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Outline

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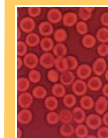


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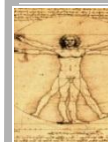
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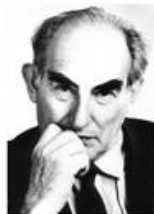
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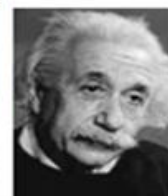
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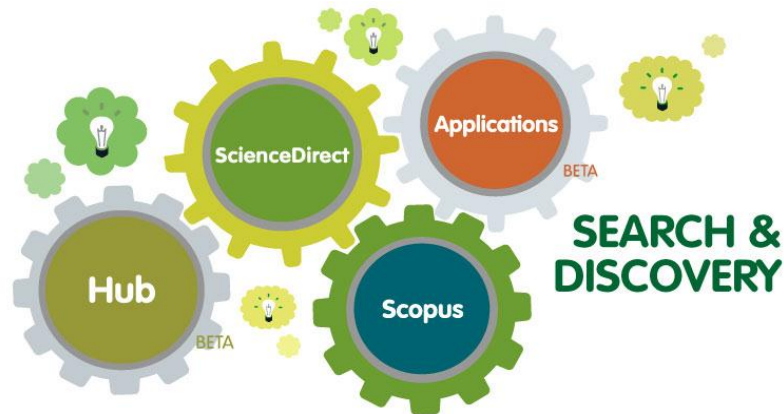
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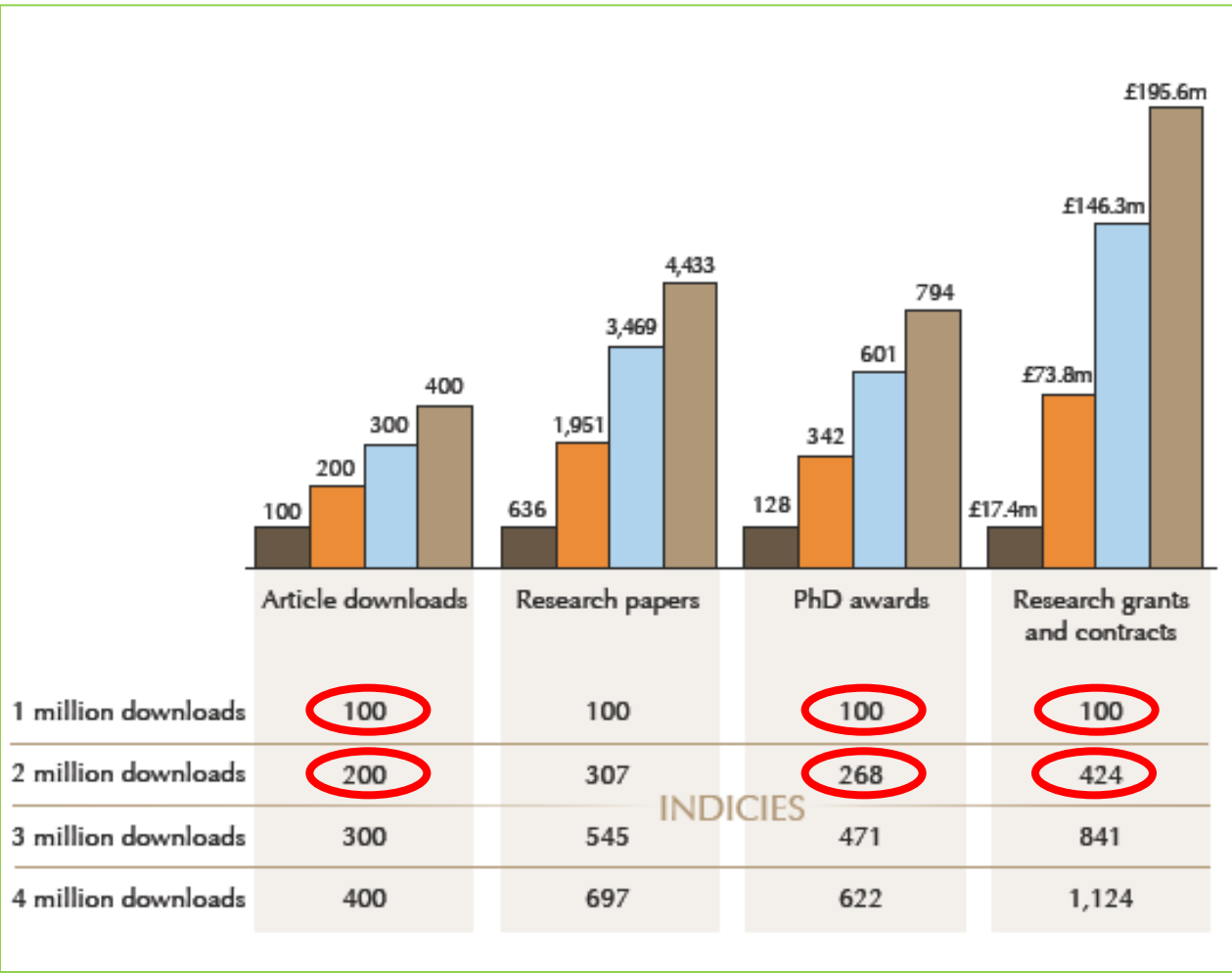
