raxmlGUI

version 1.5

manual

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Contents

Introduction

RaxmlGUI is a python application, which provides a user friendly front-end for RAxML (Stamatakis 2014a) for Maximum Likelihood based phylogenetic analyses. The GUI interacts with RAxML executables, which are incorporated in the package, or the CIPRES Science Gateway. It enables the user to select input files, set the parameters and run ML analyses locally or in the cloud, such as phylogenetic reconstructions or ancestral state reconstructions with only a few mouse clicks. A number of options and functions are automated (e. g. checking for identical sequences, or gap-only characters) and simplified (e. g. model and outgroup selection, excluding sites, setting topological constraints and partitioning a matrix). Some features extend the usage of RAxML, e. g. assembling concatenated datasets with automatic partioning, and providing analyses pipelines e. g. bootstrapping followed by computing a consensus tree, or a fast tree search followed by branch lengths estimation and computing of SH-like support values.

The GUI is meant to simplify the usage of RAxML, nevertheless it is strongly recommended to get familiar with the RAxML manual (Stamatakis 2014b) and the "hands-on session"[1] on the Exelixis page, to be aware of contents and intent of input and output files.

Requirements

- RaxmlGUI runs under Mac, Windows and Linux operating systems. The GUI automatically determines the operating system when started for the first time, and selects the respective RAxML executable.
- **Python 2.5.x or higher is required**, but please note that **Python 3.x.x is not supported**. **Under Windows make sure** that the python folder is added to your **PATH variable** (in recent python versions this is possible via a checkbox during installation). An explanation on how to do that manually you can find here.
- Additionally you can install the python library DendroPy (Sukumaran & Holder 2010) to be able to import from and export to NEXUS files (Maddison et al. 1997).
- **Furthermore, you can** set up an account for the CIPRES REST API (Miller et al. 2015), to **run RAxML** analyses **on the Cipres Science Gateway** (Miller et al. 2011) instead of using your local RAxML executable, if you install an additional python library. For further explanations see below.
- **The application can be launched** with a double click on the file "raxmlGUI.py" under Windows (during the installation of Python it should be set as the default application for the ".py" extension). Under Unix (Mac OS and Linux) the program is launched by browsing to its directory via shell, and typing "`./raxmlGUI.py`" or "`python raxmlGUI.py`". A Mac OSX application is also provided, that can be run with a double click.
- **Avoid special characters (like diacritics) and punctuation other than dots ("."") and underscore ("_") in the (path) names of the raxmlGUI folder and all input files!**

[1] http://sco.h-its.org/exelixis/web/software/raxml/hands_on.html

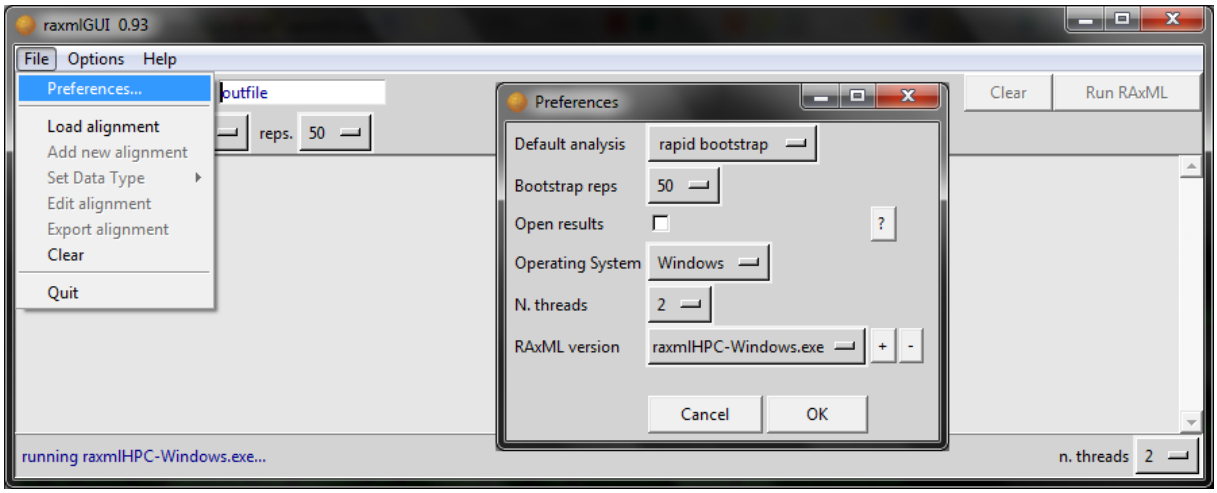

Figure 1: The preferences panel

Preferences

The preferences panel provides the possibilities to change default settings and select a RAxML executable. As default you can choose among a "normal" (Windows) or a SSE3 (Mac OSX; Berger & Stamatakis 2010) and a multithread version (Ott et al. 2007). If you choose the multithread version the number of threads used by RAxML can be set. You can use the "+" button to add additional versions of RAxML (e. g. newer binaries[2] or those compiled for special needs). The chosen binary is then automatically copied to the application contents folder "/raxml". Old or unused versions can be removed with "-" (WARNING: These executable files will be erased).

If the box "Open results" is checked, the resulting tree (e. g. best-scoring ML tree with bootstrap values) will be opened with the default application for tree files[3] (.tre extention), if you have set one.

Please note that changes made in the preferences panel become effective only after re-starting the program.

Using the CIPRES Science Gateway ***NEW in version 1.5!***

You can opt to run your analysis (so far only working for the default analysis type: "3. ML + rapid bootstrap", see below) on the CIPRES Science Gateway (Miller et al. 2011) via the REST API (Miller et al. 2015). You will need to install the necessary python toolkit, kindly provided by Terri Schwartz from the SDSC and included in the package. You will be guided through the installation when accessing the CIPRES options. Alternatively you can also install the toolkit manually by navigating to the folder "/raxmlgui/setup_python_cipres" in a command line window (using the "cd" command) and typing "python setup.py install" (without the quotes). After restarting raxmlGUI the CIPRES options should be available.

To configure the CIPRES option within raxmlGUI you can use the Utility "Configure CIPRES ID" and type in your log in information. If you don't have an account, yet, you can set one up using the button "Sign Up" or via the web page of the CIPRES REST API. **NOTE** that **the log in (user name and password) information entered will be saved in a plain text file**

[2]You can find the latest source code on Alexis Stamatakis' git repository.

[3]Widely used tree visualizers are Dendroscope (Huson et al. 2007), FigTree (Rambaut 2006), and Treeview (Page 1996). For a comprehensive list of tree visualizing and editing software see http://bioinfo.unice.fr/biodiv/Tree_-editors.html.

called "pycipres.conf" in your home folder. Especially on public computers, you should erase the file or its contents after use, which can be done from within the same utility in raxmlGUI.

You can set a maximum time for your analysis (at the bottom of the main raxmlGUI window "CIPRES CPU time"), after which the potentially unfinished job would be aborted. The maximum time is 168 hours (= 7 days). The server will give priority to shorter jobs.

Once the CIPRES REST service is configured in raxmlGUI launching an analysis on the CIPRES servers is very easy. You can load an alignment and set substitution model, partitions etc. as in a standard raxmlGUI analysis (more details below) and select an option in the "CIPRES action" button. There are currently two options to start the analysis:

1. "Run CIPRES-RAXML" will launch the analysis in a new Terminal window that will show the progress of the run. Note that this window should not be closed until the end of the run

2. "Run CIPRES-RAXML in background" will send the analysis to the CIPRES servers as a background process. This means that the analysis will continue even after you close raxmlGUI. You will be notified when the analysis is done by email (the same address you used to register to the CIPRE-REST services).

The "CIPRES action" button also provides options to check the current status of your job(s) running on the CIPRES servers and to download the results to a directory of your choice. The results of each job will be saved to folders named after the job's IDs.

Depending on where you live, you have a certain CPU time available per year (currently for 50 000 CPU hours for US citizens, 30 000 CPU hours for others. Note that parallel jobs count multiplied by the number of processes). If you exceed this time you won't be able to submit jobs any more.

