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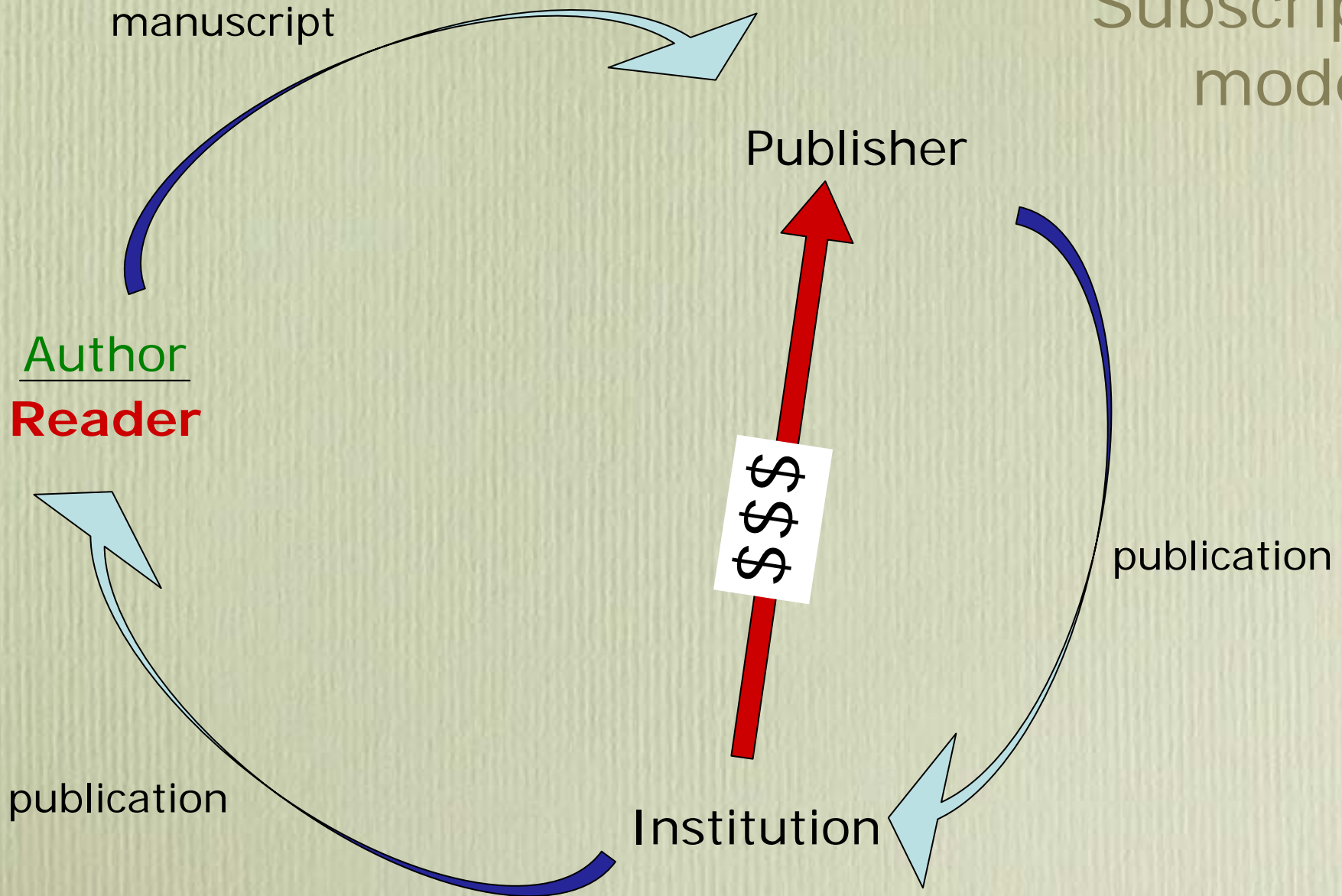
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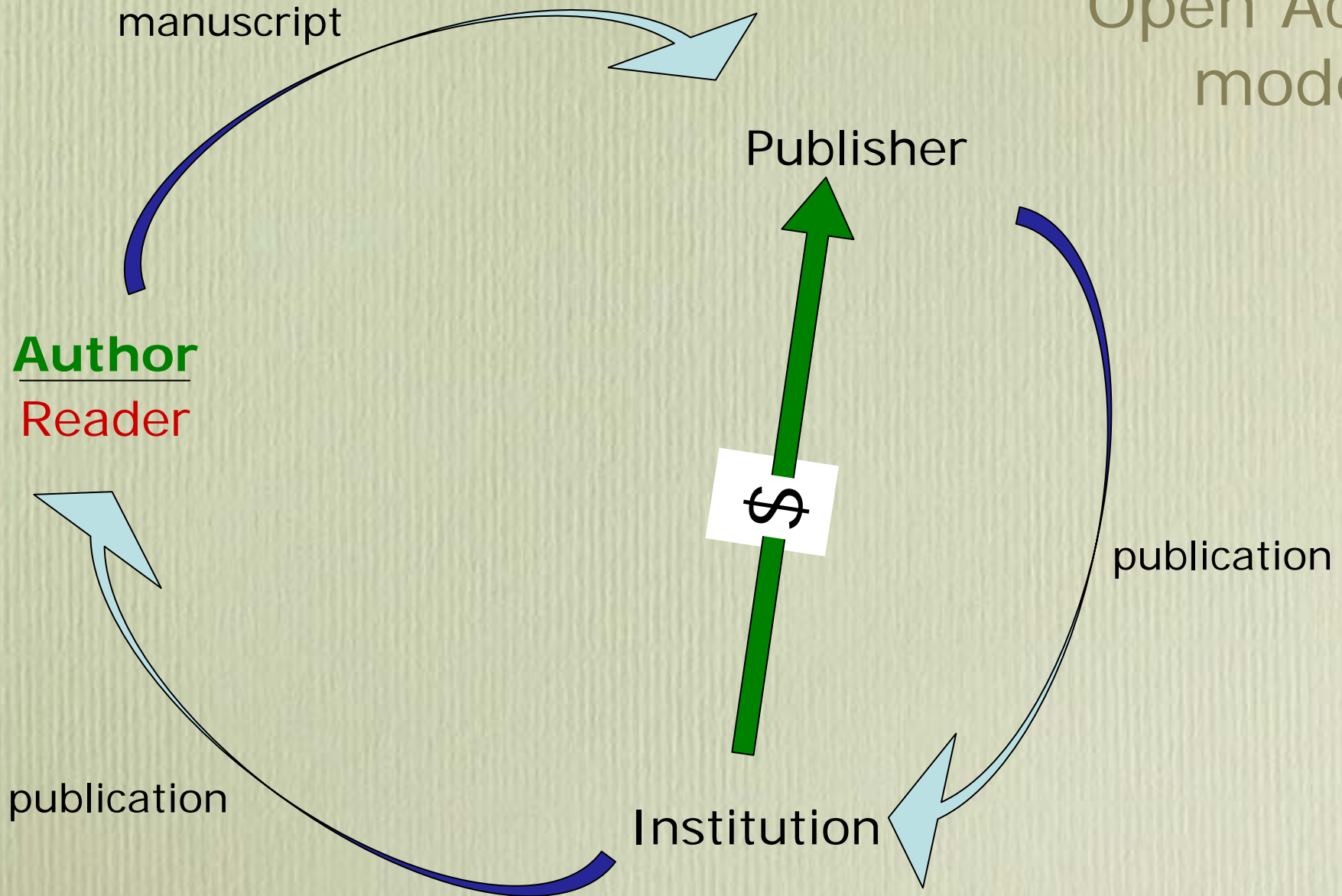