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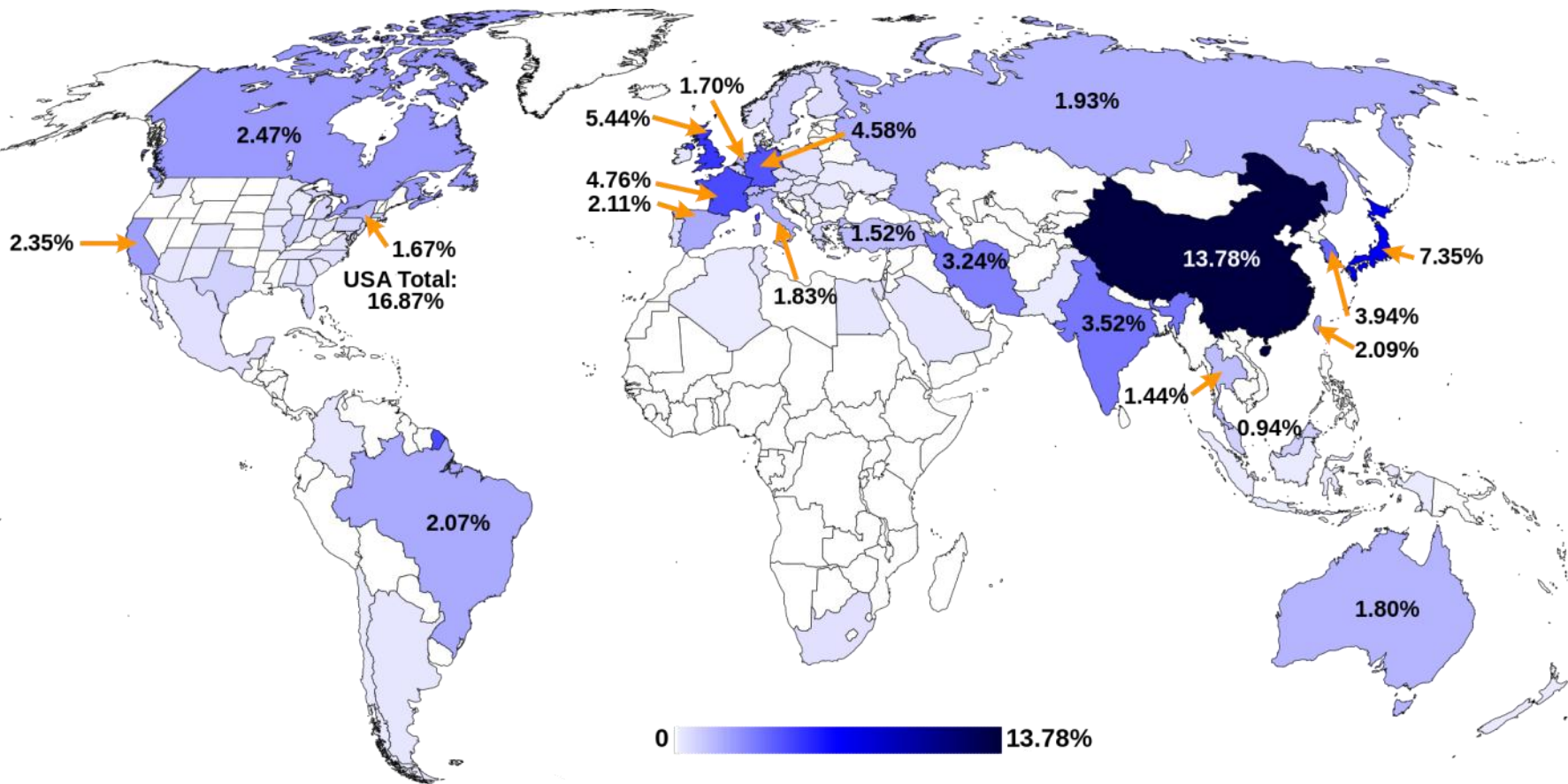
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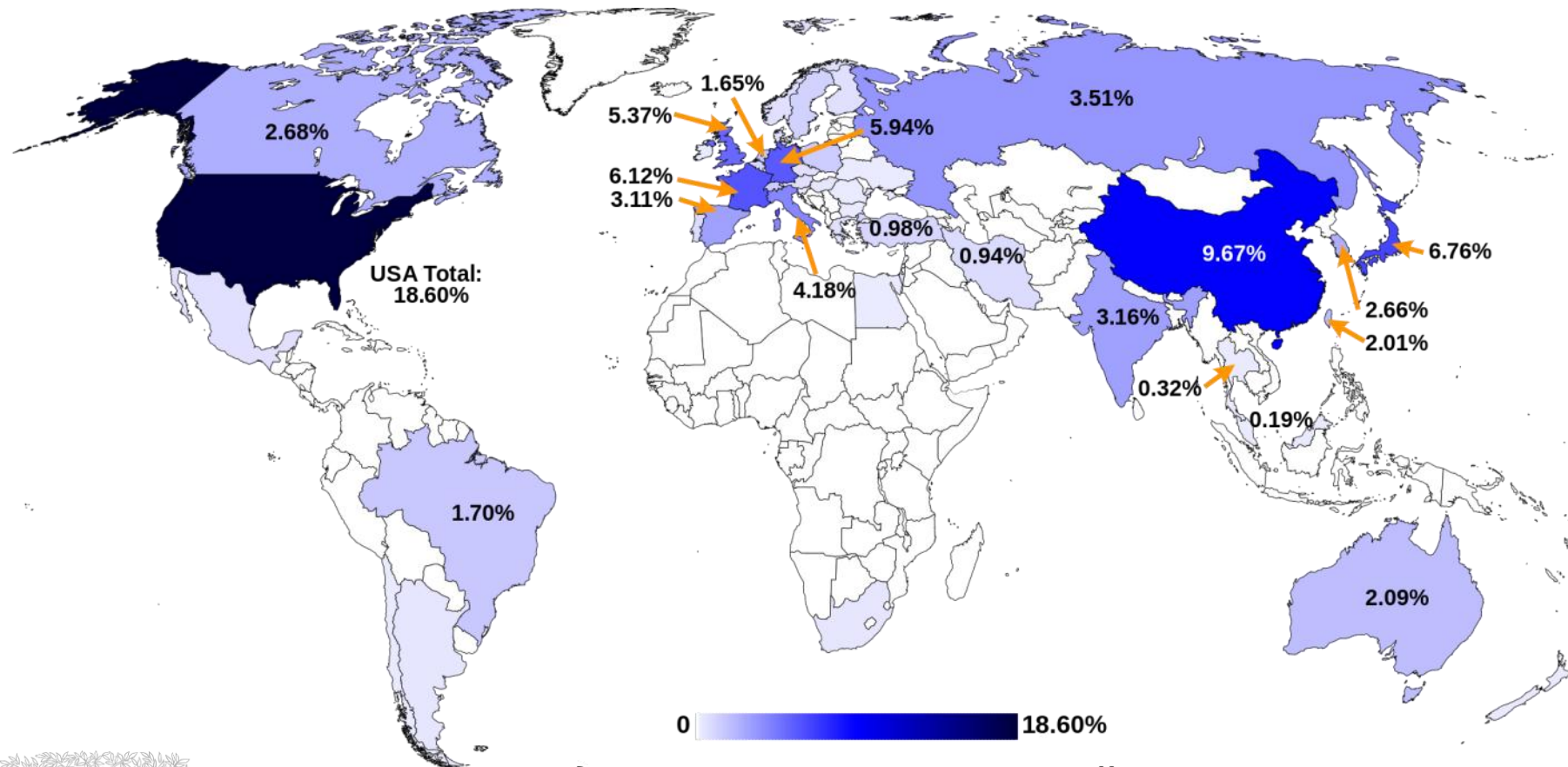
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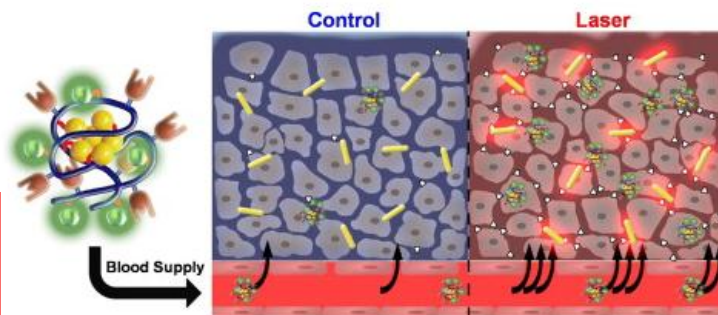
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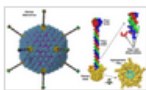
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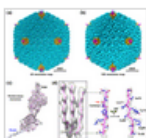
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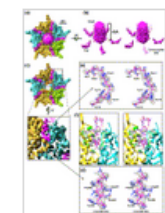
Abbreviations used

