

# Package ‘IRATER’

October 26, 2016

**Type** Package

**Title** A R Interface for the Instantaneous RATEs (IRATE) Model

**Version** 0.0.1

**Date** 2016-10-24

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**Description** A R interface to setup, run and read IRATE model runs to assess band recovery (conventional tagging) data (i.e. age-dependent or independent fishing and natural mortality rates).

**Depends** R (>= 3.0.1)

**Imports** coda, lattice, R2admb, plyr, stats

**SystemRequirements** AD Model Builder <<http://admb-project.org>>

**License** GPL

**LazyLoad** yes

**Repository** CRAN

**Date/Publication** 2016-10-26 10:07:56

**NeedsCompilation** no

## R topics documented:

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clean.admb	<i>delete IRATE (ADMB) run files</i>
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### Description

delete IRATE (ADMB) run files (not model setup files).

### Usage

```
clean.admb(setup.name)
clean.IRATE(setup.name)
```

### Arguments

setup.name	Character string defining preinstalled IRATE example setups/datasets to be run. If missing or not valid, the user will be asked to choose among valid examples. Check IRATE.examples() for valid, preinstalled IRATE examples.
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### Author(s)

Robert K. Bauer

### See Also

[compile\\_admb](#), [run\\_admb](#), [IRATE.examples](#)

### Examples

```
example.setup <- IRATE.examples()
new.setup <- new.setup.path <- example.setup[1] # select old IRATE setup to reparameterize
print(new.setup) # print setup name to be run
old.setup.path <- system.file(paste0("IRATE.examples/",new.setup,".dat"), package = "IRATER")

system(paste("mkdir -p ",new.setup.path)) # create run folder for new setup
system(paste("cp",old.setup.path, new.setup.path)) # copy old setup in new run folder
setwd(new.setup.path)

run.IRATE(new.setup) # compile and run setup
clean.IRATE(new.setup) # deletes run files (leaving only the setup file for reruns)
```

---

IRATE.examples      *list preinstalled IRATE examples*

---

**Description**

list preinstalled IRATE examples

**Usage**

IRATE.examples()

**Value**

**HoenigNonMixing** Age-dependent, harvest only (no catch-&-release) conventional tagging dataset from 1960-1964 of lake trout (*Salvelinus namaycush*), assuming an incomplete mixing of tagged fish with the wild population after being released. Based on: Hoenig et al. 1998 (incomplete mixing Table 4 for more details).

**JiangADCR** Age-dependent, harvest and catch-&-release conventional tagging dataset of Striped bass (*Morone saxatilis*) from 1991-2003, assuming an incomplete mixing of tagged fish with the wild population after being released (Similar to the JiangADH and JiangAICR data sets). Based on: Jiang et al., 2007 (Table 2 Model b).

**JiangADH** Age-dependent, harvest only (no catch-&-release) conventional tagging dataset of Striped bass (*Morone saxatilis*) from 1991-2003 (Similar to the JiangADH and JiangAICR data sets), assuming an incomplete mixing of tagged fish with the wild population after being released. Based on: Jiang et al., 2007b (Table 4 Model a).

**JiangAICR** Age-independent, harvest and catch-&-release conventional tagging dataset of Striped bass (*Morone saxatilis*) from 1991-2003 (Similar to the JiangADCR and JiangADH data sets). Based on Jiang Dissertation (Page 81 Model Fy,F'y,M91-99, M00-03).

**Author(s)**

Robert K. Bauer

**References**

Hoenig JM, Barrowman NJ, Pollock KH, Brooks EN, Hearn WS, Polacheck T. (1998) Models for tagging data that allow for incomplete mixing of newly tagged animals. *Canadian Journal of Fisheries and Aquatic Sciences* 55:1477-1483, doi: 10.1139/f97-258

Jiang H. (2005) Age-dependent tag return models for estimating fishing mortality, natural mortality, and selectivity. Ph.D. thesis, North Carolina State University, Raleigh

Jiang H, Pollock KH, Brownie C, Hightower JE, Hoenig JM, Hearn WS. (2007b) Age-dependent tag return models for estimating fishing mortality, natural mortality, and selectivity. *Journal of Agricultural, Biological, and Environmental Statistics* 12:177-194, doi: 10.1198/108571107X197382

