

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["l1", ] / (seq.length - 1)
PSJS.HKY.dim.2.nonclock.eff.lnL <- PSJS.HKY.dim.2.nonclock.summary["l1", ] / (seq.length - 1)
PSJS.HKY.rv.NOSC.dim.1.nonclock.eff.lnL <- PSJS.HKY.rv.NOSC.dim.1.nonclock.summary["l1", ] / (seq.length - 1)
PSJS.HKY.rv.NOSC.dim.2.nonclock.eff.lnL <- PSJS.HKY.rv.NOSC.dim.2.nonclock.summary["l1", ] / (seq.length - 1)
PSJS.HKY.rv.SCOK.dim.1.nonclock.eff.lnL <- PSJS.HKY.rv.SCOK.dim.1.nonclock.summary["l1", ] / (seq.length - 1)
PSJS.HKY.rv.SCOK.dim.2.nonclock.eff.lnL <- PSJS.HKY.rv.SCOK.dim.2.nonclock.summary["l1", ] / (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	2.718200e+00	6.619183e+00	1.195016e+00
## Homo D2	2.706912e+00	6.591323e+00	3.319718e+00
## lnL (D1 - D2)	-9.666460e-07	-1.250433e-06	3.876912e-03
## Heter NOSC D1	1.000000e+00	1.282491e+01	1.000000e+00
## Heter NOSC D2	1.000000e+00	1.283719e+01	1.293436e+00
## lnL (D1 - D2)	-6.299524e-08	-9.153830e-07	1.502516e-04
## Heter SCOK D1	4.206682e+00	1.233479e+01	1.422101e+00
## Heter SCOK D2	4.228217e+00	1.239234e+01	1.388763e+00
## lnL (D1 - D2)	-1.290628e-06	-5.789557e-07	4.777857e-06
##	YNL301C_YOL120C	YNL069C_YIL133C	YMR143W_YDL083C
## Homo D1	2.208291e+01	6.527762e+00	2.499954e+00
## Homo D2	3.000325e+01	6.543386e+00	2.477606e+00
## lnL (D1 - D2)	2.066991e-03	1.239731e-06	1.473688e-06
## Heter NOSC D1	9.908427e+01	1.218275e+01	4.764644e+00
## Heter NOSC D2	9.970280e+01	1.220593e+01	4.826867e+00
## lnL (D1 - D2)	-6.039285e-06	-4.577364e-07	3.161742e-07
## Heter SCOK D1	9.891786e+01	1.237519e+01	1.000000e+00
## Heter SCOK D2	6.257740e+01	1.229883e+01	1.000000e+00
## lnL (D1 - D2)	2.402390e-02	1.591868e-06	-1.682420e-07
##	YJL177W_YKL180W	YBR191W_YPL079W	YER074W_YIL069C
## Homo D1	2.871830e+00	8.105416e+00	4.336609e+01

## Homo D2	2.876216e+00	8.078559e+00	4.329623e+01
## lnL (D1 - D2)	-2.366619e-08	-5.465467e-07	-7.943210e-06
## Heter NOSC D1	1.000000e+00	1.059505e+01	5.289576e+01
## Heter NOSC D2	1.000000e+00	1.064804e+01	5.291992e+01
## lnL (D1 - D2)	-1.220317e-06	-1.098309e-05	-1.969606e-07
## Heter SCOK D1	2.468737e+00	1.064311e+01	5.295320e+01
## Heter SCOK D2	2.506476e+00	1.067691e+01	5.298438e+01
## lnL (D1 - D2)	3.357973e-07	-4.637918e-07	-2.943206e-06
##	YDR418W_YEL054C	YBL087C_YER117W	YLR333C_YGR027C
## Homo D1	2.286202e+00	1.280930e+01	7.211346e+00
## Homo D2	2.286356e+00	1.292373e+01	7.245250e+00
## lnL (D1 - D2)	-3.417742e-07	-4.140838e-06	-1.014812e-05
## Heter NOSC D1	3.757791e+00	2.916361e+01	3.543419e+01
## Heter NOSC D2	3.746113e+00	2.999653e+01	2.999629e+01
## lnL (D1 - D2)	-2.185898e-07	1.305053e-05	3.091082e-04
## Heter SCOK D1	3.314590e+00	2.821906e+01	3.486331e+01
## Heter SCOK D2	3.273311e+00	2.999609e+01	2.999610e+01
## lnL (D1 - D2)	7.909487e-07	1.288901e-04	1.980279e-04
##	YMR142C_YDL082W	YER102W_YBL072C	
## Homo D1	2.849629e+01	1.783599e+01	
## Homo D2	3.000156e+01	2.999748e+01	
## lnL (D1 - D2)	9.636334e-05	1.015029e-02	
## Heter NOSC D1	3.253834e+01	3.189525e+01	
## Heter NOSC D2	3.000144e+01	2.999924e+01	
## lnL (D1 - D2)	2.086833e-04	1.514170e-04	
## Heter SCOK D1	3.289067e+01	3.105408e+01	
## Heter SCOK D2	3.000165e+01	2.999906e+01	
## lnL (D1 - D2)	2.547296e-04	4.465986e-05	

