Transition between geographycal regions of the Delta and Gamma clades

```r
library(ape)
library(treeio)
```

```
## treeio v1.26.0 For help: https://yulab-smu.top/treedata-book/
##
## If you use the ggtree package suite in published research, please cite
## the appropriate paper(s):
##
## 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):599-603.
## doi: 10.1093/molbev/msz240
##
## 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
##
## Guangchuang Yu.  Data Integration, Manipulation and Visualization of
## Phylogenetic Trees (1st edition). Chapman and Hall/CRC. 2022,
## doi:10.1201/9781003279242
```

```r
library(ggtree)
```

```
## ggtree v3.10.0 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
##
## Guangchuang Yu.  Data Integration, Manipulation and Visualization of
## Phylogenetic Trees (1st edition). Chapman and Hall/CRC. 2022,
## doi:10.1201/9781003279242
##
## Shuangbin Xu, Lin Li, Xiao Luo, Meijun Chen, Wenli Tang, Li Zhan, Zehan
## Dai, Tommy T. Lam, Yi Guan, Guangchuang Yu. Ggtree: A serialized data
## object for visualization of a phylogenetic tree and annotation data.
## iMeta 2022, 1(4):e56. doi:10.1002/imt2.56
##
## Attaching package: 'ggtree'
```

```
## The following object is masked from 'package:ape':
##
##     rotate
library(ggplot2)
library(phylotate)
library(tidytree)
```

```
## If you use the ggtree package suite in published research, please cite
## the appropriate paper(s):
##
## Guangchuang Yu. Using ggtree to visualize data on tree-like structures.
## Current Protocols in Bioinformatics. 2020, 69:e96. doi:10.1002/cpbi.96
##
## 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 Evolution. 2018, 35(12):3041-3043.
## doi:10.1093/molbev/msy194
```

```
##
## Attaching package: 'tidytree'
```

```
## The following object is masked from 'package:treeio':
##
##     getNodeNum
```

```
## The following objects are masked from 'package:ape':
##
##     drop.tip, keep.tip
```

```
## The following object is masked from 'package:stats':
##
##     filter
library(ggnewscale)
library(stringr)
library(dplyr)
```

```
##
## Attaching package: 'dplyr'
```

```
## The following object is masked from 'package:ape':
##
##     where
```

```
## The following objects are masked from 'package:stats':
##
##     filter, lag
```

```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
library(RColorBrewer)
library(tidyr)
```

```
##
## Attaching package: 'tidyr'
```

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

```
##
##      expand
library(stringr)
library(grid)
library(tidyverse)
```

```
## -- Attaching core tidyverse packages ----------------------- tidyverse 2.0.0 --
## v forcats   1.0.0     v readr     2.1.4
## v lubridate 1.9.3     v tibble    3.2.1
## v purrr     1.0.2
```

```
## -- Conflicts ----------------------------------------- tidyverse_conflicts() --
## x tidyr::expand() masks ggtree::expand()
## x dplyr::filter() masks tidytree::filter(), stats::filter()
## x dplyr::lag()    masks stats::lag()
## x dplyr::where()  masks ape::where()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
library(phangorn)
library(RColorBrewer)
library(data.table)
```

```
##
## Attaching package: 'data.table'
##
## The following objects are masked from 'package:lubridate':
##
##      hour, isoweek, mday, minute, month, quarter, second, wday, week,
##      yday, year
##
## The following object is masked from 'package:purrr':
##
##      transpose
##
## The following objects are masked from 'package:dplyr':
##
##      between, first, last
library(ggthemes)
library(phylobase)
```

```
##
## Attaching package: 'phylobase'
##
## The following objects are masked from 'package:tidytree':
##
##      ancestor, MRCA
##
## The following object is masked from 'package:ggtree':
##
##      MRCA
##
## The following objects are masked from 'package:treeio':
##
##      ancestor, MRCA
##
```

```
## The following object is masked from 'package:ape':
##
##     edges
library(ggpubr)
```

```
##
## Attaching package: 'ggpubr'
##
## The following object is masked from 'package:ggtree':
##
##     rotate
##
## The following object is masked from 'package:ape':
##
##     rotate
meta <- read.csv("treetime_out_joint/metadata_with_clade/datsaet_phylodynamics.tsv",
    sep = "\t", header = T)
dim(meta)
```

```
## [1] 5166   11
head(meta)
```

```
##                                                                    strain
## 1   AD-AND-242_212581387701_COV-GC|EPI_ISL_5684463|Europe|NA|AY.9|2021-09-11
## 2 AD-AND-245_212871383801_COV-GC|EPI_ISL_6125409|Europe|NA|AY.124|2021-10-09
## 3 AD-AND-245_213501452101_COV-GC|EPI_ISL_8185538|Europe|NA|AY.125|2021-12-12
## 4 AD-AND-245_213501452301_COV-GC|EPI_ISL_8185535|Europe|NA|AY.122|2021-12-10
## 5   AD-AND-247_212871382801_COV-GC|EPI_ISL_6125408|Europe|NA|AY.42|2021-09-29
## 6 AD-AND-247_213001322901_COV-GC|EPI_ISL_7589517|Europe|NA|AY.124|2021-10-16
##         date       accession location region country     city subregion
## 1 2021-09-11 EPI_ISL_5684463   Europe Europe Andorra Andorra    Europe
## 2 2021-10-09 EPI_ISL_6125409   Europe Europe Andorra Andorra    Europe
## 3 2021-12-12 EPI_ISL_8185538   Europe Europe Andorra Andorra    Europe
## 4 2021-12-10 EPI_ISL_8185535   Europe Europe Andorra Andorra    Europe
## 5 2021-09-29 EPI_ISL_6125408   Europe Europe Andorra Andorra    Europe
## 6 2021-10-16 EPI_ISL_7589517   Europe Europe Andorra Andorra    Europe
##   pango_lineage last_pango_lineage        clade
## 1          AY.9               AY.9 21I (Delta)
## 2        AY.124             AY.124 21J (Delta)
## 3        AY.125             AY.125 21J (Delta)
## 4        AY.122             AY.122 21J (Delta)
## 5         AY.42              AY.42 21J (Delta)
## 6        AY.124             AY.124 21J (Delta)
```