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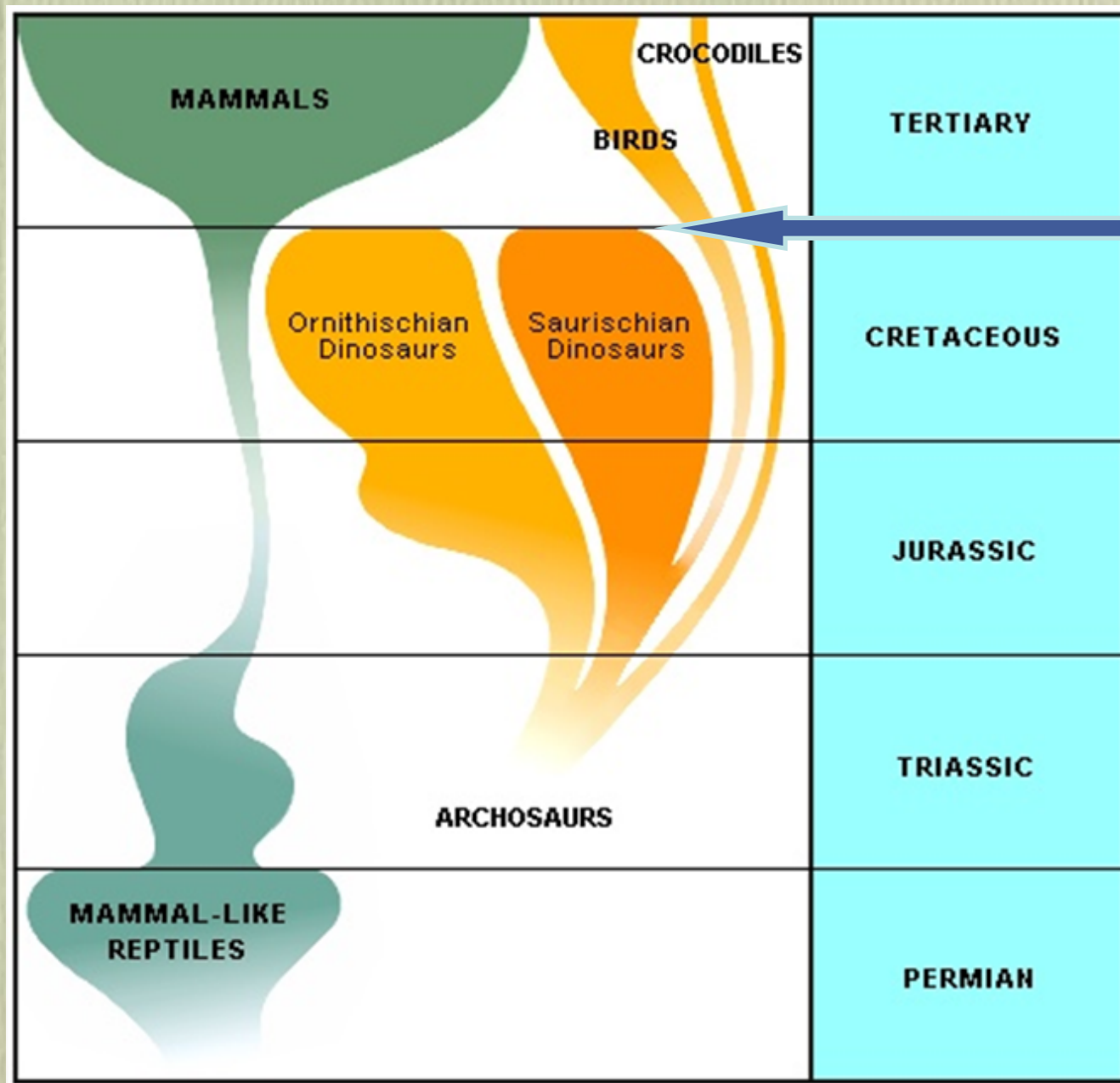
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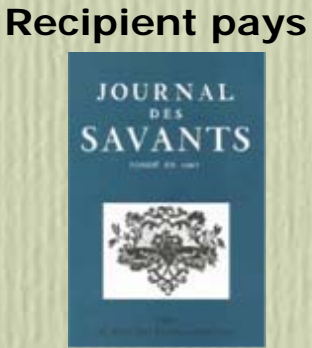


