

# stacomir : a common tool for monitoring fish migration

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## Software

- [Review](#) ↗
- [Repository](#) ↗
- [Archive](#) ↗

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## Summary

Migratory fish (like eel, salmon, shad or lamprey) are patrimonial species with cultural, scientific and economical strong interest (Keith, Persat, Feunteun, & Allardi, 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. In France, this kind of data are collected by various organizations (e.g. Migratory Associations, Amateur Fishing Federations, public institutions or research laboratories) whose purpose is to monitor fish during a long-time period. To our knowledge, there is no structured database for these data.

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, data can be accessed and updated with a JAVA interface, and results can be analyzed with the stacomirR package (R Core Team, 2017). Data ownership obviously remains that of producers and only producers can decide whether or not they want to make their data available and in which context. However, the R package is an excellent tool to share information and to compare data across multiple stations and watersheds.

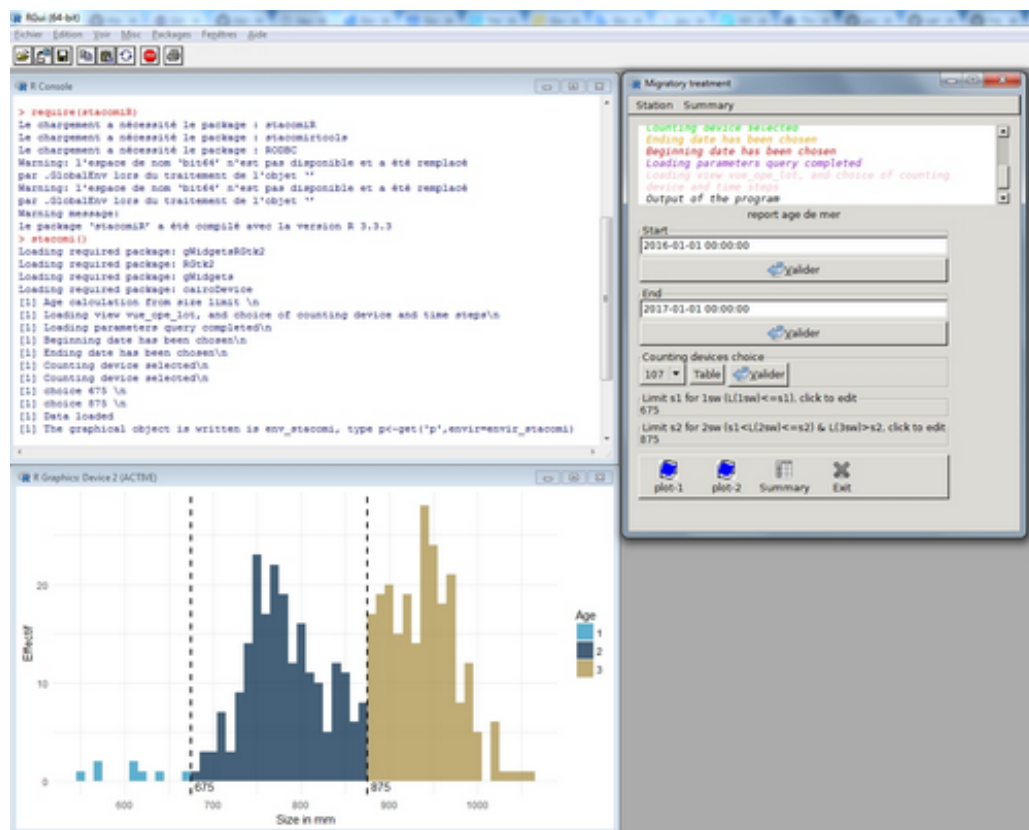
In 2018, the Stacomir project was used by people monitoring fish migration throughout France and some Spanish producers have started to use it as well. All messages delivered by the R program are available in French and in English. Some messages are also available in Spanish. The program is intended to be used both by “non experienced” R user (through a graphical interface) and people more familiar with R (through command line). All the R code automatically generated by the program 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 can be downloaded from R-Forge. To provide some help on how this package works we developed a vignette.

```
# Installation
# Get the package from CRAN
install.packages("stacomirR")
# Get the development version
install.packages("stacomirR", repos="http://R-Forge.R-project.org")

# Have a look at the vignette
library(stacomirR)
vignette("stacomir")
```

```
# Launch the graphical interface
## For user having the stacomis database
stacomis()
## For user without connection to the database
stacomis(gr_interface=FALSE,login_window=FALSE,database_expected=FALSE)
```

