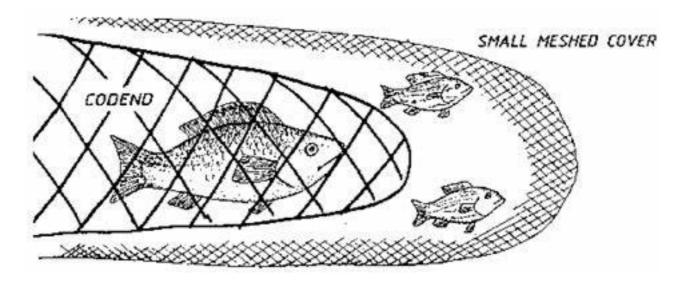
Open source software for statistical models of gear selectivity

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DTU Aqua

Selectivity model

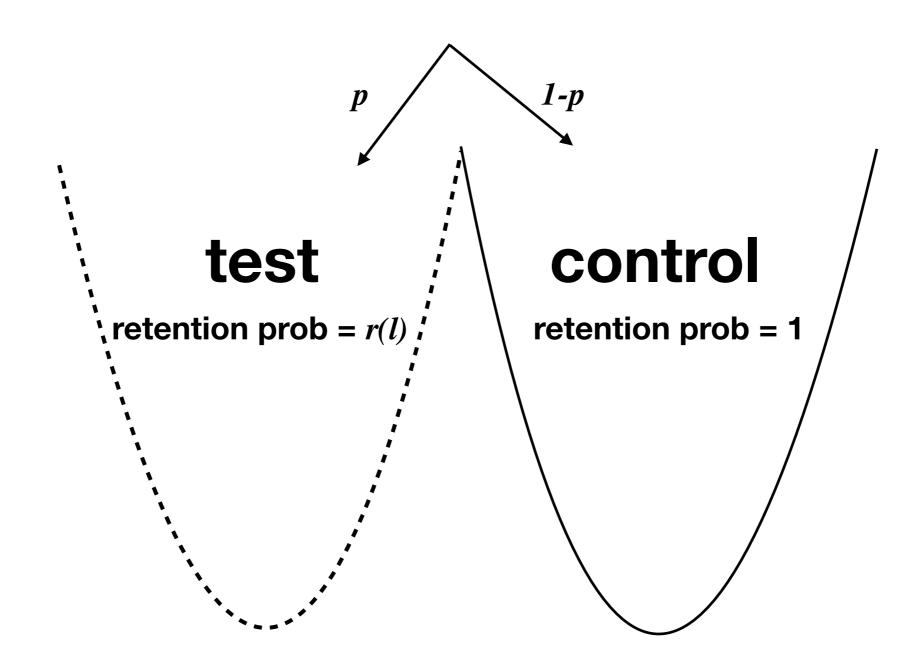


- retention probability as a function of length: r(l)
- binomial outcome
- generalized linear model (GLM)
- link function to keep probability between 0 and 1
 - e.g. logit link: $r(l) = \exp(a + bl)/(1 + \exp(a + bl))$

(image credit: <u>FAO.org</u>)

Paired gear model

(e.g. twin, trouser, alternate or parallel trawling)



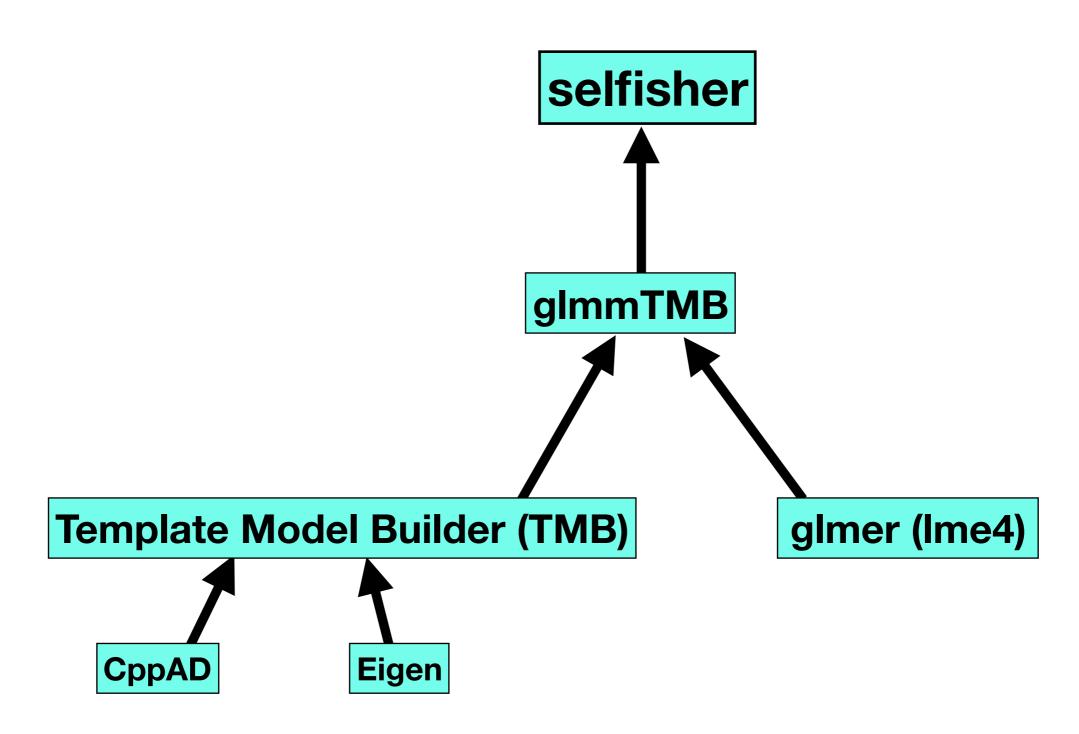
proportion of fish in test gear compared to total fish in test and control:

$$\phi = \frac{pr(l)}{pr(l) + 1 - p}$$

Estimating selectivity

- several software methods exist
- needed something for teaching
- introducing selfisher
- SELectivity of FISHERies gear in R

Open-source software pedigree of selfisher



Features of selfisher

- retention model (r)
- r links: logit, probit, c-log-log, log-log, Gompertz, Richards
- relative fishing power model (p)
- fixed and random effects on r and p
- offsets
- "double bootstrapping"
- standard regression methods

Fixed effects that could effect selectivity

- with or without stimulation devices
- net age
- total catch weight
- sea state
- substrate qualities

Standard methods

- predict(model, newdata, type)
 - "selection" = *r*
 - "prob" = *p*
 - "ratio" = r/(1-r)
 - "response" = pr/(pr+1-p)
- residuals(model, type)
 - "response"
 - "pearson"
 - "deviance"
- logLik(model)
- AICc(model)

"double bootstrap"

resample hauls with replacement

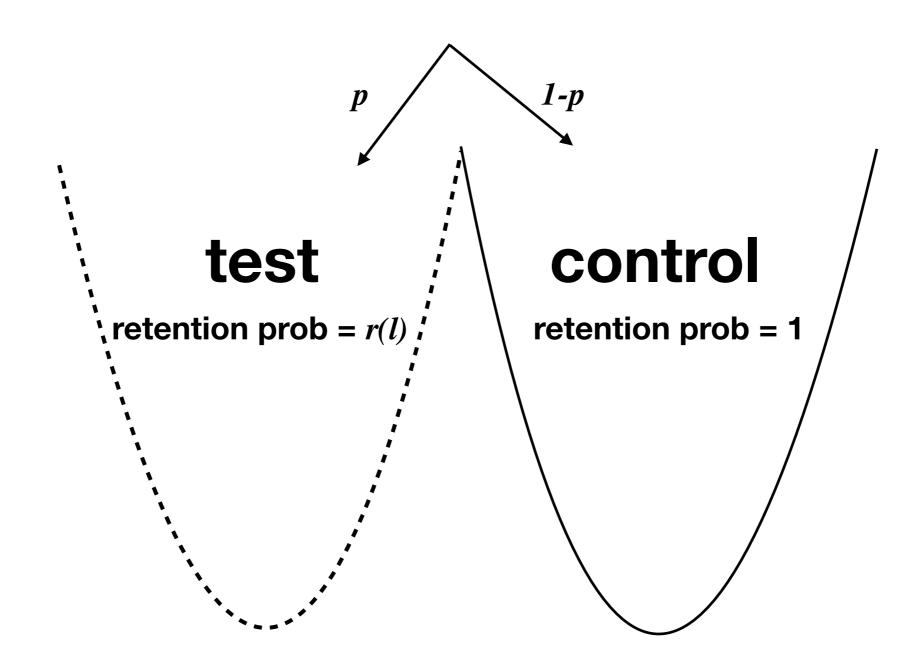
for each haul, for each length class

assume $\phi_{observed} = k_{observed}/n_{observed}$

new $\phi_{observed} = rbinom(old \phi_{observed}, n_{observed})/n_{observed}$

Paired gear model

(e.g. twin, trouser, alternate or parallel trawling)



proportion of fish in test gear compared to total fish in test and control:

$$\phi = \frac{pr(l)}{pr(l) + 1 - p}$$

Model specification details for psplit=TRUE

$$k \sim \mathsf{Binom}(\phi, n),$$
 (1)

$$\phi = \frac{pr}{pr + 1 - p},\tag{2}$$

$$logit(r) = X^{(r)}\beta^{(r)} + Z^{(r)}b^{(r)}, \qquad (3)$$

logit(p) =
$$X^{(p)}\beta^{(p)} + Z^{(p)}b^{(p)}$$
, (4)

(5)

 β s are fixed effect parameters

bs are random effects

Xs and Zs are model matricies

Simple example with psplit

haddock data from Russel Millar's website with his permission

```
data(haddock)
head(haddock)
```

```
Lengths nwide nfine
##
## 1
         24
## 2
         25
         26
## 4
         27
                   14
         28 5
                   30
         29
              19
                   49
## 6
```

Simple example with psplit

```
assume psplit=0.5
```

or estimate psplit...