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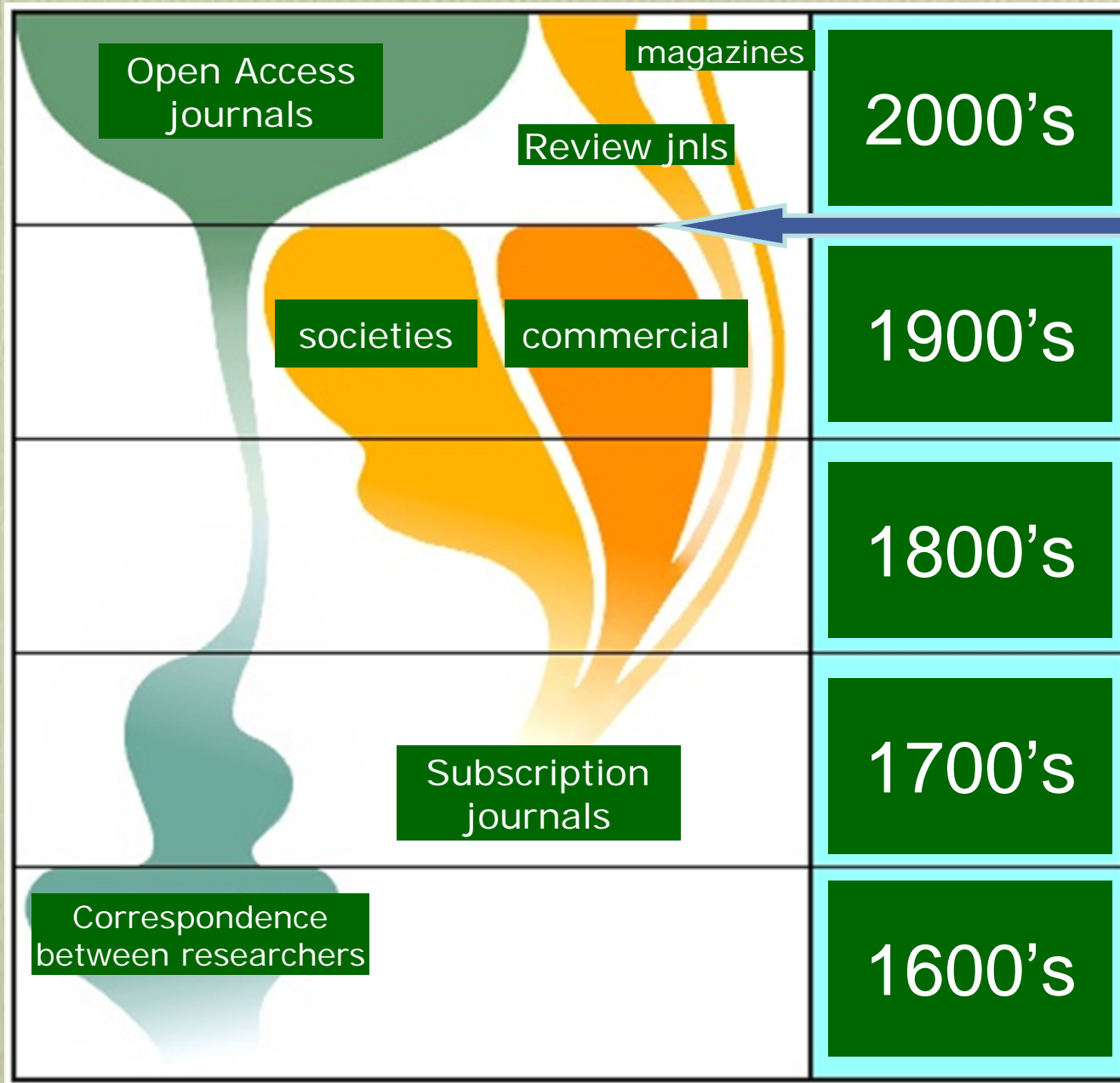




