plot bootstraps

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This is a late afternoon inquiry to see if plotting distributions of support values in trees is somewhat insightfull perhaps.

create simple tab files with bootstrap values

```
for t in analyses/*_trees/*/*.treefile
do  out=$(echo $t | sed 's/.treefile/.bootstraptab/')
    if   [ ! -f $out ]
    then egrep -o ')[0-9./]+' $t | tr -d ')' | tr '/' '\t' > $out
    fi
done
```

optionally, inspect your files for troubleshooting etc.

```
#for t in analyses/*_trees/*/*.bootstraptab
#do  head $t
#done
```

Read all tab files

now simplify these names a bit

Note that theecho = FALSE‘ parameter was added to the code chunk to prevent printing of the R code that generated the plot.

```
metatabs <- strsplit(x = files,split = '/')
rm(combitab)
```

```
## Warning in rm(combitab): object 'combitab' not found
```

```
combitab <- data.table()
for (i in 1:length(tabs)) {
  temp <- tabs[[i]]
  if (dim(temp)[2] == 1) {
   names(temp) <- 'nonparametricBootstrap'
   temp$SHaLRT <- NA
   temp$UFBootstrap <- NA
  }
  if (length(names(temp)) == 2) {
    names(temp) <- c('SHaLRT','UFBootstrap')
    temp$nonparametricBootstrap <- NA
  }
  temp$dataset   <- factor(metatabs[[i]][2])
  temp$alignment <- as.character(metatabs[[i]][3])
  temp$iqtree    <- factor(metatabs[[i]][4])

  combitab <- rbind(combitab,temp,fill=T)
  rm(temp)
}
combitab$nonparametricBootstrap <- as.numeric(combitab$nonparametricBootstrap)
combitab$SHaLRT <- as.numeric(combitab$SHaLRT)
combitab$UFBootstrap <- as.numeric(combitab$UFBootstrap)
summary(combitab)
```

```
##  nonparametricBootstrap     SHaLRT        UFBootstrap
##  Min.   :  8.00         Min.   :  0.00   Min.   : 11.00
##  1st Qu.: 39.00         1st Qu.: 71.25   1st Qu.: 73.00
##  Median : 69.00         Median : 86.40   Median : 93.00
##  Mean   : 65.11         Mean   : 77.81   Mean   : 84.15
##  3rd Qu.: 95.25         3rd Qu.: 94.65   3rd Qu.: 99.00
##  Max.   :100.00         Max.   :100.00   Max.   :100.00
##  NA's   :599            NA's   :176      NA's   :176
##                                                      dataset
##  combi_sequences_linear_trees                           : 88
##  combi-I-to-VIII-Azfi_sequences_linear_trees            :437
##  combi-I-to-VIII-Azfi-Arabidopsis_sequences_linear_trees:198
##  combi-VI-VII-Azfisuspects_trees                        : 52
##
##
##
##   alignment
##  Length:775
##  Class :character
##  Mode  :character
##
##
##
##
##
##  combi-I-to-VIII-Azfi-Arabidopsis_sequences_linear_aligned-mafft-einsi_trim-gt4_iqtree-bb2000-alrt20
##  combi-I-to-VIII-Azfi-Arabidopsis_sequences_linear_aligned-mafft-einsi_trim-gt5_iqtree-bb2000-alrt20
##  combi-I-to-VIII-Azfi-Arabidopsis_sequences_linear_aligned-mafft-einsi_trim-gt6_iqtree-bb2000-alrt20
##  combi-I-to-VIII-Azfi_sequences_linear_aligned-mafft-linsi_trim-gt4_iqtree-bb2000-alrt2000.bootstrap
##  combi-I-to-VIII-Azfi_sequences_linear_aligned-mafft-einsi_trim-gt4_iqtree-bb2000-alrt2000.bootstrap
##  combi-I-to-VIII-Azfi_sequences_linear_aligned-mafft-einsi_trim-gt6_iqtree-bb2000-alrt2000.bootstrap
##  (Other)
```

```
rm(metatabs)
```

