



Bringing the Web to the researcher

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“The Australian Digital Futures Institute (ADFI) is a cross-institutional, multidisciplinary Institute with two work-streams - one pertaining to eLearning and the other to eResearch. “

The ADFI technical team

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Outline

Summary of our work in the authoring tools area
(highlights from the presentation proposal)

- Course publishing

- Institutional repositories

- Research data registries

Lessons learned, predictions & opinions

Thoughts for eScholarship “Beyond the PDF”

- Make all resources part of a repository as soon as they are created or acquired.

- Provide a web view of all resources as early as possible in their production process.

- Provide a hub from which resources can be pushed to other services

- Make interoperable, reusable services, not monolithic systems.

Build it...



Will they come?.



Web feedback helps authors use templates

- Abstract
- Introduction
 - The network construction and analysis of molecular interactions provide a powerful system and to reveal hidden relationships between drugs, genes, proteins, and diseases would facilitate improving polypharmacology and rational drug design². In recent years, we have developed to predict the drug-target network based on ligand chemistry³⁻⁵, and the combination of chemical features of drug molecular and sequence features of protein. Computational evaluations have proven that these methods are extremely valuable. However, these methods are biased to annotated drug-target pairs, which mainly include G-protein coupled receptors (GPCR). They only cover a small portion of human proteins, and more severe in pathogens than in human. For example, among 3,999 encoded proteins in *Mycobacterium tuberculosis*, nine proteins (cmaA1, cyp51, embA, embB, embC, folK, InhA, katG and rpoC) are not in the drug-target network that is reconstructed from most of existing drug targets is more druggable targets and predicting off-target profile of new compounds on a protein-protein target data bring up questions whether or not the topology of the drug-target network is druggable.
- Results
 - A drug binding site database
 - Drugome-TB: a reliable and unbiased protein-drug interaction network
 - Drugome-TB is a scale-free and modular network
 - Highly connected proteins are potential druggable targets
 - DISCUSSION
 - Concurrent vs linear drug discovery process
 - Conventional drug discovery and development proceeds as a linear process from target identification, to optimization, to preclinical and clinical trial. It is estimated that above 90% of drug development mainly due to poor drug efficacy or safety⁵⁴. If the information of the chemical space of the target, pharmacokinetics and dynamic properties

Save as web does not have to be bad

But none of the major software vendors care...

(sorry to my friends at MS Research I know *you* do)

<http://broadcast.oreilly.com/2009/03/master-blasters.html>



We are thinking about how to embed Semantics in real world authoring systems

[http://ontologize.me/?
tl_p=http://purl.org/dc/terms/creator&
triplink=http://purl.org/triplink/v/0.1
&tl_o=http://trove.nla.gov.au/people/541658](http://ontologize.me/?tl_p=http://purl.org/dc/terms/creator&triplink=http://purl.org/triplink/v/0.1&tl_o=http://trove.nla.gov.au/people/541658)

The person or agent <http://trove.nla.gov.au/people/541658> is a creator of this resource:

<http://ptsefton.com/2010/12/09/beyond-the-pdf-proposed-session-bring-the-web-to-the-researcher-mainly-on-authoring-tools.htm>

Idea: make any heading anywhere able to declare that is about 'results':

<http://esw.w3.org/HCLSIG/SWANSIOC/Actions/RhetoricalStructure/models/blocksonontology#results>

Our contribution to Annotation

Anotar toolkit for adding text, image, video (and data)
annotation to any web system

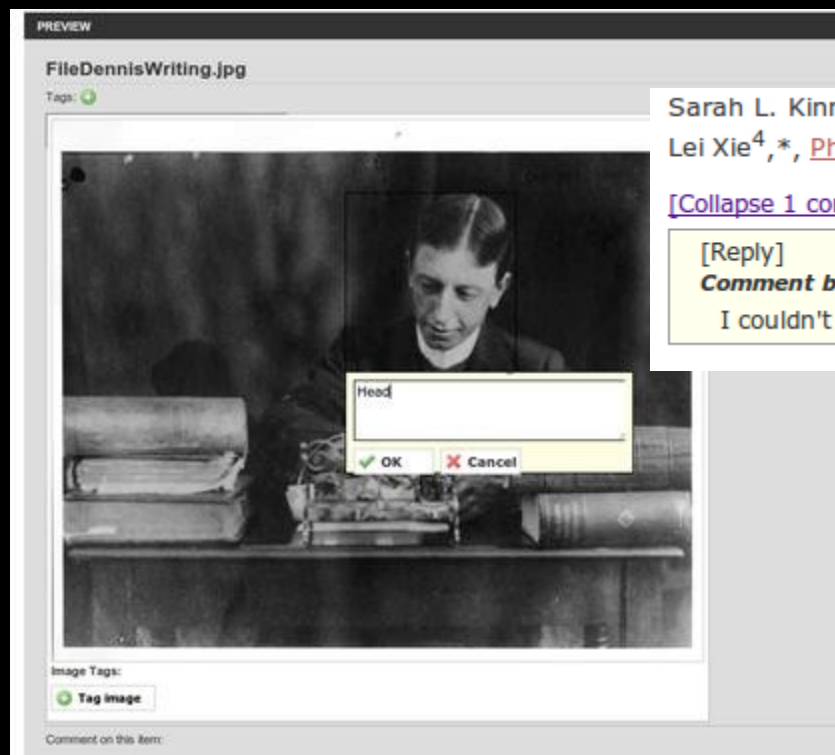
We started with systems that can be used by web developers
(jQuery):

