the Open Access publishing business model?

Traditional research publishing

- ◆ The research community transfers the rights to the research to the publisher
- ◆ The publisher covers costs by selling access to the content

Open Access research publishing

- ◆ No barriers to access
- ◆ No exclusive rights
- ◆ Publisher receives payment for the service of publication

New funding mechanisms for open access publication costs

OA Compact

Signatories of the OA Compact commit to:

"the timely establishment of durable mechanisms for underwriting reasonable publication charges for articles written by its faculty and published in fee-based open-access journals and for which other institutions would not be expected to provide funds."

Signatories of the OA Compact

- ◆ **Berkeley**
- ◆ **Columbia**
- ◆ **Cornell**
- ◆ **Dartmouth**
- ◆ **Harvard**
- ◆ **MIT**
- ◆ MSKCC
- ◆ Ottawa
- ◆ Michigan
- ◆ Barcelona
- ◆ Duke
- ◆ Calgary

The Open Access publishing industry

Open Access publishing, then and now...

2000



2010



Libertas Academica

SCIENTIFIC JOURNALS
INTERNATIONAL

Springer Open Choice

Blackwell Publishing
Online Open



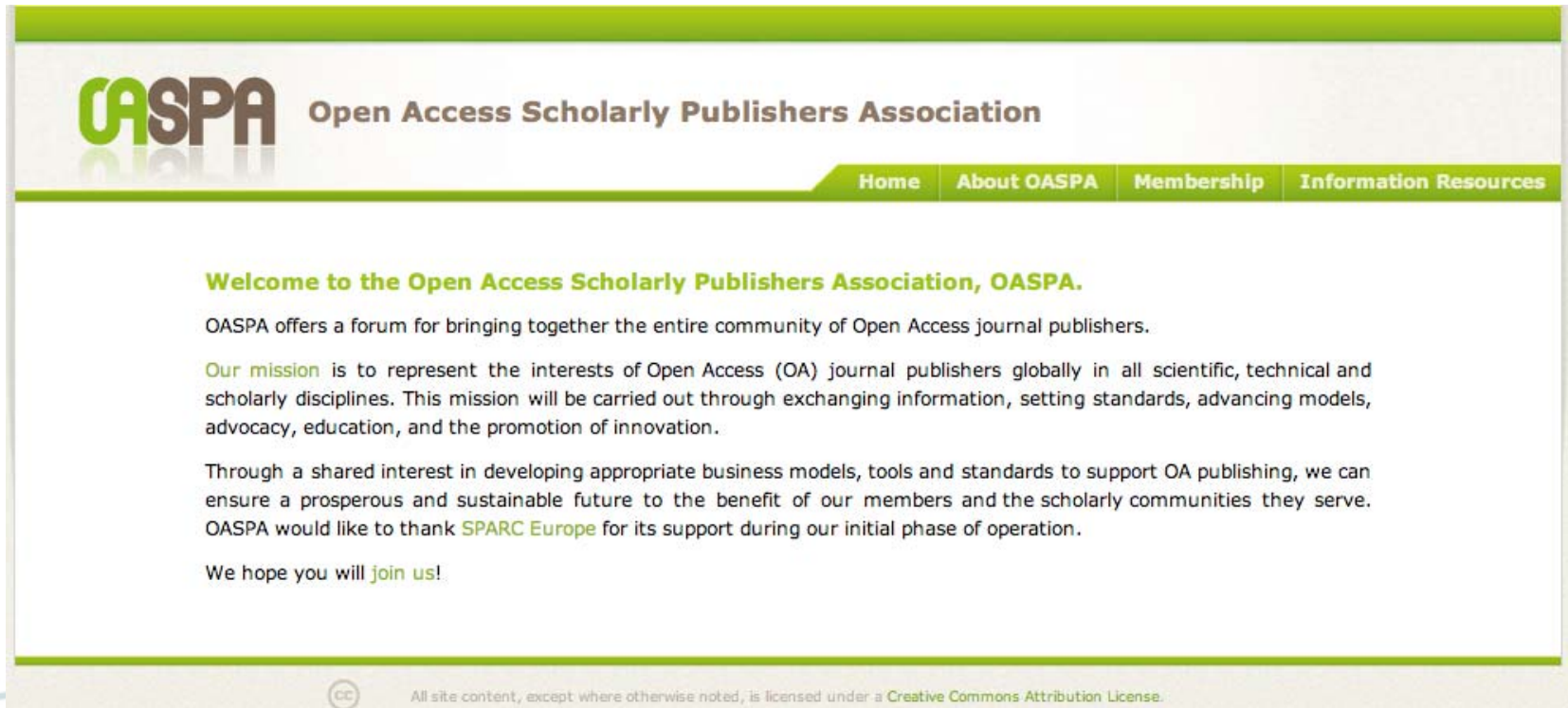
OXFORD OPEN

EXiS Open Choice



And many more...

A new industry association



The screenshot shows the homepage of the Open Access Scholarly Publishers Association (OASPA). The header features the OASPA logo on the left and the text "Open Access Scholarly Publishers Association" to its right. A navigation menu below the header includes links for "Home", "About OASPA", "Membership", and "Information Resources". The main content area contains a welcome message, a description of the association's mission, and a closing statement. At the bottom, there is a Creative Commons Attribution License notice.

