

# Package ‘fishtree’

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**Type** Package

**Title** Interface to the Fish Tree of Life API

**Version** 0.3.0

**Description** An interface to the Fish Tree of Life API to download taxonomies, phylogenies, fossil calibrations, and diversification rate information for ray-finned fishes.

**License** BSD\_2\_clause + file LICENSE

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 6.1.1

**URL** <https://fishtreeoflife.org/>

**BugReports** <https://github.com/jonchang/fishtree/issues>

**Depends** R (>= 3.4)

**Imports** ape (>= 5.2), rlang (>= 0.2.2), jsonlite (>= 1.5), utils, memoise, parallel

**Suggests** rfishbase, hisse, geiger, knitr, rmarkdown, picante, spelling, testthat

**VignetteBuilder** knitr

**Language** en-US

**NeedsCompilation** no

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**R topics documented:**

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<code>fishtree_alignment</code>	<i>Get aligned sequences from the Fish Tree of Life</i>
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**Description**

Retrieves an aligned sequence via the Fish Tree of Life API. If neither ‘species’ nor ‘rank’ are specified, returns the entire sequence matrix.

**Usage**

```
fishtree_alignment(species, rank, split = FALSE)
```

**Arguments**

<code>species</code>	(Optionally) subset the results based on a vector of species names.
<code>rank</code>	(Optionally) subset the results based on the supplied taxonomic rank.
<code>split</code>	Splits the output into a list by gene locus.

**Value**

An object of class “DNABin”, or a named list of the same if ‘split = TRUE’

**References**

Rabosky, D. L., Chang, J., Title, P. O., Cowman, P. F., Sallan, L., Friedman, M., Kashner, K., Garilao, C., Near, T. J., Coll, M., Alfaro, M. E. (2018). An inverse latitudinal gradient in speciation rate for marine fishes. *Nature*, 559(7714), 392–395. doi:10.1038/s41586-018-0273-1

**See Also**

[DNABin](#)

## Examples

```
surgeon_dna <- fishtree_alignment(rank = "Acanthuridae", split = TRUE)
surgeon_dna[[1]]
## Not run:
par(mfrow = c(9, 3), mar = c(0.5, 0.5, 1, 0.5), xaxt = "n", yaxt = "n")
for (gene in names(surgeon_dna)) {
  image(surgeon_dna[[gene]], legend = FALSE, show.labels = FALSE)
  title(gene)
}

## End(Not run)
```

---

fishtree\_complete\_phylogeny

*Get complete (stochastically-resolved) phylogenies from the Fish Tree of Life*

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## Description

Retrieves a complete, stochastically-resolved phylogeny via the Fish Tree of Life API. If neither ‘species’ nor ‘rank’ are specified, returns the entire phylogeny.

## Usage

```
fishtree_complete_phylogeny(species, rank,
  mc.cores = getOption("mc.cores", 1L))
```

## Arguments

species	(Optionally) subset the results based on a vector of species names.
rank	(Optionally) subset the results based on the supplied taxonomic rank.
mc.cores	Number of cores to use in <a href="#">mclapply</a> when subsetting the tree (default ‘1’)

## Value

An object of class “multiPhylo”.

## References

Rabosky, D. L., Chang, J., Title, P. O., Cowman, P. F., Sallan, L., Friedman, M., Kashner, K., Garilao, C., Near, T. J., Coll, M., Alfaro, M. E. (2018). An inverse latitudinal gradient in speciation rate for marine fishes. *Nature*, 559(7714), 392–395. doi:10.1038/s41586-018-0273-1

Enhanced polytomy resolution strengthens evidence for global gradient in speciation rate for marine fishes. <https://fishtreeoflife.org/rabosky-et-al-2018-update/>

**Examples**

```
## Not run:
tree <- fishtree_complete_phylogeny(rank = "Acanthuridae")
sampled_tips <- fishtree_phylogeny(rank = "Acanthuridae")$tip.label
all_tips <- tree[[1]]$tip.label
new_tips <- setdiff(all_tips, sampled_tips)
par(mfrow = c(2,2))
for (ii in 1:4) {
  plot(tree[[ii]], show.tip.label = FALSE, no.margin = TRUE)
  ape::tiplabels(pch = 19, col = ifelse(tree[[ii]]$tip.label %in% new_tips, "red", NA))
}

## End(Not run)
```

---

fishtree\_phylogeny      *Get a phylogeny from the Fish Tree of Life*

---

**Description**

Retrieves a phylogeny via the Fish Tree of Life API. If neither ‘species’ nor ‘rank’ are specified, returns the entire phylogeny.

