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Todd Vision

Department of Biology, University of North Carolina at Chapel Hill

Founder, Dryad

STM Innovations Seminar

3 December 2014

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 THIRD TARSUS.	WIDTH OF SCUTL.	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	.683	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	26.0	32.2	.766	.751	1.2272	.620	.841
44 ♀	1653	245	27.7	33.12	.7801	.7573	1.195	.638	.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	.859
51 ♀	162	252	24.8	31.9	.732	.728	1.180	.613	.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	30.52	33.41	.767	.7671	1.2073	.6401	.896
56 ♀	163	242	24.8	31.	.713	.713	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	26.0	32.1	.751	.704	1.142	.607	.819
60 ♀	155	235	22.0	30.5	.687	.683	1.042	.587	.787
61 ♀	162	247	26.	31.7	.713	.713	1.128	.607	.813
62 ♀	1532	237	24.2	30.1	.6803	.6623	1.0423	.592	.781
63 ♀	162	245	26.2	31.8	.727	.700	1.129	.610	.855
64 ♀	164	248	26.	31.8	.727	.700	1.129	.610	.855
Average . .	158	241	25.	31.4	.713	.700	1.129	.610	.855
General average for 64 birds . . .	160	245	25.	31.4	.713	.700	1.129	.610	.855

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.

Data Volume

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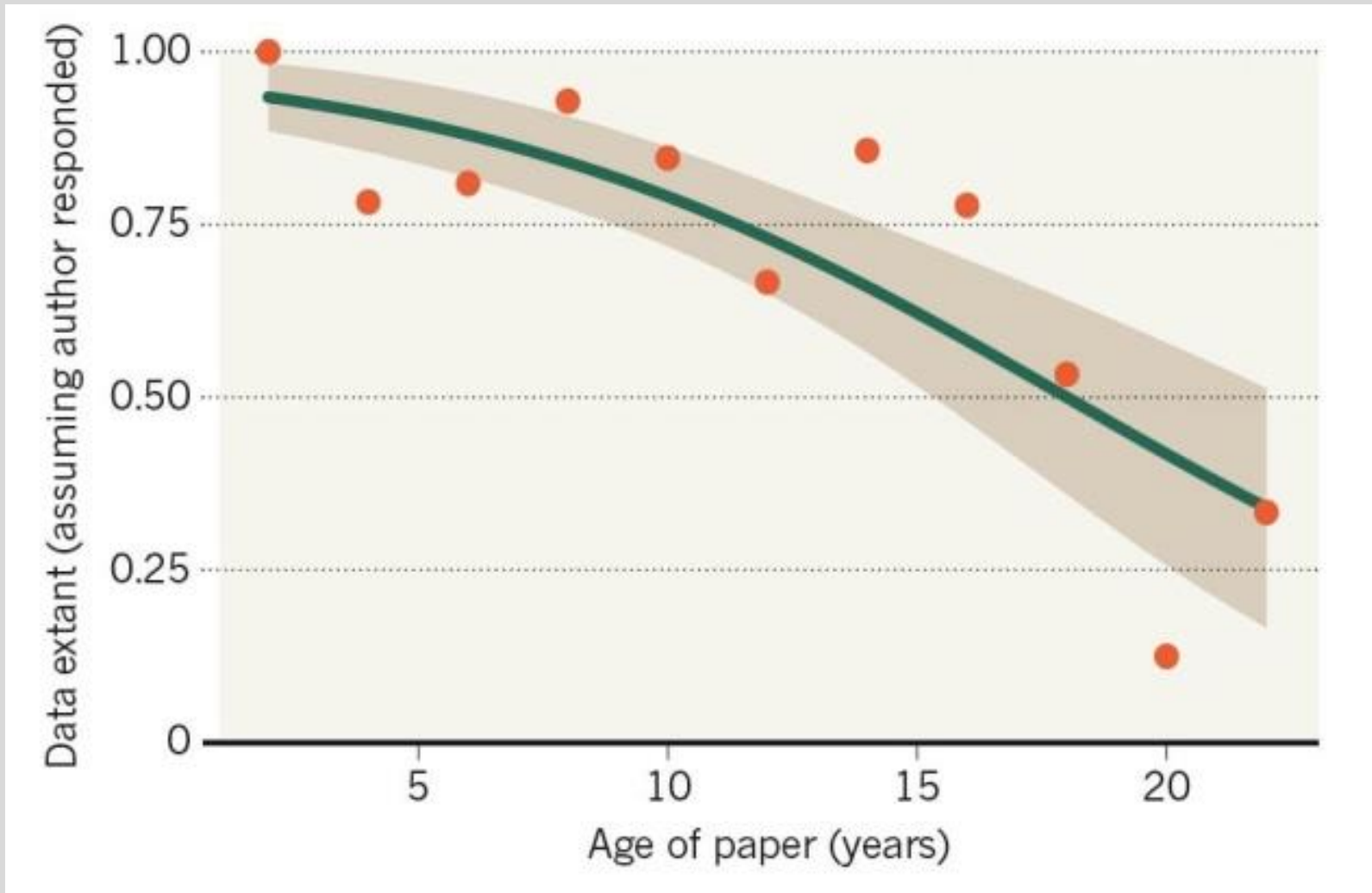
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computer science/engineering	36(31.9%)	41(36.3%)	68(58.6%)	32(27.6%)	40(34.5%)	36(31.0%)
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environmental sciences & ecology	199(42.4%)	210(44.8%)	331(70.4%)	109(23.2%)	196(41.7%)	192(40.9%)
atmospheric science	18(36.7%)	28(57.1%)	40(80.0%)	10(20.0%)	17(34.0%)	19(38.0%)
biology	73(40.6%)	65(36.1%)	134(74.4%)	31(17.2%)	82(45.3%)	53(29.3%)
medicine	4(13.3%)	17(56.7%)	17(56.7%)	9(30.0%)	9(30.0%)	8(26.7%)
Other	28(30.1%)	40(43.0%)	63(67.0%)	22(23.4%)	30(31.9%)	33(35.1%)

