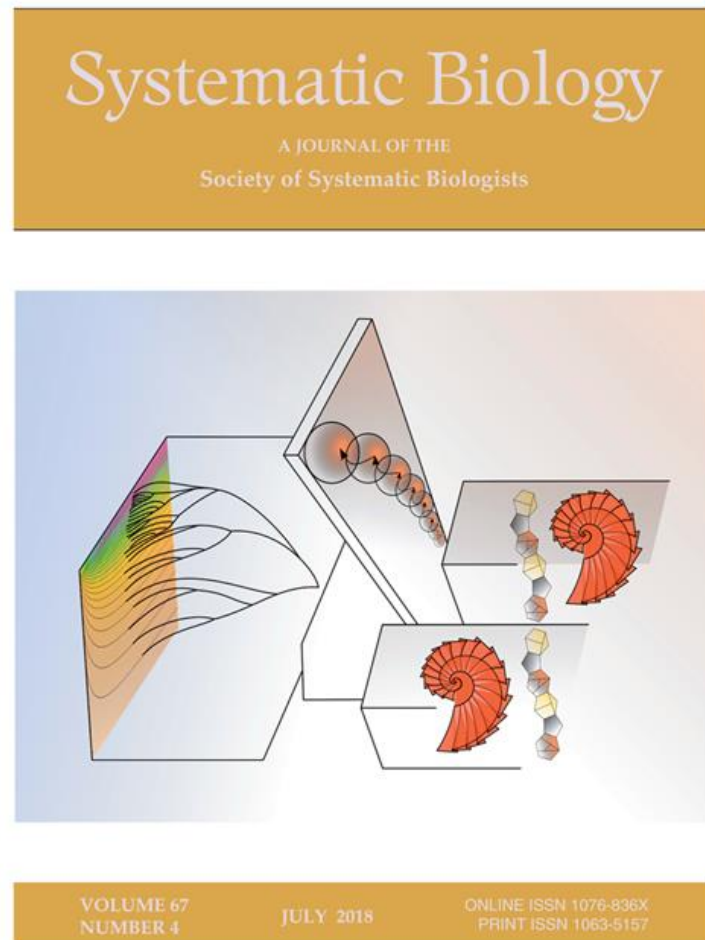


SYSTEMATIC BIOLOGY

PUBLISHER'S REPORT



2018 (JAN – JUN)

Report prepared by Julia McDonnell, Alex Beaumont, Claudia Berger, and Laura Carter

Strictly confidential

The information contained herein should not be disclosed to unauthorized persons.



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DASHBOARD

USAGE & ONLINE

- Full-text downloads: **327,945** in the first half of 2018 (compared to 528,020 in 2017), a **25% increase** compared to the same period of 2017
- Average monthly downloads: ~**54,676** in 2018 (~44,002 in 2017)

IMPACT FACTOR & CITATIONS

- 2017 Impact Factor: **8.523** (8.917 for 2016)
- Ranking, Evolutionary Biology: **4/49** (previously 3/48)

CIRCULATION

- **510** traditional institutional & migrated subscriptions (519 in the first quarter)
- **2,258** Consortia customers with access to the journal via the OUP Collection (2,428 in the first quarter)
- **1,281** institutions in developing nations accessing the journal through OUP's philanthropic initiatives (1,120 in the first quarter)

PRODUCTION

- **0.9 weeks** average publication time (median **0.5 weeks**) from receipt at OUP to Advance Access publication in 2018 so far (compared to 2.1 weeks in 2017)
- All issues have published on or ahead of schedule in 2018 so far, except for issue 2 (compared to 3 out of 6 in 2017)

MARKETING

- Email table of contents registrants: **3,561** (2.03% increase on the previous period)
- Advance article registrants: **1,442** (0.84% increase on the previous period)

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PLATFORM

So far in 2018 we have launched a number of new features to improve the user experience on the Oxford Academic platform, where *Systematic Biology* is hosted.

The most relevant of these is the new 'split view' functionality that allows users to independently navigate between article text and the figures/tables/references within that article using a two-panel format.

This view can be accessed from the navigation menu in any article published in the journal where a HTML version exists, PDF only content cannot be viewed in this format.

Species Concepts and Species Delimitation FREE

Kevin De Queiroz

Systematic Biology, Volume 56, Issue 6, 1 December 2007, Pages 879–886, <https://doi.org/10.1080/10635150701701083>

Published: 01 December 2007 **Article history** ▼

Split View PDF Cite Permissions Share ▼

Abstract

The issue of species delimitation has long been confused with that of species conceptualization, leading to a half century of controversy concerning both the definition

Users are then taken directly into split view as shown below.

Standard view PDF Cite Permissions Share ▼

Contents Figures & Tables References

Reconciliation

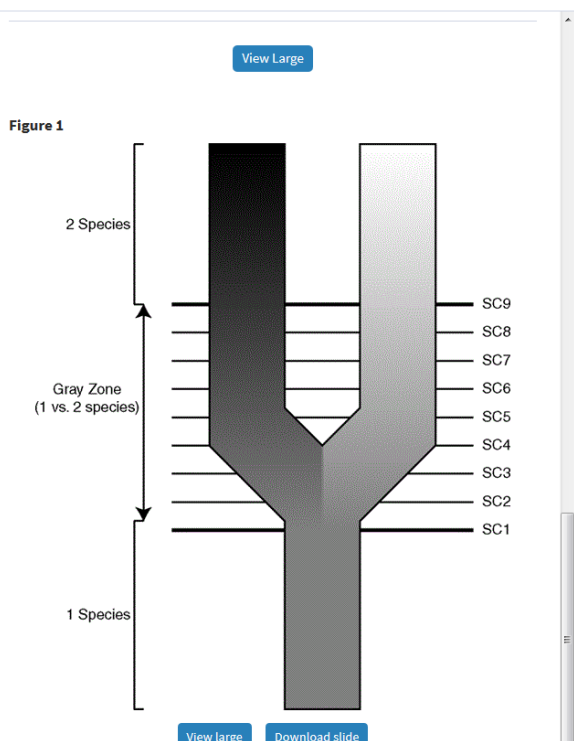
The Common Element

As I have argued previously (e.g., [de Queiroz, 1998, 1999, 2005a, 2005b, 2005c](#)), the key to reconciling the alternative species concepts is identifying a common element, which implies a single, more general, concept of species. Previous attempts to solve the species concept problem have tended instead to obscure the solution by emphasizing the differences, rather than the similarities, among rival concepts. As it turns out, all contemporary species concepts share a common element and, equally important, that shared element is fundamental to the way in which species are conceptualized. The general concept to which I refer equates species with separately evolving metapopulation lineages, or more specifically, with segments of such lineages. To clarify, here the term *lineage* refers to an ancestor–descendant series ([Simpson, 1961](#); [Hull, 1980](#)) in this case of metapopulations or simply a metapopulation extended through time (cf. [Simpson, 1951](#)). It is not to be confused with a clade or monophyletic group, which is sometimes also called a lineage but is generally made up of several lineages (separate branches). The term *metapopulation* refers to an inclusive population made up of connected subpopulations ([Levins, 1970](#); [Hanski and Gaggiotti, 2004](#)). It is used here to distinguish species, which are traditionally considered to reside at the higher end of the population–level continuum, from populations at the lower end of the continuum, such as demes and family groups. Finally, a species is not an entire metapopulation lineage but only a segment of such a lineage. The point here is that species give rise to other species, thereby forming (species level) lineages. Any given species is but one of many segments that make up such a species level lineage.

