



CC-BY, Davidk79, wikipedia

Publishing data in Dryad: infrastructure for the long tail

Todd Vision

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NESCent & UNC Chapel Hill

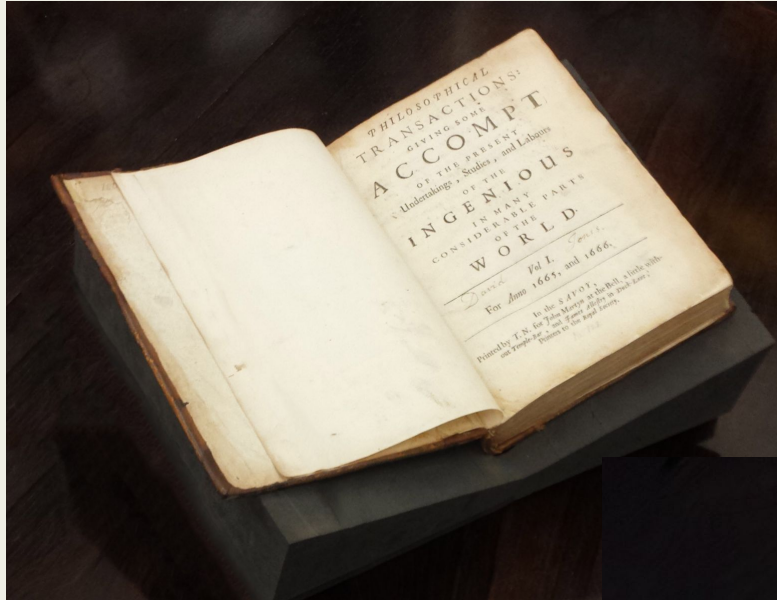
<http://orcid.org/0000-0002-6133-2581>



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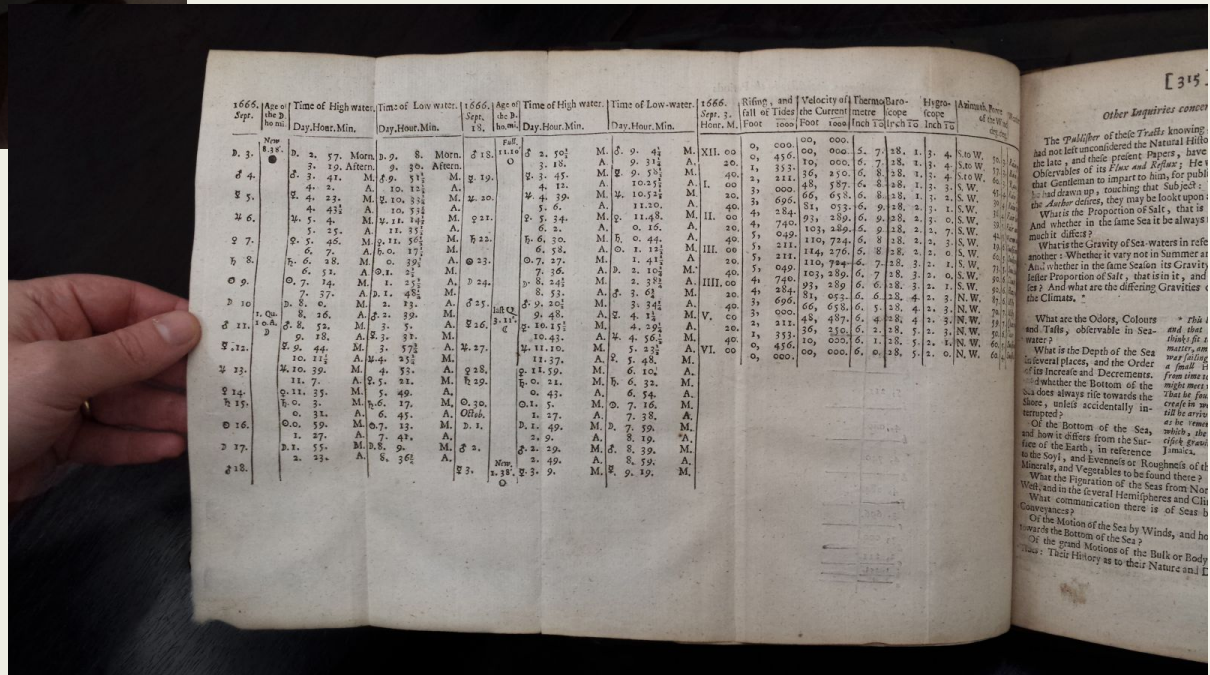
Goals

- Survey the landscape of journal policies & repositories for long tail data
- Understand what is needed to prepare a submission to Dryad and how to choose among submission options
- Understand what happens to data in Dryad after publication and how to track & get credit for data publication
- Some other data-related resources