OASPA Open Access Scholarly Publishers Association

[Home](#) [About OASPA](#) [Membership](#) [Information Resources](#)


Welcome to the Open Access Scholarly Publishers Association, OASPA.

OASPA offers a forum for bringing together the entire community of Open Access journal publishers.

Our mission is to represent the interests of Open Access (OA) journal publishers globally in all scientific, technical and scholarly disciplines. This mission will be carried out through exchanging information, setting standards, advancing models, advocacy, education, and the promotion of innovation.

Through a shared interest in developing appropriate business models, tools and standards to support OA publishing, we can ensure a prosperous and sustainable future to the benefit of our members and the scholarly communities they serve. OASPA would like to thank [SPARC Europe](#) for its support during our initial phase of operation.

We hope you will [join us!](#)

 All site content, except where otherwise noted, is licensed under a [Creative Commons Attribution License](#).

Goals of OASPA

- ◆ Represents Open Access publishers
- ◆ Agree common definition of Open Access
- ◆ Establish and enforce good standards of editorial and business practices amongst members
- ◆ Identify guidelines and best practices for publishers and institutions in managing payment of publication fees

BioMed Central's journal publishing services

The screenshot shows the BioMed Central website's publishing services page. The browser window is titled "BioMed Central | Publishing services - Mozilla Firefox" and the address bar shows "http://www.biomedcentral.com/info/publishingservices/". The page features the BioMed Central logo and tagline "The Open Access Publisher". A navigation menu includes "home", "journals A-Z", "subject areas", "advanced search", "authors", "reviewers", "libraries", "about", and "my BioMed Central". A sidebar on the left lists various services and resources, including "publishing services", "What you need to know about publishing with BioMed Central", "Publishing services Societies", "Transferring existing or starting new journals", "Browse journals", "Profiles", and "Search info pages". The main content area is titled "Publish your journal with BioMed Central" and describes the platform's experience and services. It includes two testimonials: one from Richard Kreider, Editor-in-Chief of the Journal of the International Society of Sports Nutrition (JISSN), and another from Diethard Tautz, Editor-in-Chief of Frontiers in Zoology. The page also features logos for CASPA, TRANSFER, and a grid of partner logos at the bottom.

BioMed Central
The Open Access Publisher

Welcome BioMed Central (Log on/register)
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for libraries
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press center
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• Publishing services Societies
• Publishing in partnership with societies
• Society journals: case studies
• Society journals overview
• Transferring existing or starting new journals
• Transferring existing or starting new journals
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Search info pages
Go!

CASPA
a CASIO initiative

TRANSFER
a CASIO initiative

C O P E COMMITTEE ON PUBLICATION ETHICS

Publish your journal with BioMed Central

With ten years' experience of collaborating with journal editors and societies, and with our industry leading platform and editorial services, BioMed Central is the perfect partner for developing your journal.

You will have access to a state-of-the-art platform with tools which have been optimized to allow you to run your open access journals and focus on the editorial decision making, while BioMed Central takes care of the practicalities of running the journal publishing platform and providing you with first-class editorial support services. In addition we will work closely with you and our marketing experts to draw up a strategic plan for developing readership of your journal using our proven e-marketing skills.

See additional information:
[Transferring existing or starting new journals](#)
[What to include in a journal proposal](#)
[Our editorial support services](#)
[Journal marketing and customer services](#)
[Publishing partnerships – things to consider](#)
[Open access and usage](#)
[Case studies on society journals and open access](#)

"The Journal of the International Society of Sports Nutrition (JISSN) was self-published by the Society before we moved to BioMed Central in the spring of 2007; since then we have seen both the quantity and the quality of submissions going up nicely. Also, later in 2007 BioMed Central converted our journal's back archive so that older articles were retrospectively added to PubMed Central."
Richard Kreider, Editor-in-Chief

"From the various options we considered it was clear that BioMed Central offers the most professional support. Their staff have always been very helpful and supportive, and we continue to benefit from their professional support."
Diethard Tautz, Editor-in-Chief of Frontiers in Zoology

Contact us today to discuss your requirements. Details can be found [here](#) if you would like to discuss launching a new journal with us or transferring an existing journal.

zotero

<http://www.biomedcentral.com/info/publishingservices>

BioMed Central's journal publishing services

- ◆ Online journal platform
 - Online manuscript submission
 - Online peer review
 - XML/PDF production and publication
 - Indexing and archiving
 - Article processing charge handling
- ◆ Additional services
 - Customer service (authors/reviewers/editors/readers)
 - Journal marketing
 - Journal Editorial Office assistance (optional)
 - Copy-editing (optional)

Recent author feedback on manuscript submission process

- ♦ *"Thank you for a very easy and efficient manuscript submission process. This was the easiest and fastest submission ever. Great job."*
- ♦ *"Online submission process is vastly superior (easy, well explained, download speed for Figs) to that provided by other publishers"*
- ♦ *"The submission system is impressively fast and easy to use. The selection should be changed from "very good" to "excellent"! The best submission system I ever used."*
- ♦ *"The submission process was extremely efficient and this was perhaps the easiest submission process I have come across"*

SpringerOpen

The screenshot shows the SpringerOpen website in a Mozilla Firefox browser window. The browser's address bar displays the URL <http://www.springeropen.com/>. The website header features the SpringerOpen logo on the left and the Springer logo on the right. The main content area is divided into several sections:

