

stacomIR : a common tool for monitoring fish migration

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Software

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Summary

Migratory fish (like eel, salmon, shad or lamprey) are patrimonial species with cultural, scientific and economical strong interest (Keith et al. 2011). Migratory fishes population are vulnerable as they are often more prone to human impact when migrating in rivers and to the ocean (McDowall 1992). They are often counted at stations when they perform the migrations at some of their lifestages, and these counts provide valuable indices to the population size and trend. The objective of the stacomir project is to provide a common database for people monitoring fish migration, so that data from watershed are shared, and stocks exchanging between different basins are better managed. The stacomir database, is an open-source database, it managed with a JAVA interface, and results from that database are treated directly with the stacomIR package (R Core Team 2017). The program is intended to be used by a “non experienced” R user, but all the R code automatically generated by the programm is shown to the user. Thus, it is possible to copy/paste the code and modify it (for example to change the preprogrammed colors or make more complicated changes). The package is available from CRAN and a development version is available from R-Forge.

Installation

```
install.packages("stacomIR") # get the package from CRAN
install.packages("stacomIR", repos="http://R-Forge.R-project.org") # get the devel
library(stacomIR)
```

Launch the graphical interface

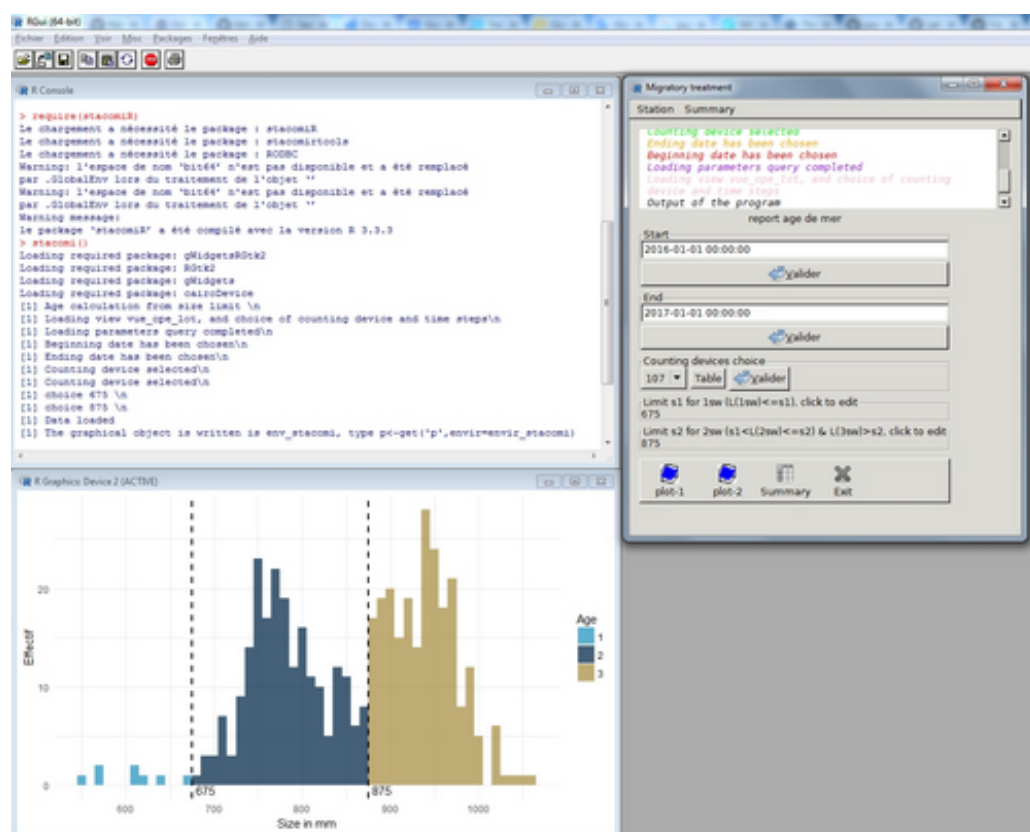
```
## For user having the stacomir database
```

```
stacomir()
```

```
## For user without connection to the database
```

```
stacomir(gr_interface=FALSE,login_window=FALSE,database_expected=FALSE)
```

Launching `stacomir()` will create the interface. The interface looks like :