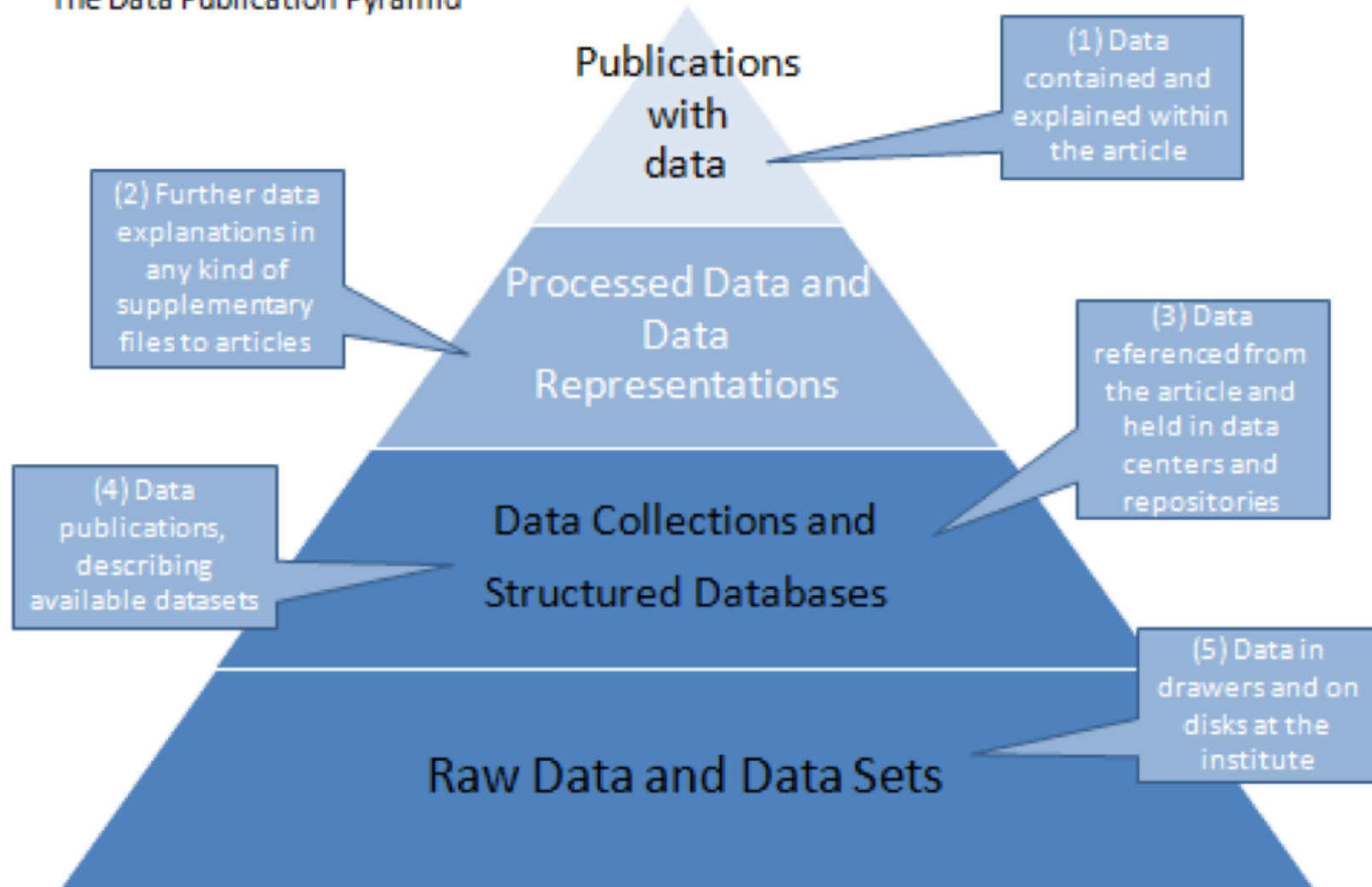


THE ROYAL SOCIETY

CELEBRATING 350 YEARS

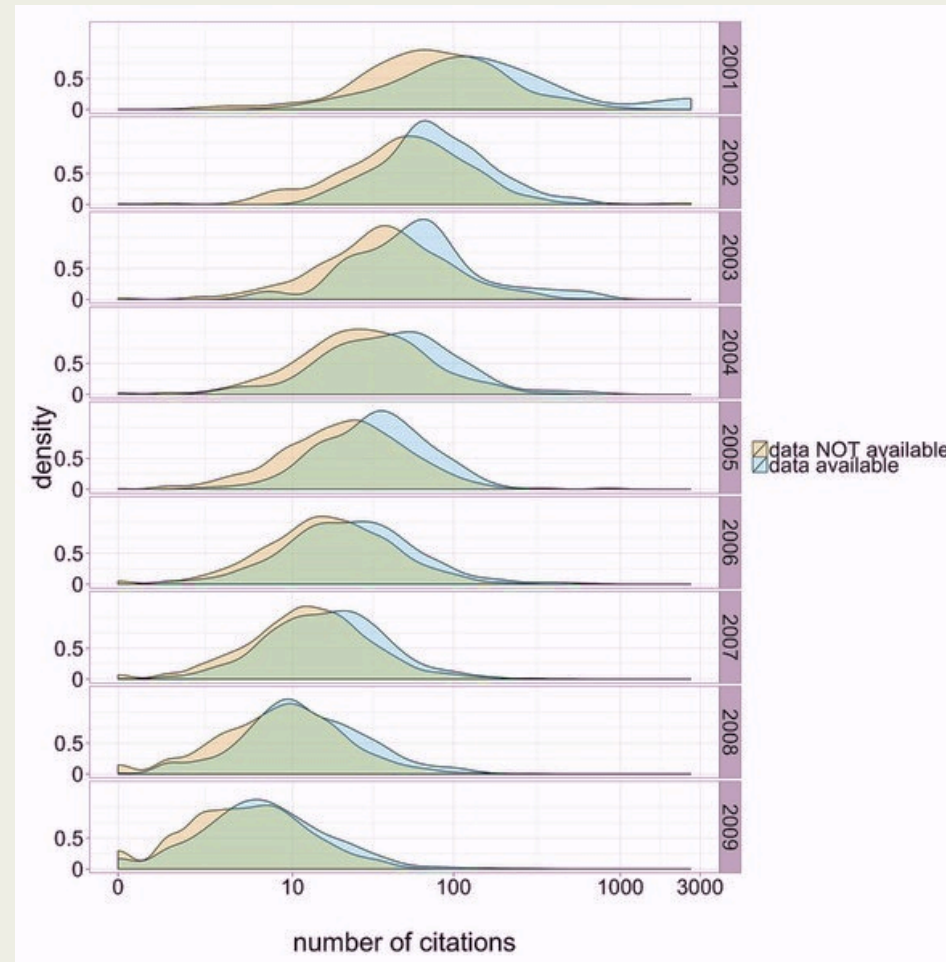


The Data Publication Pyramid



http://www.stm-assoc.org/2011_12_5_ODE_Report_On_Integration_of_Data_and_Publications.pdf

Open data citation advantage



Piwowar and Vision (2013) doi:10.7717/peerj.175

Long tail data: Bumpus' sparrows

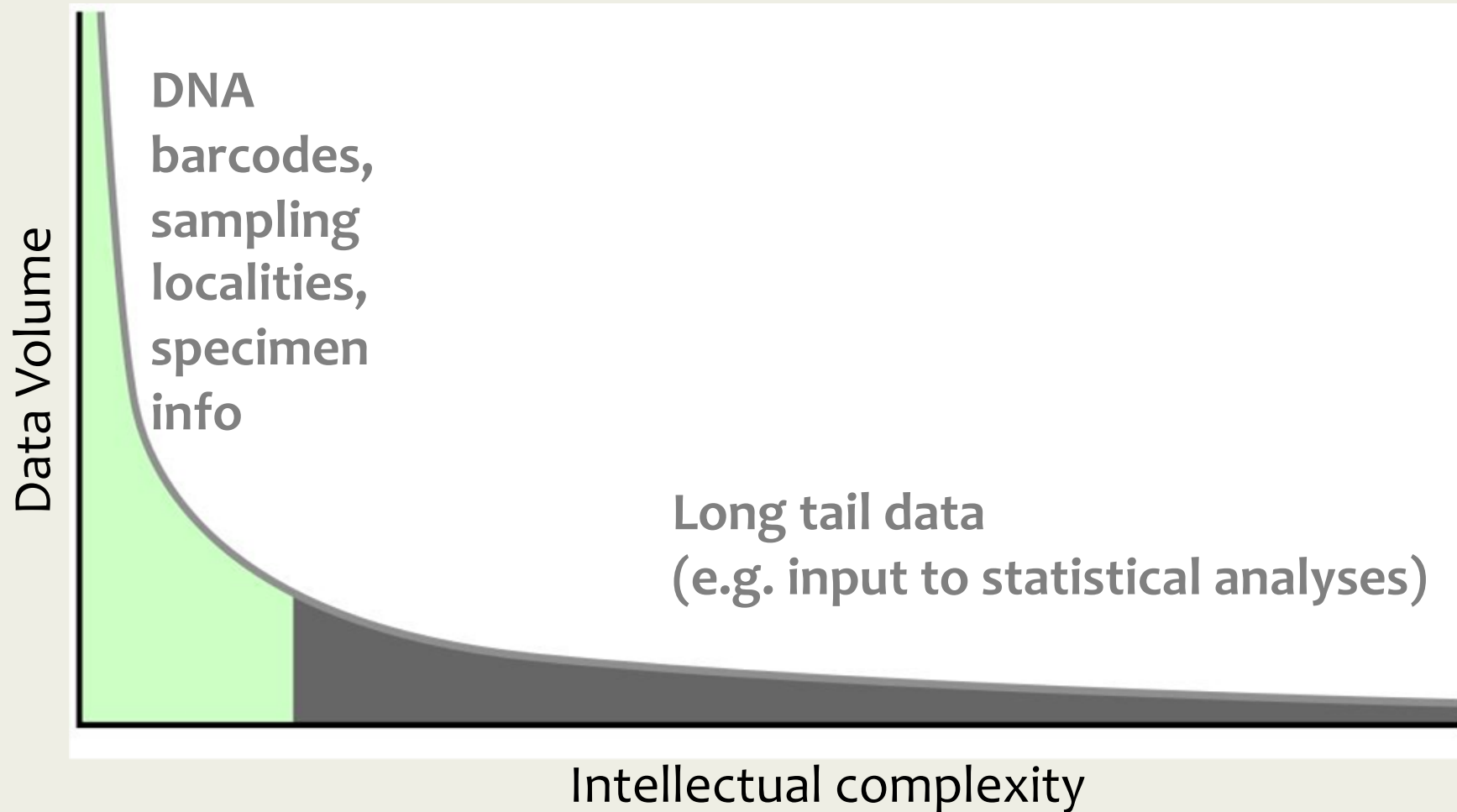
TABLE III^a.

Measurements of Twenty-eight Adult and Young Females which Perished.