The Differences

Given that all contemporary species concepts share the common view that species are (segments of) separately evolving metapopulation lineages (for evidence, see [de Queiroz, 1998](#)), it is instructive to consider how so much

Figure 1



Lineage separation and divergence (speciation) and species concepts (after [de Queiroz, 1998](#), 1999, 2005a, 2005b, 2005c).



We also continue to see improvements in many areas including:

- Search engine optimization, which triggered substantial increases in usage particularly in March 2018 when updates to the Google algorithm favourably impacted content published by OUP due to the quality of our material and platform.
- Improvements to search functionality and design.
- Enhancements to content widgets.
- GDPR compliance updates.

There have been far fewer problems with platform stability during 2018, and when problems have occurred they have been resolved much more quickly than in 2017.

Looking forwards there are various developments in the pipeline, one of which is 'SketchFab' a tool that will enable viewers to manipulate 3D models in line within the text of an article. As new functionality is launched we will update SSB and ensure you have the option to opt-in for any relevant functionality.

If there are any specific developments to the site that SSB would like to explore please let Julia McDonnell know.



Statistics at a glance:

- 6

we didn't receive a signed licence for several weeks despite multiple chasers. 'Automated Integration of Trees and Traits: A Case Study Using Paired Fin Loss Across Teleost Fishes' by Jackson *et al.* was also delayed as we were waiting for a signed licence.

Schedule

The table below shows actual issue publication date against schedule. Most issues in 2018 so far have published on or ahead of schedule. The only exception is the online publication of 67(2), which was delayed by a few days as the Project Manager at our supplier omitted to confirm the online publication with the online team. This was a one-off error and shouldn't occur again.

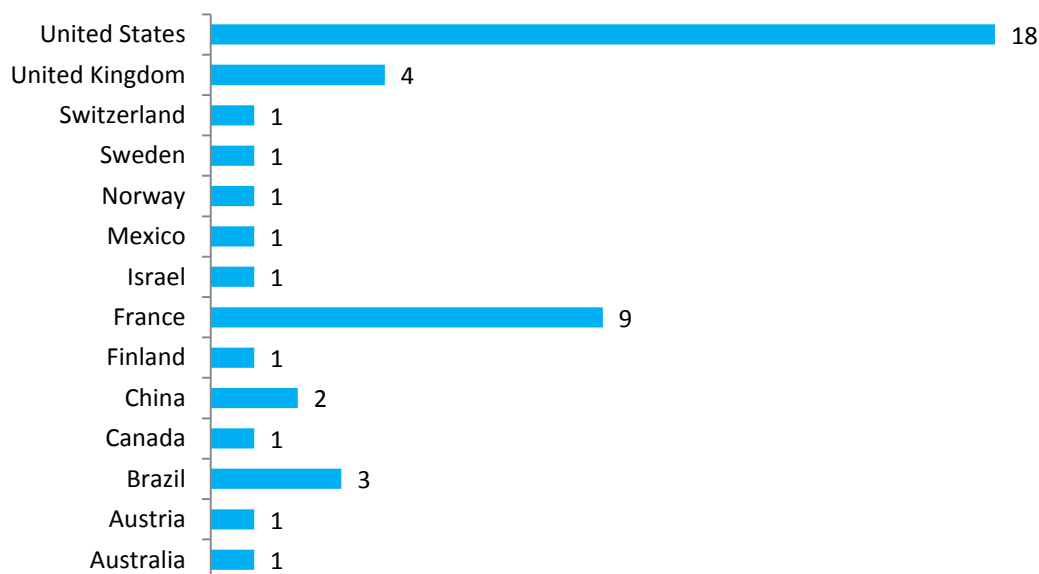
Table 1: Issue Publication Dates

| Volume/Issue | Scheduled Online | Actual Online | Scheduled Print | Actual Print |
|--------------|------------------|---------------|-----------------|--------------|
| 67/1 | 14-Dec | 14-Dec | 21-Dec | 21-Dec |
| 67/2 | 16-Feb | 21-Feb | 26-Feb | 15-Feb |
| 67/3 | 18-Apr | 16-Apr | 26-Apr | 23-Apr |
| 67/4 | 18-Jun | 15-Jun | 25-Jun | 20-Jun |

Author Distribution

The figure below shows the geographical spread of corresponding authors on all manuscripts published in *Systematic Biology* in 2018 so far.

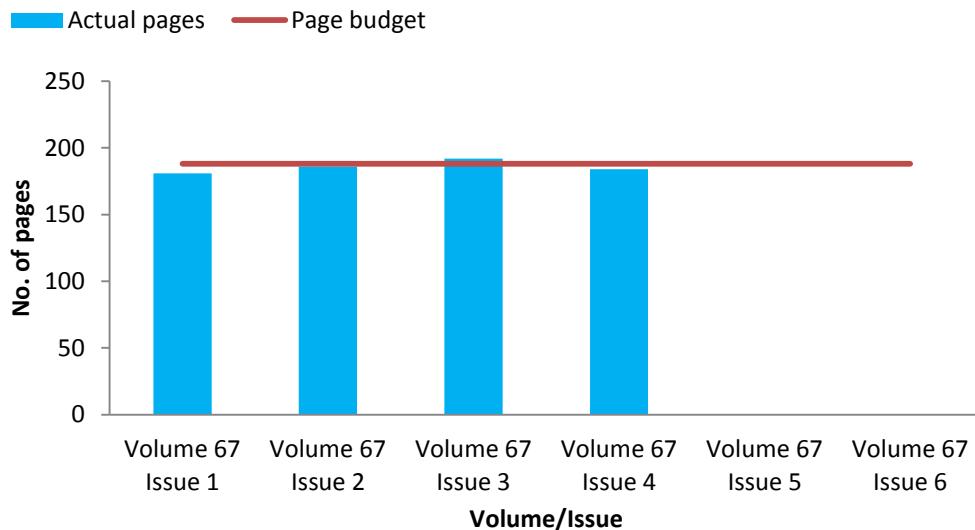
Figure 2: Geographical distribution of corresponding authors in 2018



Page Budget

The 2018 volume is currently 9 pages under budget, with **743** pages in the first four issues. This means there are **385** pages remaining for volume 67.

