

TractMLESummary

This script is used to summarize IGC tract length model with 14 Yeast data sets.

```
rm(list=ls()) # clean up workspace
setwd("/Users/xji3/GitFolders/YeastIGCTract/Code/")

finished.pairs <- readLines('../Filtered_pairs.txt')

for(dim in 1:2){
  JS.HKY.nonclock.summary <- NULL
  PSJS.HKY.nonclock.summary <- NULL
  for(pair in finished.pairs){

    summary.file.name <- paste("JS_HKY", pair, "One_rate_nonclock_summary.txt", sep = "_")
    summary_file <- paste("./summary/", summary.file.name, sep = "")
    all <- readLines(summary_file, n = -1)
    row.names <- strsplit(all[length(all)], ' ')[[1]][-1]
    summary_mat <- as.matrix(read.table(summary_file,
                                         row.names = row.names,
                                         col.names = pair))

    JS.HKY.nonclock.summary <- cbind(JS.HKY.nonclock.summary, summary_mat)

    summary.file.name <- paste("PSJS_dim" , toString(dim), "HKY", pair, "One_rate_init_30.0_nonclock_summary.txt", sep = "_")
    summary_file <- paste("./summary/", summary.file.name, sep = "")
    all <- readLines(summary_file, n = -1)
    row.names <- strsplit(all[length(all)], ' ')[[1]][-1]
    summary_mat <- as.matrix(read.table(summary_file,
                                         row.names = row.names,
                                         col.names = pair))

    PSJS.HKY.nonclock.summary <- cbind(PSJS.HKY.nonclock.summary, summary_mat)

  }
  assign(paste("PSJS.HKY.dim", toString(dim), "nonclock.summary", sep = "."), PSJS.HKY.nonclock.summary)
}
```

