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Recognising the need for a citable description of new methods and techniques in ecology and evolution, our Application papers describe new software with the intention of promoting and maximising the uptake of these new approaches.

In order to disseminate the newest advances as broadly as possible, we are pleased to be able to offer free access to all Application papers published in *Methods in Ecology and Evolution* for one month after they are assigned to an issue.

Guidelines for Authors

1. **This applies to (but is not limited to):**
a. Software: new packages or significant updates in functionality - significant is defined as "novel capabilities enabling new applications", as opposed to refinements on existing functionalities.
b. Web applications - as long as they are packaged in way that allows user to run them independently, or a case for why this is impossible is made.

2. **To be included with the submission**:
a. At a minimum, everything the reader will need to install and run the software; this includes a URL to see the source in an anonymous way (no login required), a specification of the language(s) used and their version(s), and dependencies on binaries that are not bundled with the software itself nor handled by the language package manager.
b. The code checklist must be filled in and uploaded as a 'File for the reviewers and editors'.
c. During the review process, code should be available for review on an open repository, such as Github. At acceptance, the code should be published in a suitable archive, as in our Data Archiving Policy.

3. **Structure**
a. Although we do not wish to be prescriptive about the structure, we recommend that the paper includes the application description along with one or several worked examples. Please note that the typical introduction, methods, results, discussion structure isn't required, and often is not appropriate, for Applications papers.

4. **Style guide**
a. We strongly suggest that authors follow a style guide for their language/s of choice. E.g. http://adv-r.had.co.nz/Style.html for R.

5. **Testing**
To help ensure the software is flexible and amenable to adapting in the future, tests should be included in the software:
a. Code testing is a vital part of open source software as it ensures that code is robust to changes and does what the authors expect it to do.
b. There are many ways to implement testing, for R users we recommend the following guide: https://r-pkgs.org/tests.html.
c. In addition to providing tests, some developers may want to calculate and report the coverage of their tests, for example using a tool such as CodeCov: https://about.codecov.io/.

Examples

Analysing economic costs of invasive alien species with the INVACOST R package

Boris Leroy, Andrew M. Kramer, Anne-Charlotte Vaissière, Melina Kourantidou, Franck Courchamp, Christophe Diagne

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Rpadrino: An R package to access and use PADRINO, an open access database of Integral Projection Models

Sam C. Levin, Sanne Evers, Tomos Potter, Mayra Peña Guerrero, Dylan Z. Childs, Aldo Compagnoni, Tiffany M. Knight, Roberto Salguero-Gómez

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EcoPhyloMapper: An R package for integrating geographical ranges, phylogeny and morphology

Pascal O. Title, Donald L. Swiderski, Miriam L. Zelditch

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sp0ccupancy: An R package for single-species, multi-species, and integrated spatial occupancy models

Jeffrey W. Doser, Andrew O. Finley, Marc Kéry, Elise F. Zipkin

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FLEXSDM: An R package for supporting a comprehensive and flexible species distribution modelling workflow

Santiago José Elías Velazco, Miranda Brooke Rose, André Felipe Alves de Andrade, Ignacio Minoli, Janet Franklin

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bdc: A toolkit for standardizing, integrating and cleaning biodiversity data

Bruno R. Ribeiro, Santiago José Elías Velazco, Karlo Guidoni-Martins, Geiziane Tessarolo, Lucas Jardim, Steven P. Bachman, Rafael Loyola

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MCERA5: Driving microclimate models with ERA5 global gridded climate data

David H. Klinges, James P. Duffy, Michael R. Kearney, Ilya M. D. Maclean

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Fragmented landscape generator (`flsgen`): A neutral landscape generator with control of landscape structure and fragmentation indices

Dimitri Justeau-Allaire, Grégoire Blanchard, Thomas Ibanez, Xavier Lorca, Ghislain Vieilledent, Philippe Birnbaum

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TREETOP: A Shiny-based application and R package for extracting forest information from LiDAR data for ecologists and conservationists