Figure 3: Page budget graph



Author survey

After publication, we survey our authors and ask them to rate us on the several criteria. In 2018, 14 authors have responded to the author survey, which represents a response rate of 28%. The survey asks authors to rate their experience of publishing with OUP on a scale of 1-5, where 1=Poor and 5=Excellent. Authors rated OUP as follows:

- **Speed:** 4.3
- **Quality:** 4.0
- **Service:** 4.4
- **Communication:** 4.5

Comments included:

- *"The production staff has been helpful and professional."*
- *"Everything was excellent in terms of communication and speed of publishing."*
- *"Everything was very smooth."*
- *"Everything went very smoothly and quick, I am truly impressed. All the modifications other than the Author Queries were promptly modified."*
- *"I provided vector graphics but the figures in the final pdf are blurry." (OUP Response: As standard we upload a low resolution version of the PDF—high resolution figures are available in the HTML and in print—so in response we updated this article to high resolution as a one-off and informed the author, who was happy with the end product).*

Errata and Corrigenda

There have been no corrections in 2018 so far.

Open Access

In 2018, 11 articles have been published under an OA licence via the optional OA scheme, which is uptake of approximately 22%.

Table 2: Open Access Articles Published in 2018

| Author name | Article title | DOI |
|---------------|---|-----------------------|
| Jackson, L. | Automated Integration of Trees and Traits: A Case Study Using Paired Fin Loss Across Teleost Fishes | 10.1093/sysbio/syx098 |
| dos Reis, M. | Using Phylogenomic Data to Explore the Effects of Relaxed Clocks and Calibration Strategies on Divergence Time Estimation: Primates as a Test Case | 10.1093/sysbio/syy001 |
| Stange, M. | Bayesian Divergence-Time Estimation with Genome-Wide SNP Data of Sea Catfishes (Ariidae) Supports Miocene Closure of the Panamanian Isthmus | 10.1093/sysbio/syy006 |
| Volz, E. | Modeling the growth and decline of pathogen effective population size provides insight into epidemic dynamics and drivers of antimicrobial resistance | 10.1093/sysbio/syy007 |
| Luo, A. | Comparison of Methods for Molecular Species Delimitation across a Range of Speciation Scenarios | 10.1093/sysbio/syy011 |
| McCann, J. | Dating the Species Network: Allopolyploidy and Repetitive DNA Evolution in American Daisies (<i>Melampodium</i> sect. <i>Melampodium</i> , Asteraceae) | 10.1093/sysbio/syy024 |
| Rambaut, A. | Posterior summarisation in Bayesian phylogenetics using Tracer 1.7 | 10.1093/sysbio/syy032 |
| Andermann, T. | Allele Phasing Greatly Improves the Phylogenetic Utility of Ultraconserved Elements | 10.1093/sysbio/syy039 |
| Silvestro, D. | Early arrival and climatically-linked geographic expansion of New World monkeys from tiny African ancestors | 10.1093/sysbio/syy046 |

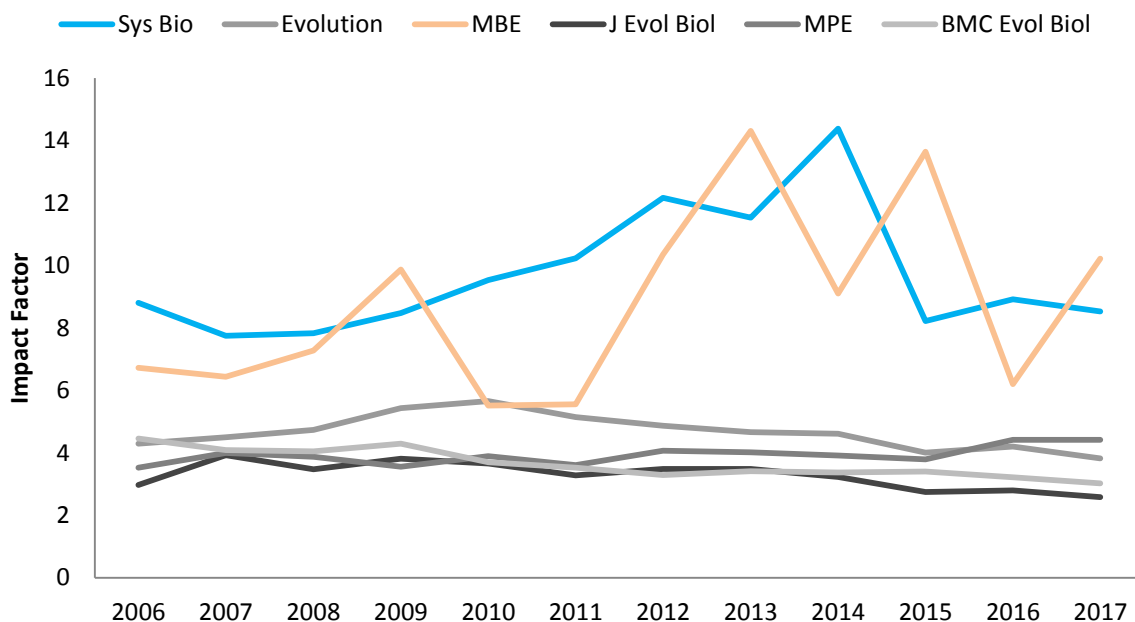
IMPACT

2017 Impact Factor

Systematic Biology's 2017 Impact Factor was announced in summer 2018. The journal received an Impact Factor of 8.523, which represents a 4.4% decrease from the previous year.

Of the 1,304 citations that contributed to the Impact Factor, 637 were self-citations, or 4.153% of the total.

Figure 4: Impact Factor Trend of *Systematic Biology* and Competitors, 2006-2017



The 2017 IF places *Systematic Biology* 4th/49 in the category 'Evolutionary Biology'.