Now show the estimated tract length and IGC initiation rates.

```
# Estimated Tract length (unit: nucleotide)
rbind(PSJS.HKY.dim.1.nonclock.summary["tract_length", ], PSJS.HKY.dim.2.nonclock.summary["tract_length", ])

##      YLR406C_YDL075W YER131W_YGL189C YML026C_YDR450W YNL301C_YOL120C
## [1,]      2.680270      6.618387      1.198002      21.37209
## [2,]      2.677647      6.603230      1.194031      30.00190
##      YNL069C_YIL133C YMR143W_YDL083C YJL177W_YKL180W YBR191W_YPL079W
## [1,]      6.961052      2.252968      2.866165      8.103450
## [2,]      6.950846      2.356362      2.854502      8.102286
##      YER074W_YIL069C YDR418W_YEL054C YBL087C_YER117W YLR333C_YGR027C
## [1,]     43.38923      2.287572     13.71813      7.21618
```

```

## [2,]          43.39314          2.310891          13.84993          7.25674
##      YMR142C_YDL082W YER102W_YBL072C
## [1,]          28.4072          17.83908
## [2,]          30.0017          29.99800

# Estimated Initial guess rate
rbind(PSJS.HKY.dim.1.nonclock.summary["init_rate", ], PSJS.HKY.dim.2.nonclock.summary["init_rate", ])

##      YLR406C_YDL075W YER131W_YGL189C YML026C_YDR450W YNL301C_YOL120C
## [1,]          2.989675          1.166681          12.49664          0.5135222
## [2,]          2.993007          1.169286          12.53704          0.3659625
##      YNL069C_YIL133C YMR143W_YDL083C YJL177W_YKL180W YBR191W_YPL079W
## [1,]          0.7348527          6.079352          3.527515          1.907803
## [2,]          0.7359258          5.812264          3.540403          1.908216
##      YER074W_YIL069C YDR418W_YEL054C YBL087C_YER117W YLR333C_YGR027C
## [1,]          0.5501929          3.528131          1.015829          1.537189
## [2,]          0.5498759          3.493682          1.006095          1.527766
##      YMR142C_YDL082W YER102W_YBL072C
## [1,]          0.5524475          0.8979608
## [2,]          0.5231800          0.5339212

# lnL comparison between 1d and 2d search
rbind(PSJS.HKY.dim.1.nonclock.summary["ll", ], PSJS.HKY.dim.2.nonclock.summary["ll", ], PSJS.HKY.dim.1.nonclock.summary["ll", ])

##      YLR406C_YDL075W YER131W_YGL189C YML026C_YDR450W YNL301C_YOL120C
## [1,] -4.249835e+05 -4.635018e+05 -6.354074e+05 -1.244172e+06
## [2,] -4.249835e+05 -4.635018e+05 -6.354074e+05 -1.244173e+06
## [3,] -3.576226e-04  5.959944e-03  3.951896e-03  1.687985e+00
##      YNL069C_YIL133C YMR143W_YDL083C YJL177W_YKL180W YBR191W_YPL079W
## [1,] -1.441304e+06 -5.308583e+05 -1.071864e+06 -7.382742e+05
## [2,] -1.441304e+06 -5.308583e+05 -1.071864e+06 -7.382742e+05
## [3,]  3.931127e-03  4.619423e-03  1.420354e-02  3.168774e-03
##      YER074W_YIL069C YDR418W_YEL054C YBL087C_YER117W YLR333C_YGR027C
## [1,] -5.210064e+05 -9.114781e+05 -5.981940e+05 -4.259553e+05
## [2,] -5.210064e+05 -9.114781e+05 -5.981940e+05 -4.259553e+05
## [3,] -3.484843e-02 -6.375714e-03  6.270676e-03 -3.536451e-03
##      YMR142C_YDL082W YER102W_YBL072C
## [1,] -1.270098e+06 -1.255272e+06
## [2,] -1.270098e+06 -1.255278e+06
## [3,]  4.850790e-02  6.016451e+00

# lnL comparison between 1d and previous model
#rbind(PSJS.HKY.dim.1.nonclock.summary["ll", ], JS.HKY.nonclock.summary["ll", ], PSJS.HKY.dim.1.nonclock.summary["ll", ])

# Compare estimated Tau value
rbind(JS.HKY.nonclock.summary["Tau", ], PSJS.HKY.dim.1.nonclock.summary["tract_length", ] * PSJS.HKY.dim.1.nonclock.summary["init_rate", ],
      PSJS.HKY.dim.2.nonclock.summary["tract_length", ] * PSJS.HKY.dim.2.nonclock.summary["init_rate", ])

##      YLR406C_YDL075W YER131W_YGL189C YML026C_YDR450W YNL301C_YOL120C
## [1,]          8.013065          7.721608          14.96955          10.97745
## [2,]          8.013137          7.721544          14.97100          10.97504

```

```
## [3,]      8.014215      7.721063      14.96961      10.97957
##      YNL069C_YIL133C YMR143W_YDL083C YJL177W_YKL180W YBR191W_YPL079W
## [1,]      5.115741      13.69655      10.10570      15.45936
## [2,]      5.115348      13.69659      10.11044      15.45979
## [3,]      5.115307      13.69580      10.10609      15.46091
##      YER074W_YIL069C YDR418W_YEL054C YBL087C_YER117W YLR333C_YGR027C
## [1,]      23.87286      8.075072      13.93793      11.09265
## [2,]      23.87244      8.070853      13.93528      11.09263
## [3,]      23.86084      8.073517      13.93435      11.08660
##      YMR142C_YDL082W YER102W_YBL072C
## [1,]      15.69432      16.01962
## [2,]      15.69349      16.01880
## [3,]      15.69629      16.01657
```