	TOTAL LENGTH.	ALAR EXTENT.	WEIGHT.	LENGTH OF BEAK AND HEAD.	LENGTH OF HUMERUS.	LENGTH OF FEMUR.	LENGTH OF TIBIO-TARSUS.	WIDTH OF SKULL.	LENGTH OF KEEL OF STERNUM.
37 ♀	155	240	26.3	31.4	.709	.710	1.125	.614	.815
38 ♀	156	240	25.8	31.5	.715	.678	1.127	.597	.812
39 ♀	160	242	26.	32.6	.740	.732	1.157	.597	.854
40 ♀	1521	2323	23.23	30.3	.6762	.688	1.048	.590	.780
41 ♀	160	250	26.5	31.7	.741	.731	1.187	.615	.886
42 ♀	155	237	24.2	31.	.727	.723	1.118	.610	.787
43 ♀	157	245	26.9	32.2	.766	.751	1.2272	.620	.841
44 ♀	1653	245	27.7	33.12	.7801	.7573	1.195	.633	.895
45 ♀	1532	2312	23.9	30.1	.6803	.6623	1.0423	.592	.781
46 ♀	162	239	26.1	30.3	.709	.685	1.092	.587	.911
47 ♀	162	243	24.6	31.6	.741	.729	1.162	.605	.840
48 ♀	159	245	23.6	31.8	.727	.700	1.129	.610	.855
49 ♀	159	247	26.	30.9	.711	.666	1.098	.580	.7492
50 ♀	155	243	25.	30.9	.730	.711	1.127	.598	.829
51 ♀	162	252	24.8	31.9	.752	.738	1.180	.615	.875
52 ♀	1521	2301	22.82	30.4	.682	.664	1.0423	.5511	.7341
53 ♀	159	242	24.8	30.8	.717	.667	1.090	.575	.809
54 ♀	155	238	24.6	31.2	.706	.702	1.102	.588	.7583
55 ♀	163	249	26.52	33.41	.767	.7671	1.2073	.6401	.896
56 ♀	163	242	24.8	31.	.713	.718	1.128	.607	.813
57 ♀	156	237	23.9	31.7	.718	.716	1.090	.611	.800
58 ♀	159	238	24.7	31.5	.726	.701	1.145	.600	.800
59 ♀	161	245	26.9	32.1	.751	.704	1.142	.607	.819
60 ♀	155	235	22.61	30.7	.695	.692	1.119	.584	.771
61 ♀	162	247	26.1	31.9	.751	.735	1.157	.618	.802
62 ♀	1534	237	24.8	30.6	.732	.718	1.172	.594	.802
63 ♀	162	245	26.2	32.5	.728	.731	1.102	.614	.832
64 ♀	164	248	26.1	32.3	.739	.707	1.159	.592	.823
Average . . .	158	241	25.3	31.4	.726	.709	1.131	.601	.820
General average for 64 birds . . .	160	245	25.8	31.5	.728	.709	1.128	.601	.834

Bumpus HC (1898) The Elimination of the Unfit as Illustrated by the Introduced Sparrow, *Passer domesticus*. *Biological Lectures from the Marine Biological Laboratory*: 209-226.

Long tail data: includes data behind figures, tables, statistical analyses; files where context matters



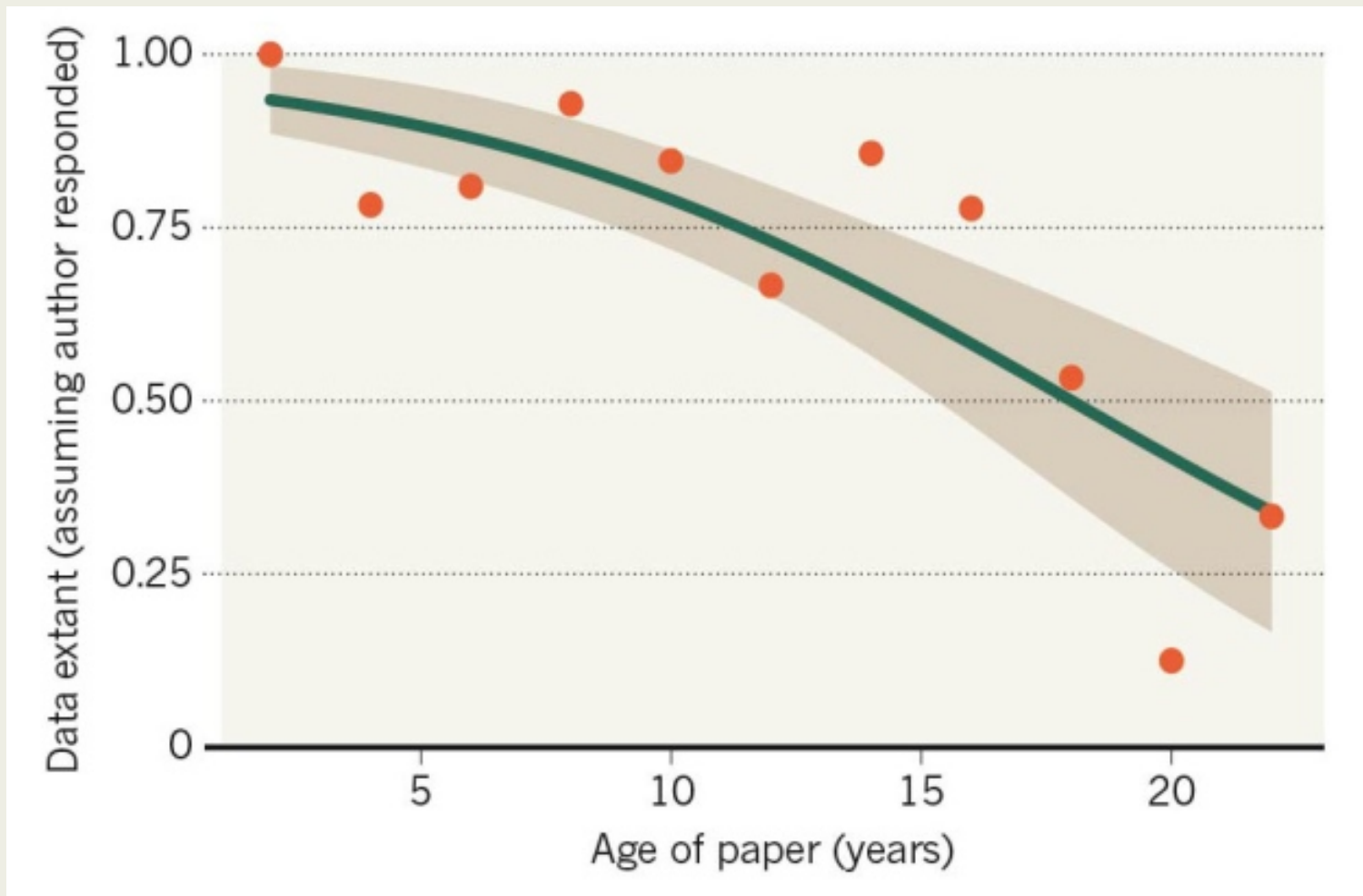
After Heidorn (2008) <http://hdl.handle.net/2142/9127>

Example: what and where are the data?

- Laist DW, Taylor C, Reynolds JE III (2013) Winter Habitat Preferences for Florida Manatees and Vulnerability to Cold. PLoS ONE 8(3): e58978

<http://doi.org/10.1371/journal.pone.0058978>

Why data publishing is a useful metaphor



Vines TH *et al.* (2013) *Current Biology* DOI:10.1016/j.cub.2013.11.014

Data papers and data journals



nature publishing group 

SCIENTIFIC DATA

 CREDIT Credit for depositing & sharing your data	 REUSE Complete, curated & standardized descriptions enable the reuse of your data
 QUALITY Rigorous community-based peer review	 DISCOVERY Helping you find datasets relevant to your research
 OPEN Available to all through a Creative Commons license	 SERVICE Rapid peer review & publication

Review Criteria: Biodiversity Data Journal

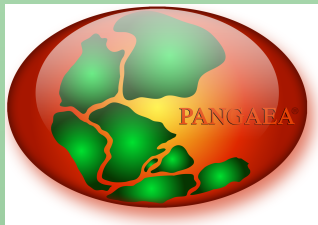
- Quality of the data
 - Are the data completely and consistently recorded within the dataset(s)?
 - Does the data resource cover scientifically important and sufficiently large region(s), time period(s) and/or group(s) of taxa to be worthy of publication?
 - Are the data consistent internally and described using applicable standards (e.g. in terms of file formats, file names, file size, units and metadata)?
 - Are the methods used to process and analyses the raw data, thereby creating processed data or analytical results, sufficiently well documented that they could be repeated by third parties?
 - Are the data correct, given the protocols? Authors are encouraged to report any tests undertaken to address this point.
 - Is the repository to which the data are submitted appropriate for the nature of the data?
- Consistency between manuscript and data
 - Does the manuscript provide an accurate description of the data?
 - Does the manuscript properly describe how to access the data?
 - Are the methods used to generate the data (including calibration, code and suitable controls) described in sufficient detail?
 - Is the dataset sufficiently novel to merit publication?
 - Have possible sources of error been appropriately addressed in the protocols and/ or the paper?
 - Is anything missing in the manuscript or the data resource itself that would prevent replication of the measurements, or reproduction of the figures or other representations of the data?
 - Are all claims made in the manuscript substantiated by the underlying data?



zenodo



Ainsley Seago



And many others

Joint Data Archiving Policy (JDAP)

Data are important products of the scientific enterprise, and they should be **preserved** and **usable** for decades in the future.