Time-scaled phylogeny was visually inspected and and the label tips were copied to voc_clades.tsv

```
tre <- read.nexus("treetime_out_joint/timetree.nexus")
t <- as_tibble(tre)
head(t)
```

```
## # A tibble: 6 x 4
##   parent  node branch.length label
##    <int> <int>         <dbl> <chr>
## 1   5167     1        0.0641 CN-Hu-1|EPI_ISL_402125|Asia|NA|B|2019-12-26
## 2   5168     2        0.160  AU-VPRL014|EPI_ISL_455603|Oceania|NA|B.1|2020-01-30
```

```
## 3    5168     3        0.0641  CN-WH01|EPI_ISL_406798|Asia|NA|B|2019-12-26
## 4    5170     4        0.00546 AE-skmc-2200543130|EPI_ISL_582623|Asia|NA|B.53|202~
## 5    5170     5        0       AE-skmc-2200522146|EPI_ISL_582611|Asia|NA|B.53|202~
## 6    5171     6        0.0433  SG-1|EPI_ISL_406973|Asia|NA|B|2020-01-23
```

```r
clades <- read.table("treetime_out_joint/voc_clades.tsv", sep = "\t", header = T)
colnames(clades) <- c("cluster", "label")
dim(clades)
```

```
## [1] 3263    2
```

Based on tip labels the MRCA was retrived

```r
nodes <- clades %>%
    group_by(cluster) %>%
    summarise(mrca = MRCA(tre, label))
head(nodes)
```

```
## # A tibble: 2 x 2
##    cluster  mrca
##    <chr>    <int>
## 1 delta     5232
## 2 gamma     8290
```
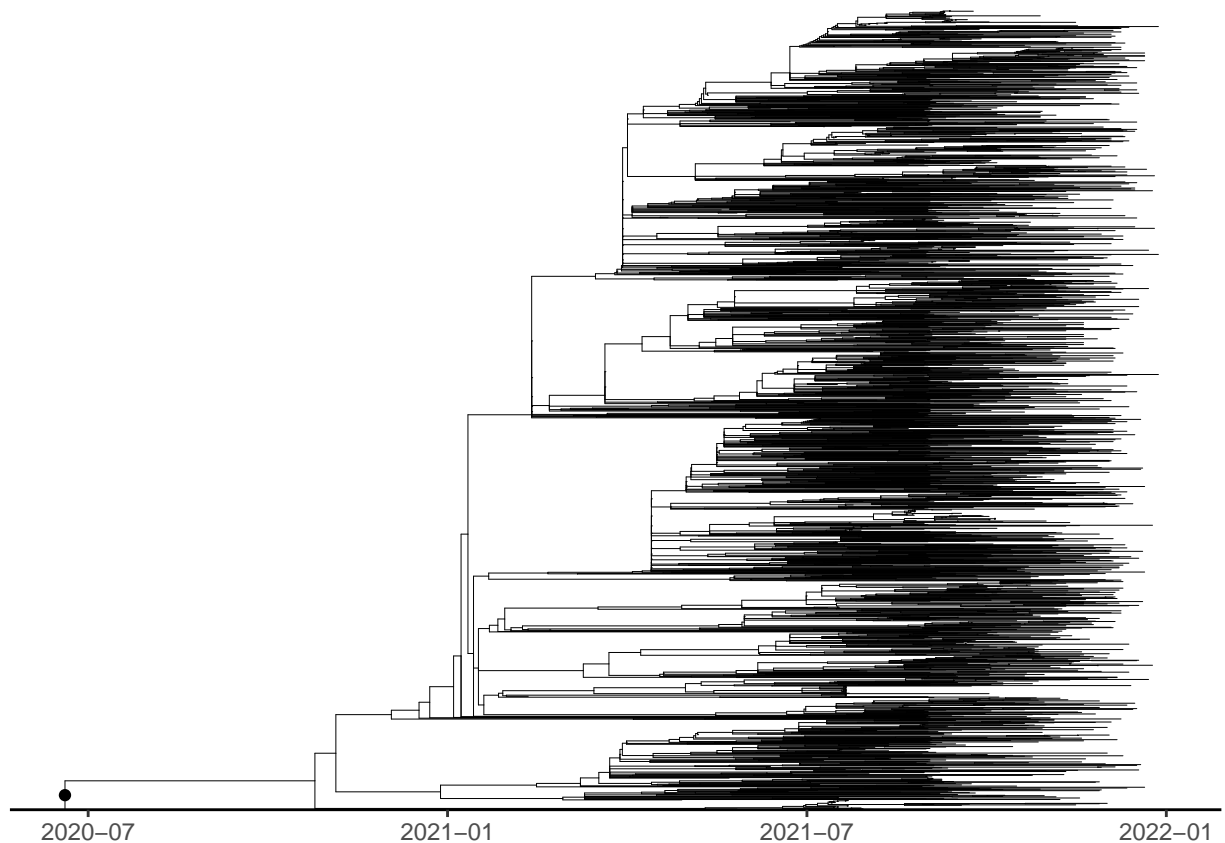
```r
dim(nodes)
```

```
## [1] 2 2
```

