

TreeVisualization

```
if (!require("BiocManager", quietly = TRUE))
  install.packages("BiocManager")
```

```
## Warning: package 'BiocManager' was built under R version 4.1.2
```

```
## Bioconductor version '3.14' is out-of-date; the current release version '3.15'
##   is available with R version '4.2'; see https://bioconductor.org/install
```

```
BiocManager::install("treeio")
```

```
## Bioconductor version 3.14 (BiocManager 1.30.18), R 4.1.0 (2021-05-18)
```

```
## Warning: package(s) not installed when version(s) same as current; use `force = TRUE`
##   to
##   re-install: 'treeio'
```

```
## Old packages: 'terra'
```

```
BiocManager::install("ggtree")
```

```
## Bioconductor version 3.14 (BiocManager 1.30.18), R 4.1.0 (2021-05-18)
```

```
## Warning: package(s) not installed when version(s) same as current; use `force = TRUE`
##   to
##   re-install: 'ggtree'
```

```
## Old packages: 'terra'
```

```
BiocManager::install("ggtreeExtra")
```

```
## Bioconductor version 3.14 (BiocManager 1.30.18), R 4.1.0 (2021-05-18)
```

```
## Warning: package(s) not installed when version(s) same as current; use `force = TRUE`
##   to
##   re-install: 'ggtreeExtra'
```

```
## Old packages: 'terra'
```

```
library("treeio")
```

```
## Warning: package 'treeio' was built under R version 4.1.2
```

```
## treeio v1.18.1 For help: https://yulab-smu.top/treedata-book/
##
## If you use treeio in published research, please cite:
##
## LG Wang, TTY Lam, S Xu, Z Dai, L Zhou, T Feng, P Guo, CW Dunn, BR Jones, T Bradley, H
Zhu, Y Guan, Y Jiang, G Yu. treeio: an R package for phylogenetic tree input and output
with richly annotated and associated data. Molecular Biology and Evolution 2020, 37(2):5
99-603. doi: 10.1093/molbev/msz240
```

```
library("ggtree")
```

```
## Warning: package 'ggtree' was built under R version 4.1.2
```

```
## Registered S3 method overwritten by 'ggtree':
##   method      from
##   identify.gg ggfun
```

```
## ggtree v3.2.1 For help: https://yulab-smu.top/treedata-book/
##
## If you use ggtree in published research, please cite the most appropriate paper(s):
##
## 1. Guangchuang Yu. Using ggtree to visualize data on tree-like structures. Current Pr
otocols in Bioinformatics. 2020, 69:e96. doi:10.1002/cpbi.96
## 2. Guangchuang Yu, Tommy Tsan-Yuk Lam, Huachen Zhu, Yi Guan. Two methods for mapping
and visualizing associated data on phylogeny using ggtree. Molecular Biology and Evoluti
on. 2018, 35(12):3041-3043. doi:10.1093/molbev/msy194
## 3. 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 a
nd other associated data. Methods in Ecology and Evolution. 2017, 8(1):28-36. doi:10.111
1/2041-210X.12628
```

```
library("ape")
```

```
## Warning: package 'ape' was built under R version 4.1.2
```

```
##
## Attaching package: 'ape'
```

```
## The following object is masked from 'package:ggtree':
##
##   rotate
```

```
## The following object is masked from 'package:treeio':  
##  
## drop.tip
```

```
library("ggtreeExtra")
```

```
## Warning: package 'ggtreeExtra' was built under R version 4.1.2
```

```
## ggtreeExtra v1.4.2 For help: https://yulab-smu.top/treedata-book/  
##  
## If you use the ggtree package suite in published research, please cite  
## the appropriate paper(s):  
##  
## 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
```

```
library(ggplot2)
```

```
## Warning: package 'ggplot2' was built under R version 4.1.2
```

```
library(ggsci)
```

```
Metadata<-read.csv("~/Documents/C-PGME/Workshop2022/WorkshopMaterials_Lorenzo/Phylogenomics/SARSCoV2_BA4.metadata.tsv",sep = "\t", header = TRUE, stringsAsFactors = T)
```