Jiang H, Pollock KH, Brownie C, Hoenig JM, Latour RJ, Wells BK, Hightower JE. (2007) Tag return models allowing for harvest and catch and release: Evidence of environmental and management impacts on striped bass fishing and natural mortality rates. *North American Journal of Fisheries Management* 27:387-396, doi: 10.1577/M06-089.1

**See Also**

[run.IRATE.example](#) and [remake.dat](#) to change the model configuration of an existing IRATE-setup

**Examples**

```
IRATE.examples()
```

---

IRATER

*IRATER - A R Interface for the Instantaneous RATES (IRATE) Model*

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**Description**

**IRATE** is a software tool, developed by Dr. Gary Nelson, to analyze band recovery (conventional tagging) data. It can estimate fishing and natural mortality rates based on likewise estimated exploitation and survival rates of (continuous) fisheries. IRATE can handle both age-independent and age-dependent instantaneous rates models (Hoenig et al., 1998; Jiang et al., 2007) to be fitted to multi-year fish tag return data. IRATE allows model development with either age-dependent harvest-only or harvest and catch-release tag returns or similar age independent models. It also allows estimation of harvest reporting rates, catch and release reporting rates, and tag retention of harvested and/or released fish. However, not all parameters in the model can be estimated simultaneously with tag data alone. Some parameters must be fixed and assumed known (usually reporting rate and tag loss) to obtain good estimates of remaining parameters. Additionally, the model can account for non-mixing of the tagged fish in the first release year and adjust for harvest and M selectivity in the age-based models. The negative log likelihood is used as the objective function to obtain maximum likelihood estimates of parameters. Several model fit statistics are provided that can be used to select the best model formulation; these include the Akaike Information Criterion (AIC), c-hat (a measure of overdispersion) and standard residuals.

Source: <http://nft.nefsc.noaa.gov/IRATE.html>

IRATER is an interface to setup IRATE model runs and execute them from within R, using the ADMB engine of IRATE. It further provides functions to read and access the model results back into R.

**Major functions:**

- [make.dat](#): writes and sets up an input data set (setup file) for IRATE model runs
- [run.IRATE](#): compile and run IRATE model from within R
- [read.par](#) & [read.rep](#): read run results

**Getting Started**

Check out the help files of the principle functions, listed above.

**Author(s)**

Robert K. Bauer

## References

<http://nft.nefsc.noaa.gov/IRATE.html>

Jiang, H.H., K.H. Pollock, C. Brownie, J.M. Hoenig, R.J. Latour, B.K. Wells, and J.E. Hightower. 2007. Tag return models allowing for harvest and catch and release: evidence of environmental and management impacts on striped bass fishing and natural mortality rates. *N. Amer. J. Fish. Man.* 27: 387-396. doi: [10.1577/M06-089.1](https://doi.org/10.1577/M06-089.1)

Hoenig, J.M., N.J. Barrowman, W.S. Hearn, and K.H. Pollock. 1998. Multiyear tagging studies incorporating fishing effort data. *Can. J. Fish. Aquat. Sci.* 55: 1466-1476. doi: [10.1139/f97-256](https://doi.org/10.1139/f97-256)

Brownie, C., D.R. Anderson, K.P. Burnham, and D.S. Robson. 1985. Statistical inference from band recovery data: a handbook. Resource publication 156 (2nd edition), US Fish and Wildlife Service. 305 p.

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make.dat	<i>writes and sets up an input data set (setup file) for IRATE model runs</i>
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---

## Description

writes and sets up an input data set (setup file) for IRATE model runs. Obligatory arguments are: setup.file.name, releases and recapture

## Usage

```
make.dat(setup.file.name, releases, recaptures, age.dependent=F, only.harvested=F, HM
, eM=T, pM, sM, Mb # natural mortality settings
, eF=T, pF, sF, Fb # fishing mortality settings
, eT=T, pT, sT, Tb # tagging mortality settings
, combine.Hrr_and_Rrr=F # combine Harvest & Release reporting rates
, eHrr=F, pHrr, sHrr, Hrrb # Harvest reporting rates
, eRrr=F, pRrr, sRrr, Rrrb # Release reporting rates
, combine.HRS_and_RRS=F # combine Harvest & Release Retention Survival
, eHRS=F, pHRS, sHRS, HRSb # Harvest Retention Survival
, eRRS=F, pRRS, sRRS, RRSb # Release Retention Survival
, incomplete.mix=F, pNonMix, sNonMix, NonMixb # Non-Mixing
, combine.HS_and_RS=T # combine Harvest & Release Selectivity
, eHS=T, sHS, HSb # age-dependent Harvest Selectivity
, eRS=F, sRS, RSb # age-dependent Release Selectivity
, eMS=T, aMS, SMS # age-dependent M Selectivity
, use.L.const=T # Likelihood Constant
)

