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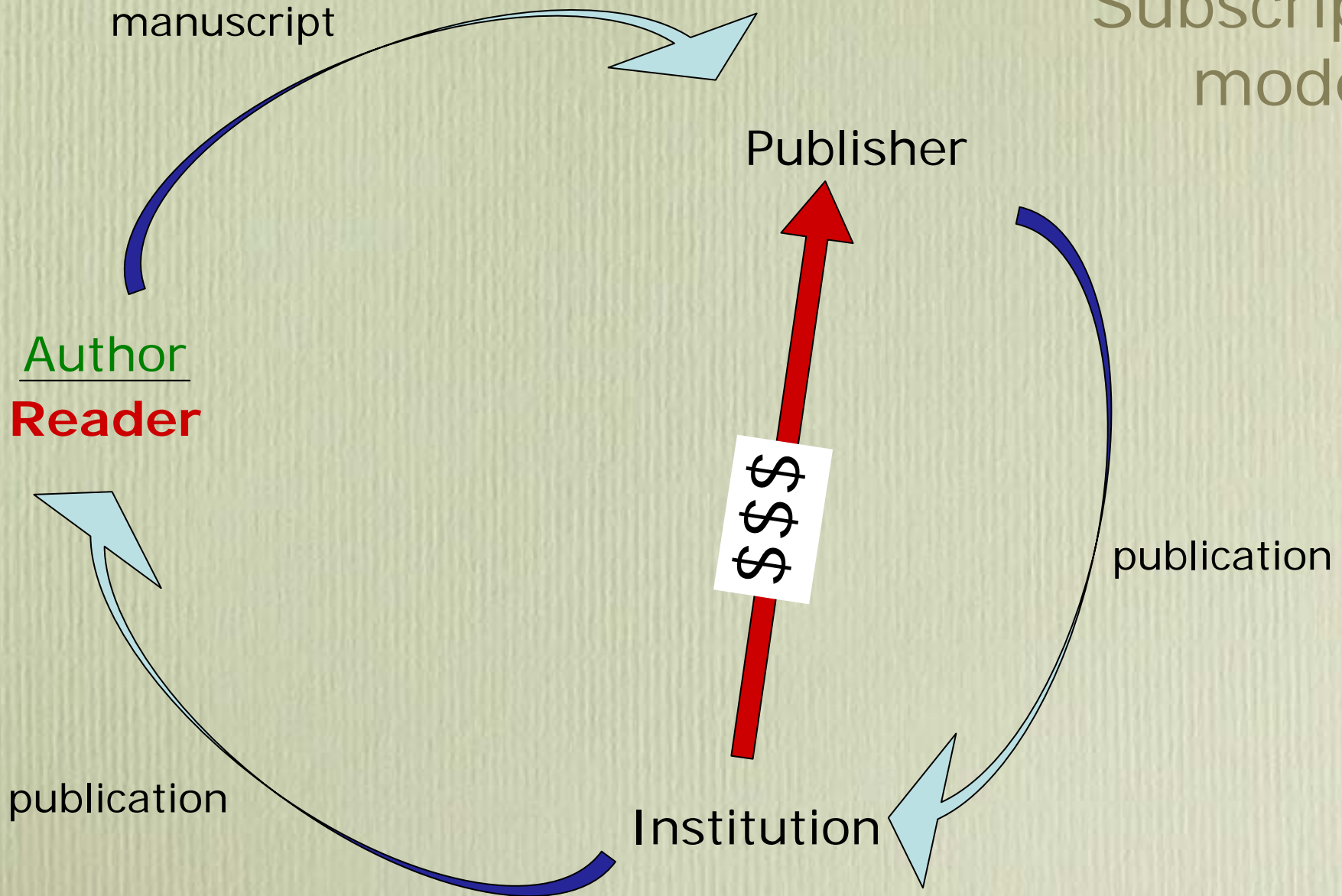
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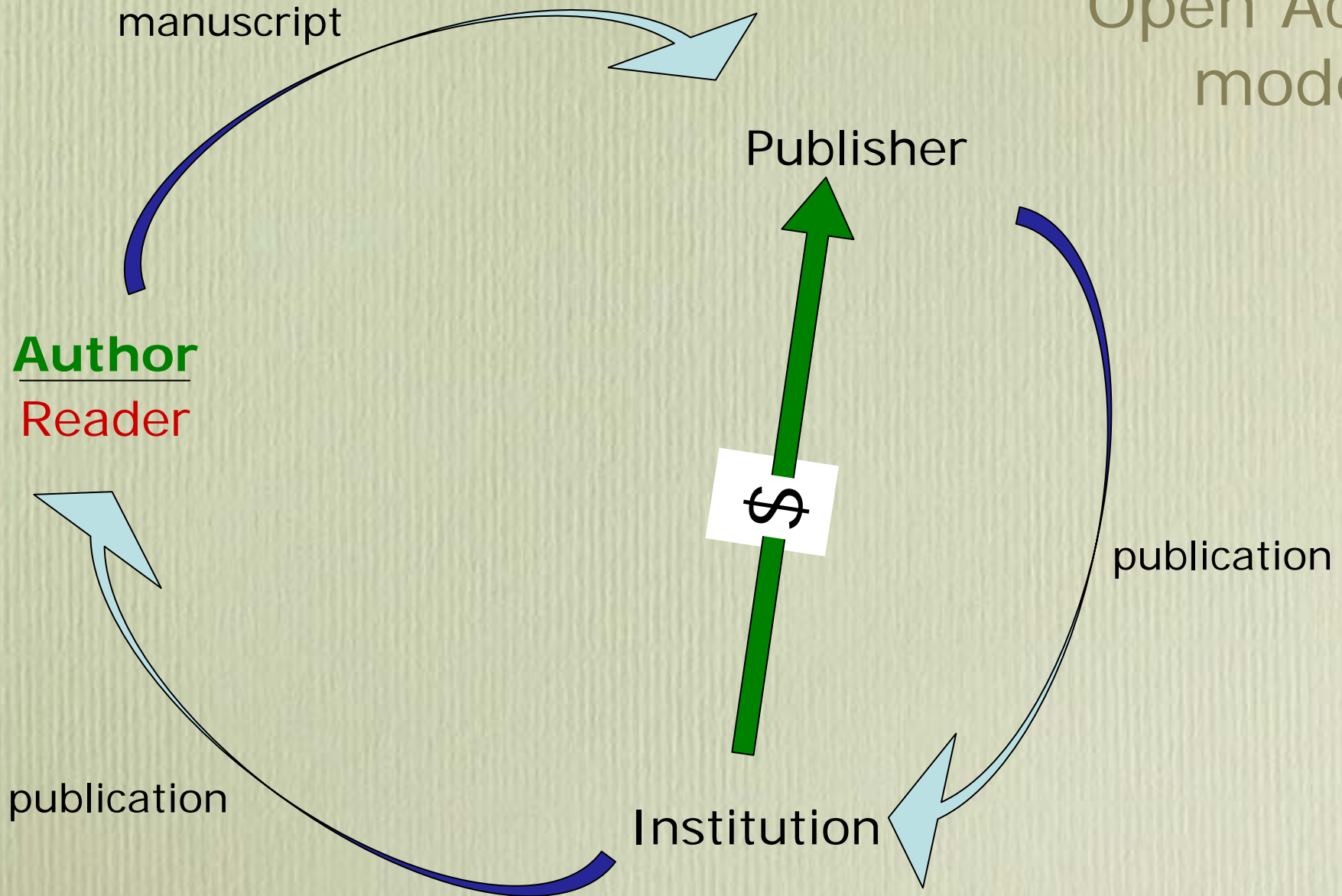