- Open access for authors in all disciplines:** A section explaining that SpringerOpen makes it easier for authors to comply with open access mandates, retain copyright, and benefit from Springer's brand. It notes that the first titles will be open to receive submissions soon and start publishing in early 2011.
- SpringerOpen Journals:** A section with a dropdown menu labeled "View a journal".
- Featured journal:** A section highlighting the "Journal of Mathematics in Industry" as a high-quality journal for industrial applications.
- SpringerOpen features:** A list of features including rigorous peer review, e-only and continuous publication, no page budgets or restrictions, and consideration by ISI and other abstracting services.
- Welcome SpringerOpen authors:** A list of benefits for authors, such as retaining copyright under Creative Commons Attribution License, free availability of articles, and an easy submission system.
- Email update:** A sign-up form for periodic news and updates.
- Open access membership:** A button to learn more about membership.
- Contact us:** A button to reach the support team.
- Download brochure:** A button to download a brochure.
- Follow us on twitter:** A link to SpringerOpen's Twitter profile.
- Twitter updates:** A section showing a recent tweet from the University of Michigan about a new fund for open access journals.

The browser's status bar at the bottom shows "Done" and various icons, including the Zotero extension.

High quality/high rejection rate journals

Peer review cascade model



Genome **Biology**

High rejection rate



BMC
Bioinformatics

BMC
Evolutionary Biology

BMC
Genomics

Moderate rejection rate



BMC
Research Notes

Low rejection rate

Rejected authors may be offered consideration in another title

- ◆ Avoids delays for authors
- ◆ Avoids wasting the time of peer reviewers
- ◆ Separates *scientific soundness* of research from *level of interest*

Additional activities/services

Journal-associated conferences

Beyond the Genome:
The true gene count, human evolution and disease genomics
11-13 October 2010
Harvard Medical School, Boston, Massachusetts

Researched with
Genome Biology

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Submit your late poster by 1st October – email matthew.mckay@biomedcentral.com

Beyond the Genome:
The true gene count, human evolution and disease genomics

Joseph B. Martin Conference Center,
Harvard Medical School, Boston, Massachusetts
11th – 13th October 2010

This international conference brings together leading researchers and industry representatives who will review recent progress in key areas of post-genomic research in biology and medicine and chart future developments, including the Human Microbiome Project and the resequencing of matched tumour and normal genomes from specific types of cancers. A cloud computing workshop, which will be open to all delegates, will provide an exciting opportunity to discuss recent and forthcoming developments in this critical and fast-moving field with policy makers and commercial and academic representatives of the genomics community and cloud platforms.

Cloud computing program announced!

Conference sponsors

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- NEW ENGLAND BioLabs
- Agilent Technologies
- BIOTEAM Enabling Science
- Caliper LifeSciences

Parasite to prevention:
Advances in the understanding of malaria
20-22 October 2010
Edinburgh Conference Centre, Heriot-Watt University, Edinburgh, UK

In association with
MALARIA JOURNAL

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Summary | About the conference | Program | Fees | Scientific committee | Bursaries | Attendees

Submit your late poster by 8th October – email matthew.mckay@biomedcentral.com

Parasite to prevention:
Advances in the understanding of malaria

20-22 October 2010
Edinburgh Conference Centre
Heriot-Watt University, Edinburgh UK

This international conference brings together leading researchers and industry representatives who will review important recent findings in parasite and vector biology, disease pathophysiology and immunology, disease treatment, prevention and control. Attendees will learn about the latest developments in key areas and initiatives that are at the forefront of malaria research.

Why Parasite to prevention?

- Internationally renowned invited speakers and scientific committee
- All participants invited to submit abstracts for oral and poster presentations. A significant number of talks will be selected from conference registrants
- Highly topical scientific program: from parasite cell biology to immunology, vaccination and control

Attendees:

- This event is a must-attend for all: postdoctoral research fellows, graduate students, principal investigators in academia and industry, clinical researchers working in malariaology.

Topics include:

- Parasite and vector cell biology
- Disease pathogenesis
- Drug discovery

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- Malaria Portal anopheles.org

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- Request further information

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Contents of Volume 10 Suppl 1

Selected papers from the Seventh Asia-Pacific Bioinformatics Conference (APBC 2009)

Research

from The Seventh Asia Pacific Bioinformatics Conference (APBC 2009)

Beijing, China. 13–16 January 2009

Edited by Michael Q Zhang, Michael S Waterman and Xuegong Zhang

[Conference website](#)
Introduction [Open Access](#)

The Seventh Asia Pacific Bioinformatics Conference (APBC2009)

Michael Q Zhang, Michael S Waterman, Xuegong Zhang

BMC Bioinformatics 2009, **10**(Suppl 1):S1 (30 January 2009)
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Genome aliquoting with double cut and join

Robert Warren, David Sankoff

BMC Bioinformatics 2009, **10**(Suppl 1):S2 (30 January 2009)
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Pathogenic *Bacillus anthracis* in the progressive gene losses and gains in adaptive evolution

GX Yu

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SE: an algorithm for deriving sequence alignment from a pair of superimposed structures

Chin-Hsien Tai, James J Vincent, Changhoon Kim, Byungkook Lee

BMC Bioinformatics 2009, **10**(Suppl 1):S4 (30 January 2009)

