Elsevier's Article of the Future

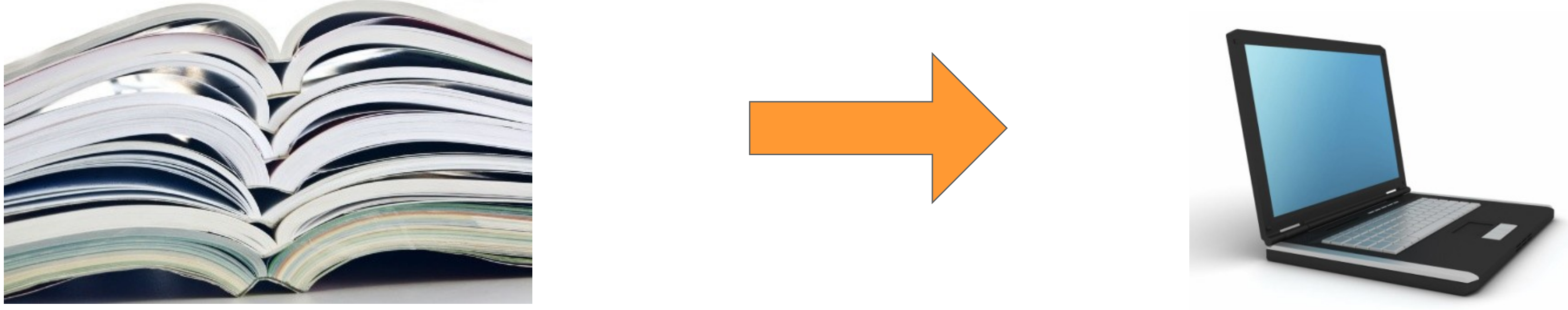
Overview of recent innovations and the road ahead

爱思唯尔未来的文章：近期创新与未来之路

Presented by: Dr. Jan Willem Wijnen, Executive Publisher Elsevier

ELSEVIER

Print to online 从纸质印刷到在线出版



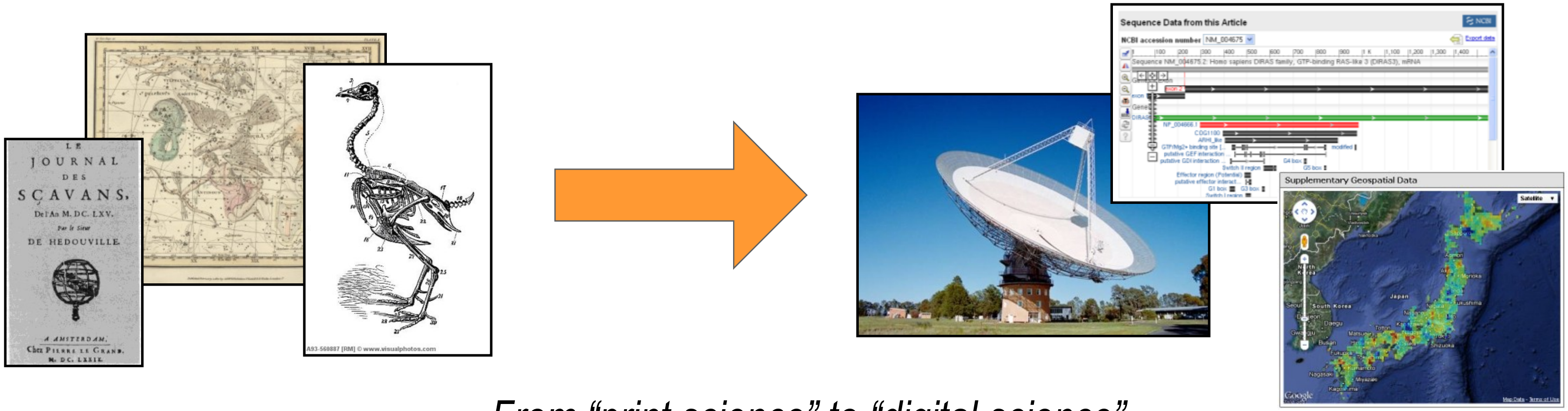
From "print science" to "digital science"

- In the past twenty year we have seen a dramatic transition from print-to-online publishing methods.
- 过去的20年，从纸质印刷到在线出版，出版模式发生了翻天覆地的变化

Digital publishing offers many new opportunities
数字出版带来新机会

- Increased speed of publication 出版速度更快
- New business models (open access, pay-per-view, bundles…) 新商业模式
- New peer-review processes 新评审流程
- Better search methods 查询更加方便
- Offering new types of information 提供新型信息

Digital content calls for a new publication format
数字内容要求新的出版形式



From "print science" to "digital science"

- Digital content allows authors to present and share more types of data, in an appropriate format
- Digital content allows readers to digest information more efficiently and gain better understanding of scientific paper
- 数字内容让作者可以通过适当的形式呈现和分享更多数据
- 数字内容让读者可以更有效地理解和消化科技论文

Roles of future publications in academic exchanges
未来出版在学术交流中的角色

- Many types of scientific information can be shared much better than in the past: 更多形式的科技信息可以更好的分享
  - Geographical information 地理信息
  - 3-Dimensional information 3D 信息
  - Software 软件
  - Data 数据
  - Plots 图表
  - Bibliographic information 书目信息
  - …

Roles of future publications in academic exchanges
未来出版在学术交流中的角色

- These days academic journals must:
  - Publish these types of digital information, to offer authors and readers the best exchange of academic knowledge.
  - Represent this information in the most suitable way/format.
  - Allow simple navigation between various sources of information
  - Be a research tool
  - Be easy to use!

