

# 1 Supplementary file of ggbreak: An R package to set tailored axis scale break easily for ggplots

## 1.1 Case study code and results

### 1.1.1 Example1: automatically wrap plot with long x axis scale

```
library(ggplot2)
library(ggbreak)
library(patchwork)

# import output data from Protscale
data <- read.table(file = "../data/7MWE_A.csv", sep = ",", header = F, fill = T)
colnames(data) <- c("Position","Score")
head(data)

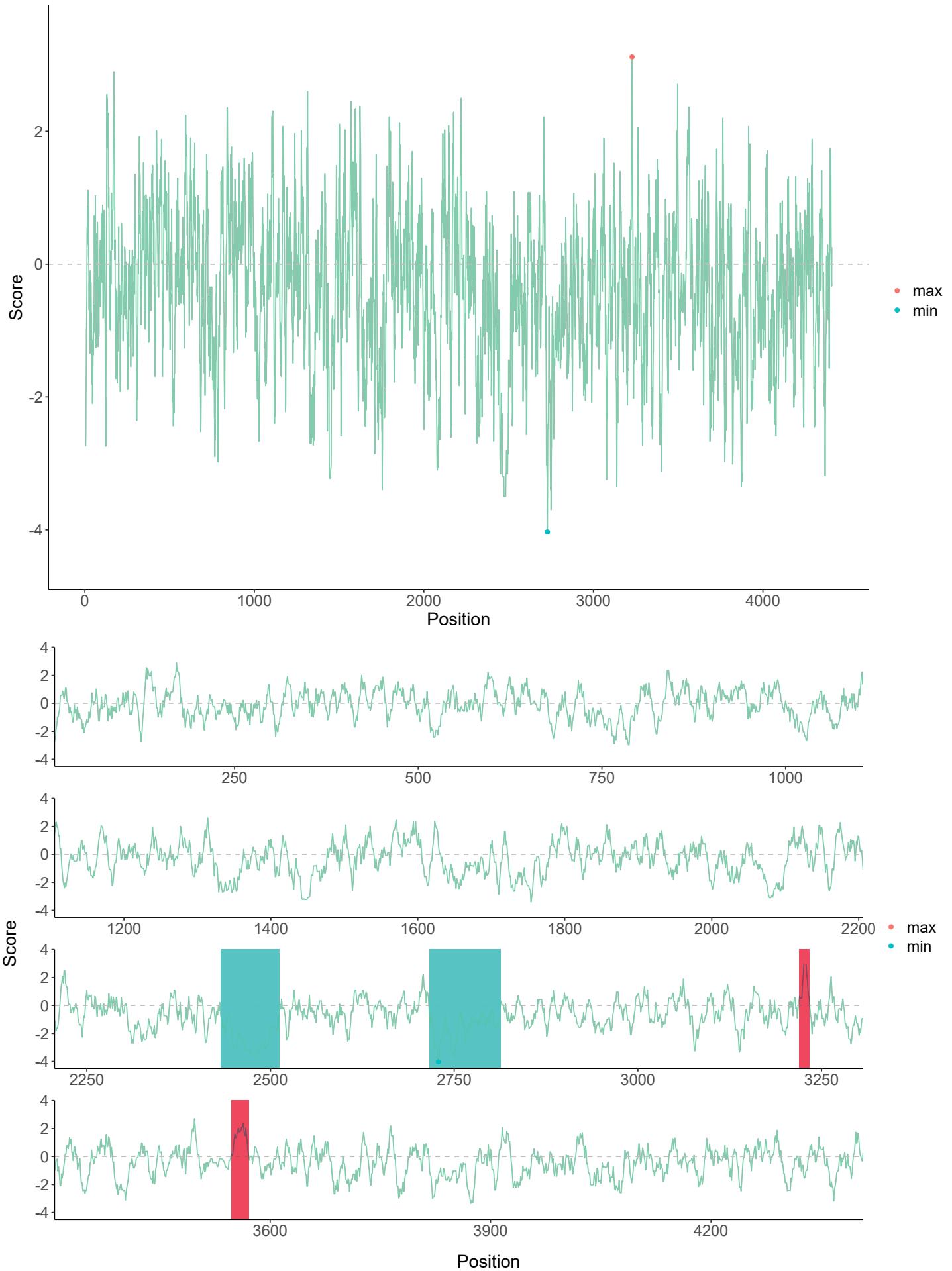
##   Position Score
## 1       5 -2.744
## 2       6 -2.533
## 3       7 -1.944
## 4       8 -1.600
## 5       9 -0.967
## 6      10 -0.967

data2 <- data.frame(c(2728,2729,3228),c(-4.033,-4.033,3.122),c("min","min","max"))
colnames(data2) <- c("Position","Score","Type")

p <- ggplot(data=data) +
  geom_line(mapping=aes(x=Position,y=Score),color="#83cbac",stat="identity") +
  geom_point(data=data2,mapping = aes(x=Position,y=Score,color=Type)) +
  theme_classic() +
  geom_hline(yintercept=0,color="grey",linetype="dashed") +
  expand_limits(y=c(-4.5,3.5)) +
  theme(axis.text.x = element_text(size = 14),
        axis.text.y = element_text(size=14),
        axis.title.x = element_text(size = 16),
        axis.title.y = element_text(size = 16),
        legend.title=element_blank(),
        legend.text=element_text(size=14))

p1 <- p + scale_wrap(n=4) +
  geom_rect(aes(xmin=2432, xmax=2512, ymin=-4.5, ymax=4),fill='#57c3c2',alpha = 0.002) +
  geom_rect(aes(xmin=2716, xmax=2813, ymin=-4.5, ymax=4),fill='#57c3c2',alpha = 0.002) +
  geom_rect(aes(xmin=3219, xmax=3233, ymin=-4.5, ymax=4),fill='#ef475d',alpha = 0.002) +
  geom_rect(aes(xmin=3547, xmax=3571, ymin=-4.5, ymax=4),fill='#ef475d',alpha = 0.002)

p/p1
```



