# 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
PSJS.HKY.rv.NOSC.dim.2.nonclock.eff.lnL <- PSJS.HKY.rv.NOSC.dim.2.nonclock.summary["ll", ]/ (seq.length
PSJS.HKY.rv.SCOK.dim.1.nonclock.eff.lnL <- PSJS.HKY.rv.SCOK.dim.1.nonclock.summary["ll", ]/ (seq.length
PSJS.HKY.rv.SCOK.dim.2.nonclock.eff.lnL <- PSJS.HKY.rv.SCOK.dim.2.nonclock.summary["ll", ]/ (seq.length

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["
   * 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["in
  * 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", "Hete
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)'.
```

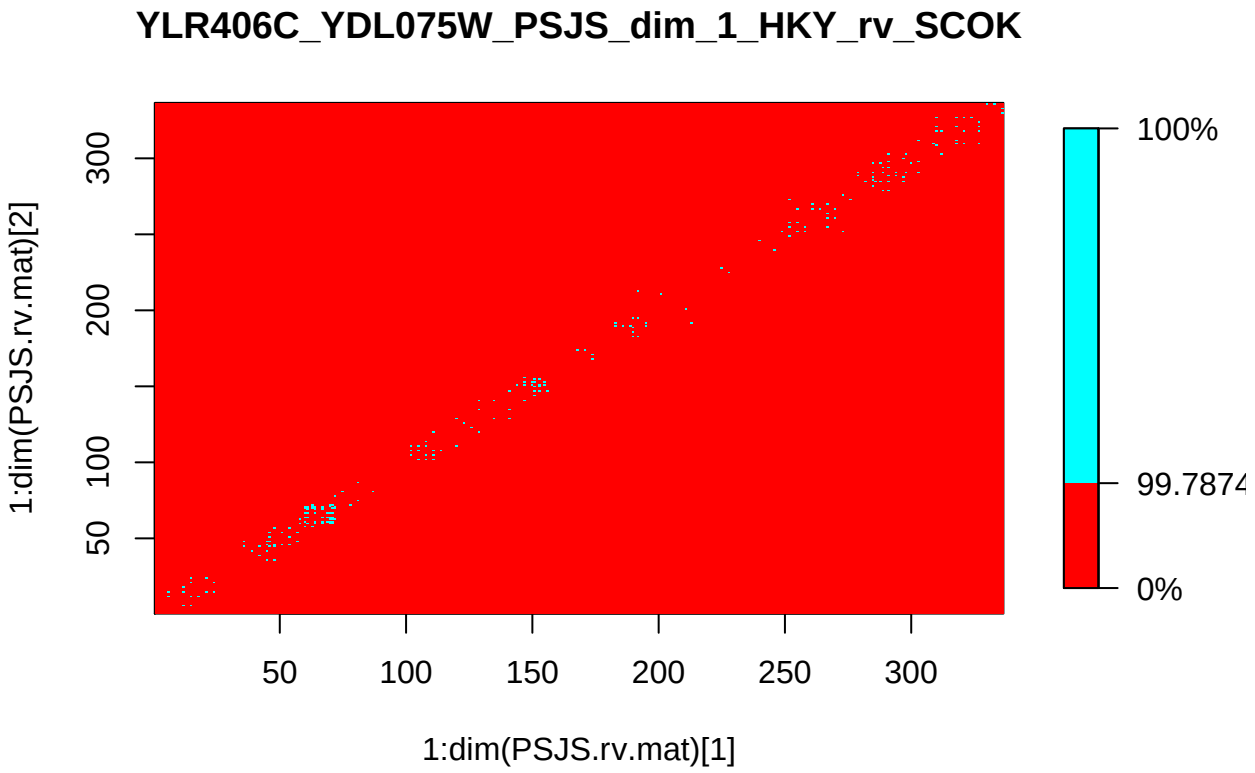
```
##
## Attaching package: 'spam'
```

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

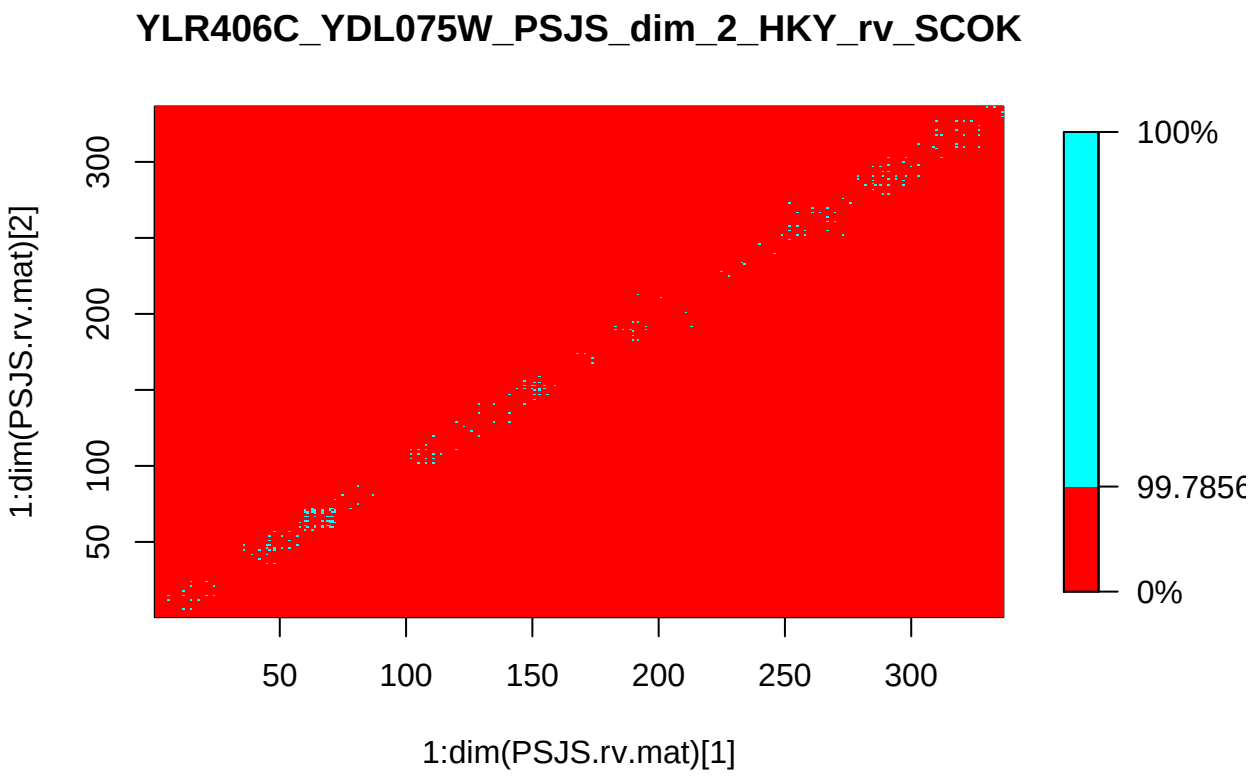
```
## Loading required package: maps
```

```
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_
    # lnL.threshold <- 1.0 / tract.length * 2

    gene.length <- get(paste("PSJS.HKY.dim.", toString(dim), ".nonclock.summary", sep = ""))["length", ]
    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))
    }
```

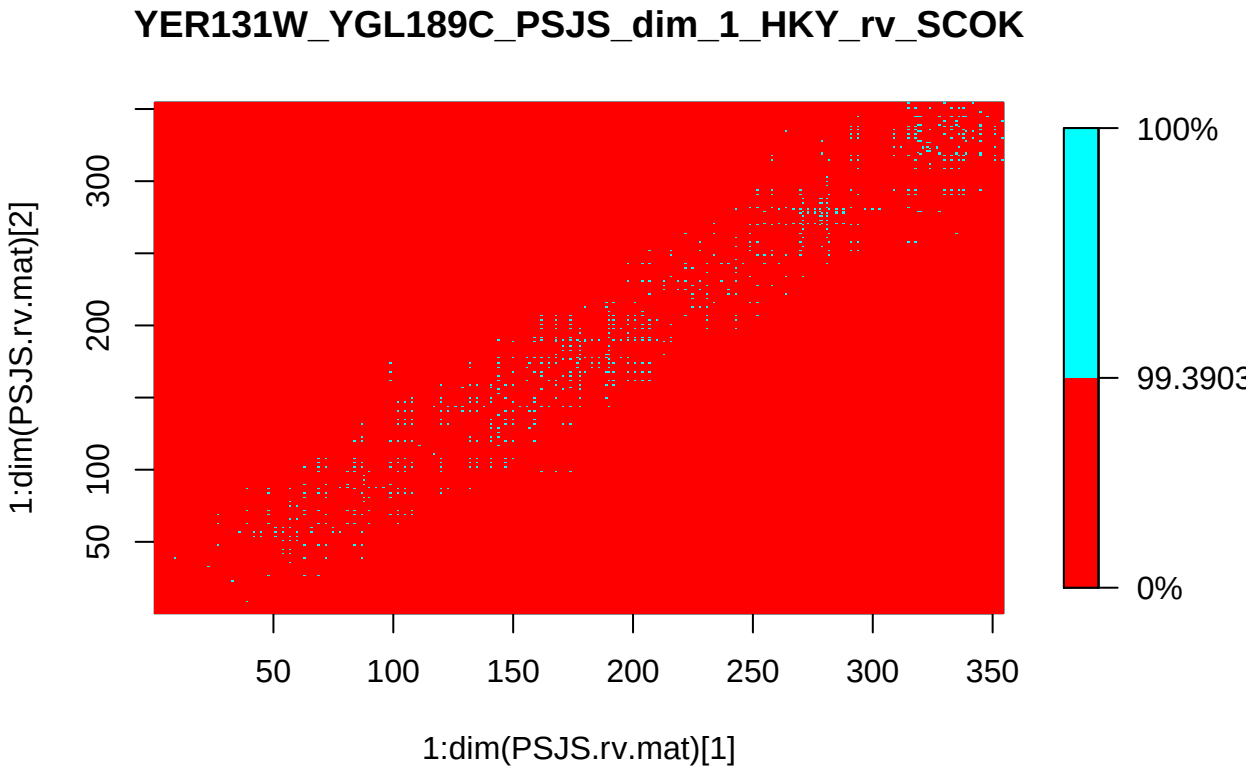
```
    Fn <- ecdf(diff.lnL.mat)
    lab.brk = c("0%", paste(toString(round(Fn(lnL.threshold) * 100, digits = 4)), "%", sep = ""), "100%
    image.plot(1:dim(PSJS.rv.mat)[1], 1:dim(PSJS.rv.mat)[2], diff.lnL.mat, breaks = brk, col = rainbow(1
               lab.breaks = lab.brk, main = paste(pair, "PSJS_dim", 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.

