Phylogenetics_SRV_viruses

Anton Zhelonkin

5/24/2022

Specifications

```
version
```

```
##                _
## platform       x86_64-pc-linux-gnu
## arch           x86_64
## os             linux-gnu
## system         x86_64, linux-gnu
## status
## major          4
## minor          2.0
## year           2022
## month          04
## day            22
## svn rev        82229
## language       R
## version.string R version 4.2.0 (2022-04-22)
## nickname       Vigorous Calisthenics
```

Requirements

```
if (!("reutils" %in% installed.packages()))
install.packages("reutils")
library(reutils)


if (!("ggtree" %in% installed.packages()))
BiocManager::install("ggtree")
library(ggtree)
```

```
## ggtree v3.4.0 For help: https://yulab-smu.top/treedata-book/
##
## If you use the ggtree package suite in published research, please cite
## the appropriate paper(s):
##
## Guangchuang Yu, David Smith, Huachen Zhu, Yi Guan, Tommy Tsan-Yuk Lam.
## ggtree: an R package for visualization and annotation of phylogenetic
## trees with their covariates and other associated data. Methods in
## Ecology and Evolution. 2017, 8(1):28-36. doi:10.1111/2041-210X.12628
##
## G Yu. Data Integration, Manipulation and Visualization of Phylogenetic
## Trees (1st ed.). Chapman and Hall/CRC. 2022. ISBN: 9781032233574
##
## S Xu, Z Dai, P Guo, X Fu, S Liu, L Zhou, W Tang, T Feng, M Chen, L
## Zhan, T Wu, E Hu, Y Jiang, X Bo, G Yu. ggtreeExtra: Compact
## visualization of richly annotated phylogenetic data. Molecular Biology
## and Evolution. 2021, 38(9):4039-4042. doi: 10.1093/molbev/msab166
```

```
sessionInfo()
```

```
## R version 4.2.0 (2022-04-22)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: Ubuntu 20.04.4 LTS
##
## Matrix products: default
## BLAS:   /usr/lib/x86_64-linux-gnu/blas/libblas.so.3.9.0
## LAPACK: /usr/lib/x86_64-linux-gnu/lapack/liblapack.so.3.9.0
##
## locale:
##  [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C
##  [3] LC_TIME=ru_RU.UTF-8        LC_COLLATE=en_US.UTF-8
##  [5] LC_MONETARY=ru_RU.UTF-8    LC_MESSAGES=en_US.UTF-8
##  [7] LC_PAPER=ru_RU.UTF-8       LC_NAME=C
##  [9] LC_ADDRESS=C               LC_TELEPHONE=C
## [11] LC_MEASUREMENT=ru_RU.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  methods   base
##
## other attached packages:
## [1] ggtree_3.4.0  reutils_0.2.3
##
## loaded via a namespace (and not attached):
##  [1] treeio_1.20.0      tidyselect_1.1.2   xfun_0.31          purrr_0.3.4
##  [5] lattice_0.20-45    ggfun_0.0.6        colorspace_2.0-3   vctrs_0.4.1
##  [9] generics_0.1.2     htmltools_0.5.2    yaml_2.3.5         utf8_1.2.2
## [13] gridGraphics_0.5-1 rlang_1.0.2        pillar_1.7.0       glue_1.6.2
## [17] DBI_1.1.2          lifecycle_1.0.1    stringr_1.4.0      munsell_0.5.0
## [21] gtable_0.3.0       evaluate_0.15      knitr_1.39         fastmap_1.1.0
## [25] parallel_4.2.0     fansi_1.0.3        Rcpp_1.0.8.3       scales_1.2.0
## [29] jsonlite_1.8.0     ggplot2_3.3.6      aplot_0.1.4        digest_0.6.29
## [33] stringi_1.7.6      dplyr_1.0.9        grid_4.2.0         cli_3.3.0
## [37] tools_4.2.0        bitops_1.0-7       yulab.utils_0.0.4  magrittr_2.0.3
## [41] RCurl_1.98-1.6     lazyeval_0.2.2     patchwork_1.1.1    tibble_3.1.7
## [45] crayon_1.5.1       ape_5.6-2          tidyr_1.2.0        pkgconfig_2.0.3
## [49] ellipsis_0.3.2     tidytree_0.3.9     ggplotify_0.1.0    assertthat_0.2.1
## [53] rmarkdown_2.14     rstudioapi_0.13    R6_2.5.1           nlme_3.1-157
## [57] compiler_4.2.0
```