Subtree containing the Delta clade was extracted

```r
delta <- extract.clade(tre, node = 5232)

d <- ggtree(delta, size = 0.1, mrsd = "2021-12-28") + scale_colour_manual() +
    theme_tree2() + geom_rootpoint(position = "identity") + xlim_tree(xlim = 2022) +
    scale_x_ggtree(labels = c("2020-01", "2020-07", "2021-01", "2021-07",
        "2022-01"), breaks = c(2020, 2020.5, 2021, 2021.5, 2022))
d
```

```r
dir.create("subtrees")
```

```
## Warning in dir.create("subtrees"): 'subtrees' ya existe
```
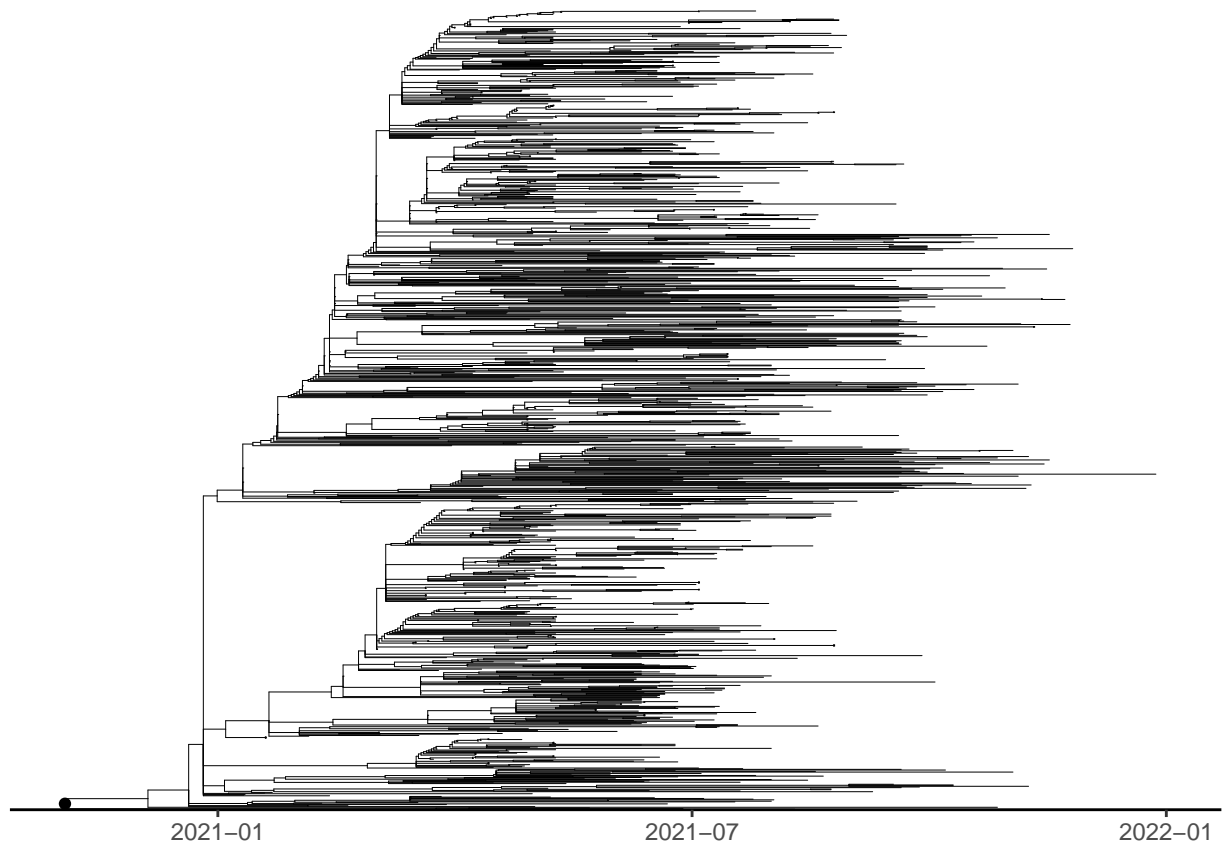
```r
write.tree(delta, "subtrees/delta_subtree.nexus")
```

Subtree containing the Gamma clade was extracted

```r
gamma <- extract.clade(tre, node = 8290)
g <- ggtree(gamma, size = 0.1, mrsd = "2021-12-28") + scale_colour_manual() +
    theme_tree2() + geom_rootpoint(position = "identity") + xlim_tree(xlim = 2022) +
    scale_x_ggtree(labels = c("2020-01", "2020-07", "2021-01", "2021-07",
        "2022-01"), breaks = c(2020, 2020.5, 2021, 2021.5, 2022))
g
```

```
write.tree(gamma, "subtrees/gamma_subtree.nexus")
```