Carlos Alberto Silva, Andrew T. Hudak, Lee A. Vierling, Ruben Valbuena, Adrian Cardil, Midhun Mohan, Danilo Roberti Alves de Almeida, Eben N. Broadbent, Angelica M. Almeyda Zambrano, Ben Wilkinson, Ajay Sharma, Jason B. Drake, Paul B. Medley, Jason G. Vogel, Gabriel Atticciati Prata, Jeff W. Atkins, Caio Hamamura, Daniel J. Johnson, Carine Klauberg

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Caleb P. Charpentier, April M. Wright

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Rafael Schouten, Virgile Baudrot, Paul Umina, James Maino

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Víctor Saldaña-Núñez, Fernando Córdova-Lepe, Felipe N. Moreno-Gómez

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Mark P. Johnson

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Rcompadre and Rage—Two R packages to facilitate the use of the COMPADRE and COMADRE databases and calculation of life-history traits from matrix population models

Owen R. Jones, Patrick Barks, Iain Stott, Tamora D. James, Sam Levin, William K. Petry, Pol Capdevila, Judy Che-Castaldo, John Jackson, Gesa Römer, Caroline Schuette, Chelsea C. Thomas, Roberto Salguero-Gómez

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Generalizing hierarchical and variation partitioning in multiple regression and canonical analyses using the `rdacca.hp` R package

Jiangshan Lai, Yi Zou, Jinlong Zhang, Pedro R. Peres-Neto

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Exploring noise, degeneracy and determinism in biological networks with the `einet` package

Brennan Klein, Anshuman Swain, Travis Byrum, Samuel V. Scarpino, William F. Fagan

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KTU: K-mer Taxonomic Units improve the biological relevance of amplicon sequence variant microbiota data

Po-Yu Liu, Shan-Hua Yang, Sung-Yin Yang

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Moritz D. Lürig

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ubms: An R package for fitting hierarchical occupancy and N-mixture abundance models in a Bayesian

framework

Kenneth F. Kellner, Nicholas L. Fowler, Tyler R. Petroelje, Todd M. Kautz, Dean E. Beyer, Jerrold L. Belant

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Carrie M. Tribble, William A. Freyman, Michael J. Landis, Jun Ying Lim, Joellë Barido-Sottani, Bjørn Tore Kopperud, Sebastian Höhna, Michael R. May

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ontoFAST: An R package for interactive and semi-automatic annotation of characters with biological ontologies

Sergei Tarasov, István Mikó, Matthew Jon Yoder

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allodb: An R package for biomass estimation at globally distributed extratropical forest plots

Erika Gonzalez-Akre, Camille Piponiot, Mauro Lepore, Valentine Herrmann, James A. Lutz, Jennifer L. Baltzer, Christopher W. Dick, Gregory S. Gilbert, Fangliang He, Michael Heym, Alejandra I. Huerta, Patrick A. Jansen, Daniel J. Johnson, Nikolai Knapp, Kamil Král, Dunmei Lin, Yadvinder Malhi, Sean M. McMahon, Jonathan A. Myers, David Orwig, Diego I. Rodríguez-Hernández, Sabrina E. Russo, Jessica Shue, Xugao Wang, Amy Wolf, Tonghui Yang, Stuart J. Davies, Kristina J. Anderson-Teixeira

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Christian John, Fraser Shilling, Eric Post

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Emilio Berti, Marco Davoli, Robert Buitenwerf, Alexander Dyer, Oskar L. P. Hansen, Myriam Hirt, Jens-Christian Svenning, Jördis F. Terlau, Ulrich Brose, Fritz Vollrath

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Juan Sebastián Ulloa, Sylvain Haupert, Juan Felipe Latorre, Thierry Aubin, Jérôme Sueur

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Sashimi: A toolkit for facilitating high-throughput organismal image segmentation using deep learning

Shawn T. Schwartz, Michael E. Alfaro

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`geomorph v4.0` and `gmShiny`: Enhanced analytics and a new graphical interface for a comprehensive morphometric experience

Erica K. Baken, Michael L. Collyer, Antigoni Kaliontzopoulou, Dean C. Adams

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`poems`: R package for simulating species' range dynamics using pattern-oriented validation