Loading a file

With the button "Load alignment" you can load a data set as input for the RAxML analysis, which must be in PHYLIP format[4]. A FASTA or NEXUS file (Maddison et al. 1997) can be loaded with the menu option "Import FASTA/NEXUS file". The latter will be converted to a PHYLIP file for which you are asked to specify a path and file name. For converting NEXUS to PHYLIP the additional python library DendroPy (Sukumaran & Holder 2010) is needed. In case it is not yet installed, you will be guided through the installation process[5]. **Please note, that blanks and special characters in taxon names in the imported file will cause errors, as they are not allowed in PHYLIP format**, please rename your taxa according to PHYLIP limitations[6].

The data type of the loaded file is determined automatically. If the file contains only one data type (i. e. nucleotides, amino acid, binary, or multistate), the alignment will be checked for readability (through the RAxML option "`-f c`"). A warning appears in case identical sequences and/or gap-only characters are detected: you can choose to run the analyses on either the original or the reduced data set. Note that if you want to exclude sites, partition the matrix and/or add additional data sets to a combined alignment, you should retain the

[4] For an example see Appendix A

[5] If you agree to install the library, the latest source code from Jeet Sukumaran's git repository is downloaded as a zip folder. You will need to unzip this folder and pass its path to raxmlGUI, when it asks for it (point the installer to the folder which contains the file "setup.py"). You can follow the installation process in the terminal/console window. You will need to restart raxmlGUI to make use of DendroPy.

[6] Prohibited characters in PHYLIP are: `, ' ) ( : ; ] [`

original file, since through this option taxa might be removed and/or coloumn numbers might change.

Analysis

Analysis settings

Seven different main analyses can be carried out through raxmlGUI:

1. "**Fast tree search**" – very fast, superficial tree search (RAxML option "-f E") followed by optional computations of branch lengths ("-f e") and SH-like support values ("-f J"; Shimodaira & Hasegawa 1999)[7]. The analysis result is comparable to FastTree (Price et al. 2010) outputs, but is expected to yield better likelihood scores.

2. "**ML search**" – Maximum likelihood reconstruction using the rapid hill-climbing algorithm ("-f d"; Stamatakis et al. 2007), optionally followed by the computation of SH-like support values (see 1.), which will be plotted on the single best-scoring tree[7]. To combine the resulting trees of independent ML searches in one file, check the box "combined output".

3. "**ML + rapid bootstrap**" (default) – Rapid bootstrap analysis and search for a best-scoring Maximum Likelihood tree (equivalent to 2.). The number of ML searches is equal to 20% of the BS replicates ("-f a"; Stamatakis et al. 2008). The bootstrap values are reported on the ML tree.

4. "**ML + slow bootstrap**" – Slow bootstrap analysis ("-b"), followed by a ML search (2.). The bootstrap support values are drawn on the most likely tree ("-f b").

5. "**Bootstrap + consensus**" – Rapid bootstrap analysis ("-x") and a subsequent majority rule consensus tree calculation from all bootstrap trees[7] ("-J MR").

6. "**Ancestral states**" – Compute marginal ancestral states based on a user provided rooted tree and a character matrix ("-f A").

7. "**Pairwise distances**" – Compute distances for all taxa pairs in the data set ("-f x"). As default a MP starting tree will be calculated, alternatively you can provide a user defined tree. This function is only available for GAMMA models.

Depending on the kind of alignment loaded you can choose the substitution model (GTR, BIN, MULTI, or PROT) with GAMMA[I] (Yang 1994), or CAT[I] (Stamatakis 2006) rate heterogeneity, or without rate heterogeneity ("-V"). For large data sets it is possible to select the RAxML option "-F" from the menu to reduce the used memory (works best in combination with CAT[I]).

If the file contains **amino acid** data, you can specify the substitution model[8] you want to apply, and whether base frequencies should be determined empirically (note that the GTR substitution models always rely on empirical frequencies). If the data type in the file is **multistate** you can choose between GTR, Ordered, and MK substitution model.

[7] Such trees can be converted to a FigTree compatible format using the menu option "Convert to FigTree".

[8] Available substitution models for amino acids are: DAYHOFF, DCMUT, JTT, MTREV, WAG, RTREV, CPREV, VT, BLOSUM62, MTMAM, LG, MTART, MTZOA, PMB, HIVB, HIVW, JTTDCMUT, FLU, GTR and GTR_UNLINKED. For the references of these see Appendix D.

You can set the **number of bootstrap replicates** with the option button "reps". You can choose a predefined number, set a user defined value, or select options of automatic "bootstopping" (Pattengale et al. 2010) according to different methods such as majority rule tree based criteria (RAxML options "`-N autoMR`" [recommended], "`-N autoMRE`", and "`-N autoMRE_IGN`") and the frequency-based criterion (option "`-N autoFC`"). If you check the box **"BS brL"** (option "`-k`"), branch lengths will be saved in the bootstrap trees (which increases computation time). Additionally you can select the **number of independent ML searches** in the second and the fourth option.

You can load a Newick file to provide a **starting tree** for the ML-search through the analysis menu (RAxML option "`-t`").

With a nucleotide alignment you can load a file in which brackets (`()`, `[]`, `{}`, `<>`) define stems and pseudo-knot regions of the sequence's **secondary structure**. The absolute number of characters of this file must be identical to the number of sites of the alignment. Nucleotide positions within the specified regions are represented by dots ("`.`").

Additional Analyses

With a file containing a set of trees (e. g. the "RAxML_bootstrap" output file from a bootstrap analysis) you can generate majority rule or strict **consensus trees** (RAxML option "`-J`"). Also you can create a **set of pruned trees**, which lack a set of rogue taxa, that decrease support values (Pattengale et al. 2011), a consensus tree from these pruned trees is automatically created.

In addition you can compute **Robinson-Foulds pairwise distances** (Robinson & Foulds 1981) between trees (option "`-f r`").

With an alignment loaded and a file containing one or more trees you can also compute **per site log Likelihoods** (option "`-f g`"). The output that can be read by CONSEL[9] (Shimodaira 2001) to calculate p-values. In addition you can compute **SH-like support values** (Shimodaira & Hasegawa 1999) on a given (best) tree (option "`-f J`").

Excluding sites

In order to exclude sites you can use the interactive panel, or load a file which has to be in the RAxML standard format:

```
1-200 333-333 500-667
```

Loading a file with this content, or specifying these ranges in the panel, will produce a new alignment file (using the RAxML flag "`-E`"), reduced by the first 200 columns, the single site 333 and the sites 500–667. The new alignment file is automatically set as input and is again checked for identical sequences and/or gap-only characters.

Partitioning the matrix

There are three different ways of defining partitions (RAxML option "`-q`"):

Maybe the easiest way is to load individual partitions one after the other as separate files with the "Add Alignment" -button. RaxmlGUI will automatically set the partitions according to the determined data type. **CAUTION! RaxmlGUI will ONLY check for identical taxon counts! Make sure taxon order and names are identical in all files!**

[9] You can use the CONSEL command "`seqmt --puzzle YOURFILE`" to convert it to CONSEL format

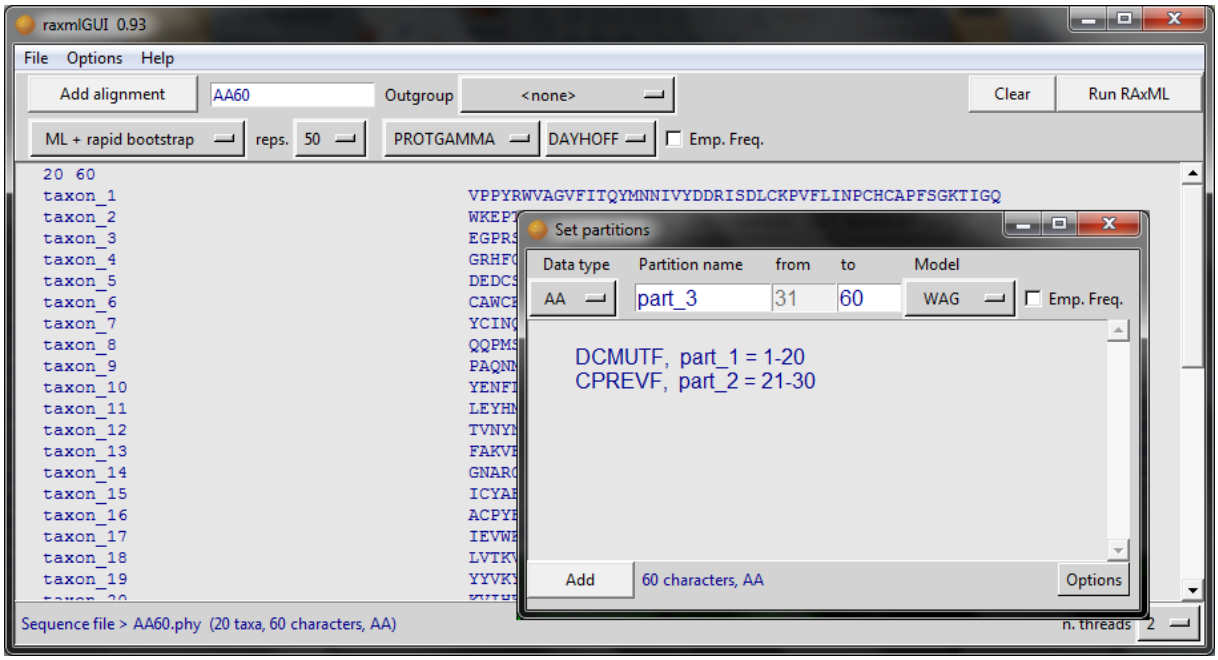

Figure 2: The partitioning panel

The second way is to load the combined data set as one and to set partitions in an interactive way with the option "Set/Edit partitions..." .