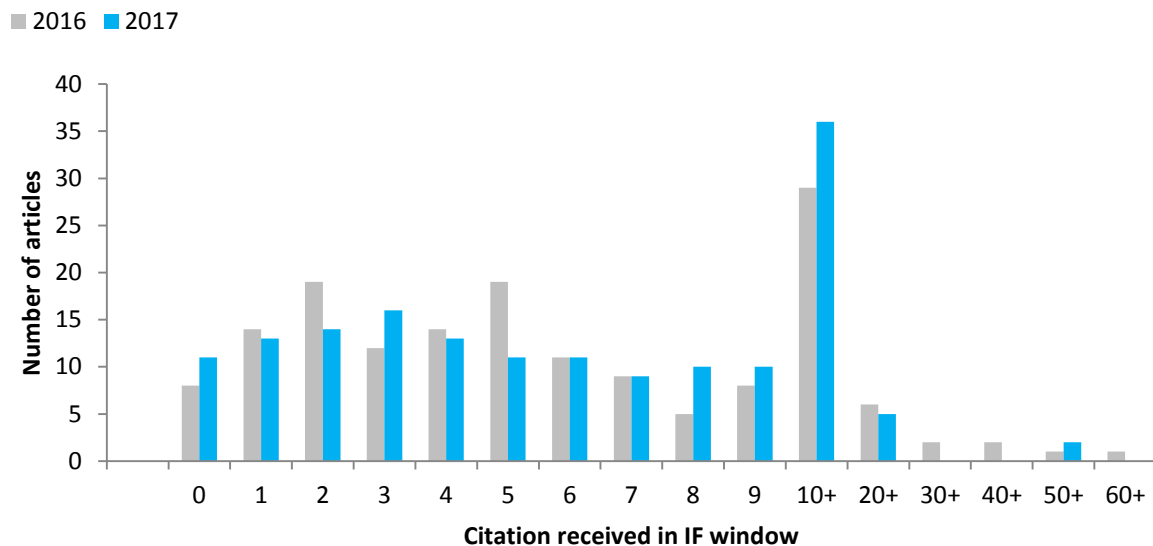
Table 3: *Systematic Biology* Ranking in 'Evolutionary Biology'

| Journal | Ranking in 'Evolutionary Biology' | Impact Factor |
|---|-----------------------------------|---------------|
| <i>Trends in Ecology & Evolution</i> | 1 | 15.938 |
| <i>Molecular Biology and Evolution</i> | 2 | 10.217 |
| <i>Annual Review of Ecology Evolution and Systematics</i> | 3 | 10.160 |
| <i>Systematic Biology</i> | 4 | 8.523 |
| <i>Molecular Ecology Resources</i> | 5 | 7.059 |
| <i>Molecular Ecology</i> | 6 | 6.131 |
| <i>Cladistics</i> | 7 | 5.877 |
| <i>Proceedings of the Royal Society B-Biological Sciences</i> | 8 | 4.847 |
| <i>Evolutionary Applications</i> | 9 | 4.694 |
| <i>Molecular Phylogenetics and Evolution</i> | 10 | 4.412 |

Citations

The following graph shows the distribution of articles in the 2016 and 2017 Impact Factor windows by number of citations received.

Figure 5: 2016-2017 Impact Factor Citation Distribution



Cited and Citing Journal

The table below shows the journals that most cited articles (in all years) from *Systematic Biology* in the left hand column and the journals most cited by *Systematic Biology* (in all years) in the right hand column.

Table 4: Cited and Citing Journals

| IF | Cited Journal (journals which most cited <i>Systematic Biology</i> in all years) | Citing Journal (journals which were most cited by <i>Systematic Biology</i> in all years) | IF |
|--------------|--|---|--------------|
| 4.412 | <i>Molecular Phylogenetic Evolution</i> | <i>Systematic Biology</i> | 8.523 |
| 2.766 | <i>PLoS One</i> | <i>Molecular Biology and Evolution</i> | 10.217 |
| 8.523 | <i>Systematic Biology</i> | <i>Proceedings of the National Academy of Sciences of the United States of America</i> | 9.504 |
| 4.122 | <i>Scientific Reports-UK</i> | <i>Nature</i> | 41.577 |
| 0.931 | <i>Zootaxa</i> | <i>Bioinformatics</i> | 5.481 |
| 3.027 | <i>BMC Evolutionary Biology</i> | <i>Evolution</i> | 3.818 |
| 4.154 | <i>Journal of Biogeography</i> | <i>Molecular Phylogenetic Evolution</i> | 4.412 |
| 2.118 | <i>PeerJ</i> | <i>Science</i> | 41.058 |
| 3.818 | <i>Evolution</i> | <i>BMC Evolutionary Biology</i> | 3.027 |
| 2.532 | <i>Biological Journal of Linnean Society</i> | <i>Genetics</i> | 4.075 |

Top Cited Articles

The table below shows the articles published in 2015 and 2016 that received the highest number of citations in 2017. In other words, these are the articles that made the highest contribution to the 2017 Impact Factor.

Table 5: Top Cited Articles, 2017

| First Author | Title | Year | Vol | Iss | Citations in 2017 | Total Citations |
|-----------------------|--|------|-----|-----|-------------------|-----------------|
| Rabosky, Daniel L. | Model Inadequacy and Mistaken Inferences of Trait-Dependent Speciation | 2015 | 64 | 2 | 53 | 164 |
| Maddison, Wayne P. | The Unsolved Challenge to Phylogenetic Correlation Tests for Categorical Characters | 2015 | 64 | 1 | 51 | 134 |
| Beaulieu, Jeremy M. | Detecting Hidden Diversification Shifts in Models of Trait-Dependent Speciation and Extinction | 2016 | 65 | 4 | 27 | 46 |
| Huang, Huateng | Unforeseen Consequences of Excluding Missing Data from Next-Generation Sequences: Simulation Study of RAD Sequences | 2016 | 65 | 3 | 25 | 53 |
| Beerenwinkel, Niko | Cancer Evolution: Mathematical Models and Computational Inference | 2015 | 64 | 1 | 23 | 61 |
| Zhang, Chi | Total-Evidence Dating under the Fossilized Birth-Death Process | 2016 | 65 | 2 | 22 | 38 |
| Szoellösi, Gergely J. | The Inference of Gene Trees with Species Trees | 2015 | 64 | 1 | 21 | 58 |
| Leache, Adam D. | Short Tree, Long Tree, Right Tree, Wrong Tree: New Acquisition Bias Corrections for Inferring SNP Phylogenies | 2015 | 64 | 6 | 19 | 53 |
| Mirarab, Siavash | Evaluating Summary Methods for Multilocus Species Tree Estimation in the Presence of Incomplete Lineage Sorting | 2016 | 65 | 3 | 18 | 56 |
| Chen, Meng-Yun | Selecting Question-Specific Genes to Reduce Incongruence in Phylogenomics: A Case Study of Jawed Vertebrate Backbone Phylogeny | 2015 | 64 | 6 | 18 | 34 |

Table 6 shows the articles published in 2016 and 2017 that received the highest number of citations in 2017. These are the articles that will make the highest contribution to the upcoming 2018 Impact Factor.