Description

This is a replication analysis of a paper by Zao et al. *"A novel simian retrovirus subtype discovered in cynomolgus monkeys (Macaca fascicularis)"*.
The plan is simple:
* download sequences by assesion numbers from GenBank (db-nucleotide)

* align sequences of the newly discovered viral strain SRV
* draw a phylogenetic tree comparing the new strain with the previously known strains

1. Data preparation

Preparing for data extraction

```
options(reutils.email = "my_email@email.com") # i`m a real person
```

Find UIDs

```
# newly discovered SRV viral whole genomes search by assession number given in the article
srv_new1 <- esearch(db = "nucleotide", term = "KU605777")
srv_new2 <- esearch(db = "nucleotide", term = "KU605778")
srv_new3 <- esearch(db = "nucleotide", term = "KU605779")
srv_new4 <- esearch(db = "nucleotide", term = "KU605780")

# previously known SRV viruses
srv1 <- esearch(db = "nucleotide", term = "M11841")
srv2 <- esearch(db = "nucleotide", term = "AF126467")
srv3 <- esearch(db = "nucleotide", term = "M12349")
srv4 <- esearch(db = "nucleotide", term = "FJ971077")
srv5 <- esearch(db = "nucleotide", term = "AB611707")
srv6_env <- esearch(db = "nucleotide", term = "AY598468")
srv7_pol <- esearch(db = "nucleotide", term = "AY594212")
serv <- esearch(db = "nucleotide", term = "U85505")

# all UIDs vector
uid <- c(srv_new1[1], srv_new2[1], srv_new3[1], srv_new4[1],
         srv1[1], srv2[1], srv3[1], srv4[1], srv5[1], srv6_env[1], srv7_pol[1], serv[1])
```

Extract FASTA sequences by uids

```
srv_new <- efetch(uid[1:4], db = "nucleotide", rettype = "fasta", retmode = "text")

srv_seq_f <- efetch(uid[1:12], db = "nucleotide", rettype = "fasta", retmode = "text")
```