  }
}
```



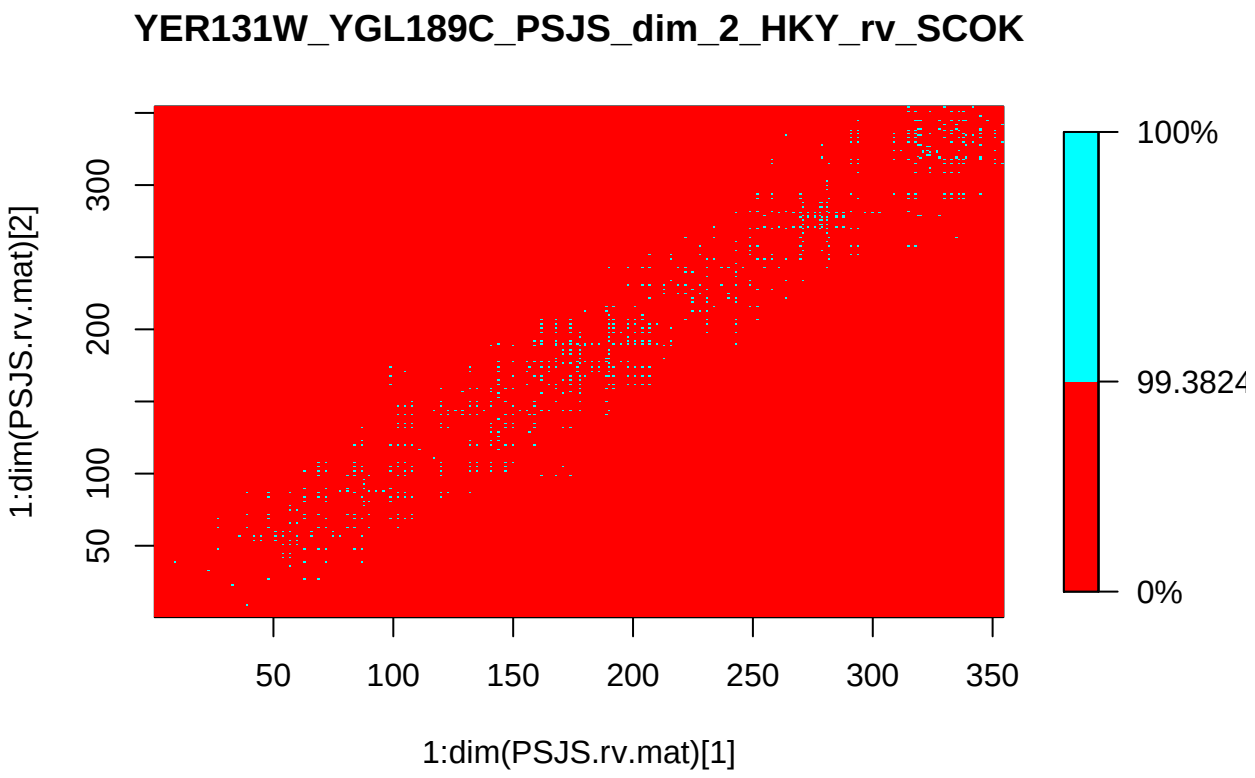

```
## [1] -0.456993043  0.005970149  1.571553690
```



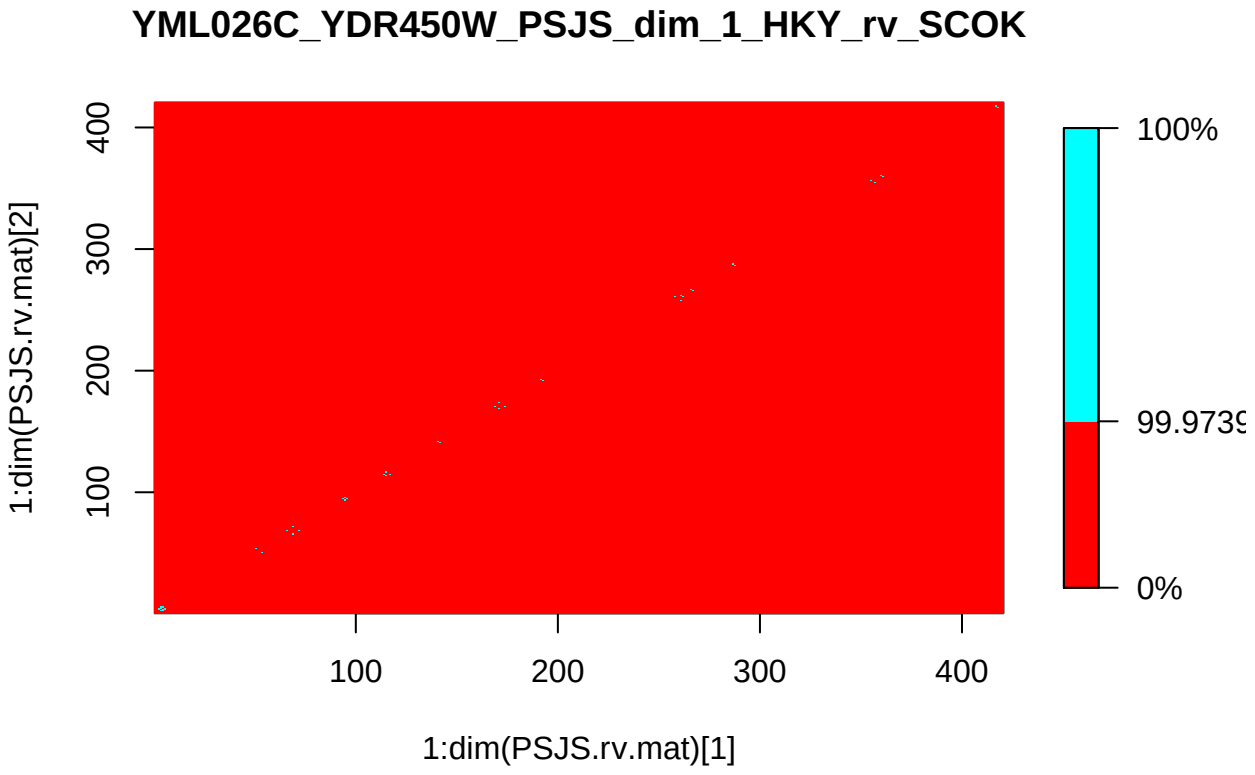

```
## [1] -0.457858026  0.005970149  1.571477120
```



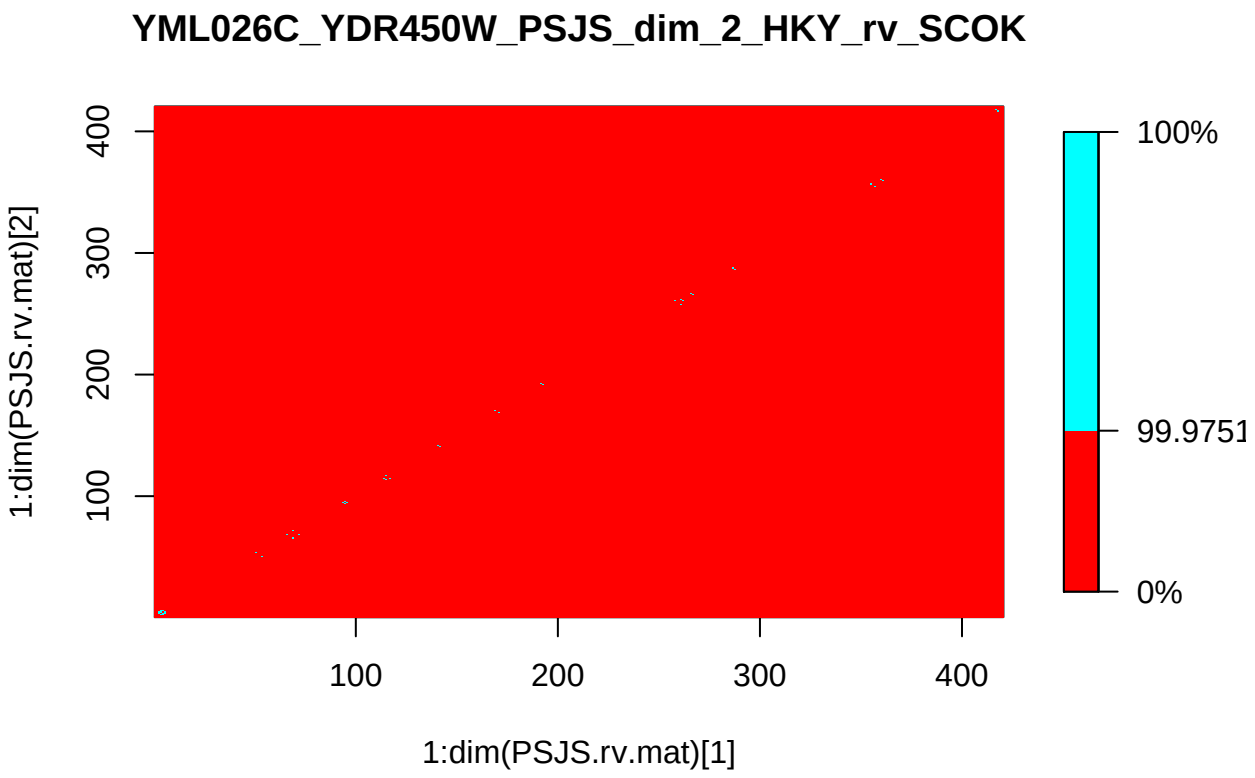