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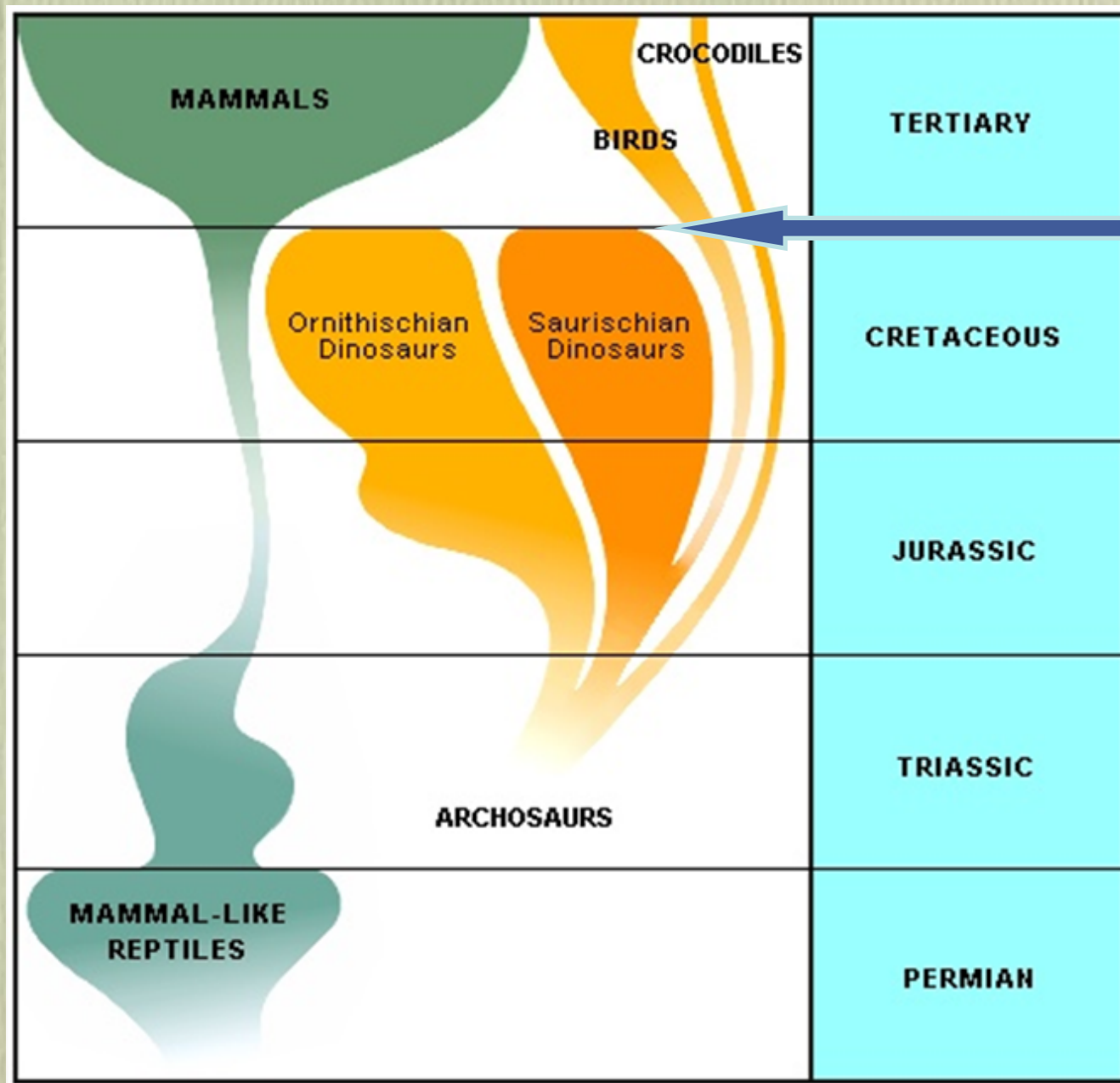
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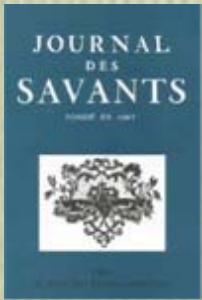