melt dataframe to long format

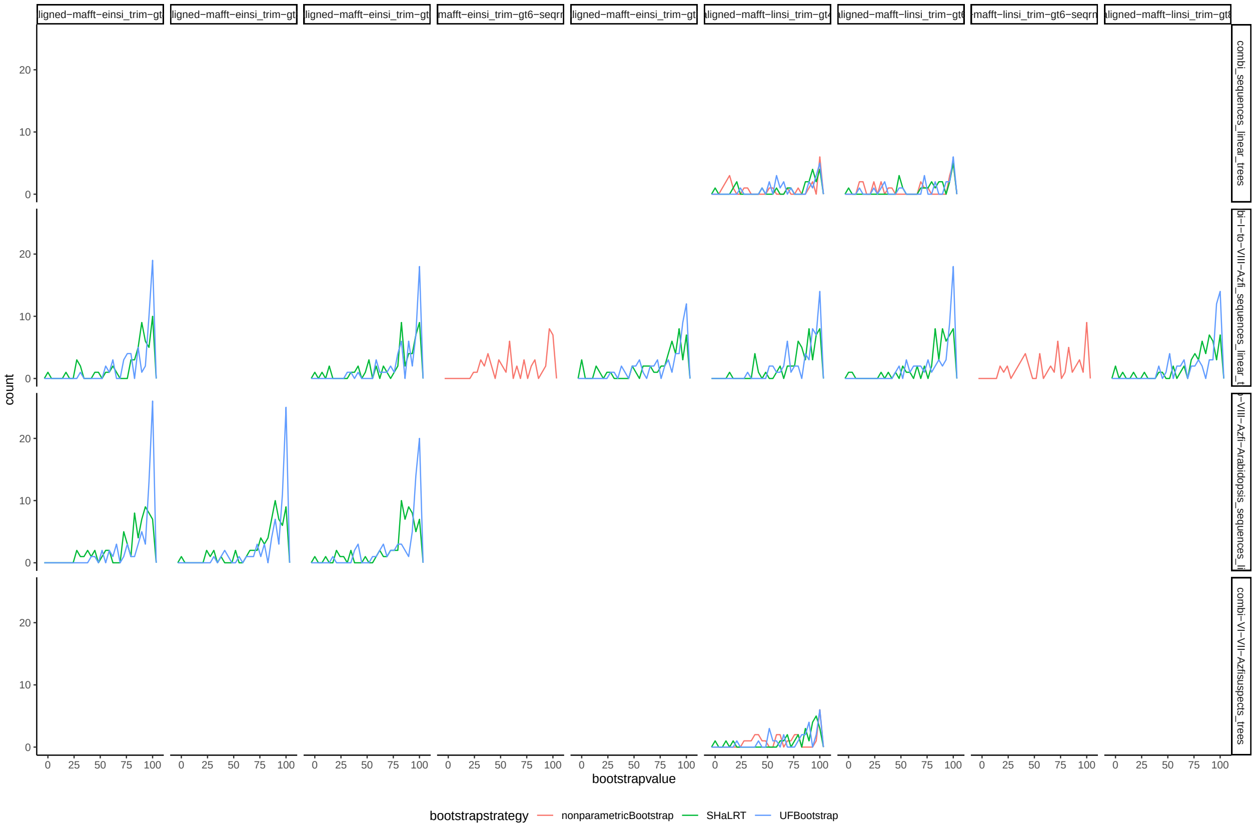
```
combitab <- melt(combitab,variable.name = 'bootstrapstrategy',id.vars = c('dataset','alignment','iqtree
```

#plot

```r
library(ggplot2)
attach(combitab)
plot <- ggplot(data=combitab,mapping = aes(x=bootstrapvalue,col=bootstrapstrategy))
plot <- plot + geom_freqpoly()
plot <- plot + theme_classic()
plot <- plot + facet_grid(dataset~alignment)
plot <- plot + theme(legend.position = 'bottom')
plot
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

