Initial population sizes

August 16, 2022

Preamble

This is an Electronic Supplement to the manuscript Marques et al. "Quantifying Deepwater Horizon oil spill induced injury on pelagic cetaceans" submitted to Marine Ecology Progress Series (MEPS).

There are 7 Electronic Supplements to the paper. The master file containing links to all the other 6 additional Electronic Supplements related to this paper is ES0_ElectronicSupplements.

You might be reading this file as a pdf or as an html. The links on this file only work if you are using the html version of it, available via the github repository or if you compiled it yourself as html and you have all the 7 html files in the same folder. Otherwise, as a pdf distributed as an Electronic Supplement to the MEPS paper, the links might not work. ***They might work. If it is possible, we can work with the MEPS Editorial Office such that we can add links below that will link to actual files, say the pdfs of each of these 7 files, on the publisher server***.

Version history

This section details the version history for static pdf files submitted as Electronic Supplement pdfs:

- 1.0 [12 Aug 2022] Version included as a pdf Electronic Supplement in the MEPS original submission

Introduction

In this document we present the distribution for the initial population sizes, population exposed and proportion exposed for each of the stocks considered in the pelagic paper.

These population sizes were obtained from the models of

Roberts, J. J.; Best, B. D.; Mannocci, L.; Fujioka, E.; Halpin, P. N.; Palka, D. L.; Garrison, L. P.; Mullin, K. D.; Cole, T. V. N.; Khan, C. B.; McLellan, W. A.; Pabst, D. A. & Lockhart, G. G. 2016 Habitat-based cetacean density models for the U.S. Atlantic and Gulf of Mexico *Scientific Reports* **6**: 22615 DOI: 10.1038/srep22615

To obtain the number of animals exposed to oil (and hence the proportion of the population exposed to oil) the estimated fraction of the population based on the density surfaces that was contained in the area considered to be affected by oil was quantified. This area is shown in the image below
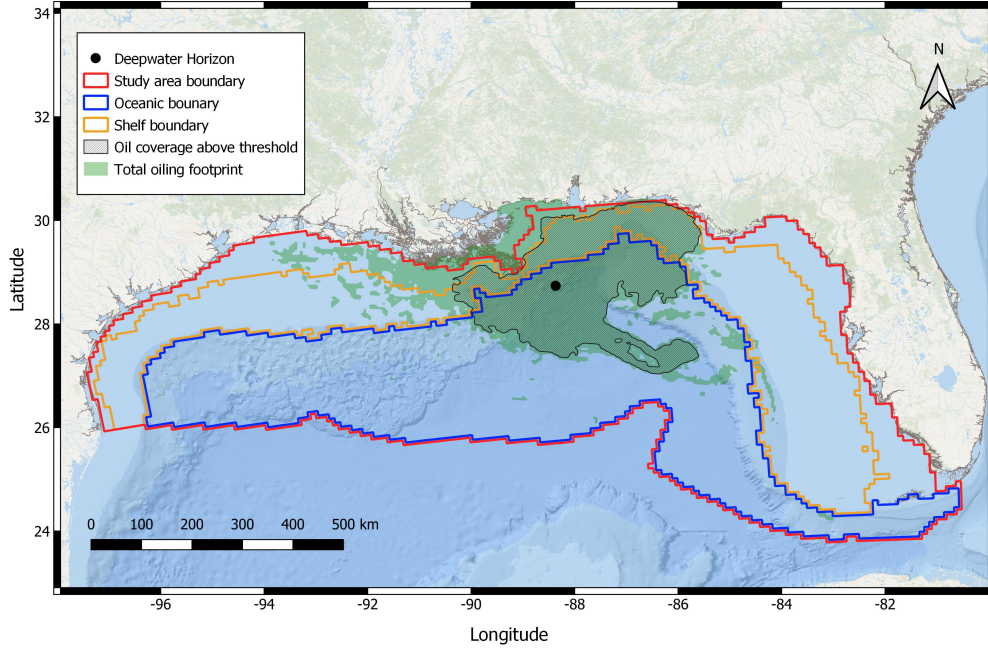
The taxonomic units considered and the corresponding codes are:

- Bwsp - beaked whales, Beaked whales sppp
- Fatt - pygmy killer whale, *Feresa attenuata*
- Ggri - Risso's dolphin, *Grampus griseus*
- Gmac - short-finned pilot whale, *Globicephala macrorhynchus*
- Kosp - Kogia whales, *Kogia* spp.
- Pele - melon-headed whale, *Peponocephala electra*
- Pmac - sperm whale, *Physeter macrocephalus*
- Satt - pantropical spotted dolphin, *Stenella attenuata*
- Sbre - rough-toothed dolphin, *Steno bredanensis*
- Scly - Clymene dolphin, *Stenella clymene*
- Scoe - striped dolphin, *Stenella coeruleoalba*
- Sfro - Atlantic spotted dolphin, *Stenella frontalis*
- Slon - spinner dolphin, *Stenella longirostris*
- Ttro - offshore bottlenose dolphins, *Tursiops truncatus*
- Ttrs - shelf bottlenose dolphins, *Tursiops truncatus*

Population size and proportion exposed

For each taxonomic unit, we present estimated total population size, the estimated population size within the area covered (above threshold) by oil, and also show maps of density to demonstrate how the above values were derived.

The realizations of population size, both for the total abundance as well as the proportion of animals exposed to oil, are in 2 separate files:

- `N_boot.csv` - 10000 bootstrap replicates of the initial population size
- `N_boot_in_oil.csv` - 10000 bootstrap replicates of the population size within the oil coverage

For each taxonomic unit, both of these files are provided in the corresponding folder at the above github repository. All taxonomic units files are inside the corresponding folder inside the folder `InOutBySp`.

To present a spatial perspective of the abundances we require 2 shapefiles (provided in the folder `InputFiles` at the above github repository) common to all pelagic taxonomic units:

- `OilCoverage.shp` - the oil coverage above a threshold
- `Study_Area_GOM_10km_Polygon` - the study area in 10 km grid cells

and two files per pelagic taxonomic unit:

- `N_bycell.csv` - the point estimate of the number of animals per grid cell, where grid cells are defined in `Study_Area_GOM_10km_Polygon`;
- `Prediction_Area.img` - the prediction area for each species

As above, these taxonomic unit specific files are in the folder `InOutBySp`, stored under a sub-folder corresponding to each taxonomic unit.

We can plot these abundance distributions and density estimates over species in turn for each taxonomic unit.

