Kia Ora!

(Hello)

Using R to Estimate Animal Population Density

Some problems with simply counting animals:

- Animals move
- Tiny animals or camouflaging animals can be very difficult to spot
- Double counting can be hard to avoid when relying on our sight alone

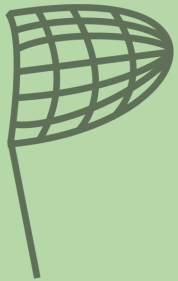
?

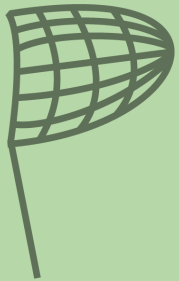
R

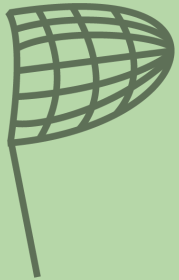
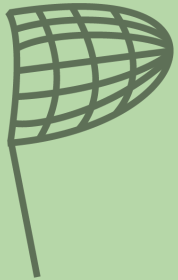
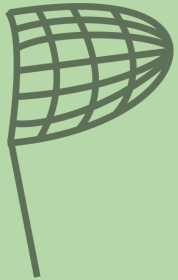
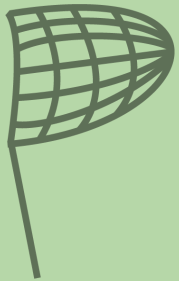
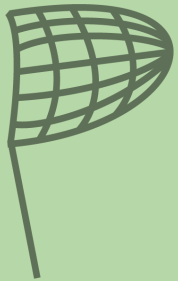
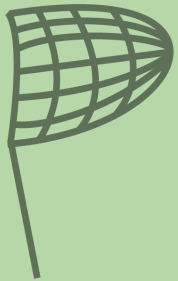
Definitions:

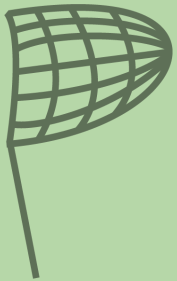
- N = The total number of animals... but where?
- A = The survey region
- Density = N/A

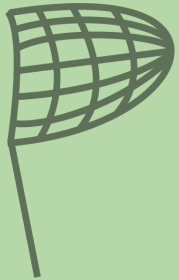
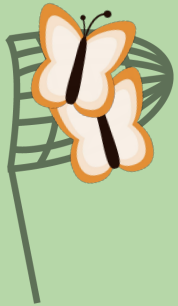
- Spatially explicit capture-recapture (SECR)
- Acoustic spatial capture-recapture (ASCR)*

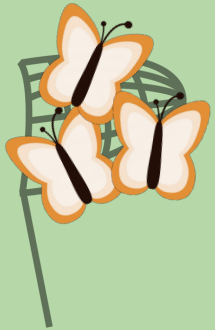
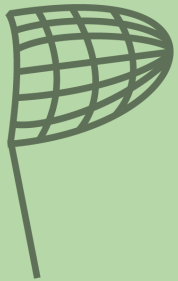
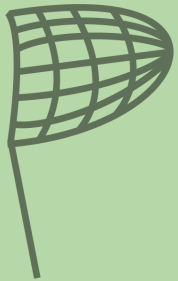


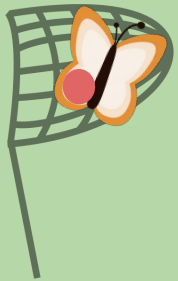
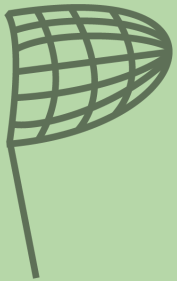


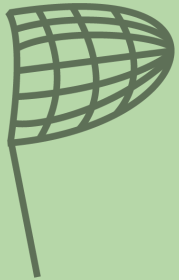
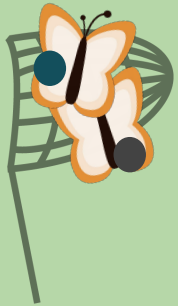
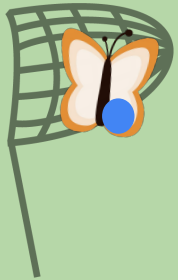
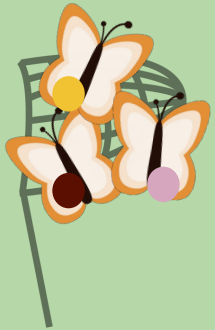
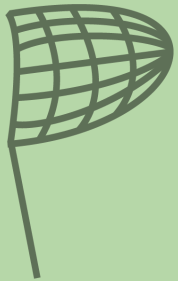
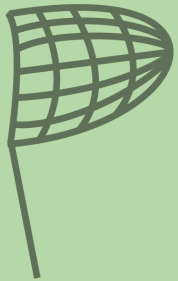







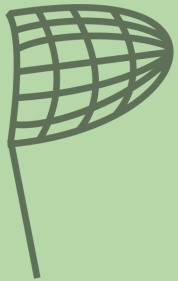


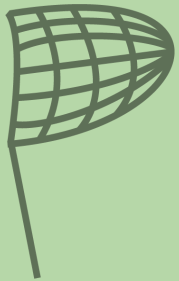



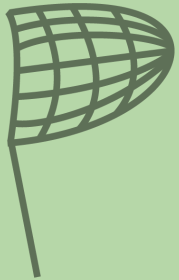
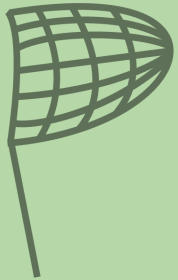
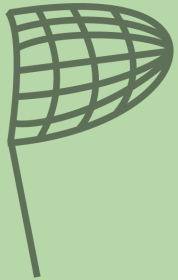
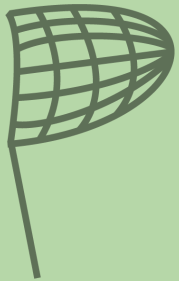
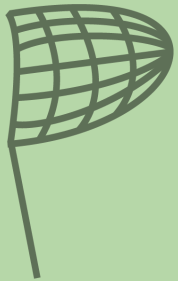
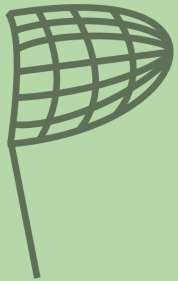