```

## Arguments

setup.file.name  
character string defining the name of the IRATE-model setup file (.dat) to be created.

releases	raw data.frame with release dates (rel.date in "Date"-format) as well as the age (numeric) of released individuals (if age dependent).
recaptures	raw data.frame with release & recapture dates (rel.date, rec.date in "Date"-format) as well as the age (numeric) of recaptured individuals and a vector harvested to indicate whether recaptured individuals were harvested or released (if age dependent).
age.dependent	whether setup file should be created for an age dependent model (default = TRUE).
only.harvested	optional, whether actual releases of recaptures should be treated as harvested or a release-recapture model should be defined. (default = TRUE).
HM	hooking-mortality value for each recapture year (default = 0.09), only required for release-recapture model, otherwise being ignored.
eM, pM, sM, Mb	eM: whether to estimate natural mortality (default = TRUE), if set TRUE: pM: beginning years of different natural mortality periods, sM: starting values of different natural mortality periods, Mb: natural mortality lower and upper boundary values for model runs.
eF, pF, sF, Fb	eF: whether to estimate fishing mortality (default = TRUE), if set TRUE: pF: beginning years of different fishing mortality periods, sF: starting values of different fishing mortality periods, Fb: fishing mortality lower and upper boundary values for model runs.
eT, pT, sT, Tb	eT: whether to estimate tagging mortality (default = TRUE), if set TRUE: pT: beginning years of different tagging mortality periods, sT: starting values of different tagging mortality periods, Tb: tagging mortality lower and upper boundary values for model runs.
combine.Hrr_and_Rrr	whether to combine Harvest & Release reporting rates (default = FALSE)
eHrr, pHrr, sHrr, Hrrb	eHrr: whether to estimate harvest reporting rates (default = FALSE), if set TRUE: pHrr: beginning years of different harvest reporting periods, sHrr: starting values of different harvest reporting periods, Hrrb: harvest reporting lower and upper boundary values for model runs.
eRrr, pRrr, sRrr, Rrrb	eRrr: whether to estimate release reporting rates (default = FALSE), if set TRUE: pRrr: beginning years of different release reporting periods, sRrr: starting values of different release reporting periods, Rrrb: release reporting lower and upper boundary values for model runs.
combine.HRS_and_RRS	whether to combine Harvest & Release Retention Survival (default = FALSE)
eHRS, pHRS, sHRS, HRSb	eHRS: whether to estimate harvest-retention survival rates (default = FALSE), if set TRUE: pHRS: beginning years of harvest-retention survival periods, sHRS: starting values of different-harvest retention survival periods, HRSb: lower and upper boundary values of harvest-retention survival rates for model runs.

eRRS, pRRS, sRRS, RRSb	eRRS: whether to estimate release-retention survival rates (default = FALSE), if set TRUE: pRRS: beginning years of release-retention survival periods, sRRS: starting values of different release-retention survival periods, RRSb: lower and upper boundary values of release-retention survival rates for model runs.
incomplete.mix, pNonMix, sNonMix, NonMixb	incomplete.mix: whether to assume incomplete mixing of tagged and wild population (default = FALSE), if set TRUE: pNonMix: beginning years of incomplete mixing periods, sNonMix: starting values of incomplete mixing periods, NonMixb: of release-retention survival rates lower and upper boundary values for model runs.
combine.HS_and_RS	whether to combine Harvest & Release Selectivity (default = TRUE)
eHS, sHS, HSb	eHS: whether to estimate age-dependent harvest selectivity rates (default = FALSE), if set TRUE: sHS: starting values of age-dependent harvest selectivity periods, HSb: lower and upper boundary values of age-dependent harvest selectivity rates for model runs.
eRS, sRS, RSb	eRS: whether to estimate age-dependent release selectivity rates (default = FALSE), if set TRUE: sRS: starting values of age-dependent release selectivity periods, RSb: lower and upper boundary values of age-dependent release selectivity rates for model runs.
eMS, aMS, SMS	eMS: whether to estimate age-dependent natural mortality rates (default = TRUE; only considered if age.dependent is set TRUE), if set TRUE: aMS: beginning age classes of age-dependent natural mortality rates (age classes are counted from 1 onwards irrespective of their age-values), SMS: starting values of (grouped) age-dependent natural mortality rates,
use.L.const	whether to set likelihood function constant (default = TRUE)