Damien A. Fordham, Sean Haythorne, Stuart C. Brown, Jessie C. Buettel, Barry W. Brook

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track2KBA: An R package for identifying important sites for biodiversity from tracking data

Martin Beal, Steffen Oppel, Jonathan Handley, Elizabeth J. Pearmain, Virginia Morera-Pujol, Ana P. B. Carneiro, Tammy E. Davies, Richard A. Phillips, Philip R. Taylor, Mark G. R. Miller, Aldina M. A. Franco, Inês Catry, Ana R. Patrício, Aissa Regalla, Iain Staniland, Charlotte Boyd, Paulo Catry, Maria P. Dias

Methods in Ecology and Evolution | Pages: 2372-2378 | DOI: 10.1111/2041-210X.13713

`ipmr`: Flexible implementation of Integral Projection Models in R

Sam C. Levin, Dylan Z. Childs, Aldo Compagnoni, Sanne Evers, Tiffany M. Knight, Roberto Salguero-Gómez

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SlicerMorph: An open and extensible platform to retrieve, visualize and analyse 3D morphology

Sara Rolfe, Steve Pieper, Arthur Porto, Kelly Diamond, Julie Winchester, Shan Shan, Henry Kirveslahti, Doug Boyer, Adam Summers, A. Murat Maga

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Grace Twiston-Davies, Matthias A. Becher, Juliet L. Osborne

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The Australian Acoustic Observatory

Paul Roe, Philip Eichinski, Richard A. Fuller, Paul G. McDonald, Lin Schwarzkopf, Michael Towsey, Anthony Truskinger, David Tucker, David M. Watson

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BRacatus: A method to estimate the accuracy and biogeographical status of georeferenced biological data

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ENMeval 2.0: Redesigned for customizable and reproducible modeling of species' niches and distributions

Jamie M. Kass, Robert Muscarella, Peter J. Galante, Corentin L. Bohl, Gonzalo E. Pinilla-Buitrago, Robert A. Boria, Mariano Soley-Guardia, Robert P. Anderson

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Linking fire behaviour and its ecological effects to plant traits, using FRaME in R

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classecol: Classifiers to understand public opinions of nature

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Carmel Farage, Daniel Edler, Anna Eklöf, Martin Rosvall, Shai Pilosof

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Daniel Edler, Johannes Klein, Alexandre Antonelli, Daniele Silvestro

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GPSeqClus: An **R** package for sequential clustering of animal location data for model building, model application and field site investigations

Justin G. Clapp, Joseph D. Holbrook, Daniel J. Thompson

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Identifying flow modules in ecological networks using Infomap

Carmel Farage, Daniel Edler, Anna Eklöf, Martin Rosvall, Shai Pilosof

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Maxime Réjou-Méchain, Ariane Tanguy, Camille Piponiot, Jérôme Chave, Bruno Hérault

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Davide Marnetto, Emilia Huerta-Sánchez

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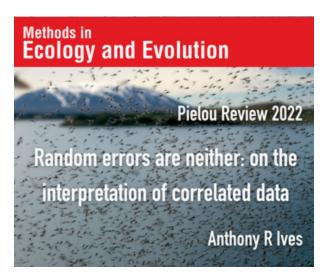Abstract | Full text | PDF | References | Request permissions

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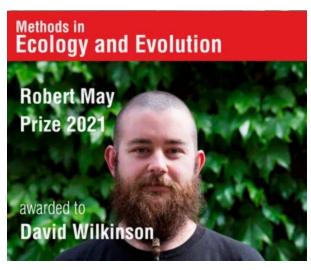
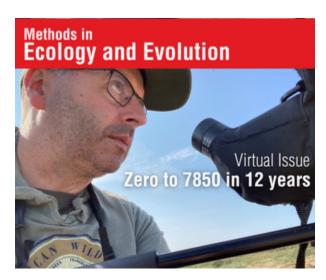Lucie Zinger, Clément Lionnet, Anne-Sophie Benoiston, Julian Donald, Céline Mercier, Frédéric Boyer

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maxnodf: An R package for fair and fast comparisons of nestedness between networks

Christoph Hoeppke, Benno I. Simmons

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