Now plot 2 dimensional lnL for 2 pairs

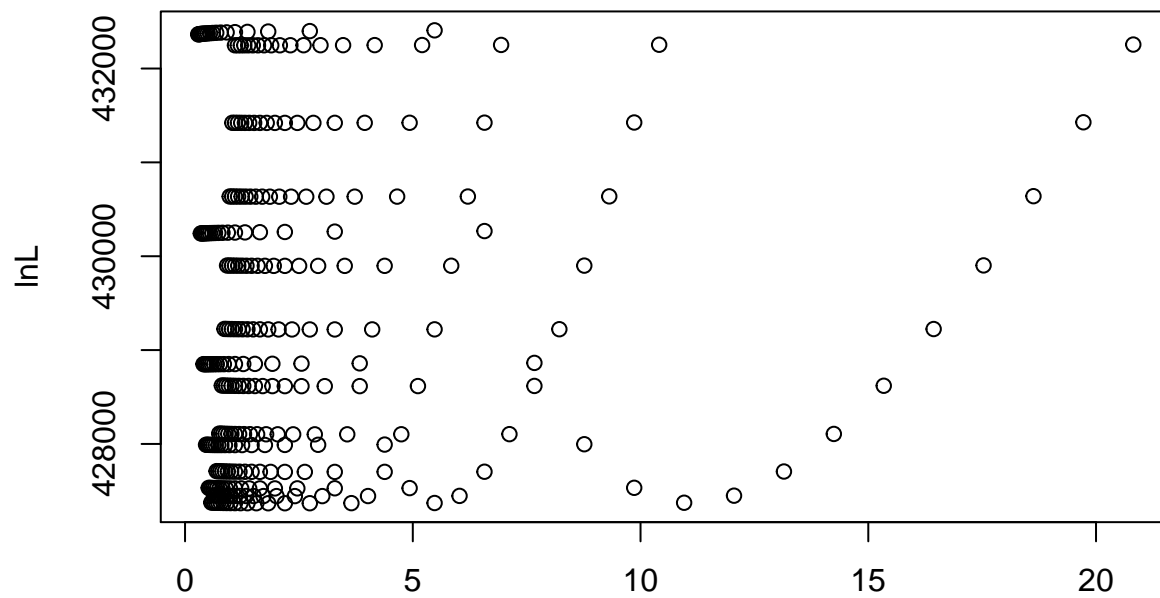
```
library("lattice")
plot.pairs <- c("YLR333C_YGR027C", "YLR406C_YDL075W")
# show estimated tract length
PSJS.HKY.nonclock.summary["tract_length", plot.pairs]
```

```
## YLR333C_YGR027C YLR406C_YDL075W
##      7.256740      2.677647
```

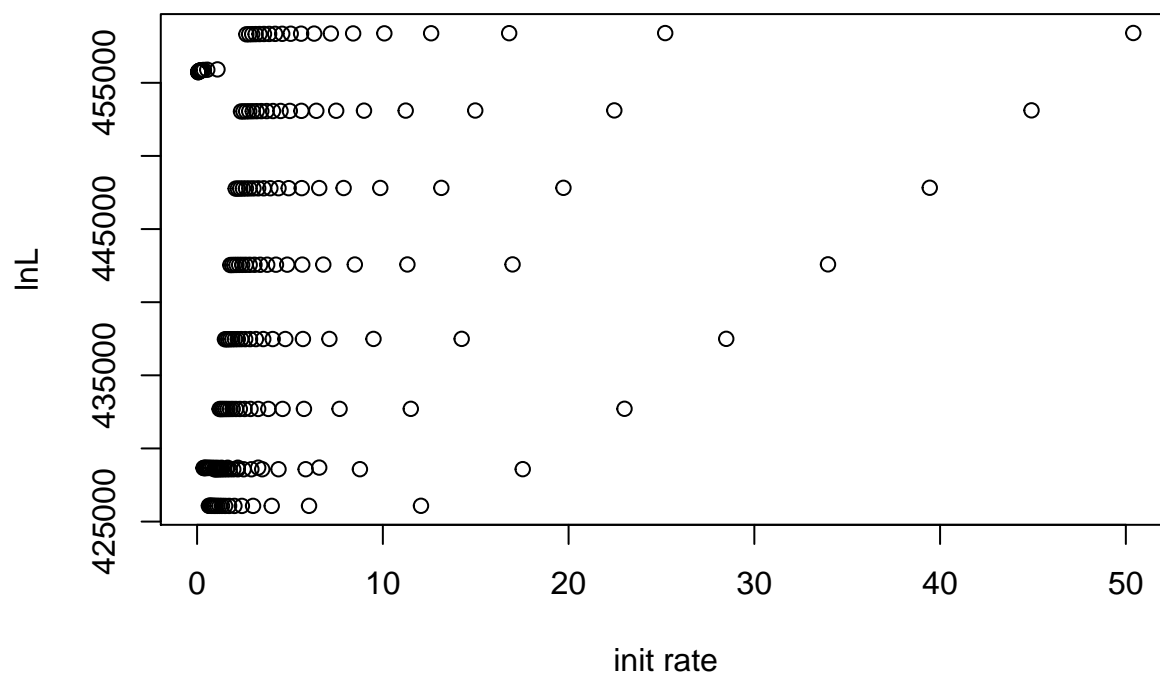
```
for( pair in plot.pairs){
  plot.file.name <- paste("./plot/", pair, "_PSJS_lnL_TractLength.txt", sep = "")
  plot.data <- read.table(plot.file.name)
  plot(plot.data[, 2], plot.data[, 3], xlab = "init rate", ylab = "lnL", main = pair)
  assign(pair, plot.data)

  plot.file.name <- paste("./plot/", pair, "_PSJS_lnL_TractLength_zoomed.txt", sep = "")
  plot.data <- read.table(plot.file.name)
  plot(plot.data[, 2], plot.data[, 3], xlab = "init rate", ylab = "lnL", main = paste(pair, "_zoomed", sep = ""))
  assign(paste(pair, "_zoomed", sep = ""), plot.data)
}
```