Introduction



Results

Observations of the N-terminal tail of the Ad5 fiber interacting with the penton base



Full model of the Ad5 fiber from



Journal of Molecular Biology

Volume 406, Issue 5, 11 March 2011, Pages 764–774



Model of the Trimeric Fiber and Its Interactions with the Pentameric Penton Base of Human Adenovirus by Cryo-electron Microscopy

Hongrong Liu^{1,2,3}, Lily Wu^{2,4}, Z. Hong Zhou^{1,2} | |

¹ Department of Microbiology, Immunology and Molecular Genetics, University of California, Los Angeles (UCLA), Los Angeles, CA 90095-7364, USA

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Abstract

Adenovirus invades host cells by first binding to host receptors through a trimeric fiber, which contains three domains: a receptor-binding knob domain, a long flexible shaft domain, and a penton base-attachment tail

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Model of the Trimeric Fiber and Its Interactions with the Pentameric Penton Base of Human Adenovirus by Cryo-electron Microscopy

Hongrong Liu^{1,2,3}, Lily Wu^{2,4} and Z. Hong Zhou^{1,2*}

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Adenovirus invades host cells by first binding to host receptors through a trimeric fiber, which contains three domains: a receptor-binding knob domain, a long flexible shaft domain, and a penton base-attachment tail domain. Although the structure of the knob domain associated with a portion of the shaft has been solved by X-ray crystallography, the *in situ* structure of the fiber in the virion is not known; thus, it remains a mystery how the trimeric fiber attaches to its underlying pentameric penton base. By high-resolution cryo-electron microscopy, we have determined the structure of the human adenovirus type 5 (Ad5) to 3.6-Å resolution and have reported the full atomic models for its capsid proteins, but not for the fiber whose density cannot be directly interpreted due to symmetry mismatch with the penton base. Here, we report the determination of the Ad5 fiber structure and its mode of attachment to the pentameric penton base by using an integrative approach of multi-resolution filtering, homology modeling, computational simulation of mismatched symmetries, and fitting of atomic models into cryo-electron microscopy density maps. Our structure reveals that the interactions between the trimeric fiber and the pentameric penton base are mediated by a hydrophobic ring on the top surface of the penton base and three flexible tails inserted into three of the five available grooves formed by neighboring subunits of penton base. These interaction sites provide the molecular basis for the symmetry mismatch and can be targeted for optimizing adenovirus for gene therapy applications.

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Introduction

Human adenovirus causes acute respiratory and gastrointestinal diseases, especially among children and immunocompromised individuals. Engineered adenovirus particles are used as gene therapy vectors for transferring genes into mammalian cells.^{1–5} Adenovirus is one of the largest (~900-Å diameter, excluding the fiber) and most complex (~150 MDa) non-enveloped, double-stranded DNA

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Abbreviations used: CryoEM, cryo-electron microscopy; Ad2, adenovirus type 2; Ad5, adenovirus type 5; 3D, three-dimensional.

Interactions between Adenovirus Fiber and Pentonbase

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viruses. Its icosahedral capsid shell contains three major proteins (hexon, penton base, and fiber) and four 'minor' proteins (IIIa, VI, VII, and IX).^{6,7} Each virion contains 240 hexon trimers (hexons) and 12 penton base pentamers (penton base), each of which is bound with one fiber trimer (fiber) (Fig. 1a and b). Hexons and pentons are joined together by three minor proteins IX, IIIa, and VIII. Two hundred forty copies of minor protein IX are located at the outer surface of the capsid, while 60 copies of minor protein IIIa and 120 copies of minor protein VIII are at the inner surface of the capsid.⁸ These minor proteins form exquisite interaction networks, which stabilize two kinds of building blocks—groups of nine hexons and groups of six capsomers (a penton base and its five surrounding hexons)—into the perfect adenovirus capsid shell.¹¹

In the virion, each fiber attaches to a penton base and plays a central role in host cell attachment and entry.^{12–14} The fiber monomer consists of three domains: an N-terminal tail, a central shaft with variable lengths, and a C-terminal knob (or head). Cryo-electron microscopy (cryoEM) structures of intact adenovirus^{5,15,16} and of a recombinant, dodecahedral particle consisting of pentons¹⁷ have revealed that the trimeric fibers attach to the pentameric penton bases. X-ray crystallography of the human adenovirus type 2 (Ad2) penton base in complex with an N-terminal polypeptide of the fiber protein has shown that a 10-aa-long N-terminal polypeptide (amino acids 10–19) binds to the groove formed by two adjacent penton base monomers.¹⁸ The extended fiber-shaft domain contains 'triple β -spiral' repeat motifs,¹⁹ each consisting of 15–20

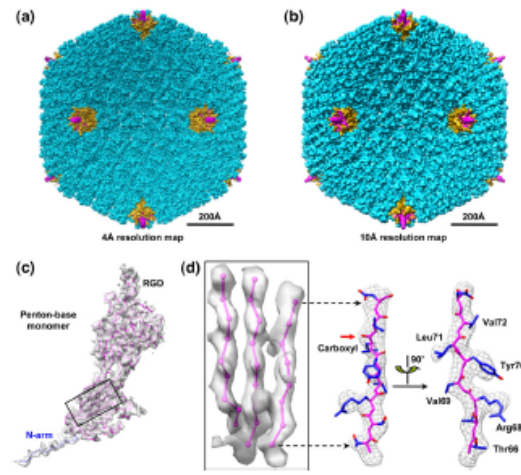
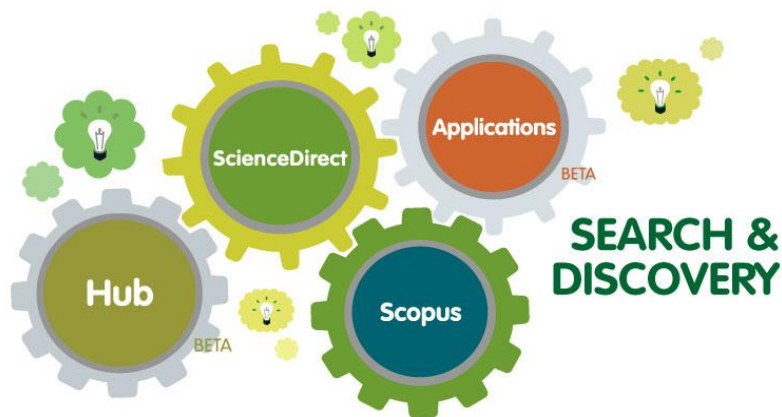


Fig. 1. Overall structure of Ad5 and the penton base protein. (a and b) Overall structure of Ad5 capsid filleted at 4.4 Å (a) and 10 Å (b), respectively, centered on a 2-fold axis of icosahedron, showing the fiber (in magenta) associating with the penton base (yellow) located at the vertices of icosahedron. The remaining capsid proteins are colored in blue. (c) Superposition of the cryoEM density map (semi-transparent) and the backbone of the atomic model (magenta sticks) of penton base protein, including the newly resolved N-arm region (blue sticks). (d) Representative enlargement of a β sheet (boxed region in (c)) showing separation of strands (left). Stick model of one strand superimposed on its density map (mesh) showing a representative carbonyl (red arrow) density (middle) and is rotated to show side chains (labeled) that are perpendicular to the β sheet (right).