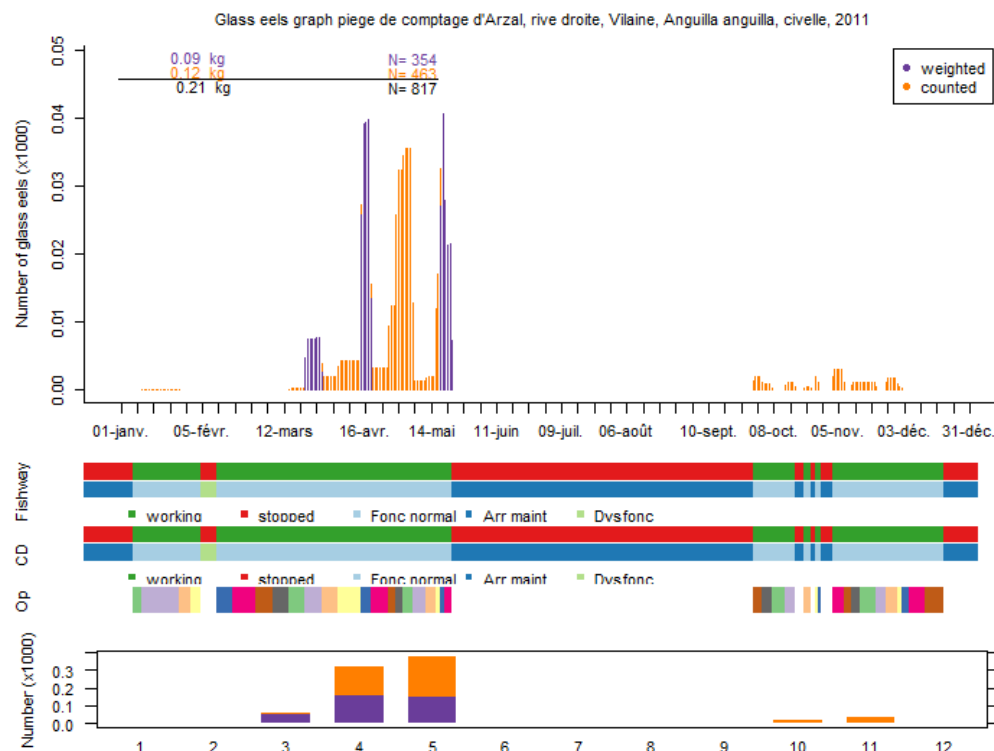


Below as an example, the glass eel migration at a glass eel trapping ladder located at the Arzal dam in the Vilaine river (France), in weight and number (top), the periods and type of operation for the fishway (DF) and the counting device (DC), and the operation (trapping periods) (middle), a summary of migration per month (bottom).

```
# Without a connection at the database we can launch these lines to generate the g
# To obtain titles in french use Sys.setenv(LANG = "fr")
data("r_mig_mult")
data("r_mig_mult_ope")
assign("report_ope",r_mig_mult_ope,envir=envir_stacomir)
data("r_mig_mult_df")
assign("report_df",r_mig_mult_df,envir=envir_stacomir)
data("r_mig_mult_dc")
assign("report_dc",r_mig_mult_dc,envir=envir_stacomir)
r_mig_mult<-calculer(r_mig_mult,silent=TRUE)

# To avoid call to dev.new() which creates a device per stage, DC, taxa, we simpli
# the object:
r_mig_mult@taxa@data<- r_mig_mult@taxa@data[1,]
r_mig_mult@stage@data<-r_mig_mult@stage@data[3,]
r_mig_mult@dc@dc_selectionne<-r_mig_mult@dc@dc_selectionne[3]

plot(r_mig_mult,plot.type="standard",silent=TRUE)
```



References

- Keith, P., H. Persat, E Feunteun, and J. (coords) Allardi. 2011. *Les Poissons d'eau Douce de France - Biotope Editions*. Biotope -Museum national d'Histoire naturelle. Inventaires et Biodiversite. <http://www.biotope-editions.com/index.php?article58/les-poissons-d-eau-douce-de-france>.
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- R Core Team. 2017. *R: A Language and Environment for Statistical Computing*. Vienna, Austria: R Foundation for Statistical Computing. <https://www.R-project.org/>.