As a condition for publication, data supporting the results in the article should be deposited in an **appropriate public archive**.

Authors may elect to **embargo** access to the data for a period up to a year after publication.

Exceptions may be granted at the discretion of the editor, especially for sensitive information.

<http://datadryad.org/pages/jdap>

Effects of JDAP since 2011

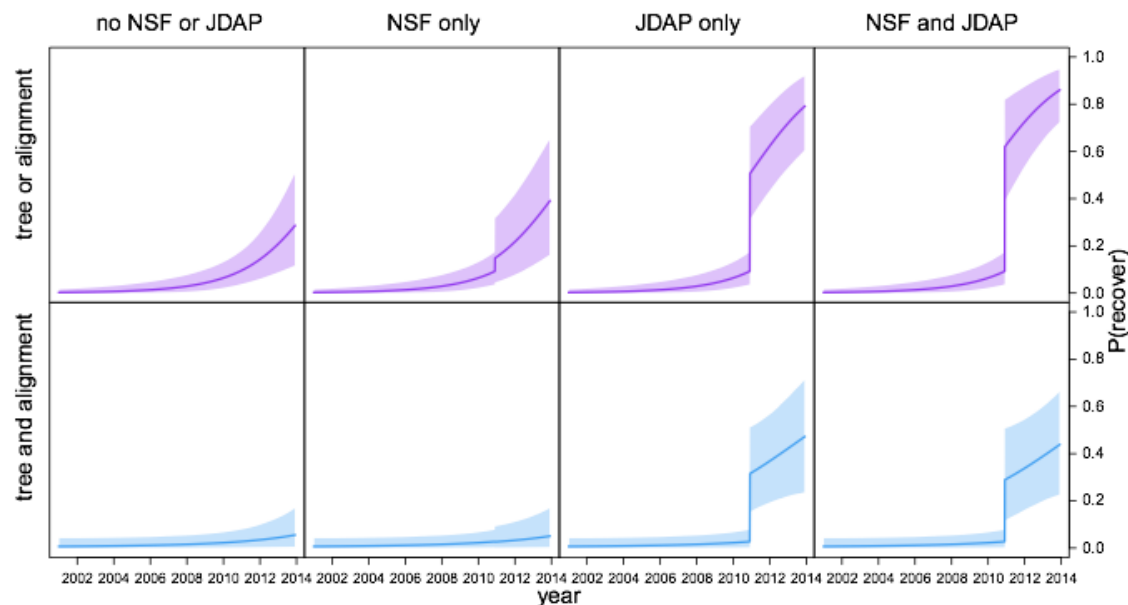


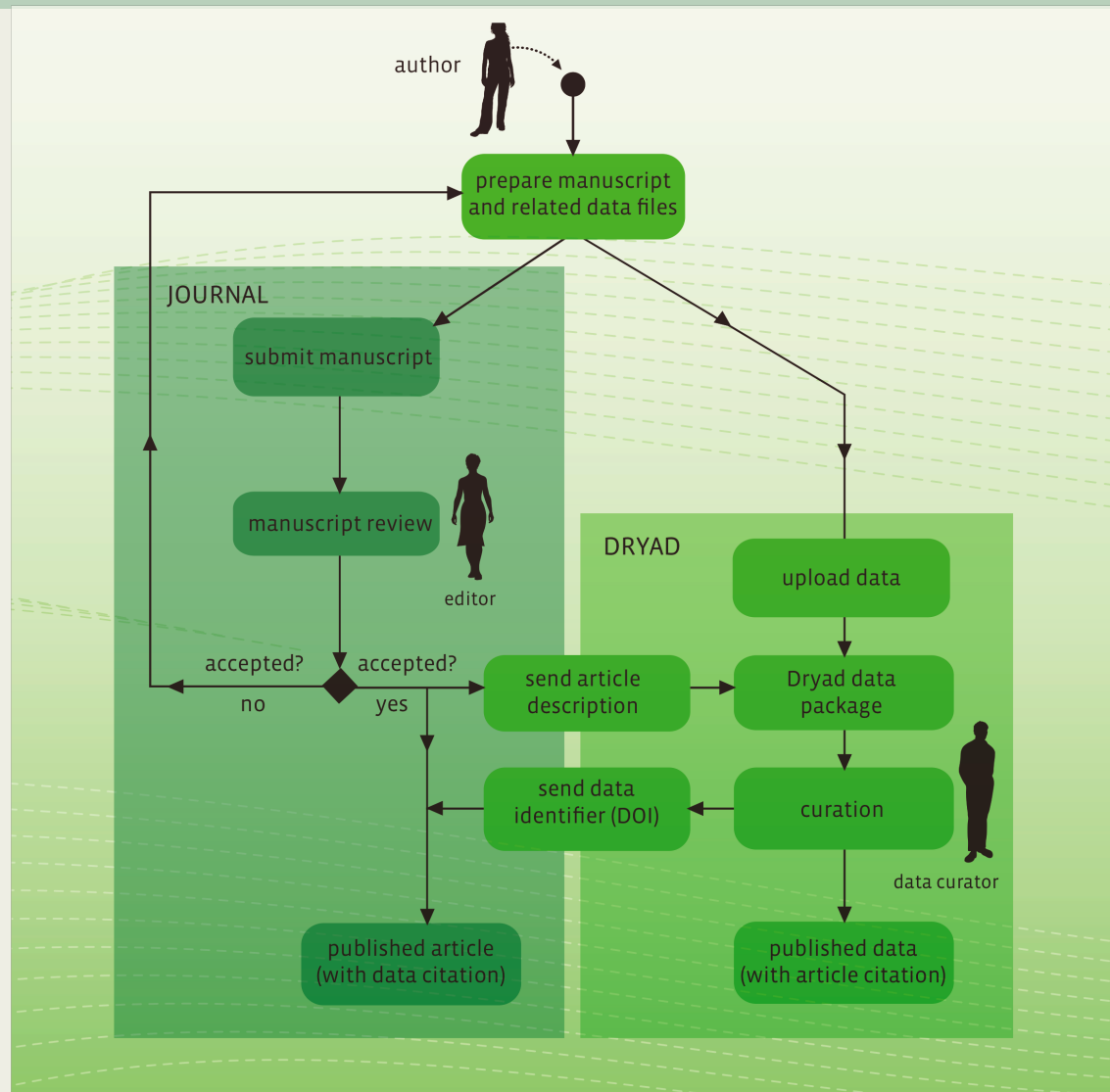
Figure 5. Availability of archived phylogenetic data as a function of age. We estimated the effect of publication age on our ability to procure partial (top panels) and complete (bottom panels) phylogenetic datasets from online archives. Overall, the probability of recovering archived phylogenetic data increases toward the present, with a conspicuous recent increase for partial datasets (left panels). The recent surge of archived phylogenetic data likely reflects recent policy changes (middle panels): studies with NSF funding are more likely to archive alignment (but not tree) files (*c.f.*, Table [S.14](#)); whereas studies published in journals with JDAP membership are dramatically more likely to archive both partial and complete phylogenetic datasets. The effects of these policy initiatives are not strictly additive (right panels): the correlation of these predictor variables suggests that studies published in JDAP journals are likely to have NSF funding. Shaded areas reflect the 95% credible intervals.

Magee *et al.* (2014) Dawn of open access to phylogenetic data. arXiv:14.1405.6623.v1

How does Dryad work?

