P2

Extent of terrestrial alien species

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Introduction

This code calculates indicator P2 of NorInAliS.

Preparations

Load data from the Alien Species List 2018 (Sandvik et al. 2020):

The AOOs (areas of occupancy) provided in the above dataset are only the *best* estimates of the *total* AOO for each species (i.e. the *median* expert judgement of the *real* AOO, including "dark figures" or unreported occurrences). However, in order to quantify uncertainty, P2 needs more than that, viz. the *low* and *high* estimates of the total AOO (i.e. lower and upper *quartiles*) as well as the *known* AOO (i.e. excluding dark figures). These values are here read from a separate file. Their source is https://artsdatabanken.no/fremmedartslista2018.

```
aoo <- read.csv2("cache/aoo.txt", as.is=T)
head(aoo)</pre>
```

```
##
                  Name known low best high
## 1
        Abies amabilis
                            4
                              20
                                    40
                                          60
## 2
        Abies balsamea
                           64 256
                                   512
                                         768
## 3 Abies cephalonica
                           12 60
                                   120
                                         180
## 4
        Abies concolor
                          100 500 1000 1500
## 5
         Abies grandis
                           24 120
                                   240
                                         360
## 6
         Abies koreana
                           12
                              24
```

Restrict data to alien species that are reproducing unaidedly in mainland Norway:

```
fab <- fab[which(fab$Status == "reproducing" & fab$Mainl),]</pre>
```

Restrict the data to terrestrial species:

Make sure that the two data frames are compatible:

```
if (all(fab$Name == aoo$Name)) {
  cat("Everything is fine.\n")
} else {
  cat("ERROR: For some reason, the two dataframes are not compatible!\n")
}
```

Everything is fine.

Define an auxiliary function:

```
# Combines text strings
"%+%" <- function(string1, string2) paste0(string1, string2)</pre>
```

Functions

Define indicator-specific functions:

The first two functions use maximum-likelihood estimation to infer the standard deviation of the AOOs, based on the best estimate (median), low estimate (1st quartile) and high estimate (3rd quartile), and assuming a log-normal distribution.

```
f <- function(s, mean, q1, q3) return(</pre>
  (q1 - qlnorm(0.25, log(mean) - exp(2*s)/2, exp(s)))^2 +
  (q3 - qlnorm(0.75, log(mean) - exp(2*s)/2, exp(s)))^2
findSD <- function(Ex, q1, q3) return(</pre>
  exp(optimise(f, c(-12, 12), mean=Ex, q1=q1, q3=q3)$min)
P2 <- function(dataset,
               column = c("known", "low", "best", "high"),
               nsim = 100000,
               maxArea = 323800) {
  # simulates AOOs for all species, which is the basis of indicator P2
  N <- nsim # random numbers per species
  M <- maxArea # maximum possible area in km^2
  aoo <- dataset[, column]</pre>
  A00 <- matrix(0, N, nrow(aoo))
  for (i in 1:nrow(aoo)) {
    if (any(is.na(aoo[i, c("low", "best", "high")]))) {
      if (is.na(aoo$best[i])) {
        if (is.na(aoo$known[i])) {
          # if no AOO is provided, assume it is O
          A00[, i] \leftarrow 0
        } else {
          # of no total AOOs are provided, assume they equal the known AOO
```

```
A00[, i] <- aoo$known[i]
        }
      } else {
        # if no low and high estimates are provided, use the best estimate
        A00[, i] <- aoo$best[i]
    } else {
      if (aoo$best[i] == 0) {
        # if the best estimate is 0, keep it 0
        A00[, i] \leftarrow 0
      } else {
        # if low, best and high estimates are provided, estimate the standard
        # deviation and generate log-normally distributed random numbers
        SD <- findSD(aoo$best[i], aoo$low[i], aoo$high[i])</pre>
        A00[, i] \leftarrow qlnorm(runif(N), log(aoo\$best[i]) - SD * SD / 2, SD)
        AOO[, i] <- sapply(AOO[, i], min, M) # constrain to area of Norway
        AOO[, i] <- ceiling(AOO[, i] / 4) * 4 # ensure multiples of 4 km<sup>2</sup>
    }
  } # i
 return(A00)
} # P2
```

Error checking and correction

Check for obvious errors in the original data:

(1) Is any low estimate greater than the corresponding best estimate?

```
w <- which(aoo$low > aoo$best)
if (length(w)) {
  print(aoo[w,])
} else {
  cat("Everything is fine.\n")
}
```

```
## Name known low best high
## 28 Acrotrichis cognata 80 40000 800 120000
```

This looks very much like a punching error in line 28. Most likely, the best estimate should have been in the middle between the low and high estimate (implying a dark figure of 1000 rather than 10). The error is corrected manually:

```
aoo$best[w] <- 80000
```