In the following we produce a plot for the initial population versus the exposed population and for the initial population versus the proportion exposed for each of the stocks considered, illustrating the potential correlation structure between these. We also output the (usually 0 or very small) number of bootstrap resamples that were removed from further analysis for each species because they represented unrealistically large population sizes. These unrealistic realizations were created due to correspondingly unrealistic GAM extrapolations in the limits of the study area.

```
## [1] "The following plots are for Bwsp"
## [1] "The spatial density for Bwsp"
```
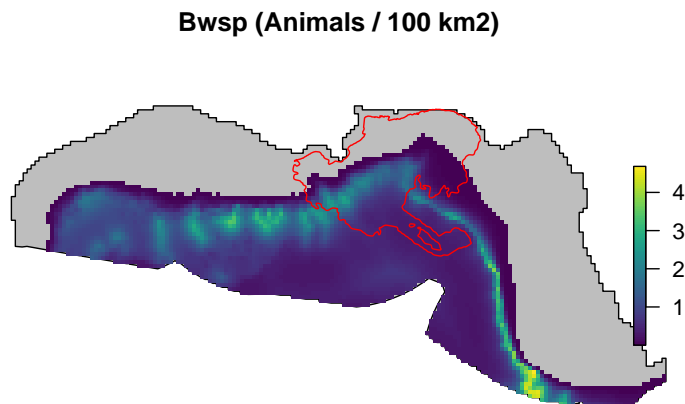
Bwsp (Animals / 100 km2)


```
## [1] "The number of exposed animals against the number of animals in the initial population"
```
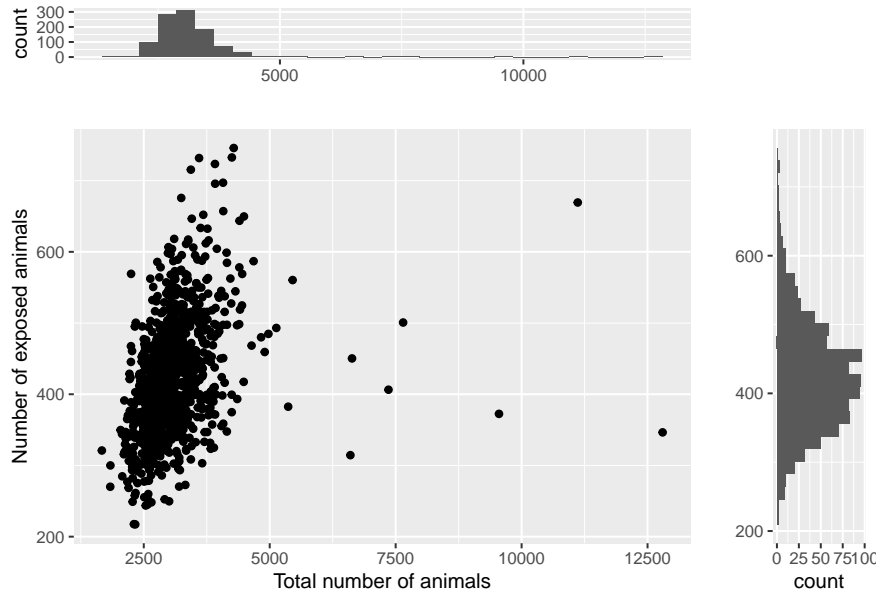
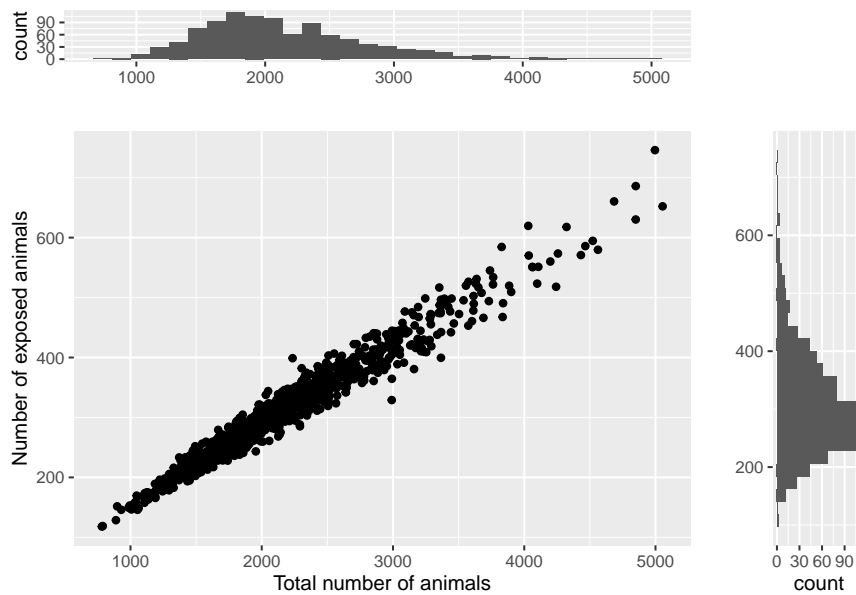## [1] "The proportion of exposed animals against the number of animals in the initial population"
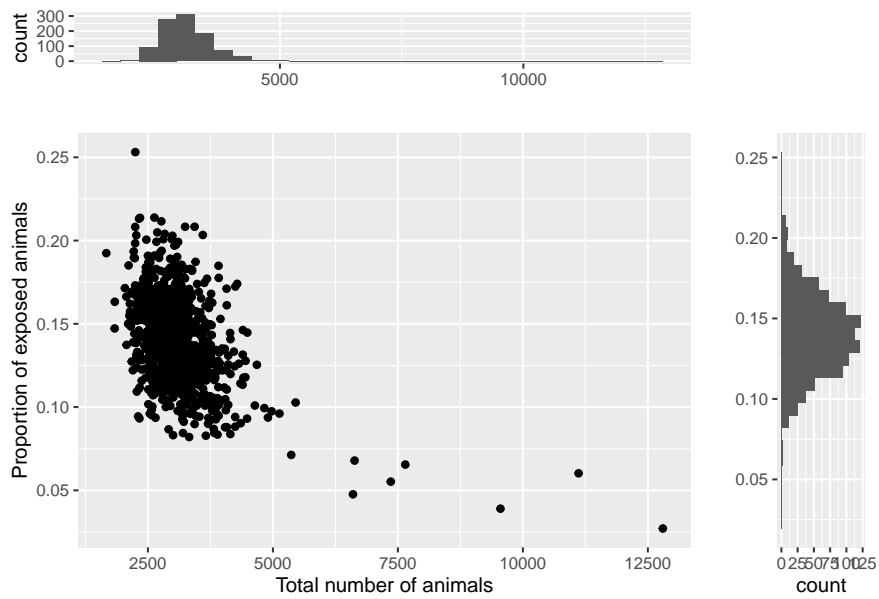
[1] "The following plots are for Fatt"
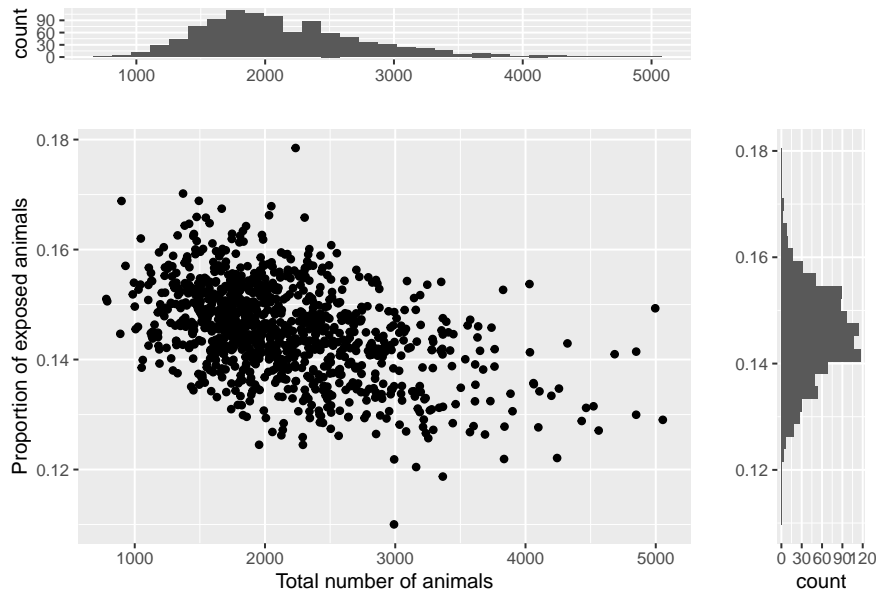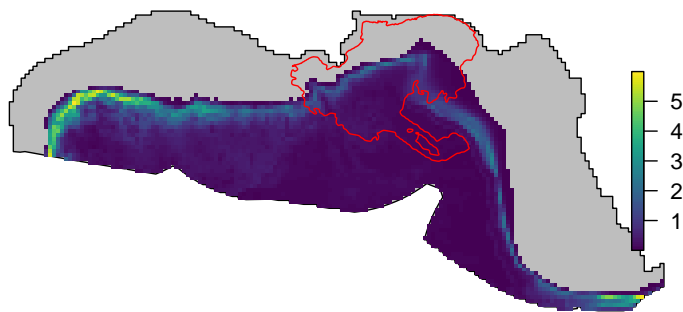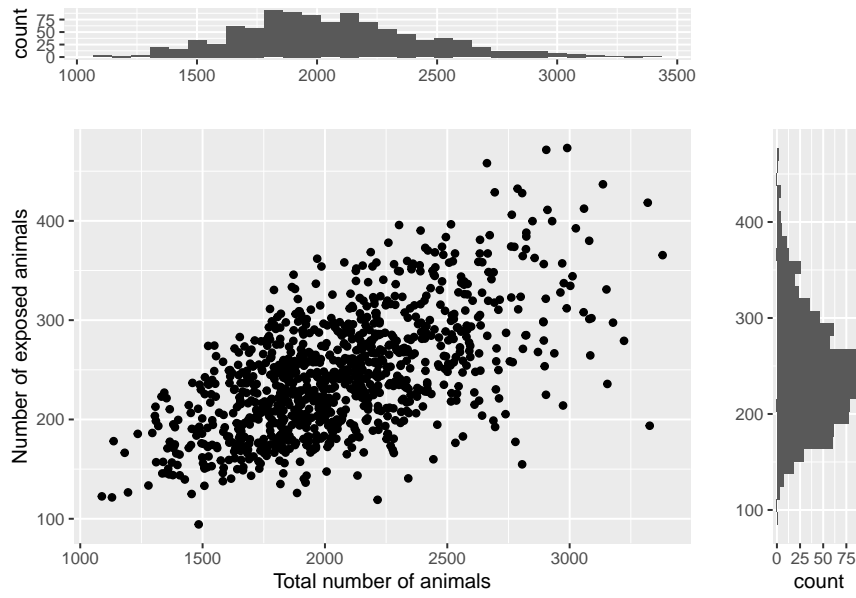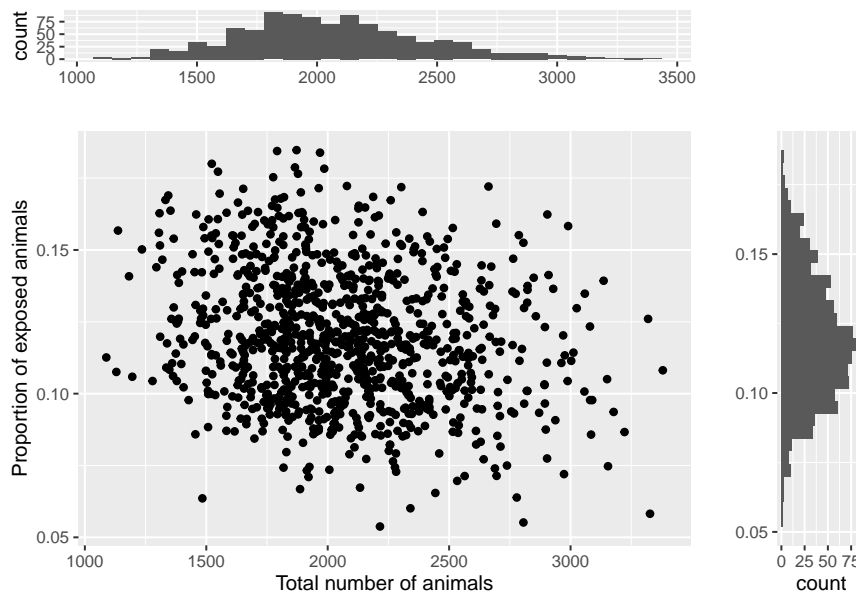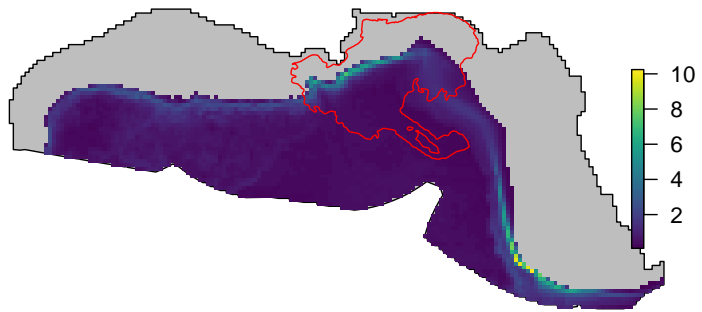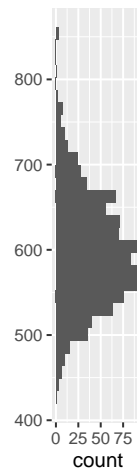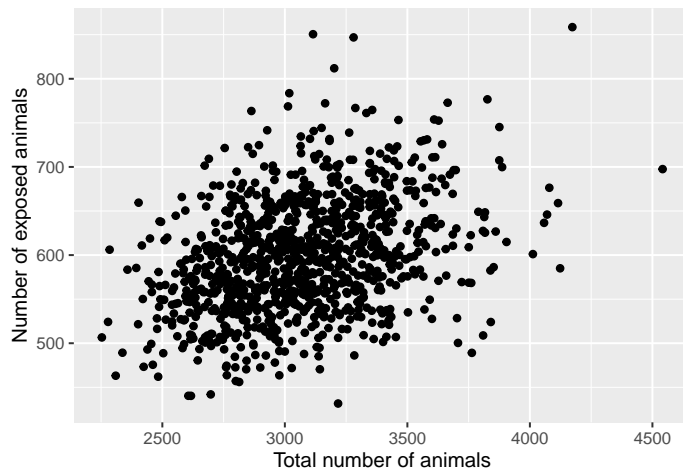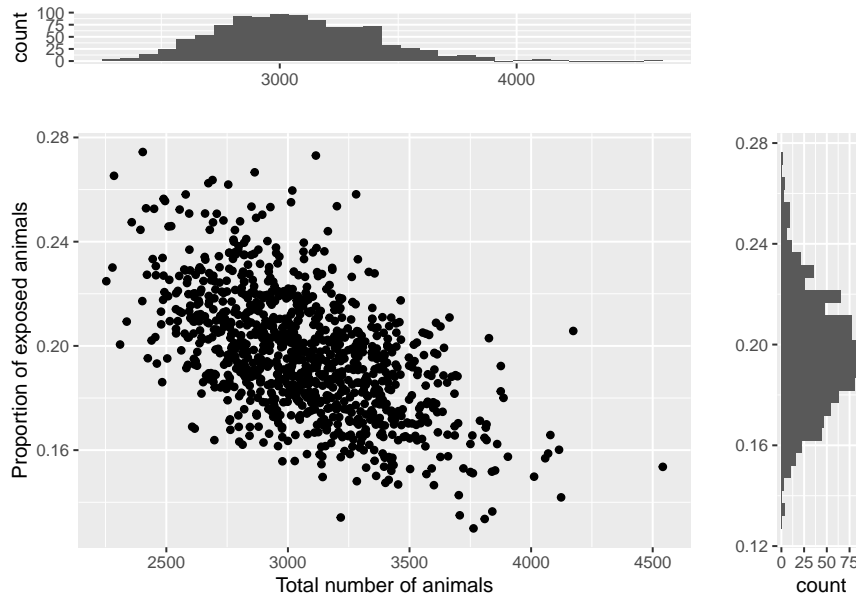## [1] "The spatial density for Fatt"