¹ $\chi^2 = 71.679, p = .000;$

² $\chi^2 = 41.985, p = .044;$

³ $\chi^2 = 43.649, p = .030.$

doi:10.1371/journal.pone.0021101.t020

Tenopir C *et al.* (2011) Data Sharing by [$n=1329$] Scientists: Practices and Perceptions. PLoS ONE doi:10.1371/journal.pone.0021101

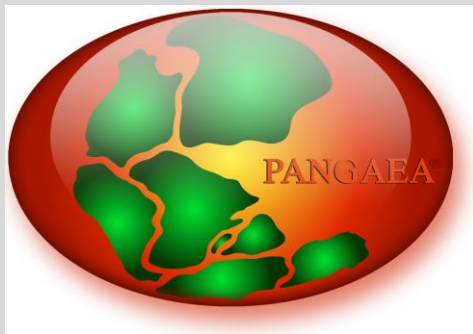
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Whitlock, M. C., M. A. McPeck, M. D. Rausher, L. Rieseberg, and A. J. Moore. 2010. Data Archiving. *American Naturalist*. 175(2):145-146.



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(GIGA)ⁿ DB



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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

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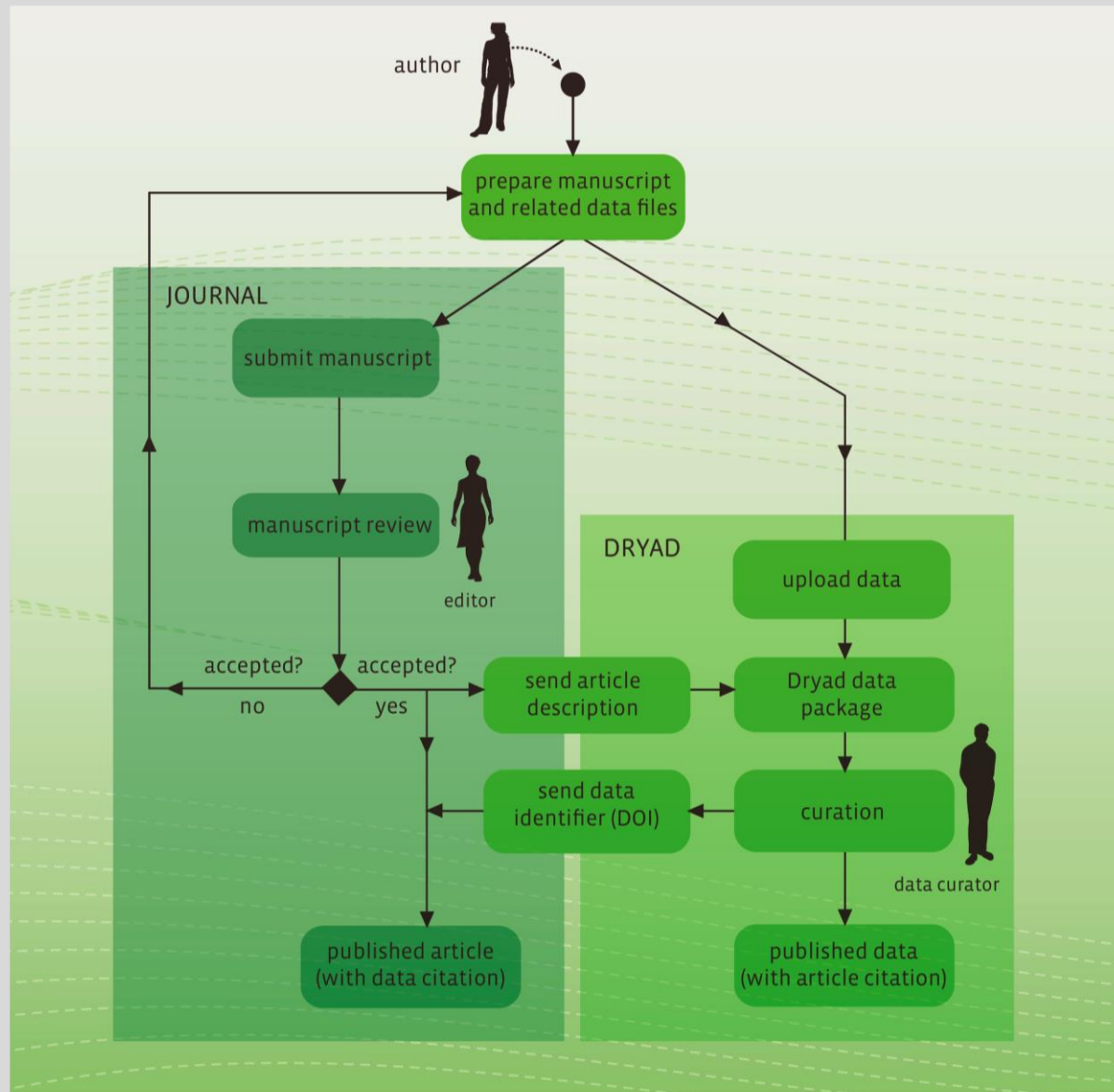
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Novel forests maintain ecosystem processes after the decline of native tree species