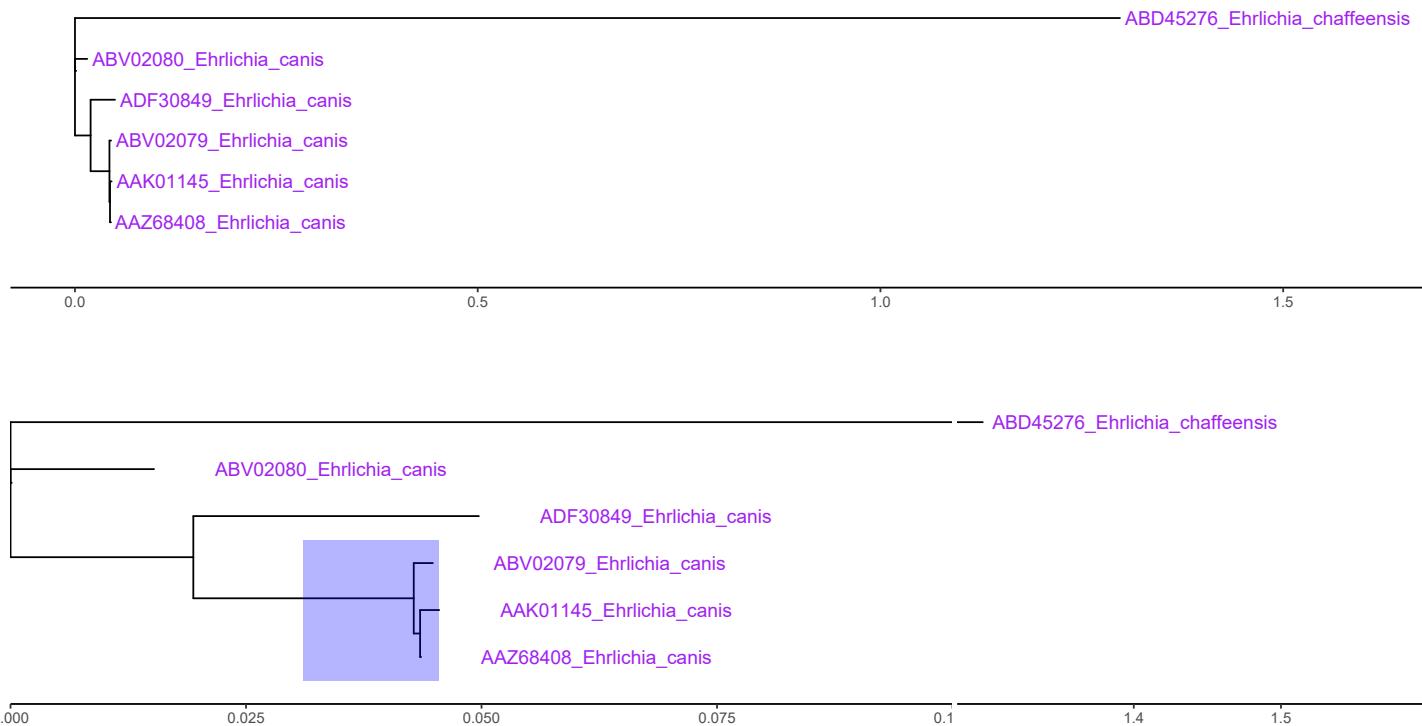
### 1.1.2 Example 2: Shrank outlier branch of phylogenetic tree

```
library("ggtree")
library("treeio")
library("ggbreak")
library("patchwork")
library("ggplot2")

treedata <- read.newick(file = "../data/gp200.nwk")
p <- ggtree(treedata, ladderize=FALSE) +
  expand_limits(x=c(0,1.6), y=c(0,8)) +
  geom_tiplab(size=4,color="purple") +
  theme_tree2()

p1 <- p + scale_x_break(breaks = c(0.1,1.28),
                         ticklabels = c(1.4,1.5),scales = 0.5) +
  geom_highlight(node=9,fill="blue",alpha = 0.3) +
  theme(
    plot.margin = margin(t = 2,
                          r = 2,
                          b = 2,
                          l = 2,
                          unit = "cm"))

p / p1
```



