

SummaryPlot

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This R script is used for generating summary plot for the Geneconv project

1, Read in tables

```
rm(list=ls()) # clean up workspace
path <-
"/Users/xji3/Genconv/NewClusterPackRun/NewPackageNewRun/OldResults01152
015/"
#path <- "G:/Geneconv/NewClusterPackRun/NewPackageNewRun/"
#HKY_clock_summary <- "HKY_clock_summary"
summary.list <- c( "HKY_nonclock_summary",
                  "HKY_clock_summary",
                  "MG94_clock_summary",
                  "MG94_nonclock_summary",
                  "Force_HKY_clock_summary",
                  "Force_HKY_nonclock_summary",
                  "Force_MG94_clock_summary",
                  "Force_MG94_nonclock_summary"
                )
#summary.list <- c("Force_MG94_clock_summary")
for (target.summary in summary.list){
  summary_file <- paste(path, target.summary, '.txt', sep = '')
  all <- readLines(summary_file, n = -1)
  col.names <- strsplit(all[1], ' ')[[1]][-1]
  row.names <- strsplit(all[length(all)], ' ')[[1]][-1]
  summary_mat <- as.matrix(read.table(summary_file,
                                     row.names = row.names,
                                     col.names = col.names))

  assign(target.summary, summary_mat)

  para.list <- c(2:20)
  for (i in para.list){
    image.name <- paste(path, 'Rscripts/', target.summary, '_',
                      row.names[i], '.png', sep = '')

    png(image.name)
    plot(summary_mat[1, ], summary_mat[i, ],
         xlab = row.names[1], ylab = row.names[i],
         main = target.summary)
    dev.off()
  }
}
```

```
}
```

Now generate summary file of only pairs that have all cases finished in HKY or MG94 models.

```
# HKY
HKY.pair.names <-
intersect(intersect(intersect(colnames(HKY_clock_summary),
                                colnames(HKY_nonclock_summary)),
                                colnames(Force_HKY_clock_summary)),
                                colnames(Force_HKY_nonclock_summary))
HKY.clock.filtered <- HKY_clock_summary[, HKY.pair.names]
HKY.nonclock.filtered <- HKY_nonclock_summary[, HKY.pair.names]
HKY.Force.clock.filtered <- Force_HKY_clock_summary[, HKY.pair.names]
HKY.Force.nonclock.filtered <- Force_HKY_nonclock_summary[,
HKY.pair.names]

write.table(HKY.clock.filtered, paste( path, "HKY_clock_filtered", sep
= ""))
write.table(HKY.nonclock.filtered, paste( path,
"HKY_nonclock_filtered", sep = ""))
write.table(HKY.Force.clock.filtered, paste( path,
"HKY_Force_clock_filtered", sep = ""))
write.table(HKY.Force.nonclock.filtered, paste( path,
"HKY_Force_nonclock_filtered", sep = ""))

# MG94
MG94.pair.names <-
intersect(intersect(intersect(colnames(MG94_clock_summary),
                                colnames(MG94_nonclock_summary)),
                                colnames(Force_MG94_clock_summary)),
                                colnames(Force_MG94_nonclock_summary))
MG94.clock.filtered <- MG94_clock_summary[, MG94.pair.names]
MG94.nonclock.filtered <- MG94_nonclock_summary[, MG94.pair.names]
MG94.Force.clock.filtered <- Force_MG94_clock_summary[,
MG94.pair.names]
MG94.Force.nonclock.filtered <- Force_MG94_nonclock_summary[,
MG94.pair.names]

write.table(MG94.clock.filtered, paste( path, "MG94_clock_filtered",
sep = ""))
write.table(MG94.nonclock.filtered, paste( path,
"MG94_nonclock_filtered", sep = ""))
write.table(MG94.Force.clock.filtered, paste( path,
"MG94_Force_clock_filtered", sep = ""))
write.table(MG94.Force.nonclock.filtered, paste( path,
"MG94_Force_nonclock_filtered", sep = ""))
```

Now analyze the results

First, show the loglikelihood improvement for each model with/without tau

HKY noncLock

(HKY.nonclock.filtered - HKY.Force.nonclock.filtered)[2,]

## YLR406C_YDL075W	YDR502C_YLR180W	YHR106W_YDR353W	YIL057C_YER067W
## 45.21	209.16	165.03	41.56
## YPL087W_YBR183W	YNL069C_YIL133C	YGR043C_YLR354C	YPR157W_YGR141W
## 49.82	90.20	58.85	75.49
## YDR099W_YER177W	YBR024W_YBR037C	YPR159W_YGR143W	YGL133W_YPL216W
## 161.47	42.12	242.58	40.79
## YNL049C_YIL109C	YPL232W_YMR183C	YIR033W_YKL020C	YMR243C_YOR316C
## 153.35	115.06	93.93	82.18
## YAL056W_YOR371C	YDR438W_YML018C		
## 26.78	24.13		

HKY cLock

(HKY.clock.filtered - HKY.Force.clock.filtered)[2,]

## YLR406C_YDL075W	YDR502C_YLR180W	YHR106W_YDR353W	YIL057C_YER067W
## 45.93	168.38	144.87	40.62
## YPL087W_YBR183W	YNL069C_YIL133C	YGR043C_YLR354C	YPR157W_YGR141W
## 42.28	78.01	39.97	62.68
## YDR099W_YER177W	YBR024W_YBR037C	YPR159W_YGR143W	YGL133W_YPL216W
## 154.92	29.14	243.60	21.22
## YNL049C_YIL109C	YPL232W_YMR183C	YIR033W_YKL020C	YMR243C_YOR316C
## 118.15	94.26	75.01	69.15
## YAL056W_YOR371C	YDR438W_YML018C		
## 30.20	11.08		