```
## [1] -2.008061364  0.005665722  2.403379539
```



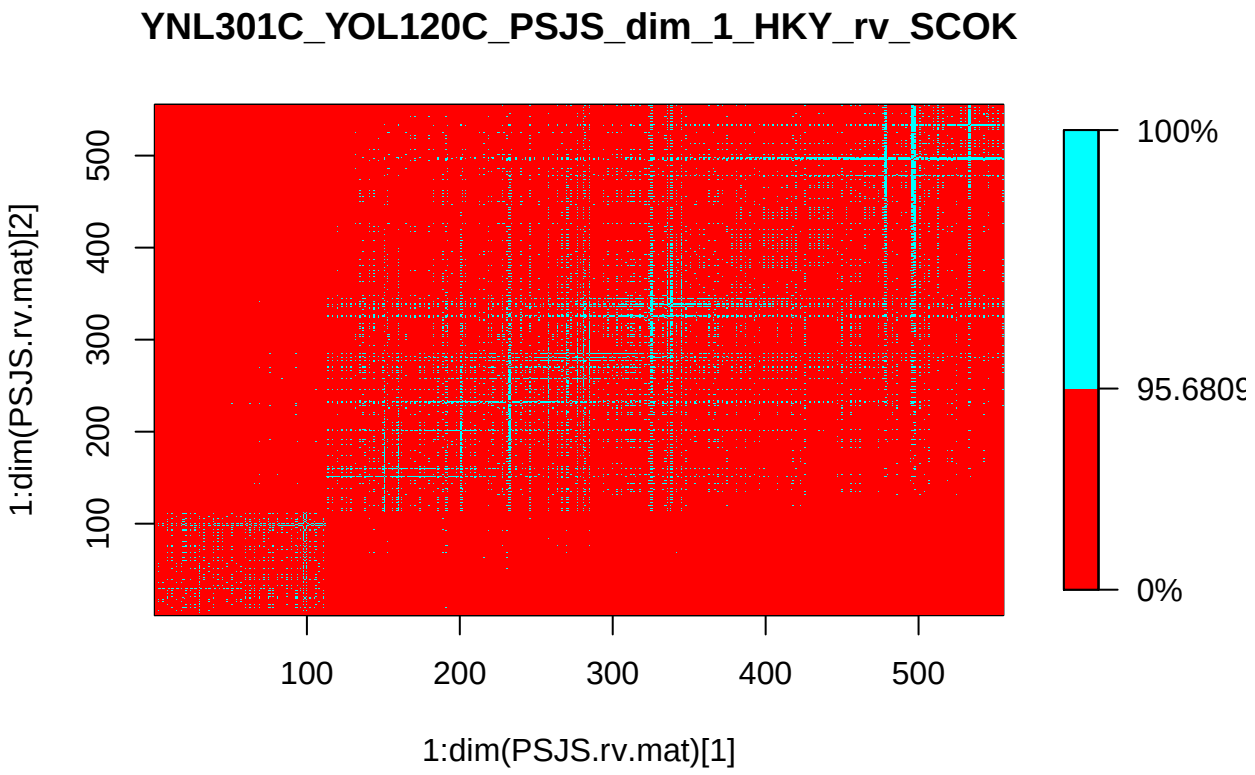

```
## [1] -2.011296533  0.005665722  2.402014322
```



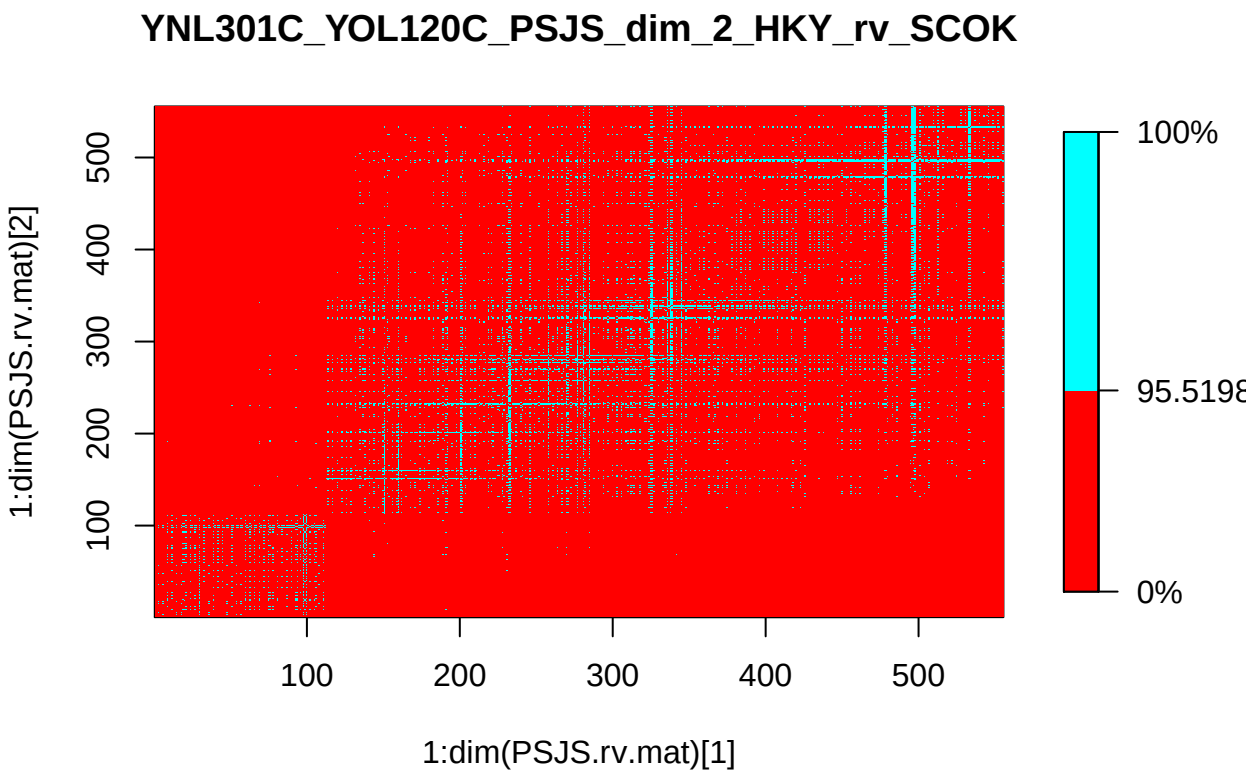

```
## [1] -0.07211660  0.00477327  0.14027934
```



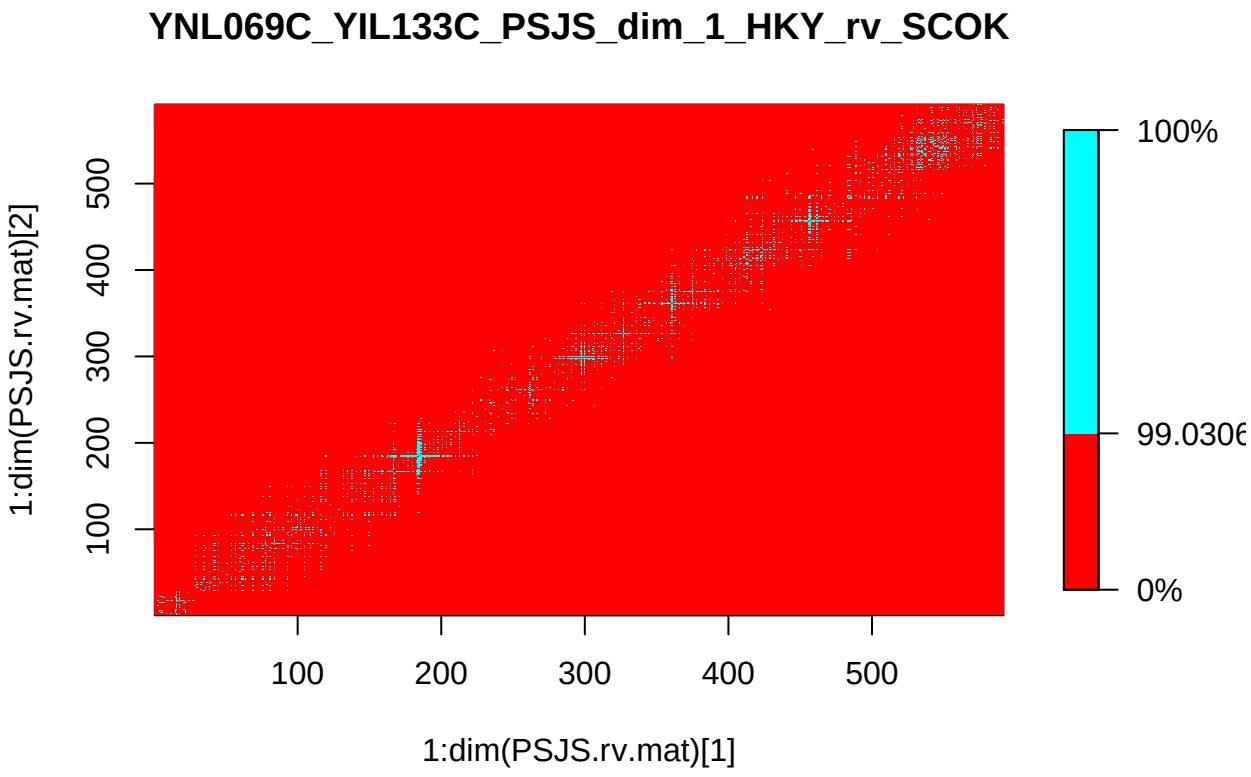

```
## [1] -0.06364769  0.00477327  0.13177736
```



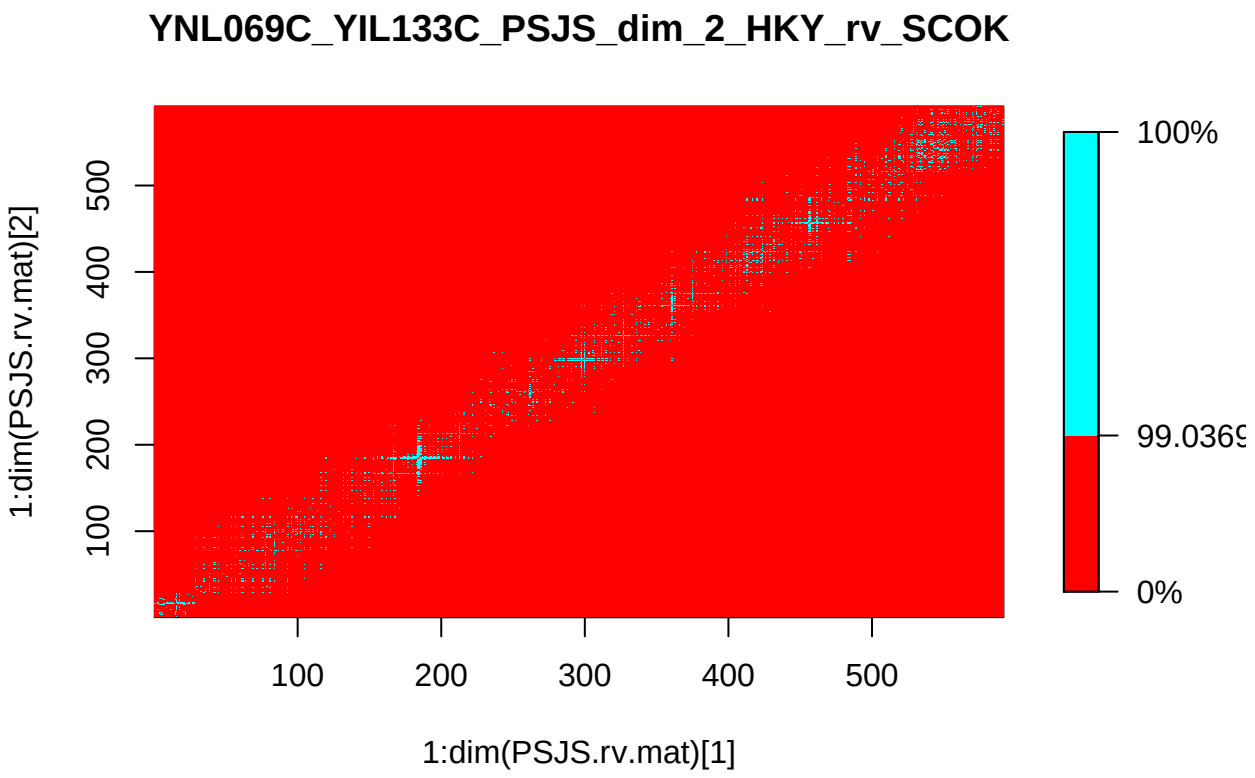