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6	View at publisher Show abstract				
<input type="checkbox"/>	The electronic properties of graphene	Castro Neto, A.H., Guinea, F.,	2009	<i>Reviews of Modern Physics</i> 81	1302

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Author	Year	Journal	Citation
Novoselov, K.S., Geim, A.K., Morozov, S.V., Jiang, D., Zhang, Y., Dubonos, S.V., Grigorieva, I.V., Firsov, A.A.	2004	Science	306 (5696), pp. 666-669 5487
Geim, A.K., Novoselov, K.S.	2007	Nature Materials	6 (3), pp. 183-191 3904
Novoselov, K.S., Geim, A.K., Morozov, S.V., Jiang, D., Katsnelson, M.I., Grigorieva, I.V., Dubonos, S.V., Firsov, A.A.	2005	Nature	438 (7065), pp. 197-200 3546
Castro Neto, A.H., Guinea, F., Peres, N.M.R., Novoselov, K.S., Geim, A.K.	2009	Reviews of Modern Physics	81 (1), pp. 109-162 1942
Novoselov, K.S., Jiang, D., Schedin, F., Booth, T.J., Khotkevich, V.V., Morozov, S.V., Geim, A.K.	2005	Proceedings of the National Academy of Sciences of the United States of America	102 (30), pp. 10451-10453 1091

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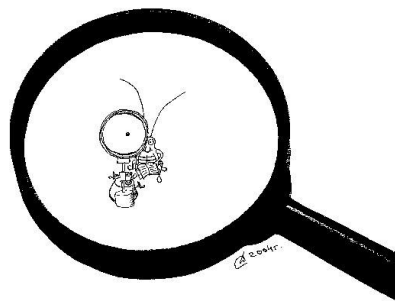
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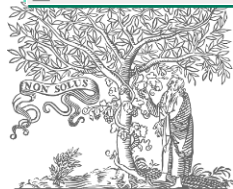
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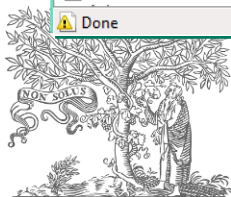
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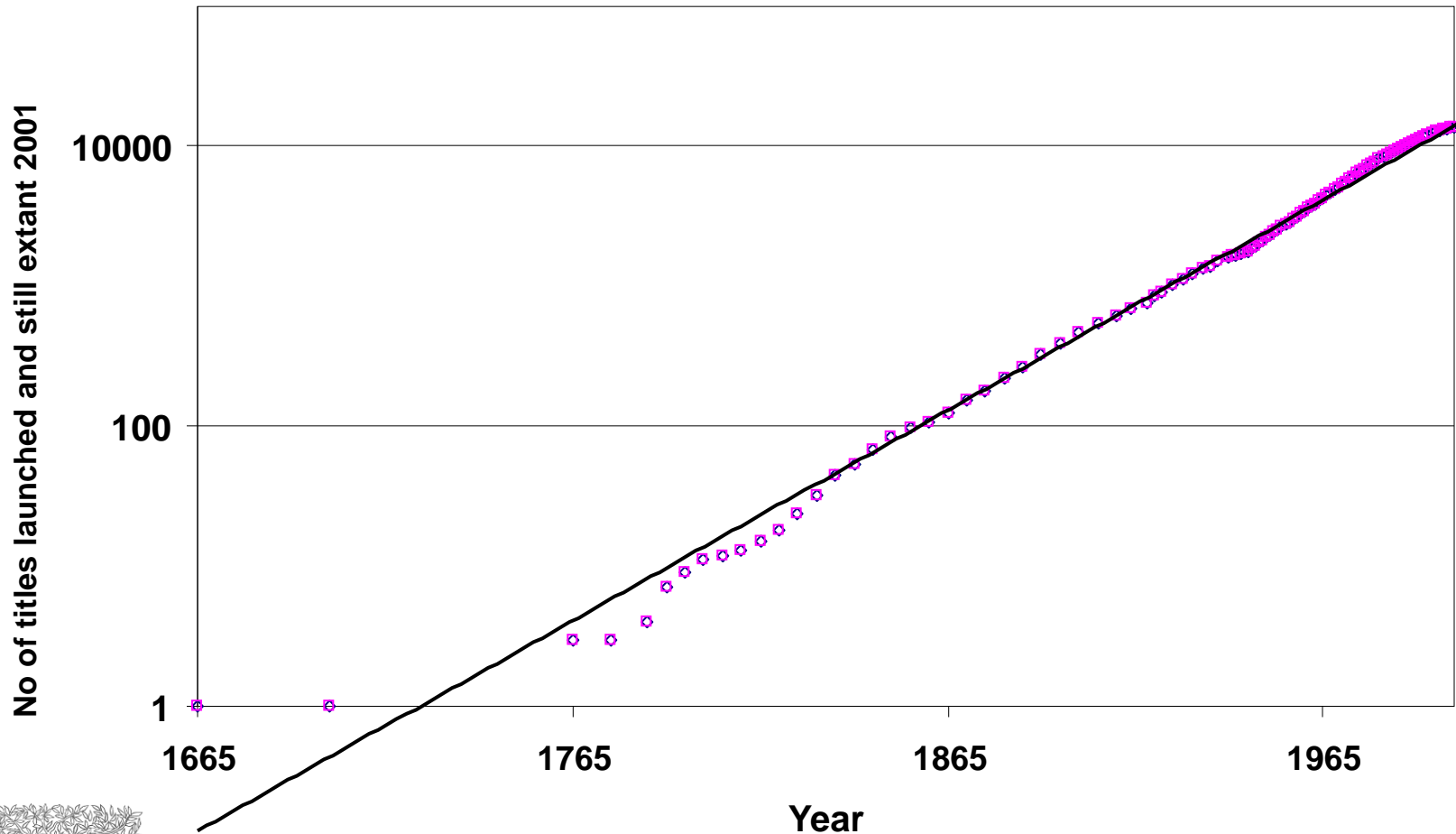


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 4. The review process
- What not to do...



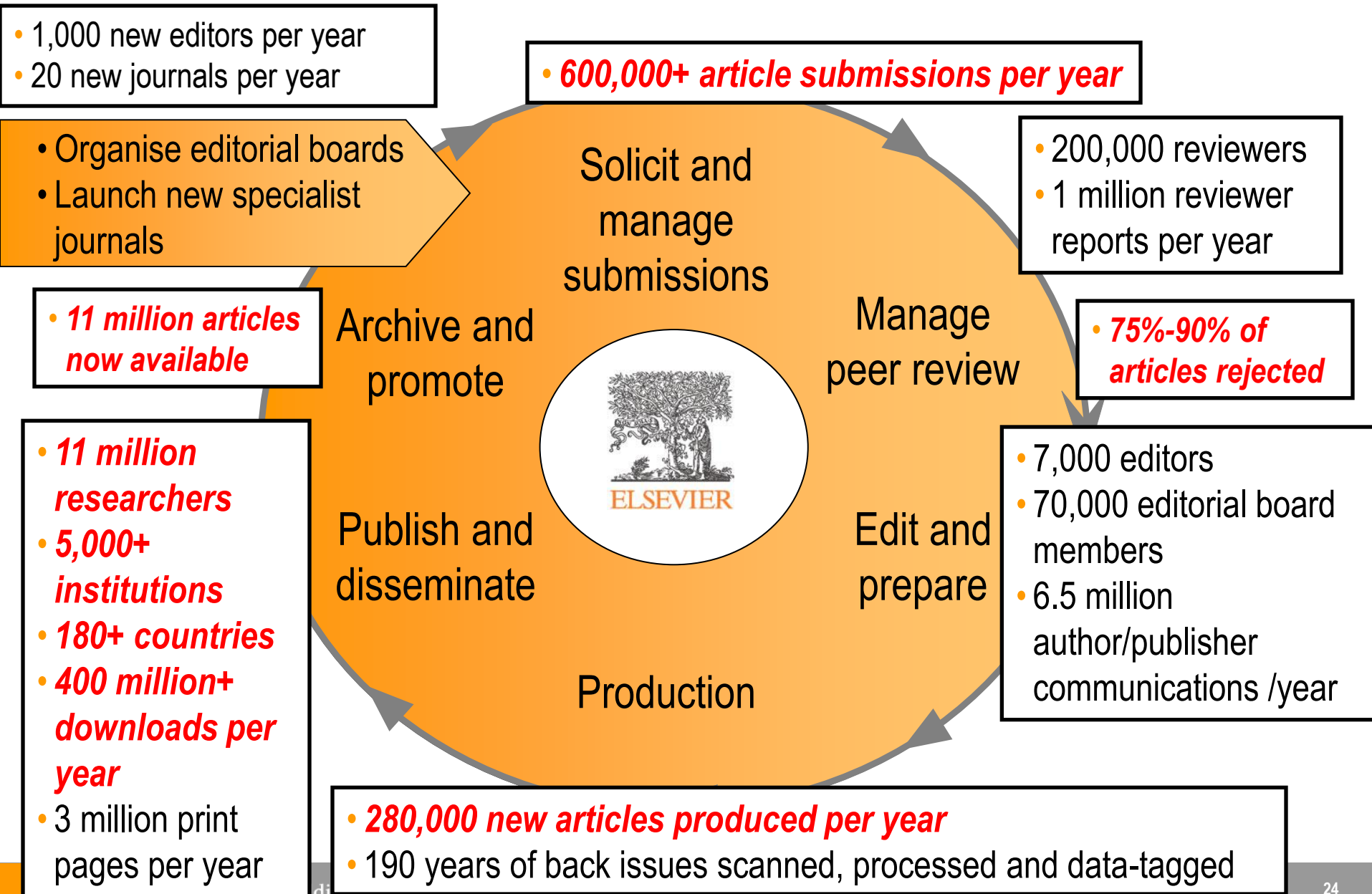
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Volume 50, Issue 1, In Progress (January 2012)