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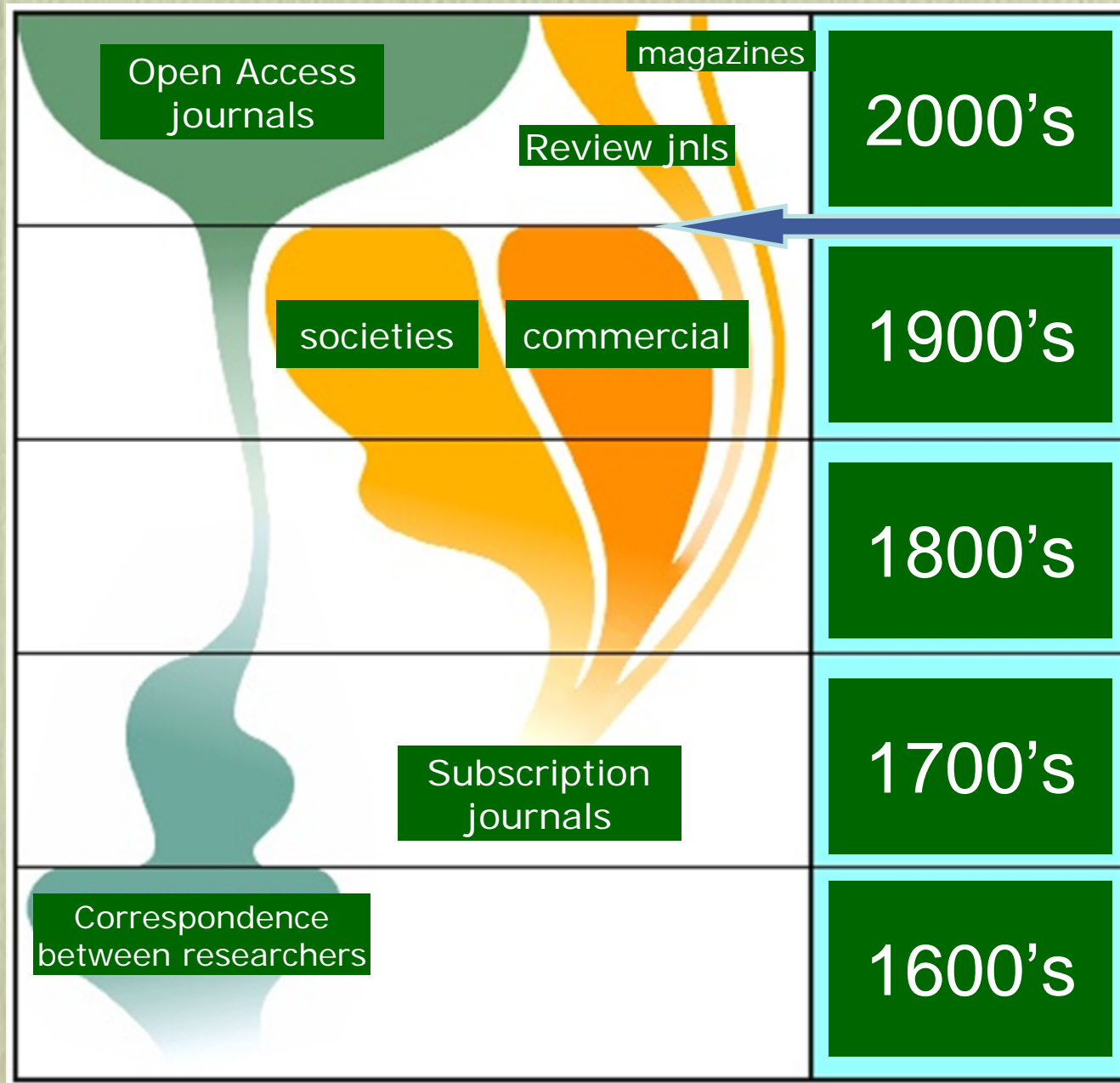
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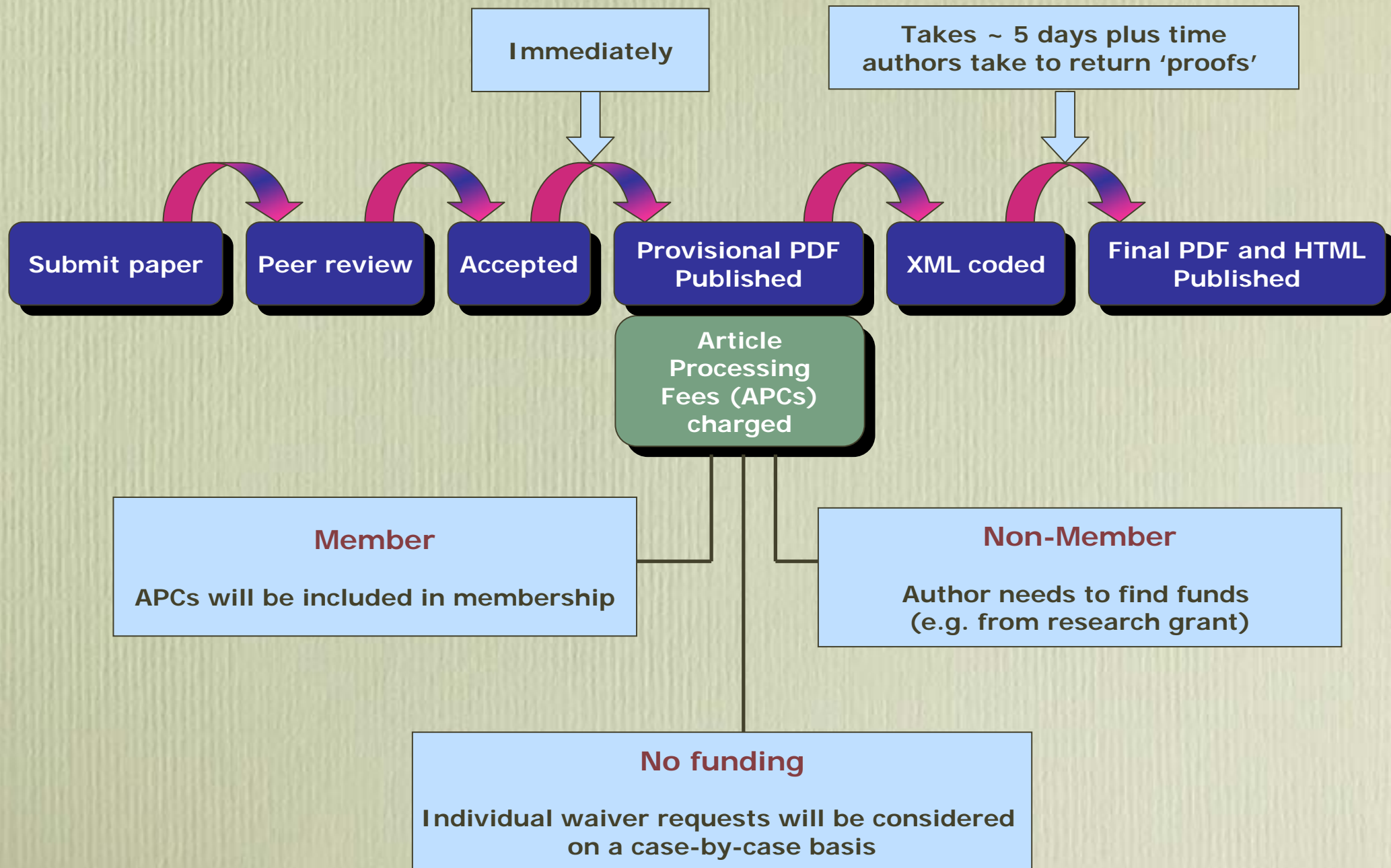
