nupoint (Version 1.0.45) package example: multi-beam data

Martin J. Cox, David L. Borchers and Natalie Kelly

March 21, 2013

1 Introduction

In this vignette we will illustrate the maximum likelihood estimation of parameters describing a density gradient function for underwater acoustic observations of shoaling animals (e.g. krill or herring). The same maximum likelihood estimation process also simultaneously accounts for decreasing detectability of shoals with range. We use the maximum likelihood estimates to calculate shoal density and biomass in a survey area.

The purpose of this vignette is to provide an example workflow to enable users to estimate shoal density using a variety of density gradient functional forms. The work flow also includes AIC-based model selection, χ^2 Goodness-of-Fit test, and non-parametric bootstrap of shoal density. In the final section, we introduce the concept of an attenuation function which deals with the situation where it is not possible to observation out to the truncation distance, w. Example code and output are provided throughout.

We start by loading the nupoint package:

```
> library(nupoint)
```

2 Example dataset description

Shoals were observed using an active underwater acoustic instrument, a multi-beam echosounder. Cox et al. [2009] decribe the multi-beam echosounder and the observation process. Example data, named krill, is included in the nupoint package is a data.frame object (see Table 1 for data summary). This example data contains $n=251$ observations and is a subset of those used by Cox et al. [2011]. Data acquisition details can be found in the same reference.

In the example data there are 11 line transects. To analyse the data, the krill shoal (or swarm) detections are collapsed in the along transect dimension. This gives us a single cross section through the water column (Figure 1) upon which the locations of the swarms are projected. The location of the ith swarm can be defined by any two of the following coordinates: θ_i, r_i, x_i, y_i (Figure 1)
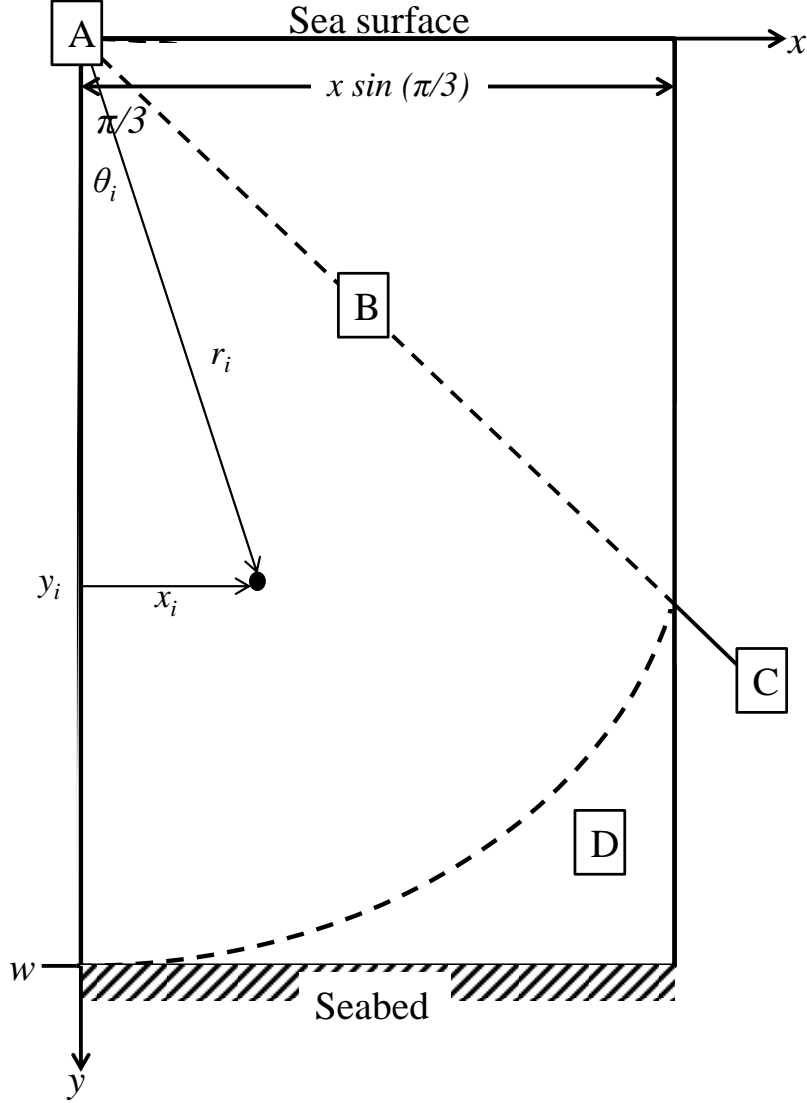
Figure 1: Multi-beam echosounder geometry and ith swarm location measurements $(\theta_i, r_i, x_i, y_i)$. One half of the multi-beam swath is shown; the swath has been folded about its vertical axis. A: location of the multi-beam echosounder head. B: Dashed line denotes the area sampled by the multi-beam echosounder. C: the maximum swath width $\theta/3$. D: No observations were possible in this region. The probability of detecting a krill swarm, $\hat{P}^*$, is calculated for the solid rectangle area (dimensions: $w \times x \sin(\pi/3)$), see Section 5.1 of this vignette and Equation 3 Cox et al. [2011]. Figure modified from Figure 2 Cox et al. [2011].

