Package: megatrees (via r-universe)

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Type Package

Title Subsets of randomly selected phylogenies from existing mega-phylogenies

Version 0.1.3

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Description There are an increasing number of mega-phylogenies available nowadays, with many of them being sets of thousands of posterior distribution phylogenies. For ecological studies, we may need to randomly select many such posterior phylogeneies to conduct analyses. This data package serves this purpose by providing a small number (100) of randomly selected posterior phylogenies (if available) so that we can readily use them for our downstream analyses without repeating the downloading and selecting processes.

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Encoding UTF-8

LazyData true

LazyDataCompression xz

Suggests ape, parallel, rtrees, testthat (>= 3.0.0), tidyverse, usethis, xfun, dplyr, stringr, remotes

Remotes daijiang/rtrees

Depends R (>= 2.10)

Config/testthat/edition 3

RoxygenNote 7.3.1

Repository https://daijiang.r-universe.dev

RemoteUrl https://github.com/daijiang/megatrees

RemoteRef HEAD

RemoteSha 5613b38ca0c0b2ded89305754aabe4a24685a140

Contents

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tree_amphibian_n100   *100 randomly selected Mega-tree of Amphibians from VertLife.*

Description

100 randomly selected Mega-tree of Amphibians from VertLife.

Usage

```
tree_amphibian_n100
```

Format

A phylogeny with class "multiPhylo". It is also a list, with the first to be the "consensus" tree (the other 99 are posterior phylogenies). Compare with a normal phylo object, each phylogeny has another data frame 'genus_family_root', which provides the root nodes information for every unique genus and family in the phylogeny. Such information can be used to insert new tips onto the phylogeny later.

Source

http://vertlife.org/data/amphibians/

References

Jetz, W., & Pyron, R. A. (2018). The interplay of past diversification and evolutionary isolation with present imperilment across the amphibian tree of life. Nature ecology & evolution, 2(5), 850-858.

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tree_bee   *The Maximum Likely Mega-tree of Bees from Bee Tree of Life*

Description

The Maximum Likely Mega-tree of Bees from Bee Tree of Life

Usage

```
tree_bee
```

Format

A maximum likely phylogeny with class "phylo". Compare with a normal phylo object, this phylogeny has another data frame 'genus_family_root', which provides the root nodes information for every unique genus and family in the phylogeny. Such information can be used to insert new tips onto the phylogeny later.

Source

http://beetreeoflife.org

References

Henríquez-Piskulich, P.; Hugall, A.F.; Stuart-Fox; D. 2023. A supermatrix phylogeny of the world's bees (Hymenoptera: Anthophila). bioRxiv 2023.06.16.545281. doi.org/10.1101/2023.06.16.545281.

---

tree_bee_n100   *100 randomly selected Mega-tree of Bees from Bee Tree of Life*

Description

100 randomly selected Mega-tree of Bees from Bee Tree of Life

Usage

```
tree_bee_n100
```

Format

A phylogeny with class "multiPhylo". It is also a list. Compare with a normal phylo object, each phylogeny has another data frame 'genus_family_root', which provides the root nodes information for every unique genus and family in the phylogeny. Such information can be used to insert new tips onto the phylogeny later.

Source

http://beetreeoflife.org

References

Henríquez-Piskulich, P.; Hugall, A.F.; Stuart-Fox; D. 2023. A supermatrix phylogeny of the world's bees (Hymenoptera: Anthophila). bioRxiv 2023.06.16.545281. doi.org/10.1101/2023.06.16.545281.

---

tree_bird_n100 *100 randomly selected Mega-tree of Birds from Bird Tree.*

Description

The first 50 phylogenies are randomly selected from those 10000 trees with Ericson backbond generated by Jetz et al. (2012); and the second 50 phylogenies are randomly selected from those 10000 trees with Hackett backbone. Node labels were added for each phylogeny.