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³Smithsonian 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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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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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 

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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) 

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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"



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African Journal of Herpetology
 Volume 63, Issue 1, 2014

Differentiation within the endemic burrowing skink *Pamelaescincus gardineri*, across the Seychelles Islands, assessed by mitochondrial and nuclear markers

DOI: 10.1080/21564574.2013.856354
 Joana Valente¹, Sara Rocha² & D. James Harris³
 pages 25-33

Abstract

Unravelling patterns of genetic differentiation across insular distributions is relevant for biogeographic and conservation reasons. In the Indian Ocean, surprisingly, little is known regarding the genetic structure of many taxa across the Seychelles Islands, despite their importance as old Gondwanan islands, part of the western Indian Ocean biodiversity hotspot. In recent molecular studies, a northern–southwestern subdivision pattern across the granitic islands has been uncovered within some species. *Pamelaescincus gardineri*, a Seychelles endemic skink and possibly one of the deepest lineages of Afro-Malagasy ‘scincoides’, is another species widespread across these islands, within which undescribed variation may occur. Both nuclear (b-mos and MCLR) and mitochondrial (Cyt-b) DNA data were used to address this issue. Mitochondrial DNA shows a marked northeastern–southwestern structure of two highly divergent clades, similar to the pattern previously described in other reptile species. Nuclear DNA seems to corroborate this pattern, although these markers were much less informative. No gene flow between the two island groups was identified, and gene flow between the two mtDNA lineages is likely, the extent of which remains to be fully explored. This will require more variable nuclear markers and more detailed sampling across the island of Mahé. A suitable assessment of morphological variation is also needed prior to any taxonomic revision of this species. From a conservation point of view, however, these lineages should already be treated as two distinct evolutionary units.

Key words
 Seychelles, phylogeography, Scincidae, *Pamelaescincus*, Cyt-b, MCLR, b-mos

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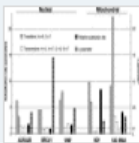
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Abstract

Keywords

- 1. Introduction
- 2. Materials and methods
 - 2.1. Taxon sampling and data acquisition
 - Table 1
 - 2.2. Sequence alignment
 - 2.3. Phylogenetic analyses
 - 2.3.1. Maximum likelihood
 - 2.3.2. Bayesian approach
 - 2.4. Statistical tests of alternative hypotheses

- 3. Results and discussion
 - 3.1. Evolutionary properties of the five genes



- 3.2. Phylogenetic results
 - 3.2.1. Results from



Molecular Phylogenetics and Evolution

Volume 28, Issue 2, August 2003, Pages 261–275



Molecular systematics of armadillos (*Xenarthra*, *Dasypodidae*): contribution of maximum likelihood and Bayesian analyses of mitochondrial and nuclear genes

Frédéric Delsuc^a, Michael J Stanhope^b, Emmanuel J.P Douzery^a

^a Laboratoire de Paléontologie, Paléobiologie et Phylogénie, Institut des Sciences de l'Evolution, Université Montpellier II, Montpellier, France

^b Queen's University of Belfast, Biology and Biochemistry, 97 Lisburn Road, Belfast BT9 7BL, UK