The third way is to load a file with the format specified in Stamatakis (2014b)[10]; note that in a partitioned analysis every site has to be assigned to one partition, i. e. sites must not be assigned to two different partitions, and no site is allowed to be not assigned to any partition.

In any case you can edit, delete, and export the partitions set.

If you successfully set a partitioning scheme on your data set, you will be asked before the run starts if you want to calculate the branch lengths independently for each partition (RAxML option "-M"). This will produce best-scoring likelihood trees with branch length optimized for each partition (identical topology).

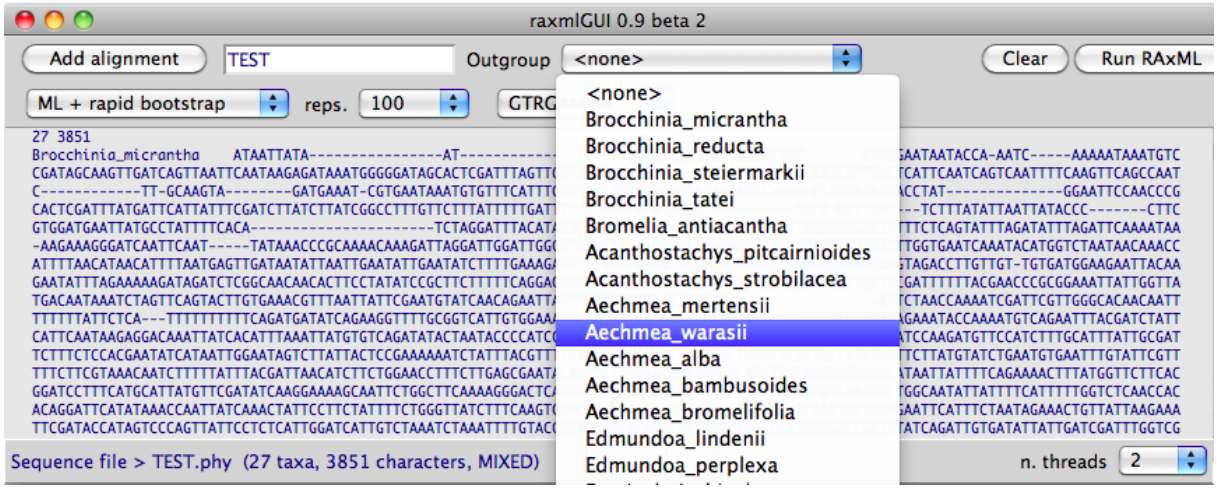

Figure 3: Outgroup selection

[10] See also Appendix B

Outgroup selection

A list of all taxa in the matrix is created in the program's toolbar for a quick single-taxon outgroup selection (RAxML option "-o"). If you want to specify more than one taxon to be in the outgroup, choose the option "select multiple outgroup" from the analysis menu. A window will open with a list of all taxa. You can mark more than one taxon by holding ⇧ (selecting ranges) or Ctrl (selecting single entries) for selecting those as outgroup. If RAxML finds the multiple outgroup not to be monophyletic, it will take the first taxon in the list as outgroup. If no outgroup is selected, the tree will be unrooted.

Setting a topological constraint

You can enforce topological constraints to your analysis through the menu option "enforce constraints". You can define taxon groups through a panel ("define topological constraint...") or by uploading a Newick formatted tree file, which can be binary or multifurcating. RAxML options "-r" or "-g" will be used for binary or multifurcating tree constraints, respectively.

Note that RAxML accepts only backbone constraints, which means, that unconstrained taxa can be placed at any position in the resulting tree, including within constrained clades. If you want to constrain monophyletic groups you can check the respective box in the panel, this will automatically append the remaining taxa to the set of constraints, so all constrained clades will result monophyletic.

Output files

You can set the name of the RAxML output files in the text field. By default the output file name is the same as the input file (without extension). The suffix "_red" is appended if identical sequences (or gap-only characters) are excluded from the analyses, and "_exc" is used when the "exclusion site" option is applied. If a RAxML info file with the same ID is found in the directory, you are prompted to change the output name before starting the analysis. For all types of output files, and their contents please refer to Stamatakis (2014b).

Utilities

In some trees RAxML associates support values to the branches, rather than to the nodes (e. g. consensus trees, and those with SH-like support values). This format is not supported by FigTree (Rambaut 2006). However, if you want to use this program, you can produce a modified version of those tree files using the menu option **"Convert to FigTree format"**.

It is possible to **export your alignment in NEXUS format**. If the necessary python library DendroPy (Sukumaran & Holder 2010) is not yet installed, you will be guided through its installation.[5]

You can **inspect the RAxML command** that will be executed in the terminal before pressing "run RAxML" with the menu option "show RAxML command". In case of pipelined analyses this can contain many commands. Further it is possible to save the command(s) to a file.

You can **export the citation** for raxmlGUI in the following formats: Text, BiBTeX, EndNote (xml), and Reference manager (RIS).

Keyboard shortcuts

Action	Short cut Win/Linux	Short cut Mac
Open alignment	Ctrl O	⌘ O
Export alignment	Ctrl S	⌘ S
Change analysis type	Ctrl A	⌘ A
Import FASTA file	Ctrl F	⌘ F
Exclude sites	Ctrl E	⌘ E
Set partitions	Ctrl P	⌘ P
Clear	Ctrl ⇧ K	⇧ ⌘ K
Quit raxmlGUI	Ctrl Q	⌘ Q
Preferences	Ctrl ⇧ P	⌘ ,
Close window	Ctrl W	⌘ W
Run analysis	Ctrl R	⌘ R
Open this raxmlGUI help	Ctrl H	⌘ ?
Import NEXUS file	Ctrl N	⌘ N
Save changes (exclude sites/ define partitions/preferences)	↵	

Contacts

If you find any problems/bugs or want to give us a feedback, please contact us: raxmlgui.help@gmail.com.
If you want to get the latest news (e. g. new releases and updates), you can subscribe to our mailing list on http://lists.sourceforge.net/lists/listinfo/raxmlgui-news.
If you have problems or questions regarding RAxML, please have a look at the RAxML google group.

If you have problems or questions regarding CIPRES, please direct them to the cipres-rest-users forum.

References

Berger S. A. and Stamatakis A. 2010. Accuracy and performance of single versus double precision arithmetics for maximum likelihood phylogeny reconstruction. *Parallel Processing and Applied Mathematics*. Ed. by R. Wyrzykowski, J. Dongarra, K. Karczewski, and J. Wasniewski. Vol. 6068. Lecture Notes in Computer Science, 270–279. doi: 10.1007/978-3-642-14403-5_29.

Huson D. H., Richter D. C., Rausch C., Dezulian T., Franz M., and Rupp R. 2007. Dendroscope: An interactive viewer for large phylogenetic trees. *BMC Bioinformatics* **8**, 460. doi: 10.1186/1471-2105-8-460.

Maddison D. R., Swofford D. L., and Maddison W. P. 1997. NEXUS: An Extensible File Format for Systematic Information. *Systematic Biology* **46**, 590–621. doi: 10.1093/sysbio/46.4.590.