### 1.1.3 Example3: Cut Manhattan plot to create more space for annotation

```
library("ggbreak")
library("patchwork")
```

```

library("ggplot2")
library("dplyr")

snp <- read.table(file = ".../data/GCST90007012_buildGRCh37.tsv",
                  header = T, fill = T)
head(snp)

##   variant_id p_value chromosome base_pair_location effect_allele    beta
## 1 rs3131972  0.3586         1          752721           A  10.880
## 2 rs11240777  0.4565         1          798959           A   8.063
## 3 rs4970383  0.3810         1          838555          -A -10.080
## 4 rs4475691  0.8293         1          846808            T   3.277
## 5 rs7537756  0.2872         1          854250           G  14.660
## 6 rs13302982  0.8938         1          861808           A   1.374
##   standard_error
## 1          11.85
## 2          10.82
## 3          11.49
## 4          15.19
## 5          13.76
## 6          10.28

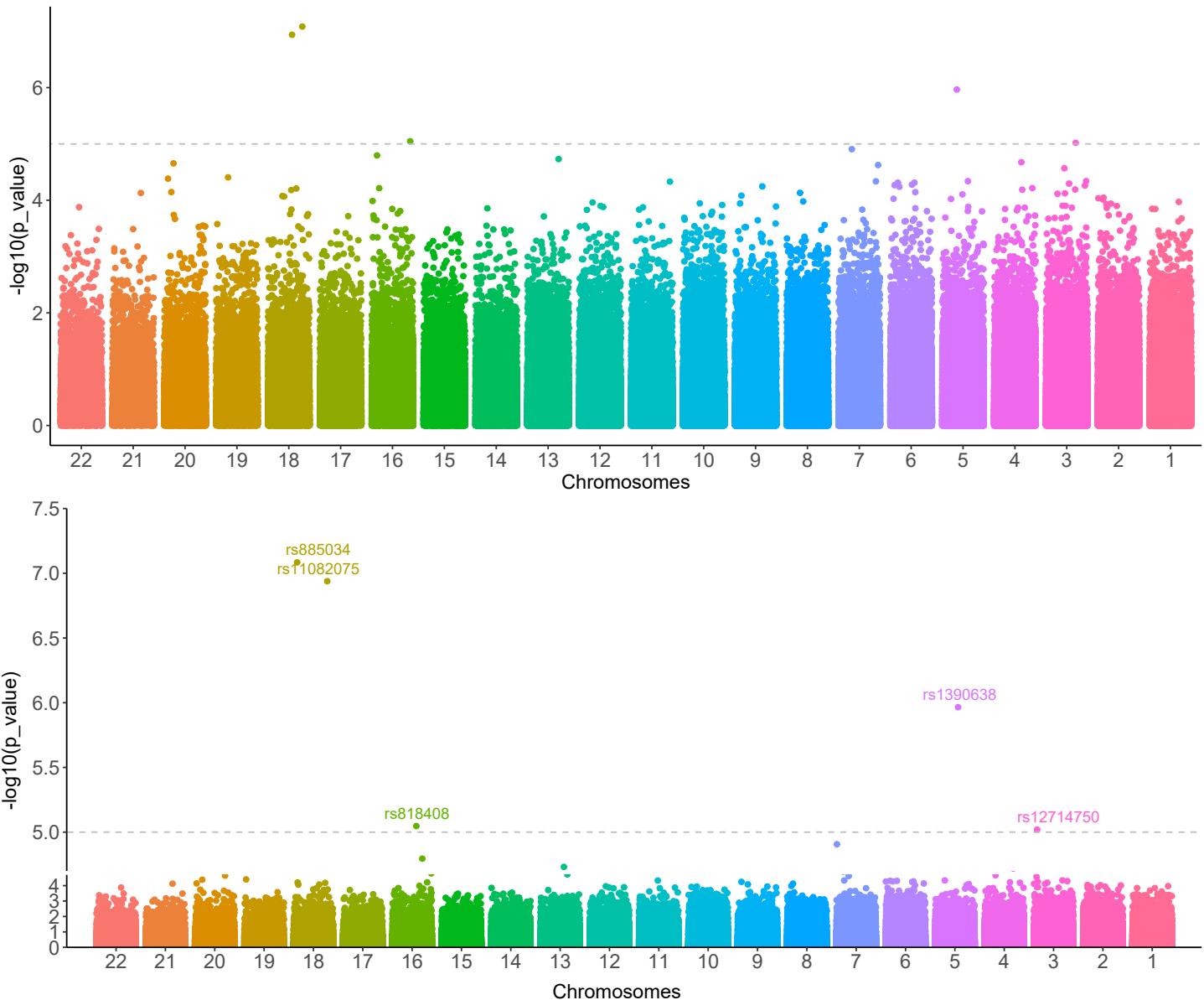
snp$chromosome <- factor(snp$chromosome,
                         levels = rev(sort(unique(snp$chromosome)))))

p1 <- ggplot(snp, aes(x=chromosome, y = -log10(p_value))) +
  geom_jitter(data=snp,
              aes(x=chromosome, y = -log10(p_value), color=chromosome)) +
  theme_classic() + xlab("Chromosomes") +
  geom_abline(intercept=5,slope = 0,color="grey",linetype="dashed") +
  theme(legend.position="none",
        axis.title.y = element_text(size = 14),
        axis.title.x = element_text(size = 14),
        axis.text = element_text(size = 14))

p2 <- p1 + scale_y_cut(breaks=c(4.7),which=c(2),scales=c(0.2)) +
  geom_text(data=snp%>%filter(-log10(p_value) >= 5),
            aes(x=chromosome, y = -log10(p_value),
                color=chromosome, label=variant_id),
            nudge_x =0.1,nudge_y = 0.1) +
  expand_limits(x=c(0, 23),y=c(0,7.5))

p1/p2