	Description	min	max
transect	Transect number	1.00	11.00
x	Shoal cross-track distance, m	0.90	77.26
y	Shoal depth, m	10.74	98.15
r	Shoal radial distance, m	11.21	99.75
theta	Shoal angle, rad	0.01	1.03
bio.g	Shoal biomass, g	1122.79	10668428.97
z	Seabed depth under shoal	70.32	128.12

Table 1: Data summary of the krill example data set.

3 Maximum likelihood estimation

We now use maximum likelihood to simultaneously estimate parameters, ϕ, for the function describing the distribution of shoals with water depth, $\pi_z(z, \phi)$, and parameters, Θ, for the detection function, $g(\sqrt{x_i^2 + y_i^2}; \Theta)$. Parameters are estimated using the `nupoint.fit` function.

We will use a half-normal form for the detection function (`nupoint.fit` argument `det.form='HNORM'`), and select a depth preference from five candidate forms: normal (`nupoint.fit` argument `grad.form='NORM'`); log-normal ('LOGNORM'); beta ('BETA'); uniform ('UNIFORM'), and a mixture distribution comprising of two normal distributions ('MNORM', and the `nupoint.fit` argument `n= 2`).

The following code is used to fit the normal parametric form for shoal distribution with depth. We start by setting the depth preference and detection functions (`norm.grad.type` and `norm.det.type`), and starting parameters (`norm.pars`), with lower and upper bounds (`norm.LB`, `norm.UB`), for the `optim` function:

```
> norm.grad.type <- "NORM" #swarm depth preference form.
> norm.det.type <- "HNORM"
> norm.pars <- c(50,20,50) #starting values for
>    #parameter vector to be estmated
>    #[1] = normal depth preference function mu;
>    #[2] = normal depth preference function sigma;
>    #[3] half-normal detection function sigma.
> norm.LB <- c(1,1,1) #lower parameter space bound.
> norm.UB <- c(120,100,100) #upper parameter space bound.
```

Finally we call the `nupoint.fit` function and simultaneously estimate the depth distribution and detection function parameters.

```
> norm.fit <- nupoint.fit(norm.pars,
+                    sight.x=krill$x,
+                    sight.y=krill$y,
+                    w=100,
```

```
+                             theta.max=pi/3,
+                             grad.type=norm.grad.type,
+                             det.type=norm.det.type,
+                             lower.b=norm.LB,
+                             upper.b=norm.UB)

--------------------------
Parallel density gradient likelihood settings
--------------------------
Depth preference parametric form: NORM
range detection function, g(r), parametric form: HNORM
Parameter starting values = 50 20 50
Angular detection function applied: FALSE
Seabed attenuation function applied: FALSE
Truncation distance = 100
Swath (max) angle, rad = 1.047198
Numerical integration grid density= 100
--------------------------
Estimating parameters
--------------------------
Maximum likelihood results
--------------------------
parameter estimates
81.736 25.144 38.194
AIC = -3.02
--------------------------
```

3.1 AIC model selection

We use AIC based model selection to chose the optimum model from the candidate set of models. In the case of krill, the prevalence of krill swarms with depth, $\pi_z(z)$, was modelled using the following parametric forms: normal, log-normal, beta, uniform and a two mixture distribution comprising of two normals. We start by running each of the candidate models.