- Then users

- Then standardizers

- Then theoreticians

Anotar



Sarah L. Kinnings¹, Li Xie², Kingston H. Fung³, Richard M. Jackson¹,
Lei Xie^{4,*}, [Philip E. Bourne](#)^{2,4,*}

[\[Collapse 1 comments...\]](#)

[Reply]

Comment by: *admin* less than a minute ago

I couldn't find Researcher IDs for most of the authors.

Web FIRST (and that means mobile and ePub too)

Sample files

ACTIONS

- Blog...
- Organise...
- Reindex
- View Solr Index

NAVIGATION

- Paper
 - Proteome-Wide Polypharmacology
 - Figures.pdf
 - FinalPaper.pdf
 - Drugome-TB_v1.docx
 - Proteome-Wide Polypharmacology C
- Data
 - Data.doc
 - supporting_data.xls
 - Provenance
 - Admin

PATH

- work
- blpdf (18)

FORMAT

- application/vnd.ms-word (7)
- application/pdf (2)
- application/vnd.ms-excel (2)
- application/vnd.ms-powerpoint (2)
- application/vnd.oasis.opendocumenttext (2)
- application/vnd.openxmlformats-officedocument.wordprocessingml (1)
- application/zip (1)
- text/html (1)

AUTHOR

- Ixie (3)
- Phil (2)

PREVIEW

Proteome-Wide Polypharmacology Drug-Target Space of Mycobacterium tuberculosis

Tags:

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Abstract

Proteome-wide analysis of protein-drug interaction network on multiple scales, from atomic systematic behaviour may provide practical solutions to rational design of polypharmacologic combinatorial landmark that integrates structural bioinformatics, molecular modelling and

ACTIONS

- Open file
- Blog...
- Reharvest
- Reindex
- View Solr Index

METADATA

Title	Protein Data Bank Advisory Committee
Creator	Phil
Description	Developing and Using Large-scale Drug-receptor Interaction Networks

ATTACHMENTS

- Manage Access
- guest
- Delete Object

PREVIEW

Protein Data Bank Advisory Committee

Tags:

Page 1

PDF version

Developing and Using Large-scale Drug-receptor Interaction Networks

Philip E. Bourne
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Lessons / opinions

Validating XML editing is not for the masses

Starting a new document paradigm is hard
(eg Wave, Etherpad, Groove)

Geek tools do not always scale or penetrate the whole market
(RSS readers, bibliography managers)

Subversion is for programmers, not authors – DropBox is for people

'Our' standards don't matter to the big players
(OAI-PMH, OAI-ORE)

