TractMLESummary

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

Now show the estimated tract length and IGC initiation rates.

# Estimated Tract length (unit: nucleotide)  
seq.length <- JS.HKY.nonclock.summary["length", ]  
PSJS.HKY.dim.1.nonclock.eff.lnL <- PSJS.HKY.dim.1.nonclock.summary["ll", ] / (seq.length - 1)  
PSJS.HKY.dim.2.nonclock.eff.lnL <- PSJS.HKY.dim.2.nonclock.summary["ll", ] / (seq.length - 1)  
PSJS.HKY.rv.NOSC.dim.1.nonclock.eff.lnL <- PSJS.HKY.rv.NOSC.dim.1.nonclock.summary["ll", ]/ (seq.length - 3)  
PSJS.HKY.rv.NOSC.dim.2.nonclock.eff.lnL <- PSJS.HKY.rv.NOSC.dim.2.nonclock.summary["ll", ]/ (seq.length - 3)  
PSJS.HKY.rv.SCOK.dim.1.nonclock.eff.lnL <- PSJS.HKY.rv.SCOK.dim.1.nonclock.summary["ll", ]/ (seq.length - 1)  
PSJS.HKY.rv.SCOK.dim.2.nonclock.eff.lnL <- PSJS.HKY.rv.SCOK.dim.2.nonclock.summary["ll", ]/ (seq.length - 1)  
  
show.mat <- rbind(PSJS.HKY.dim.1.nonclock.summary["tract\_length", ],  
 PSJS.HKY.dim.2.nonclock.summary["tract\_length", ],  
 PSJS.HKY.dim.1.nonclock.eff.lnL - PSJS.HKY.dim.2.nonclock.eff.lnL,  
 PSJS.HKY.rv.NOSC.dim.1.nonclock.summary["tract\_length",],  
 PSJS.HKY.rv.NOSC.dim.2.nonclock.summary["tract\_length",],  
 PSJS.HKY.rv.NOSC.dim.1.nonclock.eff.lnL - PSJS.HKY.rv.NOSC.dim.2.nonclock.eff.lnL,  
 PSJS.HKY.rv.SCOK.dim.1.nonclock.summary["tract\_length",],  
 PSJS.HKY.rv.SCOK.dim.2.nonclock.summary["tract\_length",],  
 PSJS.HKY.rv.SCOK.dim.1.nonclock.eff.lnL - PSJS.HKY.rv.SCOK.dim.2.nonclock.eff.lnL  
)  
row.names(show.mat) <- c("Homo D1", "Homo D2", "lnL (D1 - D2)" ,  
 "Heter NOSC D1", "Heter NOSC D2", "lnL (D1 - D2)",   
 "Heter SCOK D1", "Heter SCOK D2", "lnL (D1 - D2)"  
)  
show.mat