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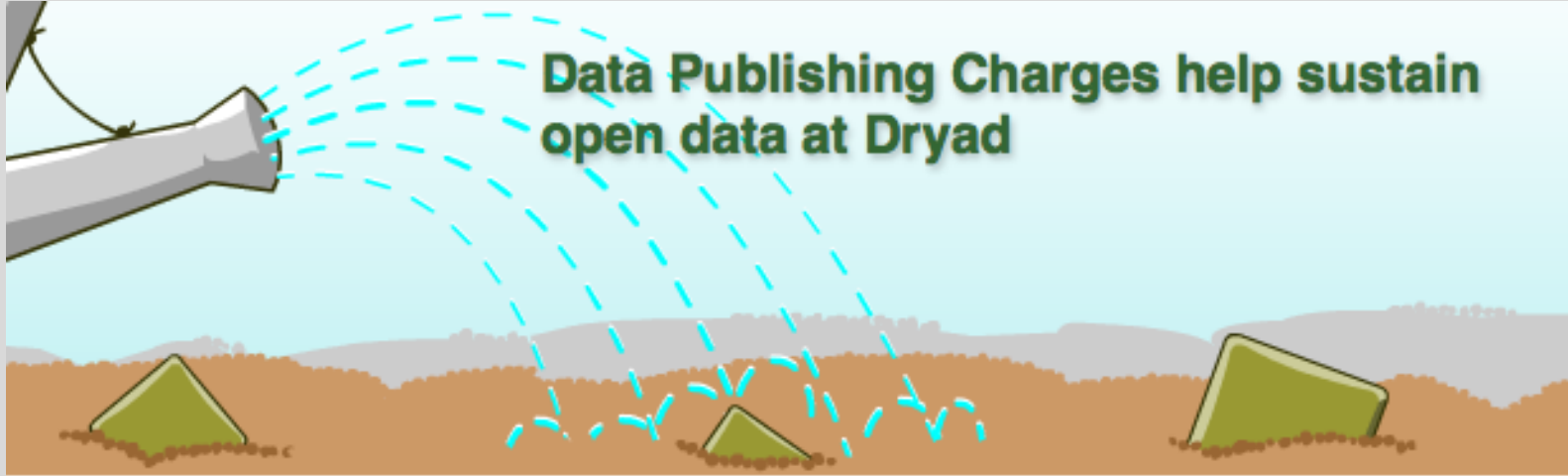
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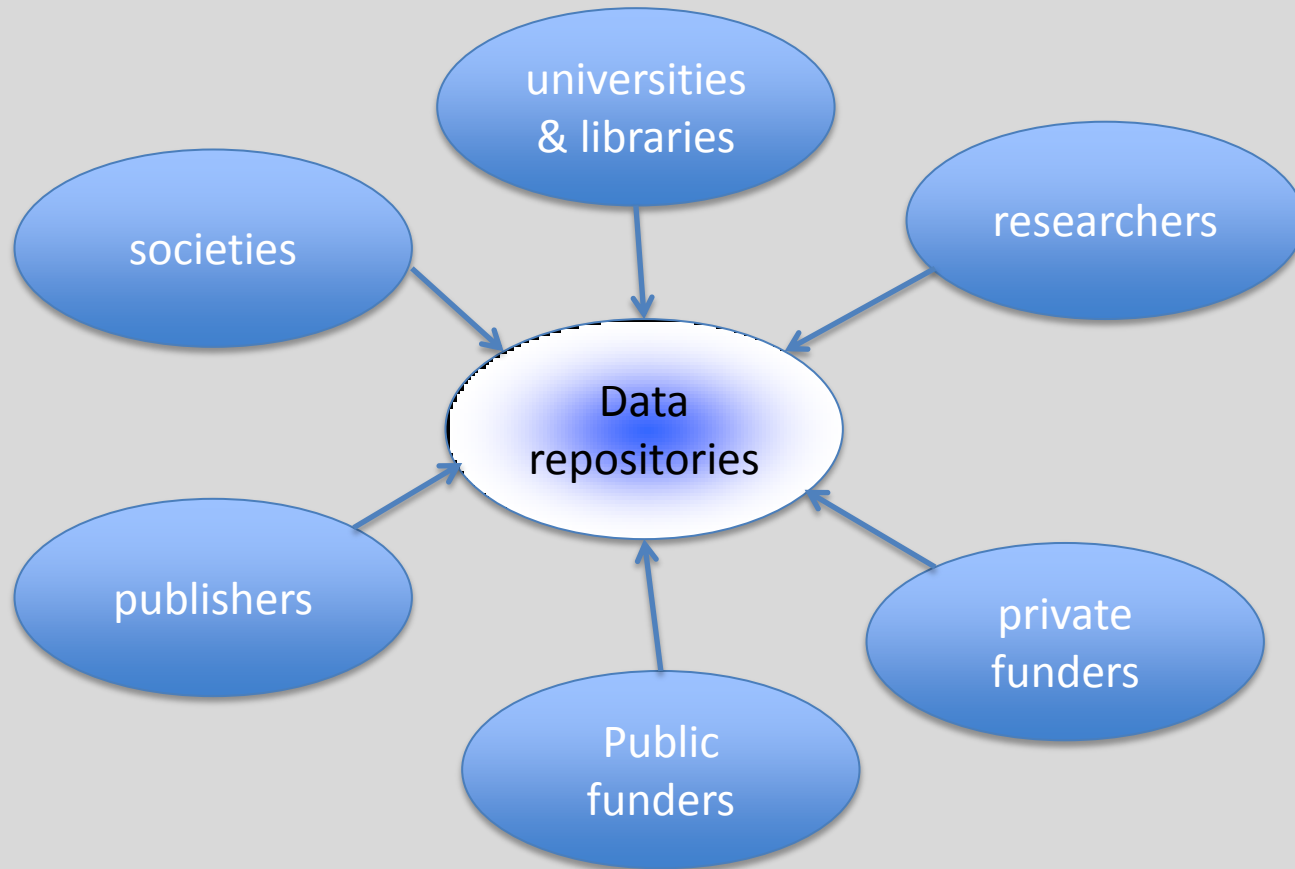


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MS Title: The coupling of endogenous genetic barriers with environmental variation: implications for interpreting loci with increased differentiation between habitats

MS Authors: Bierne, Nicolas; Welch, John; Loire, Etienne; Bonhomme, Francois; David, Patrice

Contact Author: Nicolas Bierne

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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.