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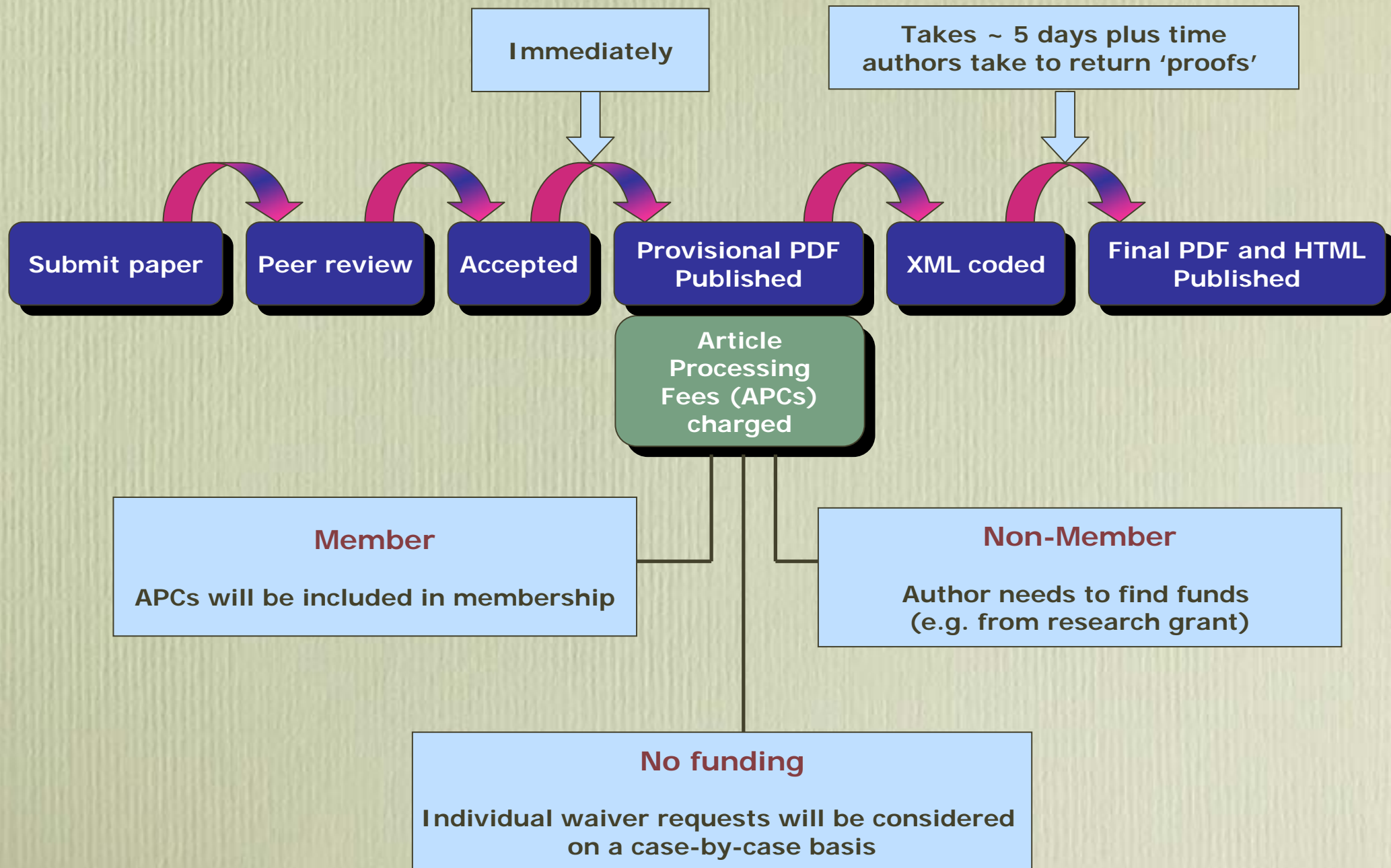
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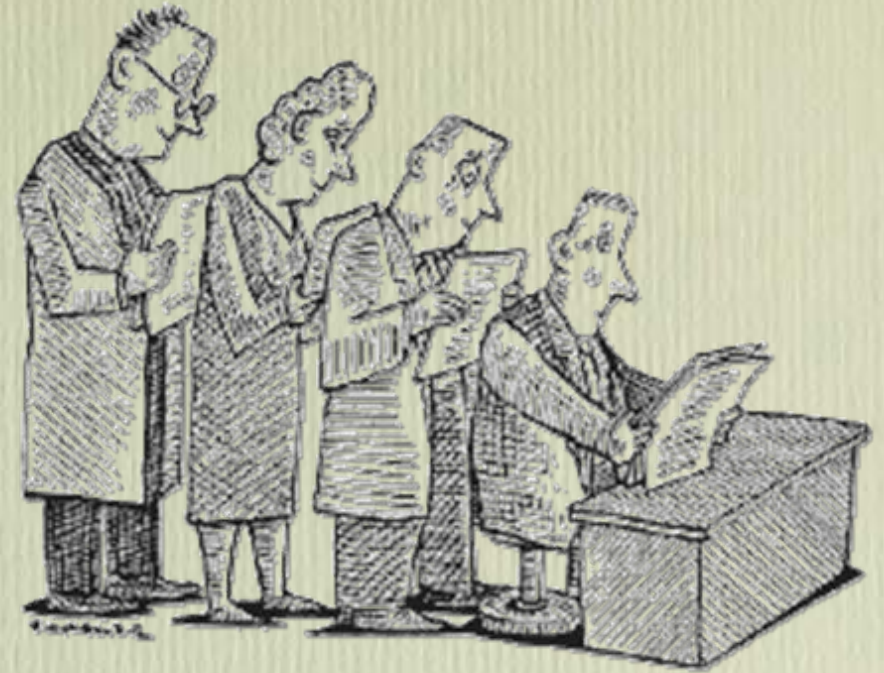