Table 6: Top Cited Articles, 2018





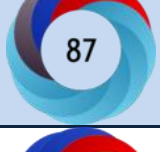


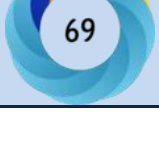
| First Author | Title | Year | Vol | Iss | Citations in 2018 | Total Citations |
|-----------------------|---|------|-----|-----|-------------------|-----------------|
| Chernomor, Olga | Terrace Aware Data Structure for Phylogenomic Inference from Supermatrices | 2016 | 65 | 6 | 22 | 36 |
| Rabosky, Daniel L. | Is BAMM Flawed? Theoretical and Practical Concerns in the Analysis of Multi-Rate Diversification Models | 2017 | 66 | 4 | 21 | 33 |
| Mirarab, Siavash | Evaluating Summary Methods for Multilocus Species Tree Estimation in the Presence of Incomplete Lineage Sorting | 2016 | 65 | 3 | 20 | 55 |
| Hohna, Sebastian | RevBayes: Bayesian Phylogenetic Inference Using Graphical Models and an Interactive Model-Specification Language | 2016 | 65 | 4 | 18 | 27 |
| Beaulieu, Jeremy M. | Detecting Hidden Diversification Shifts in Models of Trait-Dependent Speciation and Extinction | 2016 | 65 | 4 | 17 | 48 |
| Rojas, Danny | Bats (Chiroptera: Noctilionoidea) Challenge a Recent Origin of Extant Neotropical Diversity | 2016 | 65 | 3 | 17 | 29 |
| Streicher, Jeffrey W. | How Should Genes and Taxa be Sampled for Phylogenomic Analyses with Missing Data? An Empirical Study in Iguanian Lizards | 2016 | 65 | 1 | 16 | 43 |
| Meiklejohn, Kelly A. | Analysis of a Rapid Evolutionary Radiation Using Ultraconserved Elements: Evidence for a Bias in Some Multispecies Coalescent Methods | 2016 | 65 | 4 | 14 | 34 |
| To, Thu-Hien | Fast Dating Using Least-Squares Criteria and Algorithms | 2016 | 65 | 1 | 14 | 29 |
| Huang, Huateng | Unforeseen Consequences of Excluding Missing Data from Next-Generation Sequences: Simulation Study of RAD Sequences | 2016 | 65 | 3 | 13 | 54 |

Altmetrics

The Altmetric Score is a measure of the amount of attention an article has received online, in social media and from news sites, from early 2012 to date. The colors of the donut indicate the source of the attention.

The average OUP article has an Altmetric score of 6.64, while *Systematic Biology* articles score 7.30 on average. The following are the articles in *Systematic Biology* with the highest Altmetric Score (all time) over the past year.

Table 7: Top 10 Highest Altmetric Scoring Articles in the Past Year

| Score | Title |
|--|---|
|  180 | Genomic Signature of an Avian Lilliput Effect across the K-Pg Extinction |
|  100 | Bayesian Total-Evidence Dating Reveals the Recent Crown Radiation of Penguins |
|  94 | Predicting Total Global Species Richness Using Rates of Species Description and Estimates of Taxonomic Effort |
|  91 | Geomolecular Dating and the Origin of Placental Mammals |
|  91 | Model Selection in Historical Biogeography Reveals that Founder-Event Speciation is a Crucial Process in Island Clades |
|  87 | Phylogenomic Systematics of Ostariophysan fishes: Ultraconserved Elements Support the Surprising Non-monophyly of Characiformes |
|  82 | Is Permanent Parasitism Reversible? – Critical Evidence from Early Evolution of House Dust Mites |
|  80 | Rethinking phylogenetic comparative methods |
|  71 | Inferring Diversification Rate Variation From Phylogenies With Fossils |
|  69 | The Tree of Life |

ONLINE USAGE

Full-Text Downloads

- Through the first half of 2018, the journal had 327,945 full-text downloads, compared to 263,061 full-text downloads in the same period in 2017, which represents a **25% increase**.
- In 2018 so far, there have been an average of **~54,676** full-text downloads, compared to 2017's average of **~44,002**.

Usage data is routinely reprocessed to ensure accuracy when robotic usage is identified, and COUNTER compliance; as such the usage detailed here may be subject to change.

Figure 6: Total HTML and PDF Downloads, 2012-2018 ytd

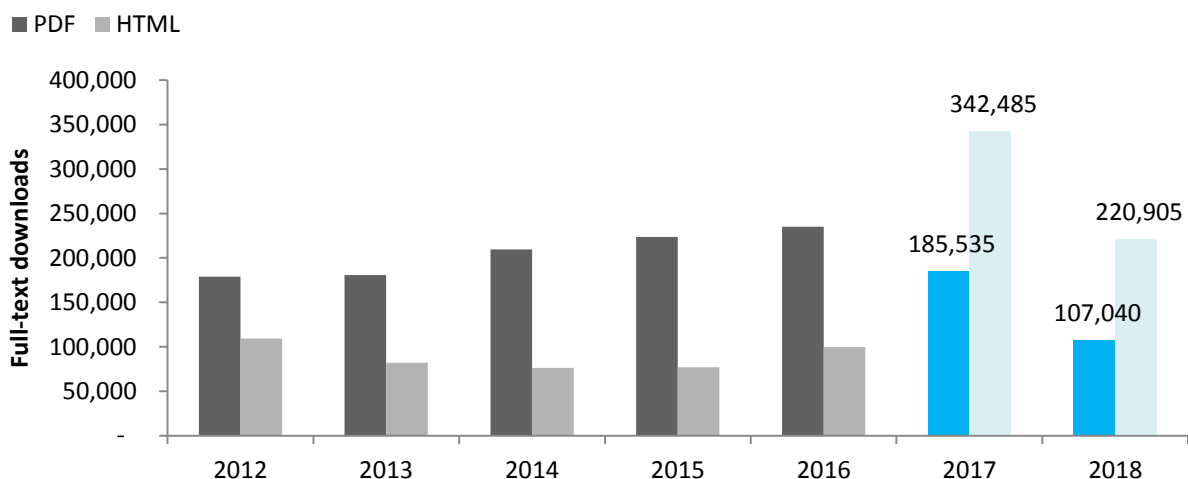
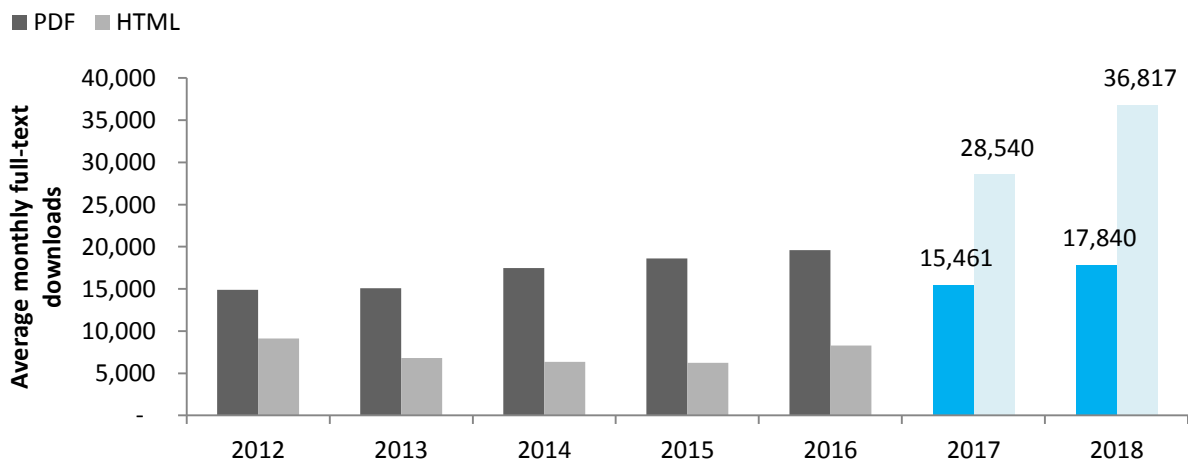