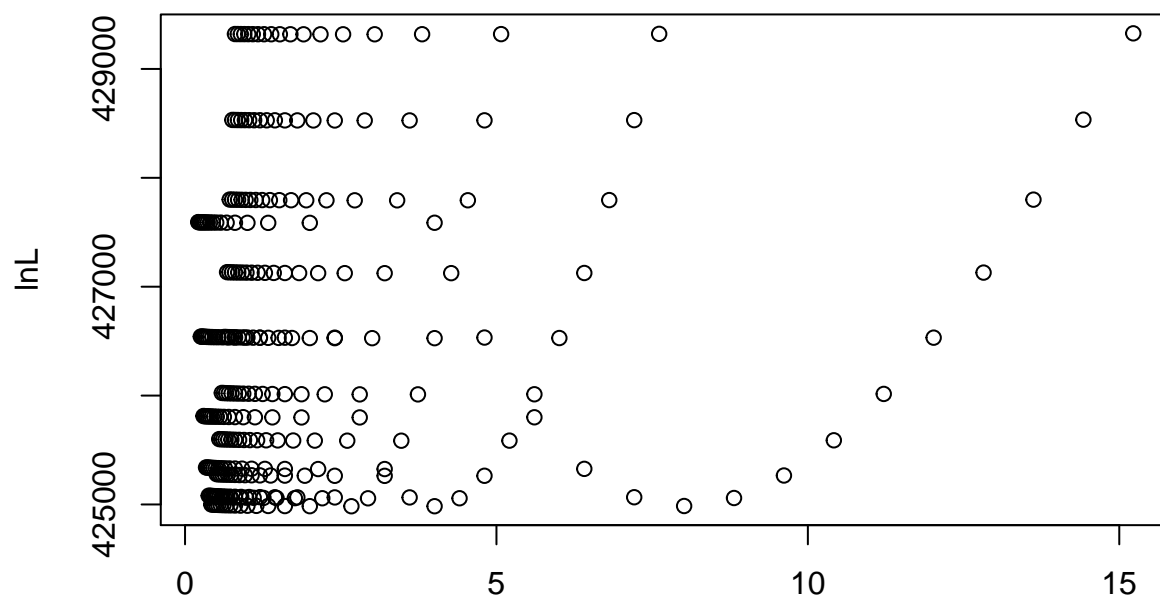
YLR333C_YGR027C



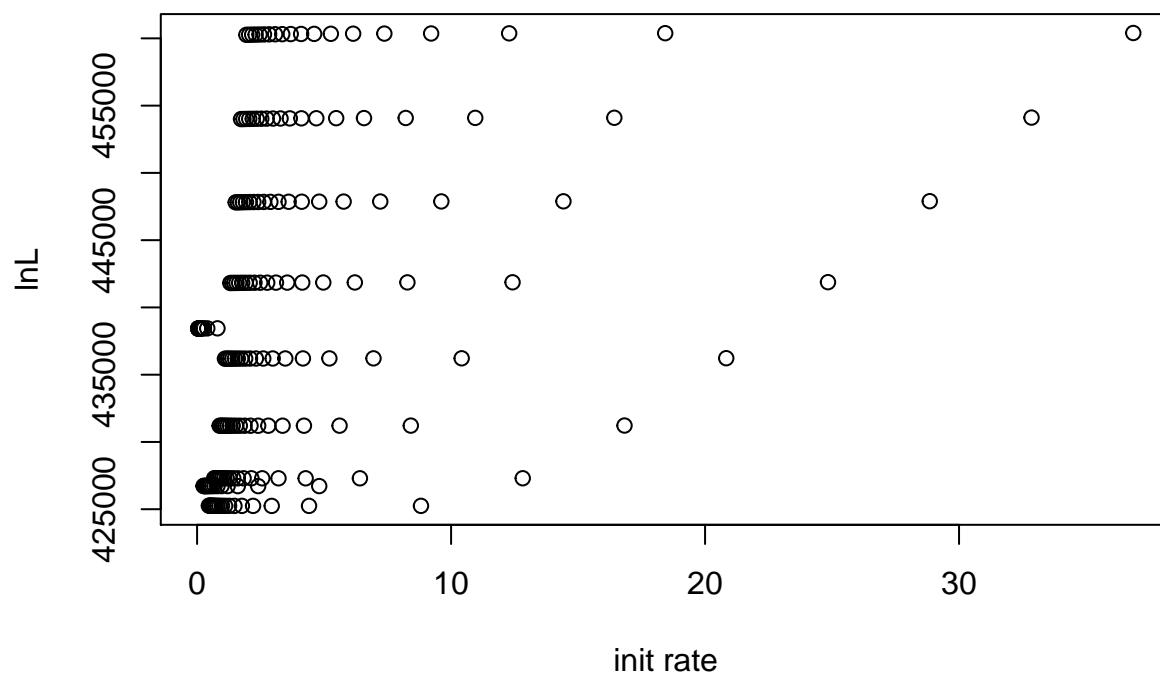
YLR333C_YGR027C_zoomed



YLR406C_YDL075W

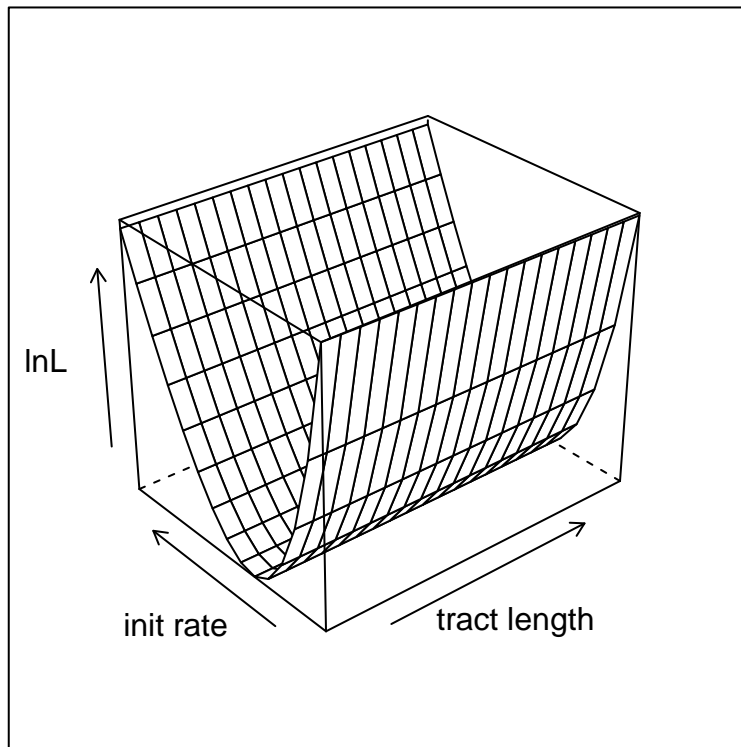


YLR406C_YDL075W_zoomed

