Let’s talk about scholarly manuscript submission
What do Authors want from the submission process?

• Speed  
• Convenience  
• No hassle
What do Funders and Institutions want from the submission process?

- Accountability
- Structured data
- Accurate data
- Granular data
Metadata – no end in sight

Conflict of interest
Funding sources
Disclosures
Animal research
Statistical methods
Data sets metadata
Ethics statements
Contributor ID (ORCID)
Institutional ID (e.g. Ringgold)
Credentials
Methodologies
Protocols
Authors and Co-contributors
Plagiarism checking
Identity validation
License data
Who’s in the middle?

**Funders:** structured, accurate granular data

**Authors:** Quick, convenient, no hassle submission

You

the publisher!

Your peer review system
OA Context

• OA is an “author services” business
• Who pays the APC?
• Pressure for lower APCs
We have a problem. Is there a magical technology solution?

Author Files (any files) → Structured XML
Clean metadata
Accurate metadata
Verified metadata

No human effort
Until then…

• Incremental tactical UI improvements
• Innovative strategic initiative from Aries
Tactical UI improvements
Announcing: “EM Ingest”

An alternative say to get submissions into your journals

Submission Partners

Submissions

Your journals
Who are “submission partners”

Language editing services
Collaborative authoring tools
Journal selectors
Pre-review services
QA services
Publisher portals
“Simple” submissions systems
How does it work?

OPTION 1
Author submits directly to journal

OPTION 2
Author submits via a Submission Partner

Submission Partner
Examples:
- Language editing service
- Pre-peer review service
- Journal selection service
- Publisher branded portal
- Collaborative authoring tool

Ingest Service
Files & JATS XML

em

STM
The global voice of scholarly publishing
<table>
<thead>
<tr>
<th>Action</th>
<th>Article Type</th>
<th>Article Title</th>
<th>Author Name</th>
<th>Transferred From</th>
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<td>Dietary protein and amino acid levels affect serum concentration and expression of GH, IGF-1, IGF-1R, and myosin, and performance of pigs</td>
<td>Sayyajit Rout, PhD, MD</td>
<td>Editage Author Services</td>
<td>Feb 25, 2015</td>
<td>Feb 25, 2015</td>
<td>Transferred Submission Received</td>
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</tbody>
</table>

Page: 1 of 1 (1 total submissions)

Display 10 results per page.
Workflow:

Transferred Submissions

Submission Partner/EM Ingest

New Submissions

Author checks and completes missing information, additional questions, and confirms
Key Ingredients

• JATS
• ORCID
• Other standards
Editage – first Submission Partner

Need help with scientific publishing?
LOOK NO FURTHER

328,000+ papers  72,000+ authors  1200+ subjects  1000+ experts  12+ years of experience
Second Submission Partner
iMotifs: an integrated sequence motif visualization and analysis environment.

Matias Piipari, Thomas A. Down, Harpreet Saini, Anton Enright, Tim J. Hubbard

Abstract

Motivation: Short sequence motifs are an important class of models in molecular biology, used most commonly for describing transcription factor binding site specificity patterns. High-throughput methods have been recently developed for detecting regulatory factor binding sites in vivo and in vitro and consequently high-quality binding site motif data are becoming available for increasing number of organisms and regulatory factors. Development of intuitive tools for the study of sequence motifs is therefore important.

iMotifs is a graphical motif analysis tool that can score motif hits in sequences. It also allows for overrepresentation and pairwise comparison of motifs without the need to convert between file formats.
Third Submission Partner…

You?
Summary

The industry has a growing problem with metadata capture …. and there is no quick fix

Submission intermediaries have a valuable role to play in solving this problem
Time’s Up!

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