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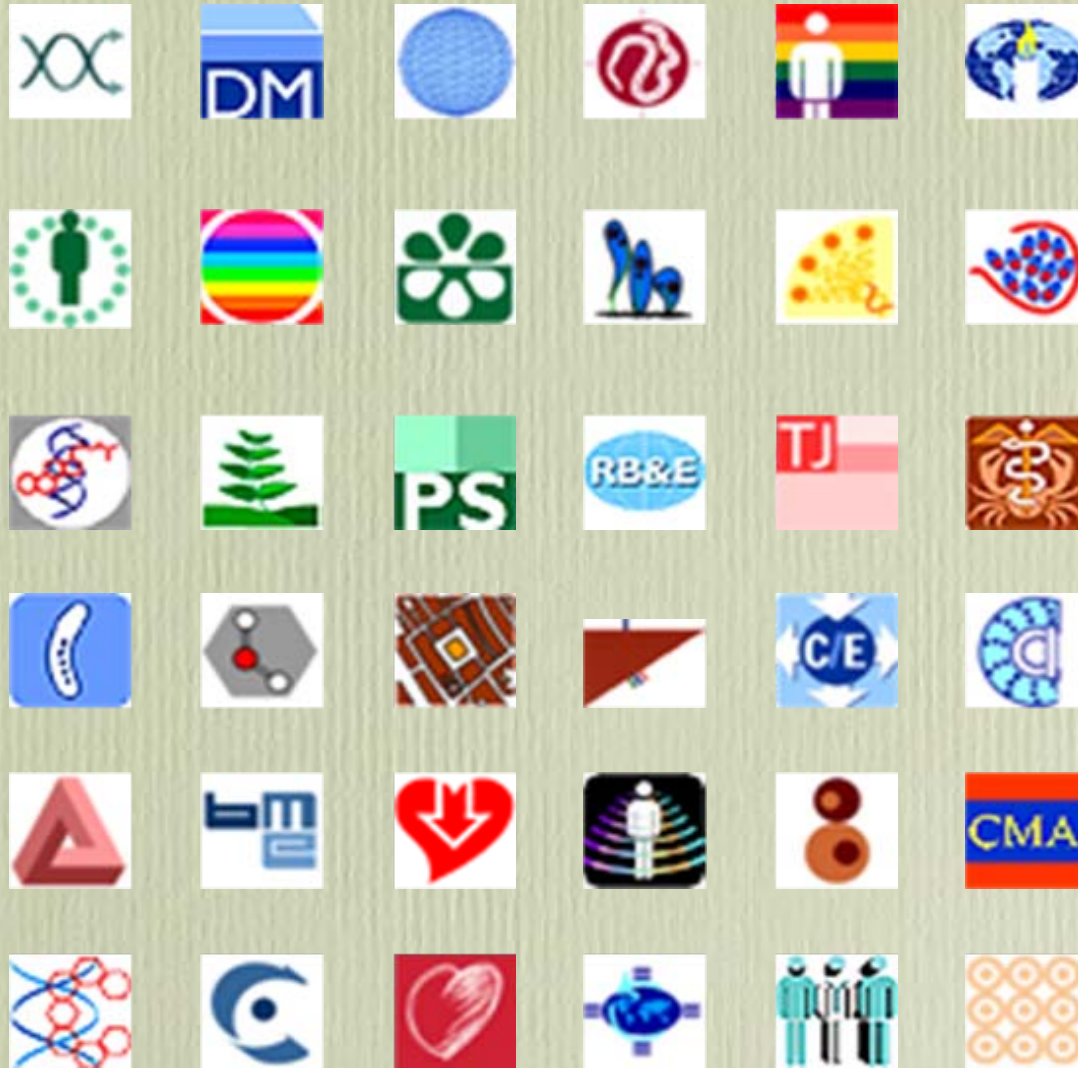
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## Identification of conserved regulatory elements by comparative genome analysis