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 Dancing together and separate again: gymnosperms exhibit frequent changes of fundamental 5S and 35S rRNA gene (rDNA) organisation.
(PMID:23512008)

Abstract 

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Garcia S, Kovařík A

Laboratori de Botànica, Facultat de Farmàcia, Universitat de Barcelona, Barcelona, Catalonia, Spain.

Heredity [2013, 111(1):23-33]

Type: Journal Article, Research Support, Non-U.S. Gov't

DOI: 10.1038/hdy.2013.11 

Abstract

In higher eukaryotes, the (S-type arrangement) or 18S-5.8S-26S genes (L-type sequencing approaches groups, including Conifer species (21 genera). The Coniferales and in Ginkgo organisation. The linked 5S embedded in the 26S-18S same (Ginkgo, Ephedra) addition, pseudogenised have been largely homologous. Comparison of 5S coding three times in the course basic units indicate relative genes in plants.



Dancing together and separate again: gymnosperms exhibit frequent changes of fundamental 5S and 35S rRNA gene (rDNA) organisation.
(PMID:23512008)

Abstract 

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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. amandaroo5@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 dispersal and consistent, showing some interspecific incoherence in recombination rate and ecological traits that do not support an approach to partners of a multipartite symbiosis. Our results help us to understand the complexity and evolution of multipartite symbioses.

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PMID: 21166729 [PubMed - indexed for MEDLINE]

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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
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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

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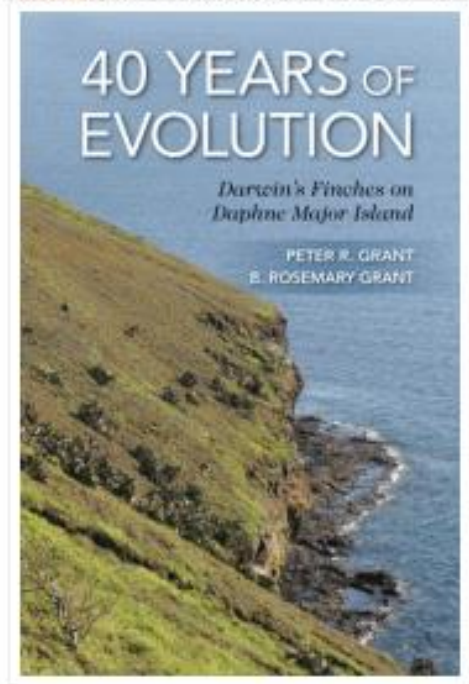
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Data from books & theses

40 Years of Data

2014/04/03 by Peggy Schaeffer | Edit

We are delighted to announce the availability of the data underlying the book "40 Years of Evolution" by Peter and Rosemary Grant.



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.