```
## Warning: Removed 951 rows containing non-finite values (stat_bin).
```



```r
rm(plot)
```

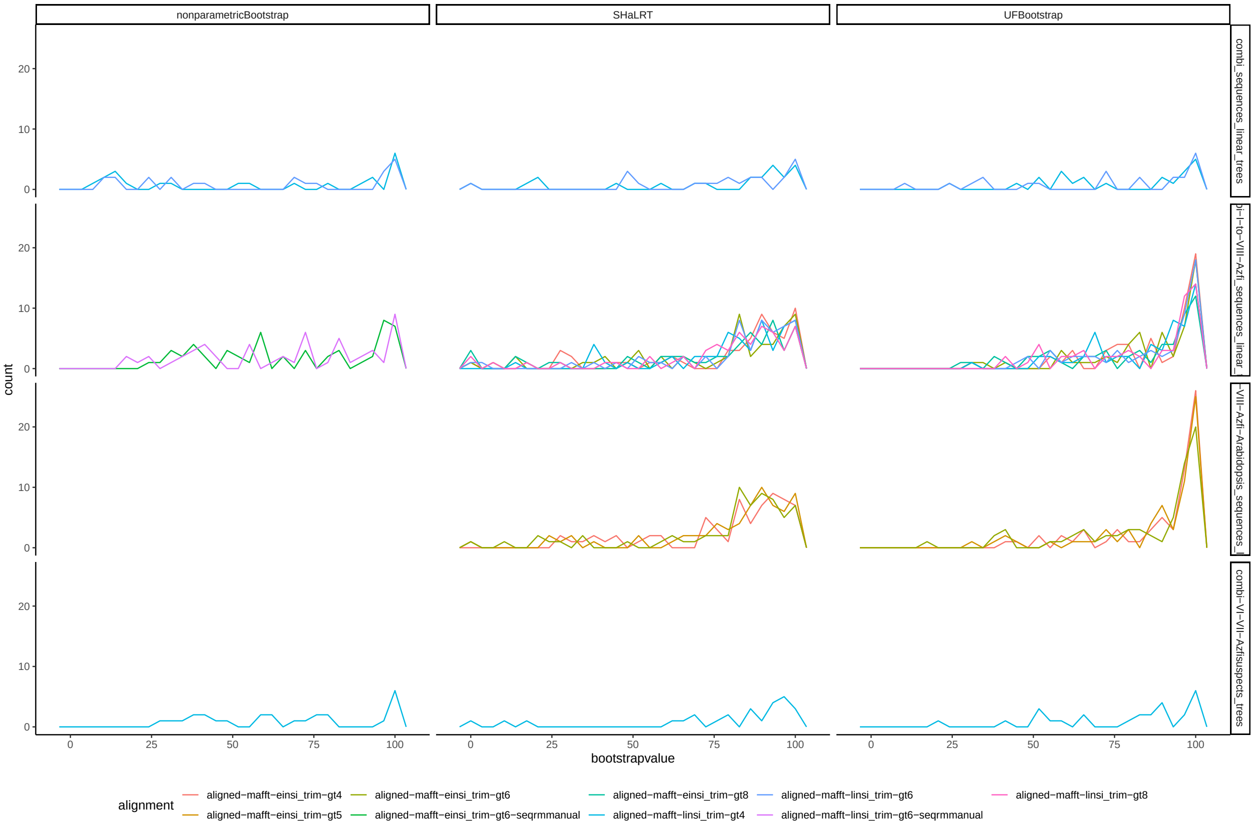
```r
library(ggplot2)
attach(combitab)
```

```
## The following objects are masked from combitab (pos = 3):
##
##     alignment, bootstrapstrategy, bootstrapvalue, dataset, iqtree
```

```r
plot <- ggplot(data=combitab,mapping = aes(x=bootstrapvalue,col=alignment))
plot <- plot + geom_freqpoly()
plot <- plot + theme_classic()
plot <- plot + facet_grid(dataset~bootstrapstrategy)
plot <- plot + theme(legend.position = 'bottom')
plot
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

```
## Warning: Removed 951 rows containing non-finite values (stat_bin).
```



```r
rm(plot)
```