Simple example output

compare the models

```
AICctab(m0, m1)
```

```
## m1 0.0 3
## m0 18.6 2
```

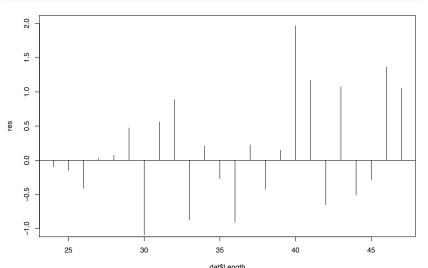
Simple example output

summary(m1)

```
## Family: binomial (logit)
## Selectivity formula:
                               prop ~ Lengths
## Relative fishing power formula:
## Data: dat
## Total: total
##
##
            ATC
                         BTC
                                  logLik deviance Pearson.ChiSq
##
          100.7
                       104.3
                                   -47.4
                                                   14.8
                                                                13.7
##
     df.resid
             21
##
##
## Selectivity model:
              Estimate Std. Error z value Pr(>|z|)
                          5.7488 -4.81 1.51e-06 ***
## (Intercept) -27.6542
## Lengths
              0.9164
                          0.1971 4.65 3.32e-06 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Relative fishing power model:
              Estimate Std. Error z value Pr(>|z|)
## (Intercept) 0.29346 0.07042 4.167 3.08e-05 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## Size at retention probability:
       p Lp.Est Lp.Std.Err
## 1 0.25 28.97665 0.2792741
## 2 0.50 30.17542 0.3557115
## 3 0.75 31.37419 0.5549850
## Selectivity range (SR):
## Estimate Std. Error
## 2.3975428 0.5156376
```

Plot residuals

```
res = residuals(m1, type="deviance")
plot(dat$Length, res, type='h', ylim=c(-1,2))
abline(0,0)
```



A multihaul example

```
data(ccmhtwdat)
ccmhtwdat=subset(ccmhtwdat, total>0)
head(ccmhtwdat, 2)

## length haul type test cover TW total prop
## 342.1 48.5 4 baseline 2 0 459.8 2 1
```

```
## 345.1 51.5 4 baseline 1 0 459.8 1 1
```

```
tail(ccmhtwdat, 2)
```

```
## length haul type test cover TW total prop
## 2138.2 26.5 22 stimulation 0 1 143 1 0
## 2142.2 30.5 22 stimulation 0 1 143 1 0
```

Mixed model for hypothesis testing

```
mmod=selfisher(prop-length*type +(1|haul), total=total, ccmhtwdat)
summary(mmod)
```

```
## Family: binomial (logit)
## Selectivity formula:
                             prop ~ length * type + (1 | haul)
## Data: ccmhtwdat
## Total: total
##
##
           ATC
                        RTC
                                logLik
                                           deviance Pearson.ChiSq
##
        1075.2
                     1097.7
                                  -532.6
                                               507.6
                                                            798 2
       df resid
##
##
           652
## Random effects:
##
## Selectivity model:
## Groups Name
                    Variance Std Dev
## haul (Intercept) 0.5041 0.71
## Number of obs: 657, groups: haul, 21
## Selectivity model:
##
                       Estimate Std. Error z value Pr(>|z|)
## (Intercept)
                      -9.30422
                                  0.37521 -24.798 < 2e-16 ***
                       ## length
## typestimulation
                       3.19766 0.75758 4.221 2.43e-05 ***
## length:typestimulation -0.22758   0.02569 -8.860 < 2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
```

Model and newdata for bootstrapping hauls

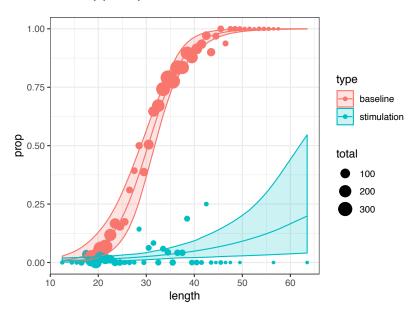
Bootstrap to get CI on predictions

```
bs=bootSel(mod, nsim=100, parallel="multicore", ncpus = 4,
    FUN=function(mod){
        predict(mod, newdata=newdata, type="selection")
        })

quants=apply(bs$t, 2, quantile, c(0.025, 0.5, 0.975))

newdata[,c("lo", "mid", "hi")]=t(quants)
```

Plot bootstrapped predictions



Maybe try other links

```
## mmod_richards 0.0 6
## mmod_loglog 9.8 5
## mmod 26.4 5
```

Installation and info

selfisher

https://github.com/mebrooks/selfisher

GLMM FAQ

http://bbolker.github.io/mixedmodels-misc/glmmFAQ.html

Future directions

- more testing and documentation
- shiny app (i.e. GUI)
- investigate "dual selection model" possibilities
- courses
- papers

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