Fatt (Animals / 100 km2)
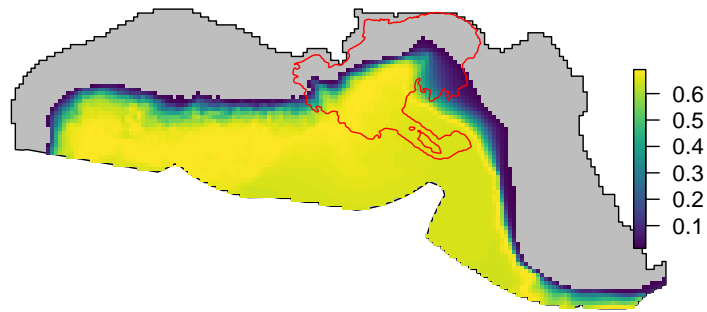
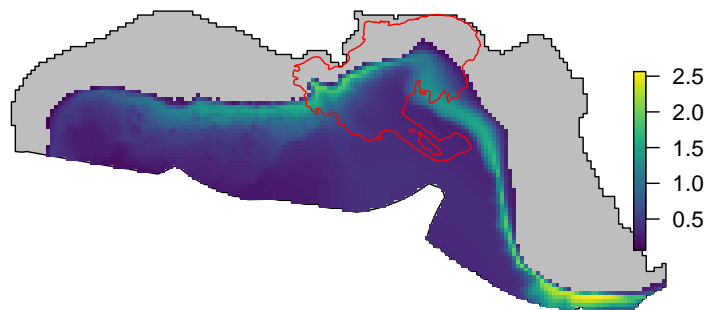## [1] "The number of exposed animals against the number of animals in the initial population"

[1] "The proportion of exposed animals against the number of animals in the initial population"

[1] "The following plots are for Gmac"
[1] "The spatial density for Gmac"

Gmac (Animals / 100 km2)

[1] "The number of exposed animals against the number of animals in the initial population"

[1] "The proportion of exposed animals against the number of animals in the initial population"
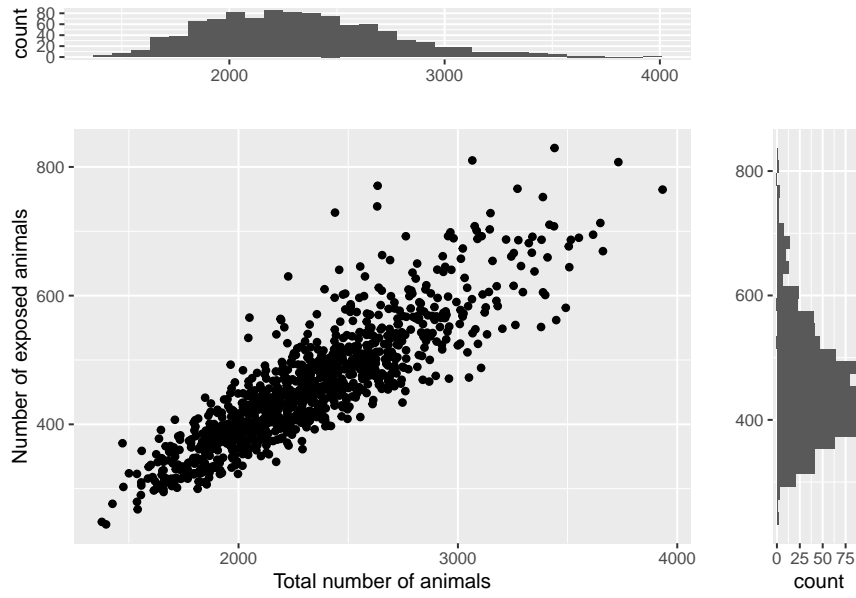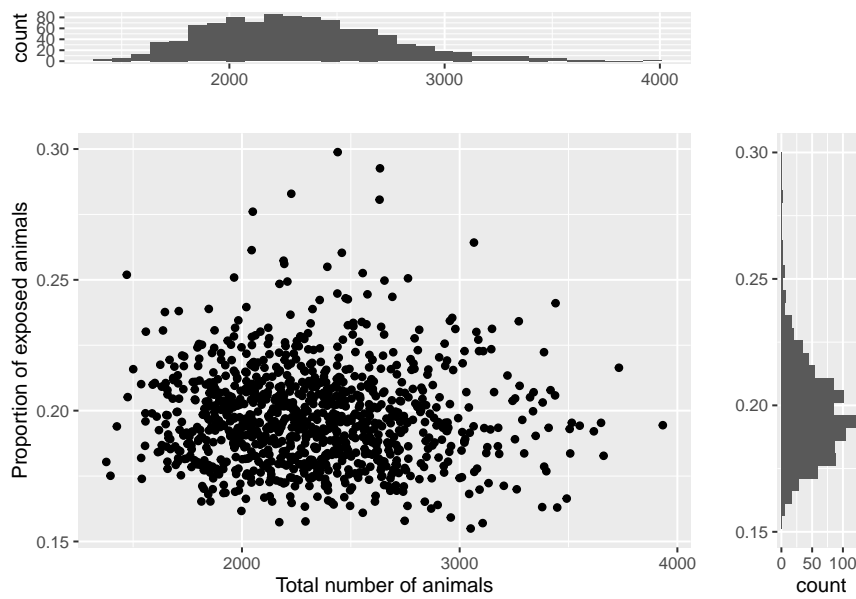

[1] "The following plots are for Ggri"
[1] "The spatial density for Ggri"

Ggri (Animals / 100 km2)

[1] "The number of exposed animals against the number of animals in the initial population"

[1] "The proportion of exposed animals against the number of animals in the initial population"

```
## [1] "The following plots are for Kosp"
## [1] "The spatial density for Kosp"
```