3.1.1 Beta

Again, we follow the same procedure of specifying the depth preference and detection functions, as well as specifying the starting parameters and upper and lower parameter space bounds.

```
> beta.grad.type <- "BETA" #swarm depth preference form.
> beta.det.type <- "HNORM" #detection function
> beta.pars <- c(2,2,50) #starting values for
>   #parameter vector to be estimated
>   #[1] = beta depth preference function shape parameter 1;
>   #[2] = beta depth preference function shape parameter 2;
```

4

```
>   #[3] = beta detection function sigma.
> beta.LB <- c(0.1,0.1,1) #lower parameter space bound.
> beta.UB <- c(20,20,100) #upper parameter space bound.
> beta.fit <- nupoint.fit(beta.pars,
+                         sight.x=krill$x,
+                         sight.y=krill$y,
+                         w=100,
+                         theta.max=pi/3,
+                         grad.type=beta.grad.type,
+                         det.type=beta.det.type,
+                         lower.b=beta.LB,
+                         upper.b=beta.UB)

--------------------------
Parallel density gradient likelihood settings
--------------------------
Depth preference parametric form: BETA
range detection function, g(r), parametric form: HNORM
Parameter starting values = 2 2 50
Angular detection function applied: FALSE
Seabed attenuation function applied: FALSE
Truncation distance = 100
Swath (max) angle, rad = 1.047198
Numerical integration grid density= 100
--------------------------
Estimating parameters
--------------------------
Maximum likelihood results
--------------------------
parameter estimates
3.857 1.633 39.058
AIC = -2.45
--------------------------
```

3.1.2 Uniform

```
> unif.grad.type <- "UNIFORM" #swarm depth preference form.
> unif.det.type <- "HNORM" #detection function
> unif.pars <- 50 #starting values for
>   #parameter vector to be estimated
>   #[1] half-normal detection function sigma.
> unif.LB <- 1 #lower parameter space bound.
> unif.UB <- 100 #upper parameter space bound.
> unif.fit <- nupoint.fit(unif.pars,
+                         sight.x=krill$x,
+                         sight.y=krill$y,
```

```
+                            w=100,
+                            theta.max=pi/3,
+                            grad.type=unif.grad.type,
+                            det.type=unif.det.type,
+                            lower.b=unif.LB,
+                            upper.b=unif.UB)

--------------------------
Parallel density gradient likelihood settings
--------------------------
Depth preference parametric form: UNIFORM
range detection function, g(r), parametric form: HNORM
Parameter starting values = 50
Angular detection function applied: FALSE
Seabed attenuation function applied: FALSE
Truncation distance = 100
Swath (max) angle, rad = 1.047198
Numerical integration grid density= 100
--------------------------
Estimating parameters
--------------------------
Maximum likelihood results
--------------------------
parameter estimates
65.825
AIC = 51.74
--------------------------
```

3.1.3 Log-normal

```
> lnorm.grad.type <- "LOGNORM" #swarm depth preference form.
> lnorm.det.type <- "HNORM"
> lnorm.pars <- c(4,2,50) #starting values for
>   #parameter vector to be estimated
>   #[1] = log-normal depth preference function log  mu;
>   #[2] = log-normal depth preference function log sigma;
>   #[3] half-normal detection function sigma.
> lnorm.LB <- c(1,0.1,1) #lower parameter space bound.
> lnorm.UB <- c(20,10,100) #upper parameter space bound.
> lnorm.fit <- nupoint.fit(lnorm.pars,
+                            sight.x=krill$x,
+                            sight.y=krill$y,
+                            w=100,
+                            theta.max=pi/3,
+                            grad.type=lnorm.grad.type,
+                            det.type=lnorm.det.type,
```

```
+                               lower.b=lnorm.LB,
+                               upper.b=lnorm.UB)

---------------------------
Parallel density gradient likelihood settings
---------------------------
Depth preference parametric form: LOGNORM
range detection function, g(r), parametric form: HNORM
Parameter starting values = 4 2 50
Angular detection function applied: FALSE
Seabed attenuation function applied: FALSE
Truncation distance = 100
Swath (max) angle, rad = 1.047198
Numerical integration grid density= 100
---------------------------
Estimating parameters
---------------------------
Maximum likelihood results
---------------------------
parameter estimates
8.34 1.206 37.314
AIC = 5.08
---------------------------
```

3.1.4   Mixture of two normal distributions

Specifying arguments for the `nupoint.fit` is a little more complex when using the normal mixture `grad.type='MNORM'` environmental preference function, but there is only one more argument, **n**, which specifies the number of mixture distributions. We start by specifying the depth preference and detection functions:

```
> det.type <-"HNORM" #detection function.
> sigma.r <- 50 #half-normal sigma detection function parameter
> grad.type <- "MNORM" #seabed depth cue distribution shape.
> nDist <- 2 #number of normal distributions.
```

We then assign a starting weight to each distribution in the mixture, $\boldsymbol{\alpha}$:

```
> wt <- rep(1/nDist,nDist) #final element removed later
```