Figure 7: Average Monthly HTML and PDF Downloads, 2012-2018 ytd



New usage metrics

As part of our move to the Oxford Academic platform, we have explored how we can improve the clarity and reliability of our usage reporting and remove some of the variance which can be attributed to robotic traffic. The new metrics we have devised are 'Visits with Content Engagement' which counts visits that include at least one full-text content page view; and 'Visits with Demand' which counts visits that include at least one full-text content page view or access denial. These metrics also show a strong increase in usage since launch of the new platform in 2017 as shown below.

Figure 8: Visits with Content Engagement and Visits with Demand, 2014-2018 ytd

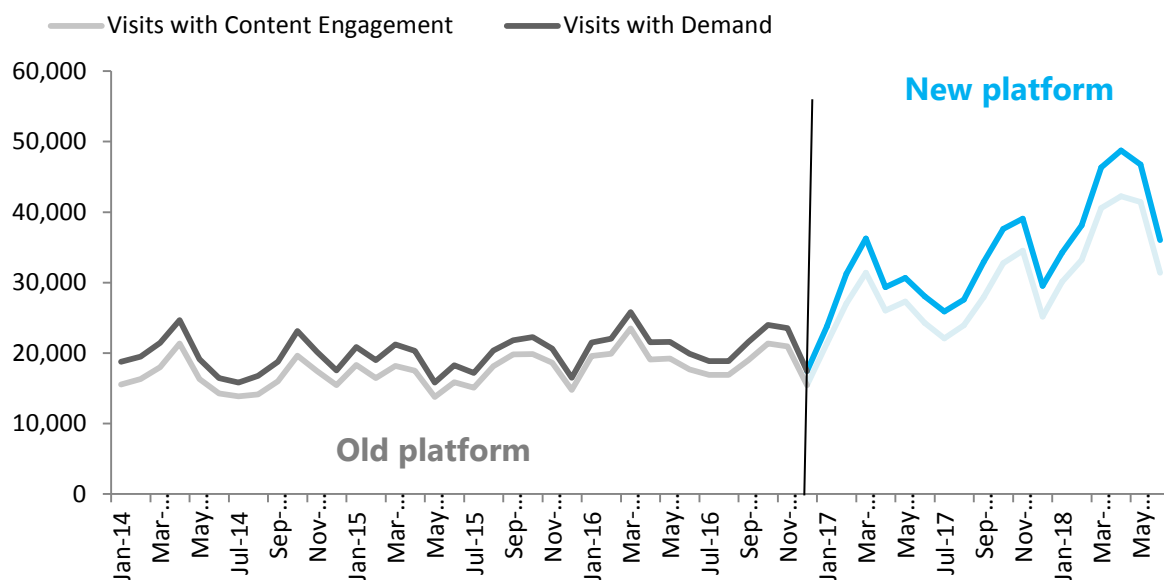


Table 8: comparison of traditional and new usage metrics by year, 2014-2018 YTD

| Year | Visits with Content Engagement | % Increase | Visits with Demand | % Increase | Full-text Downloads | % Increase |
|----------|--------------------------------|------------|--------------------|------------|---------------------|------------|
| 2014 | 198,277 | - | 232,068 | - | 285,852 | - |
| 2015 | 206,288 | 4% | 234,058 | 1% | 302,583 | 6% |
| 2016 | 229,463 | 11% | 256,599 | 10% | 334,831 | 11% |
| 2017 | 323,709 | 41% | 371,953 | 45% | 528,020 | 58% |
| 2018 YTD | 222,632 | | 252,198 | | 327,945 | |

Top Accessed Articles 2017 & 2018 ytd

Tables 9 and 10 (next page) show the top ten most downloaded articles in 2017 and 2018 ytd respectively. The download figures are a total of both PDF and HTML usage.

Table 9: Top 10 Most Accessed Articles, 2017

| First Author | Article | Year | Vol | Iss | Article Type | Downloads |
|-------------------|--|------|-----|-----|---|-----------|
| Kevin De Queiroz | Species Concepts and Species Delimitation | 2007 | 56 | 6 | Regular Manuscript | 10,387 |
| Paul D. N. Hebert | The Promise of DNA Barcoding for Taxonomy | 2005 | 54 | 5 | Point of View | 3,979 |
| David Posada | Model Selection and Model Averaging in Phylogenetics: Advantages of Akaike Information Criterion and Bayesian Approaches Over Likelihood Ratio Tests | 2004 | 53 | 5 | Regular Manuscript | 3,703 |
| Stéphane Guindon | New Algorithms and Methods to Estimate Maximum-Likelihood Phylogenies: Assessing the Performance of PhyML 3.0 | 2010 | 59 | 3 | Regular Manuscript | 3,389 |
| Fredrik Ronquist | MrBayes 3.2: Efficient Bayesian Phylogenetic Inference and Model Choice Across a Large Model Space | 2012 | 61 | 3 | Software for Systematics and Evolution | 3,367 |
| Niko Beerenwinkel | Cancer Evolution: Mathematical Models and Computational Inference | 2015 | 64 | 1 | Special Issue: Mathematical and Computational Evolutionary Biology (2013) | 3,182 |
| Stéphane Guindon | A Simple, Fast, and Accurate Algorithm to Estimate Large Phylogenies by Maximum Likelihood | 2003 | 52 | 5 | Regular Manuscript | 3,003 |
| Lintusaari, J. | Fundamentals and Recent Developments in Approximate Bayesian Computation | 2017 | 66 | 1 | Regular Manuscript | 2,824 |
| Leonardi, M. | Evolutionary Patterns and Processes: Lessons from Ancient DNA | 2017 | 66 | 1 | Regular Manuscript | 2,813 |
| Kevin de Queiroz | Nodes, Branches, and Phylogenetic Definitions | 2013 | 62 | 4 | Point of View | 2,714 |