Kosp (Animals / 100 km2)


```
## [1] "The number of exposed animals against the number of animals in the initial population"
```
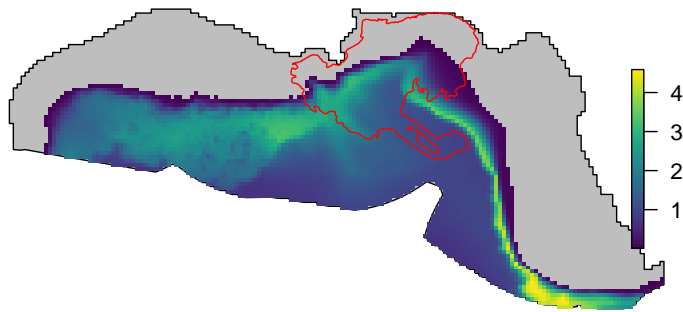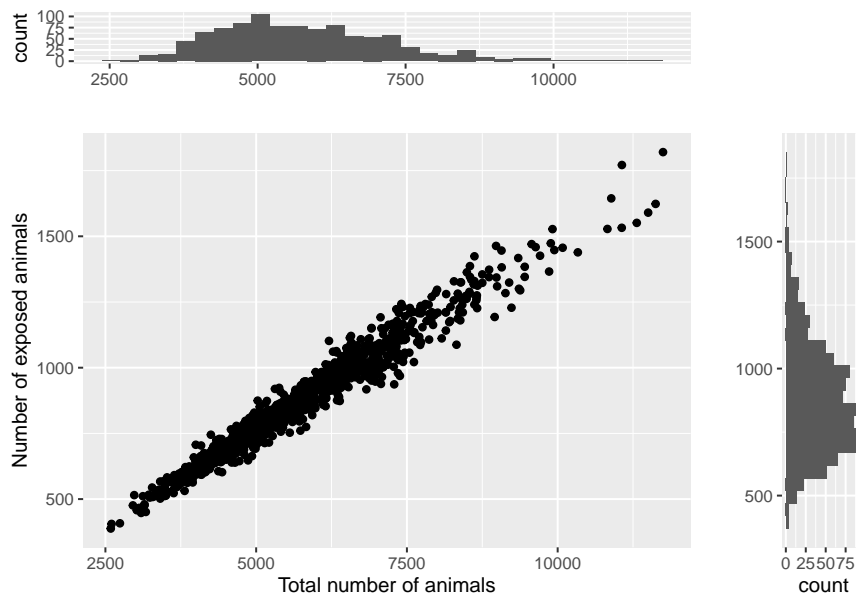
[1] "The proportion of exposed animals against the number of animals in the initial population"

[1] "The following plots are for Pele"
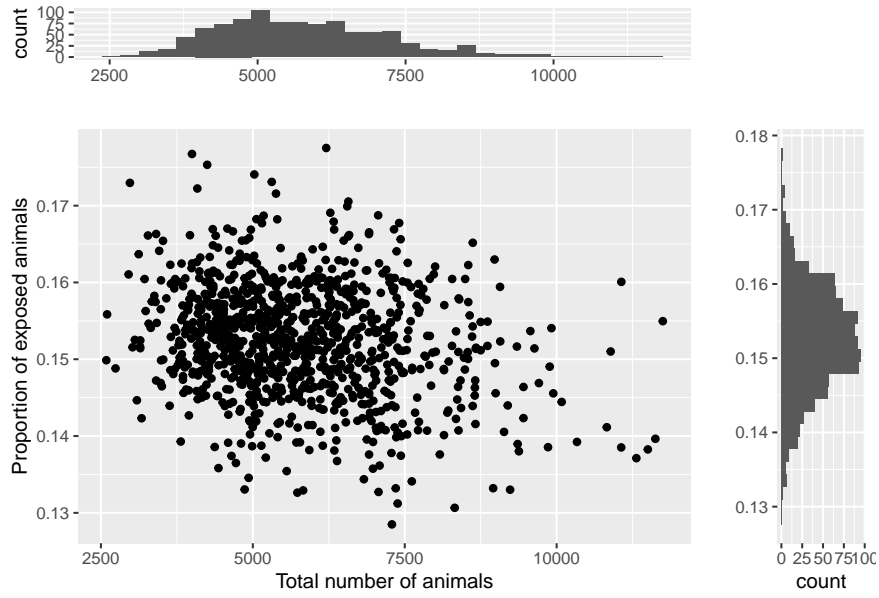## [1] "The spatial density for Pele"

Pele (Animals / 100 km2)

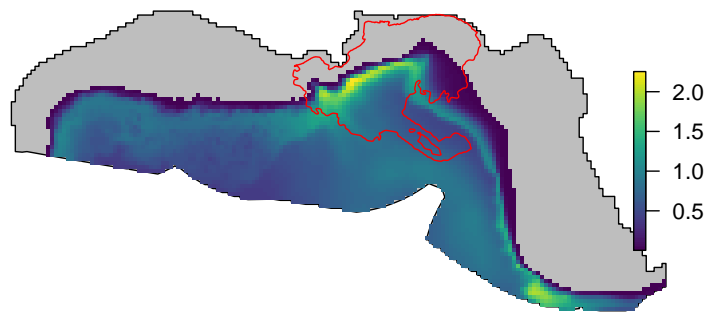## [1] "The number of exposed animals against the number of animals in the initial population"

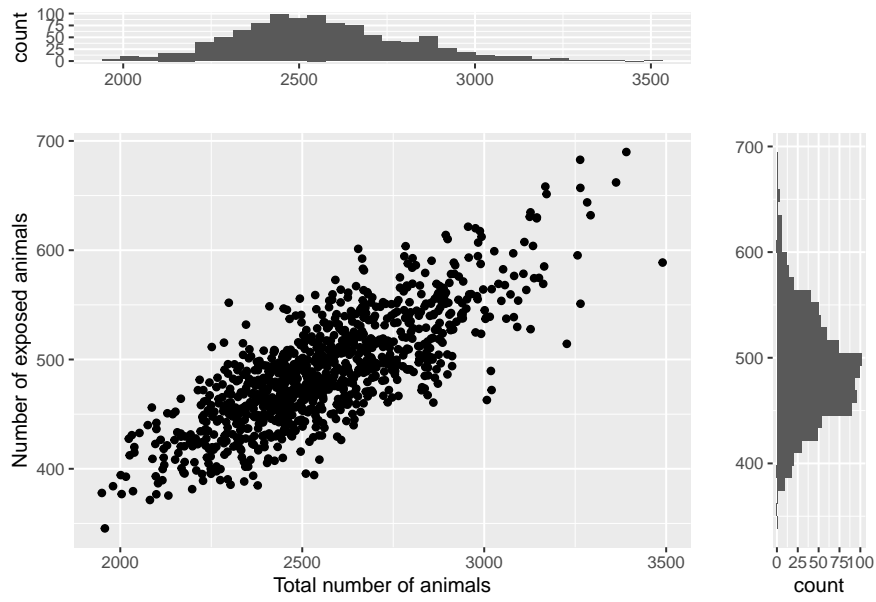## [1] "The proportion of exposed animals against the number of animals in the initial population"

```
## [1] "The following plots are for Pmac"
## [1] "The spatial density for Pmac"
```
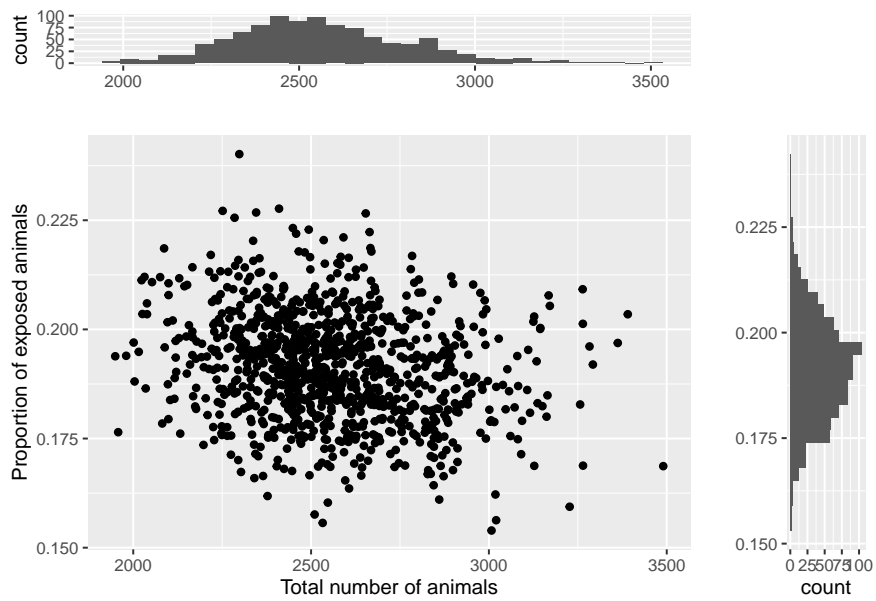
Pmac (Animals / 100 km2)


```
## [1] "The number of exposed animals against the number of animals in the initial population"
```
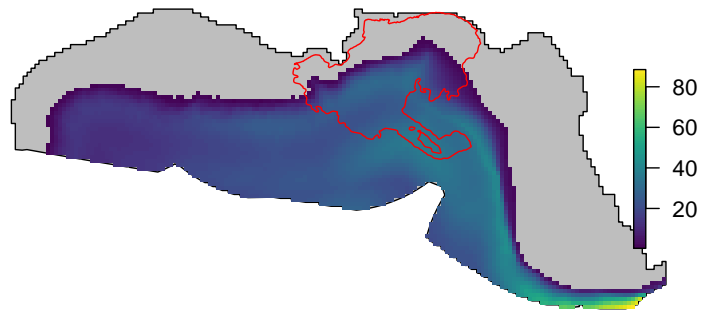
[1] "The proportion of exposed animals against the number of animals in the initial population"

[1] "The following plots are for Satt"
[1] "The spatial density for Satt"

Satt (Animals / 100 km2)

[1] "The number of exposed animals against the number of animals in the initial population"