  - 出版多种数字信息，为作者和读者提供最好的学术交流
  - 将学术信息用合适的形式呈现出来
  - 提供不同来源信息间的导航
  - 成为研究工具
  - 更易于使用

The Article of the Future: create a better platform to disseminate research
未来的文章：为科研提供更好的传播与交流平台

- Within Elsevier these new requirements for publications were bundled in the project Article-of-the-Future 爱思唯尔“未来的文章”项目
- Requirements:
  - To optimally communicate scientific research in its full richness 科研交流最优化
  - To offer <u>authors</u> a better research “outlet” 为作者提供更好的研究成果发表途径
  - To increase value to <u>users, readers, and customer</u> 为用户和读者提供价值
  - Increase attractiveness of our journals 增加期刊吸引力
- Started with Cell Press in 2009 始于2009年细胞出版社
- Full roll out to all journals mid 2012 所有期刊于2012年年中参与其中
- Continuous development of specific content innovations 持续创新

Article of the Future: Presentation, Content, Context
未来的文章：呈现形式、内容与相关信息

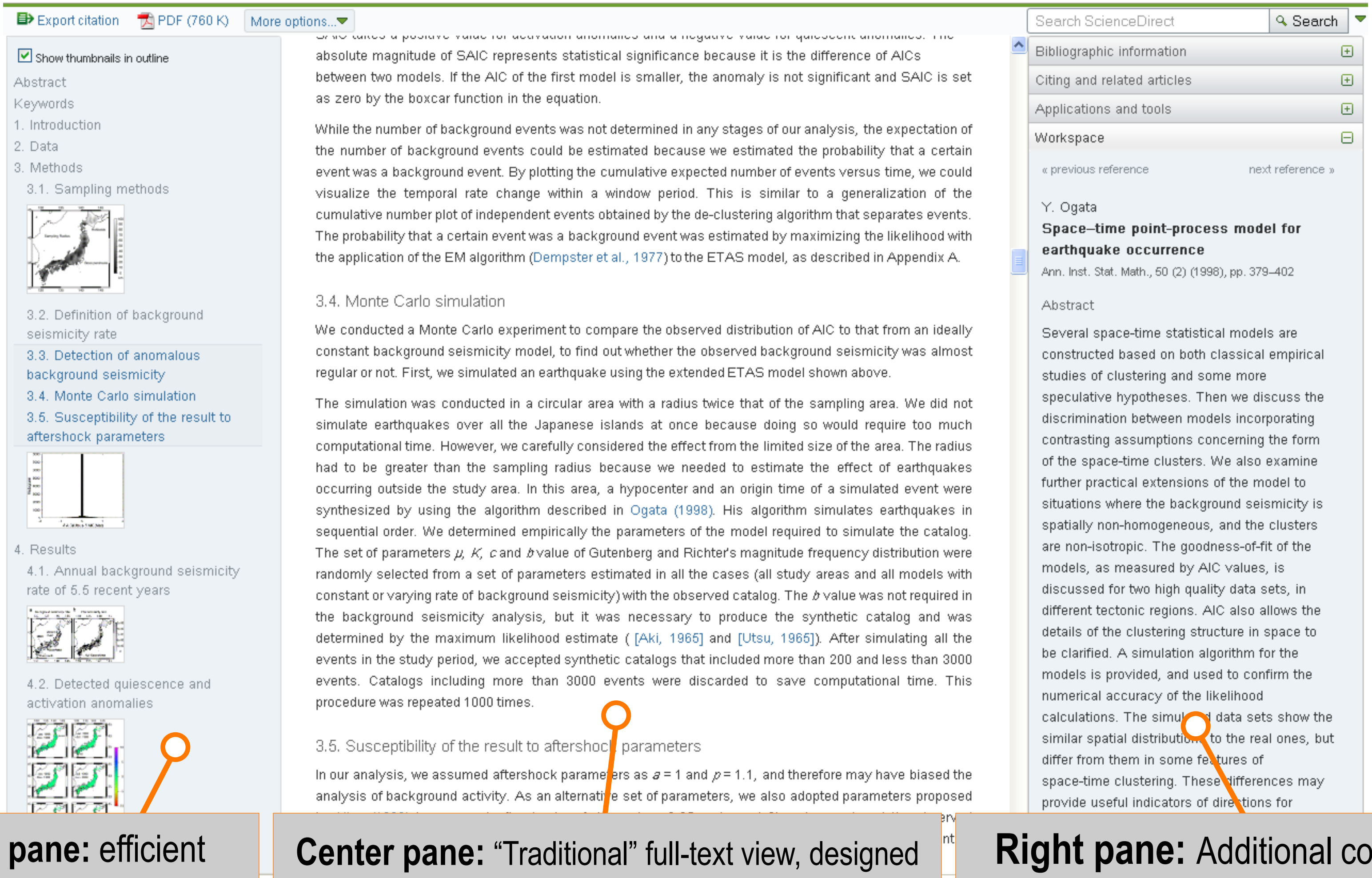
Three components of the Article of the Future concept:

- <u>Presentation</u>: Offering an optimal online browsing and reading experience
- <u>Content</u>: Support authors to share a wider range of research output – data, computer code, multimedia files, etc.
- <u>Context</u>: Connecting the online article to trustworthy scientific resources to present valuable additional information in the context of the article

- 呈现形式：提供最后的在线浏览及阅读体验
- 内容：作者可以分享的更多，比如数据、代码、多媒体信息等
- 相关信息：在线文章与来源可靠的科技信息链接，并在相关信息中呈现出来，提升附加值

Presentation: The three-pane format

呈现形式：三栏格式



SAIC takes a positive value for activation anomalies and a negative value for quiescent anomalies. The absolute magnitude of SAIC represents statistical significance because it is the difference of AICs between two models. If the AIC of the first model is smaller, the anomaly is not significant and SAIC is set as zero by the boxcar function in the equation.

While the number of background events was not determined in any stages of our analysis, the expectation of the number of background events could be estimated because we estimated the probability that a certain event was a background event. By plotting the cumulative expected number of events versus time, we could visualize the temporal rate change within a window period. This is similar to a generalization of the cumulative number plot of independent events obtained by the de-clustering algorithm that separates events. The probability that a certain event was a background event was estimated by maximizing the likelihood with the application of the EM algorithm (Dempster et al., 1977) to the ETAS model, as described in Appendix A.