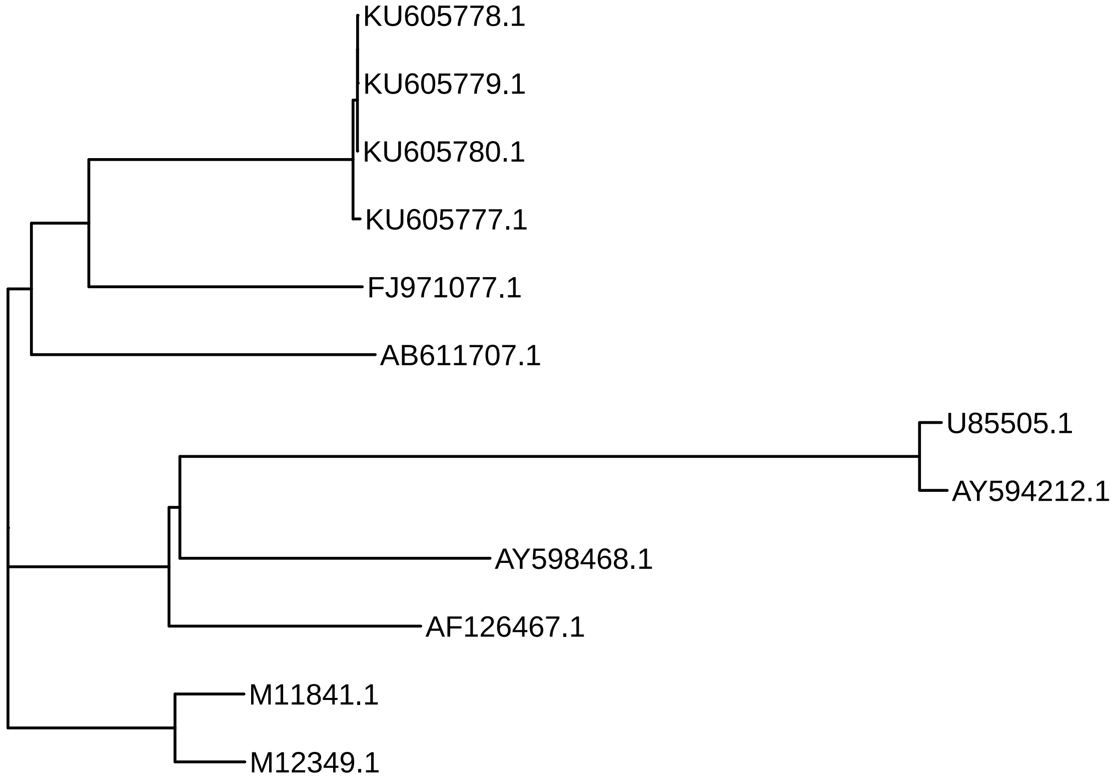
Write FASTA file with new SRV genomes and all known SRV viruses with the newly discovered ones

```
write(content(srv_new), "srv_new_sequences")

write(content(srv_seq_f), "srv_all_sequences")
```

2. Drawing tree based on modeltest-raxml pipeline

```
srv_tr <- read.tree("srv_all_raxml.raxml.bestTree")
ggtree(srv_tr) + geom_tiplab() + xlim(0,0.8)
```



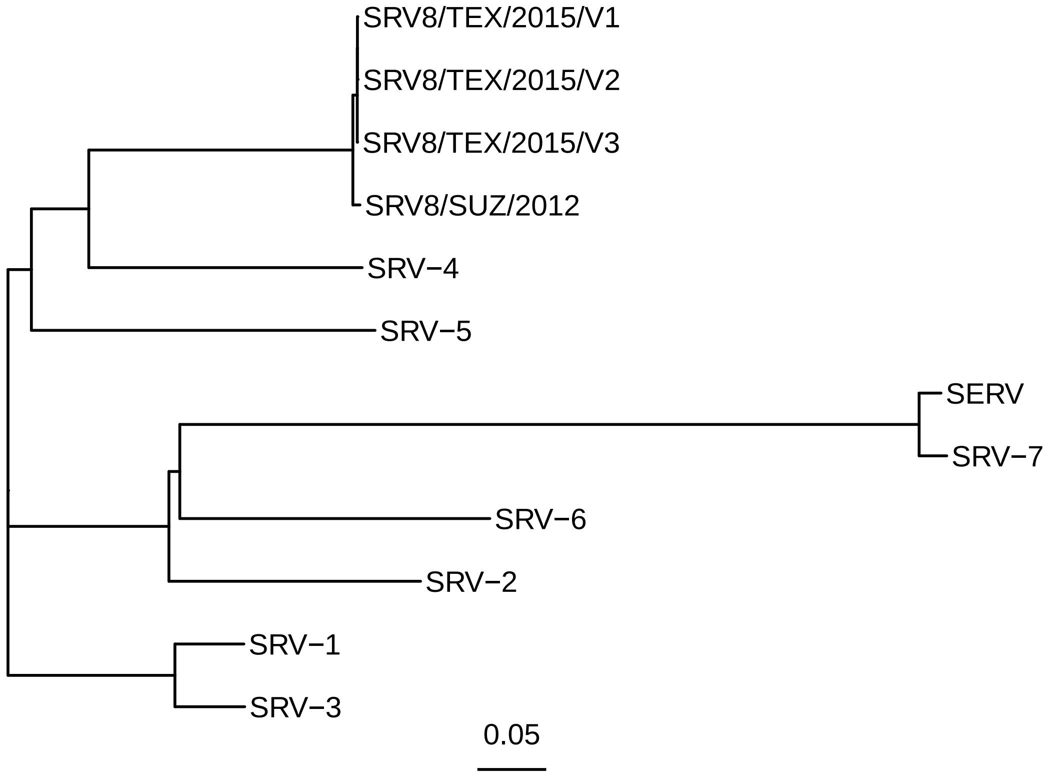
sabing tree

```
png("srv_all_raxml_bestTree.png")
ggtree(srv_tr) + geom_tiplab() + xlim(0,0.8)
dev.off()
```

```
## pdf
##   2
```