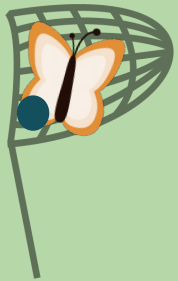
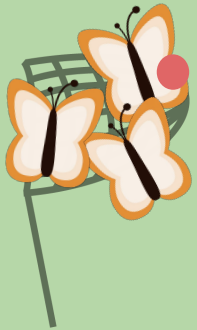



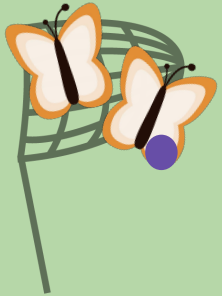
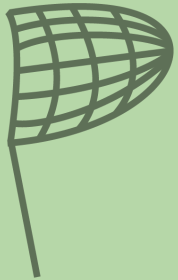







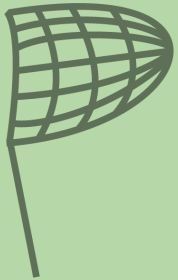
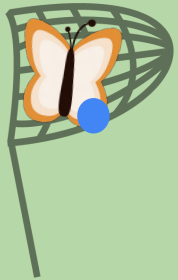
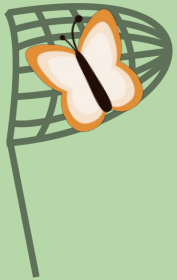


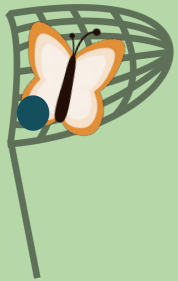
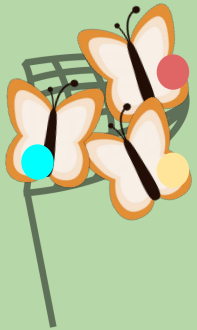
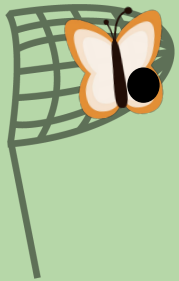


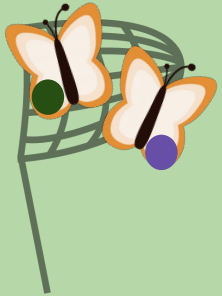
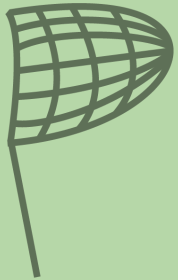
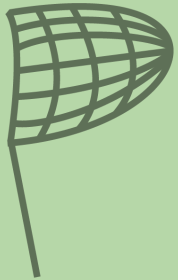
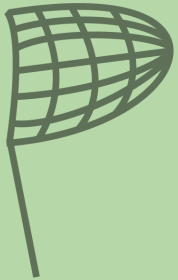
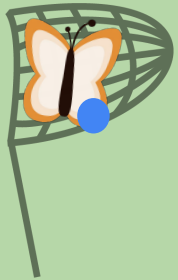
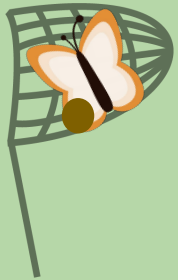







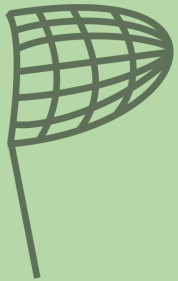



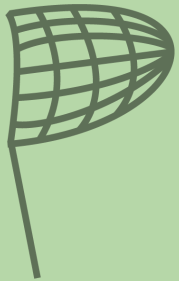



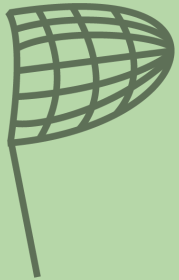
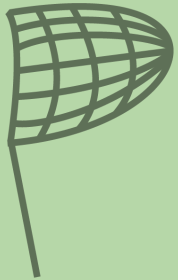
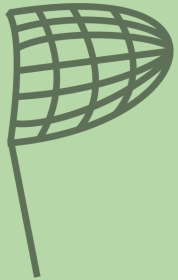
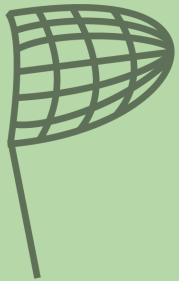
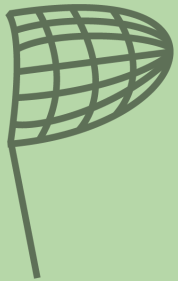
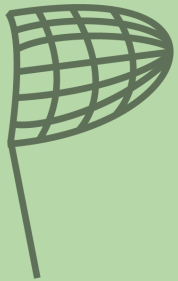








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Detection occasions

Animals

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3	0	0	1	0	1
4	0	1	0	1	1
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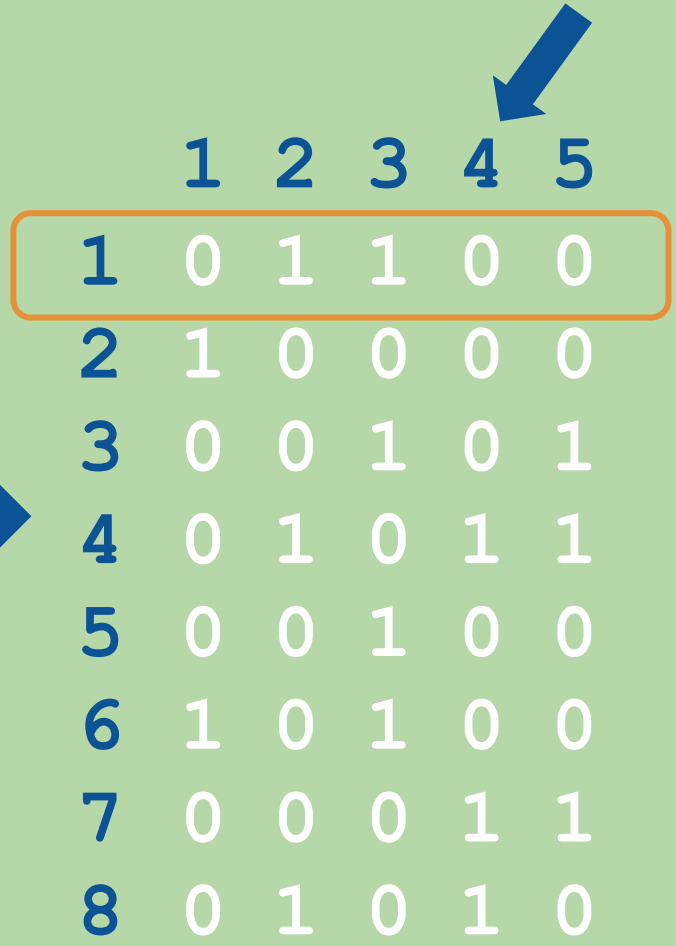
Detection occasions
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8 0 1 0 1 0
Animals
Butterfly 1 was detected on the second and third occasions only.