MG94 noncLock

(MG94.nonclock.filtered - MG94.Force.nonclock.filtered)[2,]

## YLR406C_YDL075W	YER131W_YGL189C	YDR502C_YLR180W	YML026C_YDR450W
## 17.0098	15.5082	44.6676	199.1628
## YHR106W_YDR353W	YIL057C_YER067W	YNL069C_YIL133C	YGR043C_YLR354C
## 22.1329	17.1557	59.6840	5.3063
## YDR099W_YER177W	YMR143W_YDL083C	YJR048W_YEL039C	YBR191W_YPL079W
## 16.2328	37.2294	21.4012	63.4052
## YDR418W_YEL054C	YPL232W_YMR183C	YLR284C_YOR180C	YBL087C_YER117W
## 31.1399	28.1146	0.7524	45.4327
## YGL062W_YBR218C	YER102W_YBL072C	YDR438W_YML018C	
## 446.2657	138.0125	2.9400	

MG94 cLock

(MG94.clock.filtered - MG94.Force.clock.filtered)[2,]

## YLR406C_YDL075W	YER131W_YGL189C	YDR502C_YLR180W	YML026C_YDR450W
## 17.42	15.99	241.96	315.83
## YHR106W_YDR353W	YIL057C_YER067W	YNL069C_YIL133C	YGR043C_YLR354C

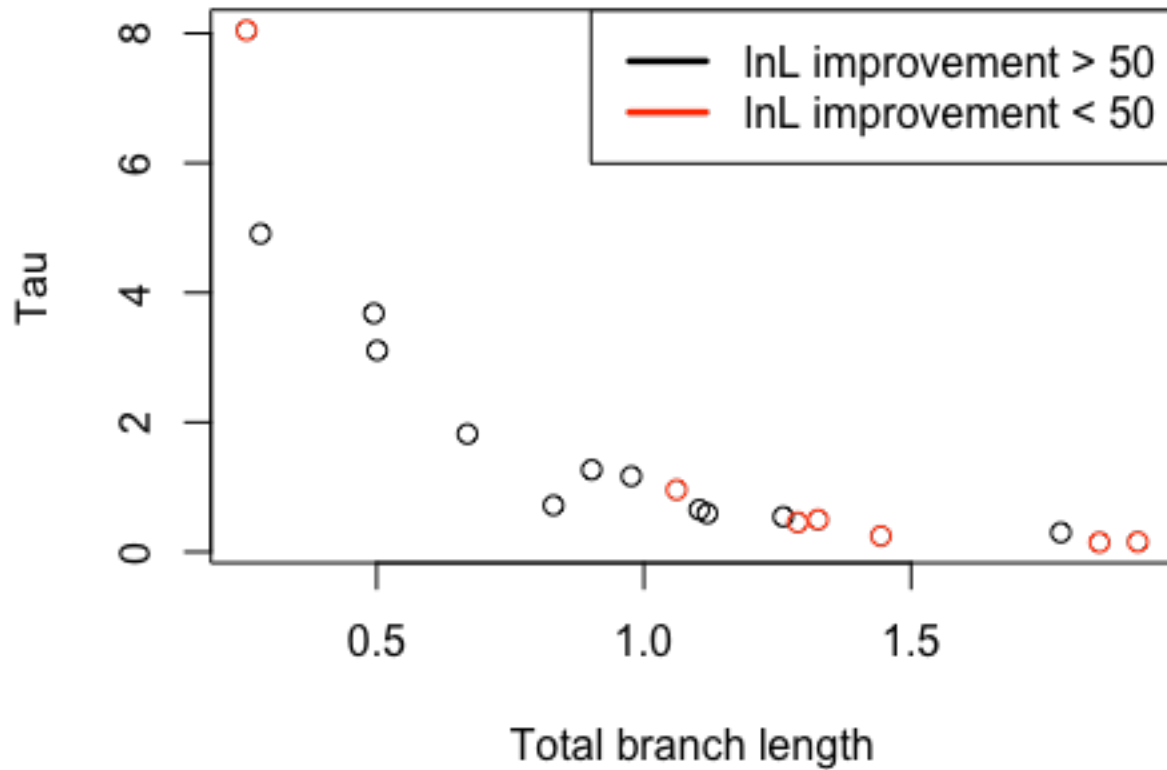
```
##          521.17          592.15          54.09          722.27
## YDR099W_YER177W YMR143W_YDL083C YJR048W_YEL039C YBR191W_YPL079W
##          209.31          45.36          192.82          69.24
## YDR418W_YEL054C YPL232W_YMR183C YLR284C_YOR180C YBL087C_YER117W
##          34.20          838.06          31.09          47.32
## YGL062W_YBR218C YER102W_YBL072C YDR438W_YML018C
##          2039.77          149.04          -87.86
```

Now plot Total blen v.s. Tau into different groups (differ by color)

HKY nonclock case

```
plot(colSums(HKY.nonclock.filtered[9:20, ]), HKY.nonclock.filtered[8,
],
     type = "n", xlab = "Total branch length", ylab = "Tau" )
col.color <- rep("black", dim(HKY.nonclock.filtered)[2])
col.color[(HKY.nonclock.filtered - HKY.Force.nonclock.filtered)[2,] <
50] <- "red"
points(x = colSums(HKY.nonclock.filtered[9:20, ]), y =
HKY.nonclock.filtered[8, ],
       type = "p", col = col.color, bg = col.color)
legend("topright", c("lnL improvement > 50", "lnL improvement < 50"),
      lty = c(1, 1),
      lwd = c(2.5, 2.5),
      col = c("black", "red"))
title("HKY nonclock")
```