**Author(s)**

Robert K. Bauer

**References**<http://nft.nefsc.noaa.gov/IRATE.html>**See Also**To check model setup files in detail see: [read.dat](#).To alter existent model setup files see: [remake.dat](#).To read model run results see: [read.rep](#) and [read.par](#).For preinstalled example runs and setup data see: [run.IRATE.example](#).To delete run files see: [clean.IRATE](#).

For more information on admb model compilation and run prodcudres see: [compile\\_admb](#) and [run\\_admb](#) from the [R2admb](#)-package

---

read.dat	<i>loads existing IRATE-model setup (incl. tag release &amp; recapture data)</i>
----------	--

---

### Description

loads an existing IRATE-model setup (incl. tag release and recapture data) as a list

### Usage

```
read.dat(setup.file.name, skip=0)
```

### Arguments

setup.file.name	character string defining the name of the existing IRATE-model input file ( <i>.dat</i> ) to be loaded.
skip	Number of lines to skip in setup file (default = 0).

### Author(s)

Robert K. Bauer

### See Also

[IRATE.examples](#), [make.dat](#), [remake.dat](#)

### Examples

```
### read a preinstalled IRATE setup example:
examples.folder <- system.file("IRATE.examples", package = "IRATER")
setwd(examples.folder)
fnames <- Sys.glob('*.*.dat')
read.dat(fnames[1])
```



---

read.par	<i>Read in parameters from an IRATE run</i>
----------	---

---

**Description**

Reads in par-file from an IRATE run

**Usage**

```
read.par(fn)
```

**Arguments**

fn                    Character string indicating the name of the .par-file to be read.

**Value**

a list containing the parameters from an IRATE run:

napram number of parameters estimated

ofv objective function value

max\_grad\_comp maximum gradient component

e\_F fishing mortality estimates

e\_M natural mortality estimates

e\_FA tag mortality

LRR1, LRR2 reporting rate

PHI1R, PHI2R phi

e\_nmixh, e\_nmixr non-mixing

sel1, sel2 catch-at-age selectivity

**Author(s)**

Robert K. Bauer

**See Also**

[read.rep](#)

---

read.rep	<i>Read report-file from an IRATE run</i>
----------	---

---

### Description

Reads in the report-file from an IRATE run

### Usage

```
read.rep(fn, skip=0, show.sm=F, short=F)
read.short.rep(fn, skip=0, show.sm=F, short=T)
```

### Arguments

fn	Character string indicating the name of the .rep-file to be read.
skip	Number of lines to skip in report file (default = 0).
show.sm	Show model report summary while reading the file.
short	read short report or long report.

### Value

a list containing the model statistics and parameter estimates from an IRATE run:

for read.short.rep or read.rep(short=T):

Log\_L, AIC, AICc, Effective\_Sample\_Size, Unpooled\_Chi\_square, Upooled\_df, Unpooled\_c\_hat,  
Pooled\_Chi\_square, Pooled\_df, Pooled\_c\_hat