Mugration analysis of the subtrees

In the subtrees directory create the subtree_delta and subtree_gamma directory and move the extracted trees.
First reconstruct ancestral states and then perform the mugration analysis

```
conda activate nextstrain
echo ""
echo ""
echo "Ancestral state reconstruction"

treetime ancestral --aln *aligned.fasta \
--tree *.nexus \
--outdir subtree_delta/ancestral_results > treetime_ancestral.log 2>&1

if [ -d "subtree_delta/ancestral_results" ]; then
echo "Ancestral state reconstruction DONE!";
else
echo "Ancestral state reconstruction FAILED!!";
fi



echo ""
echo ""
```

7

```
echo "Transition between geographical regions estimation"


treetime mugration --tree subtree_delta/ancestral_results/*.nexus \
--states ../fx_final_metadata-dataset1.tsv \
--attribute location \
--confidence \
--outdir subtree_delta/joint_mugration_region_delta \
--missing-data MD  > treetime_mugration_region_delta.log 2>&1

if [ -d "subtree_delta/joint_mugration_region_delta" ]; then
echo "Mugration using Region DONE!";
else
echo "Mugration using Region FAILED!!";
fi
```

Geographical transitions (regions) of the Delta clade

```
wt <- as.data.frame(read.table("subtrees/subtree_delta/joint_mugration_region_delta/GTR_region_delta.tx
    sep = "\t", header = T))
head(wt)
```

```
##     X      A      B      C      D      E      F      G      H      I
## 1   A 0.0000 0.0124 0.2116 0.0291 0.1266 0.0519 0.0162 0.0097 0.1157
## 2   B 0.0353 0.0000 0.0271 0.0650 0.0468 0.1671 0.0671 0.1067 0.1490
## 3   C 0.5562 0.0251 0.0000 0.0255 0.2626 0.0720 0.0856 0.0251 0.1812
## 4   D 0.0982 0.0774 0.0328 0.0000 0.0934 0.0378 0.0481 0.1173 0.1732
## 5   E 0.4811 0.0627 0.3797 0.1050 0.0000 0.2260 0.0305 0.0898 0.6912
## 6   F 0.1538 0.1746 0.0811 0.0332 0.1762 0.0000 0.1095 0.1471 0.3427
```

```
wt <- mutate_all(wt, function(x) as.numeric(as.character(x)))
```

```
## Warning: There was 1 warning in 'mutate()'.
## i In argument: 'X = (function (x) ...'.
## Caused by warning:
## ! NAs introducidos por coerción
```

```
dim(wt)
```

```
## [1]  9 10
```

```
wt$X <- NULL
sum(wt)
```

```
## [1] 11.4134
```

```
abs <- wt/sum(wt) * 100

region <- as.data.frame(read.table("subtrees/subtree_delta/joint_mugration_region_delta/GTR_region_regi
    sep = "\t", header = F))
region <- as.data.frame(region[-6, ])


split <- as.data.frame(str_split_fixed(region$`region[-6, ]`, ": ", 2))
split$V2 <- gsub("SouthAmerica", "South America", split$V2)
split$V2 <- gsub("NorthAmerica", "North America", split$V2)
colnames(abs) <- split$V2
```

```r
rownames(abs) <- split$V2
```

```r
dt2 <- abs %>%
    rownames_to_column() %>%
    gather(colname, value, -rowname)
head(dt2)
```

```
##         rowname colname     value
## 1        Africa  Africa 0.0000000
## 2     Argentina  Africa 0.3092856
## 3          Asia  Africa 4.8732192
## 4        Brazil  Africa 0.8603922
## 5        Europe  Africa 4.2152207
## 6 North America  Africa 1.3475389
```

