

Examples of Using PixgramR

Peter Hraber

2015-08-27

The examples below use data already accessible to the R interpreter. To load your own data, add these arguments to `pixgramr::pixgram()` options: `tre_file="x"` and `nts_file="x"` or `aas_file="x"`.

The tree file format is Newick and the alignment/s can be fasta or others. For supported alignment formats, see `?seqinr::read.alignment()`. Unless using the default format (fasta), change it by adding `alignment_format="x"` to `pixgramr::pixgram()` options.

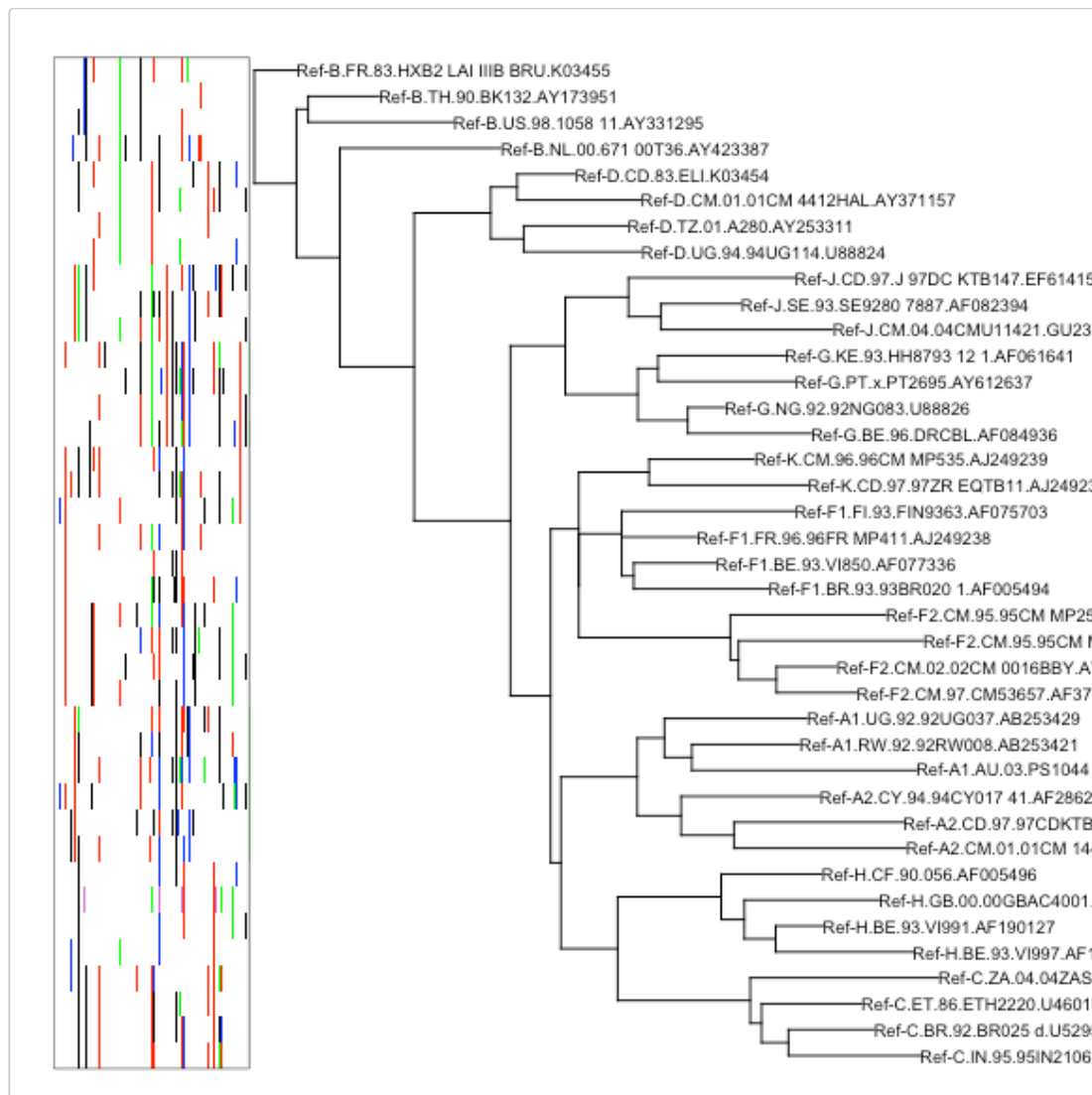
Example 1. Population-level diversity among HIV-1 reference subtypes