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Abstracts of the 16th International Charles Heidelberger Symposium on Cancer Research

Meeting abstracts

Coimbra, Portugal. 26–28 September 2010

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Volume 4 Suppl 1

Proceedings of the 13th European workshop on QTL mapping and marker assisted selection

Proceedings

Wageningen, The Netherlands. 20–21 April 2009

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Proceedings

St Louis, MO, USA. 17–20 September 2008

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Volume 3 Suppl 6

Proceedings of the 2007 and 2008 Symposia on Protein N-terminal Acetylation

Proceedings

Bergen, Norway. 24–25 May and 11–13 September 2008

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Volume 3 Suppl 5

6th International Symposium on the Intraductal Approach to Breast Cancer

Meeting abstracts



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FANTOM4



FANTOM4: Systems biology of a leukemia transcriptome and its regulation

This special collection of articles are the companion papers for the three FANTOM4 papers published with *Nature Genetics*.

FANTOM4 has used genome-wide expression profiling to measure the expression dynamics of promoter usage, mRNAs, microRNAs and other small non-coding RNAs throughout a time course of differentiation in the acute myeloid leukemia cell line THP-1. Of particular interest was the extensive use of deepCAGE (a new deep sequencing application) to identify active promoters and their expression dynamics. Computational analysis, chromatin immunoprecipitation and perturbation experiments have then been used to build network models of the transcription factors and miRNAs, their targets and their role in differentiation and maintenance of the undifferentiated state.

Research article [Open Access](#)
Core promoter structure and genomic context reflect histone 3 lysine 9 acetylation patterns

Anton Kratz, Erik Arner, Rintaro Saito, Atsutaka Kubosaki, Jun Kawai, Harukazu Suzuki, Piero Carninci, Takahiro Arakawa, Masaru Tomita, Yoshihide Hayashizaki, Carsten O Daub
BMC Genomics 2010, **11**:257 (21 April 2010)
[\[Abstract\]](#) [\[Full text\]](#) [\[PDF\]](#) [\[PubMed\]](#) [\[Related articles\]](#)

Research article [Open Access](#) **Highly accessed**
Deciphering the transcriptional circuitry of microRNA genes expressed during human monocytic differentiation

Sebastian Schmeier, Cameron R MacPherson, Magbubah Essack, Mandeep Kaur, Ulf Schaefer, Harukazu Suzuki, Yoshihide Hayashizaki, Vladimir B Bajic
BMC Genomics 2009, **10**:595 (10 December 2009)

microRNA

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How will we read scientific articles in the future?

Impact of iPad...

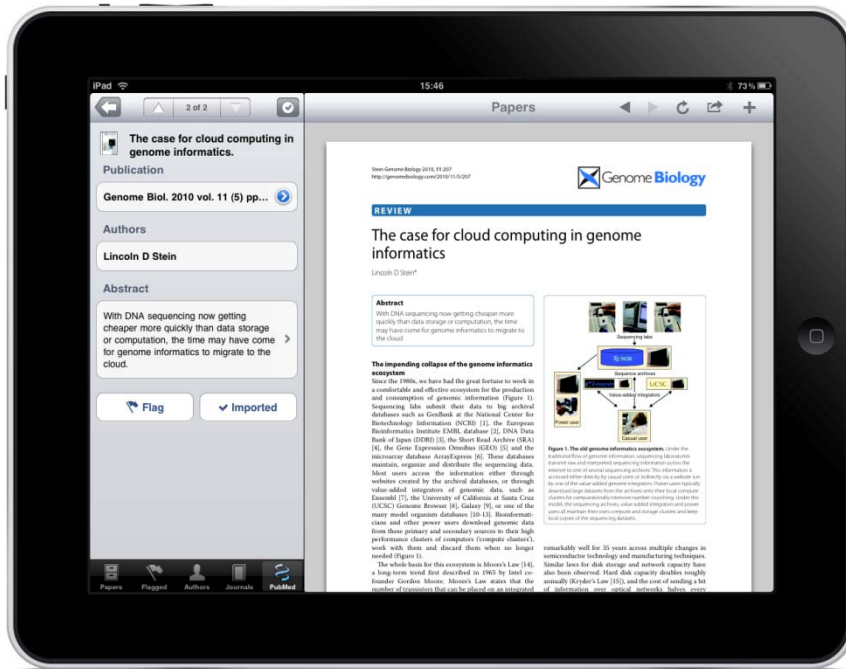
- ♦ **Books/magazines/newspapers**
 - Radical change
 - Like music, moving online...
 - Therefore changes business model
- ♦ **Scientific journals**
 - Impact is less obvious
 - Access to journals is *already* mainly online
 - But iPad and similar devices *will* affect how research is read and shared



Social/mobile reading



Social reading



What does this change mean for publishers?