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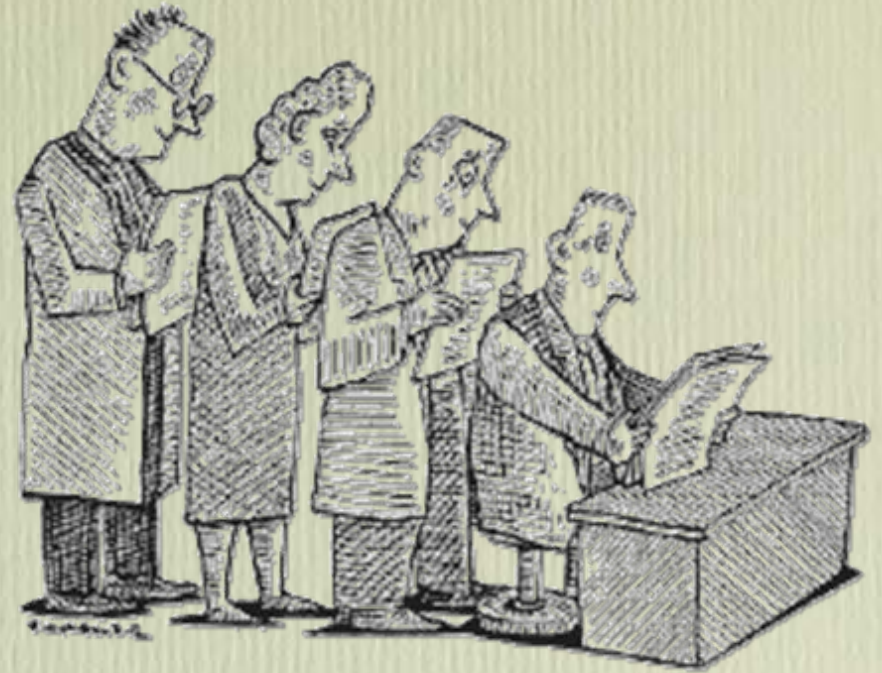
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