We distribute mixture distribution means, $\boldsymbol{\mu}$, evenly along the depth dimension:

```
> mu <- seq(10,100,length=nDist)
```

and assign an arbitrary $\boldsymbol{\sigma} = 50$ m to each distribution.

```
> sigma <- rep(50,nDist)
> pars <- as.vector(matrix(c(mu,sigma,wt),ncol=nDist,byrow=TRUE))
```

7

The final element of the vector, $\boldsymbol{\alpha}$, the weight of the nth distribution in the mixture, is removed since $\alpha_n = 1 - \sum_{i=1}^{(n-1)} \alpha_i$.

```
> pars <- c(pars[-length(pars)],sigma.r)
```

Finally, we assign lower and upper parameter space bounds. We start with the lower parameter space bound:

```
> mumin <- rep(1,nDist) #minimum mean
> sigmamin <- rep(1,nDist) #minimum sigma
> alphamin <- rep(-15,nDist) #minimum alpha
> sigma.rmin <- 1#minimum detection function parameter
```

The parameter space minima are combined into a single vector:

```
> lower.b <- as.vector(matrix(c(mumin,sigmamin,alphamin),ncol=nDist,byrow=TRUE))
> lower.b <- c(lower.b[-length(lower.b)],sigma.rmin) #remove nth weight
```

Specify the parameter space maxima:

```
> mumax <- rep(110,nDist) #maximum mean
> sigmamax <- rep(100,nDist) #maximum sigma
> alphamax <- rep(15,nDist) #maximum alpha
> sigma.rmax <- 100 #maximum detection function parameter.
```

and combine the parameter space maxima in a single vector:

```
> upper.b <- as.vector(matrix(c(mumax,sigmamax,alphamax),ncol=nDist,byrow=TRUE))
> upper.b <- c(upper.b[-length(upper.b)],sigma.rmax) #remove nth weight
```

We can now fit the two-normal mixture distribution using the above settings:

```
> mn.mbe.fit<-nupoint.fit(pars,
+                          sight.x=krill$x,
+                          sight.y=krill$y,
+                          w=100,
+                          theta.max=pi/3,
+                          grad.type=grad.type,
+                          det.type=det.type,
+                          n=nDist,
+                          lower.b=lower.b,
+                          upper.b=upper.b)

---------------------------
Parallel density gradient likelihood settings
---------------------------
Depth preference parametric form: MNORM
range detection function, g(r), parametric form: HNORM
Parameter starting values = 10 50 0.5 100 50 50
Angular detection function applied: FALSE
```

```
Seabed attenuation function applied: FALSE
Truncation distance = 100
Swath (max) angle, rad = 1.047198
Numerical integration grid density= 100
--------------------------
Estimating parameters
--------------------------
Maximum likelihood results
--------------------------
parameter estimates
10.227 99.997 -0.313 78.495 21.117 38.278
AIC = 1.19
--------------------------
```

AIC model selection results (Table 2) show that the normal distribution was optimal for describing krill swarm distribution with depth.

	AIC	dAIC	AIC weight
Normal	-3.02	0.00	0.53
Beta	-2.45	0.57	0.40
2-normal mixture	1.19	4.21	0.06
log-normal	5.08	8.10	0.01
Uniform	51.74	54.76	0.00

Table 2: AIC model delection for krill swarm prevelance with depth.

4 Goodness-of-fit

The `nupoint.gof` function is used to calculate a one-dimensional χ^2 goodness-of-fit test. The `nupoint.gof` function is available for all the perpendicular gradient functional forms. Here we calculate the one-dimensional goodness-of-fit statistic for the Normal form of the krill swarm vertical distribution model. We selected the Normal form because this form was selected under AIC (Table 2). The estimated parameters for the normal form of the krill depth distribution model, `norm.fit$par`, were $\hat{\phi} = [\ 81.74, 25.14]$, and the half-normal detection function $\hat{\Theta} = [38.19]$ were used in the goodness-of-fit calculation:

```
> norm.gof=nupoint.gof(y.obs=krill$y,
+               pars=norm.fit$par,
+               w=100,
+               grad.type='NORM',
+               det.type='HNORM',
+               n=NULL,
+               intervals=11,
+               theta.max=pi/3,
+               grid.resolution=100)


---------------------------------------------------------
nupoint: 1D Chi-squared Goodness-of-Fit results
---------------------------------------------------------
   bin.min bin.max  mids expected observed Chisq
1    10.74   18.69 14.71     0.95        2  1.15
2    18.69   26.63 22.66     3.96        4  0.00
3    26.63   34.58 30.60    10.67        9  0.26
4    34.58   42.52 38.55    21.39       26  0.99
5    42.52   50.47 46.50    28.88       28  0.03
6    50.47   58.42 54.44    41.75       34  1.44
7    58.42   66.36 62.39    44.67       41  0.30
8    66.36   74.31 70.34    40.51       46  0.74
9    74.31   82.26 78.28    30.78       41  3.39
10   82.26   90.20 86.23    19.08       16  0.50
11   90.20   98.15 94.17     8.35        4  2.27
---------------------------------------------------------
Chi-squ. statistic    =   11.06844
Number of parameters =   3
Chi-squ. df           =   7
Chi-squ. GoF p-value =   0.1356615
---------------------------------------------------------
```

