

Examples of using the plotMSY

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- R version 3.0.2 (2013-09-25), `x86_64-redhat-linux-gnu`
- Base packages: base, datasets, graphics, grDevices, grid, methods, stats, utils
- Other packages: data.table 1.8.8, FLCore 2.5.20140123, ggplot2 0.9.3.1, gridExtra 0.9.1, knitr 1.2, lattice 0.20-15, lubridate 1.3.0, MASS 7.3-27, mgcv 1.7-27, msy 0.1.10, nlme 3.1-110, plyr 1.8, R2admb 0.7.10, RColorBrewer 1.0-5, reshape2 1.2.2, scales 0.2.3, scam 1.1-6, stringr 0.6.2, xtable 1.7-1
- Loaded via a namespace (and not attached): colorspace 1.2-2, dichromat 2.0-0, digest 0.6.3, evaluate 0.4.4, formatR 0.8, gtable 0.1.2, labeling 0.2, Matrix 1.0-12, munsell 0.4.2, proto 0.3-10, stats4 3.0.2, tools 3.0.2

```
[1] "This document was created in knitr"
```

1 plotMSY

2 Quick start

Compiling and running

Compile:

```
srmsync_compile()
```

Convert FLStock object to srmsync data files, use last three years as the basis for biological and selection information (not done here, use prepared .dat files):

```
stk <- icesStocks$codNS
#FLS2srmsync(stk,y=3,"codNS","age.dat",1)
cmd <- paste('cp',paste(path.package("msy"),'extdata/age.dat',sep='/'),'.')
system(cmd)
cmd <- paste('cp',paste(path.package("msy"),'extdata/srmsync.dat',sep='/'),'.')
system(cmd)
rby <- fls2rby(stk)
rby[,c(1,2,4,5)] <- rby[,c(1,2,4,5)]/1e3
```

Run the srmsync

```
srmsync_run(sr=1,path="ricker",echo=FALSE, windose=FALSE)
srmsync_run(sr=2,path="bevholt",echo=FALSE, windose=FALSE)
srmsync_run(sr=3,path="segreg",echo=FALSE, windose=FALSE)
```

Standard plots

Plot the ssb recruitment fits (png files):

```
srmsync_plotcomposit_ssbr(rby)
```

Plot the refs and yield and ssb as a function of fishing mortality (png file):

```
srmsync_plotcomposit_yield(path="ricker",rby=rby)
srmsync_plotcomposit_yield(path="bevholt",rby=rby)
srmsync_plotcomposit_yield(path="segreg",rby=rby)
```

Plot mortality distributions (png files):

```
srmsync_plotcomposit_mort()
srmsync_plotcomposit_mort("equal")
```

Standard output

3 Slow reading

Compiling the ADMB code

The uncompiled srmsync ADMB-codes come with the **msy-package**. They can be located on your computer using the following command:

```
paste(path.package("msy"), "tpl", sep="/")
```

To compile the code as well as for further communication with the program you need to have the **R2admb** library installed and loaded as well of course the ADMB-program itself. Once these are in place compiling the code is done by:

```
srmsync_compile()
```

This command copies the tpl-files (uncompiled ADMB codes, named srmsync.tpl and srmsync2.tpl) into your current working directory and compiles them. You should now have four new files in the working directory, the two .tpl files and then srmsync and srmsync2 (or if on windose srmsync.exe and srmsync2.exe). I.e. you should have something like this in your directory:

```
## [1] "srmsync"      "srmsync.dat"  "srmsync.tpl"  "srmsync2"
## [5] "srmsync2.tpl"
```

The data files

The srmsync programs read data from separate files. Examples are provided with the **msy-package** in the following directory your computer using the following command:

```
paste(path.package("msy"), "extdata", sep="/")
```

Example output of these files are provided in the appendix. Further information about the meaning of various xxx can be found in xxxx.