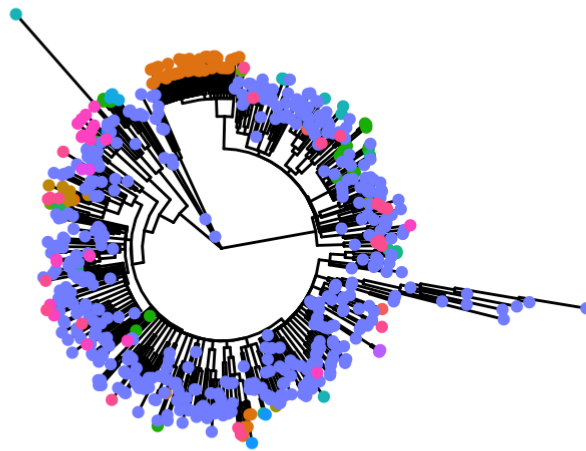
```
time_tree <- read.nexus("~/Documents/C-PGME/Workshop2022/WorkshopMaterials_Lorenzo/Phylogenomics/2022-05-03_mugration/annotated_tree.nexus")  
TreeData<-as.data.frame(as_tibble(time_tree))  
names(TreeData)[4]<-"strain"
```

```
Metadata_Tree<-merge(TreeData,Metadata,by="strain",sort = F)  
rownames(Metadata_Tree) <- Metadata_Tree$strain
```

```
p<-ggtree(time_tree,layout = "circular")%<+% Metadata_Tree +  
  geom_tippoint(aes(color=country))
```

```
## Warning: The tree contained negative edge lengths. If you want to ignore the edges,  
## you can set 'options(ignore.negative.edge=TRUE)', then re-run ggtree.
```

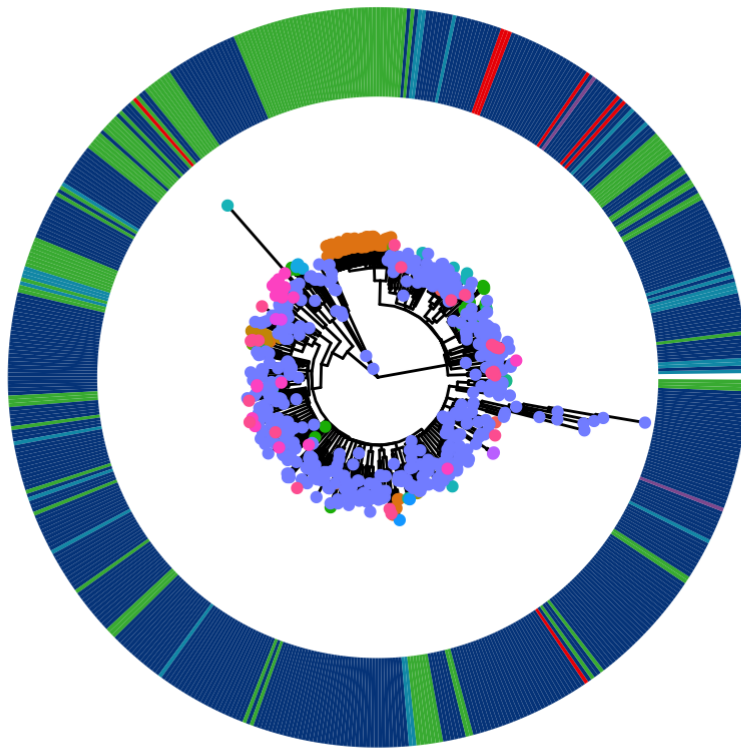
```
p
```



country

- Australia
- Austria
- Belgium
- Botswana
- Canada
- Denmark
- France
- Germany
- Israel
- Italy
- Netherlands
- South Africa
- Spain
- Switzerland
- United Kingdom
- USA

```
p + geom_fruit(
  geom=geom_tile,
  mapping=aes(fill=Metadata_Tree$region),
  width=0.2,offset = 0.2)+scale_fill_lancet()
```