**Usage**

```
fishtree_phylogeny(species, rank, type = c("chronogram", "phylogram",
    "chronogram_mrca", "phylogram_mrca"))
```

**Arguments**

species	(Optionally) subset the results based on a vector of species names.
rank	(Optionally) subset the results based on the supplied taxonomic rank.
type	Either “chronogram” or “phylogram”. A chronogram has branch lengths proportional to units of time, while a phylogram has branch lengths proportional to the amount of character change. When retrieving a phylogeny by rank, and that rank is not recovered as monophyletic, acceptable types also include “chronogram_mrca” and “phylogram_mrca”, which returns a tree with <i>*all*</i> species descending from the common ancestor of species in the specified rank.

**Details**

For maximum interoperability, ‘species’ considers spaces and underscores equivalently. Internally, the phylogenies use underscores.

**Value**

An object of class “phylo”.

## References

Rabosky, D. L., Chang, J., Title, P. O., Cowman, P. F., Sallan, L., Friedman, M., Kashner, K., Garilao, C., Near, T. J., Coll, M., Alfaro, M. E. (2018). An inverse latitudinal gradient in speciation rate for marine fishes. *Nature*, 559(7714), 392–395. doi:10.1038/s41586-018-0273-1

## See Also

[fishtree\\_rogues](#), [read.tree](#), [force.ultrametric](#)

## Examples

```
surgeons <- fishtree_phylogeny(rank = "Acanthuridae")

# Chronograms may not be ultrametric due to numerical precision issues
ape::is.ultrametric(surgeons)
ape::is.ultrametric(surgeons, tol = 0.00001)

# Difference between MRCA trees and regular trees
gobies_mrca <- fishtree_phylogeny(rank = "Gobiidae", type = "chronogram_mrca")
gobies <- fishtree_phylogeny(rank = "Gobiidae", type = "chronogram")
# MRCA trees will have more tips for non-monophyletic groups
length(gobies_mrca$tip.label) > length(gobies$tip.label)
# Drop rogue tips in the MRCA tree
rogue_gobies <- fishtree_rogues("Gobiidae")
pruned_gobies <- ape::drop.tip(gobies_mrca, rogue_gobies)
# Now the trees are identical
setequal(gobies$tip.label, pruned_gobies$tip.label)
```

---

`fishtree_rogues`

*Get rogue taxa that break the monophyly of defined taxa*

---

## Description

For groups that were recovered as paraphyletic in the phylogenetic analysis, uses the Fish Tree of Life API to identify which species prevented that clade from being recovered as monophyletic.

## Usage

```
fishtree_rogues(rank)
```

## Arguments

`rank` the (possibly paraphyletic) rank for which rogue or intruder species should be identified.

## Value

A vector of species names, potentially empty.

## References

Rabosky, D. L., Chang, J., Title, P. O., Cowman, P. F., Sallan, L., Friedman, M., Kashner, K., Garilao, C., Near, T. J., Coll, M., Alfaro, M. E. (2018). An inverse latitudinal gradient in speciation rate for marine fishes. *Nature*, 559(7714), 392–395. doi:10.1038/s41586-018-0273-1

## Examples

```

fishtree_rogues("Gobiidae") # several rogue taxa!
fishtree_rogues("Labridae") # nice and monophyletic

```

---

fishtree\_taxonomy      *Get taxonomies and other data from the Fish Tree of Life*

---

## Description

Retrieves taxonomic and other information from the Fish Tree of Life API.

