

PnTx3-6 homologs US-align phylogenetic signal tests

Code

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- see github.com/brewerlab/summer2024 for more information

Clean up workspace

```
#invisible(lapply(paste0('package:', names(sessionInfo())$otherPkgs)), detach, charact  
rm(list = ls(all = TRUE))
```

Dependencies

```
#install.packages("phylosignal", dependencies = T)  
#install.packages("readr", dependencies = T)  
#install.packages("dplyr", dependencies = T)  
#install.packages("tibble", dependencies = T)  
#install.packages("stringr", dependencies = T)
```

Importing data

US-align results

```
library(dplyr)
```

Warning: package 'dplyr' was built under R version 4.3.3

Attaching package: 'dplyr'

The following objects are masked from 'package:stats':

filter, lag

The following objects are masked from 'package:base':

intersect, setdiff, setequal, union

```
library(tibble)
```

Warning: package 'tibble' was built under R version 4.3.3

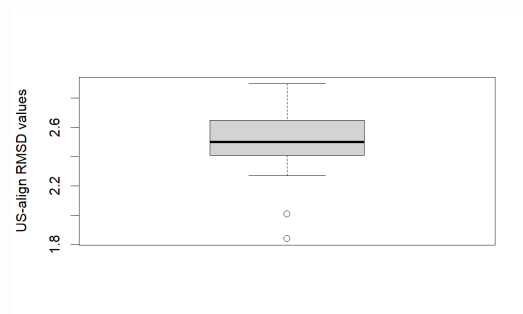
```
library(stringr)
```

Warning: package 'stringr' was built under R version 4.3.3

```
usalign_data <- read.csv("4usalign/ctenidusalignresults.csv")
```

```
usalign_data %>%  
  mutate(Name = str_replace(as.character(Name), "_model_0", "")) %>%  
  column_to_rownames("Name")
```

```
boxplot(usalign_data$RMSD, ylab="US-align RMSD values")
```



CDS-based Phylogeny

```
library(ape)
```

Warning: package 'ape' was built under R version 4.3.3

Attaching package: 'ape'

The following object is masked from 'package:dplyr':

where

library(adephylo)

Warning: package 'adephylo' was built under R version 4.3.3

Loading required package: ade4

Warning: package 'ade4' was built under R version 4.3.3

library(phylobase)

Warning: package 'phylobase' was built under R version 4.3.3

Attaching package: 'phylobase'

The following object is masked from 'package:ape':

edges

library(phylosignal)

Warning: package 'phylosignal' was built under R version 4.3.3

library(readr)

Warning: package 'readr' was built under R version 4.3.3

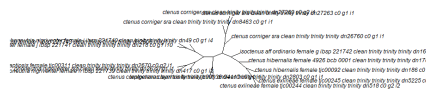
```
pntx3_6_homologs_tree <- read_file("ctenid_sequences/ickFinderCDS.correctedCDS_C
```

```
#pntx3_6_homologs_tree <- read_file("Pntx3-6_17HomologTree_rooted.tre")
```

```
pntx3_6_homologs_tree <- tolower(pntx3_6_homologs_tree)
```

```
pntx3_6_homologs_tree <- read.tree(text = pntx3_6_homologs_tree)
```

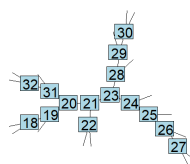
```
plot.phylo(pntx3_6_homologs_tree, align.tip.label = F, use.edge.length = F, type = "ur"
```



```
#node.labels()
```

```
plot.phylo(pntx3_6_homologs_tree, align.tip.label = F, use.edge.length = F, type = "ur"
```

