User love

I love you #mendeley.

All those folks who follow me at academia.com...try Mendeley instead. #betterUXwins

You have no idea how happy I am about the Kindle/Mendeley sync thing. #totallymademyday

I just used #Mendeley as a verb. As in, "I need to Mendeley that article". Makes sense to me.

I love how smart @mendeley_com is... it's finding my articles from my designated folder and adding them to the appropriate entries.

switched my research group over to @mendeley_com today. Everyone is really happy with how easy it is to use and share. :)

Werner Vogels

I strongly believe that Mendeley can change the face of science http://bit.ly/lLhf6 (f @mendeley_com)


Still using Mendeley even though I'm working with film criticism now and not medicine. Because I love Mendeley and I want to marry it.

Researching? Forget @wikipedia. Check @mendeley_com - you can thank me later.
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Thabo Mavundza, Agricultural Engineer
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Duncan J Watts

H<sub>R</sub>-Index: 20
G<sub>R</sub>-Index: 31

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Top 10 publications by readership:
1. Watts and Strogatz (1998) 183
4. Dodd et al. (2003) 48
5. Salganik et al. (2006) 48
8. De Choudhury et al. (2010) 41

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Duncan J Watts's alternate spellings
Duncan J. WATTS
Measuring the evolutionary rate of protein-protein interaction.

by Wenteng Qian, Xionglei He, Edwin Chan, Huailiang Xu, Jianzhi Zhang


Abstract

Despite our extensive knowledge about the rate of protein sequence evolution for thousands of genes in hundreds of species, the corresponding rate of protein function evolution is virtually unknown, especially at the genomic scale. This lack of knowledge is primarily because of the huge diversity in protein function and the consequent difficulty in gauging and comparing rates of protein function evolution. Nevertheless, most proteins function through interacting with other proteins, and protein-protein interaction (PPI) can be tested by standard assays. Thus, the rate of protein function evolution may be measured by the rate of PPI evolution. Here, we experimentally examine 87 potential interactions between Kluveromyces waltii proteins, whose one to one orthologs in the related budding yeast Saccharomyces cerevisiae have been reported to interact. Combining our results with available data from other eukaryotes, we estimate that the evolutionary rate of protein interaction is (2.6 ± 1.6) x 10^-10 per PPI per year, which is three orders of magnitude lower than the rate of protein sequence evolution measured by the number of amino acid substitutions per protein per year. The extremely slow evolution of protein molecular function may account for the remarkable conservation of life at molecular and cellular levels and allow for studying the mechanistic basis of human disease in much simpler organisms.

Reviews

should have discussed a whole genome duplication

by Giovanni Dall’Olio · 8 hours ago · Recommended: Yes · Difficulty level: Intermediate · Reviewer expertise: Intermediate

This paper provides an estimate of the rate of protein-protein interaction gain or loss between two species, S. cerevisiae and K. waltii.

The problem is that the authors did not discuss the fact that a genome-duplication event occurred between the separation of these two species. This may invalidate their conclusions about the overall PPI loss/gain rate of 2.6 ± 1.6 x 10^-10 per PPI per year. As the paper is written, a reader unaware of this genome-wide duplication would be inclined to think that this rate can be compared to other species.

Apart from this point, I liked the paper and I think it is a very good experiment. The authors did an impressive job in experimentally verifying all the interactions, and their results are valid for these two species.

References | Originality | Argumentation | Readability
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What does it mean for the future of scholarly communication?
When Tim Berners-Lee created the Web in 1991, it was with the aim of better facilitating scientific communication and the dissemination of scientific research. Put another way, the Web was designed to disrupt scientific publishing. It was not.

Here in the digital pages of the Scholarly Kitchen, for example, we covered John Wilbanks' presentation at SSP IN and Michael Nielsen's talk at the 2009 STM Conference. They were both thoughtful presentations and I agree with many of the points raised by both speakers. I think Wilbanks is right when he says that thinking of information in terms of specific containers (e.g. books, journals, etc.) presents an
Academic publishing faces two major challenges: The “Serials Crisis” and Open Access
The “Serials Crisis”: Journal subscription costs keep increasing, library budgets are shrinking.

Source: Association of Research Libraries
Open Access: Calls for free public access to (state-funded) academic research

Published online 7 April 2010 | Nature 464, 822-823 (2010) | doi:10.1038/464822a

News

US seeks to make science free for all

Moves to make research funded by the US government available to everyone could mark a turning point in a publishing revolution. Declan Butler reports.

Declan Butler

The push to open up scientific knowledge to all looks set to go into overdrive. Over the past decade, the accessibility offered by the Internet has transformed science publishing. Several efforts have already tried to harness the web's power to make research papers available for free. Now two

Harvard University is part of a group seeking ways to bolster open access to research papers.

M. FEIN/BLOOMBERG/GETTY IMAGES
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3. **Designation**: Journals provide prestige
1. Validation: Journals provide peer review
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3. Designation: Journals provide prestige
1. **Validation:** Journals provide peer review
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3. **Designation:** Journals provide prestige

Discovery through recommendation algorithms
1. Validation: Journals provide peer review
2. Filtration: Journals facilitate content discovery
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Discovery through recommendation algorithms
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THANK YOU!