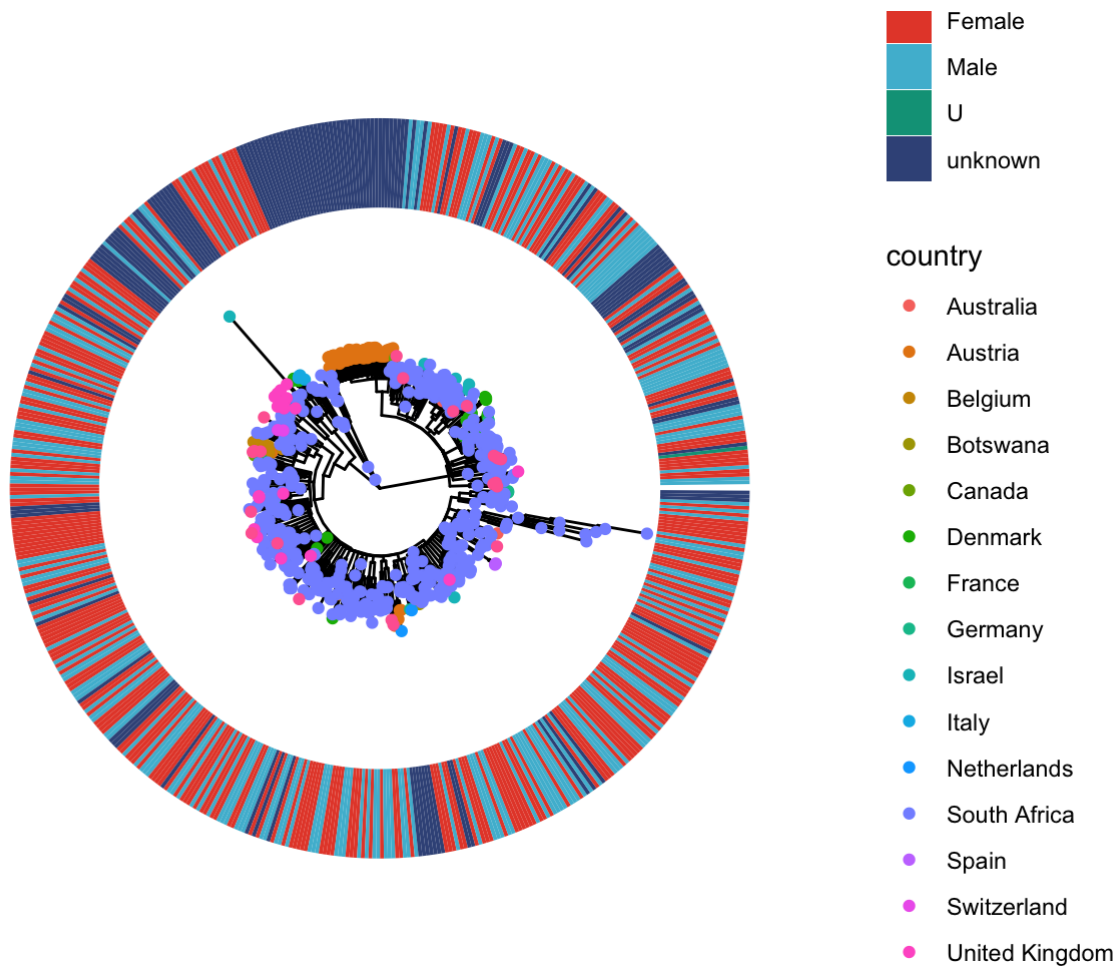


- Austria
- Belgium
- Botswana
- Canada
- Denmark
- France
- Germany
- Israel
- Italy
- Netherlands
- South Africa
- Spain
- Switzerland
- United Kingdom
- USA

Metadata_Tree\$region

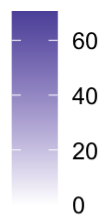
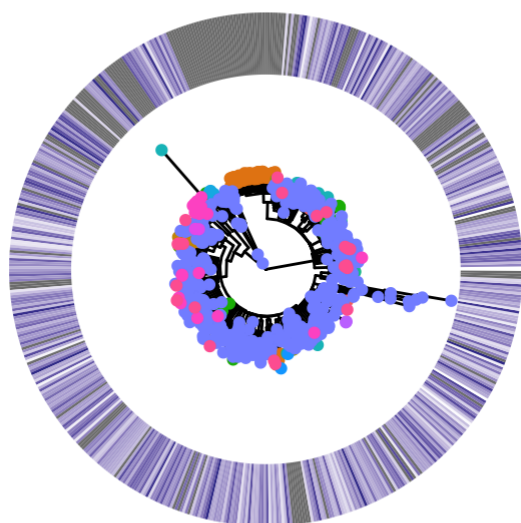
- Africa
- Asia
- Europe
- North America

```
p + geom_fruit(
  geom=geom_tile,
  mapping=aes(fill=Metadata_Tree$sex),
  width=0.2,offset = 0.2)+scale_fill_npg()
```



```
p + geom_fruit(
  geom=geom_tile,
  mapping=aes(fill=as.numeric(as.character(Metadata_Tree$age))),
  width=0.2,offset = 0.2)+scale_fill_gradient2()
```

```
## Warning in FUN(X[[i]], ...): NAs introduced by coercion
```



country

- Australia
- Austria
- Belgium
- Botswana
- Canada
- Denmark
- France
- Germany
- Israel
- Italy
- Netherlands
- South Africa
- Spain
- Switzerland
- United Kingdom