The screenshot shows the Dryad website interface. At the top is the Dryad logo and navigation links: About, For researchers, For organizations, Contact us, Login, and Sign Up. Social media icons for Twitter, Facebook, and RSS are also present. A central banner features a four-step process: 1. DEPOSIT DATA (with a bar chart icon), 2. GET PERMANENT IDENTIFIER (with a rock icon), 3. WATCH YOUR CITATIONS GROW! (with a citation icon), and 4. RELAX, YOUR DATA ARE DISCOVERABLE AND SECURE (with a padlock icon). A URL <http://dx.doi.org/10.5061/dryad.20> is shown below the steps. To the right of the banner is a green button labeled 'Submit data now' and a link 'How and why?'. Below this is a search bar with the text 'Enter keyword, author, title, DOI, etc' and a 'Go' button, with a link for 'Advanced search'. The 'Browse for data' section has buttons for 'Recently published', 'Popular', 'By Author', and 'By Journal'. Under 'Recently Published Data', three entries are listed: Bryson RW, Savary WE, Prendini L (2013) Data from: Biogeography of scorpions in the Pseudouroctonus minimus complex (Vaejoidea) from south-western North America: implications of ecological specialization for pre-Quaternary diversification. *Journal of Biogeography* doi:10.5061/dryad.q58r0; Rouger R, Jump AS (2014) Data from: A seascape genetic analysis reveals strong biogeographical structuring driven by contrasting processes in the polyploid saltmarsh species Puccinellia maritima and Triglochin maritima. *Molecular Ecology* doi:10.5061/dryad.dc56n; and Sremba AL, Martin AR, Baker CS (2014) Data from: Species identification and likely catch time period of whale bones from South Georgia. *Marine Mammal Science*. To the right, the 'Be part of Dryad' section features an illustration of a tree with data boxes and text inviting publishers, societies, universities, libraries, funders, and other stakeholder organizations to become members. It describes an active knowledge-sharing network, discounts on submission fees, and the 'Submission integration' service, which allows publishers to coordinate manuscript and data submissions, making it easier for researchers to submit data and link articles to data, and enabling confidential review of

Submission integration of publications & data



Metadata exchange via submission systems

Journal Name: Molecular Ecology
Print ISSN: 0962-1083
Online ISSN: 1095-8312
Journal Admin Email: #
Journal Editor: Tim Vines
Journal Editor Email: #
Journal Embargo Period: 0

MS Reference Number: #
MS Dryad ID: #
MS Title: The coupling of endogenous genetic barriers with environmental variation: implications for interpreting loci with increased differentiation between habitats
MS Authors: Bierne, Nicolas; Welch, John; Loire, Etienne; Bonhomme, Francois; David, Patrice

Contact Author: Nicolas Bierne
Contact Author Email: #

Contact Author Address: #
Contact Author City: #
Contact Author State: #|
Contact Author Country: #
Contact Author ZIP/Postal Code: #



Keywords: Adaptation, Ecological Genetics, Evolutionary Theory, Hybridization, Natural Selection, Population Genetics

Abstract: Genomic scans often reveal marker loci with greatly increased differentiation between populations. Often this differentiation coincides in space with contrasts in ecological factors, forming a genetic-environment association (GEA). GEAs imply a role for local adaptation, and so it is tempting to conclude that the strongly differentiated markers are themselves under ecologically-based divergent selection, or are closely linked to loci under such selection. Here, we highlight an alternative and neglected explanation: intrinsic genetic incompatibilities rather than local adaptation can be responsible for increased differentiation. Intrinsic genetic incompatibilities create tension zones whose location can shift over time. However, tension zones have a tendency to become trapped by exogenous barriers due to ecological selection. This coupling of endogenous and exogenous barriers can occur easily, even if the loci involved are unlinked. We show that (i) the coupling of endogenous and exogenous barriers can easily occur even when ecological selection is weak; (ii) when environmental heterogeneity is fine-grained, GEAs can emerge at incompatibility loci, but only locally, in places where habitats and gene pools are sufficiently intermingled to maintain linkage disequilibria between genetic incompatibilities, local-adaptation genes and neutral loci. Furthermore, the sign of linkage disequilibrium between the locally adapted and intrinsically incompatible alleles is arbitrary. Reviewing results from the literature, we find that many predictions of our model are supported, including endogenous genetic barriers that coincide with environmental boundaries, local GEA in mosaic hybrid zones, and inverted or modified GEAs at distant locations.

Data from: Towards a worldwide wood economics spectrum



Files in this package

Content in the Dryad Digital Repository is offered "as is." By downloading files, you agree to the [Dryad Terms of Service](#). To the extent possible under law, the authors have waived all copyright and related or neighboring rights to this data.  

Title	Global Wood Density Database
Downloaded	7318 times
Description	Please direct all correspondence to G. Lopez-Gonzalez <G.Lopez-Gonzalez@leeds.ac.uk>
Download	GlobalWoodDensityDatabase.xls (2.047Mb)
Details	View File Details

When using this data, please cite the original article:

Chave J, Coomes DA, Jansen S, Lewis SL, Swenson NG, Zanne AE (2009) Towards a worldwide wood economics spectrum. *Ecology Letters* 12(4): 351-366. [doi:10.1111/j.1461-0248.2009.01285.x](https://doi.org/10.1111/j.1461-0248.2009.01285.x)

Additionally, please cite the Dryad data package:

Zanne AE, Lopez-Gonzalez G, Coomes DA, Ilic J, Jansen S, Lewis SL, Miller RB, Swenson NG, Wiemann MC, Chave J (2009) Data from: Towards a worldwide wood economics spectrum. Dryad Digital Repository. [doi:10.5061/dryad.234](https://doi.org/10.5061/dryad.234)

Bidirectional linkage with publications

The screenshot shows the ScienceDirect interface for the journal *Molecular Phylogenetics and Evolution*, Volume 28, Issue 2, August 2003, Pages 261–275. The article title is "Molecular systematics of armadillos (Xenarthra, Dasypodidae): contribution of maximum likelihood and Bayesian analyses of mitochondrial and nuclear genes" by Frédéric Delsuc^a, Michael J Stanhope^b, and Emmanuel J.P Douzery^a. The article is available for purchase at \$39.95. A yellow box highlights the "Data for this Article" section, which states: "Data for this article is available at the following data repositories: Data in DRYAD". The interface includes navigation links (Home, Publications, Search, My settings, My alerts, Shopping cart), a search bar, and a sidebar with a table of contents and a "Share" section with "citeulike", "Like", and "Tweet" buttons.

Linkouts from PubMed, Genbank

The image shows two overlapping web browser windows. The top window is the PubMed abstract page for a paper titled "Comparative phylogeography, genetic differentiation and contrasting reproductive modes in three fungal symbionts of a multipartite bark beetle symbiosis." The bottom window is the GenBank record for the sequence HQ413650.1, which is a partial sequence of the 5.8S ribosomal RNA gene and internal transcribed spacer 2 of *Ophiostoma montium* isolate ss547. A yellow box highlights the "Other Literature Sources" section in the PubMed sidebar, which includes links to "Dryad Digital Repository" and "Labome Researcher Resources". Another yellow box highlights the "LinkOut to external resources" section in the GenBank sidebar, which includes links to "SILVA LSU Database" and "Dryad Digital Repository".