```r
dt2$value <- gsub(",", ".", dt2$value)
dt2$value <- as.numeric(as.character(dt2$value))
dt2$value <- round(dt2$value, 1)
head(dt2)
```

```
##         rowname colname value
## 1        Africa  Africa   0.0
## 2     Argentina  Africa   0.3
## 3          Asia  Africa   4.9
## 4        Brazil  Africa   0.9
## 5        Europe  Africa   4.2
## 6 North America  Africa   1.3
```

```r
region <- ggplot(dt2, aes(x = rowname, y = colname, fill = value)) + geom_tile(color = "white",
    lwd = 1.5, linetype = 1) + scale_fill_gradient2(low = "#075AFF", mid = "#FFFFCC",
    high = "#FF0000") + geom_text(aes(label = value), color = "black",
    size = 3) + coord_fixed() + theme(axis.text.x = element_text(angle = 90,
    vjust = 0.5, hjust = 1, size = 12), axis.text.y = element_text(size = 12),
    axis.title = element_text(size = 14), legend.text = element_text(size = 10),
    legend.title = element_blank(), panel.grid.major = element_blank(),
    panel.grid.minor = element_blank(), panel.border = element_blank(),
    panel.background = element_blank(), plot.title = element_text(size = 12)) +
    xlab("To") + ylab("From") + ggtitle("Transition rates (%) between regions - Delta")
```

```r
abs
```

```
##                  Africa Argentina      Asia    Brazil    Europe North America
## Africa        0.0000000 0.1086442 1.8539611 0.2549635 1.1092225     0.4547287
## Argentina     0.3092856 0.0000000 0.2374402 0.5695060 0.4100443     1.4640686
## Asia          4.8732192 0.2199169 0.0000000 0.2234216 2.3008043     0.6308374
## Brazil        0.8603922 0.6781502 0.2873815 0.0000000 0.8183363     0.3311897
## Europe        4.2152207 0.5493543 3.3267913 0.9199713 0.0000000     1.9801286
## North America 1.3475389 1.5297808 0.7105683 0.2908862 1.5437994     0.0000000
## Oceania       0.2497065 0.3644839 0.5020415 0.2190408 0.1235390     0.5686299
## South America 1.0373771 4.0338549 1.0251108 3.7236932 2.5347399     5.3253194
## Uruguay       1.3352726 0.6054287 0.7955561 0.5914101 2.0975345     1.3343964
##                 Oceania South America    Uruguay
## Africa        0.1419384    0.08498782  1.0137207
```

```
## Argentina     0.5879054   0.93486603   1.3054830
## Asia          0.7499956   0.21991694   1.5876075
## Brazil        0.4214345   1.02773932   1.5175145
## Europe        0.2672297   0.78679447   6.0560394
## North America 0.9593986   1.28883593   3.0026110
## Oceania       0.0000000   0.23656404   0.4266914
## South America 1.6498151   0.00000000  13.1249233
## Uruguay       0.3197995   1.41149876   0.0000000
```

```r
intro <- as.data.frame(t(abs[9, ]/sum(abs[9, ]) * 100))
intro$region <- row.names(intro)
row.names(intro) <- NULL
intro <- select(intro, region, Uruguay)