Miller M. A., Pfeiffer W., and Schwartz T. 2011. The CIPRES Science Gateway: a community resource for phylogenetic analyses. *Proceedings of the 2011 TeraGrid Conference: Extreme Digital Discovery*. TG '11. Salt Lake City, Utah: ACM, 41. isbn: 978-1-4503-0888-5. doi: 10.1145/2016741.2016785.

Miller M. A., Schwartz T., Pickett B. E., He S., Klem E. B., Scheuermann R. H., Passarotti M., Kaufman S., and O'Leary M. A. 2015. A RESTful API for access to phylogenetic tools via the CIPRES Science Gateway. *Evolutionary Bioinformatics* **11**, 43–48. doi: 10.4137/EBO.S21501.

Ott M., Zola J., Stamatakis A., and Aluru S. 2007. Large-scale maximum likelihood-based phylogenetic analysis on the IBM BlueGene/L. *Proceedings of the ACM/IEEE Supercomputing Conference*. Los Alamitos, CA, USA: IEEE Computer Society. doi: 10.1145/1362622.1362628.

Page R. D. M. 1996. Tree View: An application to display phylogenetic trees on personal computers. *Computer Applications in the Biosciences* **12**, 357–358. doi: 10.1093/bioinformatics/12.4.357.

Pattengale N. D., Aberer A. J., Swenson K. M., Stamatakis A., and Moret B. M. E. 2011. Uncovering hidden phylogenetic consensus in large datasets. *IEEE/ACM Transactions on Computational Biology and Bioinformatics* **8**, 902–911. doi: 10.1109/TCBB.2011.28.

Pattengale N. D., Alipour M., Bininda-Emonds O. R. P., Moret B. M. E., and Stamatakis A. 2010. How many bootstrap replicates are necessary? *Journal of Computational Biology* **17**, 337–354. doi: 10.1089/cmb.2009.0179.

Price M. N., Dehal P. S., and Arkin A. P. 2010. FastTree 2 – Approximately maximum-likelihood trees for large alignments. *PLoS ONE* **5**, e9490. doi: 10.1371/journal.pone.0009490.

Rambaut A. 2006. FigTree. url: http://tree.bio.ed.ac.uk/software/figtree/.

Robinson D. R. and Foulds L. R. 1981. Comparison of phylogenetic trees. *Mathematical Biosciences* **53**, 131–147. doi: 10.1016/0025-5564(81)90043-2.

Shimodaira H. 2001. Multiple comparisons of log-likelihoods and combining nonnested models with applications to phylogenetic tree selection. *Communications in Statistics, Part A – Theory and Methods* **30**, 1751–1772. doi: 10.1081/STA-100105696.

Shimodaira H. and Hasegawa M. 1999. Multiple comparisons of log-likelihoods with applications to phylogenetic inference. *Molecular Biology and Evolution* **16**, 1114–1116.

Stamatakis A. 2006. Phylogenetic models of rate heterogeneity: a high performance computing perspective. *Proceedings of the 20th IEEE/ACM International Parallel and Distributed Processing Symposium (IPDPS2006), High Performance Computational Biology Workshop*. Rhodos, Greece. doi: 10.1109/IPDPS.2006.1639535.

Stamatakis A., Blagojevic F., Nikolopoulos D. S., and Antonopoulos C. D. 2007. Exploring new search algorithms and hardware for phylogenetics: RAxML meets the IBM cell. *Journal of VLSI Signal Processing* **48**, 271–286. doi: 10.1007/s11265-007-0067-4.

Stamatakis A., Hoover P., and Rougemont J. 2008. A rapid bootstrap algorithm for the RAxML web servers. *Systematic Biology* **57**, 758–771. doi: 10.1080/10635150802429642.

Stamatakis A. 2014a. RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics* **30**, 1312–1313. doi: 10.1093/bioinformatics/btu033.

Stamatakis A. 2014b. The RAxML v8.0.X Manual, available at http://sco.h-its.org/exelixis.

Sukumaran J. and Holder M. T. 2010. DendroPy: a Python library for phylogenetic computing. *Bioinformatics* **26**, 1569–1571. doi: 10.1093/bioinformatics/btq228.

Yang Z. 1994. Maximum Likelihood phylogenetic estimation from DNA sequences with variable rates over sites: approximate methods. *Journal of Molecular Evolution* **39**, 306–314. doi: 10.1007/BF00160154.

Appendix

A A working PHYLIP example

```
6 40
1_first_row_reads_nroftaxa_blank_nrofcharacters GTGGCGGTCATTCTCATTTG
2_this_is_a_working_example__taxon_names_can_be_very_long ATTCGTGGTCATTCGTGGTC
3_not_allowed_in_names_are_blanks_and_special_characters CGTGACATTCGTGTCTTGGT
4_use_blanks_or_tabs_to_delimit_taxon_names_from_characters TCATTCGTGCGATGTCTGTG
5_there_is_no_option_for_comments_like_in_Nexus_format TGTTGCGTTGGTCATCTCAG
6_for_interleaved_format_dont_repeat_the_taxon_names TTTCTTGGGCGGTCGTTCAA

TCTCATTGGCGGTCATTGGT
ATGTTGGCGGTCATTCTCTG
ATTTGGCCTCCAGGTGTGTT
GGGTCACTCATTCGTGTTGT
TGTGATTGCGGTCATTCTCG
GTTTGGACTCATTTGCGGTC
```

B The format of the Partition file

General format

Parttype, partname = partrange

e. g.:

```
DNA, partition1 = 1-100
BIN, partition2 = 101-200
```

A slightly more complex example

```
JTT, AAgene1 = 1-500

WAGF, AAgene2withempiricalfrequencies = 501-800

MULTI, multistatepartition3 = 801-900

BIN, binarypartition4 = 901-1000

DNA, DNAgene5codon1and2 = 1001-1500\3, 1002-1500\3
DNA, DNAgene5codon3 = 1003-1500\3

DNA, DNAgene6codon1 = 1501-2000\3
DNA, DNAgene6codon2 = 1502-2000\3
DNA, DNAgene6codon3 = 1503-2000\3

DNA, DNAsplitgene7 = 2001-2200, 2800-3000
DNA, intronofgene7 = 2201-2799
```

C Selected papers that cite raxmlGUI

Agarwal I., Bauer A. M., Jackman T. R., and Karanth K. P. 2014. Insights into Himalayan biogeography from geckos: a molecular phylogeny of *Cyrtodactylus* (Squamata: Gekkonidae). *Molecular Phylogenetics and Evolution* **80**, 145–155. doi: 10.1016/j.ympev.2014.07.018.

Agarwal I. and Karanth K. P. 2014. A phylogeny of the only ground-dwelling radiation of *Cyrtodactylus* (Squamata, Gekkonidae): diversification of *Geckoella* across peninsular India and Sri Lanka. *Molecular Phylogenetics and Evolution* **82**, 193–199. doi: 10.1016/j.ympev.2014.09.016.

Aguilera F., McDougall C., and Degnan B. M. 2014. Evolution of the tyrosinase gene family in bivalve molluscs: independent expansion of the mantle gene repertoire. *Acta Biomaterialia* **10**, 3855–3865. doi: 10.1016/j.actbio.2014.03.031.

Ahrens J. B., Borda E., Barroso R., Paiva P. C., Campbell A. M., Wolf A., Nugues M. M., Rouse G. W., and Schulze A. 2013. The curious case of Hermodice carunculata (Annelida: Amphinomidae): evidence for genetic homogeneity throughout the Atlantic Ocean and adjacent basins. *Molecular Ecology* **22**, 2280–2291. doi: 10.1111/mec.12263.

Antunes Carvalho F. and Renner S. S. 2012. A dated phylogeny of the papaya family (Caricaceae) reveals the crop's closest relatives and the family's biogeographic history. *Molecular Phylogenetics and Evolution* **65**, 46–53. doi: 10.1016/j.ympev.2012.05.019.

Beer Z. W. de, Duong T. A., Barnes I., Wingfield B. D., and Wingfield M. J. 2014. Redefining *Ceratocystis* and allied genera. *Studies in Mycology* **79**, 187–219. doi: 10.1016/j.simyco.2014.10.001.

Bilewitch J. P., Ekins M. G., Hooper J. N. A., and Degnan S. M. 2014. Molecular and morphological systematics of the Ellisellidae (Coelenterata: Octocorallia): parallel evolution in a globally distributed family of octocorals. *Molecular Phylogenetics and Evolution* **73**, 106–118. doi: 10.1016/j.ympev.2014.01.023.