1 | Discrete-time local risk minimization of payment processes and applications to equity-linked life-insurance contracts
Pages 1-11
Jérome Panserra
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Highlights
 ► We develop a general theory of local risk minimization in discrete time. ► We apply this theory to the pricing and hedging of equity-linked insurance contracts. ► We prove factorization theorems simplifying the pricing and hedging of these contracts.

2 | Explaining young mortality
Pages 12-25
Colin O'Hare, Youwei Li
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Highlights
 ► Current stochastic models of mortality are inadequate when trying to fit to a wider age range. ► The logarithm of younger mortality rates shows a less linear profile and thus requires a more flexible model. ► Adding a quadratic effect adequately captures this non-linear effect. ► The proposed 4 factor model outperforms existing models on both BIC and MAPE measures.

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 4. The review process
- What not to do...



Impact Factor

- The number of current citations to articles published in a specific journal in a two year period
 - In 2009 there were 200 citations to papers published in 2008 and 275 to papers published in 2007.

divided by

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$$(200+275)/(180+205) = 1.233$$



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General Structure of a Research Article

- Title
- Abstract
- Keywords

Make them easy for indexing and searching! (informative, attractive, effective)

- Main text (IMRAD)
 - Introduction
 - Methods
 - Results
 - And
 - Discussions

**Journal space is not unlimited.
Make your article as concise as possible.**

- Conclusion
- Acknowledgement
- References
- Supplementary Data



Scientific Language – Overview

Write with clarity, objectivity, accuracy, and brevity.

- Key to successful scientific writing is to be alert for common errors:
 - Sentence construction
 - Incorrect tenses
 - Inaccurate grammar
 - Not using English

Check the Guide for Authors of the target journal for language specifications



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Save your editor and reviewers the trouble of guessing what you mean


Complaint from an editor:

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- Policies regarding authorship can vary
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 2. draft the article or revise it critically for important intellectual content; and
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All others would qualify as “Acknowledged Individuals”



Authorship - Order & Abuses

- General principles for who is listed first
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 - Conducts and/or supervises the data generation and analysis and the proper presentation and interpretation of the results
 - Puts paper together and submits the paper to journal
 - Corresponding author
 - The first author or a senior author from the institution
 - ✓ Particularly when the first author is a PhD student or postdoc, and may move to another institution soon.
- Abuses to be avoided
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- A good title should contain the **fewest** possible words that **adequately** describe the contents of a paper.
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 - Are accurate, unambiguous, specific, and complete
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- Avoid to make them
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Abstract

Tell readers what you did and the important findings

- One paragraph (between 50-300 words)
- Advertisement for your article
- A clear abstract will strongly influence if your work is considered further

What has been done

Graphite intercalation compounds (GICs) of composition $C_xN(SO_2CF_3)_2 \cdot \delta F$ are prepared under ambient conditions in 48% hydrofluoric acid, using K_2MnF_6 as an oxidizing reagent. The stage 2 GIC product structures are determined using powder XRD and modeled by fitting one dimensional electron density profiles.

A new digestion method followed by selective fluoride electrode elemental analyses allows the determination of free fluoride within products, and the compositional x and δ parameters are determined for reaction times from 0.25 to 500 h.

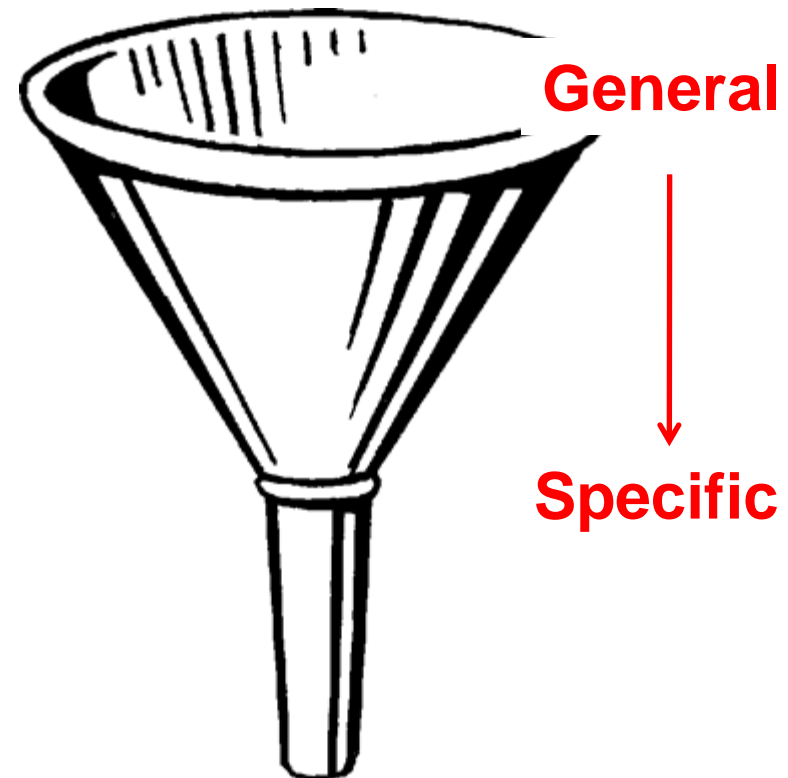
What are the main findings

Introduction

The place to convince readers that you know why your work is relevant, also for them

Answer a series of questions:

- What is the problem?
- Are there any existing solutions?
- Which one is the best?
- What is its main limitation?
- What do you hope to achieve?



Pay attention to the following

- Before you present your new data, put them into perspective first
- Be brief, it is not a history lesson
- Do not mix introduction, results, discussion and conclusions. Keep them separate
- Do not **overuse** expressions such as “novel”, “first time”, “first ever”, “paradigm shift”, etc.
- Cite only relevant references
 - Otherwise the editor and the reviewer may think you don't have a clue what you are writing about



Methods / Experimental

- Include all important details so that the reader can repeat the work.
 - Details that were previously published can be omitted but a general summary of those experiments should be included
- Avoid adding comments and discussion.
- Write in the past tense
- Consider use of Supplementary Materials
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Results – what have you found?