colnames(intro) <- c("Region", "rate")
intro$rate <- round(intro$rate, 1)
intro <- intro[-1, ]
intro
```

```
##         Region rate
## 2     Argentina  7.1
## 3          Asia  9.4
## 4        Brazil  7.0
## 5        Europe 24.7
## 6 North America 15.7
## 7       Oceania  3.8
## 8 South America 16.6
## 9       Uruguay  0.0
```

```r
bar_i <- ggplot(intro, aes(x = reorder(Region, rate), y = rate, fill = Region)) +
    geom_bar(stat = "identity") + geom_text(aes(label = rate), hjust = 1,
    size = 3.5) + theme(axis.line = element_blank(), panel.grid.major = element_blank(),
    panel.grid.minor = element_blank(), panel.border = element_blank(),
    panel.background = element_blank(), axis.text.x = element_text(hjust = 0.5),
    axis.title.x = element_text(size = 12), axis.title.y = element_text(size = 12,
        vjust = 1.5), axis.text.y = element_text(size = 10), legend.position = "none",
    plot.title = element_text(size = 10)) + scale_fill_manual(values = c(Brazil = "#fcb186",
    Europe = "#f3ffbd", `South America` = "#ec9393", Argentina = "#e6d186",
    Asia = "#eca7ba", Africa = "#d0d9b6", `North America` = "#dca76c",
    Oceania = "#ffd4d7")) + ylab("") + xlab("") + coord_flip() + ggtitle("To Uruguay")


dif <- as.data.frame(abs[, 9]/sum(abs[, 9]) * 100)
row.names(dif) <- row.names(abs)
dif$Region <- row.names(dif)
row.names(dif) <- NULL
colnames(dif) <- c("rate", "Region")
dif <- select(dif, Region, rate)
dif <- dif[order(dif$rate, decreasing = F), ]
dif <- dif[-1, ]
dif$rate <- round(dif$rate, 1)


bar_e <- ggplot(dif, aes(x = reorder(Region, rate), y = rate, fill = Region)) +
    geom_bar(stat = "identity") + geom_text(aes(label = rate), hjust = 1,
```
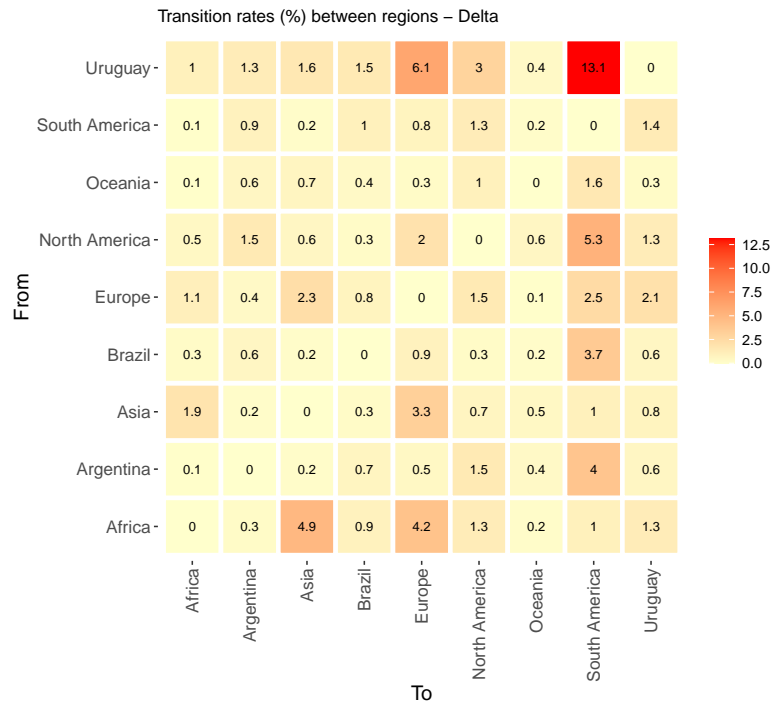
```
    size = 3.5) + theme(axis.line = element_blank(), panel.grid.major = element_blank(),
    panel.grid.minor = element_blank(), panel.border = element_blank(),
    panel.background = element_blank(), axis.text.x = element_text(hjust = 0.5),
    axis.title.x = element_text(size = 12), axis.title.y = element_text(size = 12,
        vjust = 1.5), axis.text.y = element_text(size = 10), legend.position = "none",
    plot.title = element_text(size = 10)) + scale_fill_manual(values = c(Brazil = "#fcb186",
    Europe = "#f3ffbd", `South America` = "#ec9393", Argentina = "#e6d186",
    Asia = "#eca7ba", Africa = "#d0d9b6", `North America` = "#dca76c",
    Oceania = "#ffd4d7")) + ylab("") + xlab("") + coord_flip() + ggtitle("From Uruguay")

figb <- ggarrange(bar_i, bar_e, nrow = 2)
figb <- annotate_figure(figb, left = textGrob("Region", rot = 90, vjust = 1,
    gp = gpar(cex = 1)), bottom = textGrob("Tranistion rate (%)", gp = gpar(cex = 1)))

fig1 <- ggarrange(region, figb, ncol = 2, labels = c("A", "B"), heights = c(1,
    0.6), widths = c(1, 0.6))
plot(fig1)
```
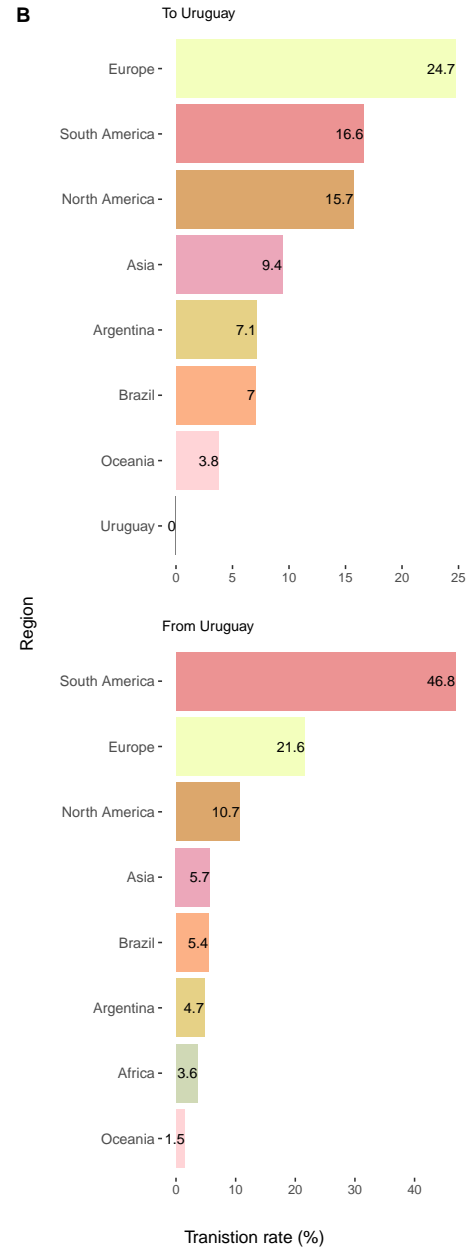
A