**Boris Lenhard\*<sup>1</sup>, Albin Sandelin\*<sup>1</sup>, Luis Mendoza<sup>1, 2</sup>, Pär Engström<sup>1</sup>, Niclas Jareborg<sup>1, 3</sup> and Wyeth W Wasserman<sup>1, 4</sup>**

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The electronic version of this article is the complete one and can be found online at: <http://jbiol.com/content/2/2/13>

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 J Biol. 2003; 2 (2): 13

## Identification of conserved regulatory elements by comparative genome analysis

Boris Lenhard,<sup>#1</sup> Albin Sandelin,<sup>#1</sup> Luis Mendoza,<sup>1,2</sup> Pär Engström,<sup>1</sup> Niclas Jareborg,<sup>1,3</sup> and Wyeth W. Wasserman<sup>#1,4</sup>

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Wyeth W. Wasserman: [wynth@cmmt.ubc.ca](mailto:wynth@cmmt.ubc.ca)

Received December 12, 2002; Revised March 21, 2003; Accepted April 8, 2003; Published May 22, 2003.  
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### Abstract

#### Background

For genes that have been successfully delineated within the human genome sequence, most regulatory sequences remain to be elucidated

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## Identification of conserved regulatory elements by comparative genome analysis

**Boris Lenhard<sup>1</sup>, Albin Sandelin<sup>1</sup>, Luis Mendoza<sup>1, 2</sup>, Pär Engström<sup>1</sup>, Niclas Jareborg<sup>1, 3</sup> and Wyeth W Wasserman<sup>1, 4</sup>** ✉

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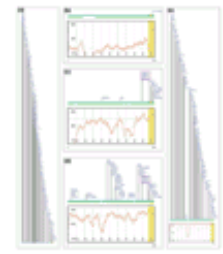
### Background

For genes that have been successfully delineated within the human genome sequence, most regulatory sequences remain to be elucidated. The annotation and interpretation process requires additional data resources and significant improvements in computational methods for the detection of regulatory regions. One approach of growing popularity is

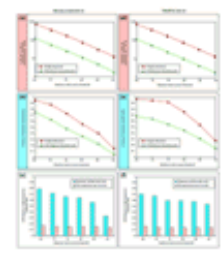
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### Figures



**Figure 1**  
Cross-species comparisons of the  $\beta$ -globin gene promoter



**Figure 2**  
The impact of phylogenetic footprinting analysis



# Economics

- Costs that have to be covered
  - editorial process, production process, web site, promotion
- Charge per article
  - related to publisher cost; variables are editorial process costs and production costs
- Waivers, reduced rates
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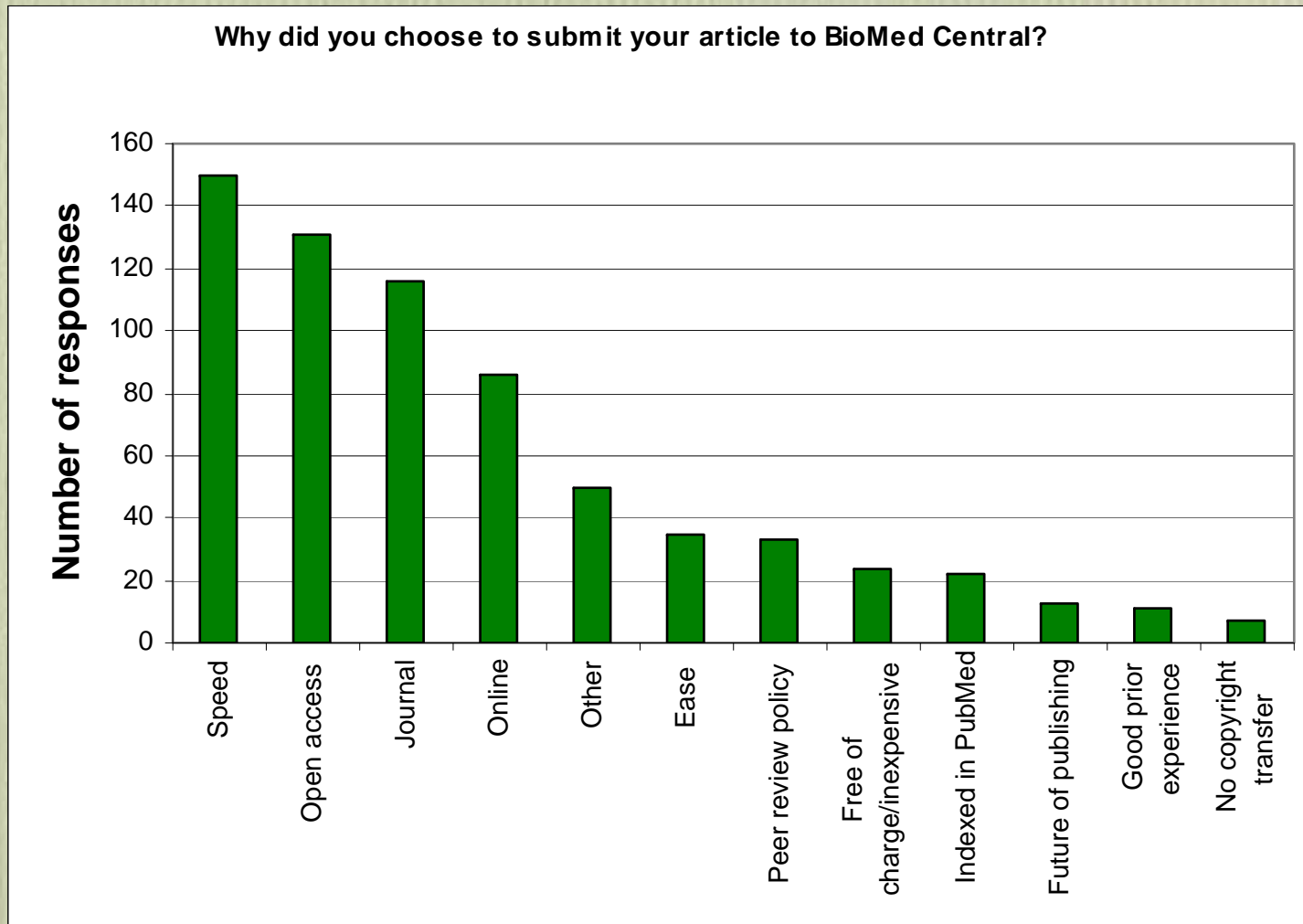


