**Inferring the extinction of species known only from a single specimen**

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Supplementary Material 1 The 236 records (in comma separated values format) of Madagascar orchid species collected during 1830–2000 that are known from a single specimen. The dataset comprises the following variables:

Species, species name;

Collection year, year collection was made;

p, probability that the species is extant, based on McCarthy method (equation 3);

Collection effort needed after 2000 to infer extinction (additional specimens), number of additional collections needed to determine whether the species is extinct;

All specimens, records of all orchid species used as a measure of collection effort;

Top 10%, records of top 10% most collected species used as a measure of effort;

OLE, records of species estimated as extant by 2000 using the optimal linear estimator (Roberts & Solow 2003) used as a measure of effort;

Ex, refers to species estimated to be extinct already, and for which no additional collection effort is required.

Supplementary Material 2 *R* script for testing extinction in species known from a single collection, based on the McCarthy method.

# Enter the exact location and the name of the file with the dataset

# below, in Line 7 (files "Dataset.csv" and "Effort.csv")

# The two csv files should have all data listed in a single column,

# without headers:

# "Dataset.csv" should contain collection years of each of the

# assessed single-collection species

# "Effort.csv" should contain collection years of all specimens used

# as a measure of collection effort

Dataset <- unlist(read.csv("/home/ijaric/Extinction/Dataset.csv", header=FALSE)); Effort <- unlist(read.csv("/home/ijaric/Extinction/Effort.csv", header=FALSE))

# Defining alpha value

alpha <- 0.05

# Establishing matrix with results

# First column will contain probability of presence of each species,

# second one will represent amount of additional collection effort

# needed to confirm extinction

results <- matrix(0,length(Dataset),2)

# Start of the loop

for(i in c(1:length(Dataset))){

 results[i,1] <- length(Effort[Effort<=Dataset[i]])/length(Effort)

 results[i,2] <- (length(Effort[Effort<=Dataset[i]])/alpha)-length(Effort)

}

# Writing the csv file with results

# Enter desired location where the file will be stored, and its name

write.csv(results, file="/home/ijaric/Extinction/Results.csv")

cat("Number of species that are extinct:", length(results[,1][results[,1]<alpha]))