Launching `stacomis()` will create the interface (if the [database provided](#) in the github installation folder is installed). The interface looks like :



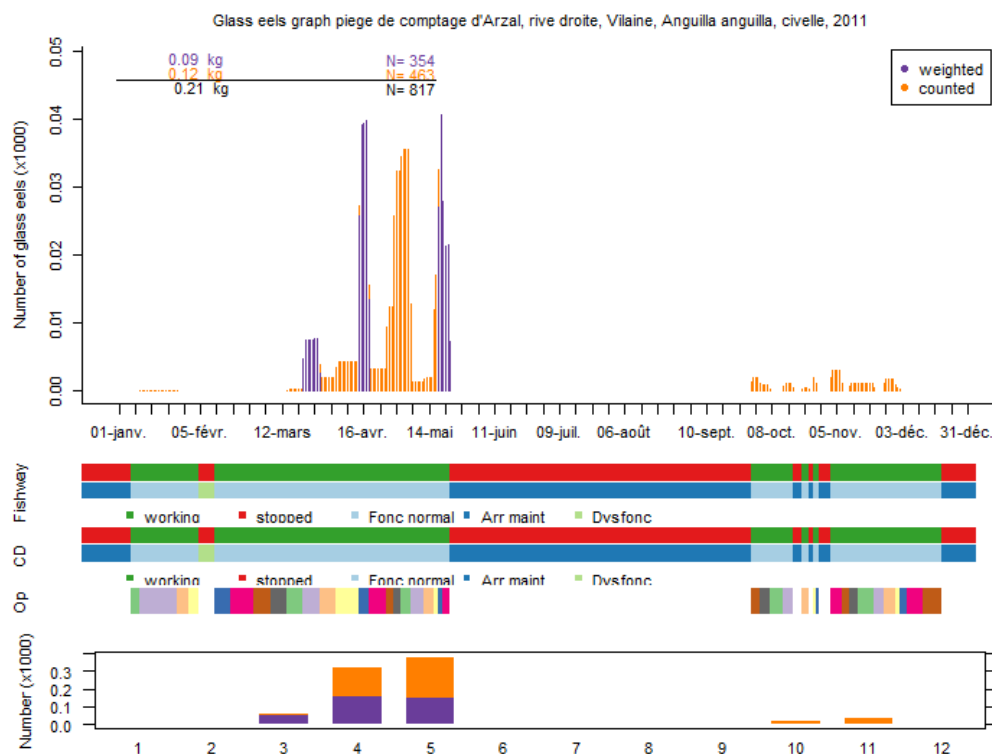
Below as an example, the glass eel migration at a glass eel trapping ladder located at the Arzal dam in the Vilaine river (France), in weight and number (top), the periods and type of operation for the fishway (DF) and the counting device (DC), and the operation (trapping periods) (middle), a summary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

```
# Without a connection at the database we can launch these lines
# to generate the graph.
# To obtain graphic titles in english uncomment the following line
#Sys.setenv(LANG = "en")
data("r_mig_mult")
data("r_mig_mult_ope")
assign("report_ope",r_mig_mult_ope,envir=envir_stacomis)
data("r_mig_mult_df")
assign("report_df",r_mig_mult_df,envir=envir_stacomis)
data("r_mig_mult_dc")
assign("report_dc",r_mig_mult_dc,envir=envir_stacomis)
r_mig_mult<-calculer(r_mig_mult,silent=TRUE)

# To avoid call to dev.new() which creates a device per stage,
```

```
# DC, taxa, we simplify 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., Persat, H., Feunteun, E., & Allardi, J. (. (2011). *Les Poissons d'eau douce de France - Biotope editions*. Inventaires et Biodiversite (Biotope -Museum national d'Histoire naturelle.). Retrieved from <http://www.biotope-editions.com/index.php?article58/les-poissons-d-eau-douce-de-france>
- McDowall, R. M. (1992). Particular problems for the conservation of diadromous fish. *Aquatic Conservation: Marine and Freshwater Ecosystems*, 2(4), 351–355. doi:10.1002/aqc.3270020405
- R Core Team. (2017). *R: A language and environment for statistical computing*. Vienna, Austria: R Foundation for Statistical Computing. Retrieved from <https://www.R-project.org/>