Here we take a look at variation in the gp41 ectodomain of the HIV-1 group M subtype reference alignment. To learn more about these data, type `help("hiv.ref")` or `?hiv.ref`.

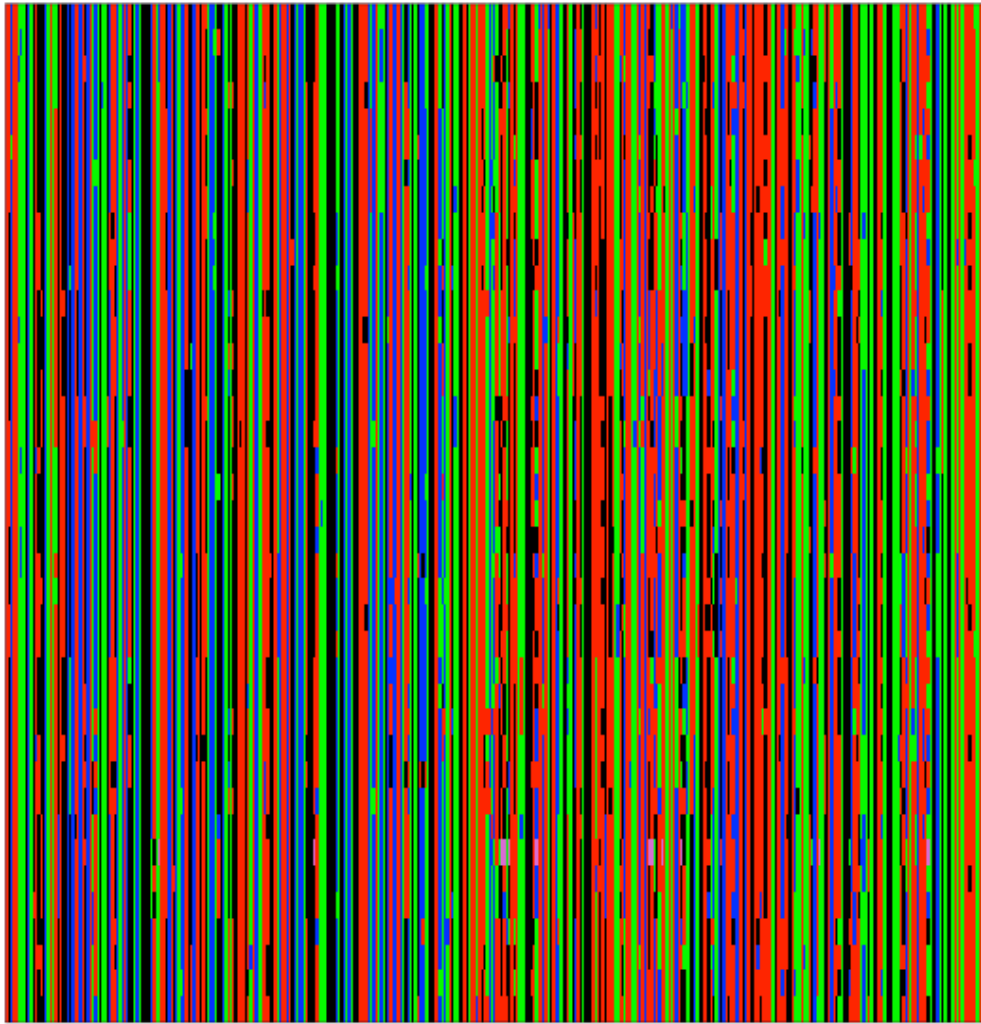
```
par(cex=1/2)
library(pixgramr, warn.conflicts=F, quietly=T)

n <- pixgramr::pixgram(tre=hiv.ref$tre, nts=hiv.ref$nts,
                      master_name="__consensus__", excise_refseq=F,
                      main="Subtype reference", sub='gp41 ectodomain')

par(mar=c(0,0,1,0), oma=c(0,0,0,0))
plot(n, xform_type=2, show_tip_label=T, raster_width=1/4)
```



```
plot(n, xform_type=0, show_tree=F, raster_width=1000)
```