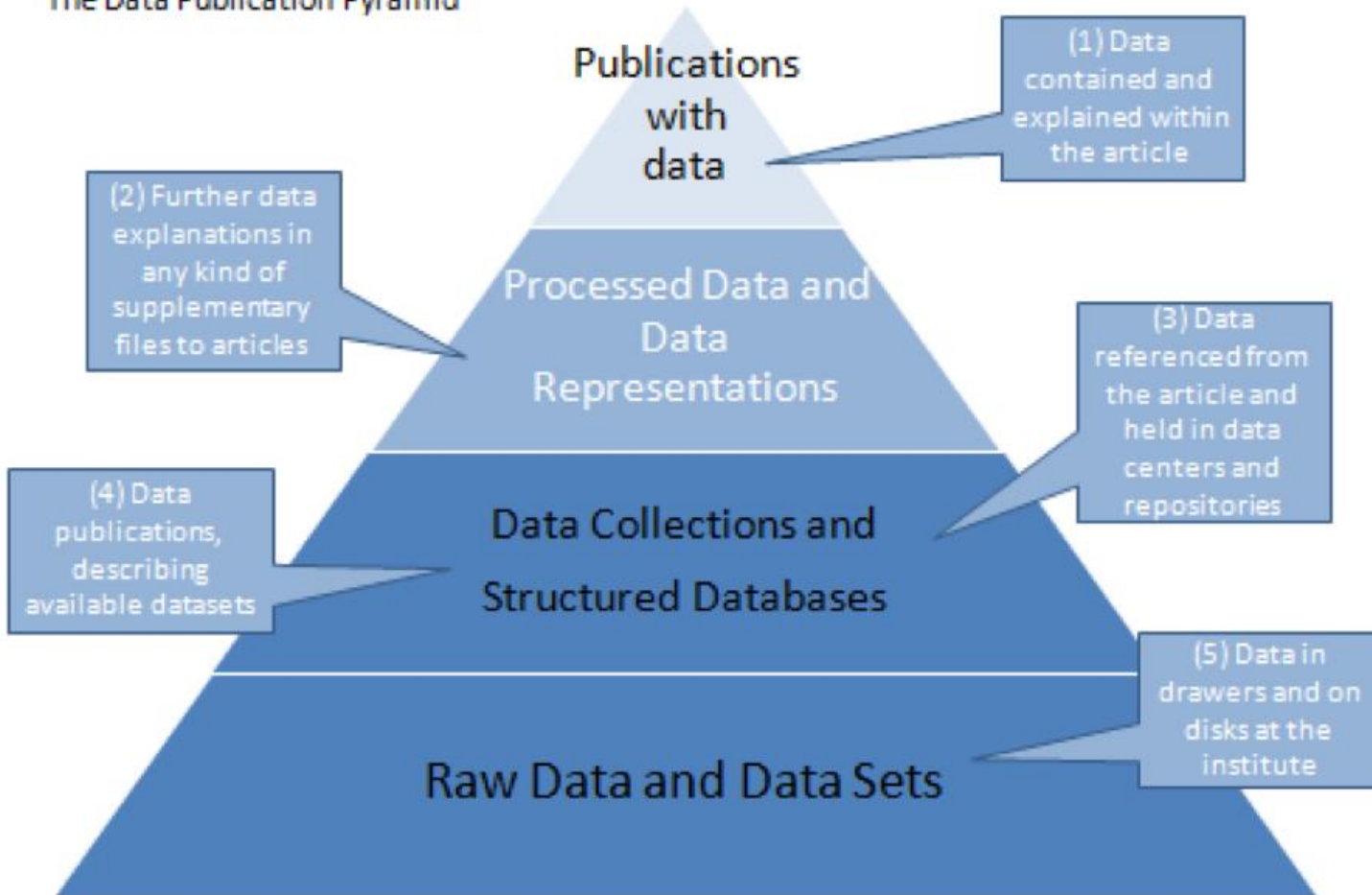


A dominant male northern elephant seal attempts to copulate with a female. Photo by Derek Roff, courtesy Princeton Univ. Press.



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.

The Data Publication Pyramid



23 April 2013, 6.40am AEST

The Reinhart-Rogoff error – or how not to Excel at economics



Data and computer code should be made publicly available at an early stage – or else ... esarastudillo

Last week we learned a famous [2010 academic paper](#), relied on by political big-hitters to bolster arguments for austerity cuts, contained significant errors; and that those errors came down to misuse of an Excel spreadsheet.

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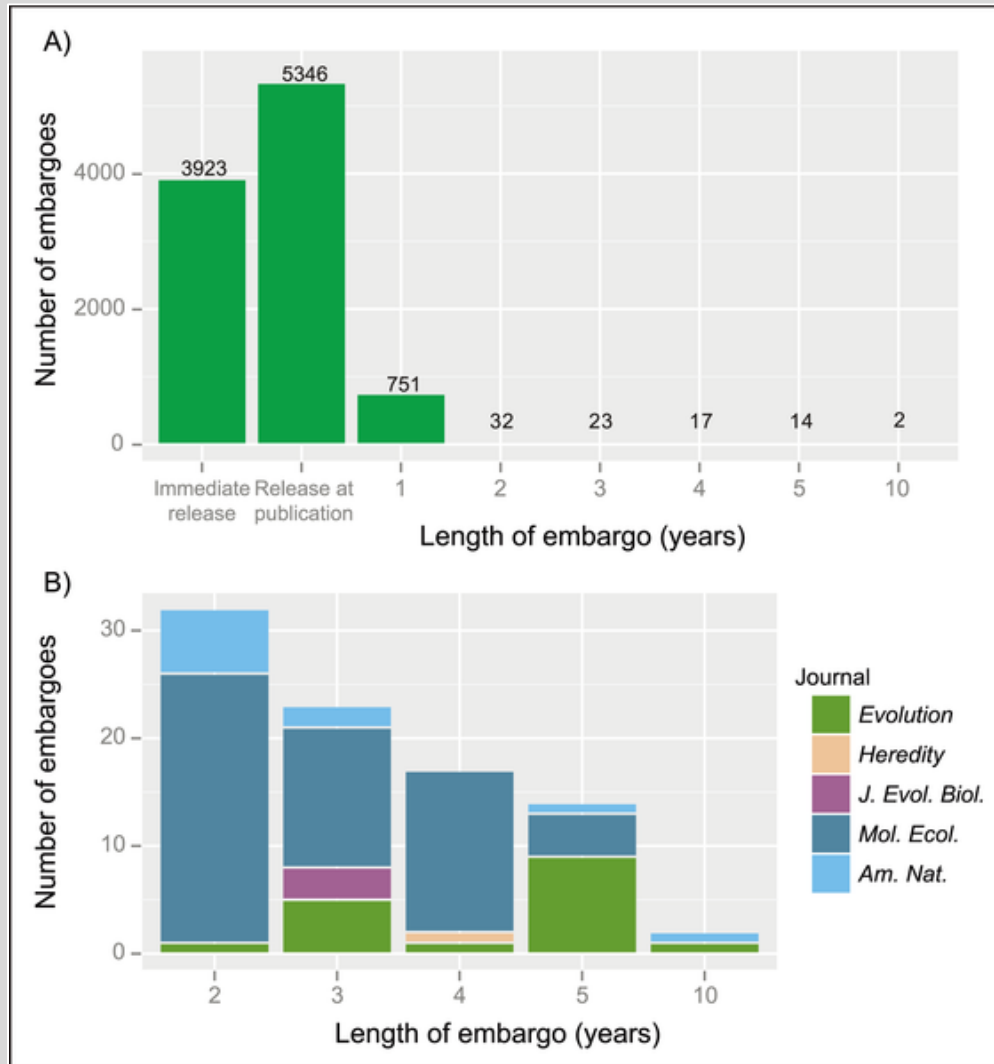
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B. Long-term embargoes (>1 year) by journal that granted them.