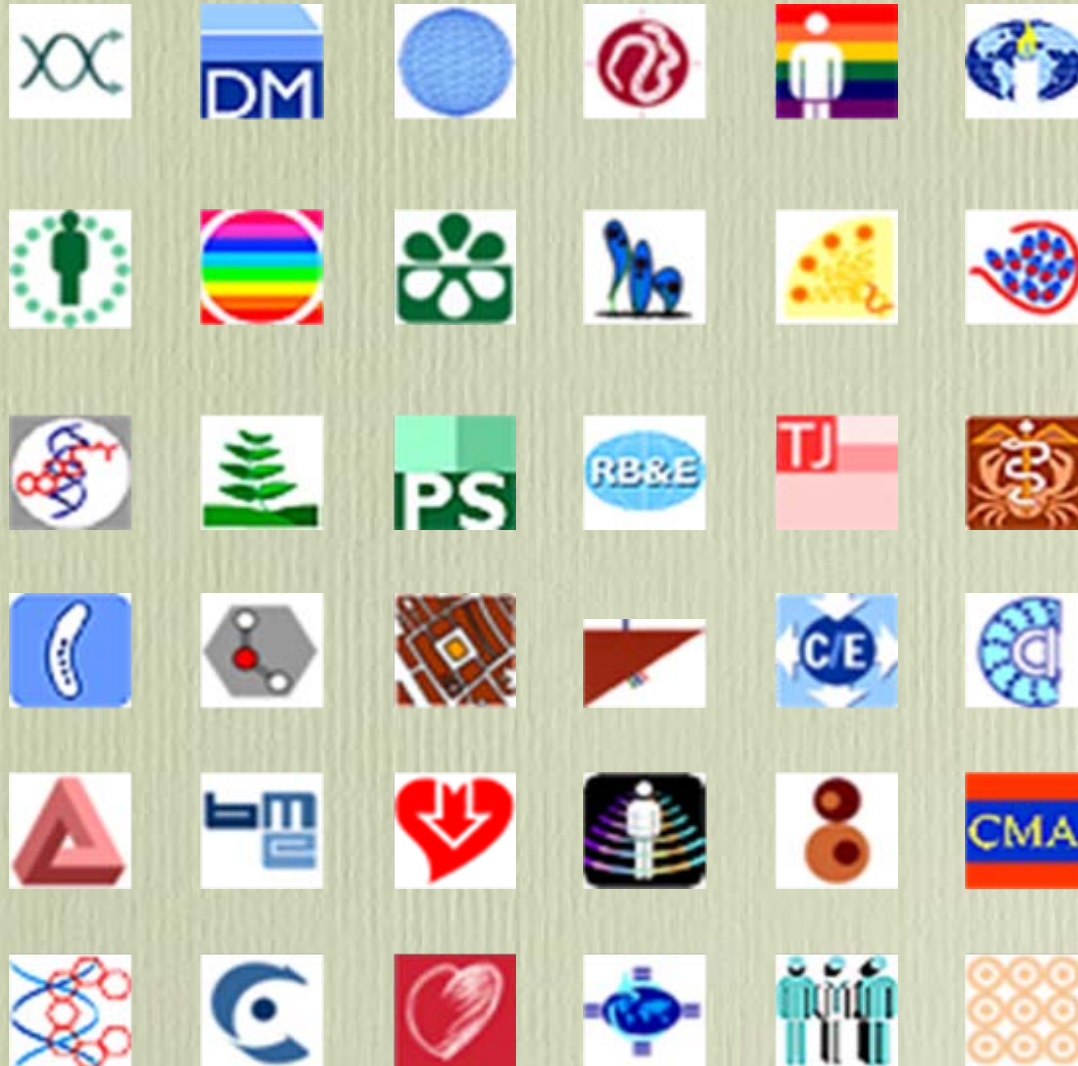
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Identification of conserved regulatory elements by comparative genome analysis