4 ggplot2 doodles

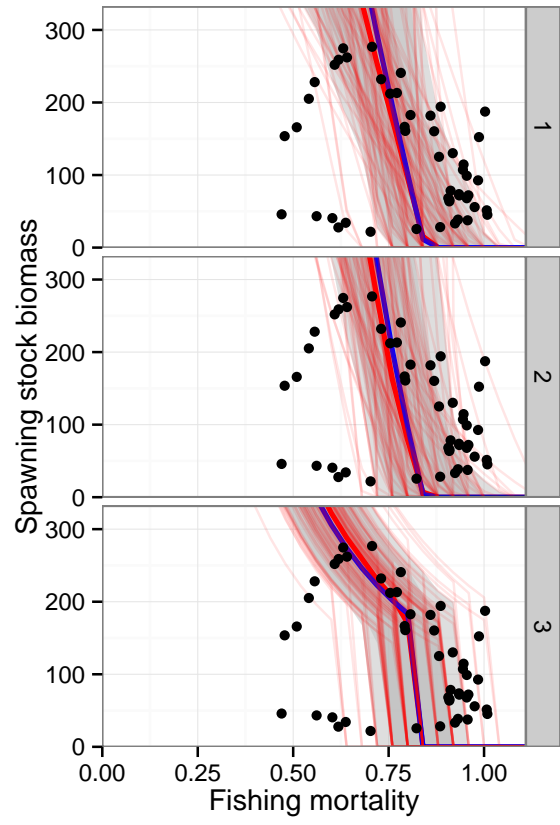
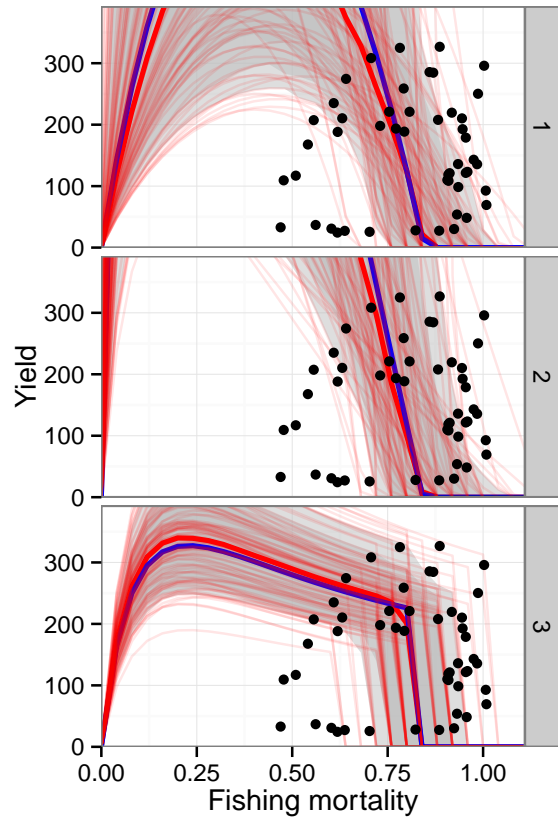
```
x1 <- srmsymc_read_yield("ricker")
x2 <- srmsymc_read_yield("bevholt")
x3 <- srmsymc_read_yield("segreg")
qs <- rbind(x1$quantiles,x2$quantiles,x3$quantiles)
d <- rbind(x1$stochastic,x2$stochastic,x3$stochastic)

plotTEST <- function(type="yield") {
  if(type == "yield") {
    x1 <- srmsymc_read_yield("ricker")
    x2 <- srmsymc_read_yield("bevholt")
    x3 <- srmsymc_read_yield("segreg")
  }
  if(type == "ssb") {
    x1 <- srmsymc_read_ssb("ricker")
    x2 <- srmsymc_read_ssb("bevholt")
    x3 <- srmsymc_read_ssb("segreg")
  }

  qs <- rbind(x1$quantiles,x2$quantiles,x3$quantiles)
  d <- rbind(x1$stochastic,x2$stochastic,x3$stochastic)

  p <- ggplot(qs,aes(variable)) +
    geom_ribbon(aes(ymin=q05,ymax=q95),fill='grey',alpha=1/2) +
    geom_ribbon(aes(ymin=q10,ymax=q90),fill='grey',alpha=1/2) +
    geom_ribbon(aes(ymin=q16,ymax=q84),fill='grey',alpha=1/2) +
    geom_line(aes(y=q50),col='red',lwd=1) +
    geom_line(aes(y=mean),col='blue',lwd=1) +
    geom_line(data=d,aes(variable,value,group=iter),alpha = 0.1,col='red') +
    facet_grid(srno ~ .)
  return(p)
}

p1 <- plotTEST("yield") + geom_point(data=rby,aes(fbar,landings)) +
  coord_cartesian(xlim=c(0,1.1*max(rby$fbar)),ylim=c(0,1.2*max(rby$landings))) +
  labs(x="Fishing mortality",y="Yield")
p2 <- plotTEST("ssb") + geom_point(data=rby,aes(fbar,ssb)) +
  coord_cartesian(xlim=c(0,1.1*max(rby$fbar)),ylim=c(0,1.2*max(rby$ssb))) +
  labs(x="Fishing mortality",y="Spawning stock biomass")
vplayout <- function(x, y) viewport(layout.pos.row = x, layout.pos.col = y)
pushViewport(viewport(layout = grid.layout(1, 2)))
print(p1, vp=vplayout(1,1))
print(p2, vp=vplayout(1,2))
```