- ◆ For last 15 years, researchers have discovered/downloaded articles online
- ◆ BUT then they read, annotated, classified and discussed largely offline
- ◆ If reading is done online, a huge amount of additional data is available
- ◆ Has potential to help both group collaboration and open discussion

Uses for social sharing data

- ◆ Article stats page
 - Download stats
 - Facebook ('Likes this' stats)
 - Tweets (bit.ly clicks)
 - Blogs (via aggregator)
 - Ratings (Mendeley, Papers, Faculty of 1000)
 - Citations (Scopus, Web of Science, Crossref, PubMed Central)
- ◆ Smart recommendations for users
 - (*cf* iTunes/Amazon/Netflix)

BioMed Central

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Gastro 2009

Come and visit BioMed Central at booth #71

BioMed Central will be exhibiting at the Gastro 2009 conference taking place in London in November. Come and visit us at booth #71 where we will be promoting our range of open access journals in the field of gastroenterology. To find out more about... [Read more](#) ▾

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BioMedCentral

@allan_marks Thanks for sharing this with us!

about 5 hours ago from web in reply to allan_marks

RT @PLOS Harvard, MIT, UC Berkeley, Cornell and Dartmouth announce commitment to Open Access <http://bit.ly/6KzmB>

about 6 hours ago from web

RT @Computer_Aid Government Digital Britain report advises donating your PCs for reuse to help the environment...<http://tinyurl.com/cq774f>

about 11 hours ago from web

#biologypix @NIHforHealth Biology Image Library published images by R. Sougrat formerly of NICHD: see his work at <http://tinyurl.com/pc3jl7>

about 13 hours ago from web

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Location London
Web <http://www.biomed...>
Bio The Open Access Publisher

226 following 676 followers

Tweets 457

Favorites

Following



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RSS feed of BioMedCentral's tweets

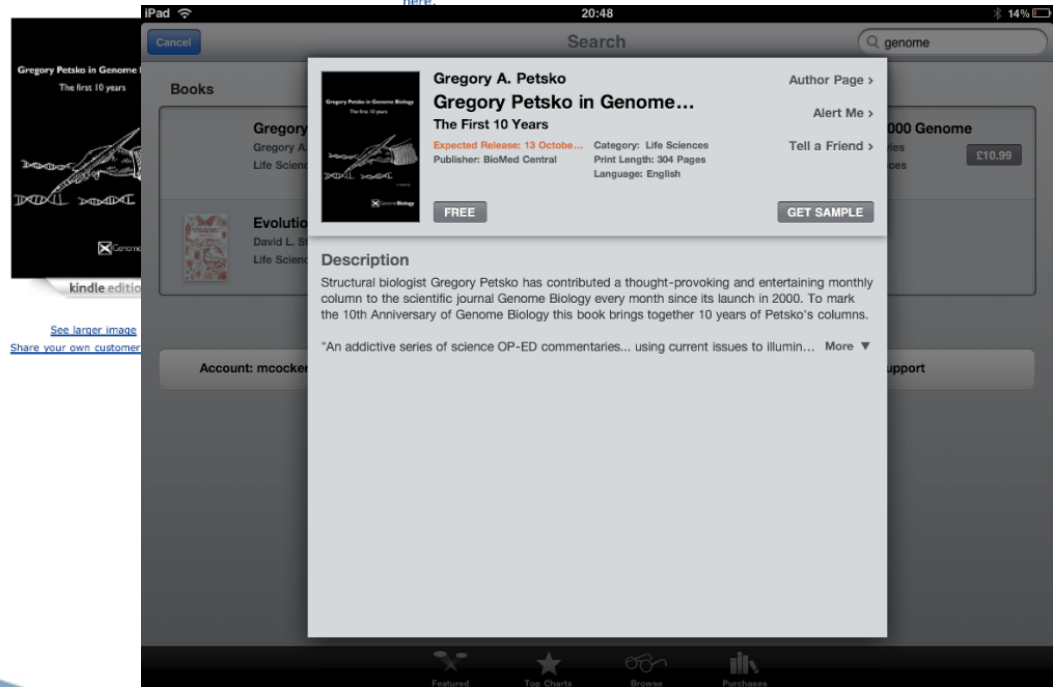
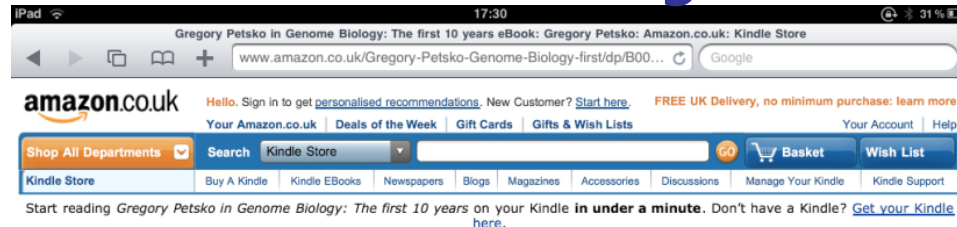
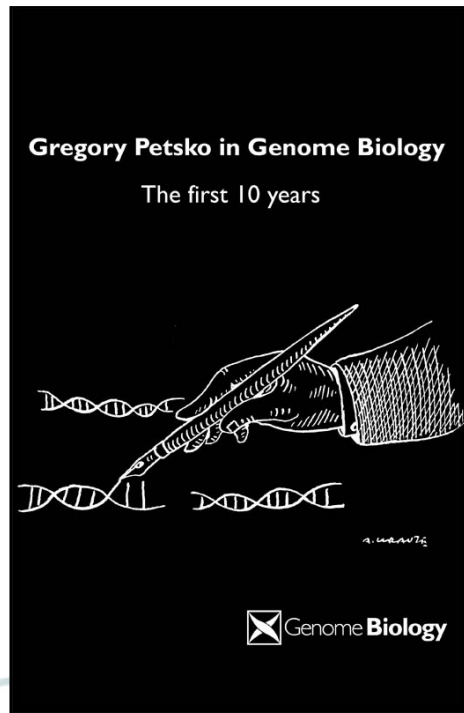
BioMed Central on mobile devices