- The following should be included
 - the **main findings**
 - Thus not all findings
 - Findings from experiments described in the Methods section
 - Highlight findings that **differ** from findings in previous publications, and **unexpected** findings
 - Results of the **statistical analysis**
 - Figures and tables are the most efficient way to present results but ...



Discussion – what do the results mean?

- **Check for the following:**
 - How do your results relate to the original question or objectives outlined in the Introduction section?
 - Do you provide interpretation for each of your results presented?
 - Are your results consistent with what other investigators have reported? Or are there any differences? Why?
 - Are there any limitations?
 - Does the discussion logically lead to your conclusion?
- **Do not**
 - Make statements that go beyond what the results can support
 - Suddenly introduce new terms or ideas



Conclusions

- Present global and specific conclusions
- Indicate uses and extensions if appropriate
- Suggest future experiments and indicate whether they are underway
- Do not summarize the paper
 - The abstract is for that purpose
- Avoid judgments about impact



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- Please **adhere to the Guide for Authors** of the journal
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- Data of secondary importance for the main scientific thrust of the article
- Or data that do not fit into the main body of the article
 - e.g. audio, video,
- Not part of the printed article
 - Will be available online with the published paper
- Must relate to, and support, the article



Suggested length of a full article

- Not the same for all journals, even in the same field
- “...25- 30 pages is the ideal length for a submitted manuscript, including **ESSENTIAL** data only.”
 - Title page
 - Abstract 1 paragraph
 - Introduction 1.5-2 manuscript pages (double-spaced, 12pt)
 - Methods 2-4 manuscript pages
 - Results and Discussion 10-12 manuscript pages
 - Conclusions 1-2 manuscript pages
 - Figures 6-8
 - Tables 1-3
 - References 20-50
- Letters or short communications have a stricter size limitation, e.g. 3,000 words and no more than 5 figures/tables.



Make every attempt to make the first submission a success

- No one gets it right the first time!
 - Write, and re-write
- Suggestions
 - After writing a first version, take several days of rest. Come back with a critical, fresh view
 - Ask colleagues and supervisor to review your manuscript. Ask them to be highly critical, and ***be open to their suggestions.***



Outline

- Scientific Publishing
 1. Kazan Federal University
 2. Elsevier's Role
- How to get Published
 1. Before you begin
 2. Select your audience & choose the right journal
 3. Prepare your manuscript
 4. The review process
- What not to do...



Cover Letter

- Submit
- Mention
- Note special interests

Professor H. D. Schmidt
School of Science and Engineering
Northeast State University
College Park, MI 10000
USA

January 1, 2008

Dear Professor Schmidt,

Enclosed with this letter you will find an electronic submission of a manuscript entitled "Mechano-sorptive creep under compressive loading - a micromechanical model" by John Smith and myself. This is an original paper which has neither previously nor simultaneously in whole or in part been submitted anywhere else. Both authors have read and approved the final version submitted.

Mechano-sorptive is sometimes denoted as accelerated creep. It has been experimentally observed that the creep of paper accelerates if it is subjected to a cyclic moisture content. This is of large practical importance for the paper industry. The present manuscript describes a micromechanical model on the fibre network level that is able to capture the experimentally observed behaviour. In particular, the difference between mechano-sorptive creep in tension and compression is analysed. John Smith is a PhD-student who within a year will present his doctoral thesis. The present paper will be a part of that thesis.

Three potential independent reviewers who have excellent expertise in the field of this paper are:

Dr. Fernandez, Tennessee Tech, email1@university.com
Dr. Chen, University of Maine, email2@university.com
Dr. Singh, Colorado School of Mines, email3@university.com

I would very much appreciate if you would consider the manuscript for publication in the *International Journal of Science*.

Sincerely yours,

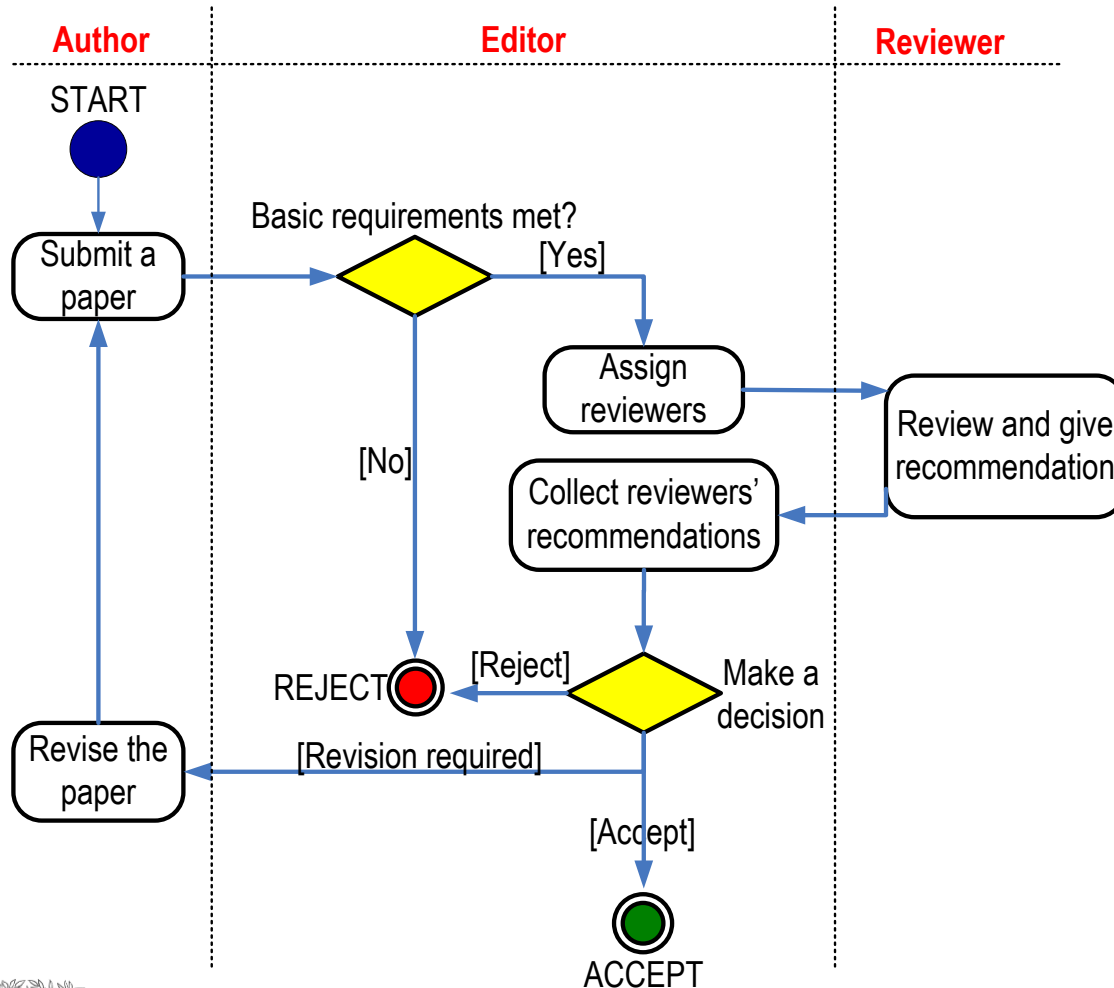
A. Professor

Final approval from all authors

Explanation of importance of research

Suggested reviewers

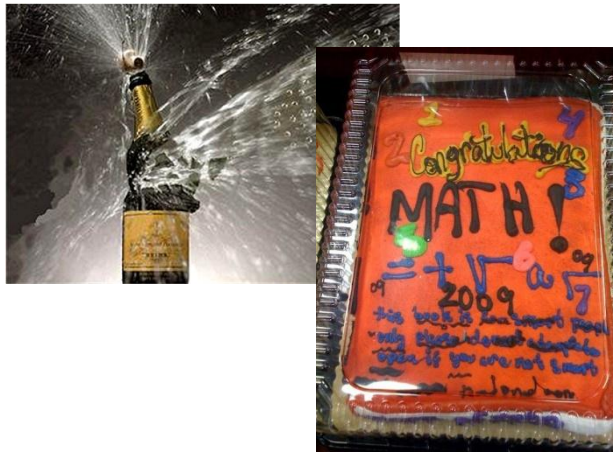
The Peer Review Process - Overview



First Decision: “Accepted” or “Rejected”