## YLR406C\_YDL075W YER131W\_YGL189C YML026C\_YDR450W  
## Homo D1 2.716147e+00 6.617908e+00 1.193170e+00  
## Homo D2 2.706976e+00 6.591345e+00 1.743004e+00  
## lnL (D1 - D2) -5.126060e-07 2.598895e-06 5.334349e-04  
## Heter NOSC D1 1.000000e+00 1.282491e+01 1.000000e+00  
## Heter NOSC D2 1.000000e+00 1.283728e+01 1.293423e+00  
## lnL (D1 - D2) -8.476650e-08 -9.196062e-07 1.502351e-04  
## Heter SCOK D1 4.221197e+00 1.233977e+01 1.422101e+00  
## Heter SCOK D2 4.227927e+00 1.239270e+01 1.388747e+00  
## lnL (D1 - D2) -1.356415e-06 -6.497521e-07 2.521877e-06  
## YNL301C\_YOL120C YNL069C\_YIL133C YMR143W\_YDL083C  
## Homo D1 2.218431e+01 6.518676e+00 1.000000e+00  
## Homo D2 3.000249e+01 6.543119e+00 2.477900e+00  
## lnL (D1 - D2) 2.082886e-03 2.575664e-06 8.508184e-04  
## Heter NOSC D1 9.918779e+01 1.219356e+01 4.764644e+00  
## Heter NOSC D2 9.970391e+01 1.220575e+01 4.826651e+00  
## lnL (D1 - D2) -6.003516e-06 -4.239378e-07 2.377469e-07  
## Heter SCOK D1 9.890040e+01 1.236399e+01 1.000000e+00  
## Heter SCOK D2 9.888296e+01 1.229864e+01 1.000000e+00  
## lnL (D1 - D2) -4.119593e-06 1.541545e-06 -1.990247e-07  
## YJL177W\_YKL180W YBR191W\_YPL079W YER074W\_YIL069C  
## Homo D1 2.872681e+00 8.111506e+00 4.332886e+01  
## Homo D2 2.876329e+00 8.078598e+00 4.329659e+01  
## lnL (D1 - D2) 1.379957e-06 2.247804e-06 -7.220908e-06  
## Heter NOSC D1 1.000000e+00 1.059558e+01 5.292347e+01  
## Heter NOSC D2 1.000000e+00 1.064791e+01 5.291987e+01  
## lnL (D1 - D2) -1.220497e-06 -1.098427e-05 -1.872650e-07  
## Heter SCOK D1 2.468737e+00 1.064311e+01 5.294623e+01  
## Heter SCOK D2 2.506450e+00 1.067706e+01 5.298442e+01  
## lnL (D1 - D2) 3.341274e-07 -4.953852e-07 -2.927730e-06  
## YDR418W\_YEL054C YBL087C\_YER117W YLR333C\_YGR027C  
## Homo D1 2.283464e+00 1.282934e+01 7.220962e+00  
## Homo D2 2.286395e+00 1.292399e+01 7.245594e+00  
## lnL (D1 - D2) 1.578160e-07 -3.389519e-06 -1.008581e-05  
## Heter NOSC D1 3.750697e+00 2.918605e+01 3.544625e+01  
## Heter NOSC D2 3.745961e+00 2.999482e+01 2.999846e+01  
## lnL (D1 - D2) -3.081539e-07 1.301859e-05 3.089821e-04  
## Heter SCOK D1 3.312490e+00 2.829440e+01 3.485149e+01  
## Heter SCOK D2 3.273311e+00 2.999373e+01 2.999769e+01  
## lnL (D1 - D2) 7.943950e-07 1.281539e-04 1.967015e-04  
## YMR142C\_YDL082W YER102W\_YBL072C  
## Homo D1 2.841439e+01 1.782834e+01  
## Homo D2 3.000179e+01 1.920406e+01  
## lnL (D1 - D2) 9.539218e-05 1.612656e-04  
## Heter NOSC D1 3.253834e+01 3.193377e+01  
## Heter NOSC D2 3.000197e+01 3.000177e+01  
## lnL (D1 - D2) 2.086143e-04 1.512709e-04  
## Heter SCOK D1 3.282120e+01 3.105408e+01  
## Heter SCOK D2 3.000454e+01 2.999993e+01  
## lnL (D1 - D2) 2.539318e-04 4.447784e-05

# Now show equivalent lnL matrix  
show.mat <- rbind(JS.HKY.nonclock.summary["ll", ],   
 PSJS.HKY.dim.1.nonclock.eff.lnL, PSJS.HKY.dim.2.nonclock.eff.lnL,   
 JS.HKY.rv.nonclock.summary["ll", ],   
 PSJS.HKY.rv.NOSC.dim.1.nonclock.eff.lnL, PSJS.HKY.rv.NOSC.dim.2.nonclock.eff.lnL,   
 PSJS.HKY.rv.SCOK.dim.1.nonclock.eff.lnL, PSJS.HKY.rv.SCOK.dim.2.nonclock.eff.lnL)  
row.names(show.mat) <- c("Homo JS", "Homo PSJS D1", "Homo PSJS D2",   
 "Heter JS",   
 "Heter NOSC D1", "Heter NOSC D2", "Heter SCOK D1", "Heter SCOK D2")  
show.mat