otherwise the full report file will be returned, containing the following

rep\_info report file information

Log\_L Log-Likelihood

K Number of parameters

AIC Akaike information criterion

AICc AIC corrected for finite sample sizes

Effective\_Sample\_Size

Unpooled\_Chi\_square

Upooled\_df

Unpooled\_c\_hat

Pooled\_Chi\_square

Pooled\_df

Pooled\_c\_hat

Harvest\_Residuals, Harvest\_Residuals\_of\_Age\_Class\_\*

Release\_Residuals, Release\_Residuals\_of\_Age\_Class\_\*

Not\_seen\_Residuals, Not\_seen\_Residuals\_of\_Age\_Class\_\*  
 Obs\_Recoveries\_of\_harvest\_fish  
 Obs\_Recoveries\_of\_release\_fish  
 Total\_Released  
 Total\_Recovered\_Tags  
 s\_matrix matrix of survival rates of the tags ( $S_{j, \text{tags}}$ )  
 S\_prob\_matrix matrix of survival rates used in the calculation of expected cell probabilities  
 Exploitation\_Rate\_of\_harvested\_fish matrix of estimated exploitation rates for harvested fish ( $U_{j, \text{tags(kept)}}$ )  
 Exploitation\_Rate\_of\_released\_fish matrix of estimated exploitation rates for released fish ( $U_{j, \text{tags(rels)}}$ )  
 Expected\_Probability\_of\_harvested\_fish matrix of cell expected probabilities for harvested tag returns ( $P_{ij}$ )  
 Expected\_Probability\_of\_released\_fish matrix of cell expected probabilities for released tag returns ( $P'_{ij}$ )  
 Not\_Seen\_Probability matrix of cell expected probabilities for not seen tag returns ( $P - \text{sum}(P_{ij} + P'_{ij})$ )  
 Expected\_Number\_of\_harvested\_fish matrix of expected number of harvested tag returns ( $E(R_{ij})$ )  
 Expected\_Number\_of\_released\_fish matrix of expected number of released tag returns ( $E(R'_{ij})$ )  
 Expected\_Number\_of\_not\_seen matrix of expected number of not seen tag returns ( $N - \text{sum}(R_{ij} + R'_{ij})$ )  
 Cell\_Likelihoods\_of\_harvested\_fish individual cell likelihood values for harvested tag returns  
 Cell\_Likelihoods\_of\_released\_fish individual cell likelihood values for released tag returns  
 Cell\_Likelihoods\_of\_not\_seen individual cell likelihood values for not seen tag returns  
 Unpooled\_Chi\_squares\_of\_Harvested\_Fish individual unpooled cell chi-square values for harvested tag returns  
 Unpooled\_Chi\_squares\_of\_Released\_Fish individual unpooled cell chi-square values for released tag returns  
 Chi\_squares\_of\_Not\_Seen individual unpooled cell chi-square values for unseen tag returns  
 Pooled\_Cells\_of\_Harvested\_Fish matrix of pooled, observed harvested tag returns  
 Pooled\_Cells\_of\_Released\_Fish matrix of pooled, observed harvested tag returns  
 Pooled\_Expected\_Cells\_of\_Harvested\_Fish matrix of pooled expected number of harvested tag returns  
 Pooled\_Expected\_Cells\_of\_Released\_Fish matrix of pooled expected number of released tag returns  
 Pooled\_Chi\_squares\_of\_Harvested\_Fish matrix of cell chi-square values for harvested tag returns  
 Pooled\_Chi\_squares\_of\_Released\_Fish matrix of pooled cell chi-square values for released tag returns  
 Pearson\_Residuals\_for\_harvested\_fish matrix of Pearson residuals for harvested tag returns  
 Pearson\_Residuals\_for\_released\_fish matrix of Pearson residuals for released tag returns  
 Pearson\_Residuals\_for\_not\_seen matrix of Pearson residuals for not seen tag returns

**Author(s)**

Robert K. Bauer

**See Also**[read.par](#)

---

remake.dat*load and reparameterize an existing IRATE-model setup file*

---

**Description**

loads an existing IRATE-model setup file (incl. tag release and recapture data) and allows to reparameterize and save it as a new setup file for IRATE model runs. Note that reparameterization will depend on the tagging dataset included in the old setup. (e.g. a "harvest and catch-&-release"-serup is not feasible with a former harvest-only data set.)

**Usage**

```
remake.dat(old.setup.name, new.setup.name, age.dependent=T,
           only.harvested=T,...)
```

**Arguments**

old.setup.name character string defining the name of the existing IRATE-model setup file (*.dat*) to be loaded.

new.setup.name character string defining the name of the IRATE-model setup file (*.dat*) to be created.

age.dependent whether setup file should be created for an age dependent model (default = *TRUE*).

only.harvested optional, whether actual releases of recaptures should be treated as harvested or a release-recapture model should be defined. (default = *TRUE*).

... Additional arguments, see Details

**Details**

HM  
hooking-mortality value for each recapture year (default = 0.09), only required for release-recapture model, otherwise being ignored.

eM, pM, sM, Mb

*eM*: whether to estimate natural mortality (default = *TRUE*),

**if set *TRUE*:**

*pM*: beginning years of different natural mortality periods,

*sM*: starting values of different natural mortality periods,

*Mb*: natural mortality lower and upper boundary values for model runs.