- ◆ Mobile-friendly article pages and My Manuscripts page being developed
- ◆ Video in all BioMed Central articles being optimized for viewing in any browser (including mobile)
- ◆ Enhancements to article and PDF metadata to integrate with social/mobile platforms
- ◆ Possible role for ePub format
- ◆ Aim to allow reviewers to annotate manuscripts as PDFs on device, then return

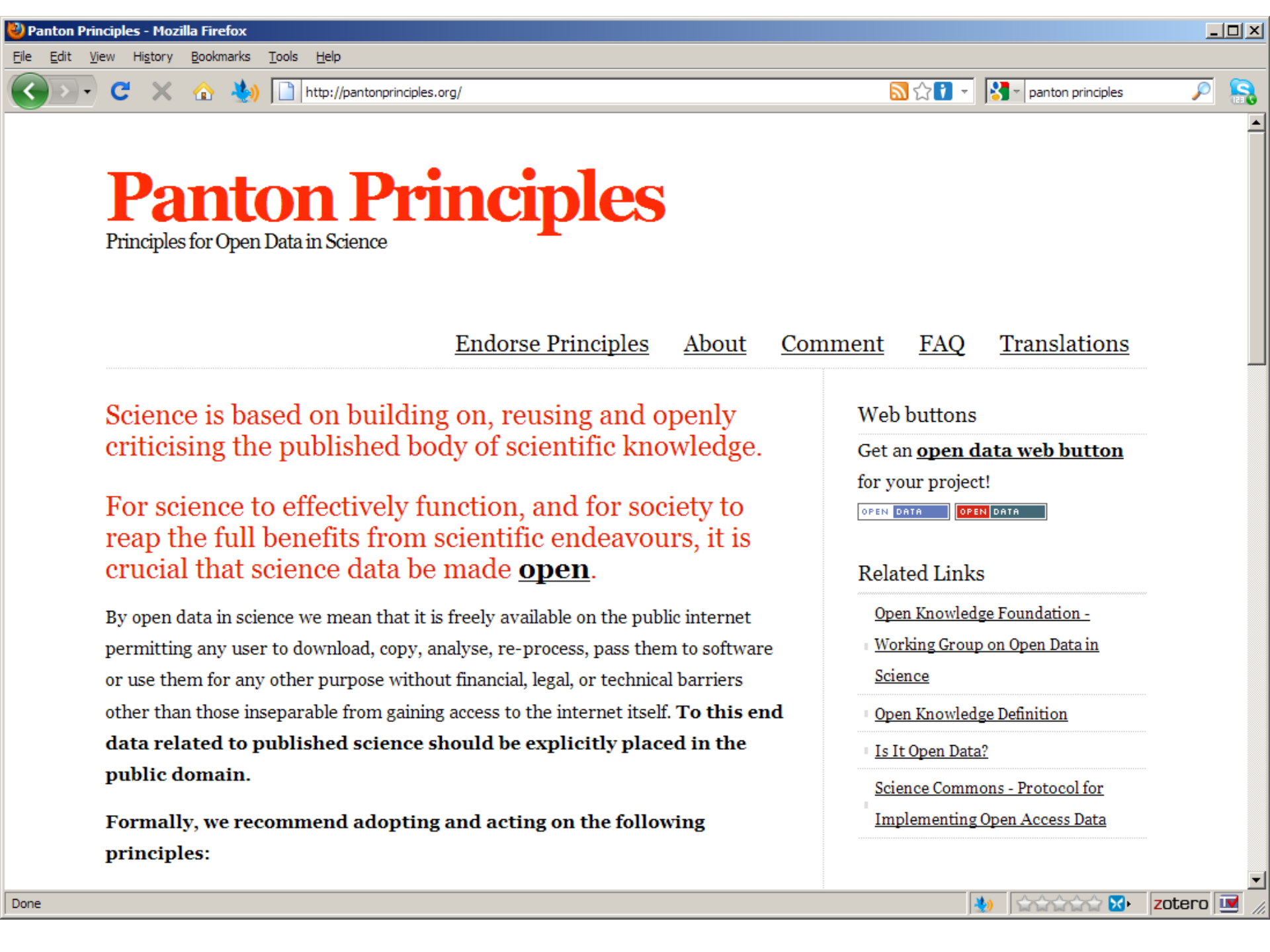
eBooks / ePub

- ◆ BioMed Central's primary focus is journals, not books
- ◆ However, supplements, special issues, and thematic series are book-like
- ◆ ePub format is at an early stage
- ◆ Limited support for complex documents
- ◆ But convenience and readability is attractive
- ◆ Automatic conversion to ePub takes advantage of investment in structured XML markup

Gregory Petsko in Genome Biology: The first 10 years



Open Data



Panton Principles

Principles for Open Data in Science

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Science is based on building on, reusing and openly criticising the published body of scientific knowledge.

For science to effectively function, and for society to reap the full benefits from scientific endeavours, it is crucial that science data be made **open**.

