Gompertz Extinction Risk Estimates for Snake River Spring/Summer Chinook Salmon Populations

Description

Make tables of extinction risk estimates using the Gompertz model applied to Snake River Spring/Summer Chinook Salmon populations.

Estimate extinction risks with quasi extinction threshold equal to <code>qet</code> over a time window equal to <code>nyears</code> a reproductive failure threshold equal to <code>rft</code> and number of bootstrap replications equal to <code>NBOOT</code>.

Usage

```
estimates.table.gompertz(qet=50,nyears=100,dela=0,rft=10,NBOOT=0)
estimates2.table.gompertz()
get.capacity.gompertz()
```

Arguments

qet	quasi-extinction threshold.
nyears	time horizon for extinction risk estimate.
dela	the Gompertz a parameter will be increased by this value while holding carrying capacity constant.
rft	reproductive failure threshold.
NBOOT	number of bootstrap replications. Default is zero bootstrap replications

Details

The defaults for qet, nyears, dela, rft, and NBOOT are 50, 100, 0, 10, and 0, respectively.

The Gompertz spawner-recruit model is parameterized as

$$R = S \exp (a + b \log(S) + \alpha + \epsilon)$$

where R represents recruits, a is intrinsic productivity, b is a density-dependent parameter, S represents spawners, α is a common year effect, and ϵ is a normally distributed random error term (Hinrichsen and Paulsen, 2020).

Do not call this function without first executing <code>source("gompertz_pva2020.s")</code>. This reads in the data file SPS_Download_DEC042017.csv, whose location should be specified by PATH, which you can specify in the gompertz_pva2020.s. The data file SPS_Download_DEC042017.csv contains the information necessary to build the spawner-recruit data for the Snake River Spring-Summer Chinook Salmon populations. After building the spawner-recruit data, <code>source("gompertz_pva2020.s")</code> then estimates the Gompertz Model parameters for the linear model. Once this is accomplished, it will be possible to call <code>estimates.table.gompertz()</code>.

The Gompertz a parameter will be set to a = a + dela, that is the maximum likelihood estimate of a will be incremented by dela. Note however, it will be assumed that carrying capacity remains constant, so that $\exp(-a/b)$ does not change.

Warning: On an ordinary laptop computer (Sys.info() [5]="x86-64"), estimates.table.gompertz will take about a minute to run when NBOOT=0. With NBOOT=1000 it will take about 16 hours to run, depending on the choice of nyears. When NBOOT=0, then estimates.table.gompertz will simply return the extinction risk estimates without 95% confidence intervals. Test how long it will take to run the model on your computer with system.time({estimates.table.gompertz()}).

estimates2.table.gompertz is a function with no arguments that calls estimates.table.gompertz using arguments nyears=24, and alternative values qet=1, rft=2; qet=10, rft=10; qet=30, rft=10; and qet=50, rft=10. These are alternatives used in the paper Hinrichsen and Paulsen (2020).

get.capacity.gompertz is a function with no arguments that returns the spawner carrying capacity estimate for the Snake River Spring/Summer Chinook Salmon populations.

Value

estimates.table.gompertz returns a list with the following elements

parmat	Parameter estimates for the Gompertz model.
extmat	A matrix of the extinction probability estimates with 95% confidence intervals. Confidence interval limits are NA if NBOOT=0.
aic	Akaike's Information Criterion (AIC) for model fit
qet	quasi-extinction threshold.
nyears	time horizon for extinction risk estimate.
dela	the Gompertz a parameter will be increased by this value while holding carrying capacity constant.
rft	reproductive failure threshold.
NBOOT	number of bootstrap replications. Default is zero bootstrap replications

get.capacity.gompertz returns a matrix with the estimated spawner carrying capacities and their confidence intervals. Carrying capacities are $K = \exp(-a/b)$.

Source

estimates.table.gompertz, estimates2.table.gompertz, and get.capacity.gompertz are based on

Hinrichsen, R. A. and Paulsen, C. M. (2020) Low carrying capacity a risk for threatened Chinook Salmon. *Ecol. Modell.* **432** (C): 109223. https://doi.org/10.1016/j.ecolmodel.2020.109223

References

Gompertz, B. (1825) On the nature of the function expressive of the law of human mortality, and on a new mode of determining the value of life contingencies. *Philos. T. R. Soc. Lond.* **115**: 513-583. https://doi.org/10.1098/rstl.1825.0026.

Hinrichsen, R. A. and Paulsen, C. M. (2020) Low carrying capacity a risk for threatened Chinook Salmon. *Ecol. Modell.* **432** (C): 109223. https://doi.org/10.1016/j.ecolmodel.2020.109223.

See Also

Not applicable.

Examples

```
## First edit the file gompertz pva2020.s set so that PATH is the location
## of the input file SPS Download DEC042017.csv. By default, this PATH is set
## to PATH="./SPS Download DEC042017.csv"
## Also make sure GPATH points at the location of the file gompertz pva2020.s
GPATH="./gompertz pva2020.s"
source (GPATH)
## return extinction risk estimates SRSS Chinook Salmon
## using a quasi-extinction threshold of 50, time window of 24 years
## reproductive failure threshold of 10, and no confidence intervals
## (NBOOT=0)
myres=estimates.table.gompertz(qet=50,nyears=24,dela=0.0,rft=10,NBOOT=0)
## display first 10 lines of parameter estimate matrix
head (myres$parmat, 10)
## display matrix of extinction risk estimates with confidence intervals
myres$extmat
## display AIC for model fit
myres$aic
```

```
## display a table of extinction risk estimates for different pairs of qet
## and rft with a time horizon of 24 years.
myres2=estimates2.table.gompertz()
##display table
myres2
##get table of spawner carrying capacities
mycap=get.capacity.gompertz()
## display table of carrying capacities
mycap
## make a plot of extinction risks versus carrying capacities
## see Figure 4a of Hinrichsen and Paulsen (2020)
plot(x=mycap[,1],y=myres$extmat[,1],main="SRSS Chinook Salmon",
     xlab="Spawner carrying capacity",ylab="Extinction risk ",
     sub="qet=50 rft=10 nyears=24")
## make a similar plot based on ranks
## see Figure 5a of Hinrichsen and Paulsen (2020)
plot(x=rank(mycap[,1]),y=rank(myres$extmat[,1]),main="SRSS Chinook Salmon",
     xlab="Spawner carrying capacity rank", ylab="Extinction risk rank",
     sub="qet=50 rft=10 nyears=24")
```