# Experience so far - payment

(June 2004)

- Waiver requests at reasonable levels
  - most for developing countries, South America, some medical research
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Research article

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The Comparative RNA Web (CRW) Site: an online database of comparative sequence and structure information for ribosomal, intron, and other RNAs

Jamie J Cannone<sup>1</sup>, Sankar Subramanian<sup>1,2</sup>, Murray N Schnare<sup>3</sup>, James R Collett<sup>2</sup>, Lisa M D'Souza<sup>1</sup>, Yushi Du<sup>2</sup>, Brian Feng<sup>1</sup>, Nan Lin<sup>1</sup>, Lakshmi V Madabusi<sup>1,4</sup>, Kirsten M Müller<sup>1,5</sup>, Nupur Paudyal<sup>1</sup>, Zhidi Shang<sup>1</sup>, Nan Yu<sup>1</sup> and Robin R Gutell<sup>1\*</sup>

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Abstract

**Background:** Comparative analysis of RNA sequences is the basis for the detailed and accurate prediction of RNA structure and the determination of phylogenetic relationships for organisms that span the entire phylogenetic tree. Underlying these accomplishments are very large, well-organized, and processed collections of RNA sequences. This data, starting with the sequences organized into a database management system and aligned to reveal their higher-order structure, and patterns of conservation and variation for organisms that span the phylogenetic tree, has been collected and analyzed. This type of information can be fundamental for and have an influence on the study of phylogenetic relationships, RNA structure, and the meeting of these two fields.

**Results:** We have prepared a large web site that disseminates our comparative sequence and structure models and data. The four major types of comparative information and systems available for the three ribosomal RNAs (16S, 16S, and 23S rRNA), transfer RNA (tRNA), and two of the catalytic weapon RNAs (group I and group II) are: (1) Current Comparative Structure Models; (2) Nucleotide Frequency and Conservation Information; (3) Sequence and Structure Data; and (4) Data Access Systems.

**Conclusions:** This online RNA sequence and structure information, the result of extensive analysis, interpretation, data collection, and computer program and web development, is accessible at our Comparative RNA Web (CRW) Site (<http://www.crnw.utmsi.utexas.edu/>). In the future, more data and information will be added to these existing categories, new categories will be developed, and additional RNAs will be studied and presented at the CRW Site.