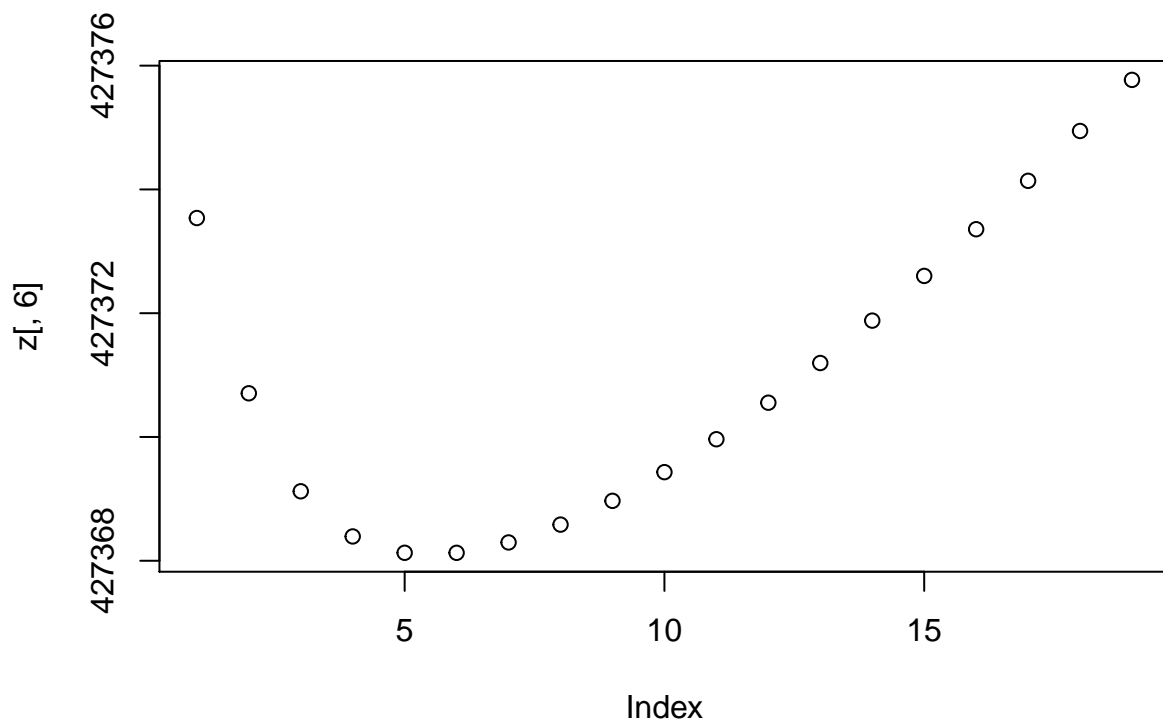


```
x <- 1:19
y <- 5:19 * 0.1
z <- matrix(YLR333C_YGR027C[1 : (length(x) * length(y))], 3], nrow = length(x), ncol = length(y), byrow = TRUE)