```
## [1] -2.463663520  0.003610108  3.173942929
```



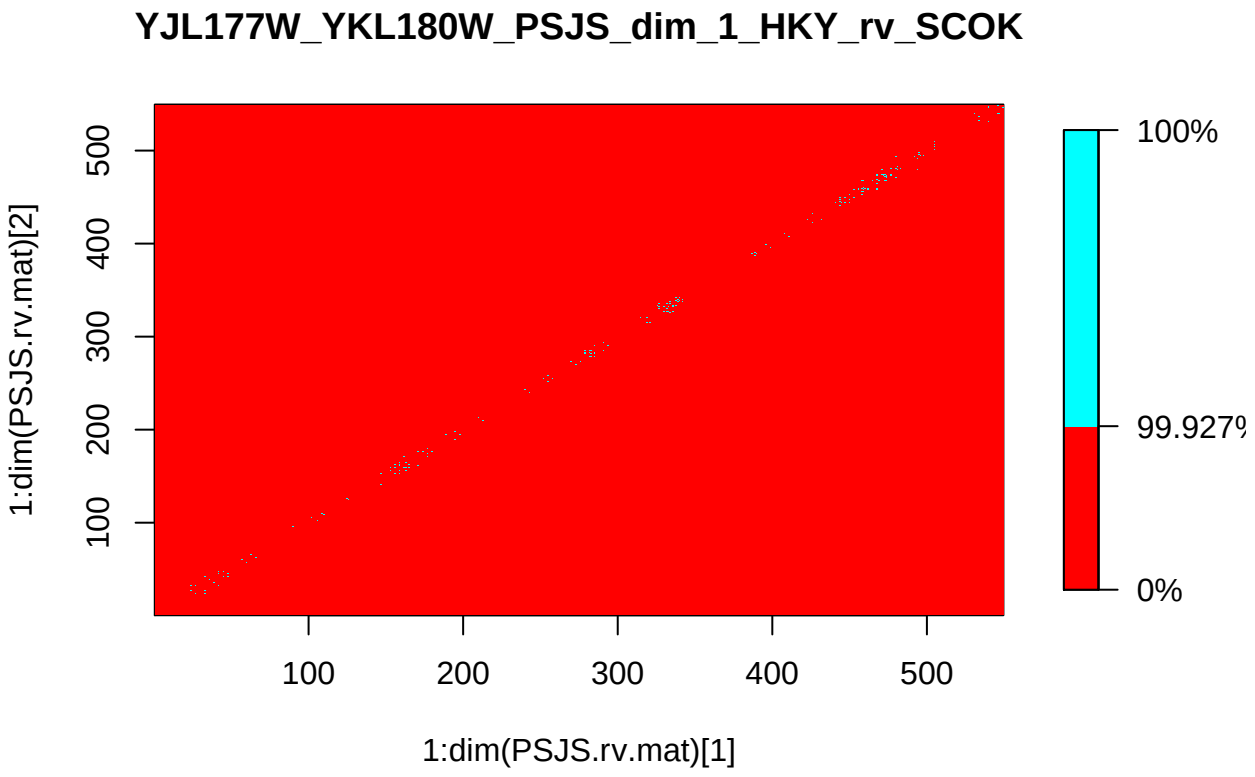

```
## [1] -2.463798990  0.003610108  3.174198705
```



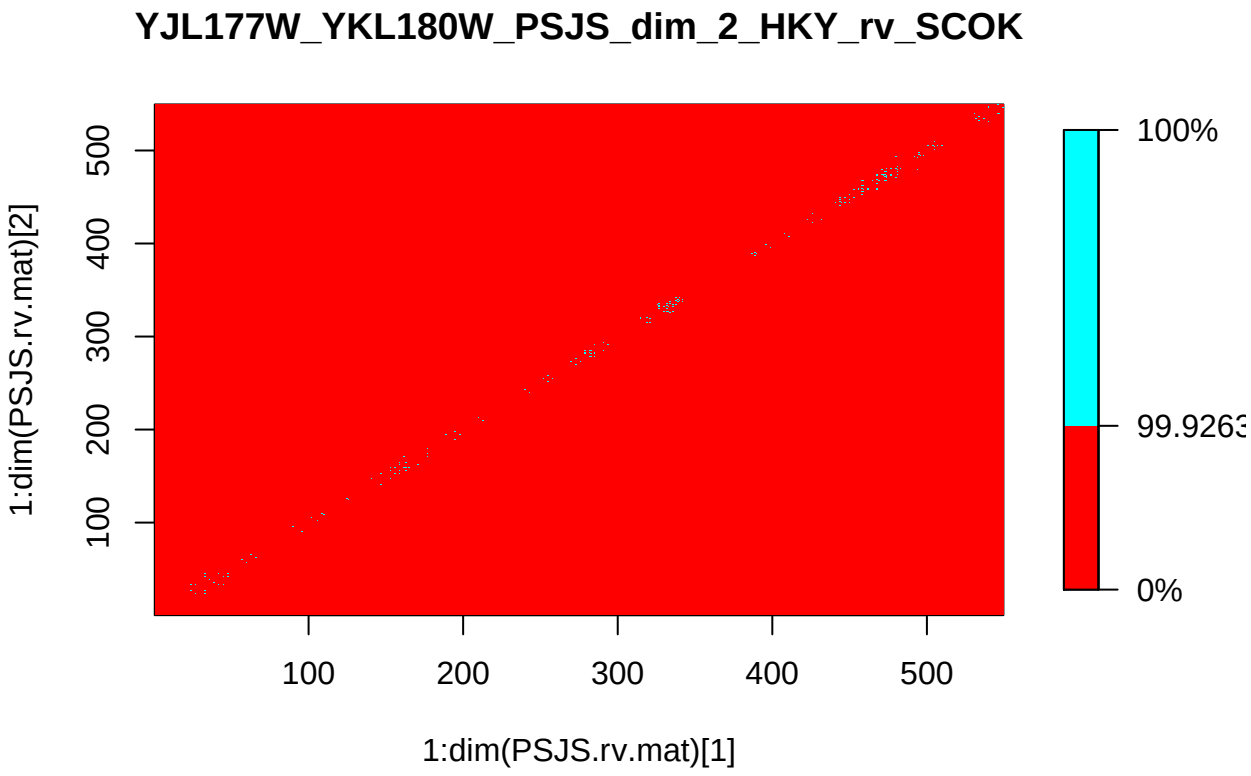

```
## [1] -1.689936713  0.003389831  3.288770362
```



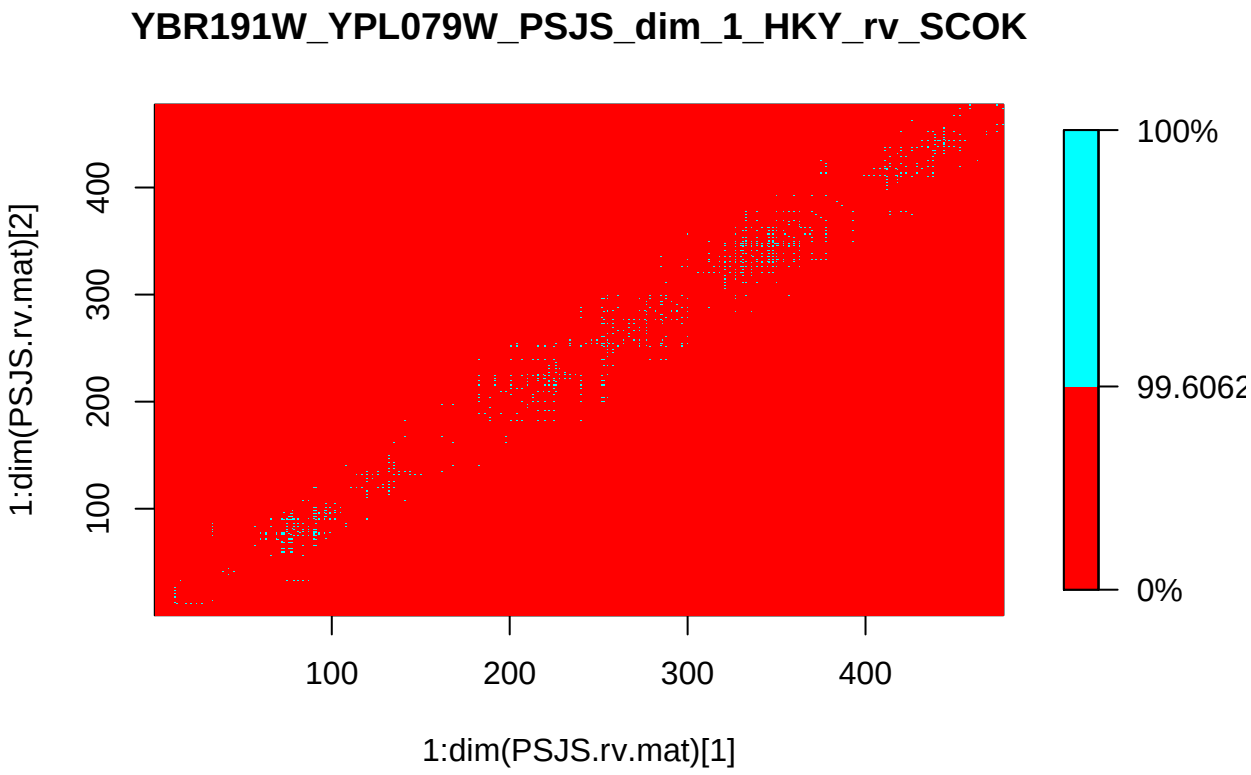