Renaming tip labels in tree

```
srv_tr_ren <- srv_tr
srv_tr_ren$tip.label <- c("SRV-5", "SRV-4", "SRV8/TEX/2015/V2", "SRV8/TEX/2015/V1",
                          "SRV8/TEX/2015/V3", "SRV8/SUZ/2012", "SRV-3", "SRV-1", "SRV-7",
                          "SERV", "SRV-6", "SRV-2")
ggtree(srv_tr_ren, ladderize=TRUE)+ geom_tiplab() + xlim(0,0.8) + geom_treescale(width = 0.05)
```



saving tree

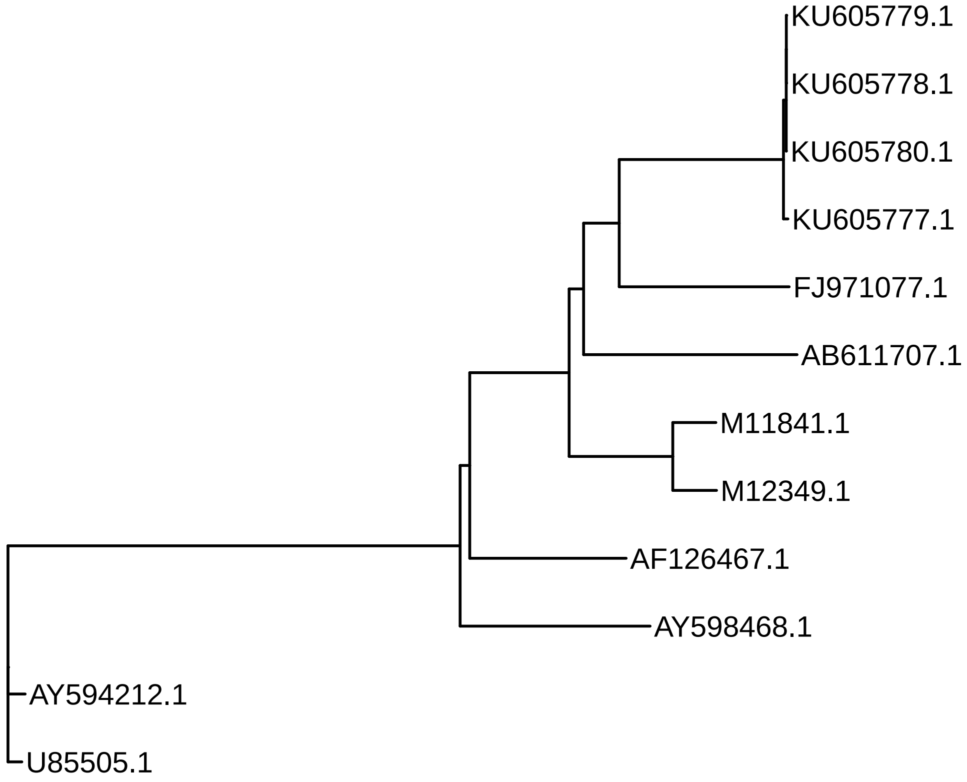
```
png("srv_all_raxml_named_bestTree.png")
ggtree(srv_tr_ren, ladderize=TRUE)+ geom_tiplab() + xlim(0,0.8) + geom_treescale(width = 0.05)
dev.off()
```

```
## pdf
##   2
```