*eF*, *pF*, *sF*, *Fb*  
*eF*: whether to estimate fishing mortality (default = *TRUE*),  
**if set *TRUE*:**  
*pF*: beginning years of different fishing mortality periods,  
*sF*: starting values of different fishing mortality periods,  
*Fb*: fishing mortality lower and upper boundary values for model runs.

*eT=T*, *pT*, *sT*, *Tb*  
*eT*: whether to estimate tagging mortality (default = *TRUE*),  
**if set *TRUE*:**  
*pT*: beginning years of different tagging mortality periods,  
*sT*: starting values of different tagging mortality periods,  
*Tb*: tagging mortality lower and upper boundary values for model runs.

combine.Hrr\_and\_Rrr whether to combine Harvest & Release reporting rates (default = *FALSE*)

*eHrr=F*, *pHrr*, *sHrr*, *Hrrb*  
*eHrr*: whether to estimate harvest reporting rates (default = *FALSE*),  
**if set *TRUE*:**  
*pHrr*: beginning years of different harvest reporting periods,  
*sHrr*: starting values of different harvest reporting periods,  
*Hrrb*: harvest reporting lower and upper boundary values for model runs.

*eRrr=F*, *pRrr*, *sRrr*, *Rrrb*  
*eRrr*: whether to estimate release reporting rates (default = *FALSE*),  
**if set *TRUE*:**  
*pRrr*: beginning years of different release reporting periods,  
*sRrr*: starting values of different release reporting periods,  
*Rrrb*: release reporting lower and upper boundary values for model runs.

combine.HRS\_and\_RRS whether to combine Harvest & Release Retention Survival (default = *FALSE*)

*eHRS=F*, *pHRS*, *sHRS*, *HRSb*  
*eHRS*: whether to estimate harvest-retention survival rates (default = *FALSE*),  
**if set *TRUE*:**  
*pHRS*: beginning years of harvest-retention survival periods,  
*sHRS*: starting values of different-harvest retention survival periods,  
*HRSb*: lower and upper boundary values of harvest-retention survival rates for model runs.

*eRRS=F*, *pRRS*, *sRRS*, *RRSb*  
*eRRS*: whether to estimate release-retention survival rates (default = *FALSE*),  
**if set *TRUE*:**  
*pRRS*: beginning years of release-retention survival periods,  
*sRRS*: starting values of different release-retention survival periods,  
*RRSb*: lower and upper boundary values of release-retention survival rates for model runs.

*incomplete.mix=F*, *pNonMix*, *sNonMix*, *NonMixb*  
*incomplete.mix*: whether to assume incomplete mixing of tagged and wild population (default = *FALSE*),  
**if set *TRUE*:**  
*pNonMix*: beginning years of incomplete mixing periods,  
*sNonMix*: starting values of incomplete mixing periods,  
*NonMixb*: of release-retention survival rates lower and upper boundary values for model runs.

combine.HS\_and\_RS whether to combine Harvest & Release Selectivity (default = *TRUE*)

eHS=F , pHS , sHS , HSb  
*eHS*: whether to estimate age-dependent harvest selectivity rates (default = *FALSE*),  
**if set *TRUE*:**  
*pHS*: beginning years of age-dependent harvest selectivity periods,  
*sHS*: starting values of age-dependent harvest selectivity periods,  
*HSb*: lower and upper boundary values of age-dependent harvest selectivity rates for model runs.

eRS=F , pRS , sRS , RSb  
*eRS*: whether to estimate age-dependent release selectivity rates (default = *FALSE*),  
**if set *TRUE*:**  
*pRS*: beginning years of age-dependent release selectivity periods,  
*sRS*: starting values of age-dependent release selectivity periods,  
*RSb*: lower and upper boundary values of age-dependent release selectivity rates for model runs.

eMS=F , aMS , SMS  
*eMS*: whether to estimate age-dependent natural mortality rates (default = *TRUE*; only considered if *age.dependent* is set *TRUE*),  
**if set *TRUE*:**  
*aMS*: beginning age classes of age-dependent natural mortality rates (age classes are counted from 1 onwards irrespective of their age-values),  
*SMS*: starting values of (grouped) age-dependent natural mortality rates,  
 use `.L.const` whether to set likelihood function constant (default = *TRUE*)