```
## [1] -1.685840742  0.003389831  3.287811317
```



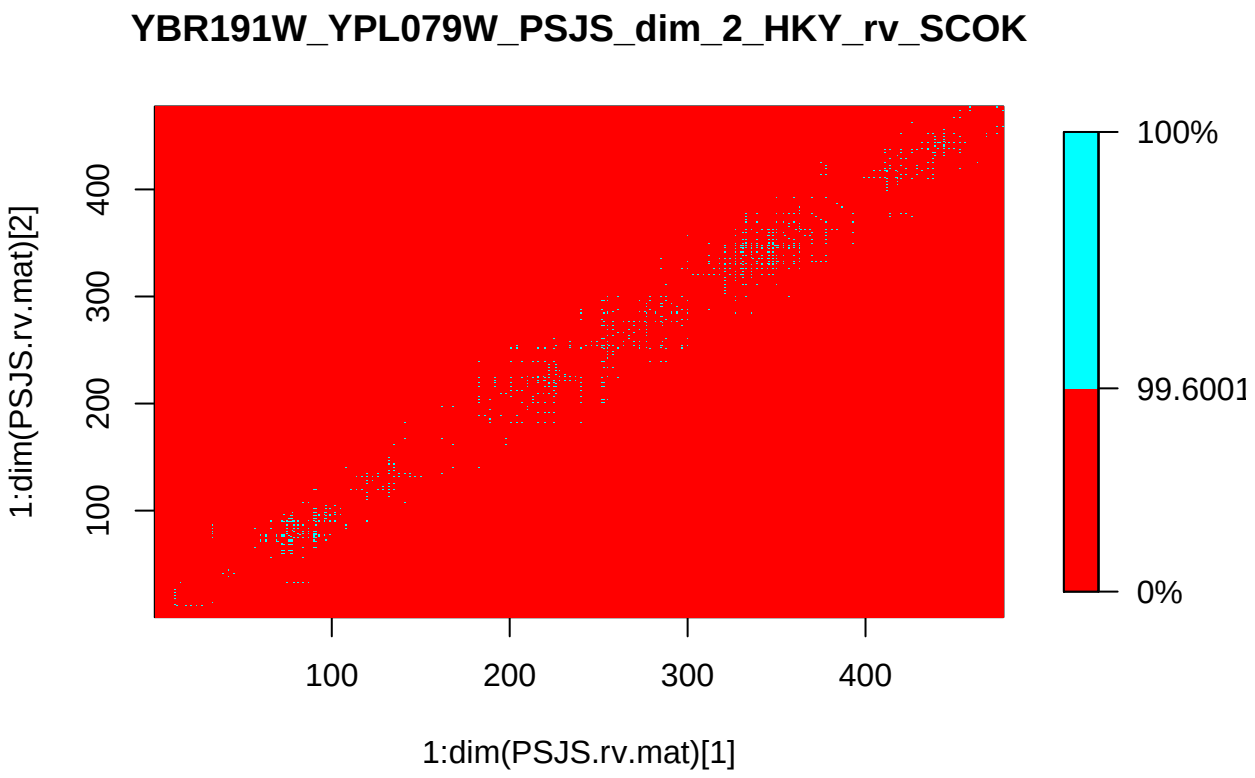

```
## [1] -0.973914187  0.003649635  1.773983046
```



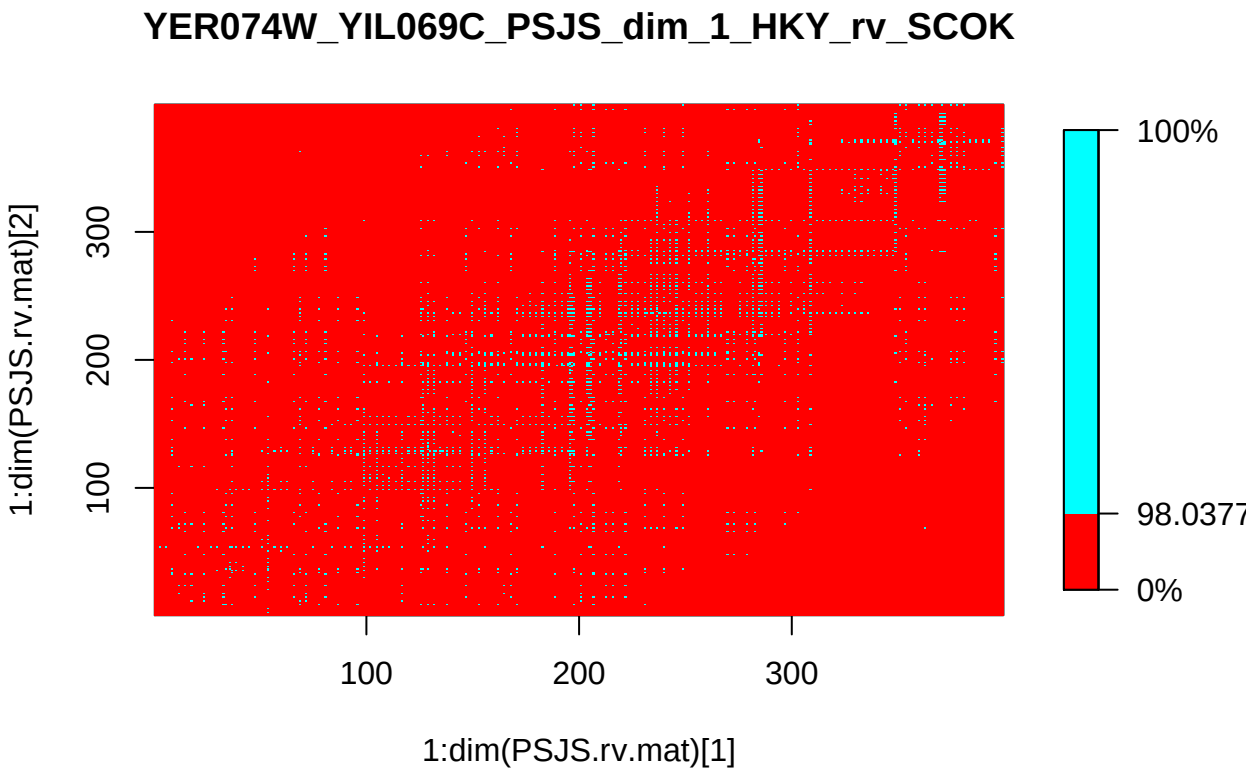

```
## [1] -0.984173760  0.003649635  1.787941306
```



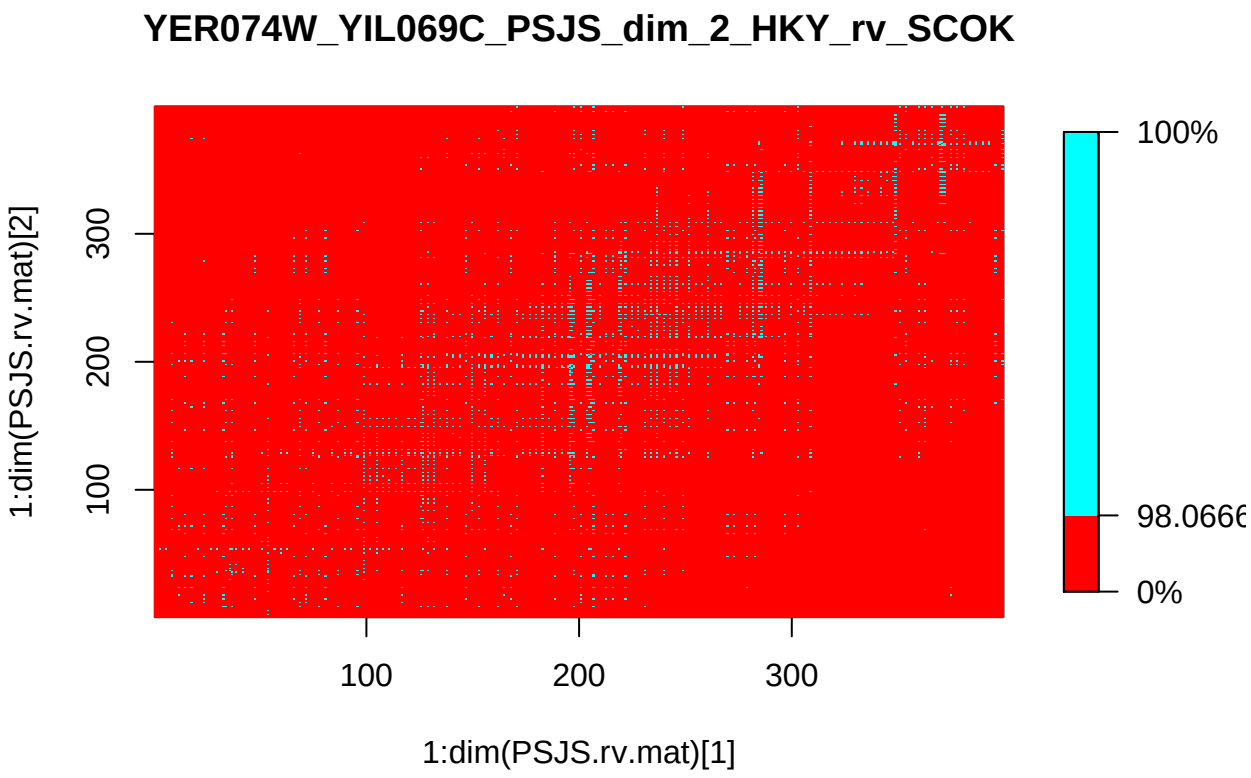