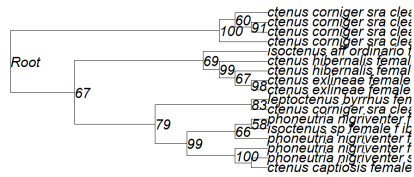
```
node.labels()
```



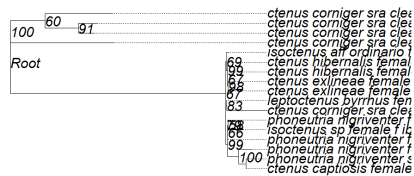
```
#edge.labels()
```

```
pntx3_6_homologs_tree_rooted <- root(pntx3_6_homologs_tree, c("ctenus_corniger_sr  
"ctenus_corniger_sra_clean_trinity_trinity_trinit  
"ctenus_corniger_sra_clean_trinity_trinity_trinit  
"ctenus_corniger_sra_clean_trinity_trinity_trinit  
resolve.root = T)
```

```
plot.phylo(pntx3_6_homologs_tree_rooted, show.node.label = T, align.tip.label = T, us
```



```
plot.phylo(pntx3_6_homologs_tree_rooted, show.node.label = T, align.tip.label = T, row
```



```
dat <- list()
dat$RMSD <- usalign_data$RMSD
dat$random <- rnorm(17, sd = sd(usalign_data$RMSD))
dat$bm <- rfractCont(pntx3_6_homologs_tree)
dat <- as.data.frame(dat)
```

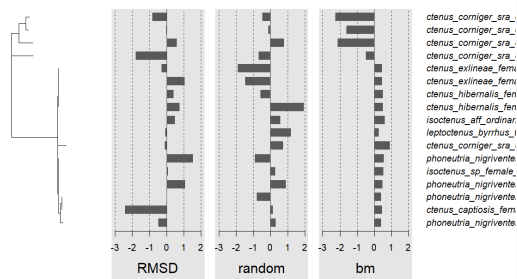
```
dat
```

```
pntx3_6_homologs_p4d <- phylo4d(pntx3_6_homologs_tree_rooted, dat)
```

```
Warning in checkTree(object) : Labels are not unique.
Warning in checkTree(object) : Labels are not unique.
```

```
barplot.phylo4d(pntx3_6_homologs_p4d)
```

```
Warning in checkTree(object) : Labels are not unique.
Warning in .local(x, ...) :
Non-unique or missing labels found, labels cannot be coerced to data row.names.
Use the label.type argument to include labels as first column of data.
```



```
phyloSignal(p4d = pntx3_6_homologs_p4d, method = "all")
```

```
Warning in checkTree(object) : Labels are not unique.
Warning in checkTree(object) : Labels are not unique.
Warning in checkTree(object) : Labels are not unique.
Warning in checkTree(object) : Labels are not unique.
Warning in checkTree(object) : Labels are not unique.
```

```
$stat
```

```
$pvalue
```

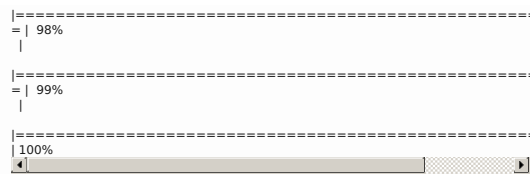
```
NA
```

```
phylosim <- phyloSim(tree = pntx3_6_homologs_tree_rooted, method = "all", nsim =
```

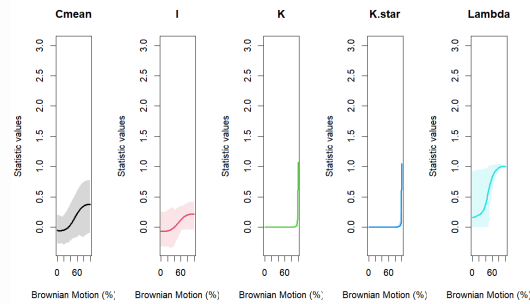


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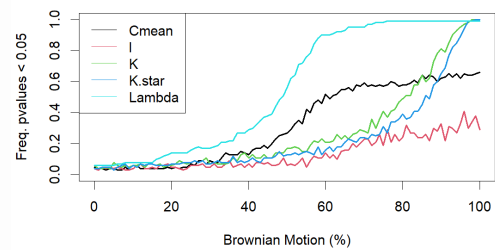
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```
plot(phylosim, stacked.methods = FALSE, quantiles = c(0.05, 0.95))
```