Detection occasions

Animals

	1	2	3	4	5
1	0	1	1	0	0
2	1	0	0	0	0
3	0	0	1	0	1
4	0	1	0	1	1
5	0	0	1	0	0
6	1	0	1	0	0
7	0	0	0	1	1
8	0	1	0	1	0

The first time we set up our nets, we only captured two butterflies: butterfly 2 and butterfly 6.

Multi-session binary capture history

Session 1	Session 2	Session 3
0 1 1 0 0	1 0 1 0 1	1 1 0 1 0
1 0 0 0 0	0 0 0 0 0	0 0 1 0 1
0 0 1 0 1	1 0 1 0 0	0 1 1 0 0
0 1 0 1 1	1 1 0 0 0	1 1 0 0 1
0 0 1 0 0	1 0 1 1 0	0 0 0 1 1
1 0 1 0 0	0 0 1 0 1	0 0 1 0 0
0 0 0 1 1	0 0 0 0 0	1 1 1 0 1
0 1 0 1 0	1 0 1 0 0	1 0 1 1 0

The `secr` package

Authors: Murray Efford, Philipp Jund, David Fletcher

https://www.otago.ac.nz/density/,
https://github.com/MurrayEfford/secr/
https://www.stats.otago.ac.nz/secrapp/

Example data

```
#Load the secr library
install.packages("secr")
library(secr)

#List available example datasets
data(package = "secr")
```

```
Data sets in package 'secr':

LStraps (skink)                 Skink Pitfall Data
OVpossumCH (OVpossum)           Orongorongo Valley Brushtail Possums
captXY (secrdemo)               SECR Models Fitted to Demonstration Data
captdata (secrdemo)             SECR Models Fitted to Demonstration Data
deermouse.ESG (deermouse)       Deermouse Live-trapping Datasets
deermouse.WSG (deermouse)       Deermouse Live-trapping Datasets
hornedlizardCH (hornedlizard)   Flat-tailed Horned Lizard Dataset
housemouse                      House mouse live trapping data
infraCH (skink)                 Skink Pitfall Data
lineoCH (skink)                 Skink Pitfall Data
ovenCH (ovenbird)               Ovenbird Mist-netting Dataset
ovenCHp (ovenbird)              Ovenbird Mist-netting Dataset
ovenbird.model.1 (ovenbird)     Ovenbird Mist-netting Dataset
ovenbird.model.D (ovenbird)     Ovenbird Mist-netting Dataset
ovenmask (ovenbird)             Ovenbird Mist-netting Dataset
ovensong.model.1 (ovensong)     Ovenbird Acoustic Dataset
ovensong.model.2 (ovensong)     Ovenbird Acoustic Dataset
possum.model.0 (possum)         Brushtail Possum Trapping Dataset
possum.model.Ds (possum)        Brushtail Possum Trapping Dataset
possumCH (possum)               Brushtail Possum Trapping Dataset
possumarea (possum)             Brushtail Possum Trapping Dataset
possummask (possum)             Brushtail Possum Trapping Dataset
possumremovalarea (possum)      Brushtail Possum Trapping Dataset
secrdemo.0 (secrdemo)           SECR Models Fitted to Demonstration Data
secrdemo.CL (secrdemo)          SECR Models Fitted to Demonstration Data
secrdemo.b (secrdemo)           SECR Models Fitted to Demonstration Data
signalCH (ovensong)             Ovenbird Acoustic Dataset
stoat.model.EX (stoatDNA)       Stoat DNA Data
stoat.model.HN (stoatDNA)       Stoat DNA Data
stoatCH (stoatDNA)              Stoat DNA Data
trapXY (secrdemo)               SECR Models Fitted to Demonstration Data
```

The *Brushtail Possum Trapping Dataset*

From the **`secr`** vignette:

Description: Data from a trapping study of brushtail possums at Waitarere, North Island, New Zealand.

Source: Landcare Research, New Zealand

The *Brushtail Possum Trapping Dataset*

Some background:

- Brushtail possums are an Australian species and considered an invasive species in New Zealand.
- Vectors of bovine tuberculosis.
- Damage native vegetation.
- Threat to native birds.

Example data

The components of the data:

- Capture histories (**`possumCH`**)
- Mask (**`possummask`**)
- Habitat perimeter (**`possumarea`**)

The Capture Histories

```
possumCH

Session =  WaitarerePossums
, , 1

     1 2 3 4 5
1501 0 0 0 0 0
1502 0 0 0 0 0
1503 0 0 0 0 0
1504 0 0 0 0 0
1506 0 0 0 0 0
1509 0 0 0 0 0
...
```

... and so on

```
summary(possumCH)

Object class        capthist
Detector type       single
Detector number     180
Average spacing     20 m
x-range             2697793 2699225 m
y-range             6077470 6078201 m

Counts by occasion
                     1   2   3   4   5 Total
n                   61  51  55  66  72   305
u                   61  19   9  14   9   112
f                   32  21  23  18  18   112
M(t+1)              61  80  89 103 112   112
losses               0   0   0   0   0     0
detections          61  51  55  66  72   305
detectors visited   61  51  55  66  72   305
detectors used     180 180 180 180 180   900

Individual covariates
 prev.tagged
 Mode :logical
 FALSE:104
 TRUE :8
```

```
summary(possumCH)

Object class       capthist
Detector type      single
Detector number    180
Average spacing    20 m
x-range            2697793 2699225 m
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detectors used      180 180 180 180 180   900

Individual covariates
 prev.tagged
 Mode :logical
 FALSE:104
 TRUE :8
```

The Mask

A mask is a defined habitat region around the detectors/traps, divided into ‘cells’.