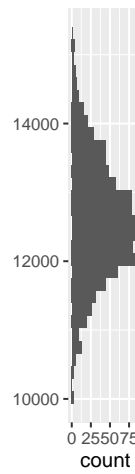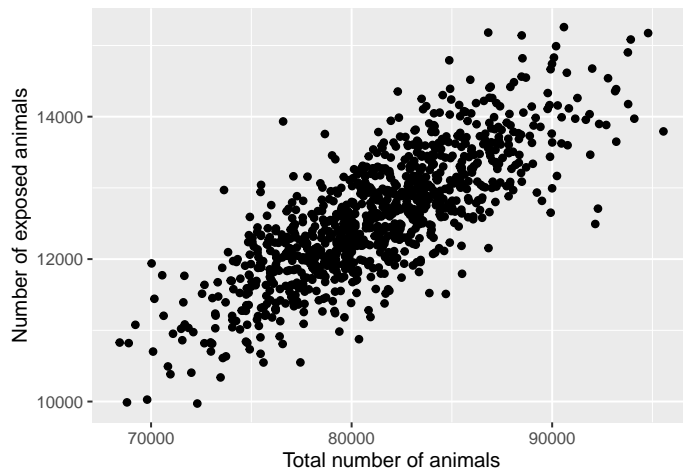## [1] "The proportion of exposed animals against the number of animals in the initial population"
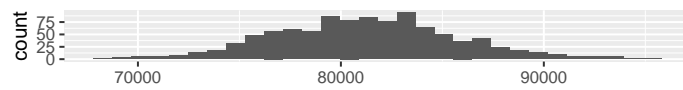
```
## [1] "The following plots are for Sbre"
## [1] "The spatial density for Sbre"
```

Sbre (Animals / 100 km2)


```
## [1] "The number of exposed animals against the number of animals in the initial population"
```

[1] "The proportion of exposed animals against the number of animals in the initial population"

[1] "The following plots are for Scly"
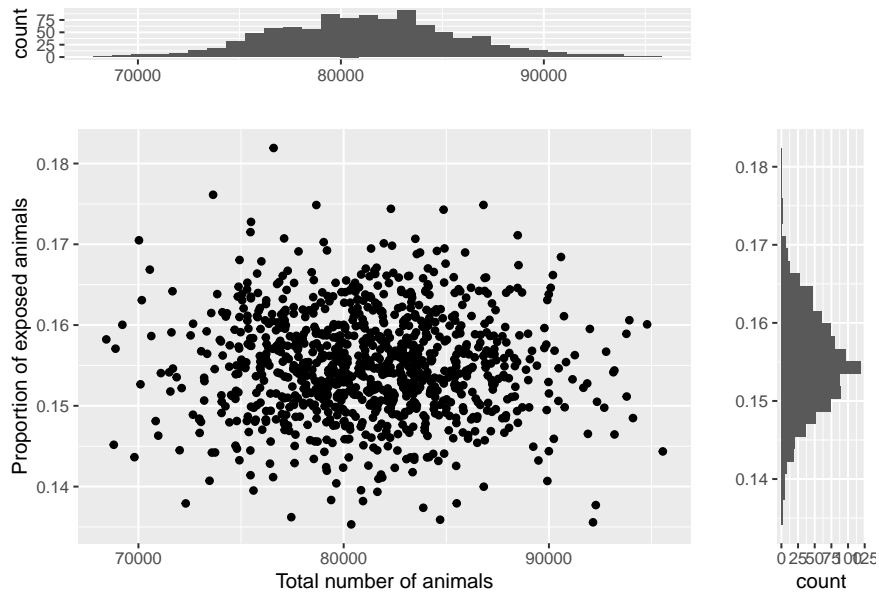## [1] "The spatial density for Scly"
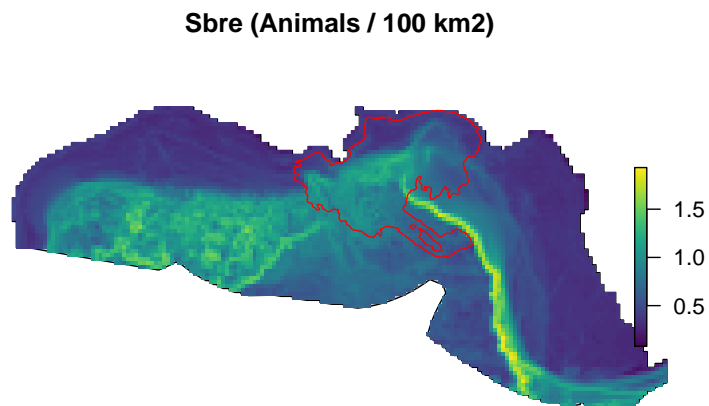
Scly (Animals / 100 km2)

[1] "The number of exposed animals against the number of animals in the initial population"
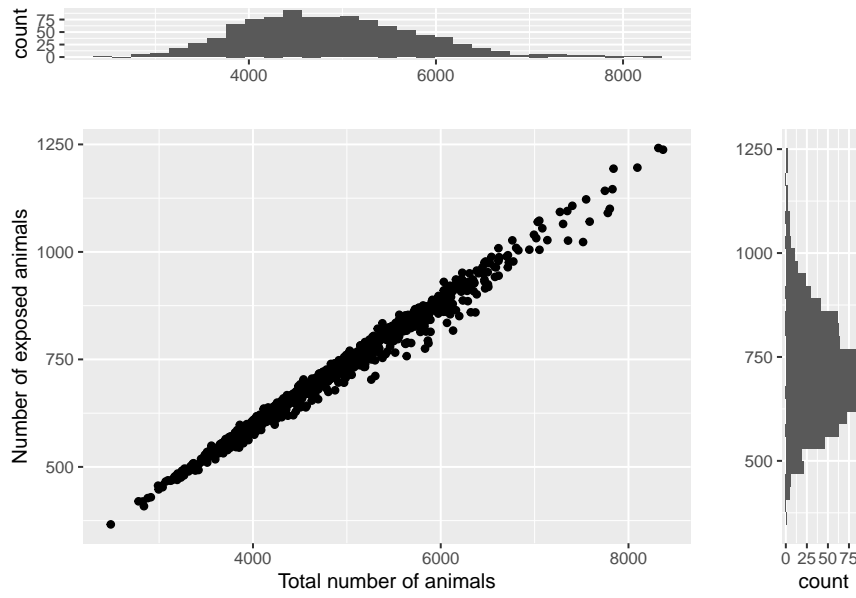

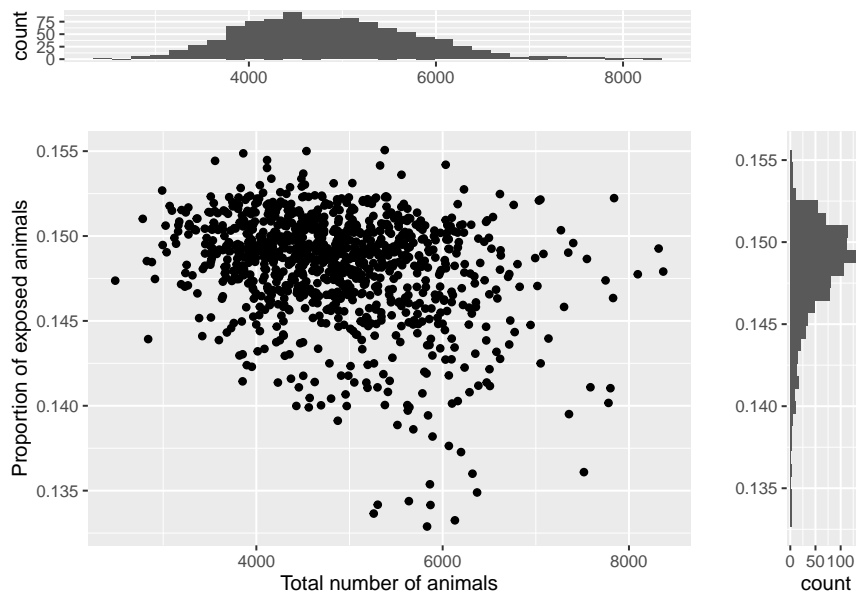## [1] "The proportion of exposed animals against the number of animals in the initial population"

```
## [1] "The following plots are for Scoe"
## [1] "The spatial density for Scoe"
```

Scoe (Animals / 100 km2)


```
## [1] "The number of exposed animals against the number of animals in the initial population"
```
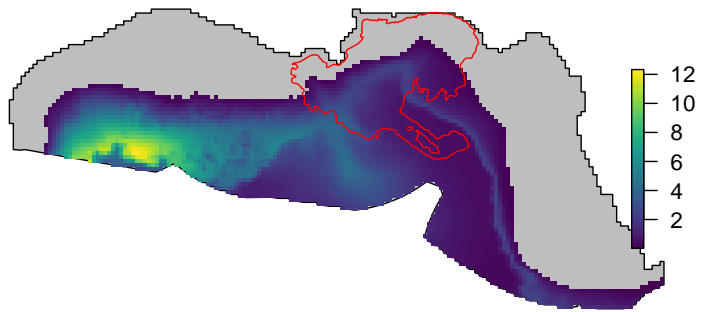
[1] "The proportion of exposed animals against the number of animals in the initial population"

[1] "The following plots are for Sfro"
[1] "The spatial density for Sfro"

Sfro (Animals / 100 km2)

[1] "The number of exposed animals against the number of animals in the initial population"