Transition rates (%) between regions – Delta

B


```
png("transition_region_delta.png", res = 800, height = 30, width = 55,
    units = "cm")
fig1
dev.off()

## pdf
##   2
```

Geographical transitions (regions) of the Gamma clade

```
wt <- as.data.frame(read.table("subtrees/subtree_gamma/joint_mugration_region_delta/GTR_region_gamma.txt
    sep = "\t", header = T))
head(wt)
```

```
##     X      A      B      C      D      E      F      G      H      I
## 1   A 0.0000 0.0752 0.1596 0.0586 0.1596 0.1507 0.1596 0.0775 0.0330
## 2   B 0.1132 0.0000 0.1132 0.3639 0.1132 0.0970 0.1132 0.5209 0.0931
## 3   C 0.1596 0.0752 0.0000 0.0586 0.1596 0.1507 0.1596 0.0775 0.0330
## 4   D 0.0195 0.0803 0.0195 0.0000 0.0195 0.0337 0.0195 0.2496 0.1470
## 5   E 0.1596 0.0752 0.1596 0.0586 0.0000 0.1507 0.1596 0.0775 0.0330
## 6   F 0.1863 0.0797 0.1863 0.1254 0.1863 0.0000 0.1863 0.1239 0.0334
```

```r
wt <- mutate_all(wt, function(x) as.numeric(as.character(x)))
```

```
## Warning: There was 1 warning in 'mutate()'.
## i In argument: 'X = (function (x) ...'.
## Caused by warning:
## ! NAs introducidos por coerción
```

```r
dim(wt)
```

```
## [1]  9 10
```

```r
wt$X <- NULL
sum(wt)
```

```
## [1] 11.4217
```

```r
abs <- wt/sum(wt) * 100

region <- as.data.frame(read.table("subtrees/subtree_gamma/joint_mugration_region_delta/GTR_region_regi
    sep = "\t", header = F))
region <- as.data.frame(region[-6, ])


split <- as.data.frame(str_split_fixed(region$`region[-6, ]`, ": ", 2))
split$V2 <- gsub("SouthAmerica", "South America", split$V2)
split$V2 <- gsub("NorthAmerica", "North America", split$V2)
colnames(abs) <- split$V2
rownames(abs) <- split$V2


dt2 <- abs %>%
    rownames_to_column() %>%
    gather(colname, value, -rowname)
head(dt2)
```

```
##          rowname colname      value
## 1         Africa  Africa 0.0000000
## 2      Argentina  Africa 0.9910959
## 3           Asia  Africa 1.3973402
## 4         Brazil  Africa 0.1707276
## 5         Europe  Africa 1.3973402
## 6  North America  Africa 1.6311057
```

```r
dt2$value <- gsub(",", ".", dt2$value)
dt2$value <- as.numeric(as.character(dt2$value))
dt2$value <- round(dt2$value, 1)
head(dt2)
```

```
##          rowname colname value
## 1         Africa  Africa   0.0
```

```
## 2      Argentina  Africa   1.0
## 3           Asia  Africa   1.4
## 4         Brazil  Africa   0.2
## 5         Europe  Africa   1.4
## 6 North America   Africa   1.6
```

```r
region <- ggplot(dt2, aes(x = rowname, y = colname, fill = value)) + geom_tile(color = "white",
    lwd = 1.5, linetype = 1) + scale_fill_gradient2(low = "#075AFF", mid = "#FFFFCC",
    high = "#FF0000") + geom_text(aes(label = value), color = "black",
    size = 3) + coord_fixed() + theme(axis.text.x = element_text(angle = 90,
    vjust = 0.5, hjust = 1, size = 12), axis.text.y = element_text(size = 12),
    axis.title = element_text(size = 14), legend.text = element_text(size = 10),
    legend.title = element_blank(), panel.grid.major = element_blank(),
    panel.grid.minor = element_blank(), panel.border = element_blank(),
    panel.background = element_blank(), plot.title = element_text(size = 12)) +
    xlab("To") + ylab("From") + ggtitle("Transition rates (%) between regions - Gamma")

abs
```

```
##                    Africa Argentina      Asia     Brazil    Europe North America
## Africa         0.0000000 0.6583959 1.3973402  0.5130585 1.3973402     1.3194183
## Argentina      0.9910959 0.0000000 0.9910959  3.1860406 0.9910959     0.8492606
## Asia           1.3973402 0.6583959 0.0000000  0.5130585 1.3973402     1.3194183
## Brazil         0.1707276 0.7030477 0.1707276  0.0000000 0.1707276     0.2950524
## Europe         1.3973402 0.6583959 1.3973402  0.5130585 0.0000000     1.3194183
## North America  1.6311057 0.6977945 1.6311057  1.0979101 1.6311057     0.0000000
## Oceania        1.3973402 0.6583959 1.3973402  0.5130585 1.3973402     1.3194183
## South America  