```
plot.phylosim(phylosim, what = "pval", stacked.methods = TRUE)
```



```
RMSD.crlg <- phyloCorrelogram(pntx3_6_homologs_p4d, trait = "RMSD")
```

```
Warning in checkTree(object) : Labels are not unique.
```

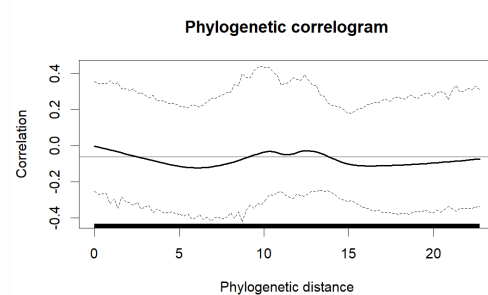
```
random.crlg <- phyloCorrelogram(pntx3_6_homologs_p4d, trait = "random")
```

```
Warning in checkTree(object) : Labels are not unique.
```

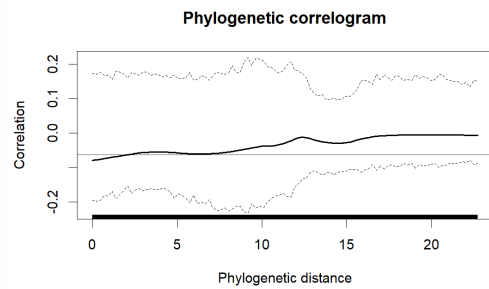
```
bm.crlg <- phyloCorrelogram(pntx3_6_homologs_p4d, trait = "bm")
```

```
Warning in checkTree(object) : Labels are not unique.
```

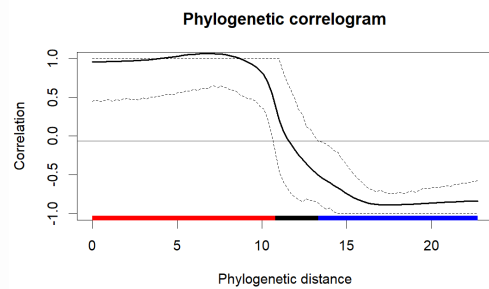
```
plot(RMSD.crlg)
```



```
plot(random.crlg)
```



```
plot(bm.crlg)
```



```
pntx3_6_homologs.ilpa <- lipaMoran(pntx3_6_homologs_p4d)
```

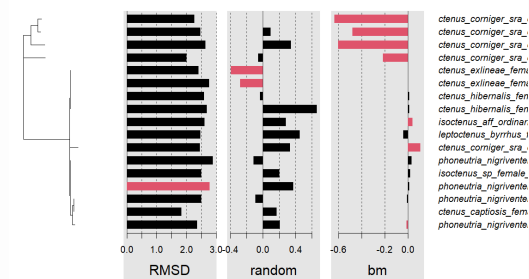
```
Warning in checkTree(object) : Labels are not unique.
Warning in .local(x, ...) :
  Non-unique or missing labels found, labels cannot be coerced to tdata row.names.
  Use the label.type argument to include labels as first column of data.
Warning in checkTree(object) : Labels are not unique.
Warning in checkTree(object) : Labels are not unique.
Warning in checkTree(object) : Labels are not unique.
```

```
carni.ilpa.p4d <- lipaMoran(pntx3_6_homologs_p4d, as.p4d = TRUE)
```

```
Warning in checkTree(object) : Labels are not unique.
Warning in .local(x, ...) :
  Non-unique or missing labels found, labels cannot be coerced to tdata row.names.
  Use the label.type argument to include labels as first column of data.
Warning in checkTree(object) : Labels are not unique.
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Warning in checkTree(object) : Labels are not unique.
Warning in checkTree(object) : Labels are not unique.
```

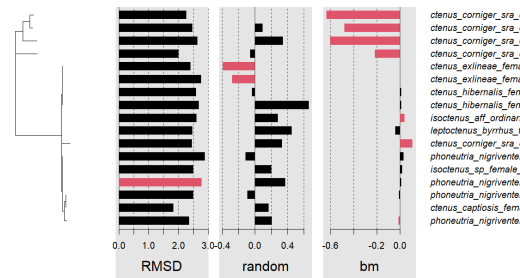
```
barplot.phylo4d(pntx3_6_homologs_p4d, bar.col=(pntx3_6_homologs.ilpa$p.value < 0
```