```
## [1] -2.324325391  0.004201681  2.941658030
```



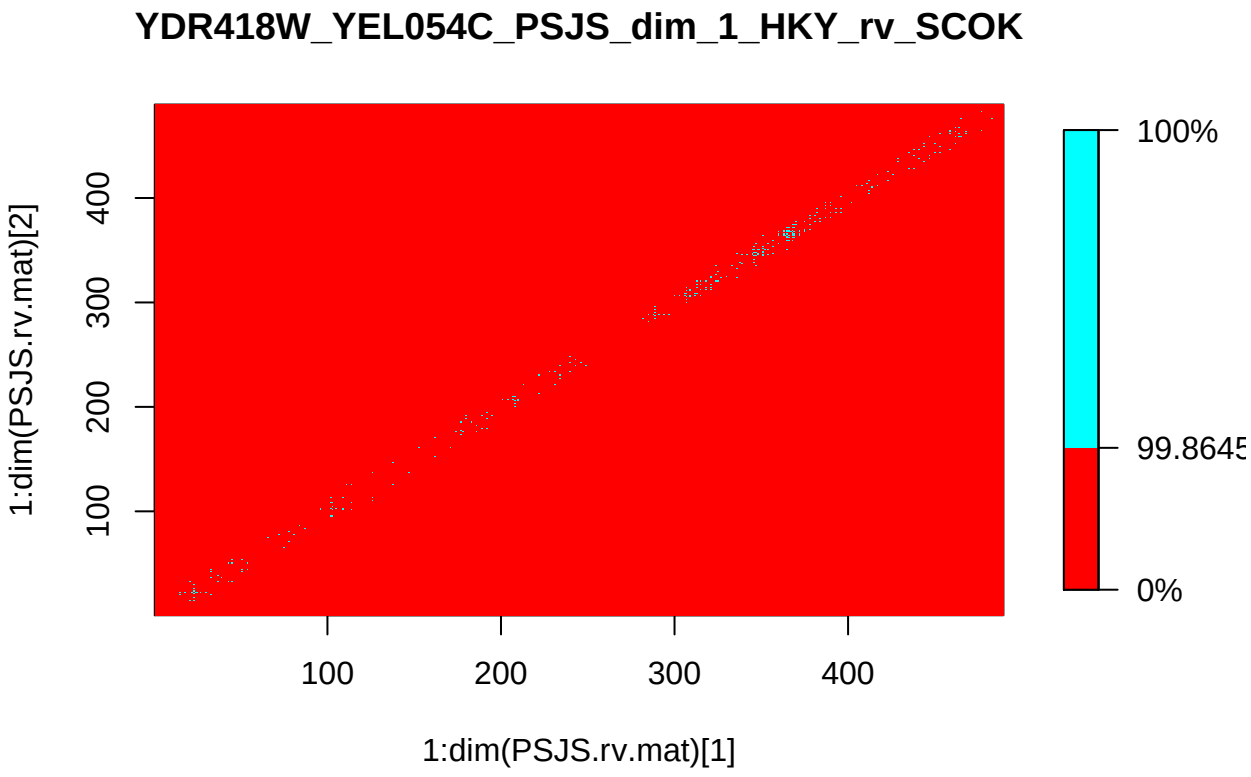

```
## [1] -2.325588464  0.004201681  2.942601503
```



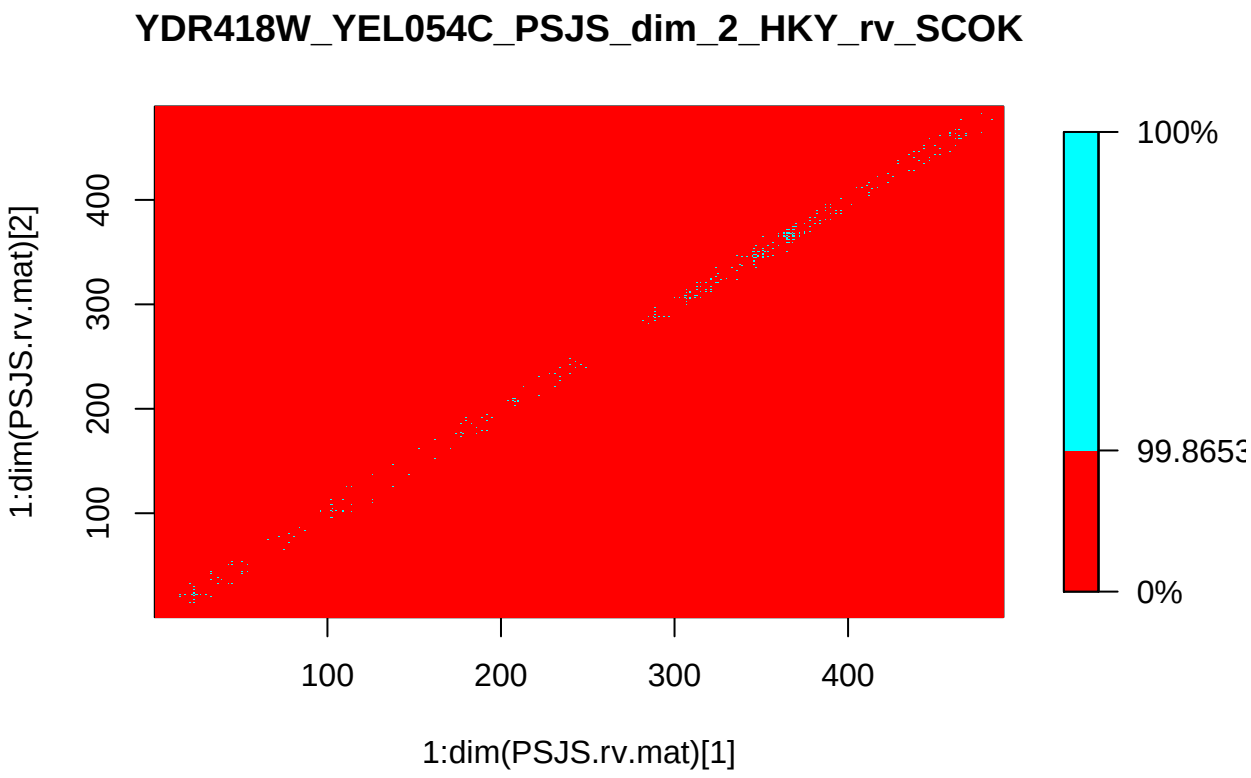

```
## [1] -0.657855050  0.005025126  3.342930735
```



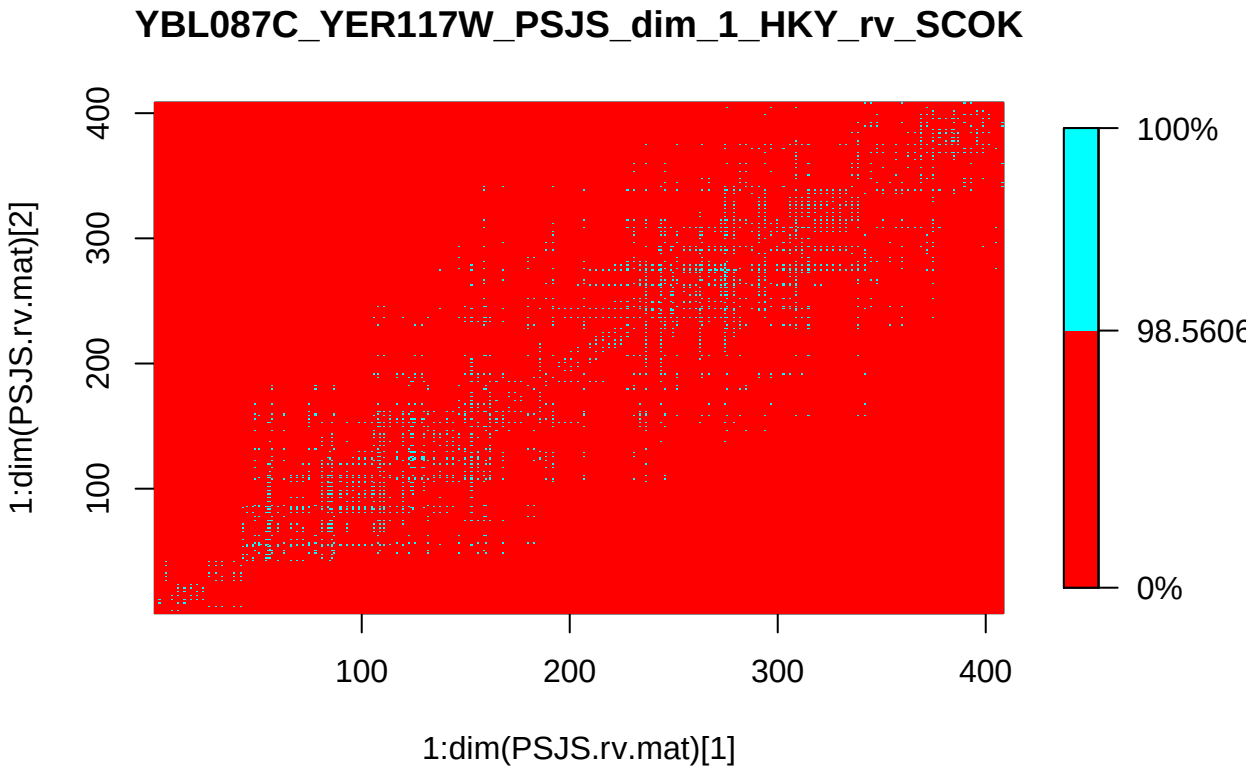

```
## [1] -0.658700093  0.005025126  3.344560919
```



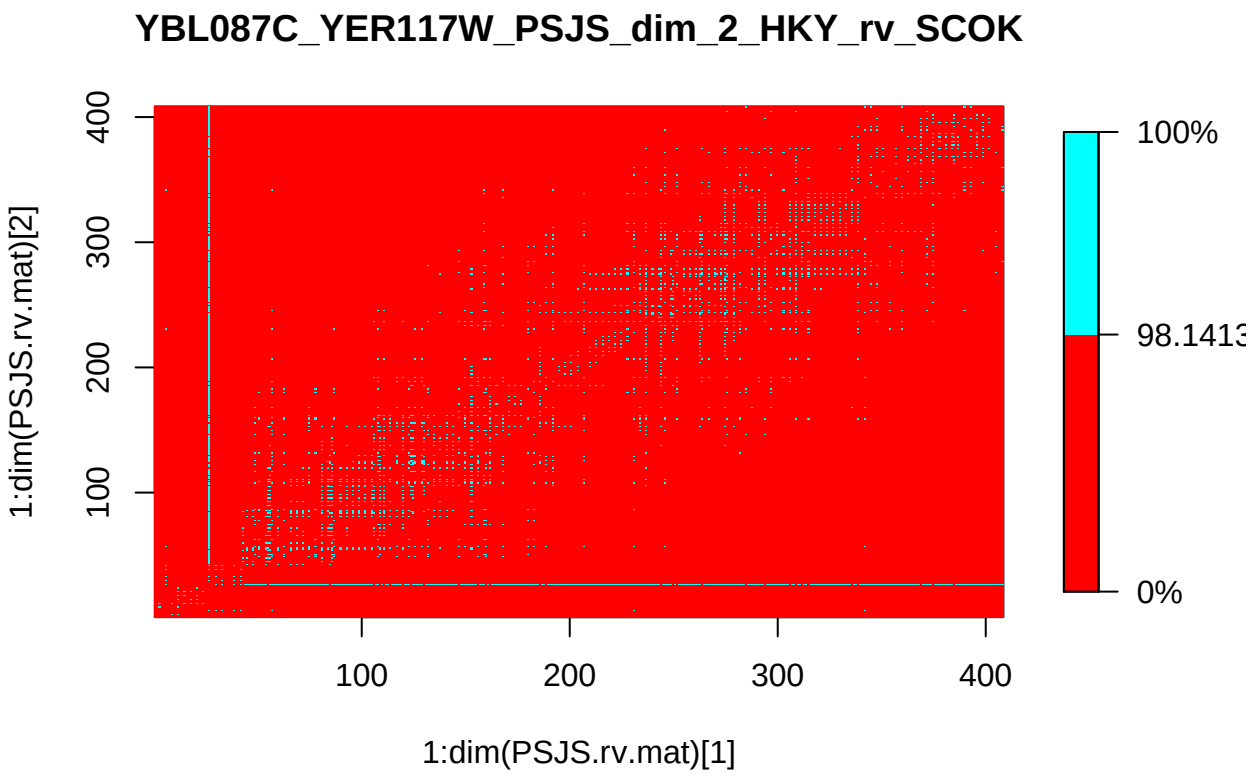