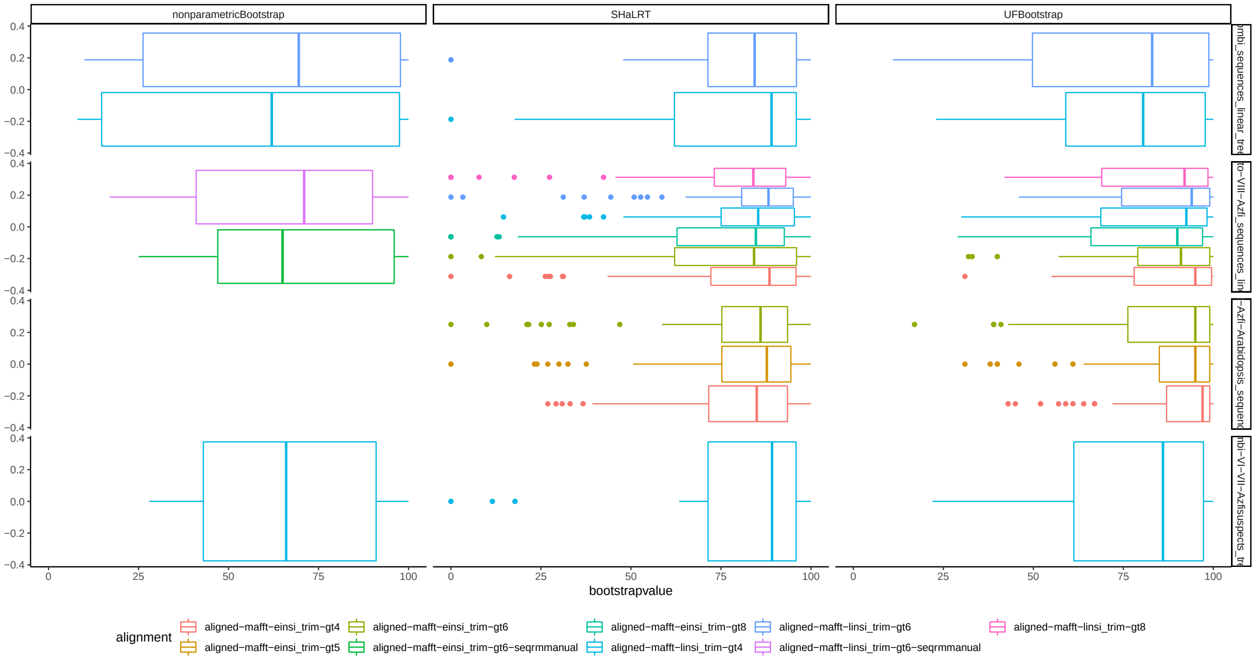
```r
library(ggplot2)
attach(combitab)
```

```
## The following objects are masked from combitab (pos = 3):
##
##     alignment, bootstrapstrategy, bootstrapvalue, dataset, iqtree
```

```
## The following objects are masked from combitab (pos = 4):
##
##     alignment, bootstrapstrategy, bootstrapvalue, dataset, iqtree
```

```r
plot <- ggplot(data=combitab,mapping = aes(x=bootstrapvalue,col=alignment))
plot <- plot + geom_boxplot()
plot <- plot + theme_classic()
plot <- plot + facet_grid(dataset~bootstrapstrategy)
plot <- plot + theme(legend.position = 'bottom')
plot
```

```
## Warning: Removed 951 rows containing non-finite values (stat_boxplot).
```



```
rm(plot)
```

All and all, plotting support values like this is not very insighfull. I'm quite surprised by how similar support distributions are for the different aligning strategies actually. Still one make some funny observations. For example the optimal trimming percentage (very naïve interpretation of optimal) differs for the different alignment strategies, but not for the two quick bootstrap methods. Perhaps the bootstrap is artificially high for leniently trimmed alignments. It seems that the UF bootstrap correlates better with the nonparemetric bootstrap, at least, if you're trying to pick an alignment strategy and use this naïve method of optimising support in your tree (which you shouldn't, at least not without inspecting the trees and the alignments as well.).