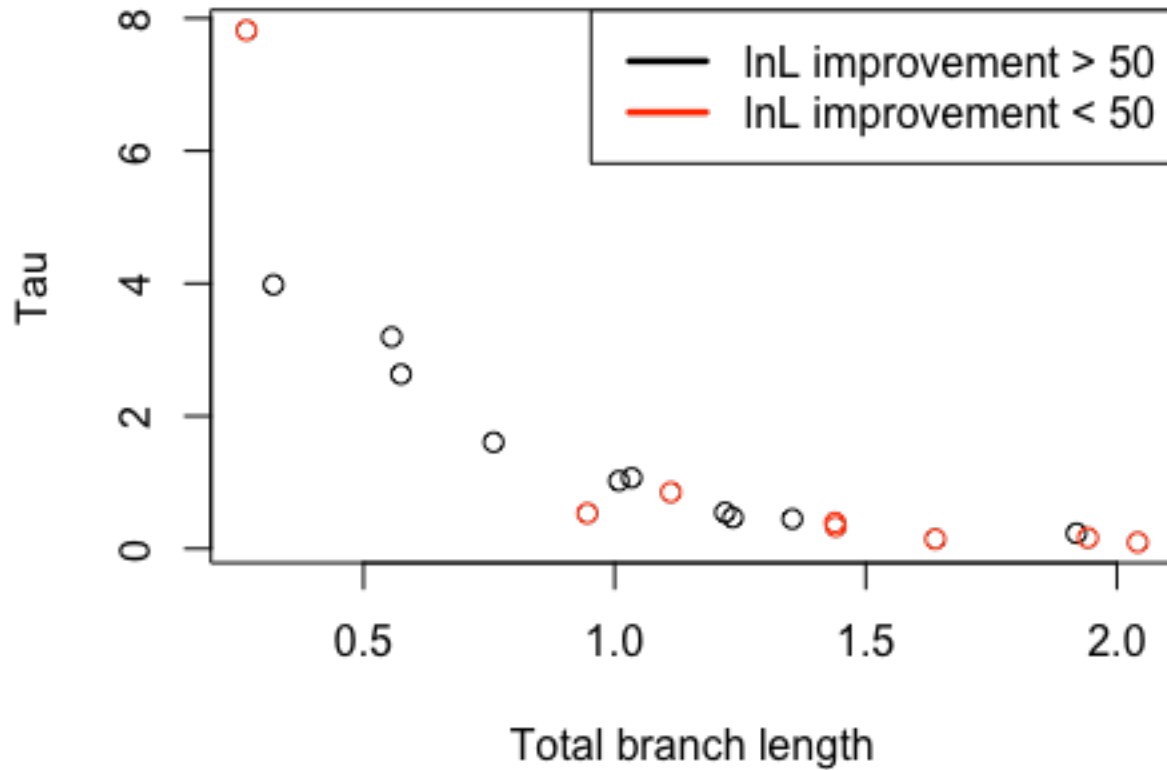
HKY nonclock



HKY clock case

```
plot(colSums(HKY.clock.filtered[9:20, ]), HKY.clock.filtered[8, ],
     type = "n", xlab = "Total branch length", ylab = "Tau" )
col.color <- rep("black", dim(HKY.clock.filtered)[2])
col.color[(HKY.clock.filtered - HKY.Force.clock.filtered)[2,] < 50] <-
"red"
points(x = colSums(HKY.clock.filtered[9:20, ]), y =
HKY.clock.filtered[8, ],
       type = "p", col = col.color, bg = col.color)
legend("topright", c("lnL improvement > 50", "lnL improvement < 50"),
      lty = c(1, 1),
      lwd = c(2.5, 2.5),
      col = c("black", "red"))
title("HKY clock")
```

