Biomass dynamic models with FLBioDym

Ispra, 18th - 22nd March, 2013

Install FLBioDym
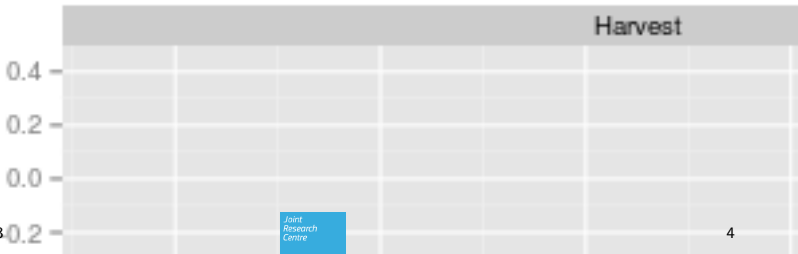
```
install.packages("FLBioDym", repos = "http://flr-project.o
```

FLBioDym

- Pella-Tomlinson (generalizes biomass dynamic models)
  - B[t+1] = B[t] + r/p$B[t]$(1-(B[t]/k)^p)) - C[t]
  - Schaeffer with $p = 1$
  - Fox with $p \sim 0$
- Interfaces with ADMB for model fit

Example

```
library(FLBioDym)
data(ple4)
ple4.bd <- FLBioDym(catch = catch(ple4), index = stock(ple4

plot(ple4.bd)
```

Joint
Research
Centre

Fitting

```r
bounds(ple4.bd)   # ple4.bd@bounds
```

```
##
## param    phase lower upper start
##   r          1    NA    NA    NA
##   k          1    NA    NA    NA
##   p          1    NA    NA    NA
##   b0         1    NA    NA    NA
##   q          1    NA    NA    NA
##   sigma      1    NA    NA    NA
```

```r
ple4.bd@bounds[, "start"] <- 10
ple4.bd@bounds[, "lower"] <- 0.1
ple4.bd@bounds[, "upper"] <- 1e+08
ple4.bd <- admbBD(ple4.bd)
```

A bit more on fitting

```
# trying different starting values and boundaries
bounds <- bounds(ple4.bd)
bounds["r", "start"] = 0.1
bounds["k", "start"] = max(catch(ple4.bd)) * 3
bounds["sigma", "start"] = 0.5
bounds["q", "start"] = 1
bounds["b0", "start"] = 0.2
bounds["p", "start"] = 1
bounds[, "lower"] = bounds[, "start"] * 0.1
bounds[, "upper"] = bounds[, "start"] * 10
ple4.bd@bounds <- bounds
ple4.bd <- admbBD(ple4.bd)
params(ple4.bd)
```

An object of class "FL

Playing with phase

```
# trying different starting values and boundaries
bounds["p", "phase"] = -1
ple4.bd@bounds <- bounds
ple4.bd <- admbBD(ple4.bd)
params(ple4.bd)

## An object of class "FLPar"
## params
##          r          k          p          b0          q
## 6.0239e-01 2.9123e+05 1.0000e+00 4.4088e-01 6.2797e+00 4
## units:  NA

plot(ple4.bd)
```

Exercise

Please do better and let me know ...