3. Drawing tree based on PhyMl3 Bootstrap

Analysis run at http://phylogeny.lirmm.fr/phylo_cgi/one_task.cgi?task_type=phyml * Substitution model: GTR
* Bootstrapped data sets: 100

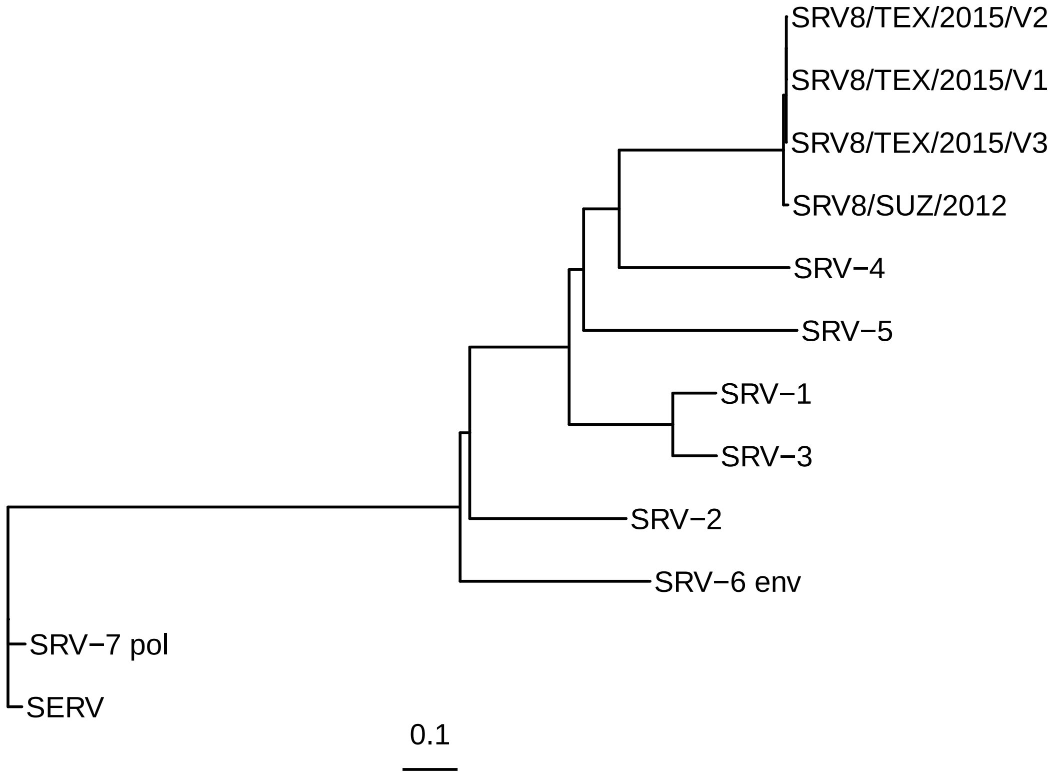
```
phy_tree <- read.tree("phyml3_all_tree.nwk")
ggtree(phy_tree) + geom_tiplab() + xlim(0,2)
```