Carr M. and Suga H. 2014. The holozoan *Capsaspora owczarzaki* possesses a diverse complement of active transposable element families. *Genome Biology and Evolution* **6**, 949–963. doi: 10.1093/gbe/evu068.

Chacón J. and Renner S. S. 2014. Assessing model sensitivity in ancestral area reconstruction using LAGRANGE: a case study using the Colchicaceae family. *Journal of Biogeography* **41**, 1414–1427. doi: 10.1111/jbi.12301.

Chen W.-J., Lavoué S., Beheregaray L. B., and Mayden R. L. 2014. Historical biogeography of a new antitropical clade of temperate freshwater fishes. *Journal of Biogeography* **41**, 1806–1818. doi: 10.1111/jbi.12333.

Chen W.-J., Lavoué S., and Mayden R. L. 2013. Evolutionary origin and early biogeography of otophysan fishes (Osariophysi: Teleostei). *Evolution* **67**, 2218–2239. issn: 1558-5646. doi: 10.1111/evo.12104.

Choi J. Y. and Aquadro C. F. 2014. The coevolutionary period of *Wolbachia pipientis* infecting *Drosophila ananassae* and its impact on the evolution of the host germline stem cell regulating genes. *Molecular Biology and Evolution* **31**, 2457–2471. doi: 10.1093/molbev/msu204.

Choi Y.-J., Klosterman S. J., Kummer V., Voglmayr H., Shin H.-D., and Thines M. 2015. Multi-locus tree and species tree approaches toward resolving a complex clade of downy mildews (Straminipila, Oomycota), including pathogens of beet and spinach. *Molecular Phylogenetics and Evolution* **86**, 24–34. doi: 10.1016/j.ympev.2015.03.003.

Chomnunti P., Hongsanan S., Aguirre-Hudson B., Tian Q., Peršoh D., Dhami M. K., Alias A. S., Xu J.-C., Liu X., Stadler M., and Hyde K. D. 2014. The sooty moulds. *Fungal Diversity* **66**, 1–36. doi: 10.1007/s13225-014-0278-5.

Cobbs C., Heath J., Stireman III J. O., and Abbot P. 2013. Carotenoids in unexpected places: gall midges, lateral gene transfer, and carotenoid biosynthesis in animals. *Molecular Phylogenetics and Evolution* **68**, 221–228. doi: 10.1016/j.ympev.2013.03.012.

Costion C. M., Edwards W., Ford A. J., Metcalfe D. J., Cross H. B., Harrington M. G., Richardson J. E., Hilbert D. W., Lowe A. J., and Crayn D. M. 2015. Using phylogenetic diversity to identify ancient rain forest refugia and diversification zones in a biodiversity hotspot. *Diversity and Distributions* **21**, 279–289. doi: 10.1111/ddi.12266.

Dai Y.-C., Xue H.-J., Vlasák J., Rajchenberg M., Wang B., and Zhou L.-W. 2014. Phylogeny and global diversity of *Polyporus* group Melanopus (Polyporales, Basidiomycota). *Fungal Diversity* **64**, 133–144. doi: 10.1007/s13225-013-0248-3.

Daranagama D. A., Camporesi E., Tian Q., Liu X., Chamyuang S., Stadler M., and Hyde K. D. 2015. *Anthostomella* is polyphyletic comprising several genera in *Xylariaceae*. *Fungal Diversity*. doi: 10.1007/s13225-015-0329-6.

Deitz K. C., Athrey G., Reddy M. R., Overgaard H. J., Matias A., Jawara M., Della Torre A., Petrarca V., Pinto J., Kiszewski A. E., Kengne P., Costanini C., Caccone A., and Slotman M. A. 2012. Genetic isolation within the malaria mosquito *Anopheles melas*. *Molecular Ecology* **21**, 4498–4513. doi: 10.1111/j.1365-294X.2012.05724.x.

Dennenmoser S., Nolte A. W., Vamosi S. M., and Rogers S. M. 2015. Phylogeography of the prickly sculpin (Cottus asper) in north-western North America reveals parallel phenotypic evolution across multiple coastal-inland colonizations. *Journal of Biogeography*. doi: 10.1111/jbi.12527.

Desiró A., Duckett J. G., Pressel S., Villarreal J. C., and Bidartondo M. I. 2013. Fungal symbioses in hornworts: a chequered history. *Proceedings of the Royal Society B* **280**, 20130207. doi: 10.1098/rspb.2013.0207.

Desiró A., Naumann M., Epis S., Novero M., Bandi C., Genre A., and Bonfante P. 2013. *Mollicutes*-related endobacteria thrive inside liverwort-associated arbuscular mycorrhizal fungi. *Environmental Microbiology* **15**, 822–836. doi: 10.1111/j.1462-2920.2012.02833.x.

Di Domenico M., Martínez A., Lana P., and Worsaae K. 2014. Molecular and morphological phylogeny of Saccocirridae (Annelida) reveals two cosmopolitan clades with specific habitat preferences. *Molecular Phylogenetics and Evolution* **75**, 202–218. doi: 10.1016/j.ympev.2014.02.003.

Du Toit N., Van Vuuren B. J., Matthee S., and Matthee C. A. 2013. Biogeography and host-related factors trump parasite life history: limited congruence among the genetic structures of specific ectoparasitic lice and their rodent hosts. *Molecular Ecology* **22**, 5185–5204. doi: 10.1111/mec.12459.

Falk B. G. and Perkins S. L. 2013. Host specificity shapes population structure of pinworm parasites in Caribbean reptiles. *Molecular Ecology* **22**, 4576–4590. doi: 10.1111/mec.12410.

Fernandes A. M., Gonzalez J., Wink M., and Aleixo A. 2013. Multilocus phylogeography of the Wedge-billed Woodcreeper *Glyphorynchus spirurus* (Aves, Furnariidae) in lowland Amazonia: widespread cryptic diversity and paraphyly reveal a complex diversification pattern. *Molecular Phylogenetics and Evolution* **66**, 270–282. doi: 10.1016/j.ympev.2012.09.033.

Fernandes A. M., Wink M., Sardelli C. H., and Aleixo A. 2014. Multiple speciation across the Andes and throughout Amazonia: the case of the spot-backed antbird species complex (*Hylophylax naevius*/*Hylophylax naevioides*). *Journal of Biogeography* **41**, 1094–1104. doi: 10.1111/jbi.12277.

Filipi K., Marková S., Searle J. B., and Kotlík P. 2014. Mitogenomic phylogenetics of the bank vole *Clethrionomys glareolus*, a model system for studying end-glacial colonization of Europe. *Molecular Phylogenetics and Evolution* **82**, 245–257. doi: 10.1016/j.ympev.2014.10.016.

Foley N. M., Thong V. D., Soisook P., Goodman S. M., Armstrong K. N., Jacobs D., Puechmaille S. J., and Teeling E. C. 2015. How and why overcome the impediments to resolution: lessons from rhinolophid and hipposiderid bats. *Molecular Biology and Evolution* **32**, 313–333. doi: 10.1093/molbev/msu329.

Grudinski M., Pannell C. M., Chase M. W., Ahmad J. A., and Muellner-Riehl A. N. 2014. An evaluation of taxonomic concepts of the widespread plant genus *Aglaia* and its allies across Wallace's Line (tribe Aglaieae, Meliaceae). *Molecular Phylogenetics and Evolution* **73**, 65–76. doi: 10.1016/j.ympev.2014.01.025.

Haddrath O. and Baker A. J. 2012. Multiple nuclear genes and retroposons support vicariance and dispersal of the palaeognaths, and an Early Cretaceous origin of modern birds. *Proceedings of the Royal Society B* **279**, 4617–4625. doi: 10.1098/rspb.2012.1630.

Hedin M. 2015. High stakes species delimitation in eyeless cave spiders (*Cicurina*, Dictynidae, Araneae) from central Texas. *Molecular Ecology* **24**, 346–361. doi: 10.1111/mec.13036.

Hedin M., Carlson D., and Coyle F. 2015. Sky island diversification meets the multispecies coalescent – divergence in the spruce-fir moss spider (*Microhexura montivaga*, Araneae, Mygalomorphae) on the highest peaks of southern Appalachia. *Molecular Ecology*. doi: 10.1111/mec.13248.