3.4. Monte Carlo simulation

We conducted a Monte Carlo experiment to compare the observed distribution of AIC to that from an ideally constant background seismicity model, to find out whether the observed background seismicity was almost regular or not. First, we simulated an earthquake using the extended ETAS model shown above.

The simulation was conducted in a circular area with a radius twice that of the sampling area. We did not simulate earthquakes over all the Japanese islands at once because doing so would require too much computational time. However, we carefully considered the effect from the limited size of the area. The radius had to be greater than the sampling radius because we needed to estimate the effect of earthquakes occurring outside the study area. In this area, a hypocenter and an origin time of a simulated event were synthesized by using the algorithm described in Ogata (1998). His algorithm simulates earthquakes in sequential order. We determined empirically the parameters of the model required to simulate the catalog. The set of parameters μ, K, c and b value of Gutenberg and Richter's magnitude frequency distribution were randomly selected from a set of parameters estimated in all the cases (all study areas and all models with constant or varying rate of background seismicity) with the observed catalog. The b value was not required in the background seismicity analysis, but it was necessary to produce the synthetic catalog and was determined by the maximum likelihood estimate ([Aki, 1965] and [Utsu, 1965]). After simulating all the events in the study period, we accepted synthetic catalogs that included more than 200 and less than 3000 events. Catalogs including more than 3000 events were discarded to save computational time. This procedure was repeated 1000 times.

3.5. Susceptibility of the result to aftershock parameters

In our analysis, we assumed aftershock parameters as $a = 1$ and $p = 1.1$, and therefore may have biased the analysis of background activity. As an alternative set of parameters, we also adopted parameters proposed

Y. Ogata

Space–time point-process model for earthquake occurrence

Ann. Inst. Stat. Math., 50 (2) (1998), pp. 379–402

Abstract

Several space-time statistical models are constructed based on both classical empirical studies of clustering and some more speculative hypotheses. Then we discuss the discrimination between models incorporating contrasting assumptions concerning the form of the space-time clusters. We also examine further practical extensions of the model to situations where the background seismicity is spatially non-homogeneous, and the clusters are non-isotropic. The goodness-of-fit of the models, as measured by AIC values, is discussed for two high quality data sets, in different tectonic regions. AIC also allows the details of the clustering structure in space to be clarified. A simulation algorithm for the models is provided, and used to confirm the numerical accuracy of the likelihood calculations. The simulated data sets show the similar spatial distribution to the real ones, but differ from them in some features of space-time clustering. These differences may provide useful indicators of directions for

Left pane: efficient navigation & browsing

左栏：导航与浏览器

Center pane: “Traditional” full-text view, designed for optimal online reading experience