Boris Lenhard*¹, Albin Sandelin*¹, Luis Mendoza^{1, 2}, Pär Engström¹, Niclas Jareborg^{1, 3} and Wyeth W Wasserman^{1, 4}

- ¹Center for Genomics and Bioinformatics, Karolinska Institutet, 171 77 Stockholm, Sweden
- ²Current address: Serono Research and Development, CH-1121 Geneva 20, Switzerland
- ³Current address: AstraZeneca Research and Development, S-151 85 Södertälje, Sweden
- ⁴Current address: Centre for Molecular Medicine and Therapeutics, University of British Columbia, Vancouver, BC V5Z 4H4, Canada

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Boris Lenhard,^{#1} Albin Sandelin,^{#1} Luis Mendoza,^{1,2} Pär Engström,¹ Niclas Jareborg,^{1,3} and Wyeth W. Wasserman^{#1,4}

¹Center for Genomics and Bioinformatics, Karolinska Institutet, 171 77 Stockholm, Sweden ²Current address: Serono Research and Development, CH-1121 Geneva 20, Switzerland ³Current address: AstraZeneca Research and Development, S-151 85 Södertälje, Sweden ⁴Current address: Centre for Molecular Medicine and Therapeutics, University of British Columbia, Vancouver, BC V5Z 4H4, Canada

Corresponding author.

[#]Contributed equally.

Wyeth W. Wasserman: wynth@cmmt.ubc.ca

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Background

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

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¹Center for Genomics and Bioinformatics, Karolinska Institutet, 171 77 Stockholm, Sweden

²Current address: Serono Research and Development, CH-1121 Geneva 20, Switzerland

³Current address: AstraZeneca Research and Development, S-151 85 Södertälje, Sweden

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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. 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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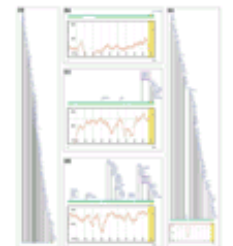


Figure 1
Cross-species comparisons of the β -globin gene promoter

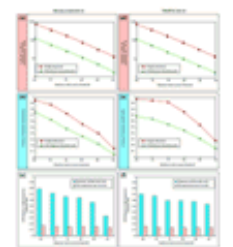


Figure 2
The impact of phylogenetic footprinting analysis



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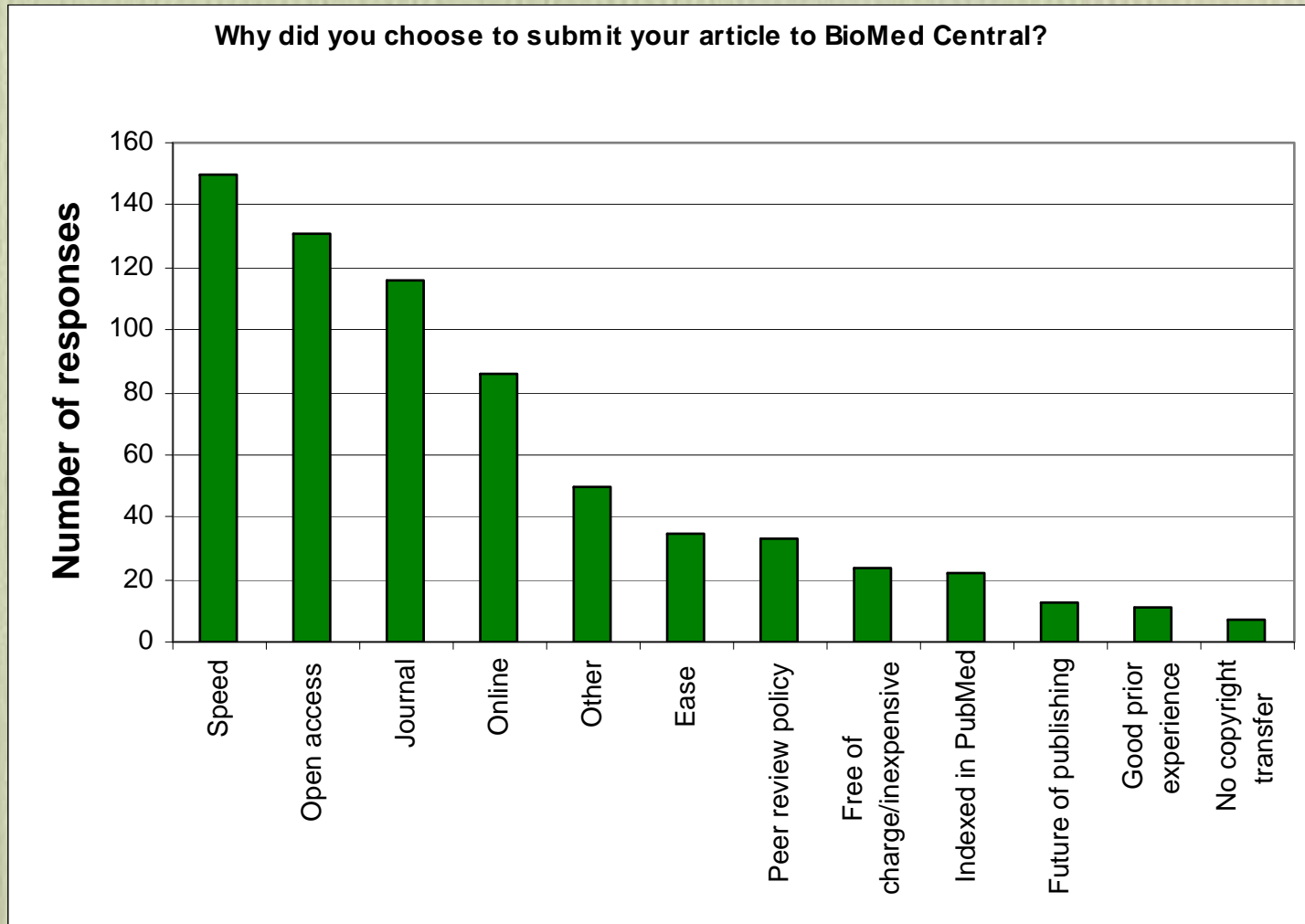