Accepted

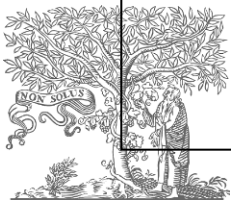
- Very rare, but it happens



- Congratulations!
 - Cake for the department
 - Now wait for page proofs and then for your article online and in print

Rejected

- Probability 75-90% ...
- Do not despair
 - It happens to everybody
- Try to understand WHY
 - Consider reviewers' advice
 - Be self-critical
- If you submit to another journal, begin as if it were a new manuscript
 - Take advantage of the reviewers' comments
 - The same reviewer may again review your manuscript!
 - Read the Guide for Authors of the new journal, again and again.



First Decision: “Major” or “Minor” Revision

- Minor revision
 - Basically, the manuscript is worth being published
 - Some elements in the manuscript must be clarified, restructured, shortened (often) or expanded (rarely)
 - Textual adaptations
 - “Minor revision” does NOT guarantee acceptance after revision!
- Major revision
 - The manuscript may be worth being published
 - Significant deficiencies must be corrected before acceptance
 - Involves (significant) textual modifications and/or additional experiments



Manuscript Revision

- Cherish the chance of discussing your work directly with other scientists in your community.
- Prepare a detailed Response Letter
 - Copy-paste each reviewer comment, and type your response below it
 - State specifically which changes you made to the manuscript
 - Include page/line numbers
 - No general statements like “Comment accepted, and Discussion changed accordingly.”
 - Provide a *scientific* response to comments to accept,
 - or a convincing, solid and polite rebuttal when you feel the reviewer was wrong.
 - Write in such a manner, that your response can be forwarded to the reviewer without prior editing
- Do not do yourself a disfavour, but cherish your work
 - You spent **weeks** and **months** in the lab or the library to do the research
 - It took you **weeks** to write the manuscript



***Why then run the risk of avoidable rejection
by not taking manuscript revision seriously?***

Rejection: not the end of the world

- Everyone has papers rejected – do not take it personally.
- Try to understand why the paper was rejected.
- Note that you have received the benefit of the editors and reviewers' time; take their advice seriously!
- Re-evaluate your work and decide whether it is appropriate to submit the paper elsewhere.
- **If so, begin as if you are going to write a new article. Read the Guide for Authors of the new journal, again and again.**



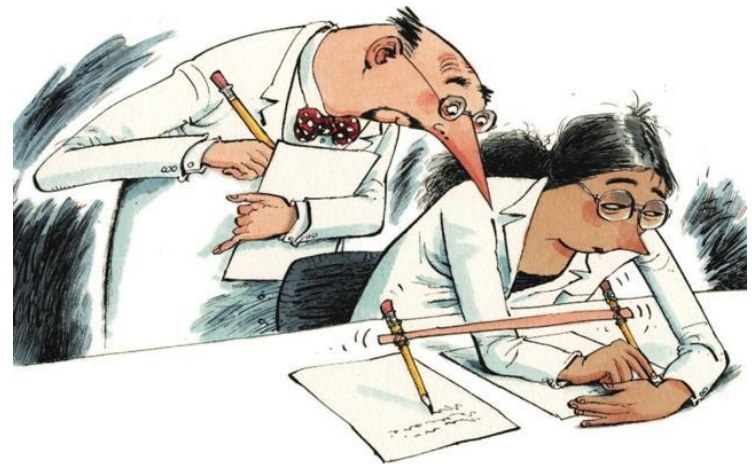
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Publish *AND* Perish! – if you break ethical rules

- International scientific ethics have evolved over centuries and are commonly held throughout the world.
- Scientific ethics are not considered to have national variants or characteristics – there is a *single ethical standard* for science.
- Ethics problems with scientific articles are on the rise *globally*.



M. Errami & H. Garner
A tale of two citations
Nature 451 (2008): 397-399



Plagiarism Detection Tools

- Elsevier is participating in 2 plagiarism detection schemes:
 - Turnitin (aimed at universities)
 - Ithenticate (aimed at publishers and corporations)

Manuscripts are checked against a database of 20 million peer reviewed articles which have been donated by 50+ publishers, including Elsevier.

All post-1994 Elsevier journal content is now included, and the pre-1995 is being steadily added week-by-week

- Editors and reviewers
- Your colleagues
- "Other" whistleblowers
 - "The walls have ears", it seems ...



doi:10.1016/j.sigpro.2005.07.019 Cite or Link Using DOI
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RETRACTED: Matching pursuit-based approach



Available online 24 August 2005.

This article has been retracted at the request of the Editor-in-Chief and Publisher. For more information, please visit <http://www.elsevier.com/locate/withdrawalpolicy>.

Reason: This article is virtually identical to the previously published article "A matching pursuit-based approach for SNR improvement in ultrasonic NDT", *Independent Nondestructive Testing International*, volume 38 (2005) 453 – 458 authored by [redacted].

The article of which the authors committed plagiarism: it won't be removed from ScienceDirect. Everybody who downloads it will see the reason of retraction...

the echoes issuing from the flaws to be detected. Therefore, it cannot be cancelled by classical time averaging or matched band-pass filtering techniques.

Many signal processing techniques have been utilized for signal-to-noise ratio (SNR) improvement in ultrasonic NDT of highly scattering materials. The most popular one is the split spectrum processing (SSP) [1–3], because it makes possible real-time ultrasonic test for industrial applications, providing quite good results. Alternatively to SSP, wavelet transform (WT) based denoising/detection methods have been proposed during recent years [4–8], yielding usually to higher improvements of SNR at the expense of an increase in complexity. Adaptive time-frequency analysis by basis pursuit (BP) [9,10] is a recent technique for decomposing a signal into an optimal superposition of elements in an over-complete waveform dictionary. This technique and some other related techniques have been successfully applied to denoising ultrasonic signals contaminated with grain noise in highly scattering materials [11,12], as an alternative to the WT technique, the computational cost of the BP algorithm being the main drawback.

In this paper, we propose a novel matching pursuit-based signal processing method for improving SNR in ultrasonic NDT of highly scattering materials, such as steel and composites. Matching pursuit is used instead of BP to reduce the complexity. Despite its iterative nature, the method is fast enough to be real-time implemented. The performance of the proposed method has been evaluated using both computer simulation and experimental results, when the input SNR (SNR_{in}) is lower than 0dB (the level of echoes from the microstructures is above the level of the echoes).