## Usage

```

fishtree_taxonomy(ranks = NULL)

```

## Arguments

ranks                      One or more taxonomic ranks to retrieve.

## Value

A list, with components containing data on the specified taxa. If ‘ranks’ is unspecified, a data frame with all valid taxa is returned instead.

## References

Rabosky, D. L., Chang, J., Title, P. O., Cowman, P. F., Sallan, L., Friedman, M., Kashner, K., Garilao, C., Near, T. J., Coll, M., Alfaro, M. E. (2018). An inverse latitudinal gradient in speciation rate for marine fishes. *Nature*, 559(7714), 392–395. doi:10.1038/s41586-018-0273-1

## Examples

```

tax <- fishtree_taxonomy(rank = "Labridae")
n_total <- length(tax$Labridae$species)
n_sampl <- length(tax$Labridae$sampled_species)
paste("There are", n_sampl, "sampled species out of", n_total, "in wrasses.")

```

---

fishtree\_tip\_rates     *Get tip rates for the Fish Tree of Life*

---

## Description

Downloads tip rates for the entire Fish Tree of Life, or for a specified subset. Tip rates can be thought of as an instantaneous speciation or extinction rate; for example, a higher tip-specific speciation rate might imply that a lineage is more likely to split a new lineage at the present time. If neither ‘species’ nor ‘rank’ are specified, returns the entire set of tip-specific diversification rates.

## Usage

```
fishtree_tip_rates(species, rank, sampled_only = TRUE)
```

## Arguments

species	(Optionally) subset the results based on a vector of species names.
rank	(Optionally) subset the results based on the supplied taxonomic rank.
sampled_only	Restricts the returned dataset to only those species that have genetic data available. Defaults to ‘TRUE’.

## Value

A data frame. Columns ending with ‘.tv’ indicate time-variable BAMM runs; those ending in ‘.tc’ are time-constant runs. The ‘dr’ column refers to the DR statistic, while ‘lambda’ and ‘mu’ are speciation and extinction, respectively.

## References

- DR rates (supplement, section 1.2.2): 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), 444–448. doi:10.1038/nature11631
- BAMM rates: Rabosky, D. L. (2014). Automatic Detection of Key Innovations, Rate Shifts, and Diversity-Dependence on Phylogenetic Trees. *PLoS ONE*, 9(2), e89543. doi:10.1371/journal.pone.0089543
- Rabosky, D. L., Chang, J., Title, P. O., Cowman, P. F., Sallan, L., Friedman, M., Kashner, K., Garilao, C., Near, T. J., Coll, M., Alfaro, M. E. (2018). An inverse latitudinal gradient in speciation rate for marine fishes. *Nature*, 559(7714), 392–395. doi:10.1038/s41586-018-0273-1
- Enhanced polytomy resolution strengthens evidence for global gradient in speciation rate for marine fishes. <https://fishtreeoflife.org/rabosky-et-al-2018-update/>

## Examples

```
# Get cichlid rates and trees
rates <- fishtree_tip_rates(rank = "Cichlidae")
tree <- fishtree_phylogeny(rank = "Cichlidae")
```

```
# Plot tree and extract plotting data
plot(tree, show.tip.label = FALSE)
obj <- get("last_plot.phylo", ape::.PlotPhyloEnv)

# Generate a color ramp
ramp <- grDevices::colorRamp(c("black", "red"), bias = 10)
tiporder <- match(rates$species, gsub("_", " ", tree$tip.label))
scaled_rates <- rates$lambda.tv / max(rates$lambda.tv, na.rm = TRUE)
tipcols <- apply(ramp(scaled_rates), 1, function(x) do.call(rgb, as.list(x / 255)))

# Place colored bars
for (ii in 1:length(tiporder)) {
  tip <- tiporder[ii]
  lines(x = c(obj$xx[tip] + 0.5, obj$xx[tip] + 0.5 + scaled_rates[ii]),
        y = rep(obj$yy[tip], 2),
        col = tipcols[ii])
}
```



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