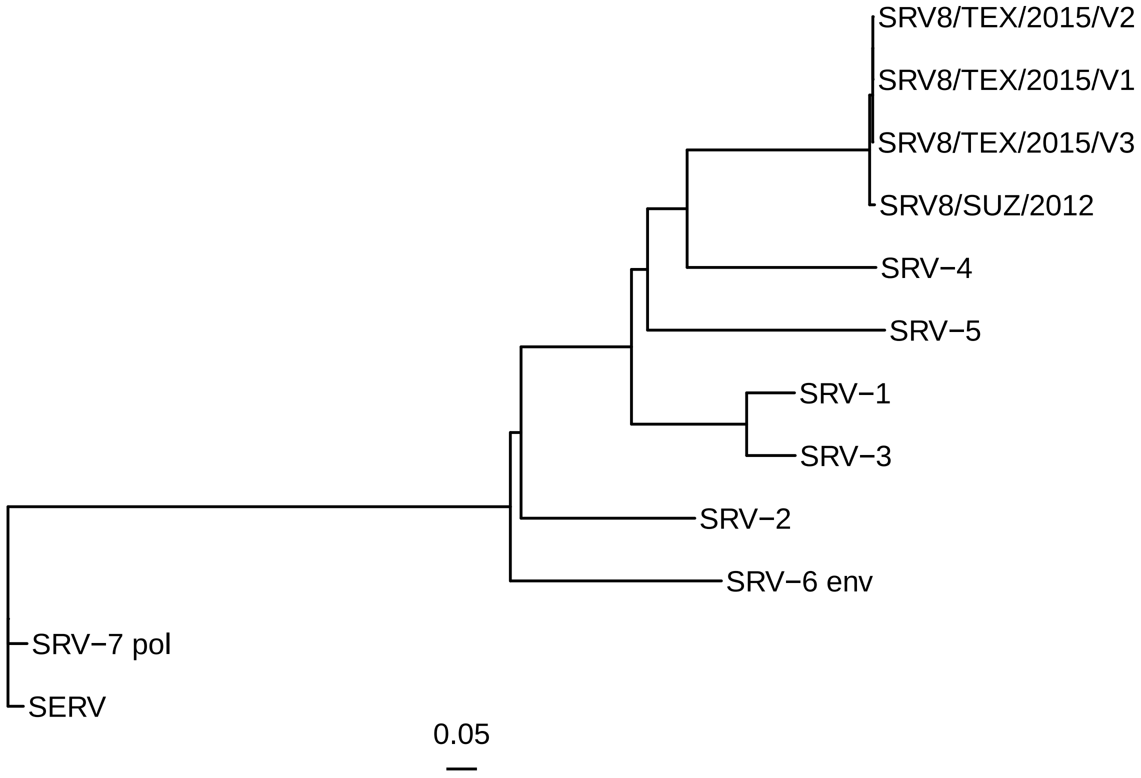
### Renaming tip labels in tree

```
phy_tree_ren <- phy_tree
phy_tree_ren$tip.label <- c("SRV-4", "SRV8/SUZ/2012", "SRV8/TEX/2015/V1",
                            "SRV8/TEX/2015/V2", "SRV8/TEX/2015/V3", "SRV-5",
                            "SRV-3", "SRV-1", "SRV-2", "SRV-6 env", "SERV",
                            "SRV-7 pol")
ggtree(phy_tree_ren, ladderize=TRUE, scale = 0.5)+ geom_tiplab() + xlim(0,2) + geom_treescale()
```

```
## Warning: Ignoring unknown parameters: scale
## Ignoring unknown parameters: scale
```



```
ggtree(phy_tree_ren, ladderize=TRUE)+ geom_tiplab() + xlim(0,1.8) +
  geom_treescale(width = 0.05)
```



saving tree

```
png("phyml3_all_tree.png")
ggtree(phy_tree_ren, ladderize=TRUE)+ geom_tiplab() + xlim(0,1.8) +
  geom_treescale(width = 0.05)
dev.off()
```

```
## pdf
##   2
```

```
png("phyml3_all_tree_res.png", width = 1200, height = 600)
ggtree(phy_tree_ren, ladderize=TRUE, size = 1.2)+ geom_tiplab(size = 10) + xlim(0,1.8) +
  geom_treescale(width = 0.05, fontsize = 10, linesize = 1.0)
dev.off()
```

```
## pdf
##   2
```