```
## [1] -0.583757669  0.004098361  1.320910183
```



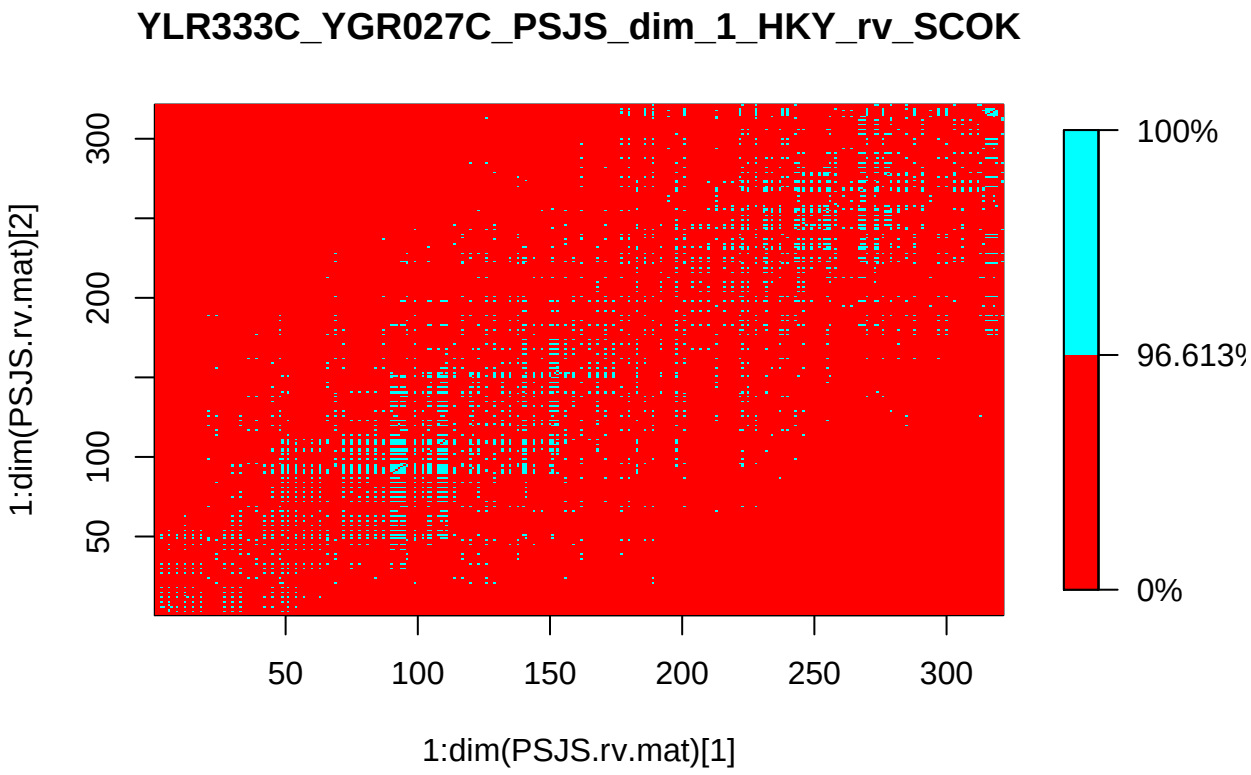

```
## [1] -0.572314332  0.004098361  1.304565473
```



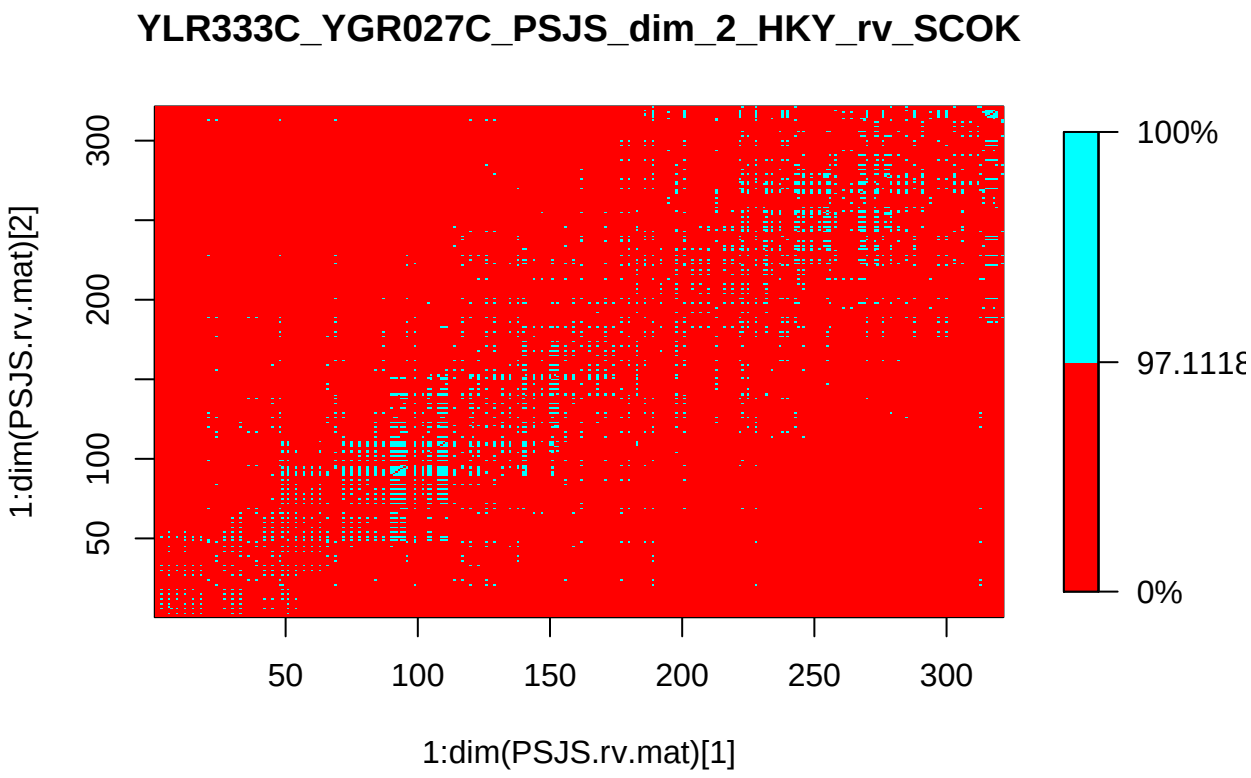

```
## [1] -3.219742257  0.004914005  2.544457671
```



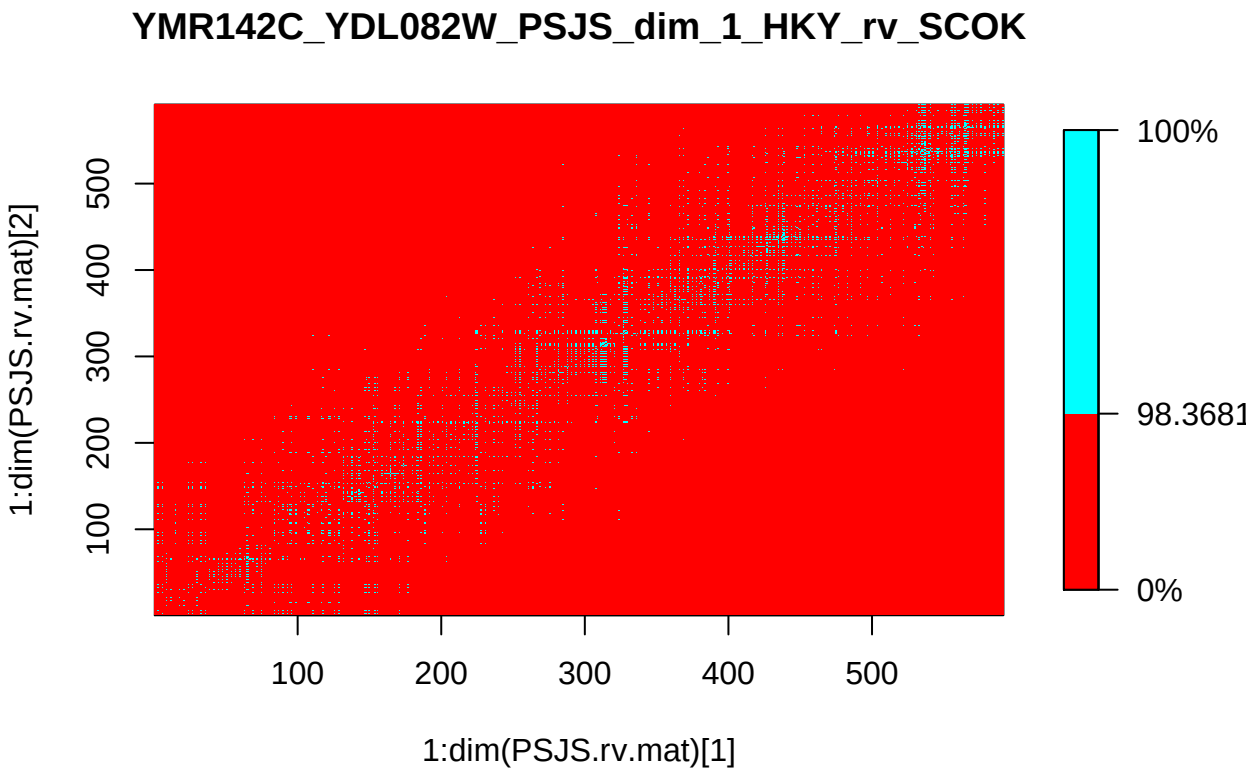