The ^{2} goodness-of-fit p-value was 0.14. A graphical output of the goodness-of-fit results is available by changing the argument `plot=TRUE` in `nupoint.gof` function (Figure 2). The `intervals` argument `nupoint.gof()` can also be used

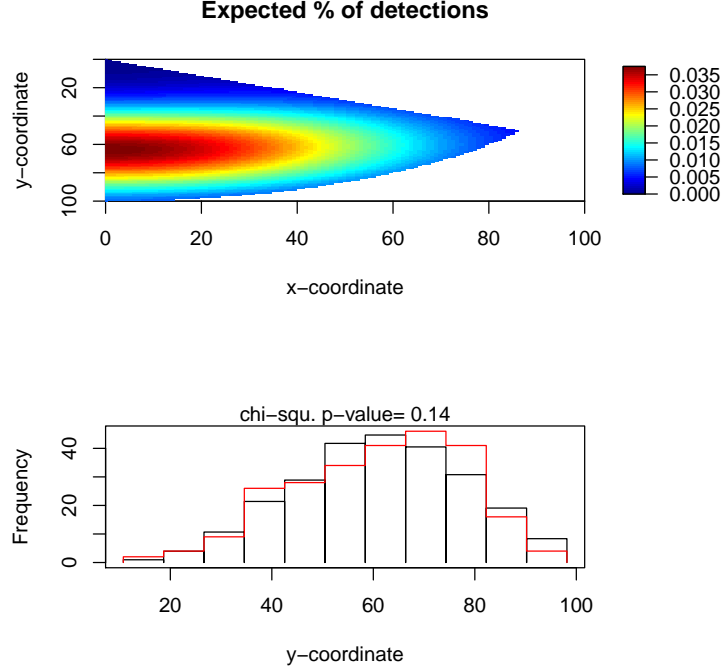to manually specify break points for the GoF bin intervals, allowing for varying bin widths.

Expected % of detections

Figure 2: Graphical display of one-dimensional χ^2 goodness-of-fit test. The upper panel is the expected percentage of detections, and lower panel a histogram of observed sightings and expected sightings.

5 Density estimation

In this example, we can estimate krill swarm volumetric (units: number of swarms per m^3 of sea) and areal swarm density (units: number of swarms per m^2 of sea surface). Once we have estimates of swarm density, we can estimate the number of swarms, $\hat{N}$ in the swarm region. Before we can calculate density, we need to estimate the probability of detecting a swarm in the rectangular area partially sampled by the multi-beam echosounder, $\hat{P}^*$ (Figure 1). Typically, we obtain $\hat{P}^*$ using parameter estimates of ϕ (vertical distribution of swarms) and Θ, (detection function) estimated using the `nupoint.fit` function.

11

5.1   Expected probability of detecting a swarm

The `nupoint.p.star` function is used to calculate, $\hat{P}^*$, (see Equation 3 of Cox et al. 2011). We use the `nupoint.p.star` function to evaluate $\hat{P}^*$ using the parameter estimates of the AIC selected optimum model (Normal vertical distribution form; Table 2)

```
> P.star=nupoint.p.star(pars.hat=norm.fit$par,
+                       grad.type=norm.grad.type,
+                       det.type=norm.det.type,
+                       w=100,theta.max=pi/3)
```

giving the estimated probability of detecting a krill swarm, $\hat{P}^*$, in the rectangular area partially sampled by the multi-beam echosounder (Figure 1) as 0.131.