```
Warning in checkTree(object) : Labels are not unique.
Warning in .local(x, ...) :
  Non-unique or missing labels found, labels cannot be coerced to tdata row.names.
  Use the label.type argument to include labels as first column of data.
```



```
barplot.phylo4d(pntx3_6_homologs_p4d, bar.col = (pntx3_6_homologs.ilpa$p.value <
```

```
Warning in checkTree(object) : Labels are not unique.
Warning in .local(x, ...) :
  Non-unique or missing labels found, labels cannot be coerced to tdata row.names.
  Use the label.type argument to include labels as first column of data.
```



```
sessionInfo()

R version 4.3.1 (2023-06-16 ucrt)
Platform: x86_64-w64-mingw32/x64 (64-bit)
Running under: Windows 11 x64 (build 22631)

Matrix products: default

locale:
[1] LC_COLLATE=English_United States.utf8
[2] LC_CTYPE=English_United States.utf8
[3] LC_MONETARY=English_United States.utf8
[4] LC_NUMERIC=C
[5] LC_TIME=English_United States.utf8

time zone: America/New_York
tzcode source: internal

attached base packages:
[1] stats    graphics  grDevices  utils      datasets  methods
[7] base

other attached packages:
[1] readr_2.1.5    phylosignal_1.3.1 phylobase_0.8.12
[4] adephylo_1.1-16 ade4_1.7-22    ape_5.8
[7] stringr_1.5.1  tibble_3.2.1  dplyr_1.1.4

loaded via a namespace (and not attached):
[1] gtable_0.3.4    bslib_0.5.1    xfun_0.41
[4] ggplot2_3.4.4    raster_3.6-26  lattice_0.21-8
[7] tzdb_0.4.0      vctrs_0.6.5    tools_4.3.1
[10] generics_0.1.3  parallel_4.3.1 fansi_1.0.6
[13] cluster_2.1.4   pkgconfig_2.0.3 Matrix_1.6-1.1
[16] uuid_1.1-1      lifecycle_1.0.4 compiler_4.3.1
[19] progress_1.2.2  munsell_0.5.0  terra_1.7-55
[22] codetools_0.2-19 permute_0.9-7   httpuv_1.6.12
[25] sass_0.4.7      htmttools_0.5.6.1 yaml_2.3.8
[28] jquerylib_0.1.4 pillar_1.9.0    later_1.3.1
[31] crayon_1.5.2    seqinr_4.2-36  tidyrr_1.3.0
[34] ellipsis_0.3.2  MASS_7.3-60    cachem_1.0.8
[37] vegan_2.6-4     boot_1.3-28.1  mime_0.12
[40] nlme_3.1-162    tidyselect_1.2.0 digest_0.6.35
[43] stringi_1.8.3   reshape2_1.4.4 purrr_1.0.2
[46] splines_4.3.1   cowplot_1.1.1  fastmap_1.1.1
[49] grid_4.3.1      colorspace_2.1-0 cli_3.6.2
[52] magrittr_2.0.3  XML_3.99-0.16.1 utf8_1.2.4
[55] prettyunits_1.2.0 scales_1.3.0   promises_1.2.1
[58] sp_2.1-1        rmarkdown_2.25 httr_1.4.7
[61] igraph_2.0.3    hms_1.1.3      mcl_0.8.7
[64] shiny_1.7.5.1   evaluate_0.23  knitr_1.45
[67] mgcv_1.8-42     rlang_1.1.2    Rcpp_1.0.11
[70] DBI_1.2.3       xtable_1.8-4   glue_1.7.0
[73] xml2_1.3.5      RNeXML_2.4.11  adegenet_2.1.10
[76] jsonlite_1.8.8  rstudioapi_0.15.0 R6_2.5.1
[79] plyr_1.8.9

LS0tDQp0aXRzZTogIlBuVHgzLTZGaG9tb2xvZ3MgVVMtYWxpZ224gcGh5bG9nZW5ldGJlIHNPZ255bCB0ZXN0cyINCm91c
```