Table 10: Top 10 Most Accessed Articles, 2018 (through June 30)

| First Author | Article | Year | Vol | Iss | Article Type | Downloads |
|-------------------|--|------------|-----|-----|--------------------|-----------|
| Kevin De Queiroz | Species Concepts and Species Delimitation | 2007 | 56 | 6 | Regular Manuscript | 8,618 |
| Kevin De Queiroz | Nodes, Branches, and Phylogenetic Definitions. | 2013 | 62 | 4 | Point of View | 6,192 |
| Paul D. N. Hebert | The Promise of DNA Barcoding for Taxonomy | 2005 | 54 | 5 | Point of View | 2,836 |
| Luo, Arong | Comparison of Methods for Molecular Species Delimitation Across a Range of Speciation Scenarios | 15-Feb-18* | | | Regular Manuscript | 2,563 |
| David Posada | Model Selection and Model Averaging in Phylogenetics: Advantages of Akaike Information Criterion and Bayesian Approaches Over Likelihood Ratio Tests | 2004 | 53 | 5 | Regular Manuscript | 2,194 |
| Stéphane Guindon | New Algorithms and Methods to Estimate Maximum-Likelihood Phylogenies: Assessing the Performance of PhyML 3.0 | 2010 | 59 | 3 | Regular Manuscript | 2,019 |
| Stange, Madlen | Bayesian Divergence-Time Estimation with Genome-Wide Single-Nucleotide Polymorphism | 2018 | 67 | 4 | Regular Manuscript | 1,960 |



| First Author | Article | Year | Vol | Iss | Article Type | Downloads |
|-----------------------|--|------|-----|-----|--|-----------|
| | Data of Sea Catfishes (Ariidae) Supports Miocene Closure of the Panamanian Isthmus | | | | | |
| Dos Reis, Mario | Using Phylogenomic Data to Explore the Effects of Relaxed Clocks and Calibration Strategies on Divergence Time Estimation: Primates as a Test Case | 2018 | 67 | 4 | Regular Manuscript | 1,956 |
| Ronquist, Fredrik | MrBayes 3.2: Efficient Bayesian Phylogenetic Inference and Model Choice Across a Large Model Space | 2012 | 61 | 3 | Software for Systematics and Evolution | 1,877 |
| Freudenstein, John V. | Characters, States and Homology | 2005 | 54 | 6 | Points of View | 1,823 |

*Advance Access

MARKETING

Highly Cited Campaign (April 2018)

To increase usage and raise the profile of *Systematic Biology*, we curated a selection of highly cited articles from the journal in recent years, which we promoted via the following methods:

- Email campaign to email alert registrants
- Email campaign sent via Clarivate to authors in related journals
- Web banners
- Twitter



Results:

In the week the emails were launched, articles received a **48% increase in downloads**. The two emails were sent to a total of 7,072 recipients; they were **opened by 29%** and **clicked by 13%**.

The web banners have received **59 clicks** and **60,991 impressions** to date. The tweets received **73 clicks**.

Full usage results will be available in the next report.



Social Media

To increase usage of *Systematic Biology*, we continually assess content for social media suitability. Articles are often selected to be shared based on their Altmetric score, in connection with the news or media, or simply due to their broad appeal.

We also retweet authors in the journal as well as others who share *Systematic Biology* articles.

Articles shared in 2018 to-date:

- [Genomic Signature of an Avian Lilliput Effect across the K-Pg Extinction](#)
Jacob S. Berv Daniel J. Field
- Sequential Monte Carlo:
 - [Effective Online Bayesian Phylogenetics via Sequential Monte Carlo with Guided Proposals](#)
Mathieu Fourment, Brian C Claywell, Vu Dinh, Connor McCoy, Frederick A Matsen IV, and Aaron E Darling
 - [Online Bayesian Phylogenetic Inference: Theoretical Foundations via Sequential Monte Carlo](#)
Vu Dinh, Aaron E Darling, and Frederick A Matsen IV
- [A Framework for Resolving Cryptic Species: A Case Study from the Lizards of the Australian Wet Tropics](#)
Sonal Singhal, Conrad J Hoskin, Patrick Couper, Sally Potter, and Craig Moritz
- [Evaluating the Impact of Genomic Data and Priors on Bayesian Estimates of the Angiosperm Evolutionary Timescale](#)
Charles S. P. Foster, Hervé Sauquet, Marlien van der Merwe, Hannah McPherson, Maurizio Rossetto, and Simon Y. W. Ho
- [Bayesian Total-Evidence Dating Reveals the Recent Crown Radiation of Penguins](#)
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Content Alerting

Content alerts are important marketing tools, not only because they encourage usage and readership of the journal, but also because we can track their impact on usage directly and use email alerting services to provide additional promotional information.

The New Issue Alert (formerly email table of contents) for *Systematic Biology* currently has **3,561** registrants – an increase of 2.03% since the last report – and the Advance Access service has **1,442** registrants – an increase of 0.84% since the last report. In total there are **3,727** individuals signed up to receive alerts from *Systematic Biology*.

Table 11: New Issue Alert Registrants, May 2016-July 2018

| Date | New Issue Alert registrants | Change (%) | AA registrants | Change (%) |
|---------------|-----------------------------|--------------|----------------|--------------|
| May 2016 | 3,039 | - | 1,312 | - |
| December 2016 | 3,073 | +34 (1.12%) | 1,321 | +9 (0.69%) |
| May 2017 | 3,202 | +129 (4.2%) | 1,367 | +46 (3.48%) |
| December 2017 | 3,406 | +204 (6.37%) | 1,411 | +44 (3.22%) |
| May 2018 | 3,490 | + 84 (2.47%) | 1,430 | + 19 (1.35%) |
| July 2018 | 3,561 | +71 (2.03%) | 1,442 | + 12 (0.84%) |

Profile

Conferences are an excellent way of maintaining and raising the global profile of a journal. *Systematic Biology* had a presence at the following conferences in 2018 to date.