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

Effects of JDAP since 2011

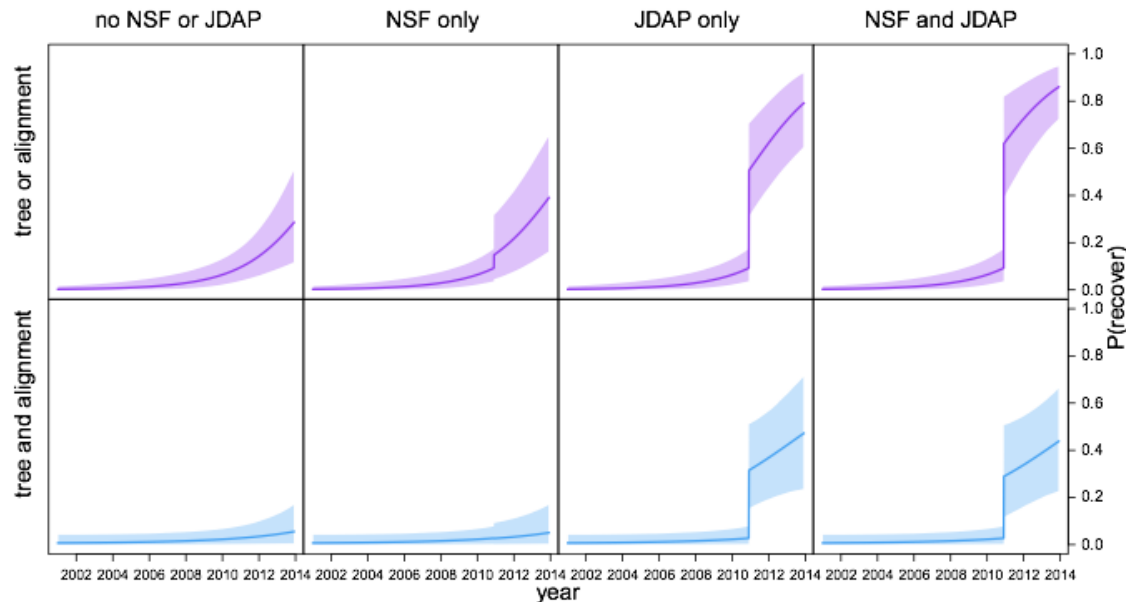
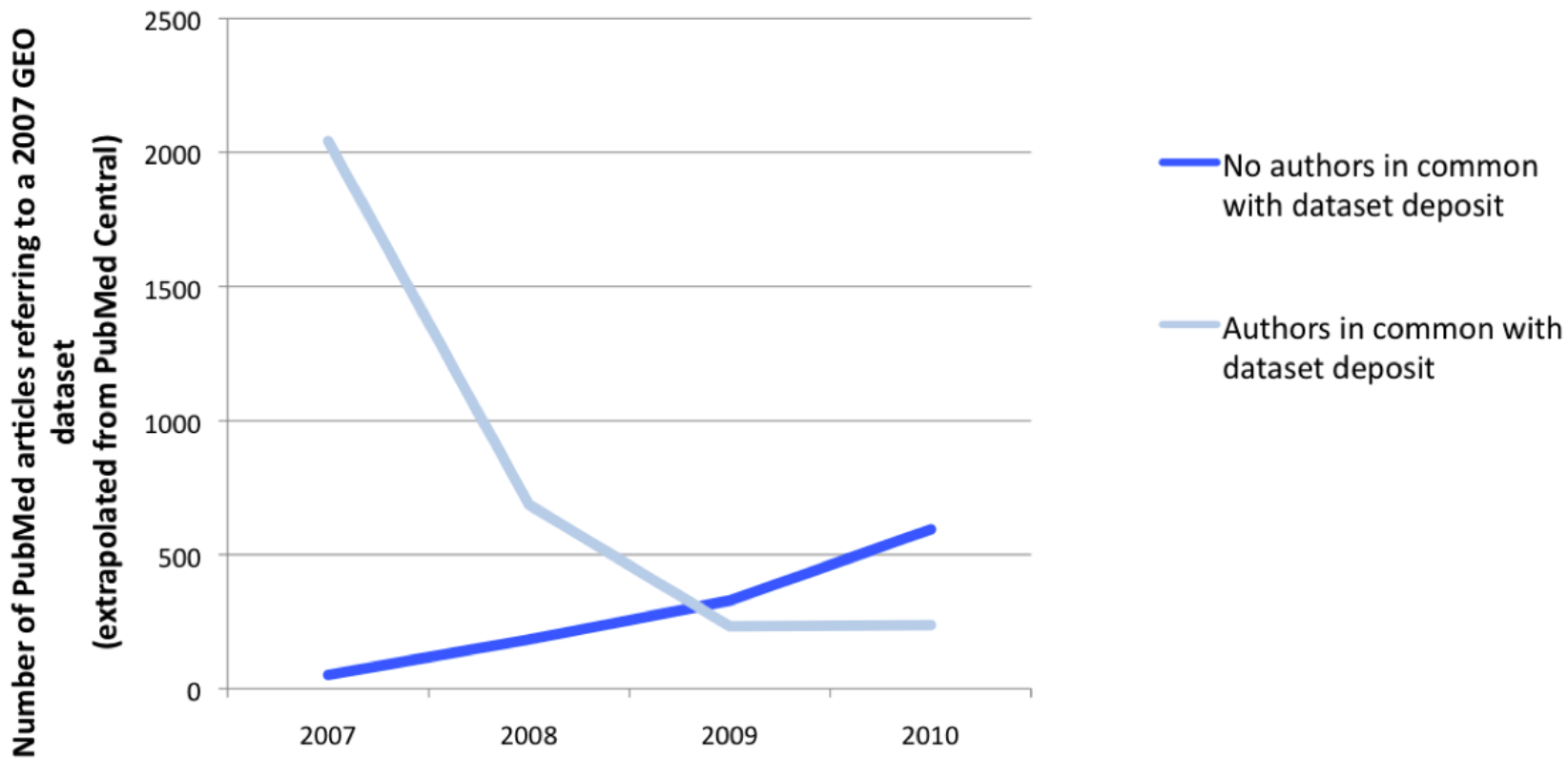