5.2   Krill swarm density estimation

We estimate krill swarm volumetric density, $\hat{D}_{s3}$, using Equation 7 in Cox et al. [2011]. We use the `nupoint.vol.density` function to estimate $\hat{D}_{s3}$. We start by determining the number of krill swarms detected in the example data `nrow(krill)`, giving $n=251$. Next we determine the line transect line length, L. Each line transect was 2.5 km long, giving $2.5 \times 11 = 27.5$ km of line transect. Now we call `nupoint.vol.density` function:

```
> (vol.den=nupoint.vol.density(n.seen=nrow(krill),
+                              L=11*2.5*1e3,
+                              w=100,
+                              theta.max=pi/3,
+                              P.star=P.star))

[1] 4.010499e-06

> #swarms per m**3 of sea.
```

The areal density of krill swarms, $\hat{D}_s$ is calculated by multiplying the volumetric density by the truncation distance (100 m) $\hat{D}_{s3}w$, giving 4e-04 krill swarms m^{-2}.

5.3   Number of swarms and biomass

The estimated number of swarms, $\hat{N}$ in the survey region with area, A, is $\hat{N} = A\hat{D}_s$. The area of survey region for the `krill` example dataset is $A=$ 3300000 m^2, making $\hat{N} = 1323$ krill swarms.

The biomass, b, (units: g) of krill in each swarm is provided in `krill$bio.g`. Cox et al. [2011] estimated mean krill swarm biomass, $E[b]$ by regression. We repeat the procedure here (Figure 3).

The regression, Figure 3, gave an expected swarm biomass $\hat{E}[b] = 204.8$ kg. hence, survey region krill biomass, $\hat{E}[b] \times \hat{N} = 271$ tonnes.
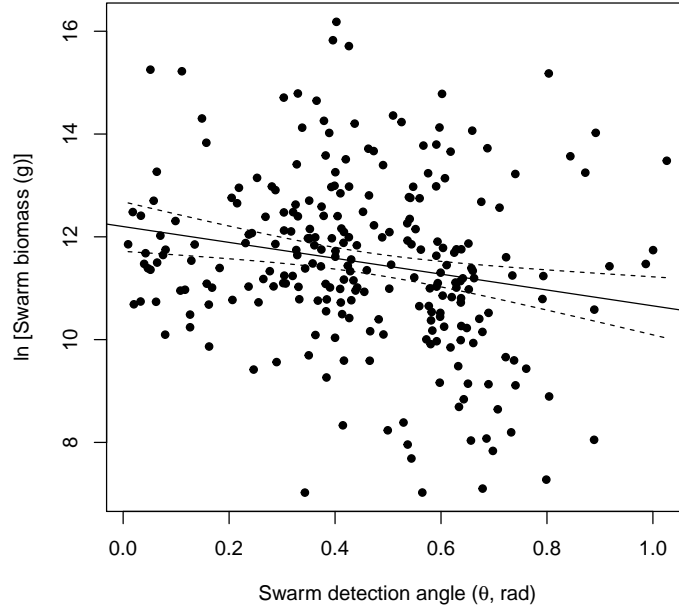
Figure 3: Estimate of mean swarm biomass: the individual krill swarm biomass estimated by using the intercept of the regression of log(swarm biomass) on the detection angle - - - - -, 95% confidence bounds. See Cox et al. [2011] for further details.

6   Variance estimation

We estimate variance of the depth distribution and detection function, as well as the variance of shoal density and abundance by non-parametric boot-strap, which has been implemented in the `nupoint.boot`. The sampling unit is specified in the blocking variable (`groupingVar`) and may be passed to the `nupoint.boot` function as either the grouping variable column name or column number. In this case the grouping variable is specified by observation day `groupingVar='transect'`.

In the following example we use the `nupoint.boot` function to calculate variance using for the normal form of depth distribution function `grad.type='NORM'`. The normal form was selected as optimum from the candidate depth preference models by AIC (Table 2):

```
> boot.res <- nupoint.boot(observations=krill,
+    nboot=100,
```

```
+    blockVar='transect',
+    initial.pars=norm.fit$par,
+    grad.type='NORM',
+    det.type='HNORM',
+    w=100,
+    theta.max=pi/3,
+    n=NULL,
+    attenuation=FALSE,
+    grid.density=100,
+    lower.b=c(1,1,1),
+    upper.b=c(120,100,100),
+    L=11*2.5*1e3,
+    A=3300000,
+    shoalBioMass='log(bio.g) ~ theta')
```