2. Matching pursuit

Matching pursuit was introduced by Mallat and Zhang [13]. Let us suppose an approximation of the ultrasonic backscattered signals $x[n]$ as a linear expansion in terms of functions $g_i[n]$ chosen from an over-complete dictionary. Let H be a Hilbert

space. We define the over-complete dictionary as a family $D = \{g_i; i=0, 1, \dots, L\}$ of vectors in H , such as $\|g_i\| = 1$.

The problem of choosing functions $g_i[n]$ that best approximate the analysed signal $x[n]$ is computationally very complex. Matching pursuit is an iterative algorithm that offers sub-optimal solutions for decomposing signals in terms of expansion functions chosen from a dictionary, where ℓ^1 norm is used as the approximation metric because of its mathematical convenience. When a well-designed dictionary is used in matching pursuit, the non-linear nature of the algorithm leads to compact and sparse signal models.

In each step of the iterative procedure, vector $g_i[n]$ which gives the largest inner product with the analysed signal is chosen. The contribution of this vector is then subtracted from the signal and the process is repeated on the residual. At the m th iteration the residue is

$$r^m[n] = \begin{cases} x[n] & m=0, \\ r^{m-1}[n] + a_{k(m)}g_{k(m)}[n], & m \neq 0, \end{cases} \quad (1)$$

where $a_{k(m)}$ is the weight associated to optimum atom $g_{k(m)}[n]$ at the m th iteration.

The weight a_k^m associated to each atom $g_k[n] \in D$ at the m th iteration is introduced to compute all the inner products with the residual $r^m[n]$:

$$a_k^m = \frac{\langle r^m[n], g_k[n] \rangle}{\langle g_k[n], g_k[n] \rangle} = \frac{\langle r^m[n], g_k[n] \rangle}{\|g_k[n]\|^2} = \langle r^m[n], g_k[n] \rangle. \quad (2)$$

The optimum atom $g_{k(m)}[n]$ (and its weight $a_{k(m)}$) at the m th iteration are obtained as follows:

$$g_{k(m)}[n] = \underset{k \in D}{\operatorname{argmin}} \|\langle r^{m-1}[n] \rangle\|^2 = \underset{k \in D}{\operatorname{argmax}} |\langle r^{m-1}[n] \rangle|^2 = \underset{k \in D}{\operatorname{argmax}} |a_k^m|. \quad (3)$$

The computation of correlations $\langle r^m[n], g_k[n] \rangle$ for all vectors $g_k[n]$ at each iteration implies a high computational effort, which can be substantially reduced using an updating procedure derived from Eq. (1). The correlation updating procedure [13] is performed as follows:

$$\langle r^{m+1}[n], g_k[n] \rangle = \langle r^m[n], g_k[n] \rangle - a_{k(m)} \langle g_{k(m)}[n], g_k[n] \rangle. \quad (4)$$

Publication ethics – How it can end

“I deeply regret the inconvenience and agony caused to you by my mistake and request and beg for your pardon for the same. As such I am facing lot many difficulties in my personal life and request you not to initiate any further action against me.

I would like to request you that all the correspondence regarding my publications may please be sent to me directly so that I can reply them immediately. To avoid any further controversies, I have decided not to publish any of my work in future.”

A “pharma” author
December 2, 2008



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A screenshot of a BBC News Europe article. The page has a red header with the BBC logo and 'NEWS EUROPE'. Below the header is a navigation bar with links for Home, UK, Africa, Asia-Pac, Europe, Latin America, Mid-East, South Asia, US & Canada, Business, and Health. The article is dated 24 February 2011 and was last updated at 11:38 GMT. The main headline is 'German minister loses doctorate after plagiarism row'. A sub-headline reads: 'Germany's defence minister has been stripped of his university doctorate after he was found to have copied large parts of his work from others.' There is a photograph of Karl-Theodor zu Guttenberg, the German defence minister, looking thoughtful. A caption below the photo states: 'Mr Guttenberg failed to name sources for parts of his PhD thesis'. The article text continues: 'Karl-Theodor zu Guttenberg, an aristocrat who lives in a Bavarian castle, admitted breaching standards but denied deliberately cheating. Analysis revealed that more than half of his thesis had long sections lifted word-for-word from the work of others. So far the German Chancellor, Angela Merkel, has stood by the minister. The University of Bayreuth decided that Mr Guttenberg had "violated scientific duties to a considerable extent". It deplored the fact that he had lifted sections of text without attribution. Last week Mr Guttenberg said he would temporarily give up his PhD title while the university investigated the charges of plagiarism. He admitted that he had made "serious mistakes". His thesis - Constitution and Constitutional Treaty: Constitutional Developments in the US and EU - was completed in 2006 and published in 2009. Chancellor Merkel insisted on Monday that she was standing by her defence minister, who was seen as something of a rising star in her conservative coalition.' On the right side of the article, there is a 'Related Stories' section with three links: 'Germany's Baron without a title', 'Plagiarism row minister drops PhD', and 'German minister denies plagiarism'.

BBC
NEWS EUROPE

Home UK Africa Asia-Pac Europe Latin America Mid-East South Asia US & Canada Business Health

24 February 2011 Last updated at 11:38 GMT

German minister loses doctorate after plagiarism row

Germany's defence minister has been stripped of his university doctorate after he was found to have copied large parts of his work from others.



Mr Guttenberg failed to name sources for parts of his PhD thesis

Karl-Theodor zu Guttenberg, an aristocrat who lives in a Bavarian castle, admitted breaching standards but denied deliberately cheating.

Analysis revealed that more than half of his thesis had long sections lifted word-for-word from the work of others.

So far the German Chancellor, Angela Merkel, has stood by the minister.

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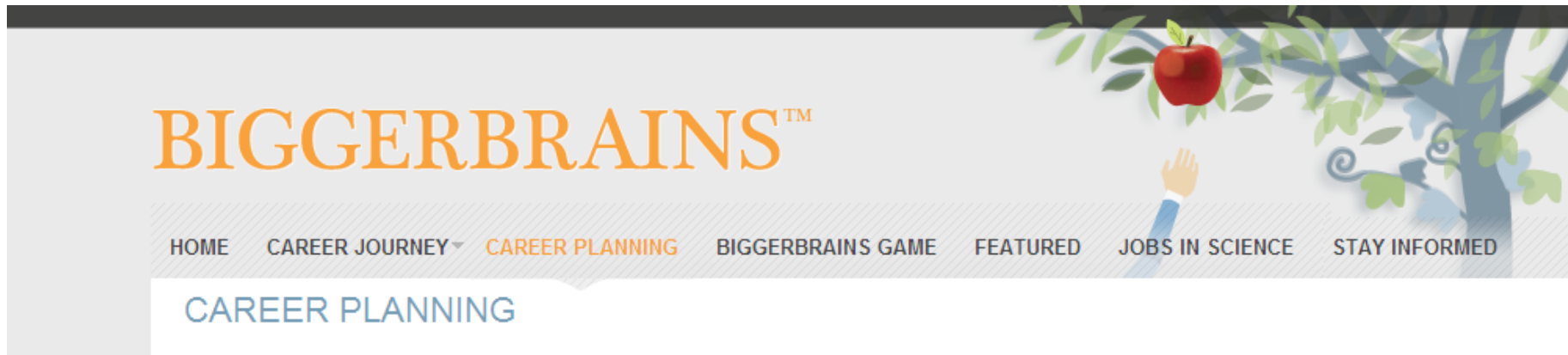
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