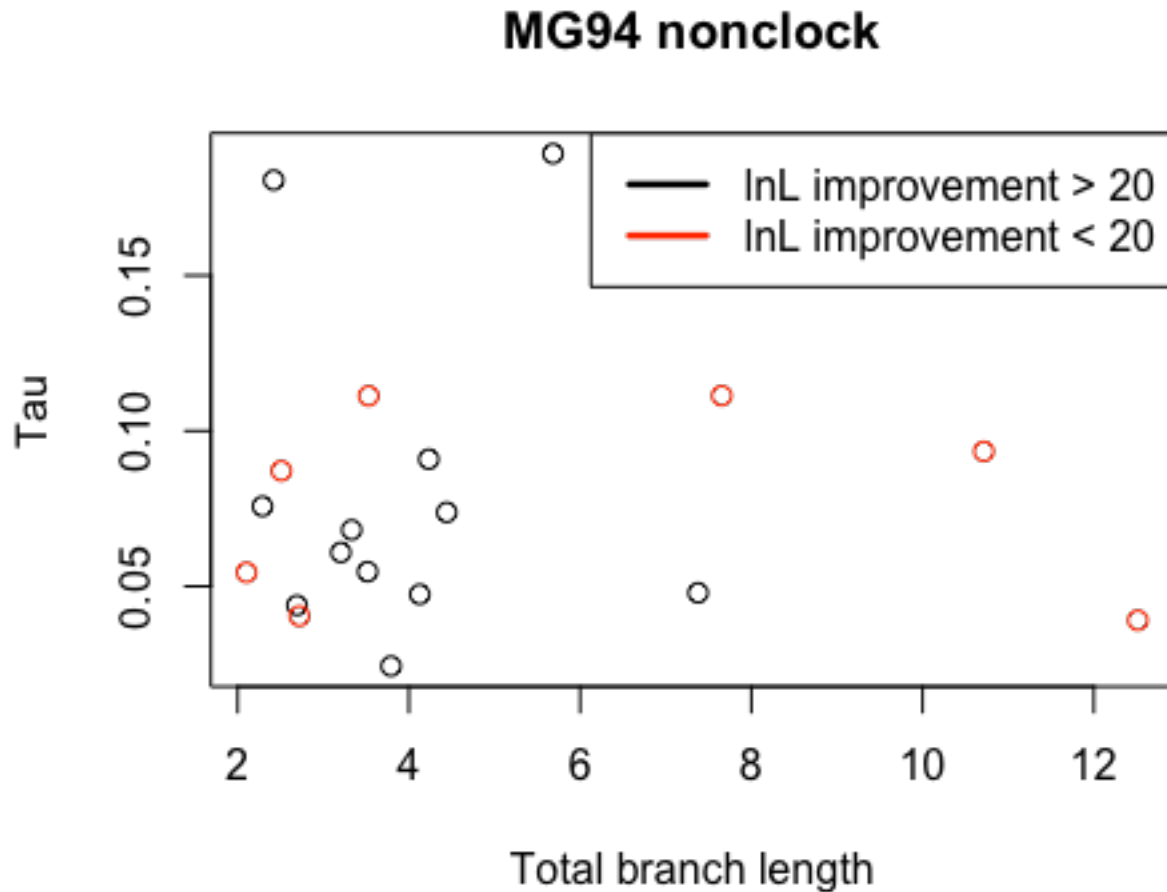
HKY clock



MG94 nonclock case

```
improvement.lmt <- 20
plot(colSums(MG94.nonclock.filtered[9:20, ]), MG94.nonclock.filtered[8,
],
     type = "n", xlab = "Total branch length", ylab = "Tau" )
col.color <- rep("black", dim(MG94.nonclock.filtered)[2])
col.color[(MG94.nonclock.filtered - MG94.Force.nonclock.filtered)[2,] <
improvement.lmt] <- "red"
points(x = colSums(MG94.nonclock.filtered[9:20, ]), y =
MG94.nonclock.filtered[8, ],
       type = "p", col = col.color, bg = col.color)
legend("topright",
      c(paste("lnL improvement > ", toString(improvement.lmt), sep =
""),
        paste("lnL improvement < ", toString(improvement.lmt), sep =
"")),
      lty = c(1, 1),
      lwd = c(2.5, 2.5),
```

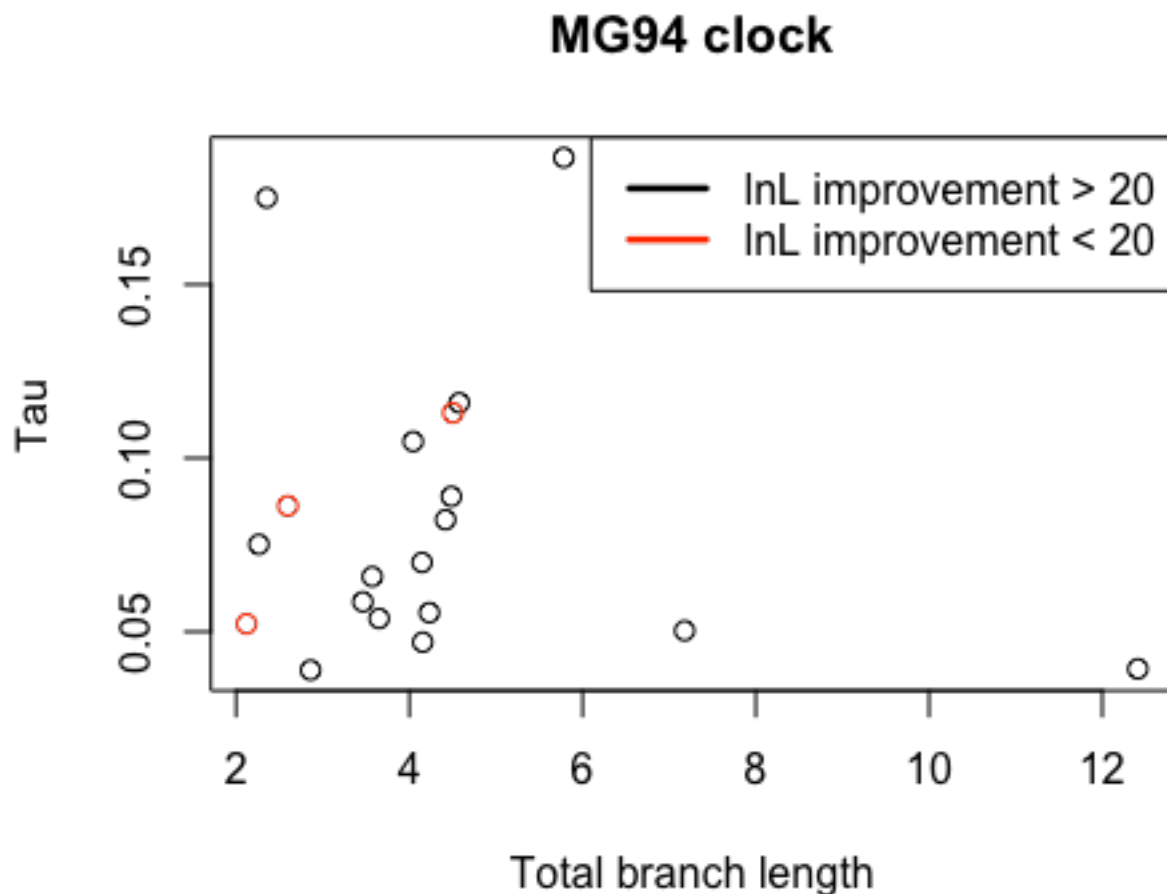
```
col = c("black", "red")
title("MG94 nonclock")
```