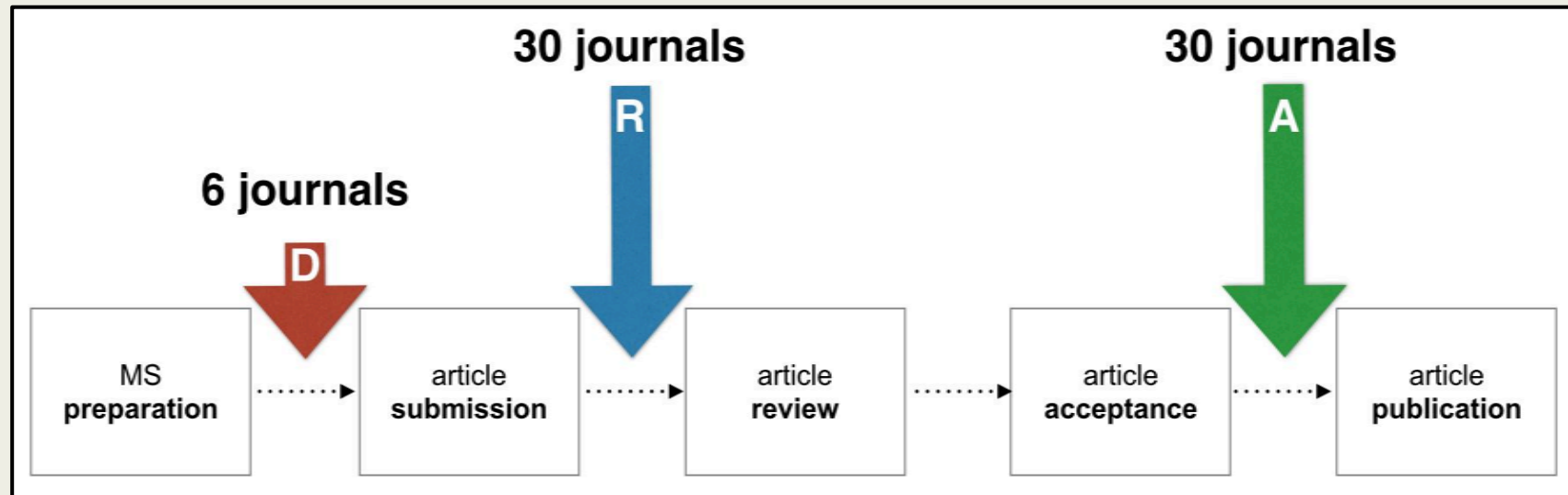
PubMed Abstract:
Mol Ecol. 2011 Feb;20(3):584-600. doi: 10.1111/j.1365-294X.2010.04953.x. Epub 2010 Dec 16.
Comparative phylogeography, genetic differentiation and contrasting reproductive modes in three fungal symbionts of a multipartite bark beetle symbiosis.
Roe AD, Rice AV, Coltman DW, Cooke JE, Sperling FA.
Department of Biological Sciences, University of Alberta, Edmonton, AB, Canada. amandaro5@gmail.com

Abstract:
Multipartite symbioses are complex symbiotic relationships involving multiple interacting partners. These types of partnerships provide excellent opportunities in which to apply a comparative approach to identify common historical patterns of population differentiation and species-specific life history traits. Using three symbiotic blue-stain fungal species (Ophiostomataceae) associated with outbreaking populations of the mountain pine beetle (*Dendroctonus ponderosae* Hopkins) in western Canada, we applied phylogenetic, population genetic and demographic approaches to clarify phylogeographic patterns among the three fungal species in northern and southern populations, despite dramatic differences in their life histories. The patterns were generally consistent, showing some interspecific incongruence in their recombination rate and ecological traits that could be related to their approach to partners of a multipartite symbiosis. These results help us to understand the complexity and evolution of multipartite symbioses.

© 2010 Blackwell Publishing Ltd.
PMID: 21166729 [PubMed - indexed for MEDLINE]

GenBank Record:
Nucleotide
Display Settings: GenBank
Ophiostoma montium isolate ss547 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence
GenBank: HQ413650.1
FASTA Graphics PopSet
Go to:
LOCUS HQ413650 918 bp DNA linear PLN 20-JAN-2011
DEFINITION Ophiostoma montium isolate ss547 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
ACCESSION HQ413650
VERSION HQ413650.1 GI:316925971
KEYWORDS .
SOURCE Ophiostoma montium
ORGANISM Ophiostoma montium
Eukaryota; Fungi; Dikarya; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
REFERENCE 1 (bases 1 to 918)
AUTHORS Roe,A.D., Rice,A.V., Coltman,D.W., Cooke,J.E. and Sperling,F.A.
TITLE Comparative phylogeography, genetic differentiation and contrasting reproductive modes in three fungal symbionts of a multipartite bark beetle symbiosis
JOURNAL Mol. Ecol. 20 (3), 584-600 (2011)
PUBMED 21166729
REFERENCE 2 (bases 1 to 918)
AUTHORS Roe,A.D., Rice,A.V., Coltman,D.W., Cooke,J.E.K. and Sperling,F.A.H.
TITLE Direct Submission

When to submit data?



Over 60 integrated journals, ~3/4 sponsored

Integrated Journals and Costs for Submitters

Show all amounts in USD\$

All journals with either [integrated data submission](#) or sponsored [Data Publishing Charges](#) are listed below. Note that for large data packages, submitters will be asked to pay an additional \$15 for the first GB beyond 10GB and \$10 for each GB thereafter.

Journal	Submission				Payment
	Integrated	Submit: R: Prior to Review A: On Acceptance	Data embargo allowed	Metadata hidden until publication	
<i>If your journal is not listed below...</i>	<i>N</i>	<i>A</i>	<i>Y</i>	<i>Y</i>	<i>\$90</i>
American Naturalist, The	Y	A	Y	N	American Society of Naturalists
Biodiversity Data Journal	N	A	Y	Y	Pensoft
Biological Journal of the Linnean Society	Y	A	Y	N	\$80
Biology Letters	Y	A	Y	Y	The Royal Society
BioRisk	Y	R	Y	N	Pensoft
BMJ Open	Y	R	N	N	\$80
Comparative Cytogenetics	Y	R	Y	N	Pensoft

Also books, theses, other vetted publications

40 Years of Data

2014/04/03 by Peggy Schaeffer | Edit

Odd couples in the animal kingdom, but not in a data repository

2013/04/30 by Peggy Schaeffer | Edit

We are celebrating the recent publication in Dryad of the first data to accompany a book [1, 2]. [Odd Couples: Extraordinary Differences Between the Sexes in the Animal Kingdom](#), from Princeton University Press, examines the occasionally surprising gender differences in animals, and what it means to be male or female in the animal kingdom. It is intended for both general and scientific readers.



A dominant male northern elephant seal attempts to copulate with a female. Photo by Derek Roff, courtesy Princeton Univ. Press.



A mature female *Argiope aurantia* (left) hanging at the hub of her orb web, with a mature male (right). Photo by Troy Bartlett, <http://www.naturecloseups.com>, courtesy Princeton Univ Press.

availability of the data underlying the book "40

Primary Grant.

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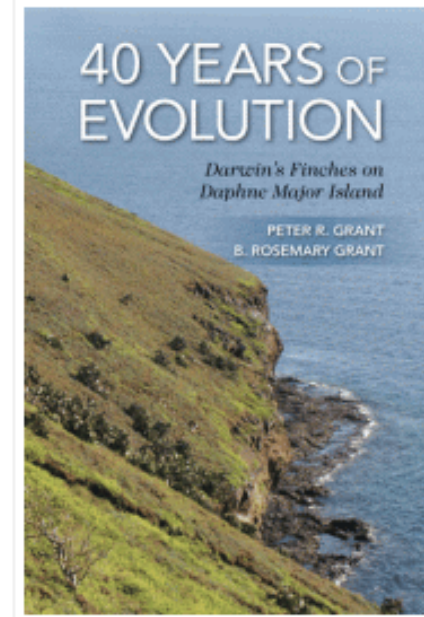
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Dryad is not just for tabular data I

Tamiflu, Relenza, and influenza: what the data do (or don't) tell us

2014/04/17 by tjvision | Edit

Business Pharmaceuticals industry

What the Tamiflu saga tells us about drug trials and big pharma

We now know the government's Tamiflu stockpile wouldn't have done us much good in the event of a flu epidemic. But the secrecy surrounding clinical trials means there's a lot we don't know about other medicines we take

Neuraminidase inhibitors for preventing and treating influenza in healthy adults and children

Tom Jefferson¹, Mark A Jones², Peter Doshi³, Chris B Del Mar⁴, Rokuro Hama⁵, Matthew J Thompson⁶, Elizabeth A Spencer⁷, Igho Onakpoya⁸, Kamal R Mahtani⁸, David Nunan⁸, Jeremy Howick⁹, Carl J Heneghan⁸

¹The Cochrane Collaboration, Roma, Italy. ²School of Population Health, The University of Queensland, Brisbane, Australia. ³Department of Pharmaceutical Health Services Research, University of Maryland School of Pharmacy, Baltimore, Maryland, USA. ⁴Centre for Research in Evidence-Based Practice (CREBP), Bond University, Gold Coast, Australia. ⁵Japan Institute of Pharmacovigilance, Osaka, Japan. ⁶Department of Family Medicine, University of Washington, Seattle, WA, USA. ⁷Department of Primary Care Health Sciences, University of Oxford, Oxford, UK. ⁸Nuffield Department of Primary Care Health Sciences, University of Oxford, Oxford, UK. ⁹Centre for Evidence-Based Medicine, University of Oxford, Oxford, UK

Contact address: Tom Jefferson, The Cochrane Collaboration, Via Puglie 23, Roma, 00187, Italy. jefferson.tom@gmail.com. jefferson@assr.it.