Figure 5. Availability of archived phylogenetic data as a function of age. We estimated the effect of publication age on our ability to procure partial (top panels) and complete (bottom panels) phylogenetic datasets from online archives. Overall, the probability of recovering archived phylogenetic data 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

Use and reuse of 2007 GEO data attributed by accession reference, extrapolated to all of PubMed



DATA NOTE

Open Access

A dataset comprising 141 magnetic resonance imaging scans of 98 extant sea urchin species

Alexander Ziegler^{1*}, Cornelius Faber², Susanne Mueller³, Nina Nagelmann² and Leif Schröder⁴

Data released on October 06, 2014

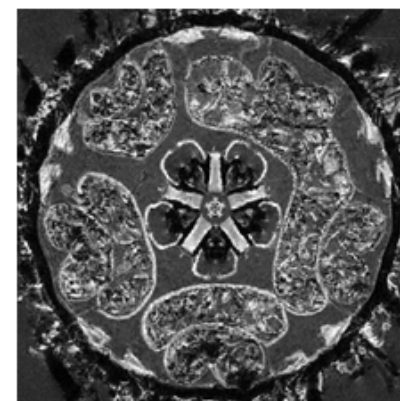
MRI scans of whole sea urchin specimens.

Ziegler, A; Faber, C; Mueller, S; Nagelmann, N; Schröder, L (2014): MRI scans of whole sea urchin specimens. *GigaScience Database*. <http://dx.doi.org/10.5524/100124> [RIS](#) [BibTeX](#) [Text](#)

Magnetic resonance imaging (MRI) is routinely used in human diagnostics, but can also be applied to study the internal anatomy of zoological specimens. Here, we present 141 MRI scans from 98 representative extant sea urchin species. The scanned specimens were whole sub-adult or adult individuals ranging in size from 5 to 43 mm. The specimens were almost entirely obtained from museum collections. Some of the samples were collected and fixed more than 135 years ago, while others were collected a few months prior to scanning. The detailed MRI acquisition and reconstruction parameters can be found in the metadata files deposited together with the raw image data. In addition, image stacks in tagged image file format (TIFF, .tif) were generated for each scan. Potential uses of the dataset include morphometric and volumetric analyses or comparative studies of internal organs.

For convenience users can choose to download all 141 datasets in a single TAR archive file called [141_MRI_scans.tgz](#) (39GB) from the FTP server.

Imaging



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Data from: Data archiving is a good investment

(2011) Piwowar, Vision, Whitlock et al. *Dryad Digital Repository*

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