Hochbach A., Schneider J., and Röser M. 2015. A multi-locus analysis of phylogenetic relationships within grass subfamily Pooideae (Poaceae) inferred from sequences of nuclear single copy gene regions compared with plastid DNA. *Molecular Phylogenetics and Evolution* **87**, 14–27. doi: 10.1016/j.ympev.2015.03.010.

Hoepflinger M. C., Geretschlaeger A., Sommer A., Hoeftberger M., Hametner C., Ueda T., and Foissner I. 2015. Molecular analysis and localization of CaARA7 a conventional RAB5 GTPase from characean algae. *Traffic* **16**, 534–554. doi: 10.1111/tra.12267.

Hongsanan S., Li Y.-M., Liu J.-K., Hofmann T., Piepenbring M., Bhat D. J., Boonmee S., Doilom M., Singtripop C., Tian Q., Mapook A., Zeng X.-Y., Bahkali A. H., Xu J.-C., Mortimer P. E., Wu X.-H., Yang J.-B., and Hyde K. D. 2014. Revision of genera in Asterinales. *Fungal Diversity* **68**, 1–68. doi: 10.1007/s13225-014-0307-4.

Humphrey P. T., Nguyen T. T., Villalobos M. M., and Whiteman N. K. 2014. Diversity and abundance of phyllosphere bacteria are linked to insect herbivory. *Molecular Ecology* **23**, 1497–1515. doi: 10.1111/mec.12657.

Jaklitsch W. M., Fournier J., Dai D.-Q., Hyde K. D., and Voglmayr H. 2015. *Valsaria* and the Valsariales. *Fungal Diversity*. doi: 10.1007/s13225-015-0330-0.

Jaklitsch W. M., Fournier J., Rogers J. D., and Voglmayr H. 2014. Phylogenetic and taxonomic revision of *Lopadostoma*. *Persoonia* **32**, 52–82. doi: 10.3767/003158514X679272.

Jaklitsch W. M., Samuels G. J., Ismaiel A., and Voglmayr H. 2013. Disentangling the *Trichoderma viridescens* complex. *Persoonia* **31**, 112–146. doi: 10.3767/003158513X672234.

Jaklitsch W. M. and Voglmayr H. 2014. Persistent hamathecial threads in the Nectriaceae, Hypocreales: *Thyronectria* revisited and re-instated. *Persoonia* **33**, 182–211. doi: 10.3767/003158514X685211.

Johansson U. S., Ekman J., Bowie R. C. K., Halvarsson P., Ohlson J. I., Price T. D., and Ericson P. G. P. 2013. A complete multilocus species phylogeny of the tits and chickadees (Aves: Paridae). *Molecular Phylogenetics and Evolution* **69**, 852–860. doi: 10.1016/j.ympev.2013.06.019.

Köhler F. and Criscione F. 2013. Plio-Pleistocene out-of-Australia dispersal in a camaenid land snail. *Journal of Biogeography* **40**, 1971–1982. doi: 10.1111/jbi.12147.

Köhler F. and Criscione F. 2014. A molecular phylogeny of camaenid land snails from north-western Australia unravels widespread homoplasy in morphological characters (Gastropoda, Helicoidea). *Molecular Phylogenetics and Evolution* **83**, 44–55. doi: 10.1016/j.ympev.2014.11.009.

Korn M., Rabet N., Ghate H. V., Marrone F., and Hundsdörfer A. K. 2013. Molecular phylogeny of the Notostraca. *Molecular Phylogenetics and Evolution* **69**, 1159–1171. doi: 10.1016/j.ympev.2013.08.006.

Kriebel R., Michelangeli F. A., and Kelly L. M. 2014. Discovery of unusual anatomical and continuous characters in the evolutionary history of *Conostegia* (Miconieae: Melastomataceae). *Molecular Phylogenetics and Evolution* **82**, 289–313. doi: 10.1016/j.ympev.2014.09.021.

Les D. H., Peredo E. L., King U. M., Benoit L. K., Tippery N. P., Ball C. J., and Shannon R. K. 2014. Through thick and thin: cryptic sympatric speciation in the submersed genus *Najas* (Hydrocharitaceae). *Molecular Phylogenetics and Evolution* **82**, 15–30. doi: 10.1016/j.ympev.2014.09.022.

Li H.-S., Xue X.-F., and Hong X.-Y. 2014. Homoplastic evolution and host association of Eriophyoidea (Acari, Prostigmata) conflict with the morphological-based taxonomic system. *Molecular Phylogenetics and Evolution* **78**, 185–198. doi: 10.1016/j.ympev.2014.05.014.

Liu J., Wang C., Fu D., Hu X., Xie X., Liu P., Zhang Q., and Li M.-H. 2015. Phylogeography of *Nanorana parkeri* (Anura: Ranidae) and multiple refugia on the Tibetan Plateau revealed by mitochondrial and nuclear DNA. *Scientific Reports* **5**, 9857. doi: 10.1038/srep09857.

Liu Y., de Bruijn I., Jack A. L. H., Drynan K., van den Berg A. H., Thoen E., Sandoval-Sierra J. V., Skaar I., van West P., Diéguez-Uribeondo J., van der Voort M., Mendes R., Mazzola M., and Raaijmakers J. M. 2014. Deciphering microbial landscapes of fish eggs to mitigate emerging diseases. *The ISME Journal* **8**, 2002–2014. doi: 10.1038/ismej.2014.44.

Lockwood J. D., Aleksić J. M., Zou J., Wang J., Liu J., and Renner S. S. 2013. A new phylogeny for the genus *Picea* from plastid, mitochondrial, and nuclear sequences. *Molecular Phylogenetics and Evolution* **69**, 717–727. doi: 10.1016/j.ympev.2013.07.004.

Maharachchikumbura S. S. N., Hyde K. D., Groenewald J. Z., Xu J.-C., and Crous P. W. 2014. *Pestalotiopsis* revisited. *Studies in Mycology* **79**, 121–186. doi: 10.1016/j.simyco.2014.09.005.

Maharachchikumbura S. S. N., Hyde K. D., Jones E. B. G., McKenzie E. H. C., Huang S.-K., Abdel-Wahab M. A., Daranagama D. A., Dayarathne M., D'souza M. J., Goonasekara I. D., Hongsanan S., Jayawardena R. S., Kirk P. M., Konta S., Liu J.-K., Liu Z.-Y., Norphanphoun C., Pang K.-L., Perera R. H., Senanayake I. C., Shang Q., Shenoy B. D., Xiao Y., Bahkali A. H., Kang J., Somrothipol S., Suetrong S., Wen T., and Xu J. 2015. Towards a natural classification and backbone tree for *Sordariomycetes*. *Fungal Diversity* **72**, 199–301. doi: 10.1007/s13225-015-0331-z.

Martins A. C., Melo G. A. R., and Renner S. S. 2014. The corbiculate bees arose from New World oil-collecting bees: implications for the origin of pollen baskets. *Molecular Phylogenetics and Evolution* **80**, 88–94. doi: 10.1016/j.ympev.2014.07.003.

Masters J. C., Génin F., Silvestro D., Lister A. M., and DelPero M. 2014. The red island and the seven dwarfs: body size reduction in Cheirogaleidae. *Journal of Biogeography* **41**, 1833–1847. doi: 10.1111/jbi.12327.

Medeiros M. C. M. P. de and Lohmann L. G. 2015. Phylogeny and biogeography of *Tynanthus* Miers (Bignonieae, Bignoniaceae). *Molecular Phylogenetics and Evolution* **85**, 32–40. doi: 10.1016/j.ympev.2015.01.010.

Meiklejohn K. A., Danielson M. J., Faircloth B. C., Glenn T. C., Braun E. L., and Kimball R. T. 2014. Incongruence among different mitochondrial regions: a case study using complete mitogenomes. *Molecular Phylogenetics and Evolution* **78**, 314–323. doi: 10.1016/j.ympev.2014.06.003.

Meiri M., Lister A. M., Collins M. J., Tuross N., Goebel T., Blockley S., Zazula G. D., van Doorn N., Guthrie R. D., Boeskorov G. G., Baryshnikov G. F., Sher A., and Barnes I. 2014. Faunal record identifies Bering isthmus conditions as constraint to end-Pleistocene migration to the New World. *Proceedings of the Royal Society B* **281**, 20132167. doi: 10.1098/rspb.2013.2167.