Editorial group: Cochrane Acute Respiratory Infections Group.

Publication status and date: New search for studies and content updated (conclusions changed), published in Issue 4, 2014.

Review content assessed as up-to-date: 22 July 2013.

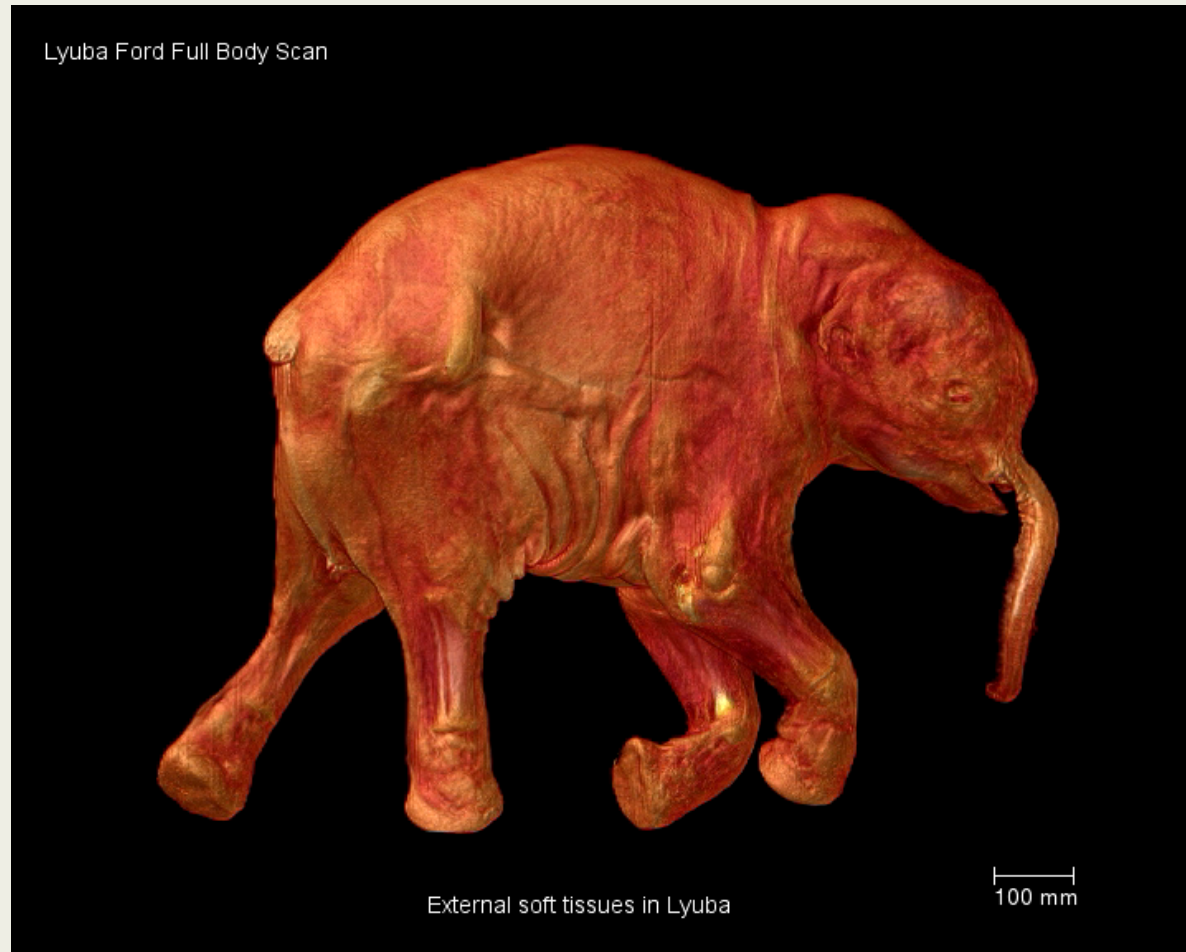
Citation: Jefferson T, Jones MA, Doshi P, Del Mar CB, Hama R, Thompson MJ, Spencer EA, Onakpoya I, Mahtani KR, Nunan D, Howick J, Heneghan CJ. Neuraminidase inhibitors for preventing and treating influenza in healthy adults and children. *Cochrane Database of Systematic Reviews* 2014, Issue 4. Art. No.: CD008965. DOI: 10.1002/14651858.CD008965.pub4.

...on of The Cochrane Collaboration,
Carl Heneghan from the University
...and their recent Cochrane
...which holds valuable lessons
...c health recommendations are

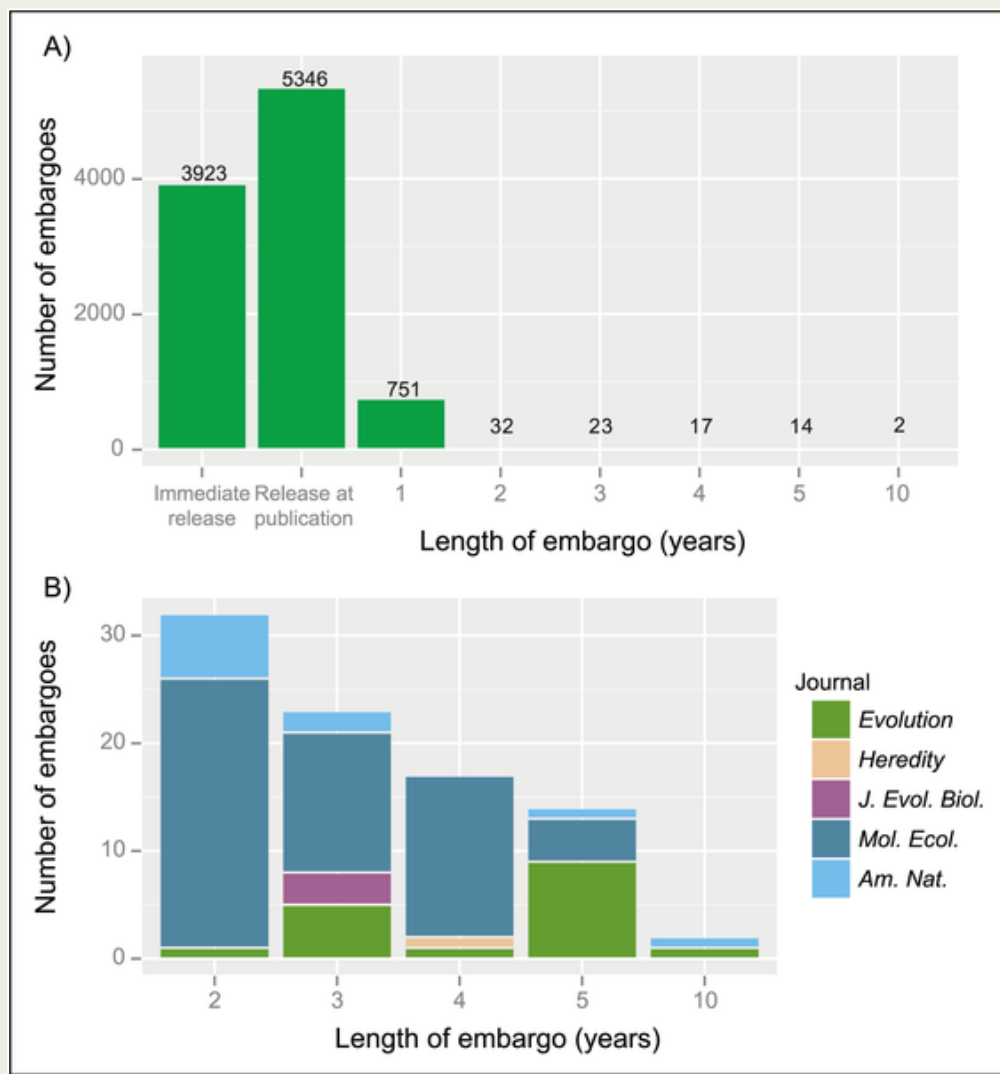


...down viral spread giving time for

Dryad is not just for tabular data II



Embargoes are the exception, not the rule



A. Embargo selections of Dryad data authors for the 10,108 files in Dryad deposited from inception to September 20, 2013. Data include only datasets related to articles published in journals for which the authors had the option of selecting an embargo.