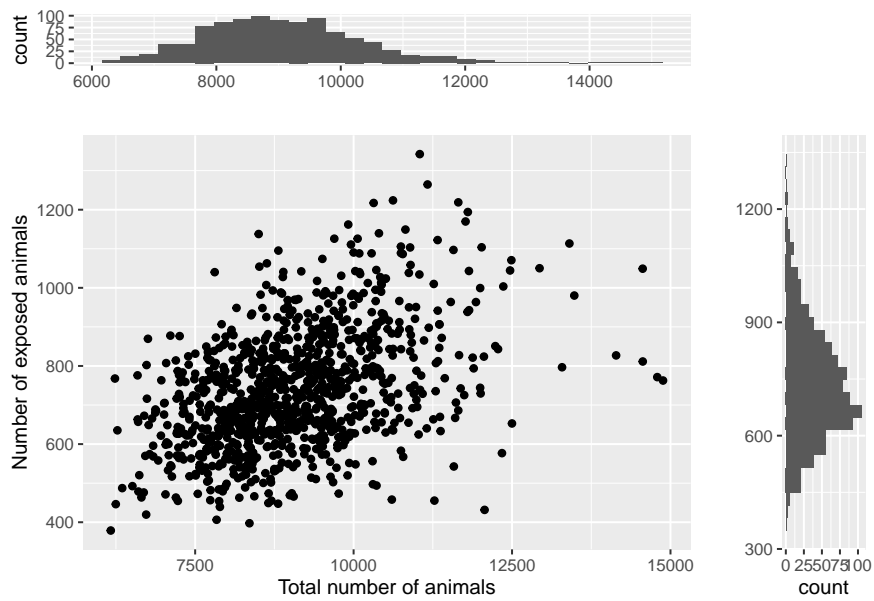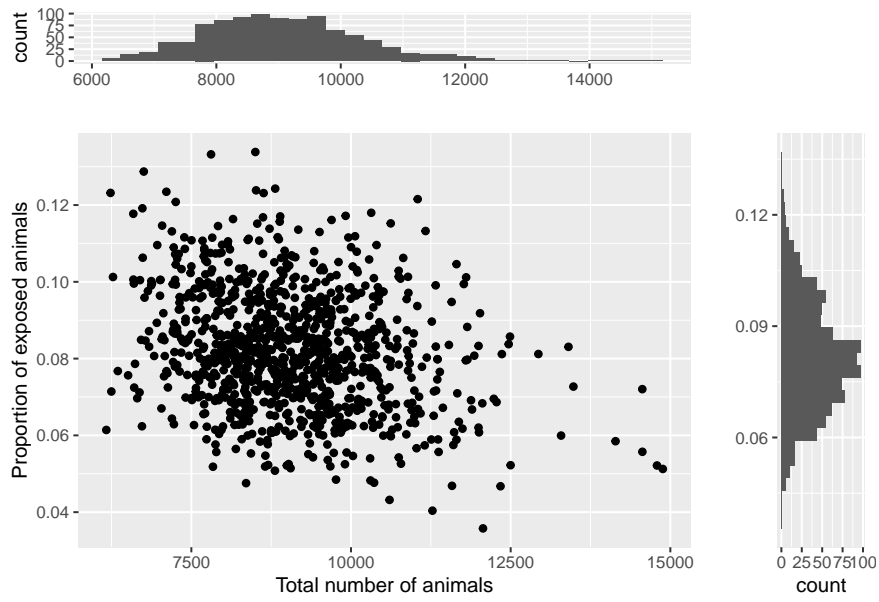## [1] "The proportion of exposed animals against the number of animals in the initial population"

```
## [1] "The following plots are for Slon"
## [1] "The spatial density for Slon"
```
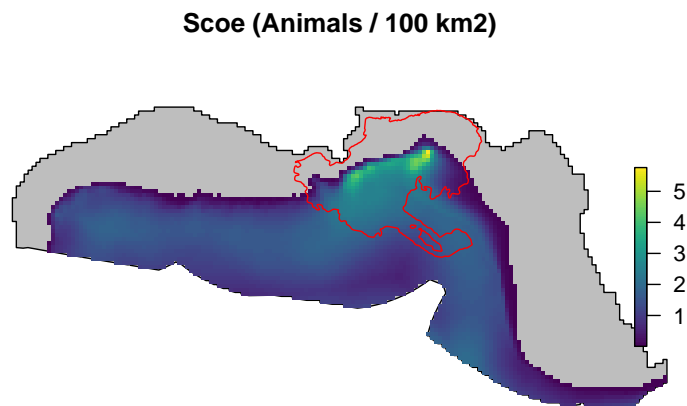
Slon (Animals / 100 km2)


```
## [1] "The number of exposed animals against the number of animals in the initial population"
```
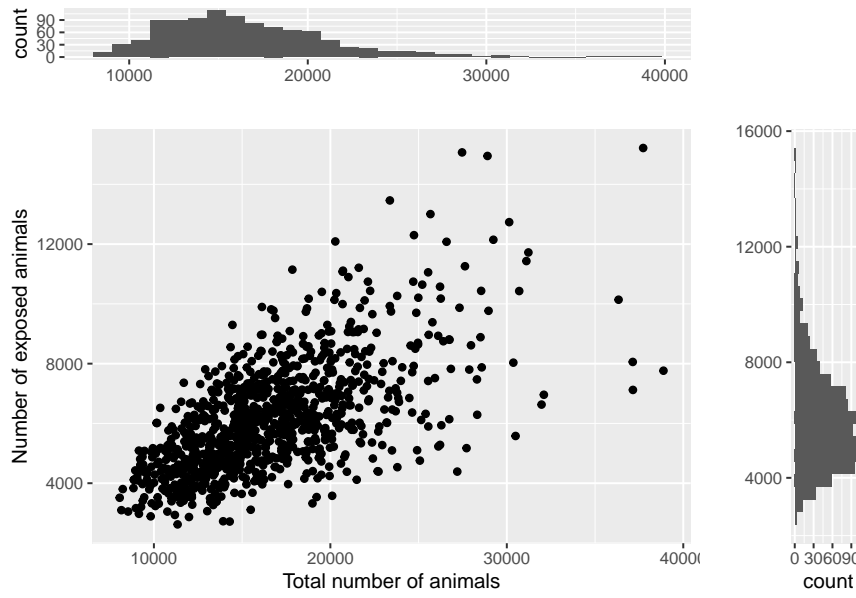
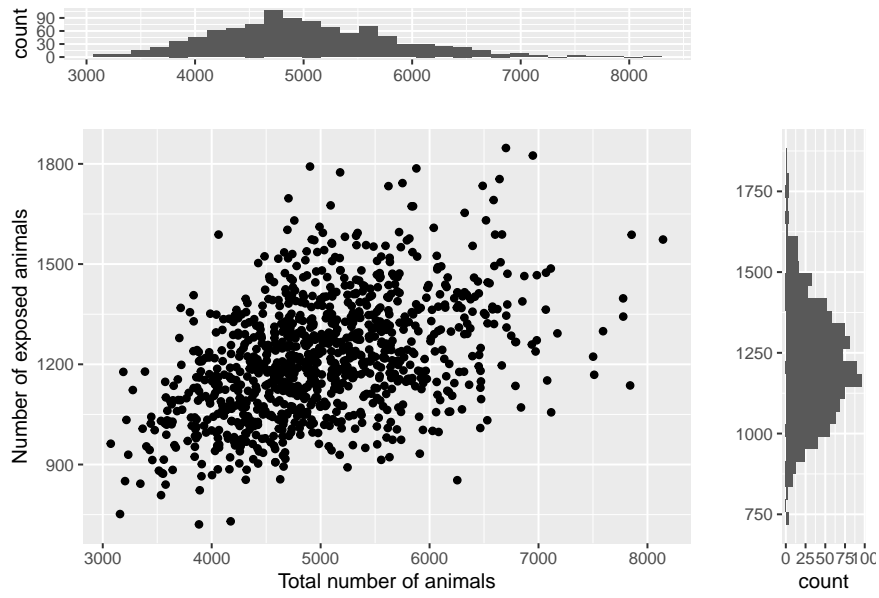## [1] "The proportion of exposed animals against the number of animals in the initial population"
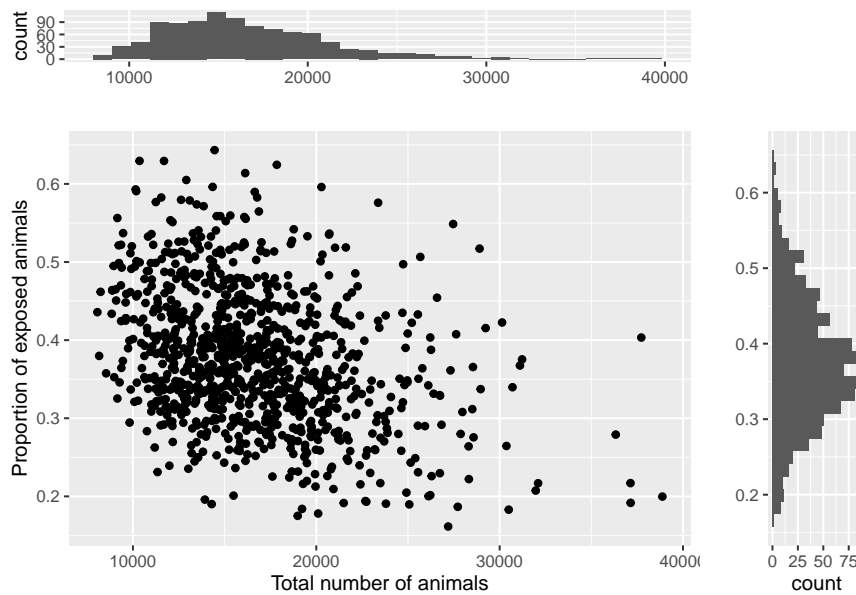
[1] "The following plots are for Ttro"
[1] "The spatial density for Ttro"