MG94 clock case

```
improvement.lmt <- 20
plot(colSums(MG94.clock.filtered[9:20, ]), MG94.clock.filtered[8, ],
     type = "n", xlab = "Total branch length", ylab = "Tau" )
col.color <- rep("black", dim(MG94.clock.filtered)[2])
col.color[(MG94.clock.filtered - MG94.Force.clock.filtered)[2,] <
improvement.lmt] <- "red"
points(x = colSums(MG94.clock.filtered[9:20, ]), y =
MG94.clock.filtered[8, ],
       type = "p", col = col.color, bg = col.color)
legend("topright",
      c(paste("lnL improvement > ", toString(improvement.lmt), sep =
""),
        paste("lnL improvement < ", toString(improvement.lmt), sep =
"")),
      lty = c(1, 1),
```

```
lwd = c(2.5, 2.5),
col = c("black", "red"))
title("MG94 clock")
```



Now see if the pairs red in HKY are also red in MG94

nonclock case

```
HKY.pair.names[(HKY.nonclock.filtered -
HKY.Force.nonclock.filtered)[2,] < 50]

## [1] "YLR406C_YDL075W" "YIL057C_YER067W" "YPL087W_YBR183W"
## [2] "YBR024W_YBR037C"
## [5] "YGL133W_YPL216W" "YAL056W_YOR371C" "YDR438W_YML018C"

MG94.pair.names[(MG94.nonclock.filtered -
MG94.Force.nonclock.filtered)[2,] < improvement.lmt]

## [1] "YLR406C_YDL075W" "YER131W_YGL189C" "YIL057C_YER067W"
## [2] "YGR043C_YLR354C"
## [5] "YDR099W_YER177W" "YLR284C_YOR180C" "YDR438W_YML018C"
```


Only 3 pairs show up in both: YLR406C_YDL075W, YIL057C_YER067W, YDR438W_YML018C.

clock case

```
HKY.pair.names[(HKY.clock.filtered - HKY.Force.clock.filtered)[2,] < 50]

## [1] "YLR406C_YDL075W" "YIL057C_YER067W" "YPL087W_YBR183W"
      "YGR043C_YLR354C"
## [5] "YBR024W_YBR037C" "YGL133W_YPL216W" "YAL056W_YOR371C"
      "YDR438W_YML018C"

MG94.pair.names[(MG94.clock.filtered - MG94.Force.clock.filtered)[2,] < improvement.lmt]

## [1] "YLR406C_YDL075W" "YER131W_YGL189C" "YDR438W_YML018C"
```

2 pairs show up in both: YLR406C_YDL075W, YDR438W_YML018C

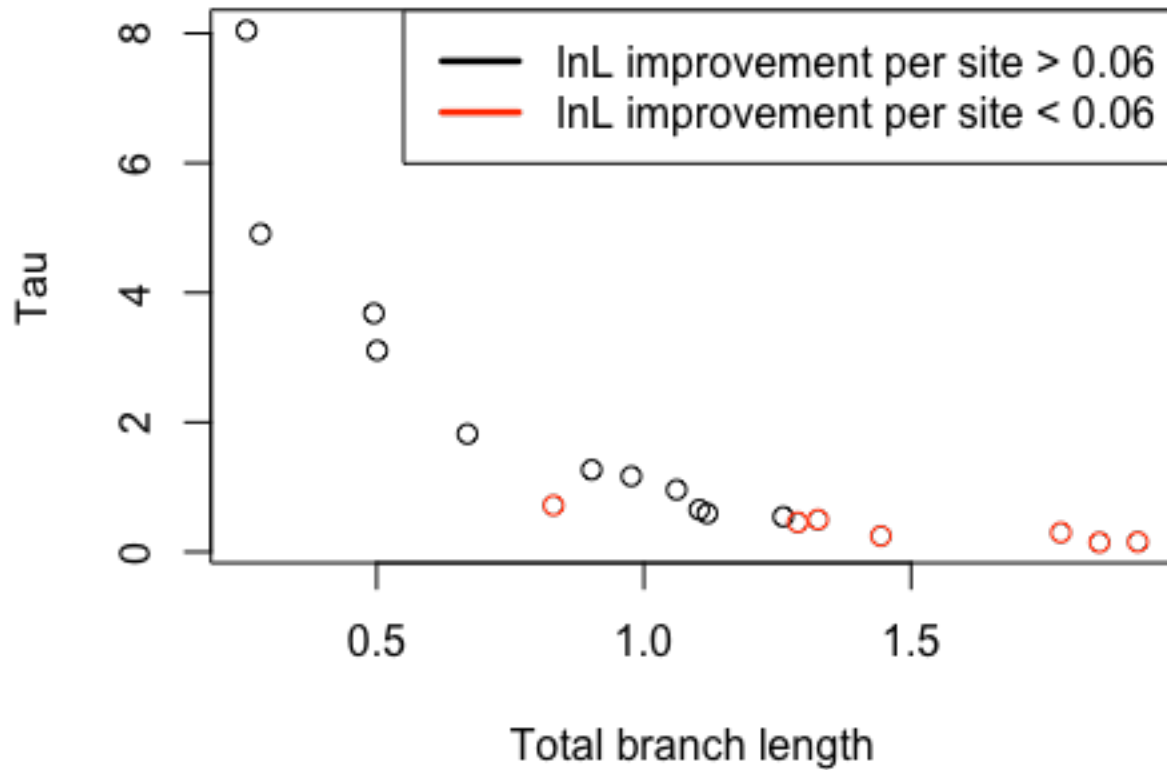
=====

Now plot Total blen v.s. Tau into different groups (differ by lnL improvement per site)