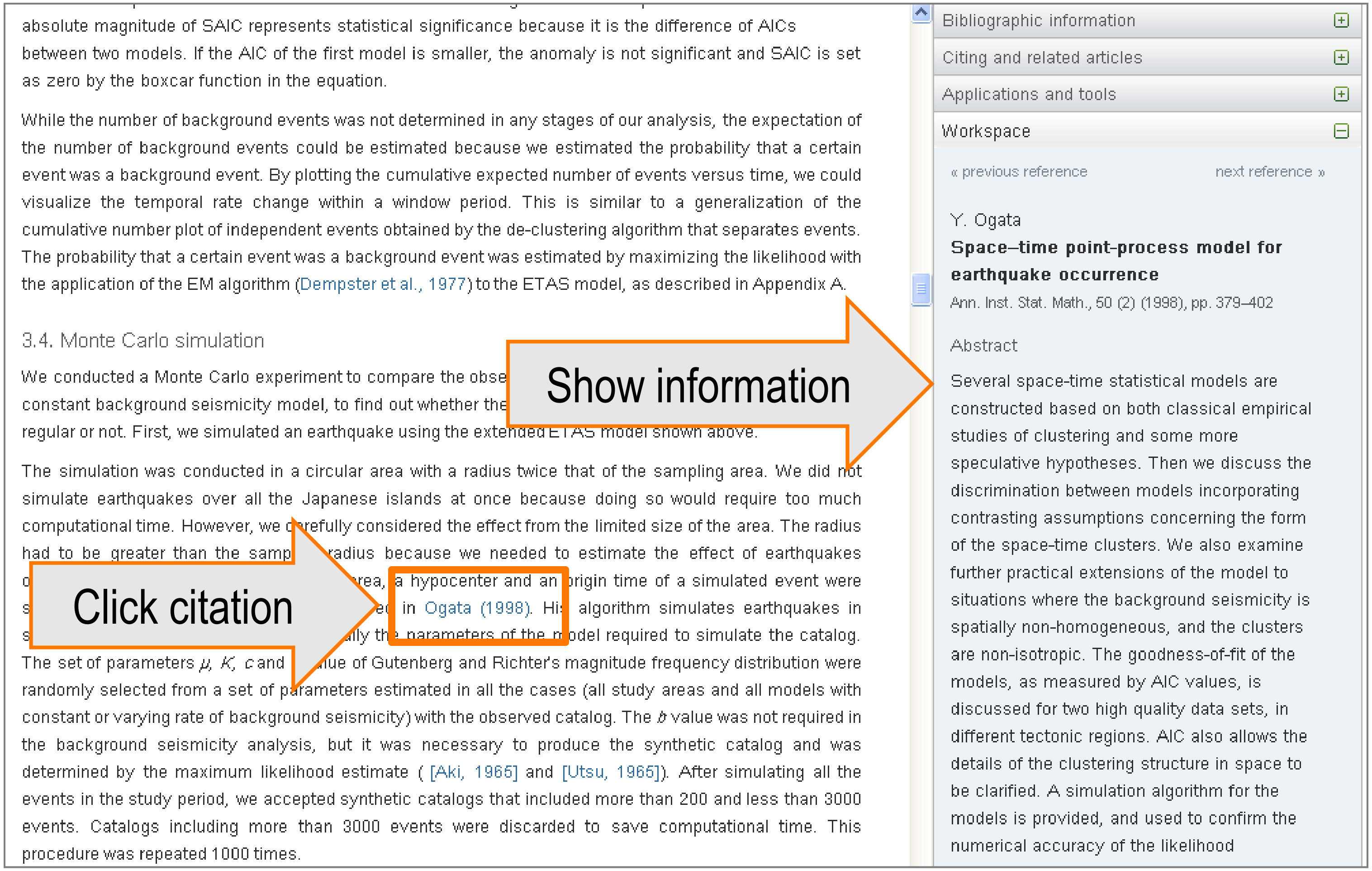
中间栏：优化后更适于在线阅读的全文

Right pane: Additional content & tools. Shown here: reference browser

右栏：相关内容和工具

Presentation: Reference browser

呈现形式：参考文献浏览器



absolute magnitude of SAIC represents statistical significance because it is the difference of AICs between two models. If the AIC of the first model is smaller, the anomaly is not significant and SAIC is set as zero by the boxcar function in the equation.

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Show information

Click citation

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点击引用文章即可在右侧呈现相关引用信息

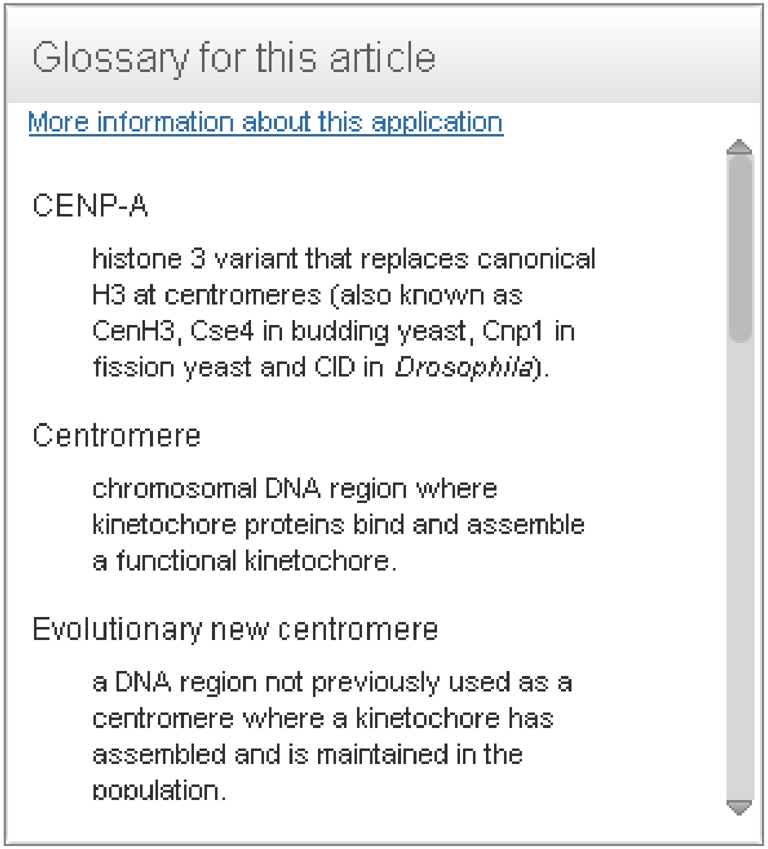
Content: Glossary Browser (All disciplines)
内容：词汇表浏览器

Enhances understanding by displaying Glossary terms next to the article

- Displays the glossary terms from the Glossary section next to the article
- Making it easier to quickly look up unknown terms while reading a paper online
- No need to scroll up and down to / from the Glossary section at the bottom of the article
- Glossary is provided by author with their manuscript

在文章旁边显示词汇表更易于读者理解

- 在文章旁边显示词汇表中的专业术语
- 在线阅读时更易于查找未知术语
- 无需翻页查找文章末尾的词汇表
- 作者在提交文章的同时提供词汇表



Glossary for this article

More information about this application

CENP-A

histone 3 variant that replaces canonical H3 at centromeres (also known as CenH3, Cse4 in budding yeast, Cnp1 in fission yeast and CID in *Drosophila*).

Centromere

chromosomal DNA region where kinetochore proteins bind and assemble a functional kinetochore.

Evolutionary new centromere

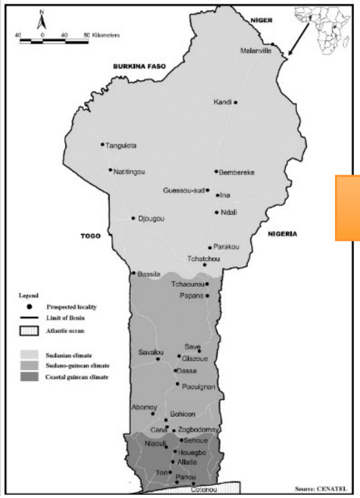
a DNA region not previously used as a centromere where a kinetochore has assembled and is maintained in the population.

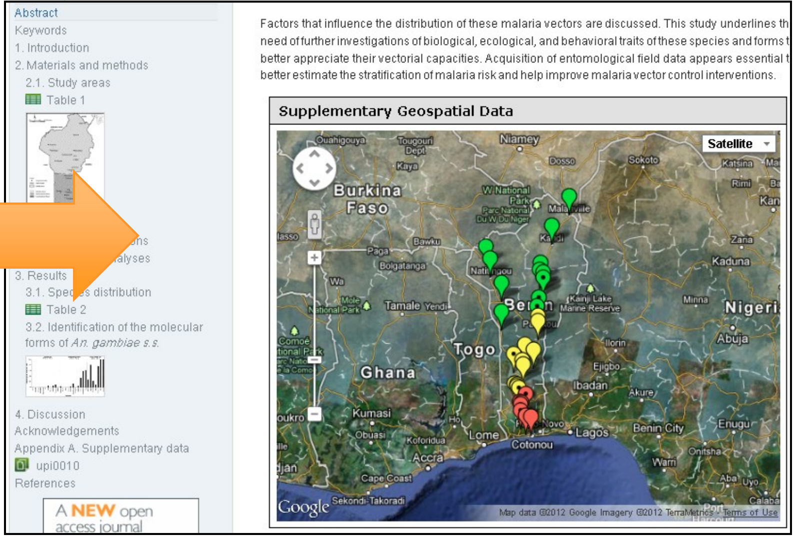
Content: Interactive (Google) Maps 内容:与谷歌地图互动