### Author(s)

Robert K. Bauer

### See Also

[IRATE.examples](#), [make.dat](#), [read.dat](#)

### Examples

```
# old.setup <- "JiangADCR" # select old IRATE setup to reparameterize
# old.setup.path <- system.file(paste0("IRATE.examples/",old.setup,".dat"), package = "IRATER")

# new.setup <- new.setup.path <- "JiangAICR_manual"
# system(paste("mkdir -p ",new.setup.path)) # create run folder for new setup
# system(paste("cp",old.setup.path, new.setup.path)) # copy old setup in new run folder

# setwd(new.setup.path)
# remake.dat(old.setup,new.setup,age.dependent = F) # reparameterize old setup
# run.IRATE(setup.new) # run new setup
```

---

run.IRATE                      *compile and run NOAA-IRATE models from within R*

---

### Description

compile and run **NOAA-IRATE** models from within R

### Usage

```
run.IRATE(setup.file, safe=F, re=F, verbose=T,
          admb_errors=c("stop", "warn", "ignore"),
          mcmc=F, mcmc.opts=mcmc.control(),
          profile=F, extra.args="")
```

### Arguments

setup.file	Character string defining IRATE setup to be run. Check <a href="#">IRATE.examples</a> for preinstalled IRATE setup examples and <a href="#">make.dat</a> to create new or <a href="#">remake.dat</a> to alter existing setup files.
safe	(logical) Compile in safe mode? (default = <i>FALSE</i> )
re	(logical) Compile in random effects (ADMB-RE) mode? (default = <i>FALSE</i> )
verbose	(logical) Verbose output? (default = <i>TRUE</i> )
admb_errors	(character) how to handle compilation/linking errors?
mcmc	(logical) run post-hoc MCMC? (default = <i>FALSE</i> )
mcmc.opts	options for MCMC run (see <a href="#">mcmc.control</a> )
profile	(logical) Run likelihood profiles? (default = <i>FALSE</i> )
extra.args	(character) extra (ADMB-) arguments for IRATE run

### Author(s)

Robert K. Bauer

### References

<http://nft.nefsc.noaa.gov/IRATE.html>

### See Also

To check model setup files see: [read.dat](#) and [make.dat](#).

To read run results see: [read.rep](#) and [read.par](#).

For preinstalled example runs see: [run.IRATE.example](#).

To delete run files see: [clean.IRATE](#).

For more information on admb model compilation and run prodcdres see: [compile\\_admb](#) and [run\\_admb](#) from the [R2admb](#)-package

**Examples**

```

example.setup <- IRATE.examples()
new.setup <- new.setup.path <- example.setup[1] # select old IRATE setup to reparameterize
print(new.setup) # print setup name to be run
old.setup.path <- system.file(paste0("IRATE.examples/",new.setup,".dat"), package = "IRATER")

system(paste("mkdir -p ",new.setup.path)) # create run folder for new setup
system(paste("cp",old.setup.path, new.setup.path)) # copy old setup in new run folder
setwd(new.setup.path)

run.IRATE(new.setup) # compile and run setup

```

---

run.IRATE.example	<i>compile and run preinstalled example IRATE-model setups</i>
-------------------	--

---

**Description**

compile and run preinstalled example IRATE-model setups

**Usage**

```
run.IRATE.example(setup.name, run.folder, ...)
```

**Arguments**

setup.name	Character string defining preinstalled IRATE example setups/datasets to be run. If missing or not valid, the user will be asked to choose among valid examples. Check IRATE.examples() for valid, preinstalled IRATE examples.
run.folder	Character string defining the folder in which the selected example shall be run. If missing a folder, named after the example setup file, will be created in the current working directory.
...	Further arguments to be passed to <a href="#">run.IRATE</a>

**Author(s)**

Robert K. Bauer

**See Also**

To check model setup files see: [read.dat](#) and [make.dat](#).  
 For run results see: [read.rep](#) and [read.par](#).  
 To delete run files see: [clean.IRATE](#).  
 For more information on admB model compilation and run prodcdres see: [compile\\_admb](#) and [run\\_admb](#) from the [R2admb](#)-package



### **Examples**

```
### setup example not specified, user will be prompted to select among existing example setups:  
# run.IRATE.example()
```

```
### example name specified  
# run.IRATE.example("JiangADCR")
```

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