```
## [1] -3.267188668  0.004914005  2.584016827
```



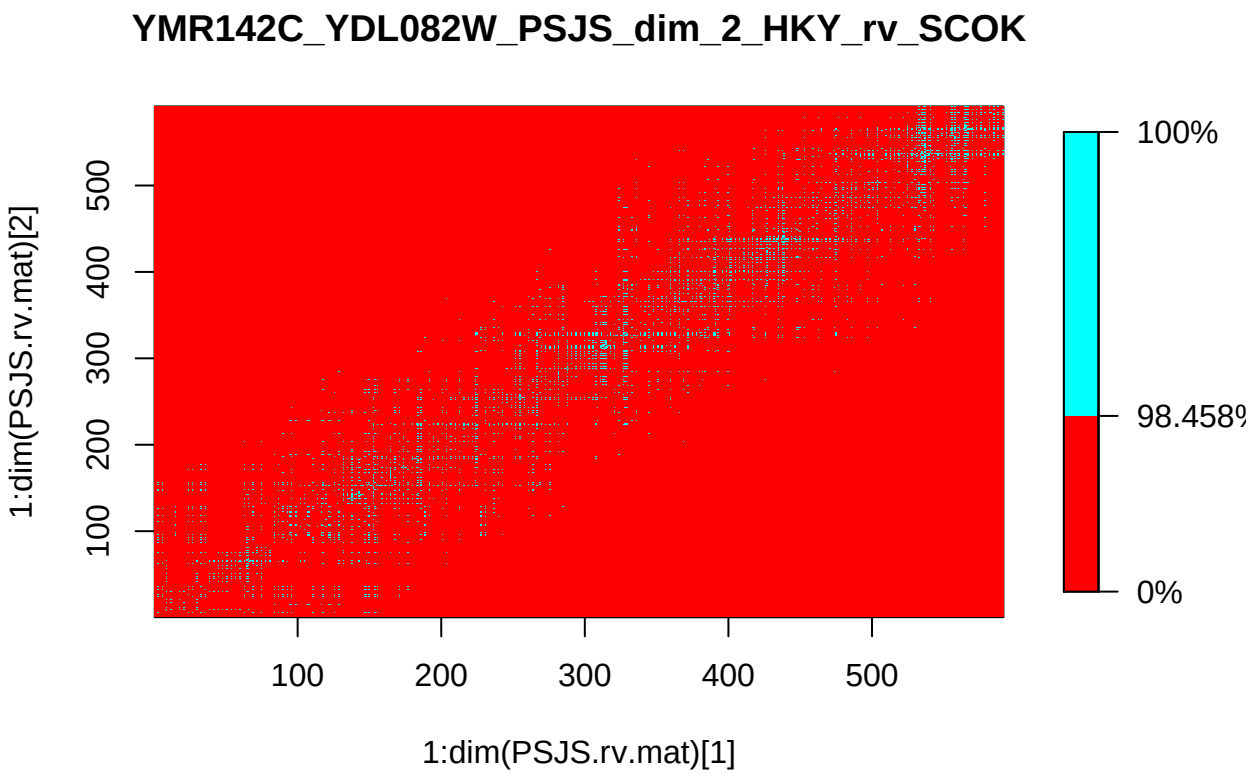

```
## [1] -1.683991  0.006250  1.625640
```



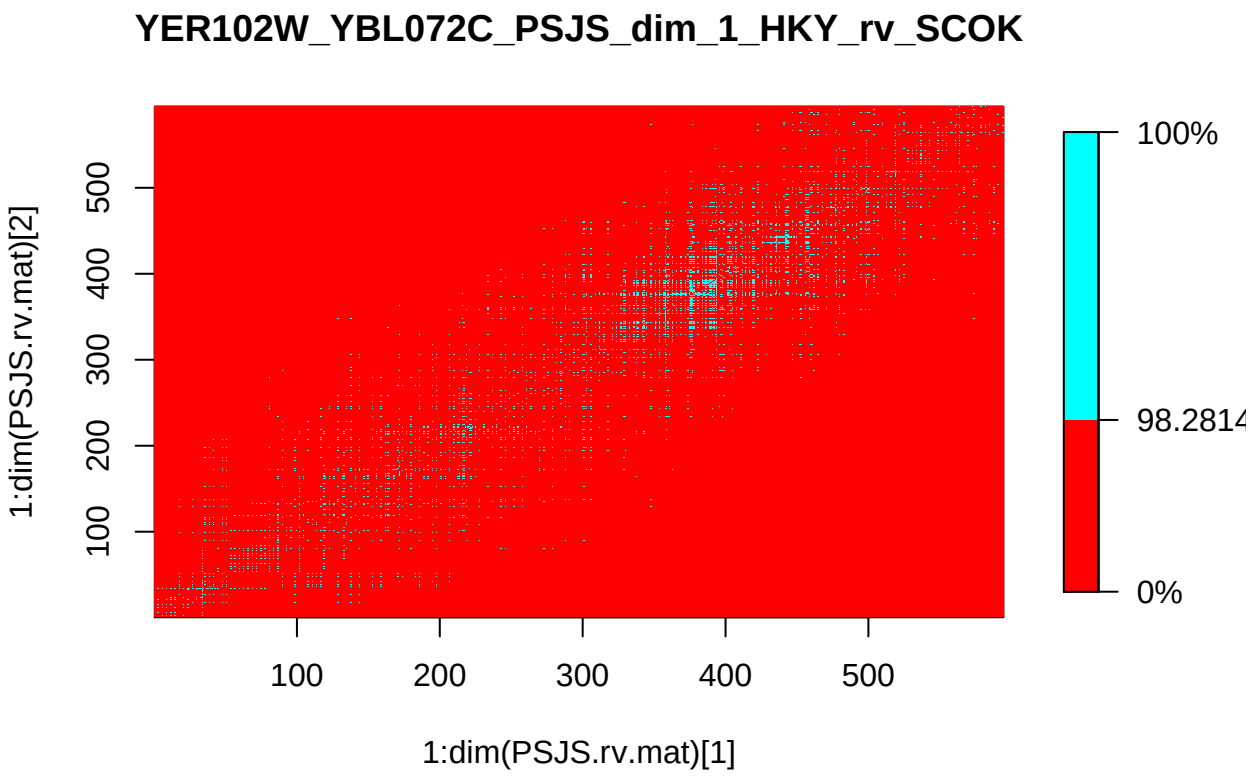

```
## [1] -1.584701  0.006250  1.602585
```



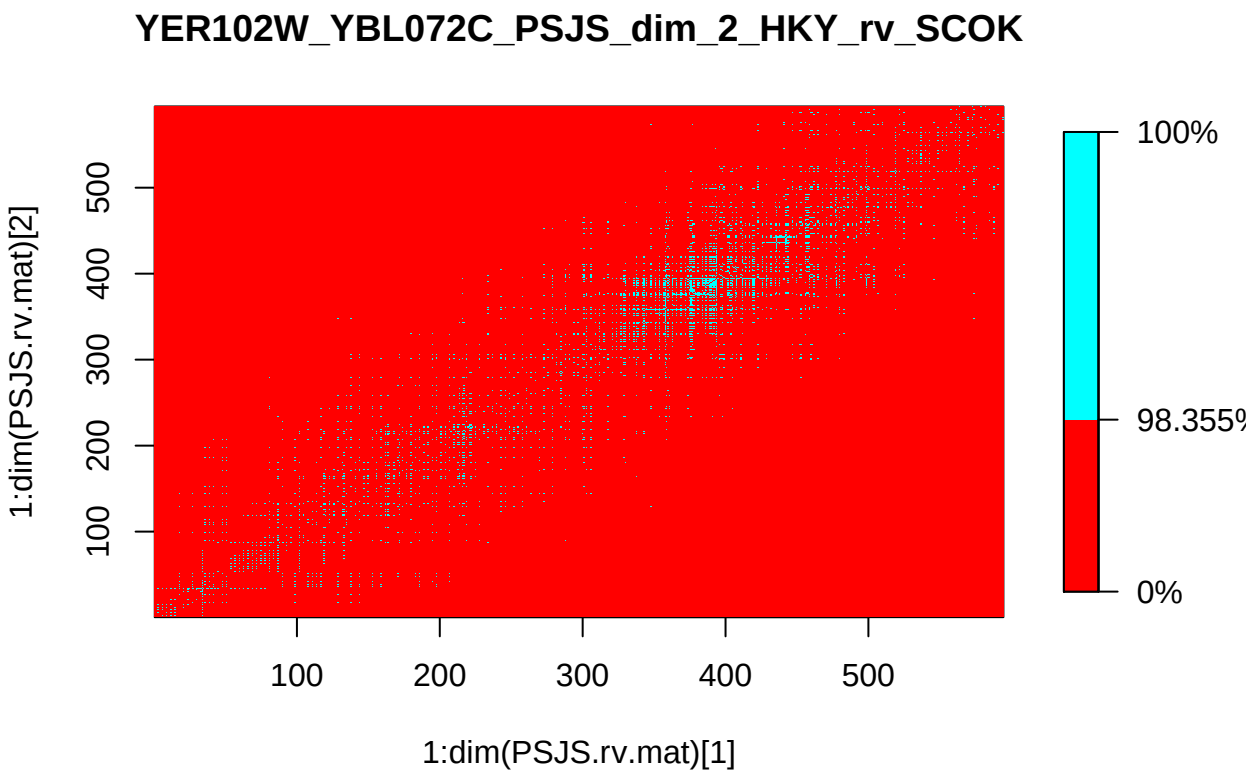

```
## [1] -2.654814234  0.003389831  4.284486594
```




```
## [1] -2.634653092  0.003389831  4.266588219
```




```
## [1] -2.415880366  0.003372681  4.057570353
```




```
## [1] -2.399946800  0.003372681  4.024576483
```

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_
#   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_
#   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 =
#   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 = "/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
                  PSJS.HKY.rv.SCOK.dim.2.nonclock.summary["tract_length",] * PSJS.HKY.rv.SCOK.dim.2.non
  * 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 13:39:42 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}
```