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The Comparative RNA Web (CRW) Site: an online database of comparative sequence and structure information for ribosomal, intron, and other RNAs

Jamie J Cannone¹, Sankar Subramanian^{1,2}, Murray N Schnare³, James R Collett², Lisa M D'Souza¹, Yushi Du², Brian Feng¹, Nan Lin¹, Lakshmi V Madabusi^{1,4}, Kirsten M Müller^{1,5}, Nupur Paudyal¹, Zhidi Shang¹, Nan Yu¹ and Robin R Gutell^{1*}

Address: ¹Department of Cellular and Molecular Biology, Section of Integrative Toxicology, University of Texas at Austin, 2500 Speedway, Austin, TX 78712-1995, USA; ²Department of Biology, Arizona State University, Tempe, AZ 85287, USA; ³Department of Biology, Dalhousie University, Halifax, Nova Scotia B3H 4R2, Canada; ⁴Department of Biology, University of Waterloo, Waterloo, Ontario N2L 3G1, Canada; ⁵Department of Biology, University of North Carolina, Chapel Hill, NC 27515, USA

*Corresponding author: jccannone@mail.utexas.edu; Sankar Subramanian: subraman@utmsi.utexas.edu; Murray N Schnare: mschnare@mail.utexas.edu; James R Collett: jcollett@mail.utexas.edu; Nan Lin: nanlin@mail.utexas.edu; Brian Feng: bfeng@mail.utexas.edu; Yushi Du: ydu@mail.utexas.edu; Lakshmi V Madabusi: lmadabusi@utdallas.edu; Kirsten M Müller: kmuller@mail.utexas.edu; Nupur Paudyal: npaudyal@mail.utexas.edu; Zhidi Shang: zshang2001@uwaterloo.ca; Nan Yu: nyu@mail.utexas.edu; Robin R Gutell: rgutell@mail.utexas.edu

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Background: Comparative analysis of RNA sequences is the basis for the detailed and accurate predictions 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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Address: ¹Department of Cellular and Molecular Biology, Section of Integrative Toxicology, 78712-1495, USA; ²Department of Biology, Arizona State University, Tempe, AZ 85287, USA; ³Department of Biology, Dalhousie University, Halifax, Nova Scotia B3H 4R2, Canada; ⁴Department of Biology, University of Waterloo, Waterloo, Ontario N2L 3G1, Canada; ⁵Department of Biology, University of Texas at Dallas, 75080-3000, Richardson, Texas, TX 75080, USA

E-mail: Jamie J Cannone - cannone@mail.scripps.edu; Sankar Subramanian - ssubram@scripps.edu; Murray N Schnare - mnschnare@scripps.edu; James R Collett - jcollett@scripps.edu; Lisa M D'Souza - ldsouza@mail.scripps.edu; Yushi Du - ydu@scripps.edu; Brian Feng - brian.feng@scripps.edu; Nan Lin - nlin@scripps.edu; Lakshmi V Madabusi - lmadabusi@scripps.edu; Kirsten M Müller - kmueller@scripps.edu; Nupur Puri - nupur.puri@scripps.edu; Zhidi Shang - zshang@scripps.edu; Nan Yu - nyu@scripps.edu; Robin R Gutell - rgutell@scripps.edu