Earth Sciences, Social Sciences, Archaeology

Turning a static image into a rich, interactive source of information

将静态图片变成内容丰富，可以互动的信息





Abstract
Keywords
1. Introduction
2. Materials and methods
2.1. Study areas
Table 1
3. Results
3.1. Species distribution
Table 2
3.2. Identification of the molecular forms of *An. gambiae s.s.*
4. Discussion
Acknowledgements
Appendix A. Supplementary data
upi0010
References

Factors that influence the distribution of these malaria vectors are discussed. This study underlines th need of further investigations of biological, ecological, and behavioral traits of these species and forms t better appreciate their vectorial capacities. Acquisition of entomological field data appears essential t better estimate the stratification of malaria risk and help improve malaria vector control interventions.

Supplementary Geospatial Data

- Present research findings in a more valuable, interactive way
- Help readers find and understand data in the context of the article
- Download data for validation & re-use of data
- Author submits KML/KMZ file as supplementary data
- Available for 100+ journals

- 研究结果以更有价值、互动性更好的方式呈现
- 帮助读者发现和理解相关数据
- 下载有效数据并加以再利用
- 作者提交 **KML/KMZ**文件作为补充数据
- 已经有**100**多种刊物提供该功能

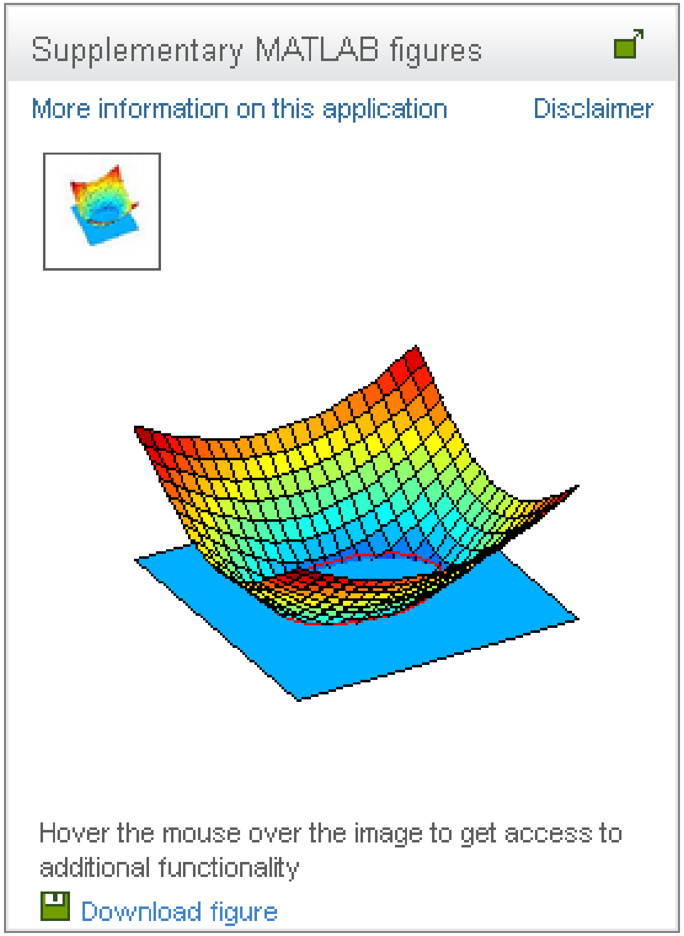
Content: MATLAB figure viewer 内容: **Matlab图片**

Engineering, applied sciences

Making plots more valuable for research

- Explore figures interactively – zoom, rotate, etc.
- Download underlying data to enable validation & re-use
- Works with author-provided .FIG files exported from MATLAB
- Currently available for 5 journals and expanding

