Attracting New Authors – through authoring tools & new technology integrations

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Chief Marketing Officer, Overleaf
Why authoring tools? How can they attract authors?

- How collaborative authoring and authoring tools that ease the writing and publishing process are on the rise.
- Authors are embracing new technology
- Happy authors are great marketers!
Why authoring tools are on the rise?

• Collaboration is on the rise
  -> more authors per paper

• Open access continues to grow
  -> new ecosystems for publishing
Collaboration on the rise...

Proportion of the world’s papers produced with more than one international author
Collaboration on the rise...
Prior to cloud-based authoring tools:
Authoring tools allow one version of the document, accessible by all.

1. Authors
2. Reviewers
3. Publishers
4. Readers
Authors have welcomed the technology!

8 million documents
700 thousand authors
180 countries
in 4 years
Continued OA Growth in Publishing Market as well:

Proportion of Articles Published in Fully OA Journals

Source: Monitoring the Transition to OA, SCImago JR, Web of Science, Delta Think analysis © 2016 Delta Think, Inc. All rights reserved. May not be reused without permission.
Open access presents infrastructure challenges for institutions, funders, and publishers.

More and different infrastructure, new offerings and more information is needed to support these OA activities – Startups and New Technology can help
Publishing Ecosystems – growth authors want

- Publishing Platforms now becoming Publishing Ecosystems - providing a suite of writing, disseminating, search, reading and sharing components.

- These ‘ecosystems’ can be obtained by allowing multiple interfaces, apps, components, products, technologies or services to connect and work together.
Publishing Ecosystems – different needs

Publishers are now differentiating between AX vs UX

• AX - Author Experience
  • Somebody who creates content by means of technology

• UX – User Experience
  • Somebody who consumes content

• Different needs – both important for a successful publishing ecosystem.

• Technology integrations are key

• Authoring Tools should integrate and provide that enhanced AX.
How to Publish

Article Guidelines

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Research Articles should present original findings in biology and medicine, such as results of basic and translational research, clinical and epidemiologic studies, or clinical trials. Null and negative findings and reanalyses of previous studies leading to new results are also encouraged.

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Those links open an authoring tool

In addition to the guidelines provided in the example abstract above, your abstract should:

- provide a synopsis of the entire article;
- begin with the broad context of the study, followed by specific background for the study;
- describe the purpose, methods and procedures, core findings and results, and conclusions of the study;
- emphasize new or important aspects of the research;
- engage the broad readership of GENETICS and be understandable to a diverse audience (avoid using jargon);
- be a single paragraph of less than 250 words;
- contain the full name of the organism studied;
- NOT contain citations or abbreviations.

**Introduction**

For the introduction, authors should be mindful of the broad readership of the journal. The introduction should set the stage for the importance of the work to a generalist reader and draw the reader in to the specific study. The scope and impact of the work should be clearly stated.

In individual organisms where a mutant is being studied, the...
Abstract

To the guidelines provided in the example abstract above, your abstract should:

- be a synopsis of the entire article;
- describe the purpose, methods and procedures, core findings, and conclusions of the study;
- emphasize any new or important aspects of the research;
- build the broad readership of GENETICS and be understandable to a diverse audience (avoid using jargon);
- be a single paragraph of less than 250 words;
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Introduction

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In individual organisms where a mutant is being studied, the rationale for the study of that mutant must be clear to a geneticist not studying that particular organism. Similarly, study...
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The khmer software package: enabling efficient nucleotide sequence analysis


1mcruso@msu.edu, Microbiology and Molecular Genetics, Michigan State University, East Lansing, MI 48824, USA

The khmer software package is a tool for the analysis of nucleotide sequence data. It provides a framework for the development of efficient algorithms for the analysis of next-generation sequencing data. The tool is designed to be flexible and scalable, allowing users to easily develop and deploy their own algorithms. The package includes a variety of tools for the analysis of nucleotide sequence data, including tools for the analysis of the diversity of microbial communities, the analysis of metagenomic data, and the analysis of single-cell sequencing data.

We have 62 co-authors on the khmer project paper! Great free LaTeX tech support from @F1000Research & @overleaf; +100

7:03 PM - 21 May 2015
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Adam Stevenson @ajsteven130 · 7h
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  "Nice! Just a couple of clicks and I just submitted my new #preprint on @overleaf to @PeerJPreprints. #openscience FTW!"
Summary

- Collaborative authoring and authoring tools that ease the writing and publishing process are on the rise.
- Authors are embracing new technology
- Happy authors are great marketers!
Thanks for listening!

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