(2) Is any high estimate less than the corresponding best estimate?

```
w <- which(aoo$high < aoo$best)
if (length(w)) {
  print(aoo[w,])
} else {
  cat("Everything is fine.\n")
}</pre>
```

```
## Name known low best high
## 55 Alphitophagus bifasciatus 20 20 1000 20
## 345 Dorytomus filirostris 4 4 40 4
```

```
## 472
                  Harmonia axyridis
                                       128 128
                                                2560
## 591
             Lithocharis nigriceps
                                                5600
                                                       112
                                       112 112
## 644 Melampsoridium hiratsukanum
                                       900 900
                                                4500
                                                       900
         Myrmecocephalus concinnus
                                                 240
                                                        12
## 680
                                        12
                                            12
## 704
                    Omalium rugatum
                                       164 164 16400
                                                       164
## 726
            Otiorhynchus armadillo
                                             8
                                                 400
                                                         8
                                         8
            Philonthus rectangulus
                                        60
                                            60
                                                3000
                                                        60
## 777
```

Here, it seems that the low and high estimate simply haven't been provided, and that, as a default, the known AOO was listed instead. In the absence of other information, we have to assume the low and high estimates to be equal to the best estimate:

```
aoo$low[w] <- aoo$high[w] <- aoo$best[w]
```

(3) By definition, AOOs are multiples of 4 square kilometres. Some figures are incompatible with this definition. We solve this by rounding upwards:

```
aoo[, 2:5] \leftarrow ceiling(aoo[, 2:5] / 4) * 4
```

(4) Is any AOO greater than the area of mainland Norway?

```
w <- which(aoo$high > 323800)
if (length(w)) {
  print(aoo[w,])
} else {
  cat("Everything is fine.\n")
}
```

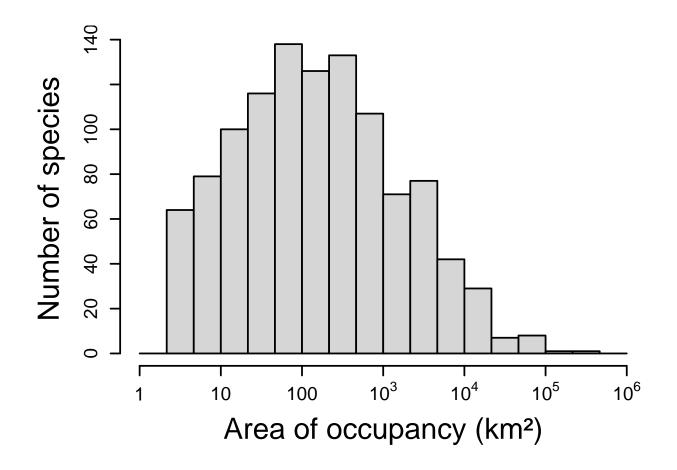
```
## Name known low best high
## 112 Atomaria lewisi 176 88000 176000 880000
```

Indeed. That is clearly an overestimate. The high estimate is reduced to (a bit less than) the area of Norway. All other estimates are possible in principle, and are thus left unchanged.

```
aoo$high[w] <- 323000
```

Show a graph of the distribution of the best estimates of total AOOs:

```
par(mai=c(0.96, 0.96, 0.06, 0.06), lwd=1.8)
H <- hist(log10(as.numeric(aoo$best)), breaks=seq(0, 6, 1/3),
    xlab="Area of occupancy (km²)", ylab="Number of species", main="",
    xaxt="n", cex.axis=1.2, cex.lab=1.8, lwd=1.8, col=grey(0.84))
axis(1, 0:6, c(1, 10, 100, expression(10^3), expression(10^4), expression(10^5),
    expression(10^6)), cex.axis=1.2, lwd=1.8)</pre>
```



Simulations

If you want P2 for high- and severe-impact species only, do this first (not run):

```
aoo <- aoo[which(fab$Impact %in% c("HI", "SE")),]
```

If you want P2 for the *remaining* species only, do this first (not run):

```
aoo <- aoo[which(fab$Impact %in% c("NK", "LO", "PH")),]</pre>
```

If you want P2 for all alien species (**default**), do none of the above.

Then start the simulation:

```
A00 <- P2(aoo)

avg <- mean(apply(A00, 1, sum))

stdev <- sd(apply(A00, 1, sum))

conf <- quantile(apply(A00, 1, sum), c(0.025, 0.25, 0.5, 0.75, 0.975))
```

Output of the results:

```
## P2 is 2410900 km^2 ± 197900 km^2 (mean ± SD)
```

```
##
## Confidence levels (in km2):
## 2.5% 25% 50% 75% 97.5%
## 2054400 2271900 2400300 2538700 2828200
```