https://www.otago.ac.nz/density/pdfs/secr-habitatmasks.pdf

```
head(possummask)

          x       y
58 2698543 6077080
59 2698563 6077080
60 2698583 6077080
61 2698603 6077080
62 2698623 6077080
63 2698643 6077080
```

The Study Area

The study area is simply the coordinates of the perimeter of the survey region.

```
head(possumarea)

         x       y
1 2697117 6075605
2 2697197 6075953
3 2697260 6076226
4 2697284 6076351
5 2697316 6076513
6 2697359 6076799
```

Visualize the study area

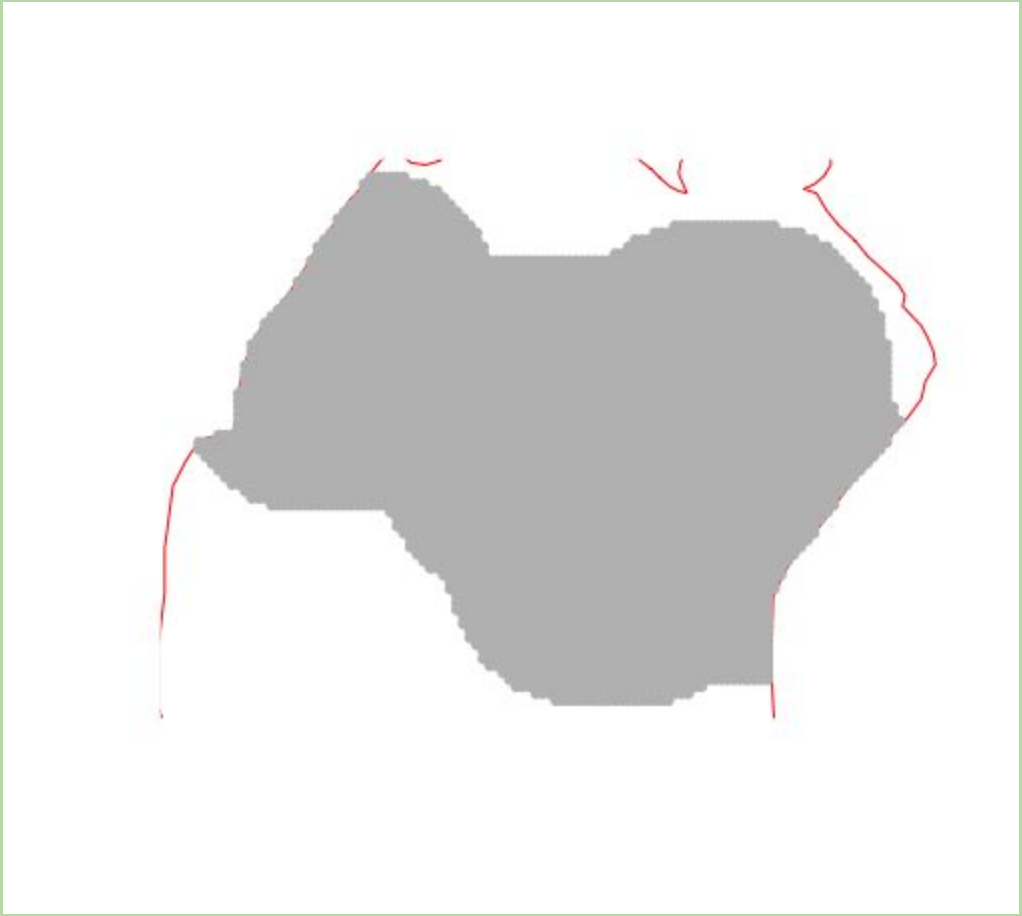
Code from the **`secr`** *vignette*

```
plot(possummask)
plot(possumCH, tracks = TRUE, add = TRUE)
plot(traps(possumCH), add = TRUE)
lines(possumarea)
```

Visualize the study area

Code from the **`secr`** *vignette*

```
plot(possummask)
plot(possumCH, tracks = TRUE, add = TRUE)
plot(traps(possumCH), add = TRUE)
lines(possumarea)
```



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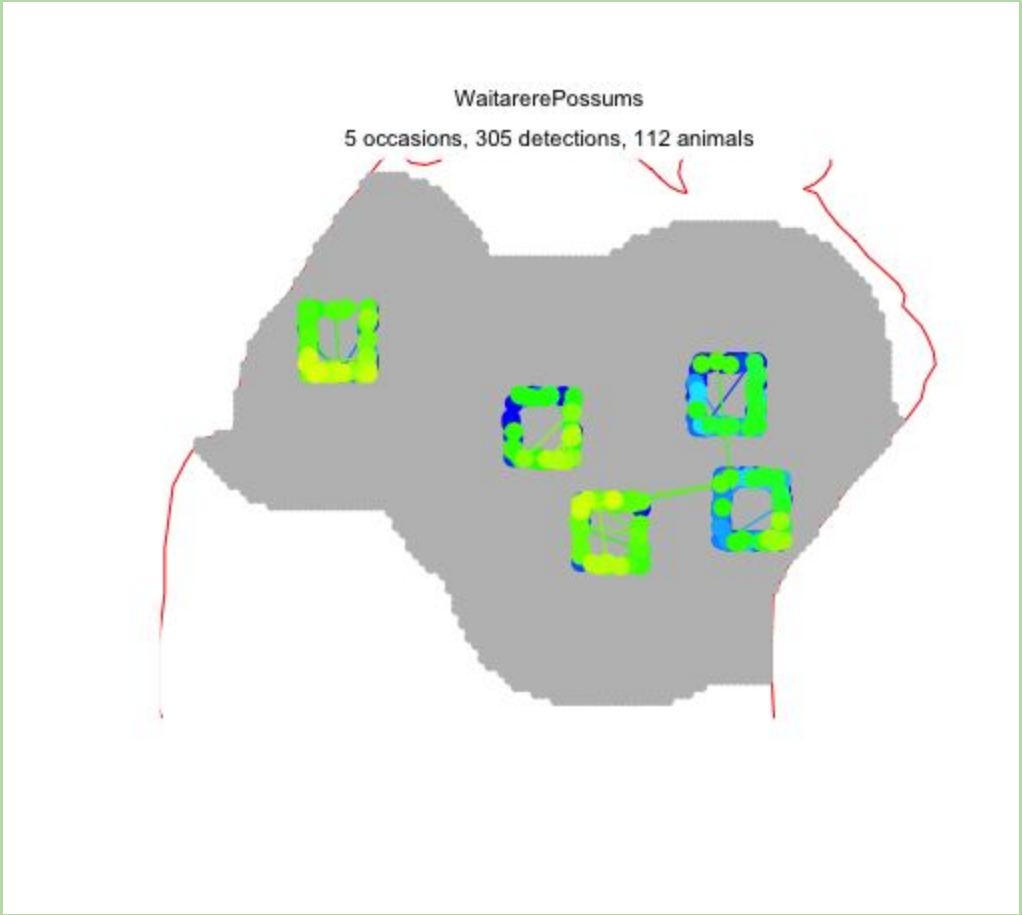
WaitarerePossums
5 occasions, 305 detections, 112 animals