Usage

```
tree_bird_n100
```

Format

A phylogeny with class "multiPhylo". It is also a list. Compare with a normal phylo object, each phylogeny has another data frame 'genus_family_root', which provides the root nodes information for every unique genus and family in the phylogeny. Such information can be used to insert new tips onto the phylogeny later.

Source

https://data.vertlife.org/

References

Jetz, W., Thomas, G. H., Joy, J. B., Hartmann, K., & Mooers, A. O. (2012). The global diversity of birds in space and time. Nature, 491(7424), 444.

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tree_butterfly	*Tree of 2244 butterfly species*

Description

This tree was generated by Kawahara et al. (2023).

Usage

```
tree_butterfly
```

Format

A phylogeny with class "phylo". It is also a list. Compare with a normal phylo object, it has another data frame 'tree_butterfly$genus_family_root', which provides the root nodes information for every unique genus and family in the phylogeny. Such information can be used to insert new tips onto the phylogeny later.

Source

https://springernature.figshare.com/articles/dataset/A_global_phylogeny_of_butterflies_reveals_their_evolutionary_history_

References

Kawahara, Akito Y., et al. "A global phylogeny of butterflies reveals their evolutionary history, ancestral hosts and biogeographic origins." Nature ecology & evolution 7.6 (2023): 903-913.

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tree_fish_12k	*Mega-tree of 11638 Fish from The Fish Tree of Life*

Description

This tree was generated by Rabosky et al. (2018). It has 11638 tips that all have sequence data. Node labels were added here.

Usage

```
tree_fish_12k
```

Format

A phylogeny with class "phylo". It is also a list. Compare with a normal phylo object, it has another data frame 'tree_fish_12k$genus_family_root', which provides the root nodes information for every unique genus and family in the phylogeny. Such information can be used to insert new tips onto the phylogeny later.

Source

https://fishtreeoflife.org/downloads/actinopt_12k_treePL.tre.xz

References

Rabosky, D. L., Chang, J., Title, P. O., Cowman, P. F., Sallan, L., Friedman, M., ... & Alfaro, M. E. (2018). An inverse latitudinal gradient in speciation rate for marine fishes. Nature, 559(7714), 392.

See Also

tree_fish_32k_n50

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tree_fish_32k_n50   *50 Mega-tree of 31516 Fish from The Fish Tree of Life*

Description

This tree was generated by Rabosky et al. (2018). It has 31516 tips, with species missing sequence data added using birth-death models. Therefore, there are 100 such posterior distribution phylogenies to account for uncertainty. The authors suggested not to use them to conduct trait evolution analyses. Here, we have randomly selected 50 of them to reduce the package size.

Usage

tree_fish_32k_n50

Format

A phylogeny with class "multiPhylo". It is also a list. Each phylogeny also has another data frame 'genus_family_root', which provides the root nodes information for every unique genus and family in the phylogeny. Such information can be used to insert new tips onto the phylogeny later.

Source

https://fishtreeoflife.org/downloads/actinopt_full.trees.xz

References

Rabosky, D. L., Chang, J., Title, P. O., Cowman, P. F., Sallan, L., Friedman, M., ... & Alfaro, M. E. (2018). An inverse latitudinal gradient in speciation rate for marine fishes. Nature, 559(7714), 392.

See Also

tree_fish_12k

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tree_mammal_n100_phylacine

100 randomly selected Mega-tree of Mammals from PHYLACINE V1.2.

Description

These 100 phylogenies are randomly selected from the 1000 trees generated by Faurby et al. (2018). Node labels were added here.

Usage

```
tree_mammal_n100_phylacine
```

Format

A phylogeny with class "multiPhylo". It is also a list. Compare with a normal phylo object, each phylogeny has another data frame 'genus_family_root', which provides the root nodes information for every unique genus and family in the phylogeny. Such information can be used to insert new tips onto the phylogeny later.