- 提高图表的可交互性：缩放、旋转等
- 下载有效数据并可再利用
- 直接使用作者提供的Matlab输出的FIG文件
- 目前5种刊物提供该功能，并在逐渐推广中



Supplementary MATLAB figures

Hover the mouse over the image to get access to additional functionality

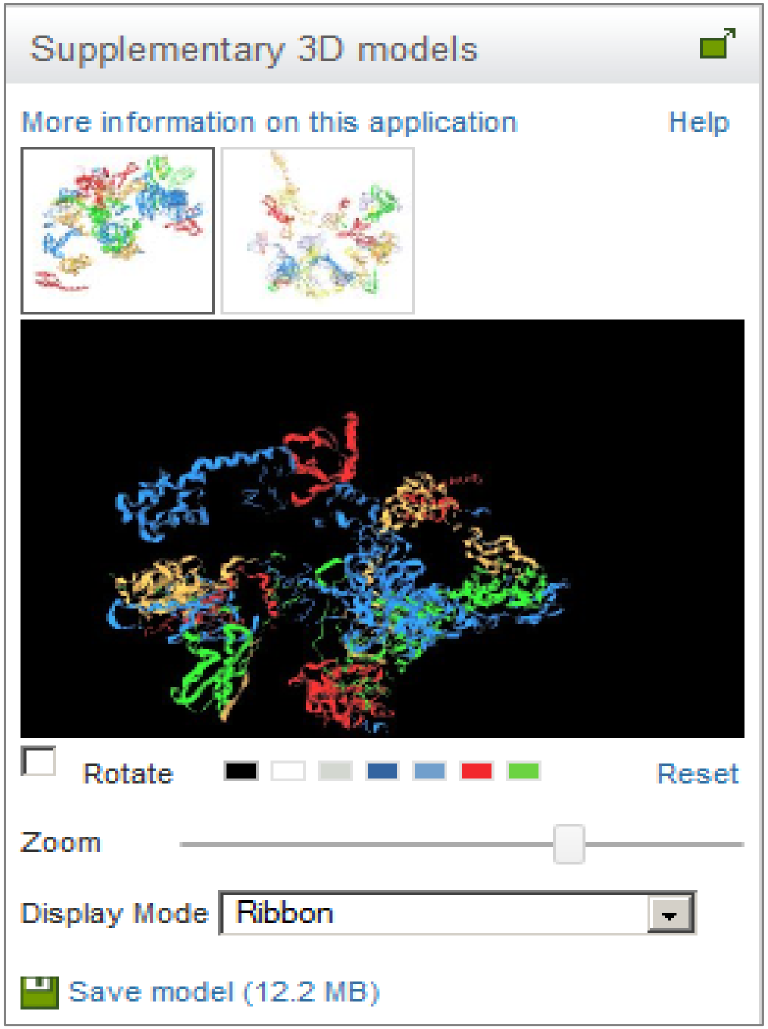
See http://www.elsevier.com/matlab

Content: Interactive Viewer for 3D Molecular Models

Molecular biology, protein sciences, … 内容：**3D分子模型**

Displays molecular structures in 3D

- Author-provided models (PDB, PSE, MOL/MOL2 format; > 100s of MBs)
- Allows for models and annotations
- Fully 3D – enlarge in canvas
- Real-time user interaction
- Supports mobile devices
- Modes: “ribbon” and “balls & sticks”
- Anaglyph stereo vision
- 8 participating journals
  - 作者提供模型
  - 可以有模型和相关注释
  - 完全**3D**：可缩放
  - 实时互动
  - 支持移动设备
  - 模式：带状或球棍模型
  - 浮雕立体效果
  - **8**种期刊参与



Display Mode: Ribbon

http://dx.doi.org/10.1016/j.jmb.2012.11.040
http://dx.doi.org/10.1016/j.str.2012.10.007

See http://www.elsevier.com/3DMolecularModels

Content: Interactive 3D Neuroimaging Viewer

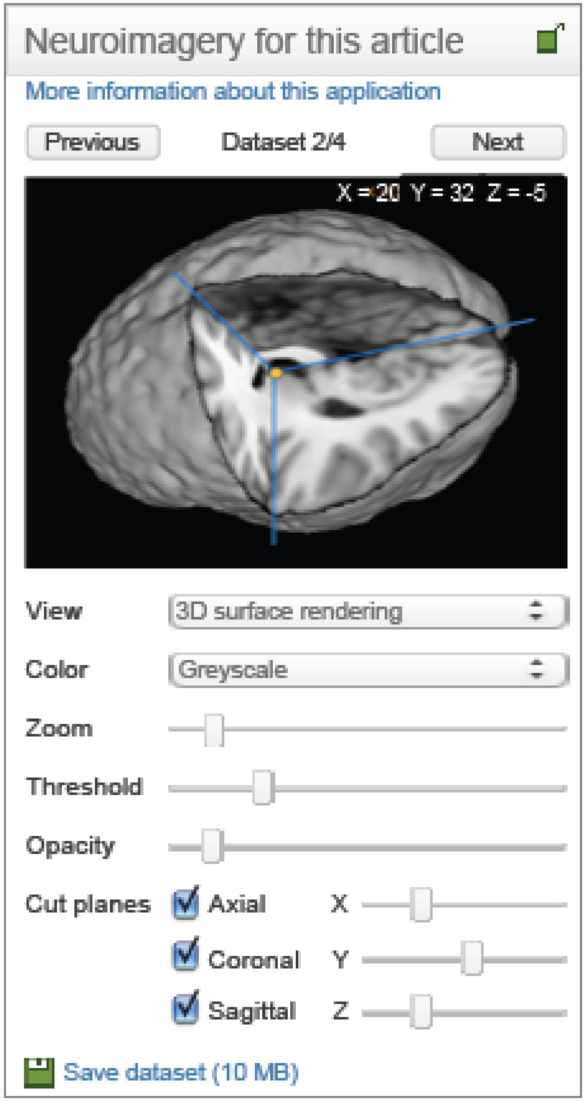
Neuroscience and neurology 内容：3D神经成像

Replacing the filmstrip of 2D images by a fully interactive 3D version of the scan

- Neuroimaging data (NIFTI files) provided by authors
- Zoom into the 3D reconstruction of the neuroimaging data
- Rotate and pan the 3D reconstruction
- Cut through the volume
- Change opacity and color mapping
- Switch between 3D and 2D views
- Download original data
- 8 neuroscience & neurology journals

可互动3D成像代替平面图像

- 作者提供的神经成像数据
- 3D数据重建：缩放和旋转
- 内部结构的呈现
- 调整透明度和成像颜色
- 3D与2D数据间的转换
- 原始数据的下载
- 8种神经科学和神经病学刊物