This time, translate the codons and color tree branches by clade.

```
clade.colors <- c("#FFC20E", "#008FD4", "#ED1C24", "#00A99D", "#F7941D",
                 "#235192", "#8DC73F", "#00A651", "#EC008C")
names(clade.colors) = sort(unique(hiv.ref$clade))

leaf.colors = sapply(seq_along(hiv.ref$tre$tip.label), function(i)
  clade.colors[hiv.ref$clade[i]])

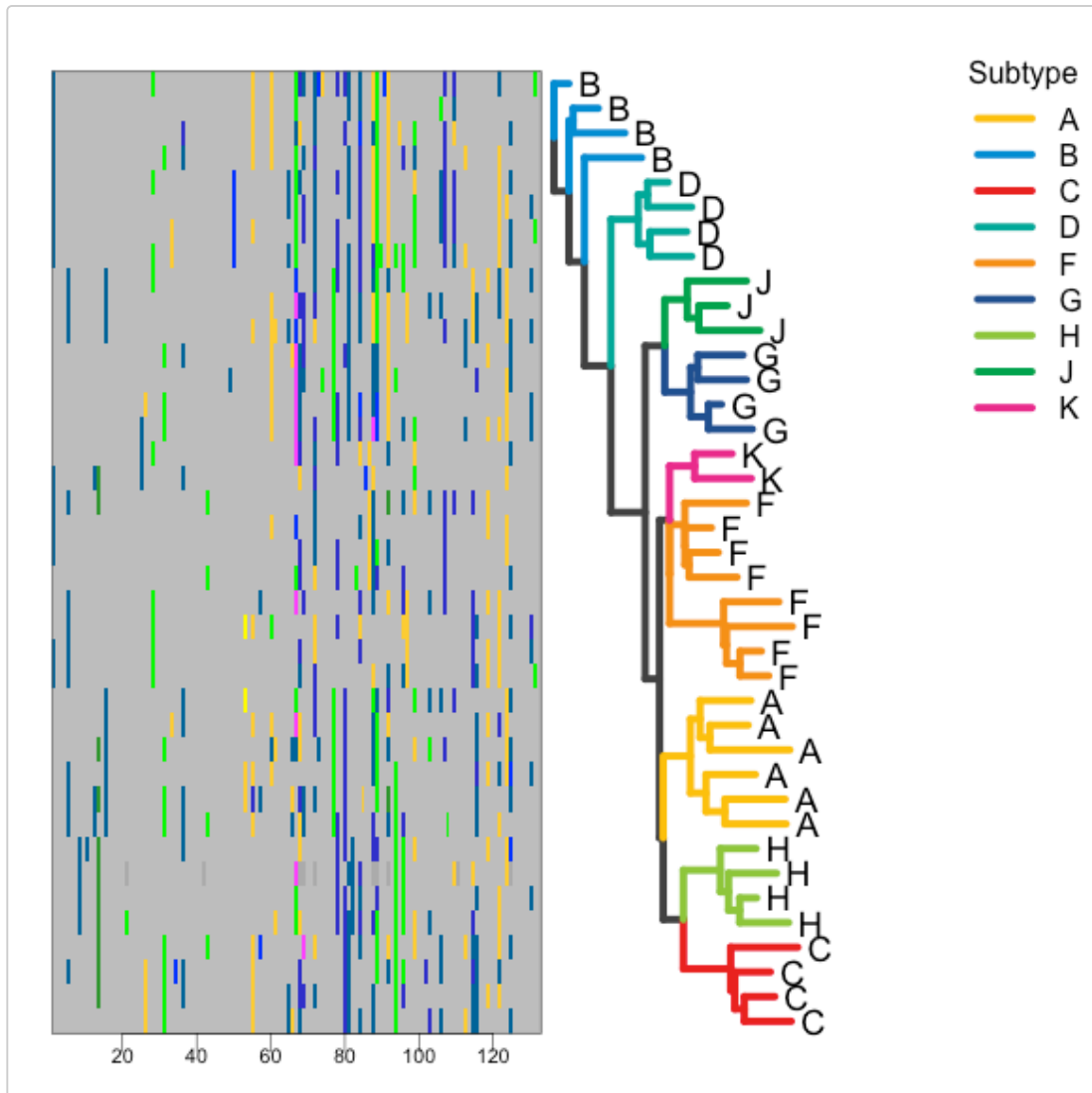
legend.attributes <- list(title='Subtype', text=names(clade.colors),
                          cols=clade.colors,
                          bg="white", bty='o', lwds=4)

p <- pixgramr::pixgram(tre=hiv.ref$tre, nts=hiv.ref$nts, is_orf=T,
                      refseq_name="Ref-B.FR.83.HXB2_LAI_IIIB_BRU.K03455",
                      master_name="__consensus__", excise_refseq=F)

hiv.ref.tip.labels <- list()
hiv.ref.tip.labels$pch = hiv.ref$clade
hiv.ref.tip.labels$bgs = NA
hiv.ref.tip.labels$col = "black"

par(mar=c(1,0,1,0), oma=c(0,0,0,0))
```

```
plot(p, xform_type=2, xform_master=T, edge_widths=4,
     leaf_colors=leaf.colors, legend_attributes=legend.attributes,
     tip_labels=hiv.ref.tip.labels, show_tip_label = T)
```