By open data in science we mean that it is freely available on the public internet permitting any user to download, copy, analyse, re-process, pass them to software or use them for any other purpose without financial, legal, or technical barriers other than those inseparable from gaining access to the internet itself. **To this end data related to published science should be explicitly placed in the public domain.**

Formally, we recommend adopting and acting on the following principles:

Web buttons

Get an **open data web button** for your project!



Related Links

- [Open Knowledge Foundation - Working Group on Open Data in Science](#)
- [Open Knowledge Definition](#)
- [Is It Open Data?](#)
- [Science Commons - Protocol for Implementing Open Access Data](#)

OPEN DATA

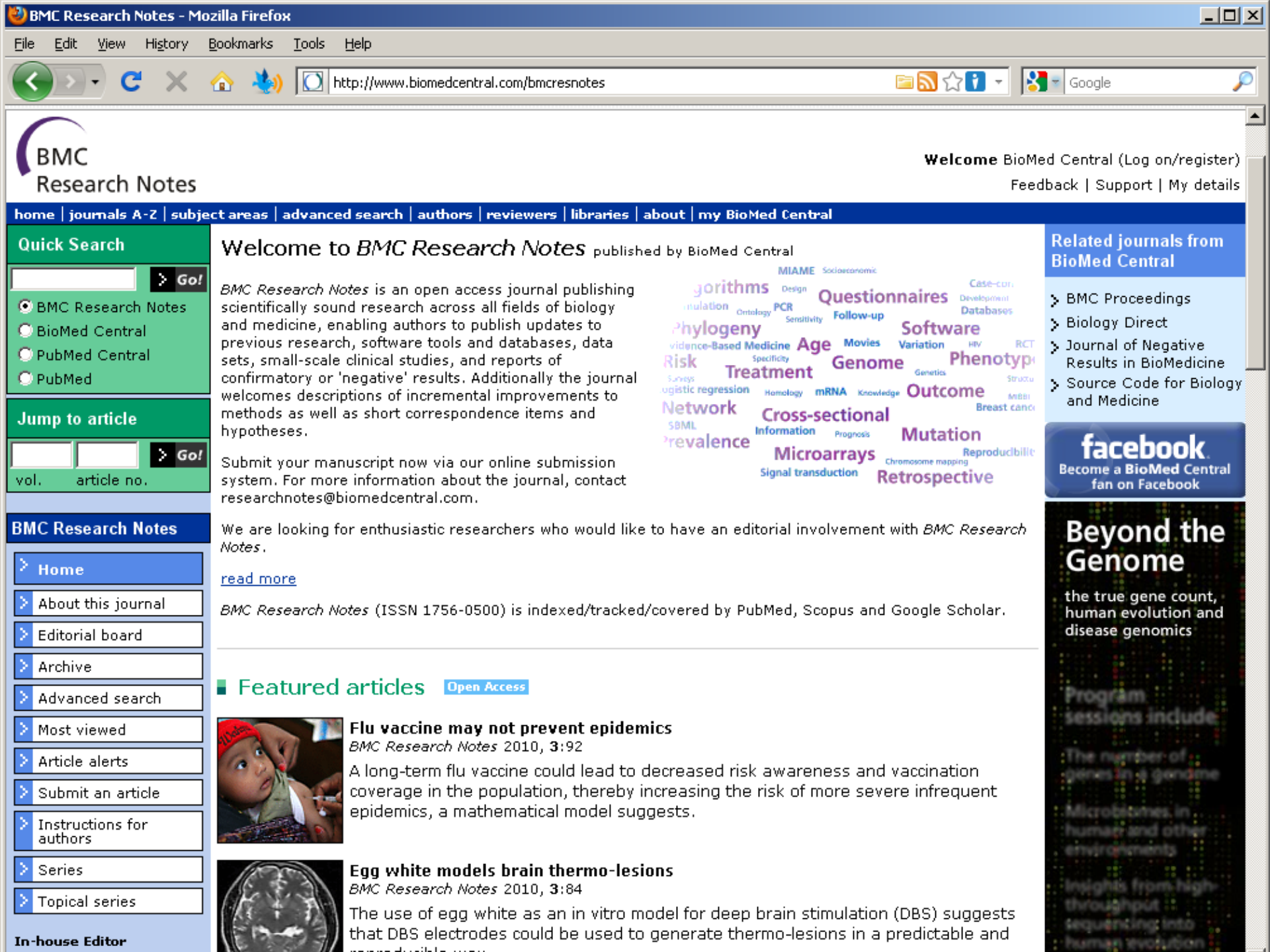


Draft position statement on Open Data

The screenshot shows a Mozilla Firefox browser window with the address bar displaying http://blogs.openaccesscentral.com/blogs/bmcblog/entry/join_the_data_debate_draft. The page content includes the BioMed Central logo and the title "BioMed Central Blog". The main heading of the post is "THURSDAY SEP 02, 2010" followed by "Join the data debate: draft position statement on open data". The text discusses the goals of the Panton Principles for Open Data, the need for careful consultation, and the draft of a position statement on data sharing and licensing. It also mentions a panel discussion on publishing primary research data at Science Online London on 3rd September 2010. On the right side, there are sections for "CATEGORIES" (All, Open Data, BioMed Central, etc.), "KEEP UP TO DATE" (Sign up for BMC Updates, Facebook, Twitter), "SEARCH", "LINKS", "Our blogs", and "Journal blogs". At the bottom of the browser window, the status bar shows "Done" and a Zotero extension icon.