APPENDIX They look like this:

```
readLines("ricke/srmsymc.dat")

## [1] "# Header: Some nice description"
## [2] "codNS # stkname: Name of the stock"
## [3] "age.dat # filename: Name of the option file (2nd file"
## [4] "1963 # ybeg: First year (yearRange[1])"
## [5] "2011 # yend: Last year (yearRange[2])"
## [6] "1 # r: Recruitment age (senhead[1])"
## [7] "7 # A: Plus group age (senhead[2])"
## [8] "1 # Ropt: S-R function type"
## [9] "1 # simopt: 0=no simulation, 1=simulation (ifelse(nits==0,0,1))"
## [10] "1 # senopt"
## [11] "1 # penopt"
## [12] "# r ssb"
## [13] " 465.56 151.90"
## [14] " 852.56 164.23"
## [15] "1069.82 203.82"
## [16] "1379.18 227.29"
## [17] "1271.87 251.45"
## [18] " 656.71 262.24"
## [19] " 606.22 258.59"
## [20] "1839.49 273.76"
## [21] "2369.05 276.23"
## [22] " 584.20 241.35"
## [23] " 875.02 213.20"
## [24] " 807.74 232.35"
## [25] "1377.80 212.99"
## [26] " 849.16 182.96"
## [27] "2096.96 161.14"
## [28] "1271.87 160.33"
## [29] "1435.47 166.71"
## [30] "2273.88 181.50"
## [31] " 885.58 194.66"
## [32] "1407.04 188.34"
## [33] " 819.13 154.97"
## [34] "1426.88 132.46"
## [35] " 378.51 126.63"
## [36] "1692.98 115.73"
## [37] " 671.32 108.99"
## [38] " 462.31 100.61"
## [39] " 767.58 94.28"
## [40] " 333.70 80.18"
## [41] " 370.28 73.64"
## [42] " 792.54 71.11"
## [43] " 446.86 68.60"
## [44] " 944.11 72.11"
## [45] " 557.94 81.06"
## [46] " 403.53 79.22"
## [47] "1059.17 75.21"
## [48] " 170.59 61.27"
## [49] " 303.46 55.94"
## [50] " 548.53 49.66"
## [51] " 208.98 41.73"
## [52] " 255.76 42.57"
## [53] " 119.13 36.90"
## [54] " 200.19 31.98"
## [55] " 137.45 29.76"
```

```
## [56] " 344.90  26.24"
## [57] " 147.12  32.83"
## [58] " 178.80  38.25"
## [59] " 191.19  47.19"
## [60] " 326.44  51.79"
## [61] " 165.71  56.33"
```

and:

```
readLines("ricker/age.dat")

## [1] "#Header: Some nice description"
## [2] "2 # fno: Number of fleets (nstocks)"
## [3] "1 # sno: Fleets for yield per recruit stats (always 1)"
## [4] "0 # f: proportional fishing mortality before spawning time (pf)"
## [5] "0 # m: proportional natural mortality before spawning time (pm)"
## [6] "# Selection pattern"
## [7] "0.0273348519362187 0.2186788154897490 "
## [8] "0.3006833712984050 0.4783599088838270 "
## [9] "0.8251708428246010 0.2716400911161730 "
## [10] "1.0216400911161700 0.1025056947608200 "
## [11] "1.1070615034168600 0.0358769931662870 "
## [12] "1.1924829157175400 0.0307517084282460 "
## [13] "1.1788154897494300 0.0444191343963554 "
## [14] "# cv Selection pattern"
## [15] "0.175 0.175 "
## [16] "0.097 0.097 "
## [17] "0.076 0.076 "
## [18] "0.079 0.079 "
## [19] "0.085 0.085 "
## [20] "0.109 0.109 "
## [21] "0.109 0.109 "
## [22] "# Weight at age"
## [23] "0.747 0.286 "
## [24] "1.306 0.755 "
## [25] "2.634 1.726 "
## [26] "4.236 3.542 "
## [27] "6.104 5.964 "
## [28] "7.642 6.674 "
## [29] "9.701 8.823"
## [30] "# cv Weight at age"
## [31] "0.112 0.255 "
## [32] "0.143 0.282 "
## [33] "0.137 0.419 "
## [34] "0.097 0.542 "
## [35] "0.062 0.480 "
## [36] "0.050 0.345 "
## [37] "0.040 0.792 "
## [38] "# Biological data"
## [39] "#      M,      mat,      wSSB"
## [40] "1.0385 0.01 0.339"
## [41] "0.6975 0.05 0.964"
## [42] "0.4895 0.23 2.404"
## [43] "0.2325 0.62 4.173"
## [44] "0.2000 0.86 6.112"
## [45] "0.2000 1.00 7.647"
## [46] "0.2000 1.00 9.770"
## [47] "# cv Biological data"
```

```
## [48] "# cvM, cvmat, cvwSSB"  
## [49] "0.1 0.0 0.112"  
## [50] "0.1 0.1 0.143"  
## [51] "0.1 0.1 0.137"  
## [52] "0.1 0.1 0.097"  
## [53] "0.1 0.0 0.062"  
## [54] "0.1 0.0 0.050"  
## [55] "0.1 0.0 0.040"
```