B. Long-term embargoes (>1 year) by journal that granted them.

Data: Vision TJ, Scherle R, Mannheimer S (2013) Embargo selections of Dryad data authors. FigShare. <http://doi.org/10.6084/m9.figshare.805946>.

Article: Roche DG, Lanfear R, Binning SA, Haff TM, et al. (2014) Troubleshooting Public Data Archiving: Suggestions to Increase Participation. PLoS Biol 12(1): e1001779

ReadMe files

- One per data package or one per file
- Recommendations
 - Plain text
 - For each filename, a short description of contents
 - For tabular data: definitions of column headings and row labels; data codes (including missing data); and measurement units
 - Data processing steps not described elsewhere that may affect interpretation of results
 - What if any associated datasets are stored elsewhere
 - Whom to contact with questions
- Côrtes *et al.* <http://dx.doi.org/10.5061/dryad.b003f>

Example: Review a data package

- Corrêa Côrtes M, Uriarte M, Lemes MR, Gribel R, Kress WJ, Smouse PE, Bruna EM (2013) Data from: Low plant density enhances gene dispersal in the Amazonian understory herb *Heliconia acuminata*. Dryad Digital Repository.

<http://dx.doi.org/10.5061/dryad.b003f>

Giving credit for data: citation

Ecological Monographs, 82(2), 2012, pp. 221–228
© 2012 by the Ecological Society of America

Novel forests maintain ecosystem processes after the decline of native tree species

JOSEPH MASCARO,^{1,4} R. FLINT HUGHES,² AND STEFAN A. SCHNITZER^{1,3}

¹*Department of Biological Sciences, University of Wisconsin, Milwaukee, Wisconsin 53211 USA*

²*Institute for Pacific Islands Forestry, USDA Forest Service, Hilo, Hawaii 96720 USA*

³*Smithsonian Tropical Research Institute, Apartado 2072, Balboa, Republic of Panama*

Abstract. The positive relationship between species diversity (richness and evenness) and critical ecosystem functions, such as productivity, carbon storage, and nutrient cycling, is often used to predict the consequences of extinction. At regional scales, however, plant species richness is mostly increasing rather than decreasing because successful plant species introductions far outnumber extinctions. If these regional increases in richness lead to local

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Taking credit for data I

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Sharma J., Thomas W.K. (2012) Dramatic Shifts in Benthic Microbial Eukaryote Communities following the Deepwater Horizon Oil Spill. *PLoS ONE*, 7(6):e38550. <http://dx.plos.org/10.1371/journal.pone.0038550> Data available at 

Taking credit for data II



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Keywords: plant biology, genome evolution, bioinformatics, scholarly communication

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Genome-scale phylogenetics: Inferring the plant tree of life from 18,896 gene trees: Systematic Biology 2011

DOI: [10.1093/sysbio/syq072](https://doi.org/10.1093/sysbio/syq072)

<http://www.scopus.com/inward/record.url?eid=2-s2.0-79951569533&partnerID=MN8TOARS>

Burleigh, J.G. and Bansal, M.S. and Eulenstein, O. and Hartmann, S. and Wehe, A. and Vision, T.J., (2011). "Genome-scale phylogenetics: Inferring the plant tree of life from 18,896 gene trees", Systematic Biology, vol. 60, no. 2, pp. 117-125

Data from: Genome-scale phylogenetics: inferring the plant tree of life from 18,896 gene trees 2010

DOI: [10.5061/DRYAD.7881](https://doi.org/10.5061/DRYAD.7881)

Burleigh, J. Gordon; Bansal, Mukul S.; Eulenstein, Oliver; Hartmann, Stefanie; Wehe, André; Vision, Todd J.; , (2010). "Data from: Genome-scale phylogenetics: inferring the plant tree of life from 18,896 gene trees"



Tracking data citation and reuse I

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Data from: Crossing the divide: gene flow produces intergeneric hybrid in feral transgenic creeping bentgrass population.

From Repository: [Dryad](#).
By: Zapiola, Maria L; Mallory-Smith, Carol A

Dryad
DOI: <http://dx.doi.org.libproxy.lib.unc.edu/10.5061/dryad.kg521>
Viewed Date: 24 Oct 2012
Published: 2012

Abstract
Gene flow is the most frequently expressed public concern related to the deregulation of transgenic events (Snow 2002; Ellstrand 2003). However, assessing the potential for transgene escape is complex because it depends on the opportunities for unintended gene flow, and establishment and persistence of the transgene in the environment (Warwick et al. 2008). Creeping bentgrass (*Agrostis stolonifera* L.), a turfgrass species widely used on golf courses, has been genetically engineered to be resistant to glyphosate, a nonselective herbicide. Outcrossing species, such as creeping bentgrass (CB), which have several compatible species, have greater chances for gene escape and spontaneous hybridization (i.e. natural, unassisted sexual reproduction between taxa in the field), which challenges transgene containment. Several authors have emphasized the need for evidence of

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Tracking data citation and reuse II

ImpactStory.

Emilio M. Bruna

Overview

Map

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8 Datasets

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Welcome to the Canadian Healthy Oceans Network website!

The Canadian Healthy Oceans Network, or **CHONE** (pronounced Ko-nee), is an NSERC strategic network focused on biodiversity science for the sustainability of Canada's three oceans. CHONE, a marine worm that occurs in all of Canada's three oceans is the equivalent of the canary in the coal mine: it indicates a healthy benthic habitat.



The network includes about 150 researchers from 14 universities across Canada, the federal Department of Fisheries and Oceans, and seven other government laboratories, to carry out thirty-five collaborative research projects in three interconnected themes.



CHONE's research in Canada's three oceans: the Pacific, the Arctic and the Atlantic, showing Discovery Corridors in white. These locations are focal areas for biodiversity research.

Animal Without a Brain Can "Sneeze," Surprising Study Shows
Jan 15, 2014

CHONE's Dr. Verena Tunnicliffe to receive The Murray A. Newman Award
Dec 20, 2013

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Nov 29, 2013

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Example: Dryad submission

- Let's resubmit this one:
 - Corrêa Côrtes M, Uriarte M, Lemes MR, Gribel R, Kress WJ, Smouse PE, Bruna EM (2013) Data from: Low plant density enhances gene dispersal in the Amazonian understory herb *Heliconia acuminata*. Dryad Digital Repository. <http://dx.doi.org/10.5061/dryad.b003f>

Other resources: best practice docs

- Borer, ET *et al.* (2009) Some simple guidelines for effective data management. *Bulletin of the ESA* 48, 205-214
- Hook, LA *et al.* (2010) Best Practices for Preparing Environmental Data Sets to Share and Archive.
<http://daac.ornl.gov/PI/BestPractices-2010.pdf>
- Penev L *et al.* (2011) Pensoft Data Publishing Policies and Guidelines for Biodiversity Data.
http://www.pensoft.net/J_FILES/Pensoft_Data_Publishing_Policies_and_Guidelines.pdf
- Whitlock MC (2010) Data archiving in ecology and evolution: best practices *Trends in Ecology & Evolution* 26, 61-65.
- See also DataONE resources:
<http://www.dataone.org/best-practices>

Other resources: re3data.org



Integrated Digitized Biocollections

General **Institutions** Terms Standards

Name of repository	Integrated Digitized Biocollections
Additional name(s)	iDigBio
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Subject(s)	Life Sciences Biology
Description	The National Resource for Advancing Digitization of Biodiversity Collections (ADBC) funded by the National Science Foundation. Through ADBC, data and images for millions of biological specimens are being made available in electronic format for the research community, government agencies, students, educators, and the general public
Contact	https://www.idigbio.org/contact
Content type(s)	Audiovisual data Images
Keyword(s)	biodiversity evolution paleontology
Repository size	23.925.716 Specimen Records; 3.419.648 Media Records; 348 Recordsets
Repository type(s)	disciplinary
Mission statement for designated community	https://www.idigbio.org/about/mission
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Type of data, sample, physical collection, software, collection materials, and other materials to be produced in the course of the project.

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- <https://dmptool.org/plans/8332.pdf>

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Questions?

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