wireframe(z, row.values = x, col.values = y, xlab = "tract length", ylab = "init rate", zlab = "lnL", main = "YLR406C_YDL075W")
```

YLR333C_YGR027C

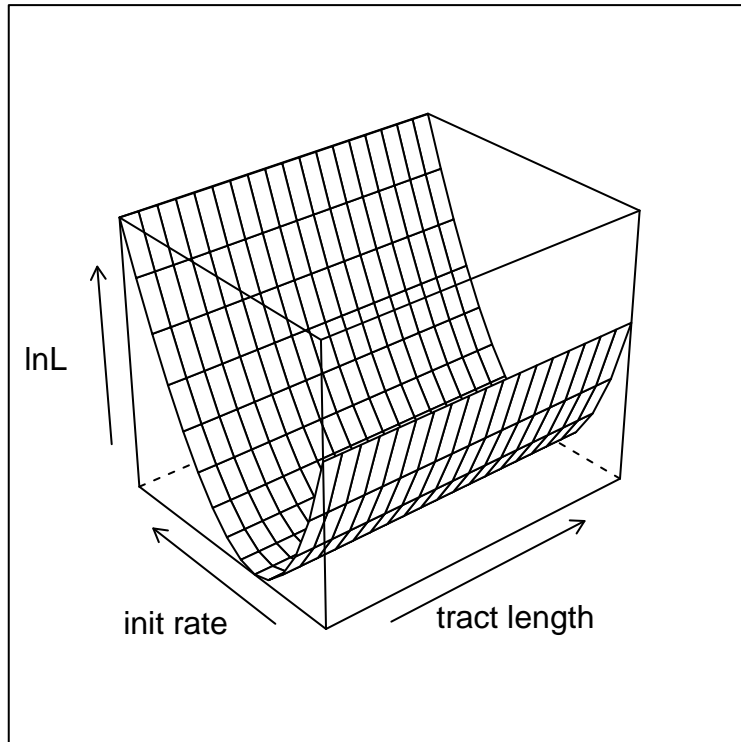


```
# plot the ridge  
plot(z[, 6])
```