HKY nonclock case

```
plot(colSums(HKY.nonclock.filtered[9:20, ]), HKY.nonclock.filtered[8, ],
     type = "n", xlab = "Total branch length", ylab = "Tau" )
col.color <- rep("black", dim(HKY.nonclock.filtered)[2])
col.color[((HKY.nonclock.filtered - HKY.Force.nonclock.filtered)[2,] /
HKY.nonclock.filtered[1, ]) < 0.06] <- "red"
points(x = colSums(HKY.nonclock.filtered[9:20, ]), y =
HKY.nonclock.filtered[8, ],
       type = "p", col = col.color, bg = col.color)
legend("topright", c("lnL improvement per site > 0.06",
                    "lnL improvement per site < 0.06"),
      lty = c(1, 1),
      lwd = c(2.5, 2.5),
      col = c("black", "red"))
title("HKY nonclock")
```

HKY nonclock



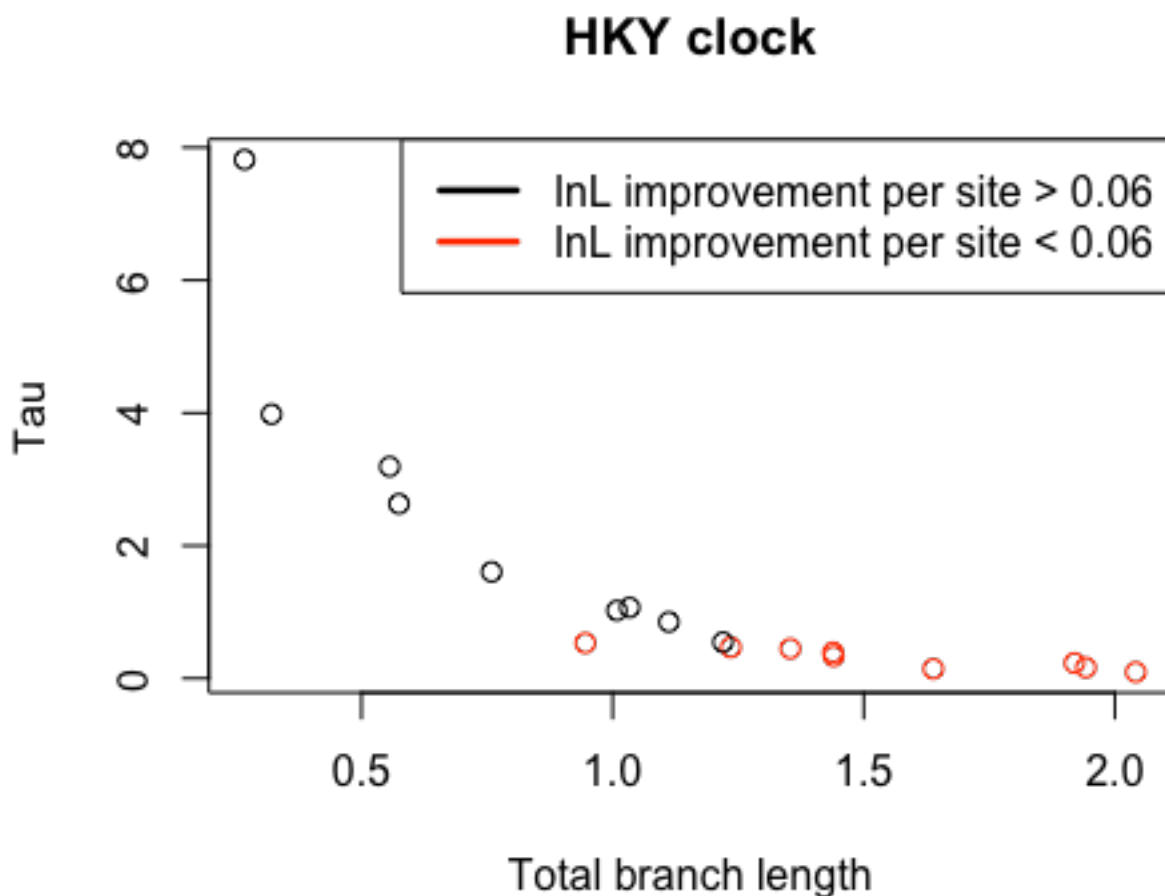
```
# lnL improvement per site
((HKY.nonclock.filtered - HKY.Force.nonclock.filtered)[2, ] /
HKY.nonclock.filtered[1, ])

## YLR406C_YDL075W YDR502C_YLR180W YHR106W_YDR353W YIL057C_YER067W
##      0.13337      0.18252      0.17245      0.08823
## YPL087W_YBR183W YNL069C_YIL133C YGR043C_YLR354C YPR157W_YGR141W
##      0.05409      0.15185      0.05909      0.06093
## YDR099W_YER177W YBR024W_YBR037C YPR159W_YGR143W YGL133W_YPL216W
##      0.21108      0.05014      0.12123      0.01368
## YNL049C_YIL109C YPL232W_YMR183C YIR033W_YKL020C YMR243C_YOR316C
##      0.06107      0.13457      0.03502      0.07266
## YAL056W_YOR371C YDR438W_YML018C
##      0.01355      0.02331
```