Source

https://github.com/MegaPast2Future/PHYLACINE_1.2/blob/master/Data/Phylogenies/Complete_phylogeny.nex

References

Faurby, S., Davis, M., Pedersen, R. Ø., Schowanek, S. D., Antonelli, A., & Svenning, J. C. (2018). PHYLACINE 1.2: The phylogenetic atlas of mammal macroecology. Ecology, 99(11), 2626-2626.

See Also

tree_mammal_n100_vertlife

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tree_mammal_n100_vertlife

100 randomly selected Mega-tree of Mammals from VertLife.

Description

The first 50 phylogenies are randomly selected from those 10000 trees with Node Dating Exponential backbone provided by Upham et al. (2019); and the second 50 phylogenies are randomly selected from those 10000 trees with Fossil Birth Death Zhou et al.'s backbone. Node labels were added for each phylogeny.

Usage

```
tree_mammal_n100_vertlife
```

Format

A phylogeny with class "multiPhylo". It is also a list. Compare with a normal phylo object, each phylogeny has another data frame 'genus_family_root', which provides the root nodes information for every unique genus and family in the phylogeny. Such information can be used to insert new tips onto the phylogeny later.

Source

https://vertlife.org/data/mammals/

References

Upham, N. S., Esselstyn, J. A., & Jetz, W. (2019). Inferring the mammal tree: species-level sets of phylogenies for questions in ecology, evolution, and conservation. PLoS biology, 17(12), e3000494.

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  tree_plant_otl   *Mega-tree of Plants based on Open Tree of Life*

Description

This tree was based on Brown and Smith (2018), which in turn was based on the Open Tree of Life. It was copied from 'V.PhyloMaker::GBOTB.extended'. After then, node labels were added for empty ones.

Usage

```
tree_plant_otl
```

Format

A phylogeny with class "phylo". It is also a list. Compare with a normal phylo object, it has another data frame 'tree_plant_otl$genus_family_root', which provides the root nodes information for every unique genus and family in the phylogeny. Such information can be used to insert new tips onto the phylogeny later.

Source

https://github.com/jinyizju/V.PhyloMaker/tree/master/data

References

Smith, S. A., & Brown, J. W. (2018). Constructing a broadly inclusive seed plant phylogeny. American Journal of Botany, 105(3), 302-314.

Jin, Y., & Qian, H. (2019). V. PhyloMaker: an R package that can generate very large phylogenies for vascular plants. Ecography.

tree_reptile_n100	*100 randomly selected Mega-tree of Reptiles (Squamates) from VertLife.*

Description

100 randomly selected Mega-tree of Reptiles (Squamates) from VertLife.

Usage

```
tree_reptile_n100
```

Format

A phylogeny with class "multiPhylo". It is also a list. Compare with a normal phylo object, each phylogeny has another data frame 'genus_family_root', which provides the root nodes information for every unique genus and family in the phylogeny. Such information can be used to insert new tips onto the phylogeny later.

Source

https://vertlife.org/data/squamates/

References

Tonini, J. F. R., Beard, K. H., Ferreira, R. B., Jetz, W., & Pyron, R. A. (2016). Fully-sampled phylogenies of squamates reveal evolutionary patterns in threat status. Biological Conservation, 204, 23-31.

tree_shark_ray_n100	*100 randomly selected Mega-tree of Sharks, Rays, and Chimaeras from VertLife.*

Description

100 randomly selected Mega-tree of Sharks, Rays, and Chimaeras from VertLife.

Usage

```
tree_shark_ray_n100
```

Format

A phylogeny with class "multiPhylo". It is also a list. Compare with a normal phylo object, each phylogeny has another data frame 'genus_family_root', which provides the root nodes information for every unique genus and family in the phylogeny. Such information can be used to insert new tips onto the phylogeny later.

Source

https://vertlife.org/data/sharks//

References

Stein, R. W., Mull, C. G., Kuhn, T. S., Aschliman, N. C., Davidson, L. N., Joy, J. B., ... & Mooers, A. O. (2018). Global priorities for conserving the evolutionary history of sharks, rays and chimaeras. Nature ecology & evolution, 2(2), 288-298.

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