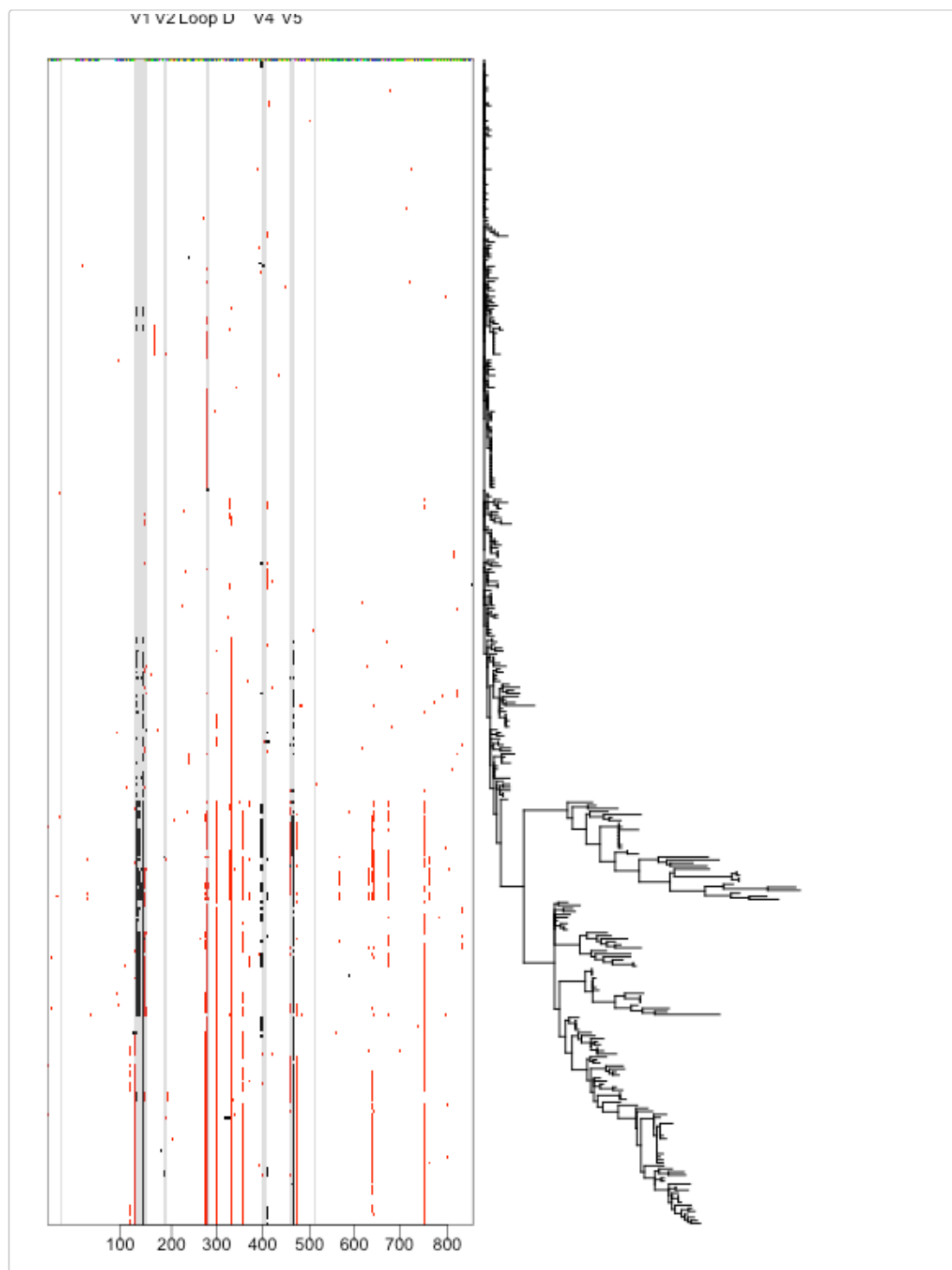


Example 2. Within-host envelope glycoprotein (Env) sequences

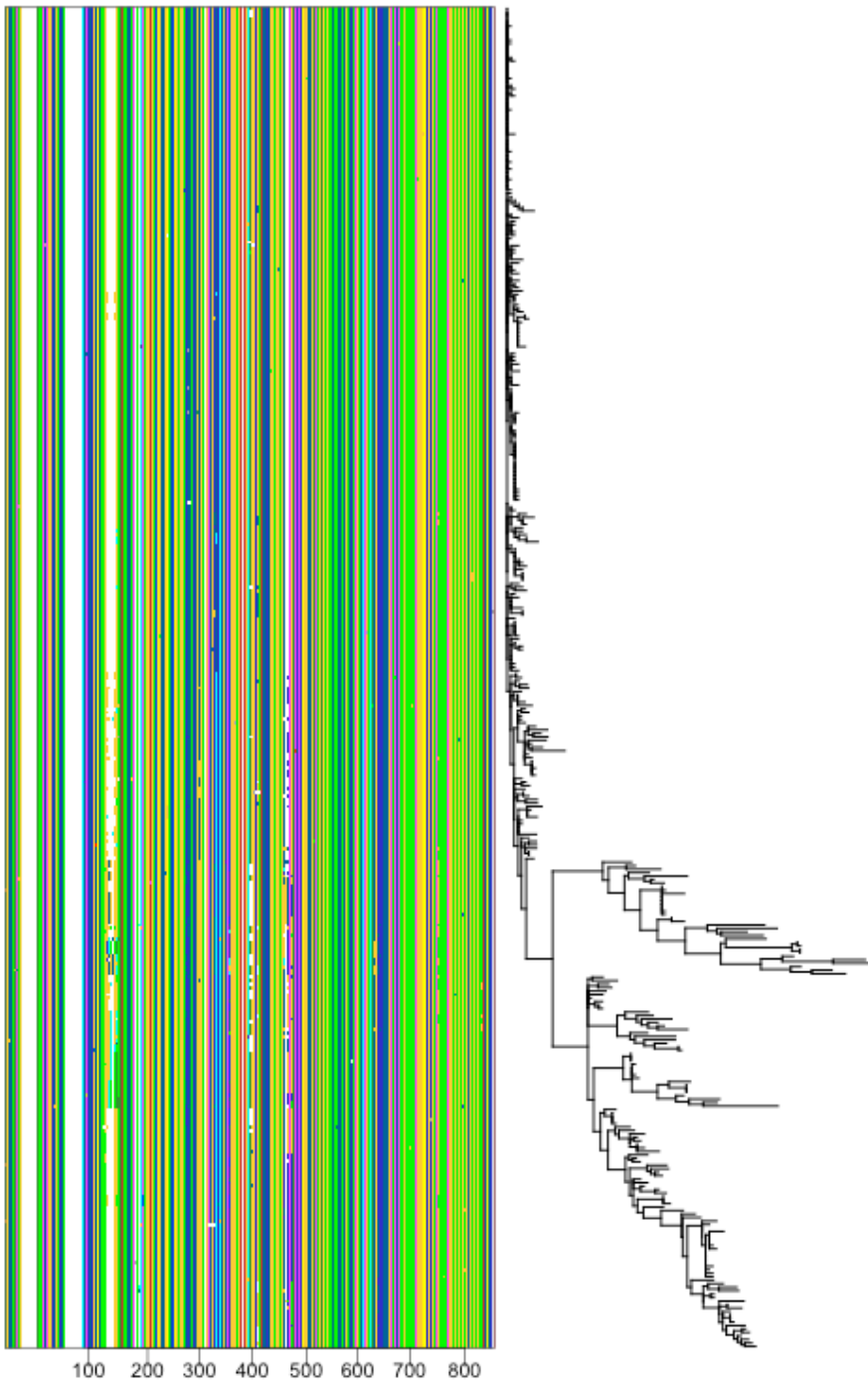
CH505 Env shows descent from a single transmitted-founder virus over three years post-infection.

To learn more about these data, type `help("CH505")` or `?CH505`.