Dataset 2/4

X = 20 Y = 32 Z = -5

View: 3D surface rendering

Color: Greyscale

Cut planes: ☑ Axial X, ☑ Coronal Y, ☑ Sagittal Z

Content: The Collage Executable Paper 内容: 制作可执行文章

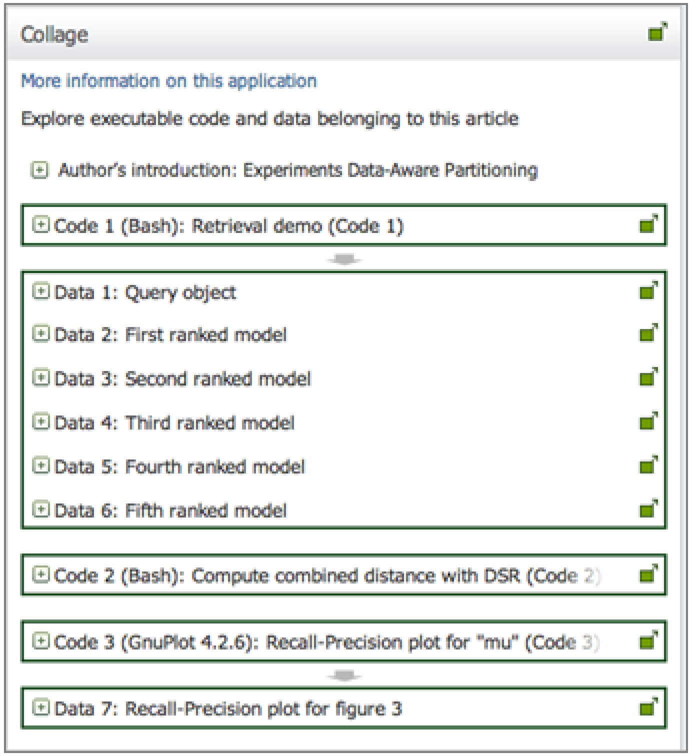
Computer Science

Capturing the full computational workflow, improving research reproducibility

- Authors include code and data with their article
- Capture full workflow from input data to results
- Readers can change parameters and re-execute experiment to validate results and build new insights
- Pilot Special Issue in Computers & Graphics

获取完整计算流程，提高研究的可重复性

- 作者随文章提供代码和数据
- 获取完整的计算流程等
- 读者可以调整参数重新运算以验证结果，并可能获取新的结果。
- 在计算机和图形图像的特刊中进行试验



Collage

More information on this application

Explore executable code and data belonging to this article

⊞ Author's introduction: Experiments Data-Aware Partitioning

⊞ Code 1 (Bash): Retrieval demo (Code 1)

⊞ Data 1: Query object
⊞ Data 2: First ranked model
⊞ Data 3: Second ranked model
⊞ Data 4: Third ranked model
⊞ Data 5: Fourth ranked model
⊞ Data 6: Fifth ranked model

⊞ Code 2 (Bash): Compute combined distance with DSR (Code 2)

⊞ Code 3 (GnuPlot 4.2.6): Recall-Precision plot for "mu" (Code 3)

⊞ Data 7: Recall-Precision plot for figure 3

See http://www.elsevier.com/executablepaper

Content (coming up): Interactive plots 内容: 互动图表

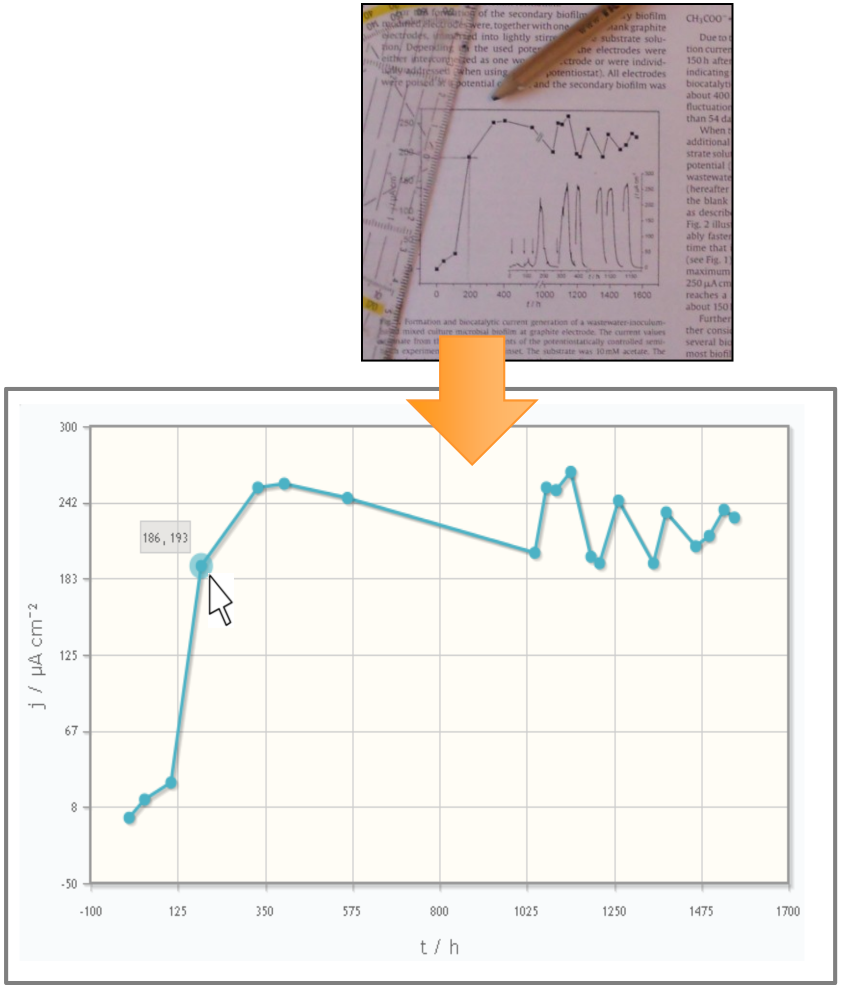
All disciplines

Making plots more useful for research

- Allow readers to access data that used to be “buried” in plots
- Data cursor
- Switch plot <> table view
- Download data
- Interactive visualization capabilities

让图表更利于研究

- 读者可以获取图表背后的数据
- 数据游标
- 图片和表格的切换
- 数据下载
- 图表的交互可视能力



UNDER DEVELOPMENT

Context: Banner linking with data repositories

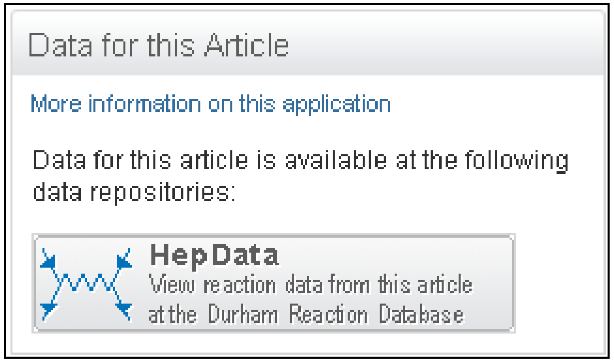
All disciplines 相关信息：标题与数据库链接

Enabling one-click access to relevant primary data

- Banners linking out to data repositories
- Landing page collects data that is directly relevant for the article
- Enable reproducibility of research, and re-use of data
- For selected data repositories in all scientific domains

