

MBE Editor's Report

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Revenue from *Molecular Biology and Evolution* (MBE) accounted for nearly 94% of all income received in 2008 by the Society for Molecular Biology and Evolution. We continue to benefit from expert management by Senior Editor Cathy Kennedy and her team at Oxford University Press (OUP). On the Society side, Editorial Assistant Elizabeth Raffaele remains the anchor of the MBE Editorial Office, managing the peer review process and coordinating with the OUP Production team.

Vital statistics

In 2008, MBE's impact factor rose to 7.280. Among journals in the Evolutionary Biology category of the Thomson Reuters ISI Web of Knowledge, MBE ranks just below *Systematic Biology* (7.822) and two review journals.

With respect to the SJR importance index of SCImago (2007), which weights citations by the importance of the citing journal, MBE ranks second among journals in Ecology, Evolution, Behavior and Systematics. MBE also ranks second with respect to the *H* index (Hirsch 2005), which increases with both the number of citations and the number of highly-cited articles.

Table 1 shows the six-year record of original scientific publications (excluding errata and editorials). The flow of submissions in 2008 remained strong, with a stable number of Open Access (OA) articles. The number of color figures continued to climb, to 263, in excellent agreement with the projection of 261, based a linear regression over the preceding five years (Uyenoyama 2008).

Table 2 provides further information about the 269 papers published in 2008, distinguishing among Research Articles (Research), Letters, and Reviews, as well as OA and non-OA.

Of 1,072 decisions in 2008, 792 were rendered on first submissions (a category which includes previously-rejected manuscripts with resubmission encouraged). Table 3 shows the distribution across decisions. Almost all of the Accept category represents manuscripts resubmitted following a Reject and Resubmit decision.

Publishing in MBE

Editorial Board appointments: Eddie Holmes, Laura Katz, Spencer Muse, Stephanie Santorico, Diethard Tautz, and Ziheng Yang have resigned as Associate Editors. On behalf of the Society and the community it serves, I extend my sincere thanks to them for their judgment and many contributions over the years.

Joining the Editorial Board are Alexei Drummond, Daniel Falush, Matthew Hahn, James McInerney, Helen Piontkivska, Oliver Pybus, Willie Swanson, Naoki Takebayashi, and John True. I am most grateful to them for offering their expertise, in several vibrant and emerging research areas.

TeX/LaTeX resources: Authors may now download from the Journal website (<http://mbe.oxfordjournals.org/>) an MBE template, together with .cls and .bst files. We are grateful for the expressions of appreciation already received from authors, which I pass on with my own thanks to Cindy Gross of OUP Production.

Publication embargoes: Authors submitting analyses of community resources including pre-publication releases of genome sequence data are encouraged to follow the principles summarized in accepted guidelines, including those of the National Human Genome Research Institute (<http://www.genome.gov/>). Authors may now flag upon submission a manuscript possibly subject to a publication embargo. Upon acceptance, the corresponding author of such a manuscript must work with the MBE Editorial Office and OUP Production to ensure its publication on Advance Access and in the online and print versions of MBE at the appropriate time.

Greater itemization in invoices: To date, invoicing errors have generally gone undetected until six months or more after the closing of a volume, at the point of the detailed examination by Liz Raffaele and myself of the accounting report from OUP. To reduce the effect of such errors on the community of authors MBE serves, we are instituting a billing format that includes more detailed itemization, designed to make publication fees more transparent to authors. I appreciate the efforts of Pam Sutherland (Operations Director at OUP) to oversee the immediate implementation of these enhancements and also to develop procedures to reduce the error rate itself.

Editorial policies

Available on the MBE website (<http://mbe.oxfordjournals.org/>) are updated Instructions to Authors.

Scope: MBE welcomes analyses of data or new methodologies for such analyses, with the primary objective of illuminating the process of evolution. Conclusions must derive from a well-defined inferential framework. As is the case in virtually all biological disciplines, the evidentiary basis of MBE papers is increasingly genomic in scale. At any scale, well-supported inferences about the nature of the evolutionary process remain the overarching objective, with investigations for which the primary contribution is phylogenetic reconstruction or description of patterns of molecular variation likely to find a better fit in other venues.

Reviews: Reviews addressing key research areas are generally invited, but I welcome discussion with authors of possible review topics. Publication charges are waived for accepted reviews, which are made freely available on the MBE website.

Ethical publication: As a member of the Committee on Publication Ethics (COPE, <http://publicationethics.org/>),

Table 1. Recent Trajectory.

Volume	20	21	22	23 ^a	24	25
Year	2003	2004	2005	2006	2007	2008
Manuscripts received	645	727	800	863	908	901
Articles ^b	229	236	259	247	284	269
Open Access				15	36	37
Acceptance rate (%)	35.5	32.5	32.4	28.6	31.3	29.9
Article pages published	2145	2349	2533	2339	2834	2724

^a Excluding Young Investigator articles^b Research Articles, Letters, and Reviews

MBE draws upon the guidelines suggested by this organization. Over past two years, the incidence has increased of inappropriate use of text or material from published literature without proper citation. All such incidents have involved inexperienced investigators or inadequate oversight by more senior co-authors, all of whom of course share responsibility for the content of any submission. MBE maintains a zero-tolerance policy on unethical practices. We are adopting the use of software designed to detect plagiarism, provided through the CrossRef service CrossCheck (<http://www.crossref.org/crosscheck.html>).

Appeals: Formal appeals to the Editor-in-Chief of final decisions on manuscripts should address procedural problems in the conduct of peer review (e.g., conflicts of interest or breaches of confidentiality). Substantive concerns (e.g., assessment of the science or appropriateness for MBE) lie primarily within the purview of the Associate Editors.

Standards for data accessibility: Data and other resources supporting articles published in MBE must be made available, together with a sufficiently detailed description of their nature and acquisition to permit replication of results. Beyond this minimal universal standard, deposition of such resources in public archives offers ben-

Table 2. Content.

	Non-Open Access			Open Access	
	Research	Letter	Review	Research	Letter
Number of articles	212	18	2	33	4
Average page length	10.6	3.9	10.5	10.8	3.8
Color figures/article	0.9	0.4	2.5	1.6	1.0

Table 3. Decisions on Initial Submissions.

Decision	Number	Percentage
Accept	15	1.9
Minor Revision	173	21.8
Major Revision	62	7.8
Reject and Resubmit	158	20.0
Reject	197	24.9
AE Reject ^a	124	15.7
EiC Reject ^b	63	8.0

^a Associate Editor reject without review^b Editor in Chief reject without review

efits to the authors of the original article describing their analysis. For example, a recent study indicated that public availability of data was associated with a 69% increase in citations (Piwowar et al. 2007).

At its 2007 meeting in Halifax, Nova Scotia, the SMBE Council joined several other organizations in evolutionary biology in establishing a partnership with Dryad (<http://www.datadryad.org/repo/>), a joint project of the National Evolutionary Synthesis Center (NESCent, <https://www.nescent.org>) and the University of North Carolina Metadata Research Center (<http://ils.unc.edu/mrc/>). A four-year grant from the Biological Databases and Informatics program of the National Science Foundation (USA) presently supports the development of the Dryad digital repository of scientific data. Ultimately, this repository will enable searches, using a variety of biological relevant keys (e.g., gene, taxon, geographical location of samples), of the data themselves, even apart from the original article in which they appeared. To ensure accessibility of archived data in perpetuity, the format of data files will be automatically updated. MBE authors will soon be invited to upload data supporting their articles to the Dryad digital repository.

References

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