HKY clock case

```
plot(colSums(HKY.clock.filtered[9:20, ]), HKY.clock.filtered[8, ],
     type = "n", xlab = "Total branch length", ylab = "Tau" )
col.color <- rep("black", dim(HKY.clock.filtered)[2])
```

```
col.color[((HKY.clock.filtered - HKY.Force.clock.filtered)[2,] /
HKY.clock.filtered[1, ]) < 0.06] <- "red"
points(x = colSums(HKY.clock.filtered[9:20, ]), y =
HKY.clock.filtered[8, ],
      type = "p", col = col.color, bg = col.color)
legend("topright", c("lnL improvement per site > 0.06",
                    "lnL improvement per site < 0.06"),
      lty = c(1, 1),
      lwd = c(2.5, 2.5),
      col = c("black", "red"))
title("HKY clock")
```



```
# lnL improvement per site
((HKY.clock.filtered - HKY.Force.clock.filtered)[2,] /
HKY.clock.filtered[1, ])

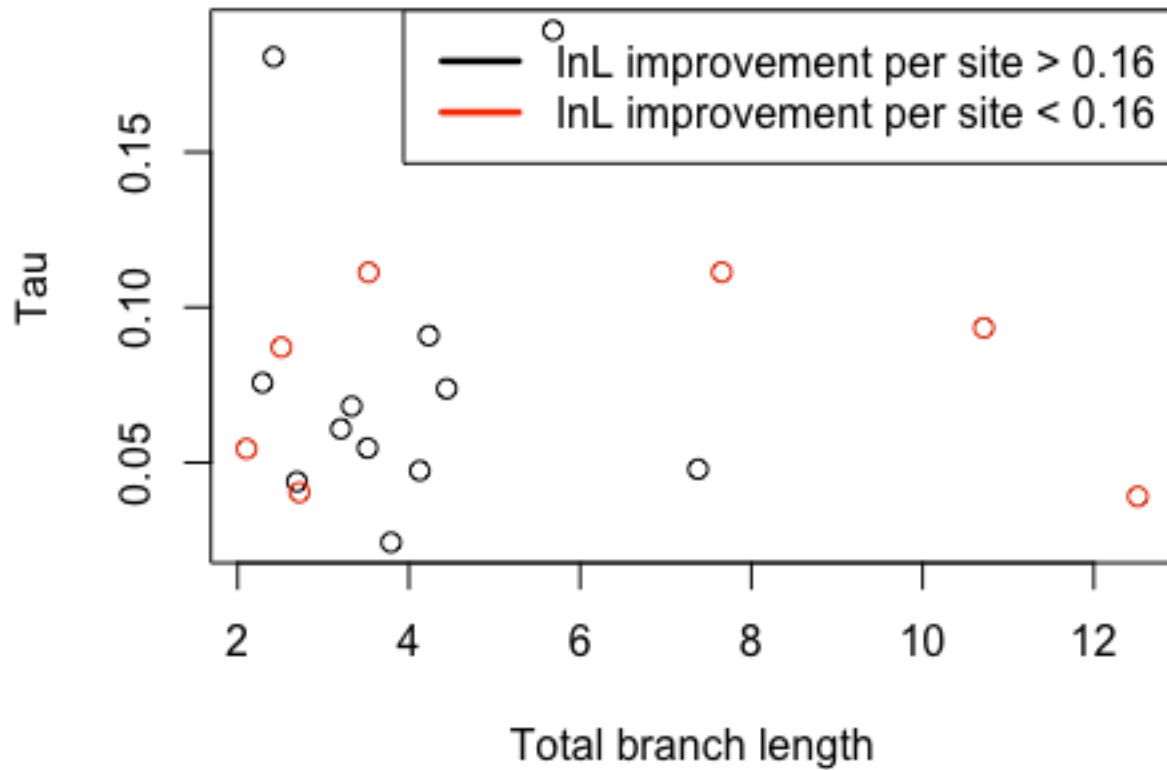
## YLR406C_YDL075W YDR502C_YLR180W YHR106W_YDR353W YIL057C_YER067W
##      0.135487      0.146931      0.151376      0.086245
## YPL087W_YBR183W YNL069C_YIL133C YGR043C_YLR354C YPR157W_YGR141W
##      0.045908      0.131323      0.040133      0.050586
```

```
## YDR099W_YER177W YBR024W_YBR037C YPR159W_YGR143W YGL133W_YPL216W
##          0.202513          0.034693          0.121737          0.007116
## YNL049C_YIL109C YPL232W_YMR183C YIR033W_YKL020C YMR243C_YOR316C
##          0.047052          0.110245          0.027969          0.061142
## YAL056W_YOR371C YDR438W_YML018C
##          0.015277          0.010706
```

MG94 nonclock case

```
improvement.lmt <- 0.16
plot(colSums(MG94.nonclock.filtered[9:20, ]), MG94.nonclock.filtered[8,
],
     type = "n", xlab = "Total branch length", ylab = "Tau" )
col.color <- rep("black", dim(MG94.nonclock.filtered)[2])
col.color[((MG94.nonclock.filtered - MG94.Force.nonclock.filtered)[2,]
/ MG94.nonclock.filtered[1]) < improvement.lmt] <- "red"
points(x = colSums(MG94.nonclock.filtered[9:20, ]), y =
MG94.nonclock.filtered[8, ],
       type = "p", col = col.color, bg = col.color)
legend("topright",
      c(paste("\nL improvement per site > ",
toString(improvement.lmt), sep = ""),
        paste("\nL improvement per site < ",
toString(improvement.lmt), sep = "")),
      lty = c(1, 1),
      lwd = c(2.5, 2.5),
      col = c("black", "red"))
title("MG94 nonclock")
```