BioMed Central encourages the publication of datasets

- ◆ Electronic version of article is authoritative
- ◆ Authors are encouraged to include additional files containing underlying data
- ◆ Where possible data is presented in a convenient embedded form (movies, chemical structures, KML etc)
- ◆ “Mini-websites” also allow authors to embed supporting data



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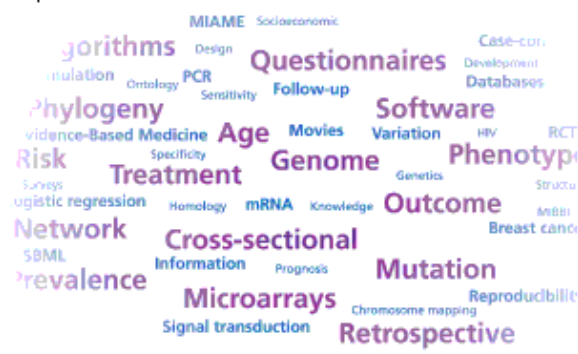
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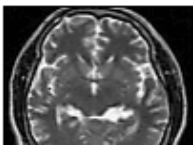
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Flu vaccine may not prevent epidemics

BMC Research Notes 2010, **3**:92

A long-term flu vaccine could lead to decreased risk awareness and vaccination coverage in the population, thereby increasing the risk of more severe infrequent epidemics, a mathematical model suggests.



Egg white models brain thermo-lesions

BMC Research Notes 2010, **3**:84

The use of egg white as an in vitro model for deep brain stimulation (DBS) suggests that DBS electrodes could be used to generate thermo-lesions in a predictable and reproducible way.

Beyond the Genome

the true gene count, human evolution and disease genomics


Program sessions include:
The number of genes in the human genome
Microbes in human evolution
The human genome: a new paradigm
The human genome: a new paradigm

Plans to extend reusability of data

- ◆ BioMed Central is working with the community to develop explicit guidelines to facilitate data reuse within particular disciplines
- ◆ A series of articles are being commissioned for *BMC Research Notes*

Cloud computing and reproducibility

Stein Genome Biology 2010, 11:207
http://genomebiology.com/2010/11/5/207

 Genome Biology

REVIEW

The case for cloud computing in genome informatics

Lincoln D Stein*

Abstract
With DNA sequencing now getting cheaper more quickly than data storage or computation, the time may have come for genome informatics to migrate to the cloud.

The impending collapse of the genome informatics ecosystem
Since the 1980s, we have had the great fortune to work in a comfortable and effective ecosystem for the production and consumption of genomic information (Figure 1). Sequencing labs submit their data to big archival databases such as GenBank at the National Center for Biotechnology Information (NCBI) [1], the European Bioinformatics Institute EMBL database [2], DNA Data Bank of Japan (DDBJ) [3], the Short Read Archive (SRA) [4], the Gene Expression Omnibus (GEO) [5] and the microarray database ArrayExpress [6]. These databases maintain, organize and distribute the sequencing data. Most users access the information either through websites created by the archival databases, or through value-added integrators of genomic data, such as Ensembl [7], the University of California at Santa Cruz (UCSC) Genome Browser [8], Galaxy [9], or one of the many model organism databases [10-13]. Bioinformaticians and other power users download genomic data from these primary and secondary sources to their high performance clusters of computers ('compute clusters'), work with them and discard them when no longer needed (Figure 1).

The whole basis for this ecosystem is Moore's Law [14], a long-term trend first described in 1965 by Intel co-founder Gordon Moore. Moore's Law states that the number of transistors that can be placed on an integrated circuit board is increasing exponentially, with a doubling time of roughly 18 months. The trend has held up remarkably well for 35 years across multiple changes in semiconductor technology and manufacturing techniques. Similar laws for disk storage and network capacity have also been observed. Hard disk capacity doubles roughly annually (Kryder's Law [15]), and the cost of sending a bit of information over optical networks halves every 9 months (Butter's Law [16]).

Genome sequencing technology has also improved dramatically, and the number of bases that can be sequenced per unit cost has also been growing at an exponential rate. However, until just a few years ago, the doubling time for DNA sequencing was just a bit slower than the growth of compute and storage capacity. This

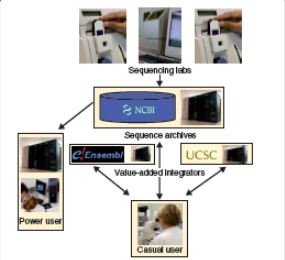



Figure 1. The old genome informatics ecosystem. Under the traditional flow of genome information, sequencing laboratories transmit raw and interpreted sequencing information across the internet to one of several sequencing archives. This information is accessed either directly by casual users or indirectly via a website run by one of the value-added genome integrators. Power users typically download large datasets from the archives onto their local compute clusters for computationally intensive number crunching. Under this model, the sequencing archives, value-added integrators and power users all maintain their own compute and storage clusters and keep local copies of the sequencing datasets.

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- ◆ Expands access to high performance computing
- ◆ Huge potential to make computational research more comparable and reproducible
- ◆ Sharing of data *and* executable code
- ◆ Need to define best practices for publication
- ◆ Frameworks such as Galaxy will play an important role