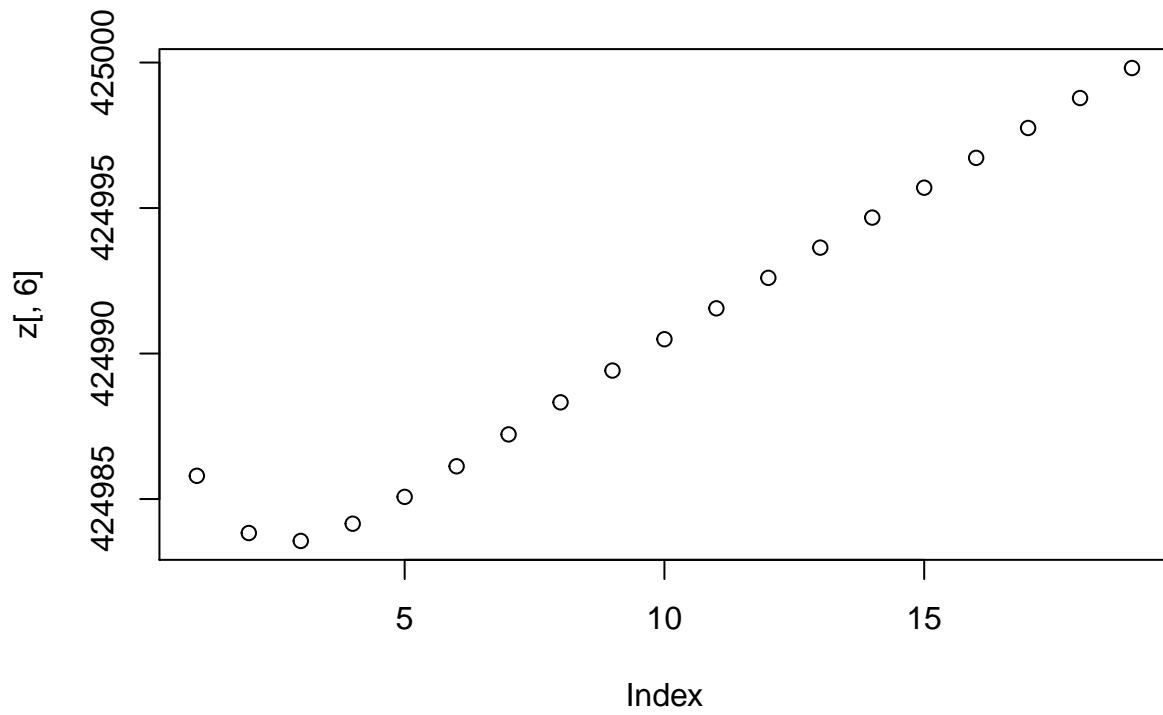


```
z <- matrix(YLR406C_YDL075W[1 : (length(x) * length(y)), 3], nrow = length(x), ncol = length(y), byrow = TRUE)
wireframe(z, row.values = x, col.values = y, xlab = "tract length", ylab = "init rate", zlab = "lnL", mesh = TRUE)
```

YLR406C_YDL075W



```
# plot the ridge
plot(z[, 6])
```



```
#image(x, y, z)
```

```
# Now export data
```

```
save.image(file = "./TractSummary.RData")
```