Now show equivalent lnL matrix

```
show.mat <- rbind(JS.HKY.nonclock.summary["l1", ],
  PSJS.HKY.dim.1.nonclock.eff.lnL, PSJS.HKY.dim.2.nonclock.eff.lnL,
  JS.HKY.rv.nonclock.summary["l1", ],
  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.1.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	-1516.489
## 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	-1196.952	-1223.815	-1375.031
## Heter SCOK D2	-1196.952	-1223.815	-1375.031
##	YNL301C_YOL120C	YNL069C_YIL133C	YMR143W_YDL083C
## Homo JS	-2245.814	-2442.924	-1323.835
## Homo PSJS D1	-2245.796	-2442.889	-1323.836
## 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	-2134.214	-2340.480	-1223.483
## Heter SCOK D2	-2134.214	-2340.480	-1223.483
##	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	-1847.114	-1475.115	-1239.145
## Heter SCOK D2	-1847.114	-1475.115	-1239.145
##	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	-1742.535	-1379.644	-1254.466
## Heter SCOK D2	-1742.535	-1379.644	-1254.466
##	YMR142C_YDL082W	YER102W_YBL072C	
## Homo JS	-2152.783	-2116.872	
## Homo PSJS D1	-2152.708	-2116.816	
## Homo PSJS D2	-2152.708	-2116.826	
## Heter JS	-2033.878	-2037.260	
## Heter NOSC D1	-2033.824	-2037.172	
## Heter NOSC D2	-2033.824	-2037.173	
## Heter SCOK D1	-2040.721	-2044.073	
## Heter SCOK D2	-2040.721	-2044.073	

```

# 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	8.012614	7.721439	14.97145
## Homo PSJS D2 Tau	8.014535	7.720756	14.97138
## Heter JS Tau	5.099441	5.269409	12.84695
## Heter PSJS NOSC Tau	5.099286	5.269885	12.84721
## Heter PSJS SCOK Tau	5.101680	5.269348	12.84988
##	YNL301C_YOL120C	YNL069C_YIL133C	YMR143W_YDL083C
## Homo JS Tau	10.977195	5.115744	13.696544

## Homo PSJS D2 Tau	10.980822	5.116213	13.693381
## Heter JS Tau	7.938067	3.626380	9.192845
## Heter PSJS NOSC Tau	7.940762	3.626650	9.194454
## Heter PSJS SCOK Tau	7.949545	3.626577	9.192774
##	YJL177W_YKL180W	YBR191W_YPL079W	YER074W_YIL069C
## Homo JS Tau	10.113116	15.45949	23.87185
## Homo PSJS D2 Tau	10.112268	15.46063	23.86057
## Heter JS Tau	6.451423	13.64155	20.89786
## Heter PSJS NOSC Tau	6.451208	13.64292	20.89544
## Heter PSJS SCOK Tau	6.451289	13.64255	20.89143
##	YDR418W_YEL054C	YBL087C_YER117W	YLR333C_YGR027C
## Homo JS Tau	8.074947	13.93825	11.092744
## Homo PSJS D2 Tau	8.074333	13.93398	11.086801
## Heter JS Tau	5.163330	11.05823	9.875537
## Heter PSJS NOSC Tau	5.162529	11.05068	9.862555
## Heter PSJS SCOK Tau	5.163026	11.05023	9.860501
##	YMR142C_YDL082W	YER102W_YBL072C	
## Homo JS Tau	15.69461	16.01937	
## Homo PSJS D2 Tau	15.69650	16.01623	
## Heter JS Tau	14.36769	14.76518	
## Heter PSJS NOSC Tau	14.36903	14.76436	
## Heter PSJS SCOK Tau	14.36888	14.76357	

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.ru.NOSC.nonclock.summary["tract_length", pair])
#   plot.file.name <- paste("./plot/", pair, "/", pair, "_PSJS_HKY_lnL_ru_NOSC_nonclock_dim_1_offratio_")
#   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_ru_NOSC_nonclock_dim_1_offratio_")
# plot.data <- read.table(plot.file.name)
# #plot(plot.data[, 2], plot.data[, 3], xlab = "init rate", ylab = "lnL", main = paste(pair, "_zoomed"))
# 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")
# # plot the ridge
# plot(x, z[, 3])
# }
```

```
# Now export data  
save.image(file = "./TractSummary.RData")
```