MG94 nonclock



```
# LnL improvement per site
((MG94.nonclock.filtered - MG94.Force.nonclock.filtered)[2,] /
MG94.nonclock.filtered[1])

## YLR406C_YDL075W YER131W_YGL189C YDR502C_YLR180W YML026C_YDR450W
##      0.150529      0.137241      0.395289      1.762502
## YHR106W_YDR353W YIL057C_YER067W YNL069C_YIL133C YGR043C_YLR354C
##      0.195866      0.151820      0.528177      0.046959
## YDR099W_YER177W YMR143W_YDL083C YJR048W_YEL039C YBR191W_YPL079W
##      0.143653      0.329463      0.189391      0.561108
## YDR418W_YEL054C YPL232W_YMR183C YLR284C_YOR180C YBL087C_YER117W
##      0.275574      0.248802      0.006659      0.402059
## YGL062W_YBR218C YER102W_YBL072C YDR438W_YML018C
##      3.949254      1.221350      0.026018
```

MG94 clock case

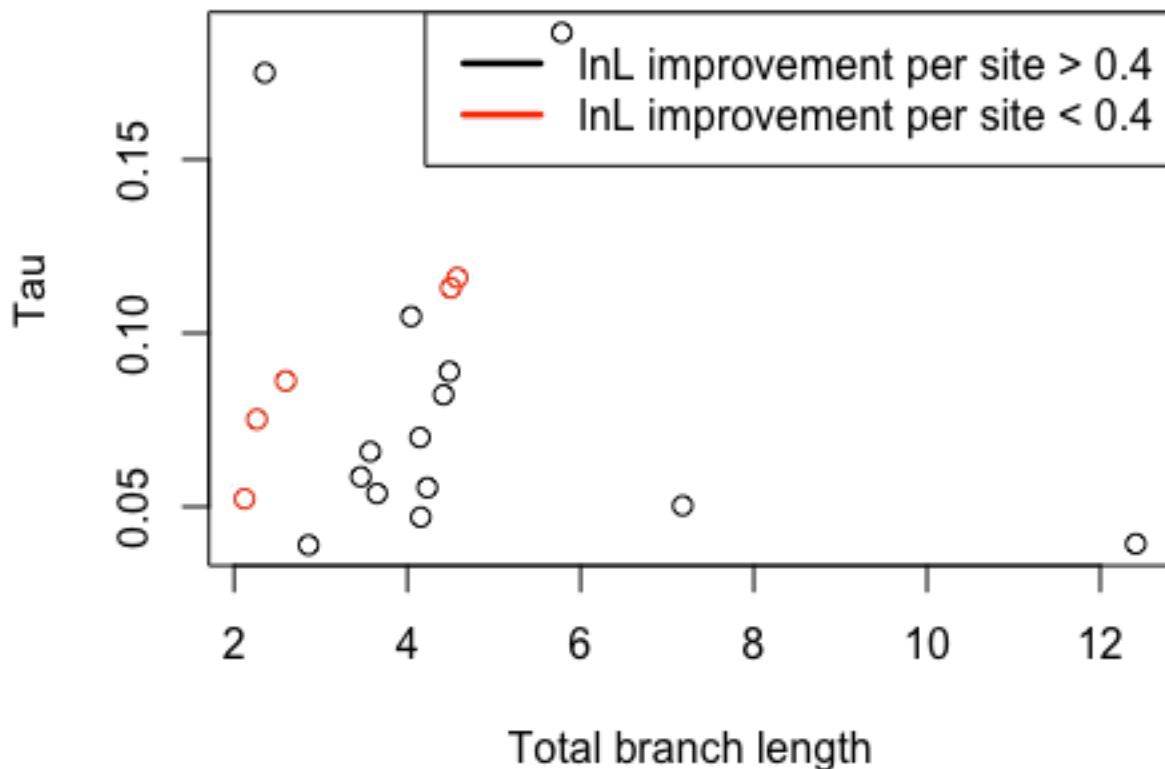
```
improvement.lmt <- 0.4
plot(colSums(MG94.clock.filtered[9:20, ]), MG94.clock.filtered[8, ],
     type = "n", xlab = "Total branch length", ylab = "Tau" )
```

```

col.color <- rep("black", dim(MG94.clock.filtered)[2])
col.color[((MG94.clock.filtered - MG94.Force.clock.filtered)[2,] /
MG94.clock.filtered[1]) < improvement.lmt] <- "red"
points(x = colSums(MG94.clock.filtered[9:20, ]), y =
MG94.clock.filtered[8, ],
      type = "p", col = col.color, bg = col.color)
legend("topright",
      c(paste("lnL improvement per site > ",
toString(improvement.lmt), sep = ""),
      paste("lnL improvement per site < ",
toString(improvement.lmt), sep = "")),
      lty = c(1, 1),
      lwd = c(2.5, 2.5),
      col = c("black", "red"))
title("MG94 clock")

```

MG94 clock



```

# lnL improvement per site
((MG94.clock.filtered - MG94.Force.clock.filtered)[2,] /
MG94.clock.filtered[1])

```

##	YLR406C_YDL075W	YER131W_YGL189C	YDR502C_YLR180W	YML026C_YDR450W
##	0.1542	0.1415	2.1412	2.7950
##	YHR106W_YDR353W	YIL057C_YER067W	YNL069C_YIL133C	YGR043C_YLR354C
##	4.6121	5.2403	0.4787	6.3917
##	YDR099W_YER177W	YMR143W_YDL083C	YJR048W_YEL039C	YBR191W_YPL079W
##	1.8523	0.4014	1.7063	0.6128
##	YDR418W_YEL054C	YPL232W_YMR183C	YLR284C_YOR180C	YBL087C_YER117W
##	0.3027	7.4165	0.2752	0.4188
##	YGL062W_YBR218C	YER102W_YBL072C	YDR438W_YML018C	
##	18.0510	1.3189	-0.7776	