Metallinou M., Červenka J., Crochet P.-A., Kratochvíl L., Wilms T., Geniez P., Shobrak M. Y., Brito J. C., and Carranza S. 2015. Species on the rocks: Systematics and biogeography of the rock-dwelling *Ptyodactylus* geckos (Squamata: Phyllodactylidae) in North Africa and Arabia. *Molecular Phylogenetics and Evolution* **85**, 208–220. doi: 10.1016/j.ympev.2015.02.010.

Millanes A. M., Truong C., Westberg M., Diederich P., and Wedin M. 2014. Host switching promotes diversity in host-specialized mycoparasitic fungi: uncoupled evolution in the *Biatoropsis-Usnea* system. *Evolution* **68**, 1576–1593. doi: 10.1111/evo.12374.

Moradmand M., Schönhofer A. L., and Jäger P. 2014. Molecular phylogeny of the spider family Sparassidae with focus on the genus *Eusparassus* and notes on the RTA-clade and 'Laterigradae'. *Molecular Phylogenetics and Evolution* **74**, 48–65. doi: 10.1016/j.ympev.2014.01.021.

Morinière J., Michat M. C., Jäch M. A., Bergsten J., Hendrich L., and Balke M. 2015. Anisomeriini diving beetles — an Atlantic – Pacific Island disjunction on Tristan da Cunha and Robinson Crusoe Island, Juan Fernández? *Cladistics*. doi: 10.1111/cla.12074.

Norlinder E., Nygren A., Wiklund H., and Pleijel F. 2012. Phylogeny of scale-worms (Aphroditiformia, Annelida), assessed from 18SrRNA, 28SrRNA, 16SrRNA, mitochondrial cytochrome c oxidase subunit I (COI), and morphology. *Molecular Phylogenetics and Evolution* **65**, 490–500. doi: 10.1016/j.ympev.2012.07.002.

Phookamsak R., Liu J.-K., McKenzie E. H. C., Manamgoda D. S., Ariyawansa H. A., Thambugala K. M., Dai D.-Q., Camporesi E., Chukeatirote E., Wijayawardene D. N. N., Bahkali A. H., Mortimer P. E., Xu J.-C., and Hyde K. D. 2014. Revision of Phaeosphaeriaceae. *Fungal Diversity* **68**, 159–238. doi: 10.1007/s13225-014-0308-3.

Pickering S., Hué S., Kim E.-Y., Reddy S., Wolinsky S. M., and Neil S. J. D. 2014. Preservation of Tetherin and CD4 counter-activities in circulating *Vpu* alleles despite extensive sequence variation within HIV-1 Infected individuals. *PLoS Pathogens* **10**, e1003895. doi: 10.1371/journal.ppat.1003895.

Pisano J., Condamine F. L., Lebedev V., Bannikova A., Quére J.-P., Shenbrot G. I., Pagès M., and Michaux J. R. 2015. Out of Himalaya: the impact of past Asian environmental changes on the evolutionary and biogeographical history of Dipodoidea (Rodentia). *Journal of Biogeography* **42**, 856–870. doi: 10.1111/jbi.12476.

Planas E. and Ribera C. 2014. Uncovering overlooked island diversity: colonization and diversification of the medically important spider genus *Loxosceles* (Arachnida: Sicariidae) on the Canary Islands. *Journal of Biogeography* **41**, 1255–1266. doi: 10.1111/jbi.12321.

Reyes-Velasco J., Meik J. M., Smith E. N., and Castoe T. A. 2013. Phylogenetic relationships of the enigmatic longtailed rattlesnakes (*Crotalus ericsmithi*, *C. lannomi*, and *C. stejnegeri*). *Molecular Phylogenetics and Evolution* **69**, 524–534. doi: 10.1016/j.ympev.2013.07.025.

Reynolds R. G., Niemiller M. L., and Revell L. J. 2014. Toward a Tree-of-Life for the boas and pythons: Multilocus species-level phylogeny with unprecedented taxon sampling. *Molecular Phylogenetics and Evolution* **71**, 201–213. doi: 10.1016/j.ympev.2013.11.011.

Roncal J., Couderc M., Baby P., Kahn F., Millán B., Meerow A. W., and Pintaud J.-C. 2015. Palm diversification in two geologically contrasting regions of western Amazonia. *Journal of Biogeography*. doi: 10.1111/jbi.12518.

Rosnow J. J., Edwards G. E., and Roalson E. H. 2014. Positive selection of Kranz and non-Kranz C_4 phosphoenolpyruvate carboxylase amino acids in Suaedoideae (Chenopodiaceae). *Journal of Experimental Botany* **65**, 3595–3607. doi: 10.1093/jxb/eru053.

Ruch J., Riehl T., May-Collado L. J., and Agnarsson I. 2014. Multiple origins of subsociality in crab spiders (Thomisidae). *Molecular Phylogenetics and Evolution* **82**, 330–340. doi: 10.1016/j.ympev.2014.10.015.

Salgado-Salazar C., Rossman A. Y., Samuels G. J., Hirooka Y., Sanchez R. M., and Chaverri P. 2015. Phylogeny and taxonomic revision of *Thelonectria discophora* (Ascomycota, Hypocreales, Nectriaceae) species complex. *Fungal Diversity* **70**, 1–29. doi: 10.1007/s13225-014-0280-y.

Sánchez-Baracaldo P., Ridgwell A., and Raven J. A. 2014. A Neoproterozoic transition in the marine nitrogen cycle. *Current Biology* **24**, 652–657. doi: 10.1016/j.cub.2014.01.041.

Schaer J., Perkins S. L., Decher J., Leendertz F. H., Fahr J., Weber N., and Matuschewski K. 2013. High diversity of West African bat malaria parasites and a tight link with rodent *Plasmodium* taxa. *Proceedings of the National Academy of Sciences of the USA* **110**, 17415–17419. doi: 10.1073/pnas.1311016110.

Scheunert A. and Heubl G. 2014. Diversification of *Scrophularia* (Scrophulariaceae) in the Western Mediterranean and Macaronesia – Phylogenetic relationships, reticulate evolution and biogeographic patterns. *Molecular Phylogenetics and Evolution* **70**, 296–313. doi: 10.1016/j.ympev.2013.09.023.

Schneider J. V., Bissiengoud P., Carmo E. Amarale M. do, Tahira A., Fay M. F., Thines M., Sosef M. S. M., Zizka G., and Chatrou L. W. 2014. Phylogenetics, ancestral state reconstruction, and a new infrafamilial classification of the pantropical Ochnaceae (Medusagynaceae, Ochnaceae s.str., Quiinaceae) based on five DNA regions. *Molecular Phylogenetics and Evolution* **78**, 199–214. doi: 10.1016/j.ympev.2014.05.018.

Silvestro D., Zizka G., and Schulte K. 2014. Disentangling the effects of key innovations on the diversification of Bromelioideae (Bromeliaceae). *Evolution* **68**, 163–175. doi: 10.1111/evo.12236.

Sinn B. T., Kelly L. M., and Freudenstein J. V. 2015. Putative floral brood-site mimicry, loss of autonomous selfing, and reduced vegetative growth are significantly correlated with increased diversification in Asarum (Aristolochiaceae). *Molecular Phylogenetics and Evolution* **89**, 194–204. doi: 10.1016/j.ympev.2015.04.019.

Slancarova V., Zdanska J., Janousek B., Talianova M., Zschach C., Zluvova J., Siroky J., Kovacova V., Blavet H., Danihelka J., Oxelman B., Widmer A., and Vyskot B. 2013. Evolution of sex determination systems with heterogametic males and females in *Silene*. *Evolution* **67**, 3669–3677. doi: 10.1111/evo.12223.

Solodovnikov A., Yue Y., Tarasov S., and Ren D. 2013. Extinct and extant rove beetles meet in the matrix: Early Cretaceous fossils shed light on the evolution of a hyperdiverse insect lineage (Coleoptera: Staphylinidae: Staphylininae). *Cladistics* **29**, 360–403. doi: 10.1111/j.1096-0031.2012.00433.x.

Stearns J. C., Davidson C. J., McKeon S., Whelan F. J., Fontes M. E., Schryvers A. B., Bowdish D. M. E., Kellner J. D., and Surette M. G. 2015. Culture and molecular-based profiles show shifts in bacterial communities of the upper respiratory tract that occur with age. *The ISME Journal*. doi: 10.1038/ismej.2014.250.