一键获取相关数据

- 标题与数据库的链接
- 登陆页面搜集与文章相关的数据
- 研究可重复，数据可再利用
- 所有的科学领域均提供筛选后的数据库



Data for this Article

More information on this application

Data for this article is available at the following data repositories:

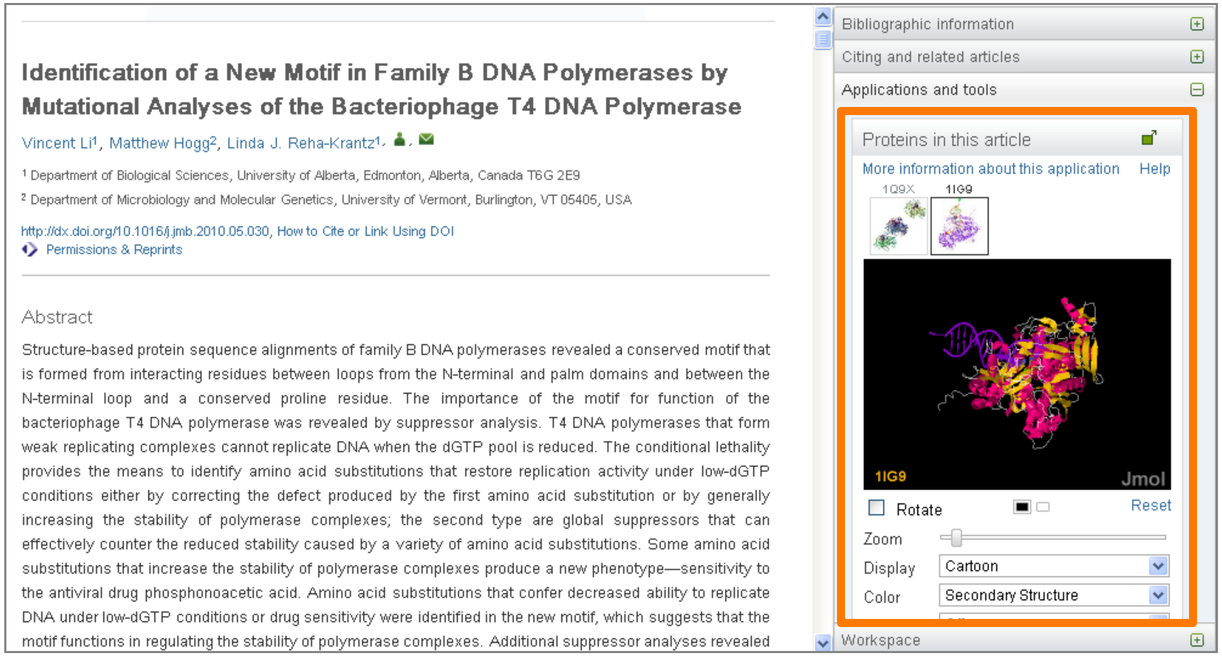
Data for this Article

More information on this application

Data for this article is available at the following data repositories:

See http://www.elsevier.com/databaselinking

Context: Data integration & visualization
Life Sciences 相关信息：数据整合与可视化



Identification of a New Motif in Family B DNA Polymerases by Mutational Analyses of the Bacteriophage T4 DNA Polymerase

Vincent Li[1], Matthew Hogg[2], Linda J. Reha-Krantz[1],

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[2] Department of Microbiology and Molecular Genetics, University of Vermont, Burlington, VT 05405, USA

http://dx.doi.org/10.1016/j.jmb.2010.05.030, How to Cite or Link Using DOI
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Abstract

Structure-based protein sequence alignments of family B DNA polymerases revealed a conserved motif that is formed from interacting residues between loops from the N-terminal and palm domains and between the N-terminal loop and a conserved proline residue. The importance of the motif for function of the bacteriophage T4 DNA polymerase was revealed by suppressor analysis. T4 DNA polymerases that form weak replicating complexes cannot replicate DNA when the dGTP pool is reduced. The conditional lethality provides the means to identify amino acid substitutions that restore replication activity under low-dGTP conditions either by correcting the defect produced by the first amino acid substitution or by generally increasing the stability of polymerase complexes; the second type are global suppressors that can effectively counter the reduced stability caused by a variety of amino acid substitutions. Some amino acid substitutions that increase the stability of polymerase complexes produce a new phenotype—sensitivity to the antiviral drug phosphonoacetic acid. Amino acid substitutions that confer decreased ability to replicate DNA under low-dGTP conditions or drug sensitivity were identified in the new motif, which suggests that the motif functions in regulating the stability of polymerase complexes. Additional suppressor analyses revealed

Display: Cartoon
Color: Secondary Structure

- Biology, biochemistry
- 20+ journals
- In collaboration with Protein Data Bank

- Explore protein structures relevant to the article – zoom, rotate, etc.
- Structure and other protein data integrated from Protein Data Bank
- Author-tagged

- 了解文章中相关蛋白的结构，可缩放、旋转等
- 从蛋白数据银行中整合蛋白数据和结构
- 作者标记

Conclusion 结论

Future academic publications will allow:

- Smooth exchange of various types of digital information.
- Linking to external sources of information
- Interactive data
- Easy readability and navigation
- Become a research tool, next to information carrier.

- 各种数字信息之间的交流更顺畅
- 与多种外部信息互联
- 互动型信息
- 易读且可导航
- 不仅是信息载体，也是研究工具