We used the estimated parameters for the normal distribution, [81.74, 25.14, 38.19], as the initial parameters `initial.pars=norm.fit$par` argument. Total line transect length, the `L` argument, has units m and the survey region area argument, `A` has units m^2. The choice of length and mass units is unimportant, but should be consistently applied. In the above example, expected shoal biomass $\hat{E}[b]$ was calculated for each transect interaction using the linear regression form specified in the `shoalBioMass` argument. Alternatively, a fixed value could have been specified, which would have resulted in the same $\hat{E}[b]$ being used in all bootstrap calculations. We obtain variance estimates for each of the depth preference gradient and half-normal detection function parameters (Table 3.) as well as density (not shown), abundance and biomass estimates.

	point.est	CV.percent	min	max
depth gradient mean	81.74	16.83	66.65	120.00
depth gradient sigma	25.14	23.73	16.61	43.92
detection sigma	38.19	7.64	32.94	51.16
P*	0.13	33.11	0.06	0.31
N hat	1323.46	31.54	571.09	3277.31
E[b], kg	204.80	23.48	126.53	337.86
Area B, tonnes	271.05	35.90	122.88	645.31

Table 3: Bootstrap results for the normal density gradient and half-normal detection function.

7 Attenuation function

During some surveys it may not be possible to always observe out to the truncation distance, w. Typically this situation will occur because of an obstruction that prevents observation beyond it, which in the krill example given

here, is the seabed. If a survey is conducted in open ocean then this is unlikely to be an issue, but nearshore surveys, such as Cox et al. [2009], the seabed depth varied along the transect line. `nupoint` follows the approach of Cox et al. [2011], and treats along-transect seabed depth as a random variable and uses a cumulative distribution to model the probability that the sea at a randomly chosen location was no less than y metres deep.

For convenience in the following example seabed depth under each krill swarm, `krill$z`, were used as observations to model attenuation, but any set of observations describing seabed depth could be used, not just seabed depth observations at a krill swarms. For example, Cox et al. [2011] used seabed depth observations, at 100 m along-transect intervals independently of where swarms were observed. In `nupoint` parameters for a seabed attenuation function are estimated using `make.atten.f()`. One of the outputs of `make.atten.f()` is to return a function called `atten.f` to the R workspace.

To take attenuation is taken into account, `nupoint.fit()` and `nupoint.env.fit()` call `atten.f()` from the R workspace. This means that `make.atten.f()` must be called before `nupoint.fit()`. In future `nupoint` releases, `make.atten.f()` will be incorporated into `nupoint.fit` and associated goodness-of-fit and bootstrap functions.

We start the example by checking the `workspace` for the `atten.f`:

```
> 'atten.f' %in% ls()
```

```
[1] FALSE
```

then fit create an attenuation function:

```
> atten.fit=make.atten.f(prep.dist=krill$z,form='norm',starting.pars=c(90,10))
```

```
the following seabed attenuation function has been returned to the R workspace:
atten.f<<- function(seabedDepth) 1-pnorm(seabedDepth,95.1141535839473,10.5625798419803)
```

Finally, check to see if `atten.fit` returned a the attenuation function `atten.f()` to the workspace:

```
> 'atten.f' %in% ls()
```

```
[1] TRUE
```

Using the `make.atten.f()` argument `plot=TRUE`, the empirical cumulative distribution function (ECDF) is plotted (Figure 4).

Now we call `nupoint.fit()` to estimate parameters for density gradient and detection functions under seabed atenuation. We start by using the same `nupoint.fit()` arguments as the `nupoint.fit()` call in Section 3:

```
> norm.grad.type <- "NORM" #swarm depth preference form.
> norm.det.type <- "HNORM"
> norm.pars <- c(50,20,50) #starting values for
```
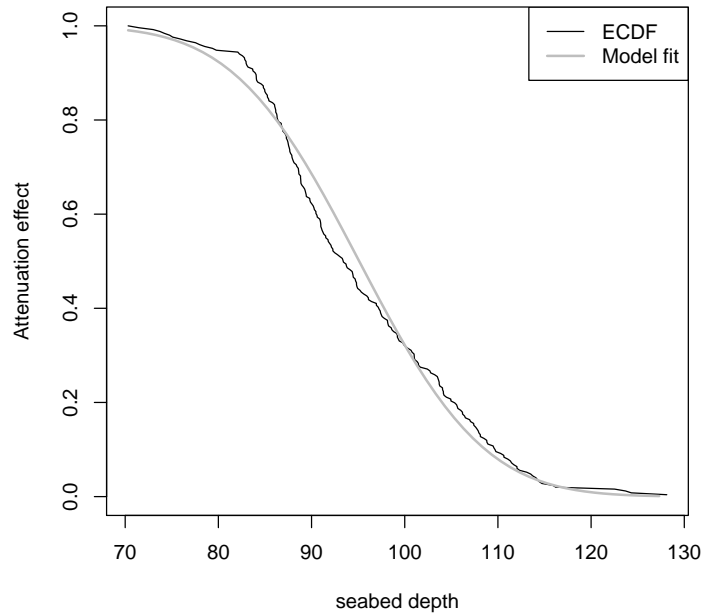
Figure 4: The empirical cumulative distribution function used to model seabed attenuation.

```
>    #paramter vector to be estmated
>    #[1] = normal depth preference function mu;
>    #[2] = normal depth preference function sigma;
>    #[3] half-normal detection function sigma.
> norm.LB <- c(1,1,1) #lower parameter space bound.
> norm.UB <- c(120,100,100) #upper parameter space bound.
```