## YLR406C\_YDL075W YER131W\_YGL189C YML026C\_YDR450W  
## Homo JS -1268.614 -1313.057 -1516.485  
## Homo PSJS D1 -1268.607 -1313.036 -1516.485  
## Homo PSJS D2 -1268.607 -1313.036 -1516.486  
## Heter JS -1189.812 -1216.912 -1368.469  
## Heter NOSC D1 -1189.812 -1216.885 -1368.469  
## Heter NOSC D2 -1189.812 -1216.885 -1368.469  
## Heter SCOK D1 -1189.806 -1216.881 -1368.468  
## Heter SCOK D2 -1189.806 -1216.881 -1368.468  
## YNL301C\_YOL120C YNL069C\_YIL133C YMR143W\_YDL083C  
## Homo JS -2245.814 -2442.924 -1323.835  
## Homo PSJS D1 -2245.796 -2442.889 -1323.835  
## Homo PSJS D2 -2245.798 -2442.889 -1323.836  
## Heter JS -2126.642 -2332.607 -1217.381  
## Heter NOSC D1 -2126.504 -2332.566 -1217.378  
## Heter NOSC D2 -2126.504 -2332.566 -1217.378  
## Heter SCOK D1 -2126.509 -2332.547 -1217.381  
## Heter SCOK D2 -2126.509 -2332.547 -1217.381  
## YJL177W\_YKL180W YBR191W\_YPL079W YER074W\_YIL069C  
## Homo JS -1955.960 -1551.020 -1309.130  
## Homo PSJS D1 -1955.957 -1550.996 -1309.061  
## Homo PSJS D2 -1955.957 -1550.996 -1309.061  
## Heter JS -1840.376 -1468.945 -1233.000  
## Heter NOSC D1 -1840.376 -1468.921 -1232.920  
## Heter NOSC D2 -1840.376 -1468.921 -1232.920  
## Heter SCOK D1 -1840.373 -1468.917 -1232.918  
## Heter SCOK D2 -1840.373 -1468.917 -1232.918  
## YDR418W\_YEL054C YBL087C\_YER117W YLR333C\_YGR027C  
## Homo JS -1867.785 -1469.782 -1331.133  
## Homo PSJS D1 -1867.783 -1469.768 -1331.110  
## Homo PSJS D2 -1867.783 -1469.768 -1331.110  
## Heter JS -1735.398 -1372.911 -1246.666  
## Heter NOSC D1 -1735.393 -1372.853 -1246.639  
## Heter NOSC D2 -1735.393 -1372.853 -1246.639  
## Heter SCOK D1 -1735.393 -1372.864 -1246.626  
## Heter SCOK D2 -1735.393 -1372.865 -1246.626  
## YMR142C\_YDL082W YER102W\_YBL072C  
## Homo JS -2152.783 -2116.872  
## Homo PSJS D1 -2152.708 -2116.816  
## Homo PSJS D2 -2152.708 -2116.816  
## Heter JS -2033.878 -2037.260  
## Heter NOSC D1 -2033.824 -2037.172  
## Heter NOSC D2 -2033.824 -2037.173  
## Heter SCOK D1 -2033.803 -2037.179  
## Heter SCOK D2 -2033.803 -2037.179

