Garcia Program Description

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What you will learn in this presentation

- How to use github
- How to use R
- How to compute MRE's in R
- How to compute CYER's in R

Downloading requisite files directly from github

Downloading requisite files from github via R

install.packages("pkgbuild") # pkgbuild is not available (for R version 3.5.0) install.packages("devtools") # make sure you have the latest version from CRAN library(devtools) # load package devtools::install_github("r-lib/pkgbuild") # install updated version of pkgbuild from GitHub library(pkgbuild) # load package find_rtools() # should be TRUE, assuming you have Rtools 3.5 devtools::install_github("eriqande/rubias") installed.packages()["rubias", "Version"] # must be "0.1.0.900" in order to handle haploid data library(rubias) # load package and use!

MRE Calculations

- What you'll need

ERA output Fishery lookup file Escapement data Stock lookup file R functions

- Options

Load R functions

```
source("Code/GarciaFunLibrary.R")
```

Reading ERA output into R

```
#Read in HRJ files in a directory
 by=readHRJdir(userDir="Data/", nFisheries=79,
                straysinescap=TRUE, Age6="include")
```

```
## Reading 1 HRJ File of 4 : LYFB1.HRJ
## Reading 2 HRJ File of 4 : LYFC1.HRJ
## Reading 3 HRJ File of 4 : SRHB1.HRJ
## Reading 4 HRJ File of 4 : SRHC1.HRJ
```

```
#Convert to CY layout
 cy=convertHRJ_BYtoCY(x=by)
#Convert HRJ from R to Access format
 z.cy=convertHRJ_RtoAccess(x=cy, writeCSV=FALSE, userDir=N
#add the 'preferred' table to the Access format
 z.cy = addPTableHRJ(x=z.cy, hrjclass = "Access")
```

readHRJdir()

```
readHRJdir(userDir="Data/", nFisheries=79,
                  straysinescap=TRUE, Age6="include")
```

convertHRJ_BYtoCY()

```
convertHRJ_BYtoCY(x=by)
```

convertHRJ_RtoAccess()

```
convertHRJ_RtoAccess(x=cy, writeCSV=FALSE, userDir=NULL)
```

convertHRJ_RtoAccess()

```
addPTableHRJ(x=z.cy, hrjclass = "Access")
```

Slide with Plot

```
plot(pressure)
```