We then call `nupoint.fit()` to simultaneously estimate the depth distribution, ϕ, and detection function parameters, Θ:

```
> norm.fit.atten <- nupoint.fit(norm.pars,
+                     sight.x=krill$x,
+                     sight.y=krill$y,
+                     sight.z=krill$z,
+                     w=100,
+                     theta.max=pi/3,
+                     grad.type=norm.grad.type,
+                     det.type=norm.det.type,
```

```
+                        lower.b=norm.LB,
+                        upper.b=norm.UB)

---------------------------
Parallel density gradient likelihood settings
---------------------------
Depth preference parametric form: NORM
range detection function, g(r), parametric form: HNORM
Parameter starting values = 50 20 50
Angular detection function applied: FALSE
Seabed attenuation function applied: TRUE
function(seabedDepth) 1-pnorm(seabedDepth,95.1141535839473,10.5625798419803)
<environment: 0x07e20ed8>
Truncation distance = 100
Swath (max) angle, rad = 1.047198
Numerical integration grid density= 100
---------------------------
Estimating parameters
---------------------------
Maximum likelihood results
---------------------------
parameter estimates
93.758 29.525 38.274
AIC = 482.89
---------------------------
```

When considering attenuation by the seabed, estimated mean krill swarm depth, $\hat{\phi}_1$, increased to 93.8 m, *cf* 81.7 m without attenuation. When data seabed depth data is passed into nupoint.ft() via the sight.z argument, nupoint.ft() calls atten.f() from the R workspace. We use nupoint.gof() to calculate χ^2 goodness-of-fit, for the norm.fit.atten object:

```
> norm.atten.gof=nupoint.gof(y.obs=krill$y,
+                 pars=norm.fit.atten$par,
+                 w=100,
+                 grad.type='NORM',
+                 det.type='HNORM',
+                 n=NULL,
+                 intervals=11,
+                 attenuation=TRUE,
+                 theta.max=pi/3,
+                 grid.resolution=100)

-------------------------------------------------------
nupoint: 1D Chi-squared Goodness-of-Fit results
-------------------------------------------------------
   bin.min bin.max  mids expected observed Chisq
```

```
1      10.74    18.69 14.71      1.17       2   0.58
2      18.69    26.63 22.66      4.40       4   0.04
3      26.63    34.58 30.60     10.99       9   0.36
4      34.58    42.52 38.55     20.98      26   1.20
5      42.52    50.47 46.50     27.72      28   0.00
6      50.47    58.42 54.44     40.16      34   0.95
7      58.42    66.36 62.39     44.21      41   0.23
8      66.36    74.31 70.34     42.05      46   0.37
9      74.31    82.26 78.28     33.12      41   1.88
10     82.26    90.20 86.23     19.48      16   0.62
11     90.20    98.15 94.17      6.72       4   1.10
--------------------------------------------------------
Chi-squ. statistic   =  7.331244
Number of parameters =  3
Chi-squ. df          =  7
Chi-squ. GoF p-value =  0.3952244
--------------------------------------------------------
```

resulting in a χ^2 goodness-of-fit p-value = 0.4.

References

M. J. Cox, D. A. Demer, J. D. Warren, G. R. Cutter, and A. S. Brierley. Multibeam echosounder observations reveal interactions between Antarctic krill and air-breathing predators. *Marine Ecology Progress Series*, 378:199–209, 2009.

M.J. Cox, D.L. Borchers, D.A. Demer, G.R. Cutter, and A.S. Brierley. Estimating the density of Antarctic krill (Euphausia superba) from multi-beam echo-sounder observations using distance sampling methods. *Journal of the Royal Statistical Society: Series C (Applied Statistics)*, 60(2):301–316, 2011.