# Compare estimated Tau value  
# Estimated Tract length (unit: nucleotide)   
show.mat <- rbind(  
 JS.HKY.nonclock.summary["Tau",],  
 PSJS.HKY.dim.2.nonclock.summary["tract\_length", ] \* PSJS.HKY.dim.2.nonclock.summary["init\_rate",],  
 JS.HKY.rv.nonclock.summary["Tau",] \* 3.0 / colSums(rbind(1, JS.HKY.rv.nonclock.summary[c("r2", "r3"),])),  
 (PSJS.HKY.rv.NOSC.dim.2.nonclock.summary["tract\_length",] \* PSJS.HKY.rv.NOSC.dim.2.nonclock.summary["init\_rate", ]  
 \* 3.0 / colSums(rbind(1, PSJS.HKY.rv.NOSC.dim.2.nonclock.summary[c("r2", "r3"), ]))),   
 PSJS.HKY.rv.SCOK.dim.2.nonclock.summary["tract\_length",] \* PSJS.HKY.rv.SCOK.dim.2.nonclock.summary["init\_rate", ]  
 \* 3.0 / colSums(rbind(1, PSJS.HKY.rv.SCOK.dim.2.nonclock.summary[c("r2", "r3"), ]))  
)  
row.names(show.mat) <- c("Homo JS Tau", "Homo PSJS D2 Tau", "Heter JS Tau", "Heter PSJS NOSC Tau", "Heter PSJS SCOK Tau")  
show.mat

## YLR406C\_YDL075W YER131W\_YGL189C YML026C\_YDR450W  
## Homo JS Tau 8.009604 7.718943 14.97063  
## Homo PSJS D2 Tau 8.013992 7.720717 14.97064  
## Heter JS Tau 5.099108 5.269134 12.83681  
## Heter PSJS NOSC Tau 5.099494 5.269976 12.84692  
## Heter PSJS SCOK Tau 5.101011 5.269659 12.84640  
## YNL301C\_YOL120C YNL069C\_YIL133C YMR143W\_YDL083C  
## Homo JS Tau 10.979078 5.115600 13.696391  
## Homo PSJS D2 Tau 10.980671 5.115197 13.696316  
## Heter JS Tau 7.943329 3.627058 9.192430  
## Heter PSJS NOSC Tau 7.940951 3.626537 9.193698  
## Heter PSJS SCOK Tau 7.940280 3.626416 9.193133  
## YJL177W\_YKL180W YBR191W\_YPL079W YER074W\_YIL069C  
## Homo JS Tau 10.118415 15.46016 23.87190  
## Homo PSJS D2 Tau 10.113094 15.46073 23.86086  
## Heter JS Tau 6.451872 13.64246 20.90049  
## Heter PSJS NOSC Tau 6.451223 13.64287 20.89540  
## Heter PSJS SCOK Tau 6.451251 13.64291 20.89149  
## YDR418W\_YEL054C YBL087C\_YER117W YLR333C\_YGR027C  
## Homo JS Tau 8.079769 13.93613 11.093217  
## Homo PSJS D2 Tau 8.074370 13.93386 11.087009  
## Heter JS Tau 5.163078 11.05276 9.875265  
## Heter PSJS NOSC Tau 5.162050 11.05020 9.863170  
## Heter PSJS SCOK Tau 5.163026 11.04945 9.860981  
## YMR142C\_YDL082W YER102W\_YBL072C  
## Homo JS Tau 15.69469 16.02066  
## Homo PSJS D2 Tau 15.69624 16.01818  
## Heter JS Tau 14.36723 14.76525  
## Heter PSJS NOSC Tau 14.36942 14.76508  
## Heter PSJS SCOK Tau 14.36978 14.76392

Now plot triangular lnL increase for pairs

pair <- "YER074W\_YIL069C"  
pair <- "YBL087C\_YER117W"  
dim <- 1  
  
library(fields)

## Loading required package: spam

## Loading required package: grid

## Spam version 1.4-0 (2016-08-29) is loaded.  
## Type 'help( Spam)' or 'demo( spam)' for a short introduction   
## and overview of this package.  
## Help for individual functions is also obtained by adding the  
## suffix '.spam' to the function name, e.g. 'help( chol.spam)'.