Ttro (Animals / 100 km2)
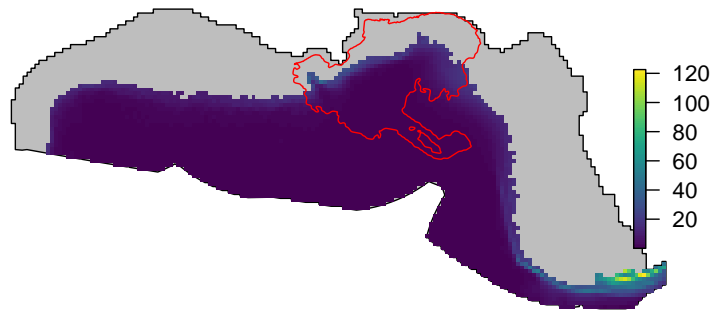
[1] "The number of exposed animals against the number of animals in the initial population"
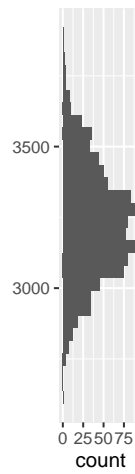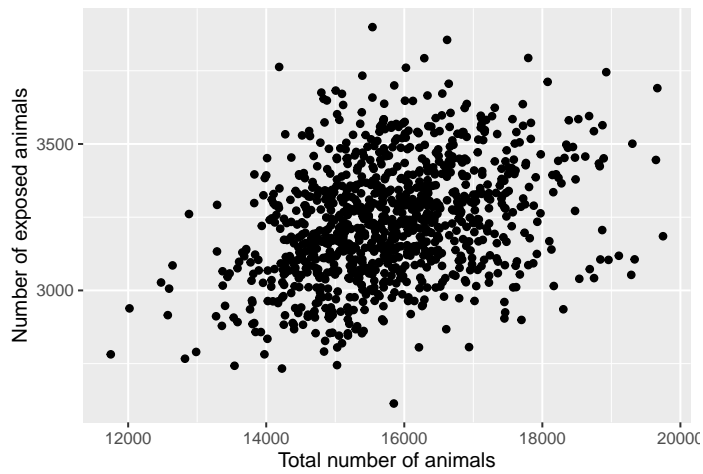
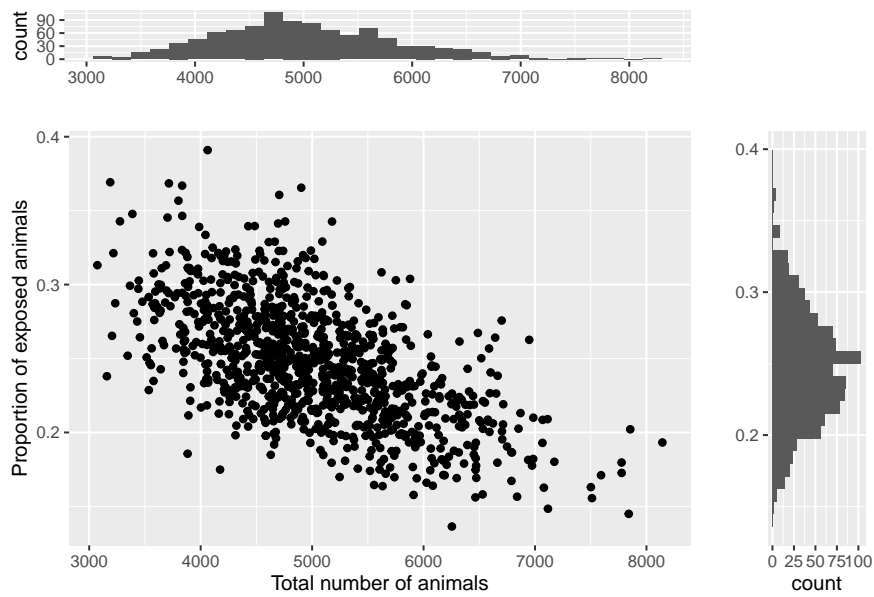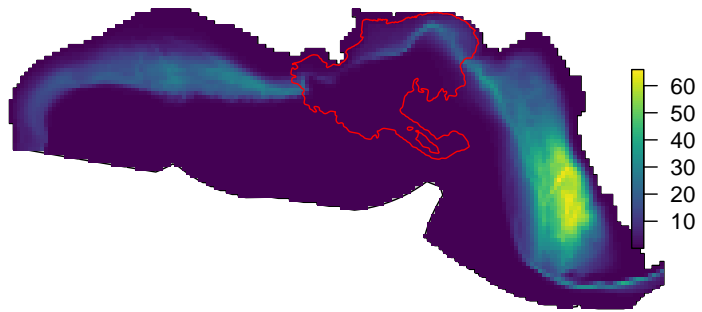## [1] "The proportion of exposed animals against the number of animals in the initial population"
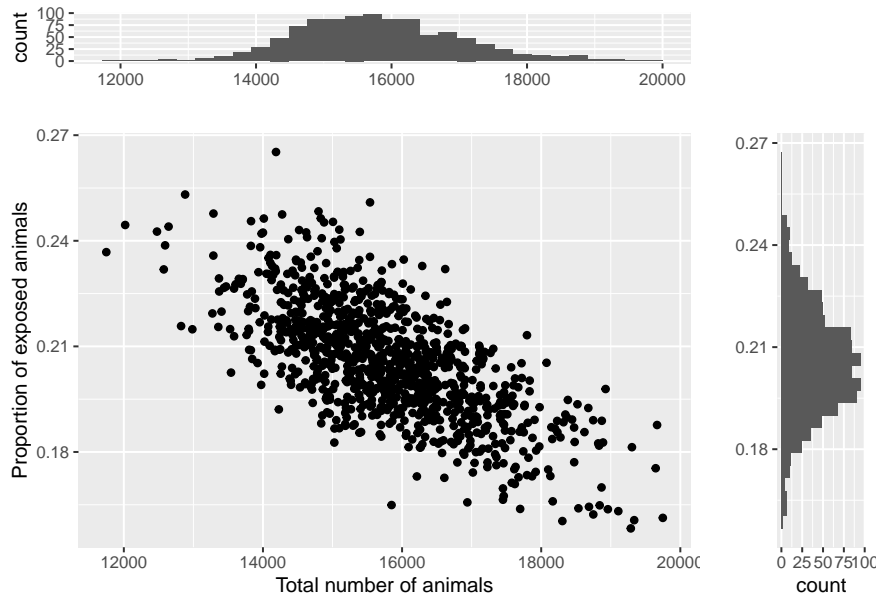
```
## [1] "The following plots are for Ttrs"
## [1] "The spatial density for Ttrs"
```