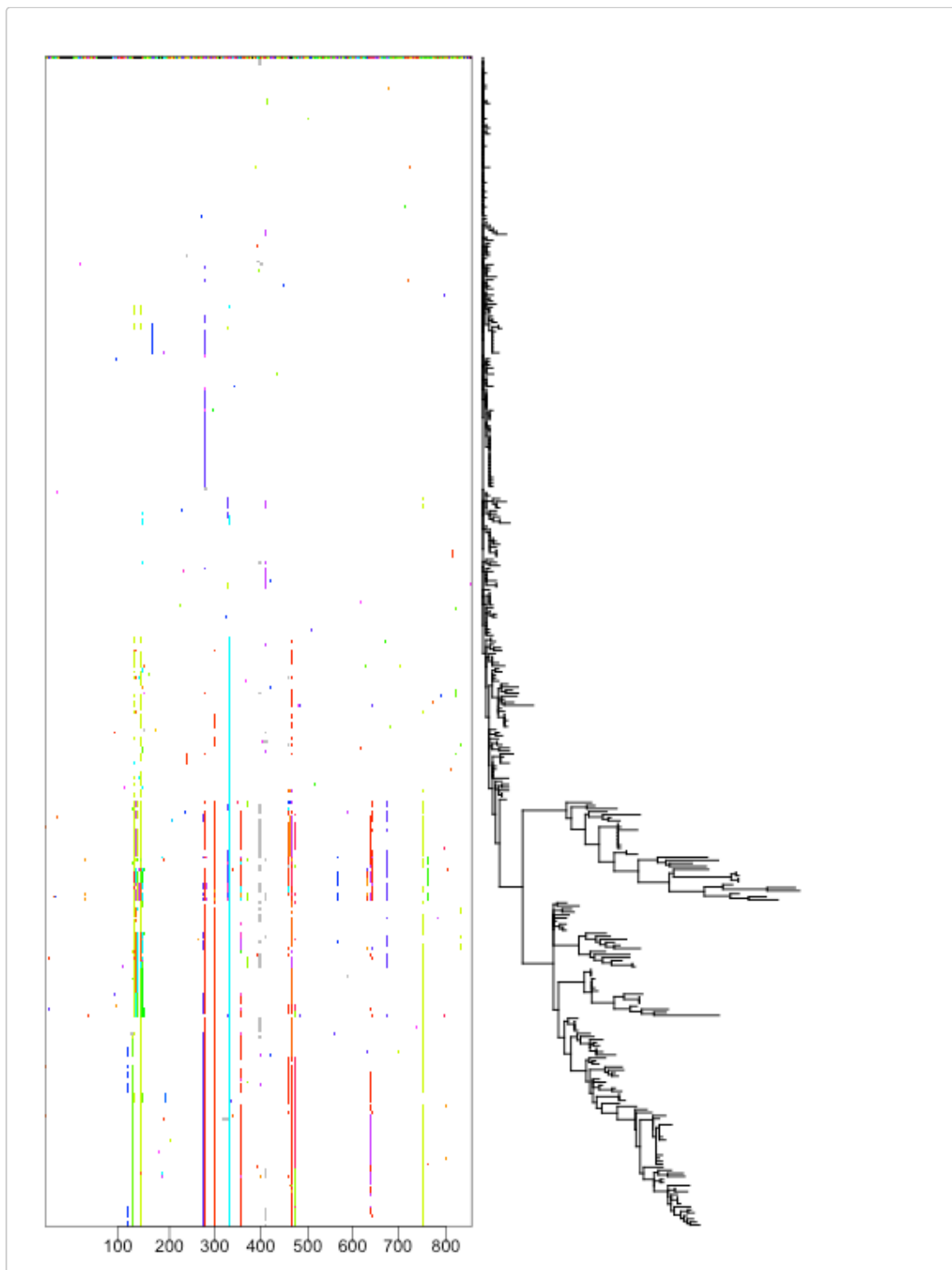
```
library(pixgramr, warn.conflicts=F, quietly=T)
p <- pixgramr::pixgram(tre=CH505$tre, aas=CH505$aas, excise_refseq=T)
par(mar=c(0,0,0,0), oma=c(0,0,0,0))
plot(p, xform_type=1, xform_master=F, annotate_env=T)
```



```
plot(p, xform_type=0, xform_master=F)
```



```
plot(p, xform_type=2, xform_master=F, color_lut_type="taylor")
```



In this view, leaf colors show the passage of time:

```
library(pixgramr)

wpi.colors=c( "#EC008C", "#ED1C24", "#F7941D", "#FFC20E", "#CADB2A",
              "#8DC73F", "#00A651", "#00A99D", "#31B6E9", "#008FD4",
              "#235192", "#662D91", "black", "#666666", "#888888")

names(wpi.colors) = sort(unique(CH505$wpi))

CH505.colors = sapply(seq_along(CH505$tre$tip.label), function(i)
  wpi.colors[CH505$wpi[i]])
```

```

legend.attributes <- list(text=names(wpi.colors), cols=wpi.colors,
                          bg="white", bty='o', lwds=3/2, title='WPI')

scale.bar <- list(pos=c(1/20,7), lwd=1, len=5/953, cex=4/5, text="5 aas")
par(mar=c(0,0,0,0), oma=c(0,0,0,0))
plot(CH505.pixgram <- pixgramr::pixgram(aas=CH505$aas,
                                       tre=CH505$tre, xform_type=3,
                                       raster_width=5/4,
                                       raster_margin=1/100, main="CH505",
                                       sub="Env gp160"),
    leaf_colors=CH505.colors,
    legend_attributes=legend.attributes,
    scale_bar=scale.bar, no_margin=T, xform_master=T, annotate_env=T)

```