##   
## Attaching package: 'spam'

## The following objects are masked from 'package:base':  
##   
## backsolve, forwardsolve

## Loading required package: maps

# for (pair in finished.pairs[-6]){  
# for (dim in 1:2){  
# # JS.lnL <- get(paste(pair, "JS\_HKY\_nonclock\_lnL", sep = "\_"))  
# # row.lnL <- JS.lnL[, 2] %\*% matrix(1, 1, dim(JS.lnL)[1])  
# # col.lnL <- t(row.lnL)  
# # JS.mat <- row.lnL + col.lnL  
# #   
# # PSJS.lnL <- get(paste(pair, "PSJS\_dim", toString(dim), "HKY\_nonclock\_lnL", sep = "\_"))  
# # PSJS.mat <- matrix(0, dim(JS.lnL)[1], dim(JS.lnL)[1])  
# # for(i in 1:dim(PSJS.lnL)[1]){  
# # PSJS.mat[PSJS.lnL[i, 1] + 1, PSJS.lnL[i, 2] + 1] <- PSJS.lnL[i, 3]  
# # }  
# # PSJS.mat <- PSJS.mat + t(PSJS.mat)  
# #   
# # diff.lnL.mat <- PSJS.mat - JS.mat  
# # image.plot(1:dim(PSJS.mat)[1], 1:dim(PSJS.mat)[2], diff.lnL.mat, breaks = quantile(diff.lnL.mat))  
# # breaks <- c(0:20 \* max(diff.lnL.mat) / 20, 0:19 \* (-min(diff.lnL.mat) / 20) + min(diff.lnL.mat))  
# # hist(diff.lnL.mat, breaks = breaks)  
#   
# # Now PSJS RV SCOK model  
#   
# JS.rv.lnL <- get(paste(pair, "JS\_HKY\_rv\_nonclock\_lnL", sep = "\_"))  
# row.lnL <- JS.rv.lnL[, 2] %\*% matrix(1, 1, dim(JS.rv.lnL)[1])  
# col.lnL <- t(row.lnL)  
# JS.rv.mat <- row.lnL + col.lnL  
# diag(JS.rv.mat) <- 0.0  
#   
# PSJS.rv.lnL <- get(paste(pair, "PSJS\_dim", toString(dim), "HKY\_rv\_SCOK\_nonclock\_lnL", sep = "\_"))  
# PSJS.rv.mat <- matrix(0, dim(JS.rv.lnL)[1], dim(JS.rv.lnL)[1])  
# for(i in 1:dim(PSJS.rv.lnL)[1]){  
# PSJS.rv.mat[PSJS.rv.lnL[i, 1] + 1, PSJS.rv.lnL[i, 2] + 1] <- PSJS.rv.lnL[i, 3]  
# }  
# PSJS.rv.mat <- PSJS.rv.mat + t(PSJS.rv.mat)  
#   
#   
# diff.lnL.mat <- PSJS.rv.mat - JS.rv.mat  
# to.plot.mat <- diff.lnL.mat  
# to.plot.mat[to.plot.mat < 0.01] <- 0  
# # brk = quantile( c(diff.lnL.mat), c(0., 0.98, 1.0))  
# # #lab.brk = paste(names(brk), round(brk, digits = 2), sep = ":")  
# # lab.brk = names(brk)  
#   
# # tract.length <- get(paste("PSJS.HKY.dim.", toString(dim), ".nonclock.summary", sep = ""))["tract\_length", pair]  
# # lnL.threshold <- 1.0 / tract.length \* 2  
#   
# gene.length <- get(paste("PSJS.HKY.dim.", toString(dim), ".nonclock.summary", sep = ""))["length", pair]  
# lnL.threshold <- 1.0 / (gene.length - 1) \* 2  
# if(lnL.threshold > max(diff.lnL.mat)){  
# brk = quantile( c(diff.lnL.mat), c(0., 0.99, 1.0))  
# }else{  
# brk = c(min(diff.lnL.mat), lnL.threshold, max(diff.lnL.mat))  
# }  
#   
#   
# Fn <- ecdf(diff.lnL.mat)  
# lab.brk = c("0%", paste(toString(round(Fn(lnL.threshold) \* 100, digits = 4)), "%", sep = ""), "100%")  
# image.plot(1:dim(PSJS.rv.mat)[1], 1:dim(PSJS.rv.mat)[2], diff.lnL.mat, breaks = brk, col = rainbow(2),   
# lab.breaks = lab.brk, main = paste(pair, "PSJS\_dim", toString(dim), "HKY\_rv\_SCOK", sep = "\_"))  
# print(brk)  
# #hist(diff.lnL.mat)  
# #write.table(diff.lnL.mat, paste("./", pair, "\_matlab\_test.txt", sep = ""), row.names = FALSE, col.names = FALSE, sep = "\t")  
#   
# }  
# }