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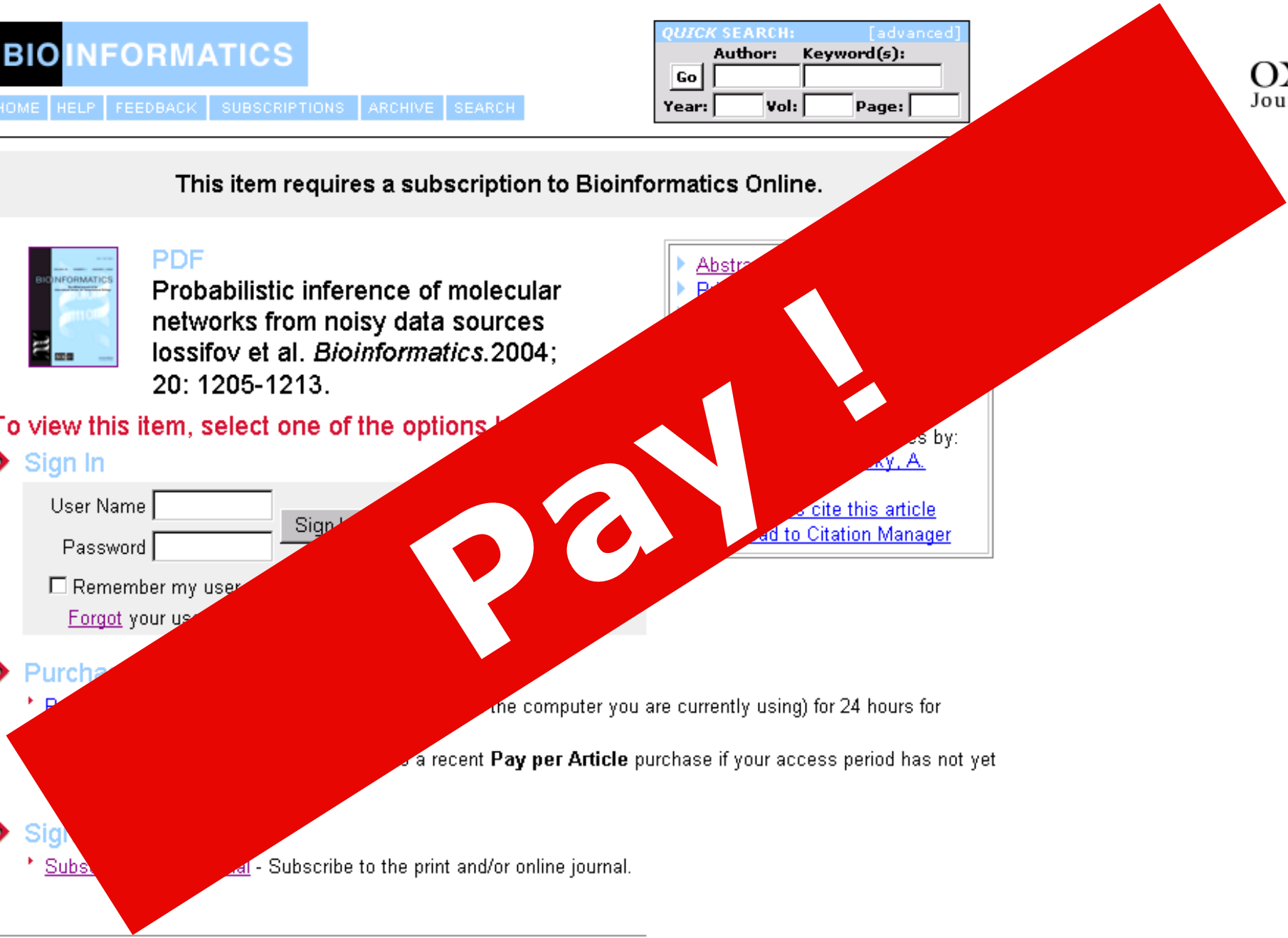
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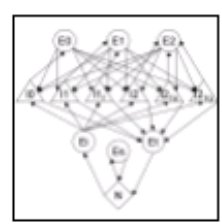
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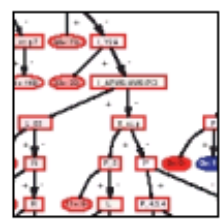
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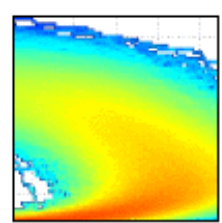
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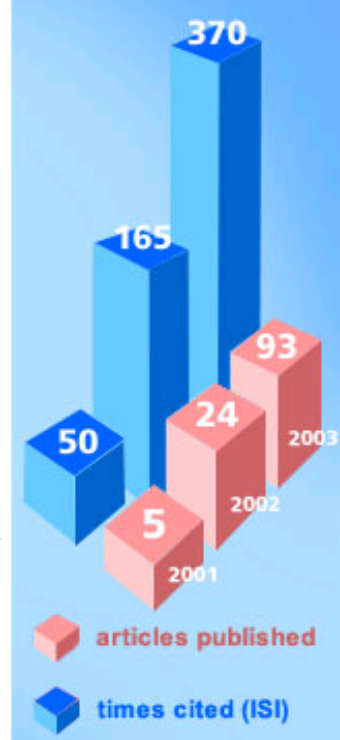
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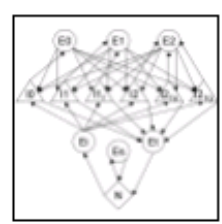
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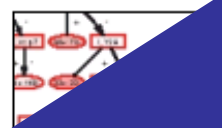
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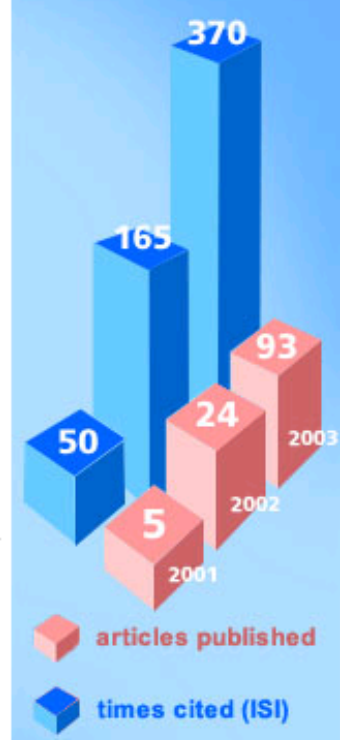
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