Table 12: Conferences 2018 to date

| Conference | City | Date |
|---|---------------------|------------|
| Society for Integrative and Comparative Biology (SICB) | San Francisco, USA | 03.01.2018 |
| 11th International Biocuration Conference | Shanghai, China | 11.04.2018 |
| Experimental Biology (FASEB) | San Diego, USA | 21.04.2018 |
| European Congress Of Conservation Biology | Jyväskylä, Finland | 12.06.2018 |
| Plant Biology Europe 2018 | Copenhagen, Denmark | 18.06.2018 |
| American Society Of Mammalogists | New York, NY, USA | 25.06.2018 |
| Society For Experimental Biology | Florence, Italy | 03.07.2018 |
| International Conference On Intelligent Systems For Molecular Biology | Chicago, IL, USA | 06.07.2018 |
| Society For Molecular Biology And Evolution | Yokohama, Japan | 08.07.2018 |
| American Society Of Plant Biologists | Montreal, Canada | 14.07.2018 |
| American Genetic Association | Waimea, HI, USA | 22.07.2018 |

SSB Conference 2018

To support the SSB Standalone Conference in June, we produced a web banner to display on the *Systematic Biology* website. **Results:** The web banner received **44 clicks** and **40,998 impressions**.



SALES HIGHLIGHTS

Member subscriptions

In addition to institutional subscribers, the journal is offered to members of the Society of Systematic Biologists as part of their membership package. Table 13 provides a breakdown of the member subscriptions in 2018 and the total for 2017.

Table 13: Member Subscriptions, 2017-2018 ytd

| | Membership | Format | Total |
|-------------------|-------------------|----------------|------------|
| 2017 | Student member | Online only | 167 |
| | | Print & online | 79 |
| | Regular member | Online only | 181 |
| | | Print & online | 228 |
| | Emeritus member | Online only | 0 |
| | | Print & online | 17 |
| | Lifetime member | Online only | 6 |
| | | Print & online | 20 |
| | Sustaining member | Print & online | 5 |
| | Honorary member | | 5 |
| | Prize winners | | 3 |
| 2017 Total | | | 711 |
| 2018 | Student member | Online only | 248 |
| | | Print & online | 65 |
| | Regular member | Online only | 239 |
| | | Print & online | 186 |
| | Emeritus member | Online only | 4 |
| | | Print & online | 15 |
| | Lifetime member | Online only | 4 |
| | | Print & online | 26 |
| | Sustaining member | Print & online | 2 |
| | Honorary member | | 5 |
| | Prize winners | | 5 |
| 2018 Total | | | 799 |

Subscriptions by type

Figure 9 (next page) shows the number of 'traditional' subscribers taking print, online and combined subscriptions from 2012-2018 ytd. In 2018 so far, 46 subscribers continued to take a print subscription through either the Print only or Combined subscription options. However, the vast majority of institutions now access the journal via our OUP collection as demonstrated by Figure 10 (next page) which shows the split of subscribers by type.

Figure 9: Traditional institutional access by format, 2012-2018 ytd

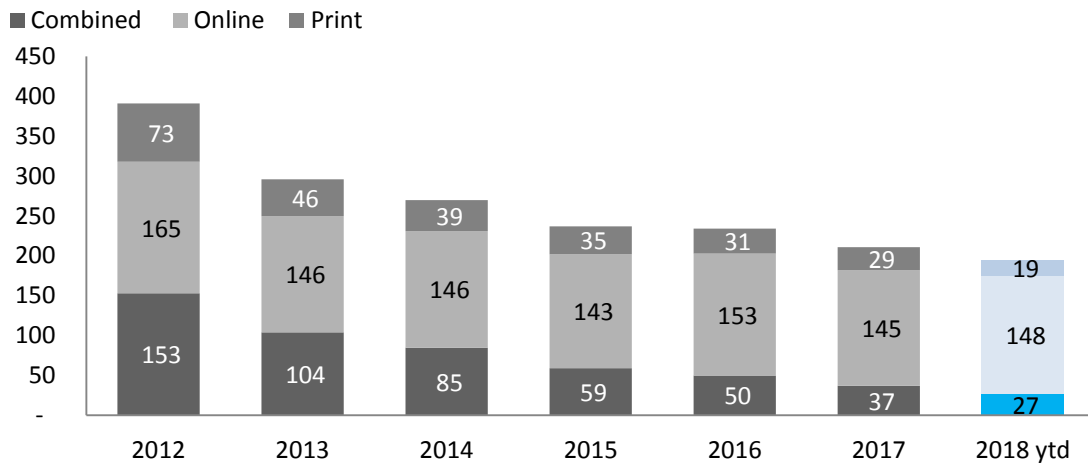
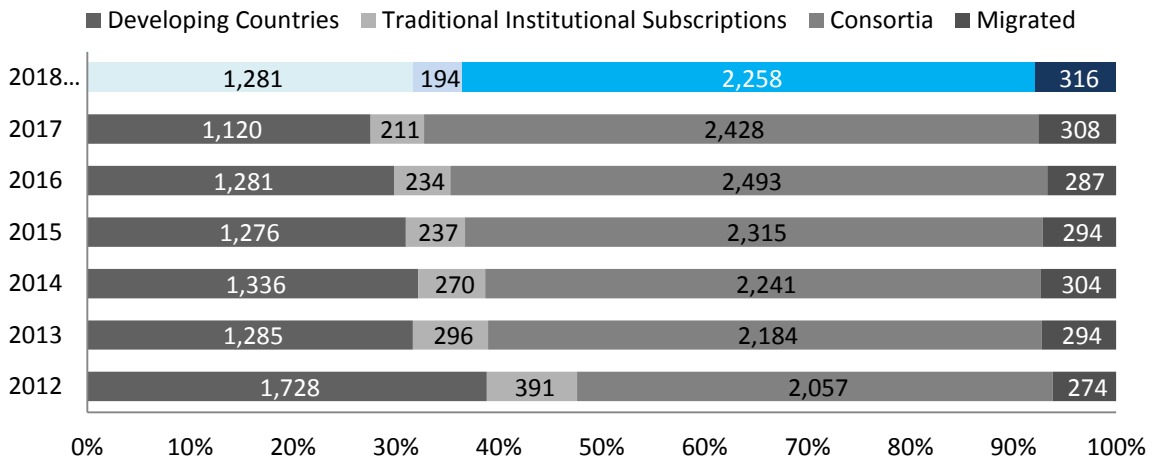


Figure 10: Institutional subscriptions by type, 2012-2018 ytd



Regional breakdown of institutions with access

The figure below shows the geographical spread of traditional subscribers and consortia subscribers in 2018.

Figure 11: Institutional subscriptions by region, 2017 (left) and 2018 ytd (right)