Now plot 2 dimensional lnL for 2 pairs

# library("lattice")  
# plot.pairs <- c("YLR333C\_YGR027C", "YLR406C\_YDL075W")  
# plot.pairs <- finished.pairs  
# # show estimated tract length  
# PSJS.HKY.nonclock.summary["tract\_length", plot.pairs]  
# for( pair in plot.pairs){  
# print(PSJS.HKY.rv.NOSC.nonclock.summary["tract\_length", pair])  
# plot.file.name <- paste("./plot/", pair, "/", pair, "\_PSJS\_HKY\_lnL\_rv\_NOSC\_nonclock\_dim\_1\_offratio\_0.5.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, "/", pair, "\_PSJS\_HKY\_lnL\_rv\_NOSC\_nonclock\_dim\_1\_offratio\_0.1\_zoomed\_in.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)  
#   
# x <- 1:6 \* 6 + 9  
# y <- 1:4 \* 0.05 + 0.85  
# to.plot.mat <- get(pair)  
# z <- matrix(to.plot.mat[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 = pair)  
# # plot the ridge  
# plot(x, z[, 3])  
# }

# Now export data  
save.image(file = "/Users/xji3/Dropbox/Public/SharedWithJeff/TractSummary.RData")

03232017 construct a table for my talk

library(xtable)

##   
## Attaching package: 'xtable'

## The following object is masked from 'package:spam':  
##   
## display

show.mat <- NULL  
show.mat <- cbind(JS.HKY.rv.nonclock.summary["ll",],  
 PSJS.HKY.rv.SCOK.dim.2.nonclock.eff.lnL,  
 JS.HKY.rv.nonclock.summary["Tau",] \* 3.0 / colSums(rbind(1, JS.HKY.rv.nonclock.summary[c("r2", "r3"),])),  
 PSJS.HKY.rv.SCOK.dim.2.nonclock.summary["tract\_length",] \* PSJS.HKY.rv.SCOK.dim.2.nonclock.summary["init\_rate", ]  
 \* 3.0 / colSums(rbind(1, PSJS.HKY.rv.SCOK.dim.2.nonclock.summary[c("r2", "r3"), ])),  
 PSJS.HKY.rv.SCOK.dim.2.nonclock.summary["tract\_length",]  
 )  
colnames(show.mat) <- c("HKY + RV + SSJS lnL", "HKY + RV + PSJS IGC", "Tau", "Effective Tau",  
 "Estimated Tract Length")  
show.mat