0.9438175 4.2130331 0.9438175  9.1510020 0.9438175     1.2204838
## Uruguay        0.9762119 1.8272236 0.9762119 13.0847422 0.9762119     0.7993556
##                   Oceania South America   Uruguay
## Africa          1.3973402      0.678533 0.2889237
## Argentina       0.9910959      4.560617 0.8151151
## Asia            1.3973402      0.678533 0.2889237
## Brazil          0.1707276      2.185314 1.2870238
## Europe          1.3973402      0.678533 0.2889237
## North America   1.6311057      1.084777 0.2924258
## Oceania         0.0000000      0.678533 0.2889237
## South America   0.9438175      0.000000 0.9324356
## Uruguay         0.9762119      2.264111 0.0000000
```

```r
intro <- as.data.frame(t(abs[9, ]/sum(abs[9, ]) * 100))
intro$region <- row.names(intro)
row.names(intro) <- NULL
intro <- select(intro, region, Uruguay)
colnames(intro) <- c("Region", "rate")
intro$rate <- round(intro$rate, 1)
intro <- intro[-1, ]
intro
```

```
##           Region rate
## 2      Argentina  8.4
## 3           Asia  4.5
## 4         Brazil 59.8
## 5         Europe  4.5
## 6 North America   3.7
```

```
## 7         Oceania  4.5
## 8 South America 10.3
## 9         Uruguay  0.0
```

```r
bar_i <- ggplot(intro, aes(x = reorder(Region, rate), y = rate, fill = Region)) +
    geom_bar(stat = "identity") + geom_text(aes(label = rate), hjust = 1,
    size = 3.5) + theme(axis.line = element_blank(), panel.grid.major = element_blank(),
    panel.grid.minor = element_blank(), panel.border = element_blank(),
    panel.background = element_blank(), axis.text.x = element_text(hjust = 0.5),
    axis.title.x = element_text(size = 12), axis.title.y = element_text(size = 12,
        vjust = 1.5), axis.text.y = element_text(size = 10), legend.position = "none",
    plot.title = element_text(size = 10)) + scale_fill_manual(values = c(Brazil = "#fcb186",
    Europe = "#f3ffbd", `South America` = "#ec9393", Argentina = "#e6d186",
    Asia = "#eca7ba", Africa = "#d0d9b6", `North America` = "#dca76c",
    Oceania = "#ffd4d7")) + ylab("") + xlab("") + coord_flip() + ggtitle("To Uruguay")



dif <- as.data.frame(abs[, 9]/sum(abs[, 9]) * 100)
row.names(dif) <- row.names(abs)
dif$Region <- row.names(dif)
row.names(dif) <- NULL
colnames(dif) <- c("rate", "Region")
dif <- select(dif, Region, rate)
dif <- dif[order(dif$rate, decreasing = F), ]
dif <- dif[-1, ]
dif$rate <- round(dif$rate, 1)


bar_e <- ggplot(dif, aes(x = reorder(Region, rate), y = rate, fill = Region)) +
    geom_bar(stat = "identity") + geom_text(aes(label = rate), hjust = 1,
    size = 3.5) + theme(axis.line = element_blank(), panel.grid.major = element_blank(),
    panel.grid.minor = element_blank(), panel.border = element_blank(),
    panel.background = element_blank(), axis.text.x = element_text(hjust = 0.5),
    axis.title.x = element_text(size = 12), axis.title.y = element_text(size = 12,
        vjust = 1.5), axis.text.y = element_text(size = 10), legend.position = "none",
    plot.title = element_text(size = 10)) + scale_fill_manual(values = c(Brazil = "#fcb186",
    Europe = "#f3ffbd", `South America` = "#ec9393", Argentina = "#e6d186",
    Asia = "#eca7ba", Africa = "#d0d9b6", `North America` = "#dca76c",
    Oceania = "#ffd4d7")) + ylab("") + xlab("") + coord_flip() + ggtitle("From Uruguay")

figb <- ggarrange(bar_i, bar_e, nrow = 2)
figb <- annotate_figure(figb, left = textGrob("Region", rot = 90, vjust = 1,
    gp = gpar(cex = 1)), bottom = textGrob("Tranistion rate (%)", gp = gpar(cex = 1)))

fig1 <- ggarrange(region, figb, ncol = 2, labels = c("A", "B"), heights = c(1,
    0.6), widths = c(1, 0.6))
plot(fig1)
```
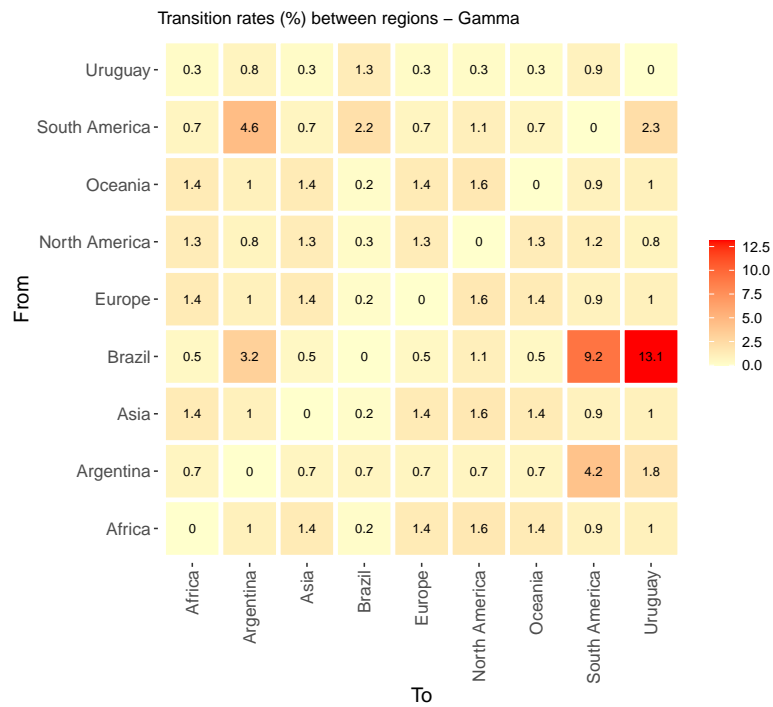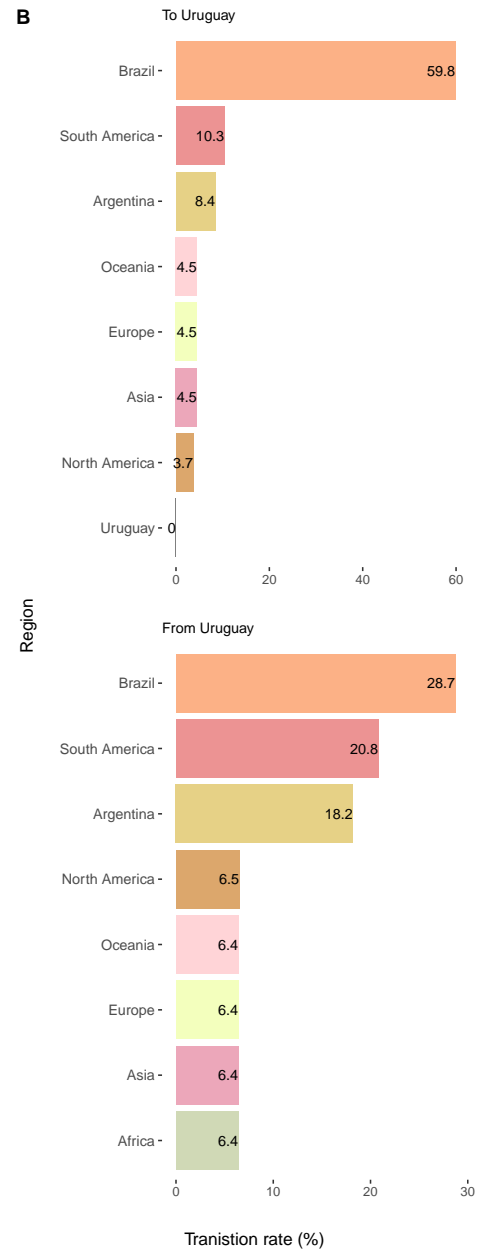
A

Transition rates (%) between regions – Gamma

B

To Uruguay

From Uruguay


```
png("transition_region_gamma.png", res = 800, height = 30, width = 55,
    units = "cm")
fig1
dev.off()
```

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