Suija A., Ertz D., Lawrey J. D., and Diederich P. 2015. Multiple origin of the lichenicolous life habit in Helotiales, based on nuclear ribosomal sequences. *Fungal Diversity* **70**, 55–72. doi: 10.1007/s13225-014-0287-4.

Summers M. M., Messing C. G., and Rouse G. W. 2014. Phylogeny of Comatulidae (Echinodermata: Crinoidea: Comatulida): a new classification and an assessment of morphological characters for crinoid taxonomy. *Molecular Phylogenetics and Evolution* **80**, 319–339. doi: 10.1016/j.ympev.2014.06.030.

Tamar K., Carranza S., Bosch H. in den, Sindaco R., Moravec J., and Meiri S. 2015. Hidden relationships and genetic diversity: molecular phylogeny and phylogeography of the Levantine lizards of the genus *Phoenicolacerta* (Squamata: Lacertidae). *Molecular Phylogenetics and Evolution*. doi: 10.1016/j.ympev.2015.05.002.

Trovant B., Orensanz J. M. L., Ruzzante D. E., Stotz W., and Basso N. G. 2014. Scorched mussels (Bivalvia: Ivalvia: Mytilidae: Brachidontinae) from the temperate coasts of South America: phylogenetic relationships, trans-Pacific connections and the footprints of Quaternary glaciations. *Molecular Phylogenetics and Evolution* **82**, 60–74. doi: 10.1016/j.ympev.2014.10.002.

Ure A. E. and Forslund O. 2012. Lack of methylation in the upstream region of human papillomavirus type 6 from aerodigestive tract papillomas. *Journal of Virology* **86**, 13790–13794. doi: 10.1128/JVI.01938-12.

Velo-Antón G., Godinho R., Harris D. J., Santos X., Martínez-Freiria F., Fahd S., Larbes S., Pleguezuelos J. M., and Brito J. C. 2012. Deep evolutionary lineages in a Western Mediterranean snake (*Vipera latastei/monticola* group) and high genetic structuring in Southern Iberian populations. *Molecular Phylogenetics and Evolution* **65**, 965–973. doi: 10.1016/j.ympev.2012.08.016.

Voglmayr H., Rossman A. Y., Castlebury L. A., and Jaklitsch W. M. 2012. Multigene phylogeny and taxonomy of the genus *Melanconiella* (Diaporthales). *Fungal Diversity* **57**, 1–44. doi: 10.1007/s13225-012-0175-8.

Wagner N., Silvestro D., Brie D., Ibisch P. I., Zizka G., Weising K., and Schulte K. 2013. Spatiotemporal evolution of *Fosterella* (Bromeliaceae) in the Central Andean biodiversity hotspot. *Journal of Biogeography* **40**, 869–880. doi: 10.1111/jbi.12052.

Yamasaki H., Hiruta S. F., and Kajihara H. 2013. Molecular phylogeny of kinorhynchs. *Molecular Phylogenetics and Evolution* **67**, 303–310. doi: 10.1016/j.ympev.2013.02.016.

Zhang F., Chen Z., Dong R.-R., Deharveng L., Stevens M. I., Huang Y.-H., and Zhu C.-D. 2014. Molecular phylogeny reveals independent origins of body scales in Entomobryidae (Hexapoda: Collembola). *Molecular Phylogenetics and Evolution* **70**, 231–239. doi: 10.1016/j.ympev.2013.09.024.

Zhou L.-W., Vlasák J., Decock C., Assefa A., Stenlid J., Abate D., Wu S.-H., and Dai Y.-C. 2015. Global diversity and taxonomy of the *Inonotus linteus* complex (Hymenochaetales, Basidiomycota): *Sanghuangporus* gen. nov., *Tropicoporus excentrodendri* and *T. guanacastensis* gen. et spp. nov., and 17 new combinations. *Fungal Diversity*. doi: 10.1007/s13225-015-0335-8.

D References for Amino Acid substitution models

DAYHOFF: Dayhoff M. O., Schwartz R. M., and Orcutt B. C. 1978. A model of evolutionary change in proteins. *Atlas of Protein Sequence and Structure*. Ed. by M. O. Dayhoff. Vol. 5 suppl. 2. National Biomedical Research Foundation, 345–352. URL: http://citeseerx.ist.psu.edu/viewdoc/summary?doi=10.1.1.145.4315.

DCMUT: Kosiol C. and Goldman N. 2005. Different versions of the Dayhoff rate matrix. *Molecular Biology and Evolution* **22**, 193–199. DOI: 10.1093/molbev/msi005.

JTT: Jones D. T., Taylor W. R., and Thornton J. M. 1992. The rapid generation of mutation data matrices from protein sequences. *Computer Applications in the Biosciences* **8**, 275–282. DOI: 10.1093/bioinformatics/8.3.275.

MTREV: Adachi J. and Hasegawa M. 1995. Model of amino acid substitution in proteins encoded by mitochondrial DNA. *Journal of Molecular Evolution* **42**, 459–468. DOI: 10.1007/BF02498640.

WAG: Whelan S. and Goldman N. 2001. A general empirical model of protein evolution derived from multiple protein families using a maximum-likelihood approach. *Molecular Biology and Evolution* **18**, 691–699. URL: http://mbe.oxfordjournals.org/content/18/5/691.

RTREV: Dimmic M. W., S. R. J., P. M. D., and A. G. R. 2002. rtREV: a substitution matrix for inference of retrovirus and reverse transcriptase phylogeny. *Journal of Molecular Evolution* **55**, 65–73. DOI: 10.1007/s00239-001-2304-y.

CPREV: Adachi J., Waddell P., Martin W., and Hasegawa M. 2000. Plastid genome phylogeny and a model of amino acid substitution for proteins encoded by chloroplast DNA. *Journal of Molecular Evolution* **50**, 348–358. DOI: 10.1007/s002399910038.

VT: Müller T. and Vingron M. 2000. Modeling amino acid replacement. *Journal of Computational Biology* **7**, 761–776. DOI: 10.1089/10665270050514918.

BLOSUM62: Henikoff S. and Henikoff J. G. 1992. Amino acid substitution matrices from protein blocks. *Proceedings of the National Academy of Sciences of the U.S.A.* **89**, 10915–10919. URL: http://www.pnas.org/content/89/22/10915.

MTMAM: Yang Z., Nielsen R., and Hasegawa M. 1998. Models of amino acid substitution and applications to mitochondrial protein evolution. *Molecular Biology and Evolution* **15**, 1600–1611. URL: http://mbe.oxfordjournals.org/content/15/12/1600.short.

LG: Le S. and Gascuel O. 2008. An improved general amino acid replacement matrix. *Molecular Biology and Evolution* **25**, 1307–1320. DOI: 10.1093/molbev/msn067.

MTART: Abascal F., Posada D., and Zardoya R. 2007. MtArt: a new model of amino acid replacement for Arthropoda. *Molecular Biology and Evolution* **24**, 1–5. DOI: 10.1093/molbev/msl136.

MTZOA: Rota-Stabelli O., Yang Z., and Telford M. J. n.d. MtZoa: a general mitochondrial amino acid substitutions model for animal evolutionary studies. *Molecular Phylogenetics and Evolution* **52**, 268–272. DOI: 10.1016/j.ympev.2009.01.011.

PMB: Veerassamy S., Smith A., and Tillier E. R. 2003. A transition probability model for amino acid substitutions from blocks. *Journal of Computational Biology* **10**, 997–1010. DOI: 10.1089/106652703322756195.

HIVB, HIVW: Nickle D. C., Heath L., Jensen M. A., Gilbert P. B., Mullins J. I., and Kosakovsky Pond S. L. 2007. HIV-specific probabilistic models of protein evolution. *PLoS ONE* **2**, e503. doi: 10.1371/journal.pone.0000503.

FLU: Dang C. C., Le Q. S., Gascuel O., and Le V. S. 2010. FLU, an amino acid substitution model for influenza proteins. *BMC Evolutionary Biology* **10**, 99. doi: 10.1186/1471-2148-10-99.

GTR: Tavaré S. 1986. Some probabilistic and statistical problems on the analysis of DNA sequences. *Lectures on Mathematics in the Life Sciences* **17**, 57–86.

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