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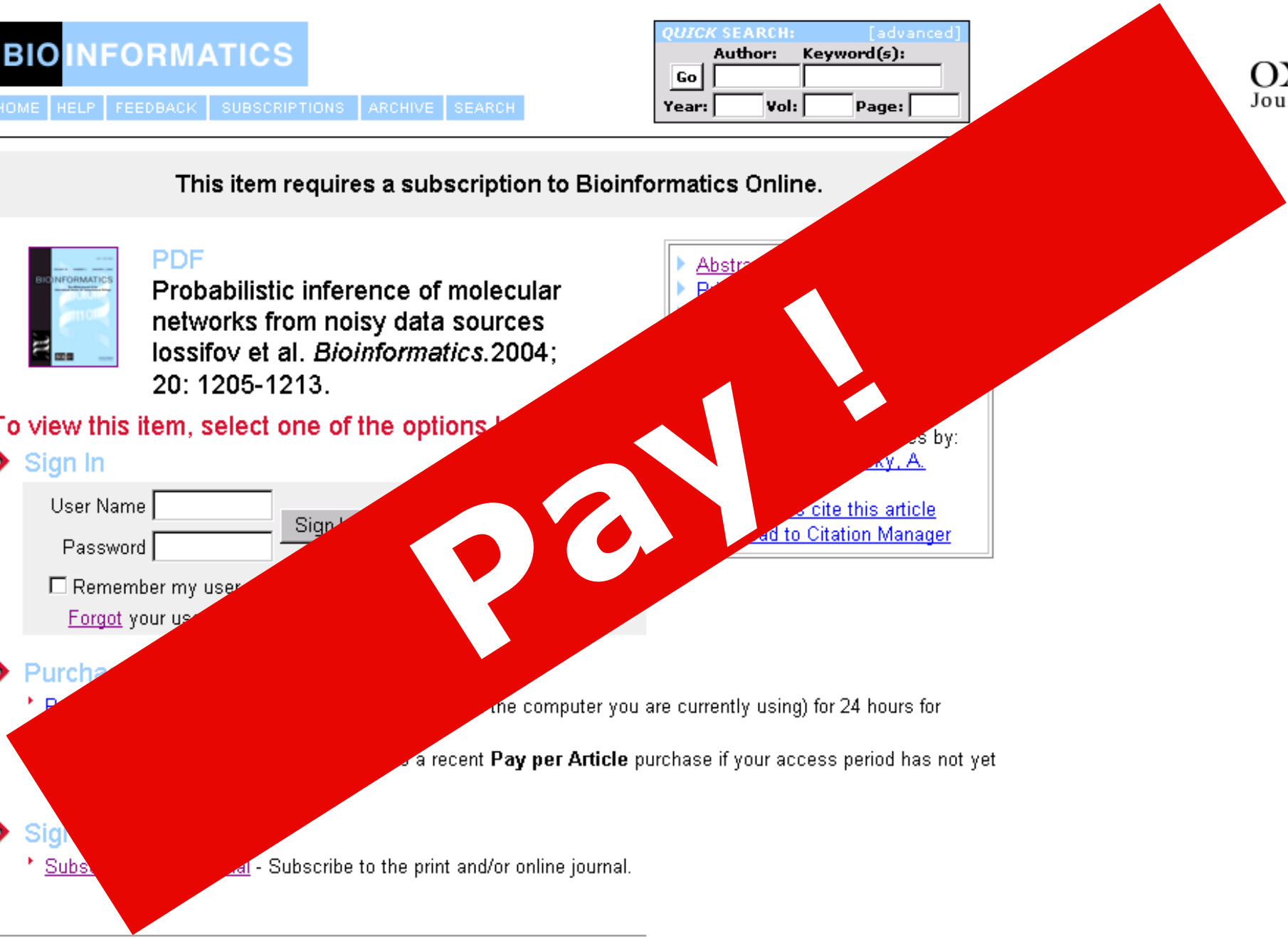
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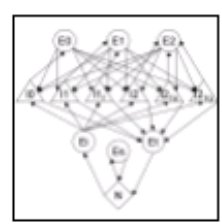
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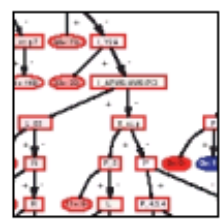
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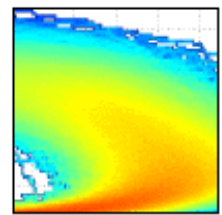
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*BMC Bioinformatics* 2004, **5**:59

Using a gene-finding program trained on one species to predict genes in another species can produce highly inaccurate results, but the new SNAP gene finder is designed to adapt easily to a variety of genomes.



**Predicting protein partners**  
*BMC Bioinformatics* 2004, **5**:38

A probabilistic decision tree approach to the prediction of co-complexed protein pairs in yeast has been developed, validated and shown to have some advantages over other methods.



**Modelling biochemistry**  
*BMC Bioinformatics* 2004, **5**:24

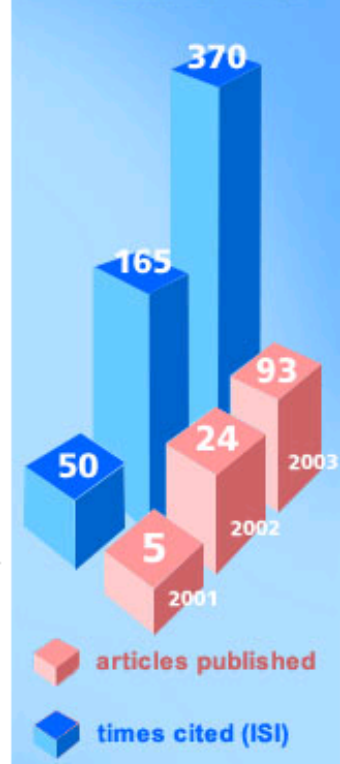
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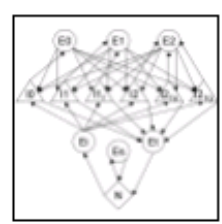
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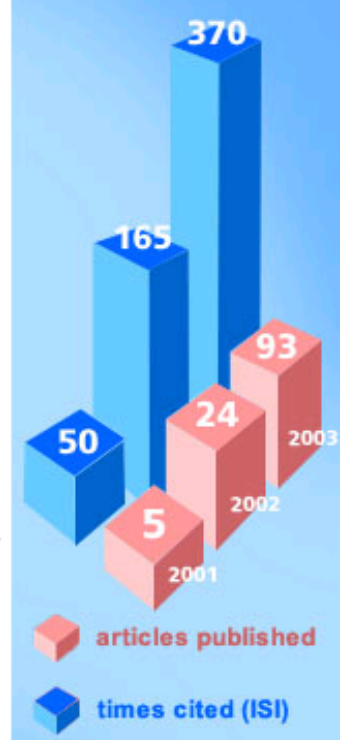
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