Ttrs (Animals / 100 km2)
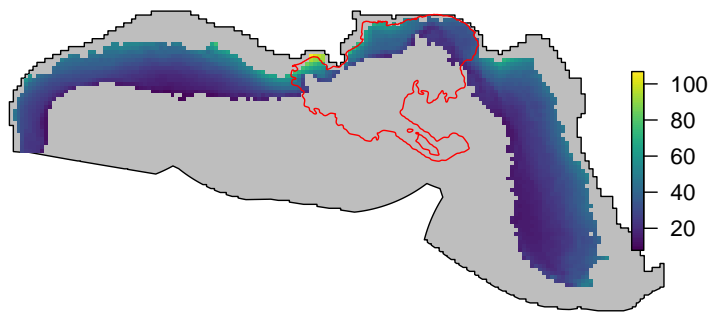

```
## [1] "The number of exposed animals against the number of animals in the initial population"
```
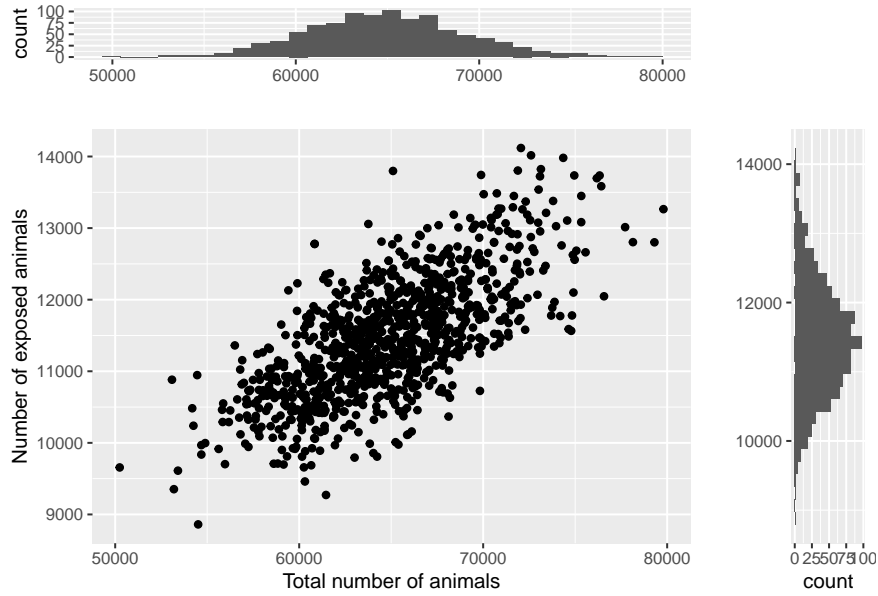
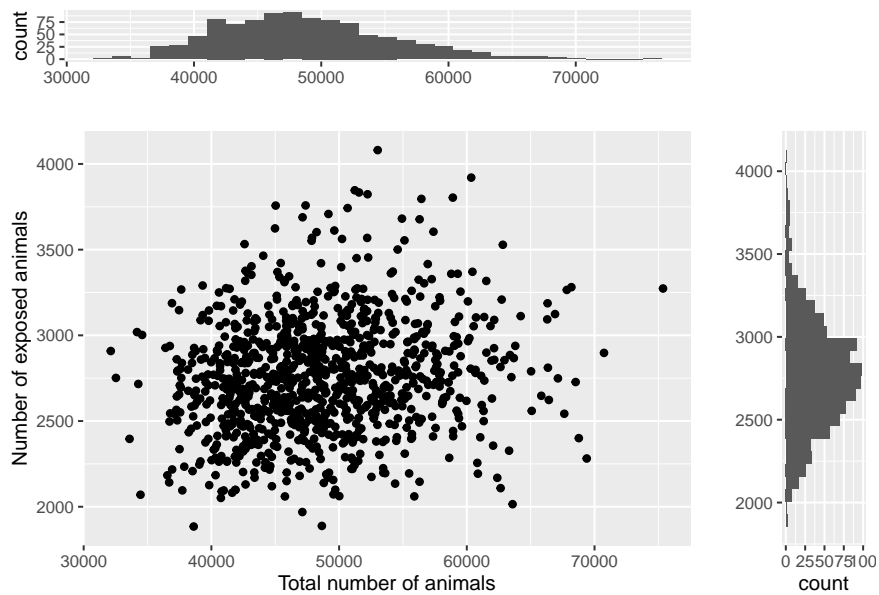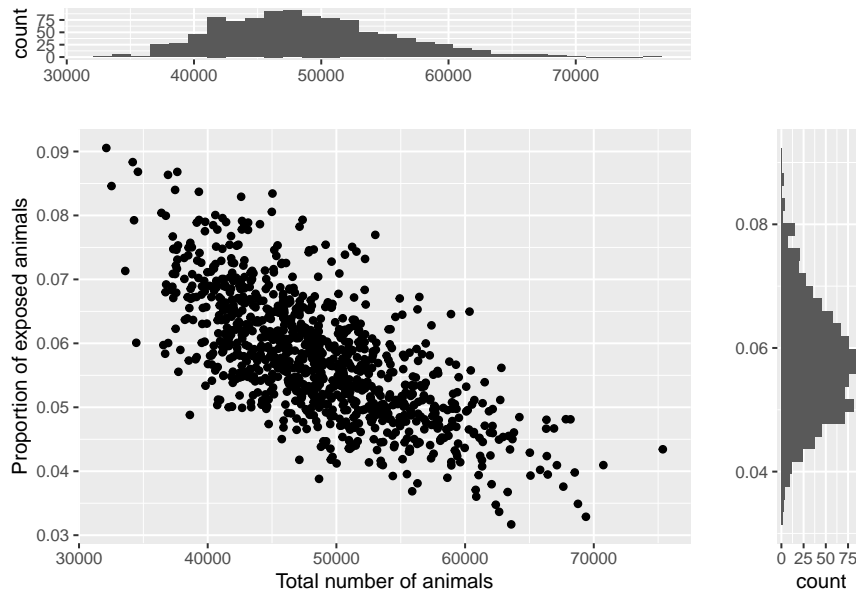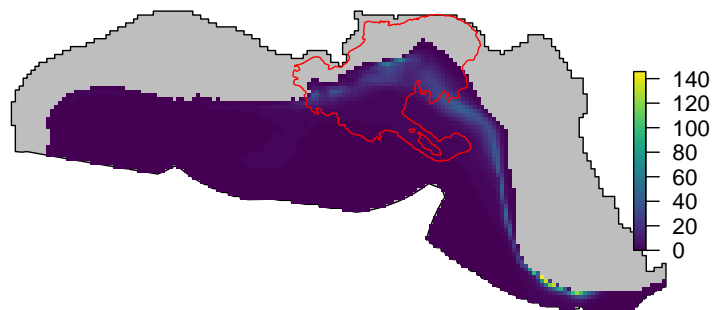## [1] "The proportion of exposed animals against the number of animals in the initial population"
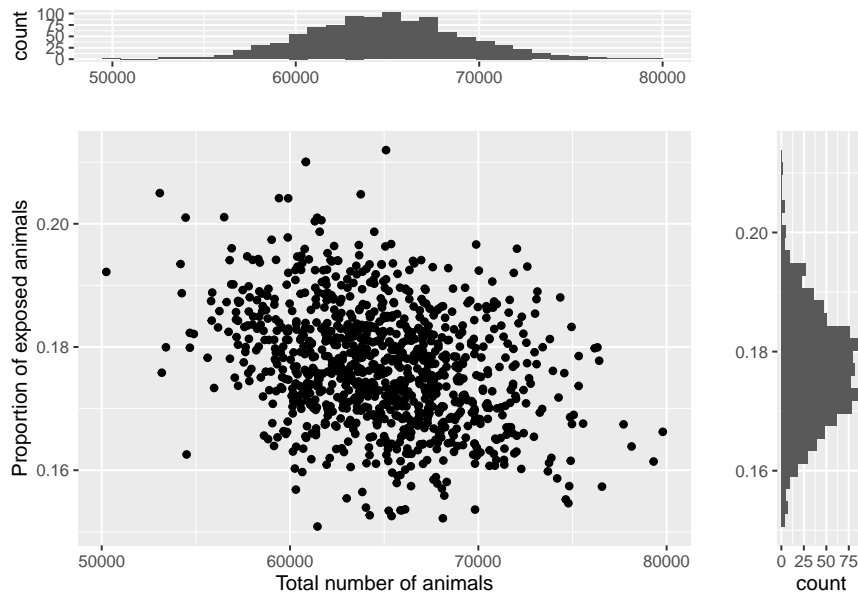

Summary tables

We present below a summary table with the estimated mean for the initial population size (N), the exposed population size (Ne) and the proportion exposed (Pe) for each of the taxonomic units considered. A summary table describing how many iterations were above the limit considered to be unrealistic and caused by GAM extrapolations and hence were removed from the analysis is also presented below.

Producing values for tables in the paper

The following code is used for producing the content for the first table of the main paper, regarding the initial population sizes and proportion exposed (and corresponding precision).

Table 1: Estimated mean for the initial population size (N), the exposed population size (Ne) and the proportion exposed (Pe) for each of the taxonomic units considered. The sufix cv, L and U stand for the empirical Coefficient of Variation and Lower and Upper confidence interval bounds. These intervals were obtained by the quantile method.

Sp	NL	N	NU	Ncv	NeL	Ne	NeU	Necv	PeL	Pe	PeU	Pecv
Bwsp	2236	3098	4323	23.2	286	424	604	19.1	0.093	0.140	0.191	18.5
Fatt	1137	2152	3762	31.1	170	310	520	28.6	0.128	0.145	0.161	5.9
Gmac	1378	2065	2910	18.7	146	245	374	24.2	0.077	0.120	0.165	19.3
Ggri	2489	3063	3759	10.6	486	598	730	10.8	0.154	0.197	0.248	11.9
Kosp	1650	2322	3288	18.1	312	458	687	20.3	0.166	0.197	0.240	9.7
Pele	3483	5784	9074	25.5	531	879	1363	24.8	0.138	0.152	0.166	4.8
Pmac	2117	2561	3094	9.5	396	489	595	10.3	0.168	0.191	0.216	6.4
Satt	72954	81233	90464	5.5	10875	12589	14353	6.9	0.142	0.155	0.168	4.2
Sbre	3271	4867	6804	19.0	491	720	1005	18.5	0.140	0.148	0.152	2.2
Scly	6873	9065	11826	14.1	474	737	1087	20.4	0.054	0.082	0.113	18.6
Scoe	3579	5011	6751	16.5	907	1219	1588	14.6	0.174	0.247	0.323	16.0
Sfro	37527	48688	62825	13.7	2150	2763	3501	12.0	0.041	0.058	0.078	16.4
Slon	9589	16501	27477	27.9	3411	6090	10430	29.8	0.217	0.377	0.555	22.5
Ttro	13705	15791	18445	7.6	2867	3232	3633	6.1	0.173	0.206	0.239	7.8
Ttrs	56992	64897	73804	6.6	9943	11466	13195	7.2	0.159	0.177	0.195	5.4

Table 2: Treshold value defining extreme realizations and number of realizations considered extreme, for each of the taxonomic units considered.

Sp	limit	above.limit
Bwsp	13210	3
Fatt	5494	0
Gmac	3997	0
Ggri	4684	0
Kosp	4468	1
Pele	13166	0
Pmac	3779	0
Satt	103746	0
Sbre	9486	0
Scly	15565	1
Scoe	9237	1
Sfro	81942	0
Slon	40384	2
Ttro	21756	0
Ttrs	86434	0

Table 1

Initial population sizes

```
Table1N <-  paste0(round(sumNsPes$N,0),"; ",round(sumNsPes$Ncv,1),
                " (",round(sumNsPes$NL,0)," ,",round(sumNsPes$NU),")")
#note we remove the last row which has the Ttru for Barataria Bay
write.table(Table1N,"Table1N.txt",sep="\t",row.names = FALSE,quote = FALSE,col.names = FALSE)
```

About the Proportion exposed

```
Table1P <-  paste0(round(sumNsPes$Pe,3),"; ",round(sumNsPes$Pecv,1),
                " (",round(sumNsPes$PeL,3)," ,",round(sumNsPes$PeU,3),")")
#note we remove the last row which has the Ttru for Barataria Bay
write.table(Table1P,"Table1P.txt",sep="\t",row.names = FALSE,quote = FALSE,col.names = FALSE)
```

Additional Tables

The following code is used for producing a table containing the values for initial population size and proportion exposed used as input in the supplementary information file ES5_GetInjury.

```
write.table(sumNsPes,"Table4GetInjury.txt",sep="\t",
            row.names = FALSE,quote = FALSE,col.names = TRUE)
```

References

Roberts, J. J.; Best, B. D.; Mannocci, L.; Fujioka, E.; Halpin, P. N.; Palka, D. L.; Garrison, L. P.; Mullin, K. D.; Cole, T. V. N.; Khan, C. B.; McLellan, W. A.; Pabst, D. A. & Lockhart, G. G. 2016 Habitat-based cetacean density models for the U.S. Atlantic and Gulf of Mexico *Scientific Reports* **6**: 22615 DOI: 10.1038/srep22615