You can't make HTML from arbitrary Word or TeX documents

Natural language is not tree-shaped

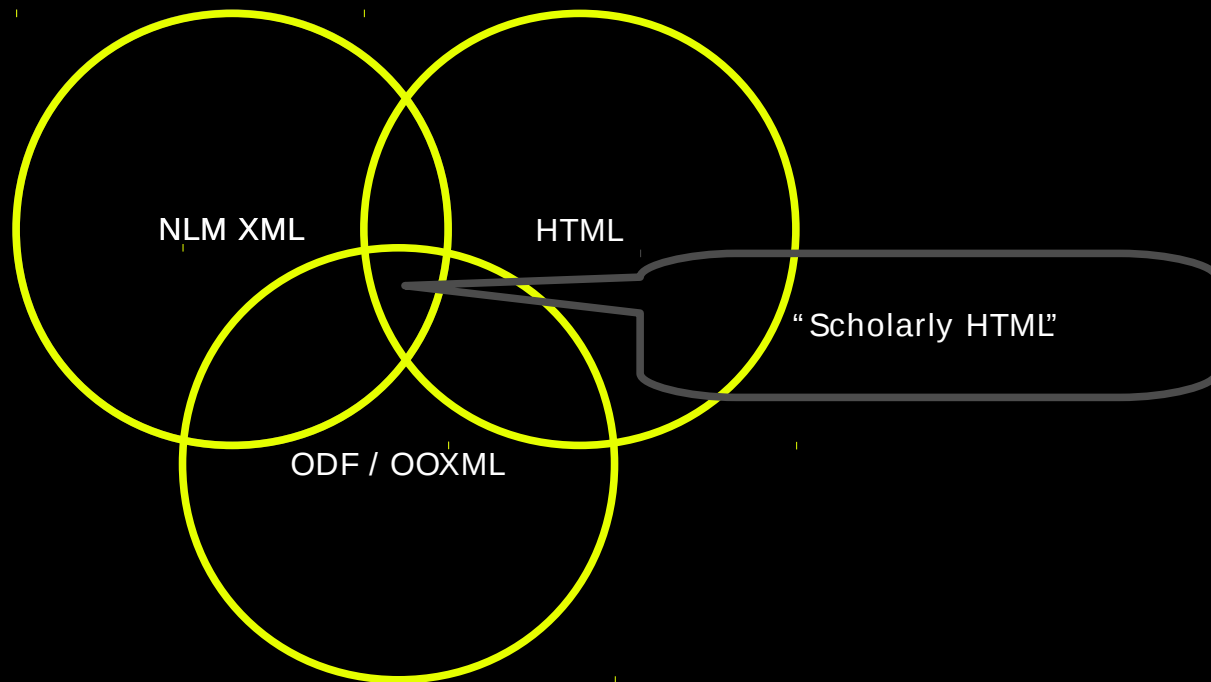


The good news?

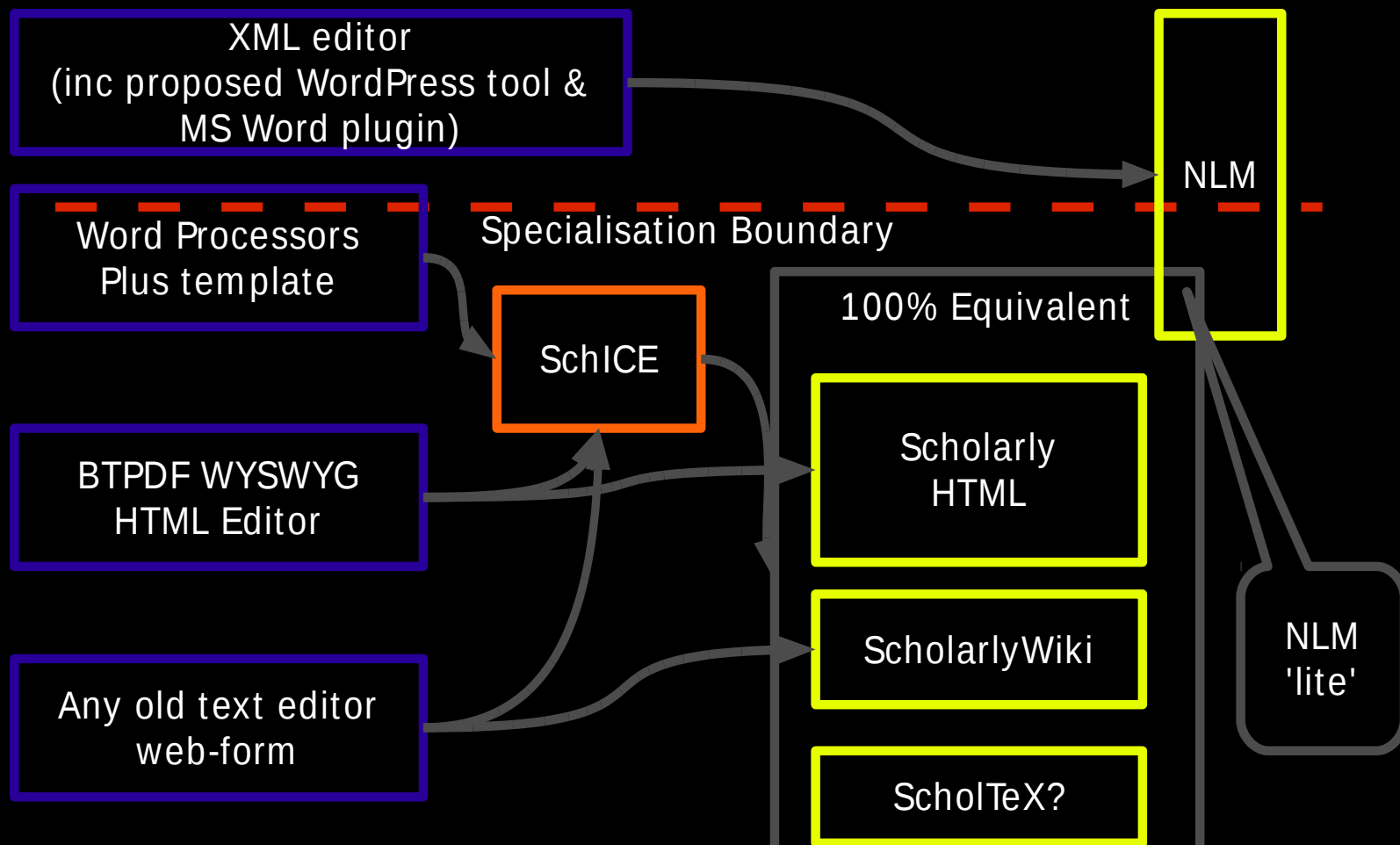
Authors probably are ready for a structured, fluid WYSIWYM editor



Can we talk about “Scholarly HTML” this week?



What we can build: Interop



Bringing together docs and data

Declarative semantics over ordering

Use declarative typed links to data – let the viewing application do something

Consider the limits of mainstream authoring systems
– we *will* be dealing with them

Be *of* the web not just *on* it.

Homeless? Feral? Misguided?



Self-deposit does work





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