```



#### 1.1.4 Example 4: Inserting broken axes in barplot with ggbreak

```
library("ggbreak")
library("ggplot2")

data1 <- read.table(file = "../data/data1.txt",
                     header = TRUE, sep = "\t", dec = ".")
data1$Species.name <- factor(data1$Species.name,
                             levels = rev(unique(data1$Species.name)))
load("../data/sigdata.rda")

p1 <- ggplot(data=data1,aes(x=Species.name,weight = Mean, fill = group)) +
  geom_bar(position = 'dodge') +
  labs( y = 'Relative abundance(%)', x = NULL) +
  theme_classic() +
  coord_flip() +
  theme(
    axis.text.x = element_text(size=14),
    axis.text.y = element_text(size=14),
    axis.title.x = element_text(size=14))
```

```

p2 <- ggplot(data=data1,aes(x=Species.name,weight = log10(Mean+1), fill = group)) +
  geom_bar(position = 'dodge') +
  labs( y = 'log10(Relative abundance+1)', x = NULL) +
  theme_classic() + coord_flip() +
  theme(
    axis.text.x = element_text(size =14),
    axis.text.y = element_text(size =14),
    axis.title.x = element_text(size=14))

```

```

p3 <- p1 + scale_y_break(c(32, 84),scales=0.5,ticklabels=c(84,85,86)) +
  scale_y_break(c(3.5, 10),scales=0.5,ticklabels = c(15,25))

```

```

p4 <- p3 + geom_text(data=sigdata,mapping=aes(x=Species,y=Mean,label=sig),vjust=-0.1)

```

```

p1 / p3 | p2 / p4

```