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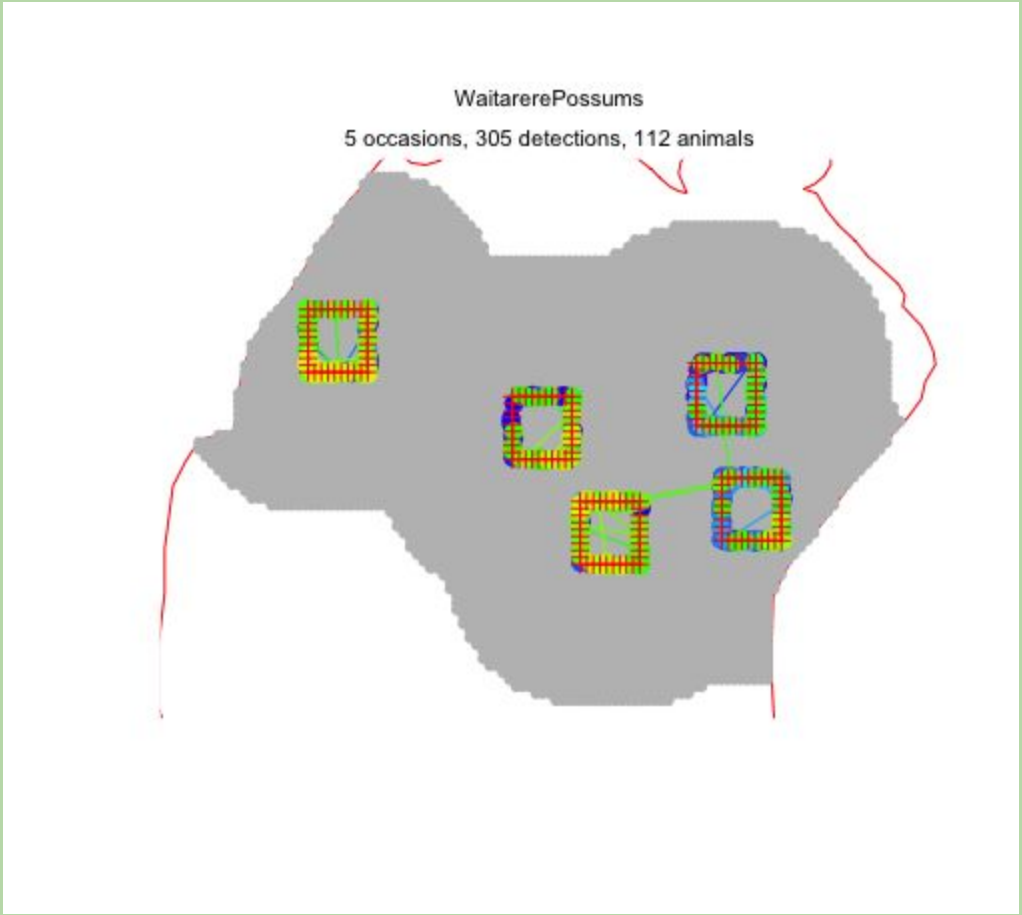
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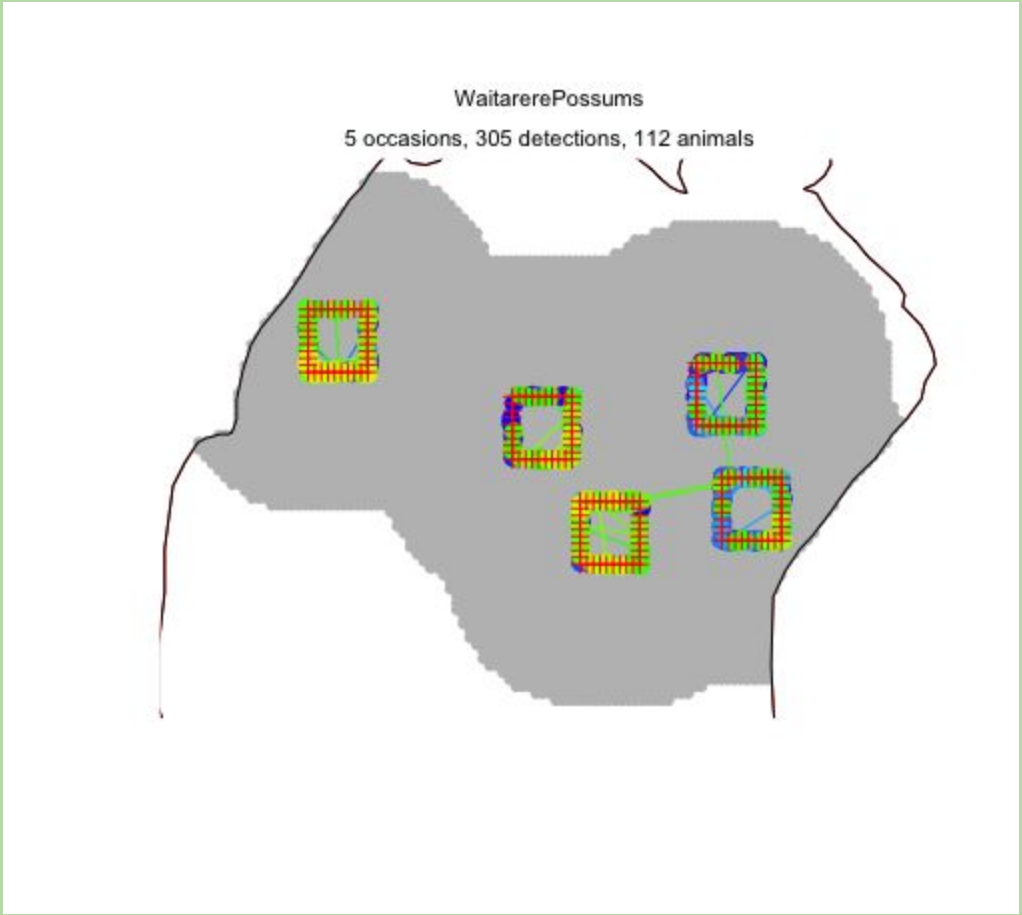
```


WaitarerePossums
5 occasions, 305 detections, 112 animals

Create some models

The Null Model