## HKY + RV + SSJS lnL HKY + RV + PSJS IGC Tau  
## YLR406C\_YDL075W -1189.812 -1189.806 5.099108  
## YER131W\_YGL189C -1216.912 -1216.881 5.269134  
## YML026C\_YDR450W -1368.469 -1368.468 12.836811  
## YNL301C\_YOL120C -2126.642 -2126.509 7.943329  
## YNL069C\_YIL133C -2332.607 -2332.547 3.627058  
## YMR143W\_YDL083C -1217.381 -1217.381 9.192430  
## YJL177W\_YKL180W -1840.376 -1840.373 6.451872  
## YBR191W\_YPL079W -1468.945 -1468.917 13.642456  
## YER074W\_YIL069C -1233.000 -1232.918 20.900494  
## YDR418W\_YEL054C -1735.398 -1735.393 5.163078  
## YBL087C\_YER117W -1372.911 -1372.865 11.052761  
## YLR333C\_YGR027C -1246.666 -1246.626 9.875265  
## YMR142C\_YDL082W -2033.878 -2033.803 14.367232  
## YER102W\_YBL072C -2037.260 -2037.179 14.765252  
## Effective Tau Estimated Tract Length  
## YLR406C\_YDL075W 5.101011 4.227927  
## YER131W\_YGL189C 5.269659 12.392702  
## YML026C\_YDR450W 12.846401 1.388747  
## YNL301C\_YOL120C 7.940280 98.882961  
## YNL069C\_YIL133C 3.626416 12.298639  
## YMR143W\_YDL083C 9.193133 1.000000  
## YJL177W\_YKL180W 6.451251 2.506450  
## YBR191W\_YPL079W 13.642911 10.677062  
## YER074W\_YIL069C 20.891490 52.984421  
## YDR418W\_YEL054C 5.163026 3.273311  
## YBL087C\_YER117W 11.049450 29.993728  
## YLR333C\_YGR027C 9.860981 29.997693  
## YMR142C\_YDL082W 14.369779 30.004538  
## YER102W\_YBL072C 14.763920 29.999934

x.rescale <- xtable(show.mat)  
print(x.rescale, scalebox = 0.7)

## % latex table generated in R 3.3.0 by xtable 1.8-2 package  
## % Thu Mar 23 13:44:35 2017  
## \begin{table}[ht]  
## \centering  
## \scalebox{0.7}{  
## \begin{tabular}{rrrrrr}  
## \hline  
## & HKY + RV + SSJS lnL & HKY + RV + PSJS IGC & Tau & Effective Tau & Estimated Tract Length \\   
## \hline  
## YLR406C\\_YDL075W & -1189.81 & -1189.81 & 5.10 & 5.10 & 4.23 \\   
## YER131W\\_YGL189C & -1216.91 & -1216.88 & 5.27 & 5.27 & 12.39 \\   
## YML026C\\_YDR450W & -1368.47 & -1368.47 & 12.84 & 12.85 & 1.39 \\   
## YNL301C\\_YOL120C & -2126.64 & -2126.51 & 7.94 & 7.94 & 98.88 \\   
## YNL069C\\_YIL133C & -2332.61 & -2332.55 & 3.63 & 3.63 & 12.30 \\   
## YMR143W\\_YDL083C & -1217.38 & -1217.38 & 9.19 & 9.19 & 1.00 \\   
## YJL177W\\_YKL180W & -1840.38 & -1840.37 & 6.45 & 6.45 & 2.51 \\   
## YBR191W\\_YPL079W & -1468.94 & -1468.92 & 13.64 & 13.64 & 10.68 \\   
## YER074W\\_YIL069C & -1233.00 & -1232.92 & 20.90 & 20.89 & 52.98 \\   
## YDR418W\\_YEL054C & -1735.40 & -1735.39 & 5.16 & 5.16 & 3.27 \\   
## YBL087C\\_YER117W & -1372.91 & -1372.86 & 11.05 & 11.05 & 29.99 \\   
## YLR333C\\_YGR027C & -1246.67 & -1246.63 & 9.88 & 9.86 & 30.00 \\   
## YMR142C\\_YDL082W & -2033.88 & -2033.80 & 14.37 & 14.37 & 30.00 \\   
## YER102W\\_YBL072C & -2037.26 & -2037.18 & 14.77 & 14.76 & 30.00 \\   
## \hline  
## \end{tabular}  
## }  
## \end{table}