```
#Create a null model
possum.null <- secr.fit(capthist = possumCH, model
= list(D~1, g0~1, sigma~1), mask = possummask,
trace = F)
summary(possum.null)
```

Note: you can find this model already pre-fitted in the **secr** *package. It is called* **possum.model.0**

Create some models

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Note: you can find this model already pre-fitted in the **secr** *package. It is called* **possum.model.0**

Output part 1:

```
$traps
 Detector Number Spacing UsagePct
   single    180      20      100

$capthist
 Occasions Detections    Animals  Detectors       Moves   Animals2
         5        305        112        180         184         80

$mask
 Cells Spacing  Area
  5120      20 204.8

$modeldetails
    CL fixed distribution hcov
 FALSE  none      poisson
```

Output part 2:

```
$AICtable
            model   detectfn npar    logLik      AIC     AICc
 D~1 g0~1 sigma~1 halfnormal    3 -1097.107 2200.214 2200.437

$coef
             beta    SE.beta        lcl        ucl
D       0.5257912 0.10283337  0.3242415  0.7273409
g0     -1.4354960 0.14050246 -1.7108757 -1.1601162
sigma   3.9415010 0.04961677  3.8442539  4.0387481

$predicted
       link   estimate SE.estimate        lcl        ucl
D       log  1.6917969  0.17443411  1.3829813  2.0695701
g0    logit  0.1922438  0.02181808  0.1530502  0.2386462
sigma   log 51.4958399  2.55663044 46.7238130 56.7552466
```

Output part 2:

```
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                 model   detectfn npar    logLik      AIC     AICc
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g0     logit  0.1922438  0.02181808  0.1530502  0.2386462
sigma    log 51.4958399  2.55663044 46.7238130 56.7552466
```

The Detection Function

A detection function models the probability of detection from the distance of the animal to the detector.

Common detection functions:

- Halfnormal
- Hazard rate
- Exponential
- Uniform

Detectors don’t have to be traps

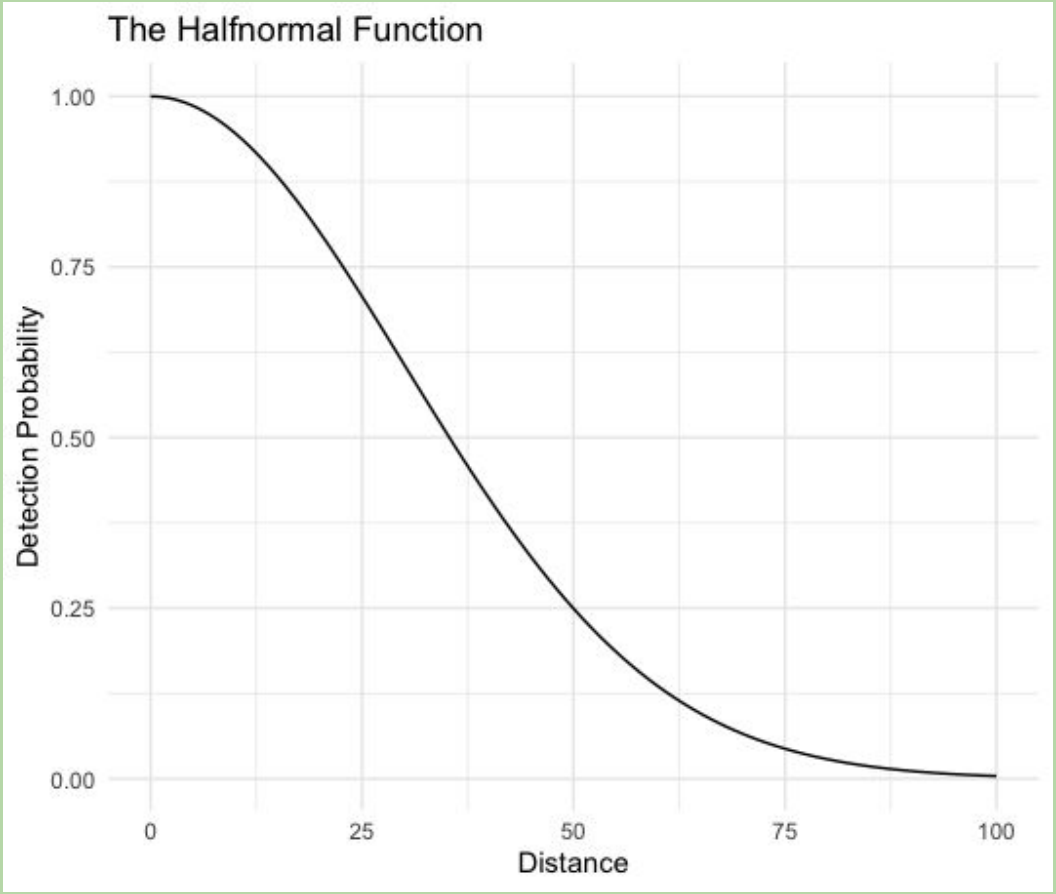
Other examples of detectors include:

- Camera traps
- Hair snares
- Microphones*

Halfnormal Detection Function

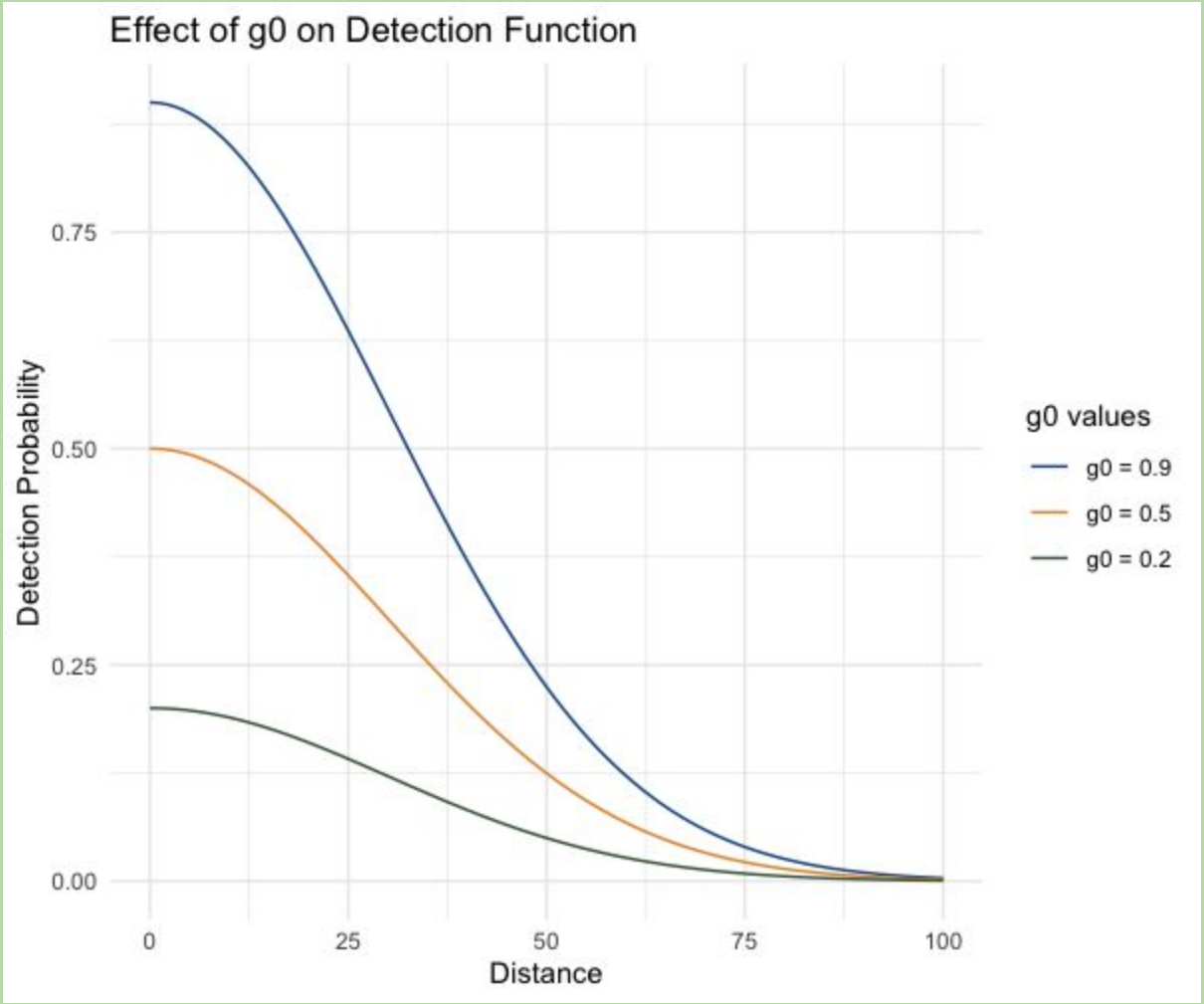
$$g(d) = g_0 \exp\left(\frac{-d^2}{2\sigma^2}\right)$$

Halfnormal Detection Function



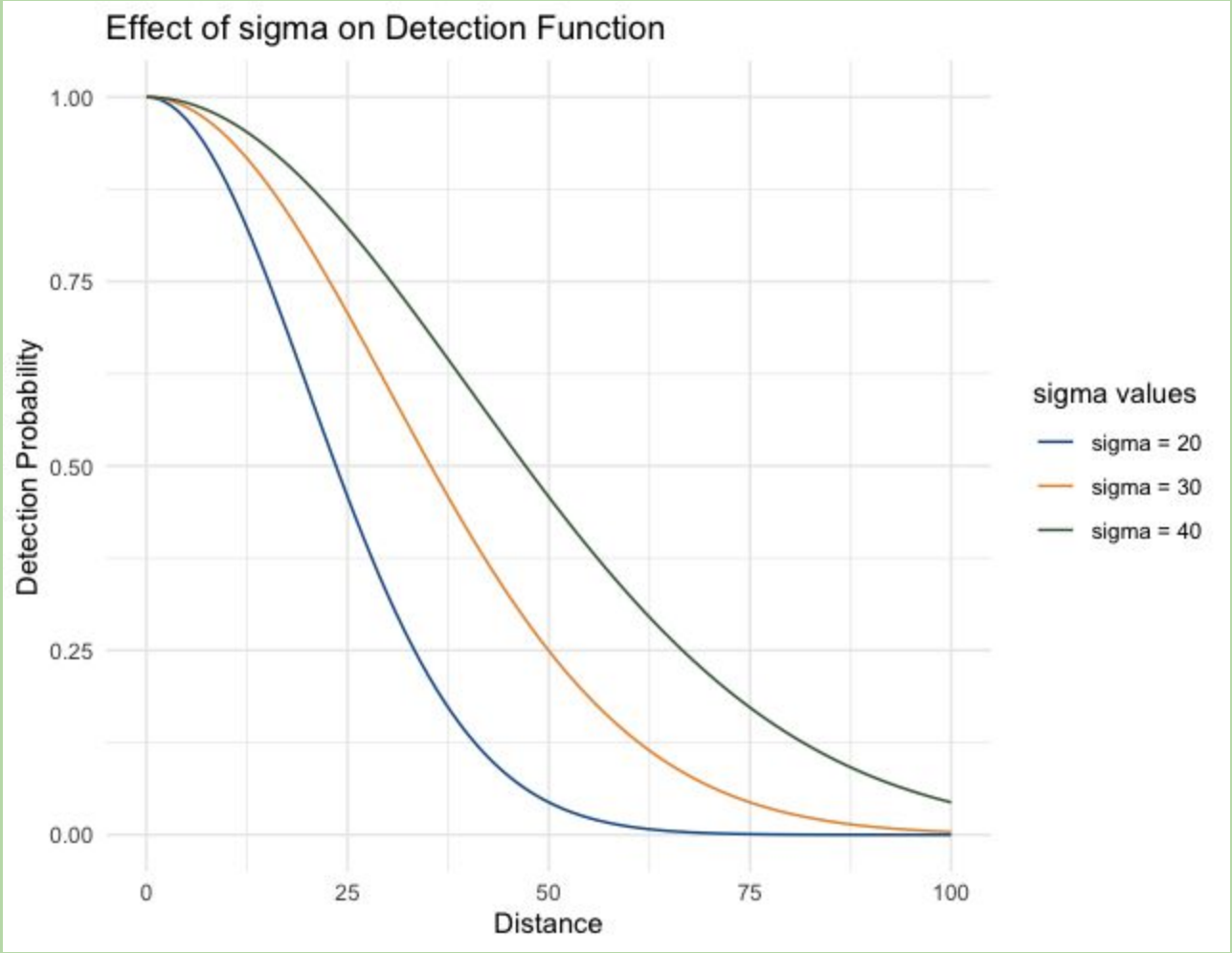
Detection Function Parameters: **g0**

g0 is the probability of trapping/detecting the animal when its distance from the trap is zero, i.e. it is the ‘baseline detection probability’


Effect of g0 on Detection Function
Detection Probability
0.75
0.50
0.25
0.00
0
25
50
75
100
Distance
g0 values
g0 = 0.9
g0 = 0.5
g0 = 0.2

Detection Function Parameters: **sigma (σ)**

Sigma is the scale at which the detection probability decreases as the distance between the animal and the detector/trap decreases


Effect of sigma on Detection Function
1.00
0.75
0.50
0.25
0.00
Detection Probability
0
25
50
75
100
Distance
sigma values
sigma = 20
sigma = 30
sigma = 40

Output part 2:

```
$AICtable
            model   detectfn npar    logLik      AIC     AICc
 D~1 g0~1 sigma~1 halfnormal    3 -1097.107 2200.214 2200.437

$coef
             beta    SE.beta        lcl        ucl
D       0.5257912 0.10283337  0.3242415  0.7273409
g0     -1.4354960 0.14050246 -1.7108757 -1.1601162
sigma   3.9415010 0.04961677  3.8442539  4.0387481

$predicted
       link   estimate SE.estimate        lcl        ucl
D       log  1.6917969  0.17443411  1.3829813  2.0695701
g0    logit  0.1922438  0.02181808  0.1530502  0.2386462
sigma   log 51.4958399  2.55663044 46.7238130 56.7552466
```

Create some models

Using covariates in models

```
#Create a model using a covariate
possum.ds <- secr.fit(capthist = possumCH, model =
list(D ~ d.to.shore), mask = possummask,
    link = list(D = "identity"), method =
"Nelder-Mead", trace = FALSE)
summary(possum.ds)
```

Note: you can find this model already pre-fitted in the **secr** *package. It is called* **possum.model.Ds**

Create some models

Using covariates in models

```
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 Detector Number Spacing UsagePct
   single    180      20      100

$capthist
 Occasions Detections    Animals  Detectors       Moves   Animals2
         5        305        112        180         184         80

$mask
 Cells Spacing  Area
  5120      20 204.8

$modeldetails
    CL fixed distribution hcov
 FALSE  none      poisson
```

Output part 2:

```
$AICtable
                      model   detectfn npar    logLik      AIC     AICc
 D~d.to.shore g0~1 sigma~1 halfnormal    4 -1096.511 2201.021 2201.395

$coef
                       beta      SE.beta          lcl           ucl
D              2.0396902453 0.2300789442  1.588743801  2.4906366896
D.d.to.shore -0.0008351331 0.0002804306 -0.001384767 -0.0002854992
g0           -1.4347928503 0.1406632548 -1.710487764 -1.1590979369
sigma         3.9421270063 0.0497832001  3.844553727  4.0397002856

$predicted
          link  estimate SE.estimate        lcl        ucl
D     identity  1.490883   0.1760654  1.1458014  1.8359651
g0       logit  0.192353   0.0218525  0.1531005  0.2388312
sigma      log 51.528085   2.5668232 46.7378219 56.8093137
```

Compare Models

We can compare models to determine which one is the best fit for the possum data using the *Akaike Information Criterion (AIC).*

```
AIC(possum.null, possum.ds)
modelAverage(possum.null, possum.ds)
```

Compare Models

We can compare models to determine which one is the best fit for the possum data using the *Akaike Information Criterion (AIC).*

```
AIC(possum.null, possum.ds)
modelAverage(possum.null, possum.ds)
```

	model	detectfn	npar	logLik	AIC	AICc	dAICc	AICcwt
possum.null	D~1 g0~1 sigma~1	halfnormal	3	-1097.107	2200.214	2200.437	0.000	0.6175
possum.ds	D~d.to.shore g0~1 sigma~1	halfnormal	4	-1096.511	2201.021	2201.395	0.958	0.3825

Compare Models

We can compare models to determine which one is the best fit for the possum data using the *Akaike Information Criterion (AIC).*

```
AIC(possum.null, possum.ds)
modelAverage(possum.null, possum.ds)
```

	estimate	SE.estimate	lcl	ucl
D	2.4471863	1.26968527	0.9398882	6.3717371
g0	0.1922856	0.02183131	0.1530693	0.2387171
sigma	51.5081714	2.56057924	46.7290795	56.7760321

	estimate	SE.estimate	lcl	ucl
D	2.4471863	1.26968527	0.9398882	6.3717371
g0	0.1922856	0.02183131	0.1530693	0.2387171
sigma	51.5081714	2.56057924	46.7290795	56.7760321

Brief Notes on Acoustic Capture-Recapture

- We can't always physically see or capture animals, but sometimes we can hear them, .e.g. tiny frogs or huge whales.
- Capture histories give us information about estimated bearings, estimated distances, and received signal strengths.
- We estimate call density, rather than animal density.
- We have to independently collect data on call rate.
- We can then estimate animal density by dividing call density by call rate.

R Packages for ASCR Models

- **`ascr`** (https://github.com/b-steve/ascr)
- **`acre`** (https://github.com/b-steve/acre)

Credits and References

Ben Stevenson, The University of Auckland
Professor James Russell, The University of Auckland

The University of Otago (2023, July 14). *DENSITY: spatially explicit capture-recapture*. https://www.otago.ac.nz/density/

Efford M (2023). *secr: Spatially explicit capture-recapture models*. R package version 4.6.1, https://CRAN.R-project.org/package=secr.

Ngā Mihi

(Thank You)