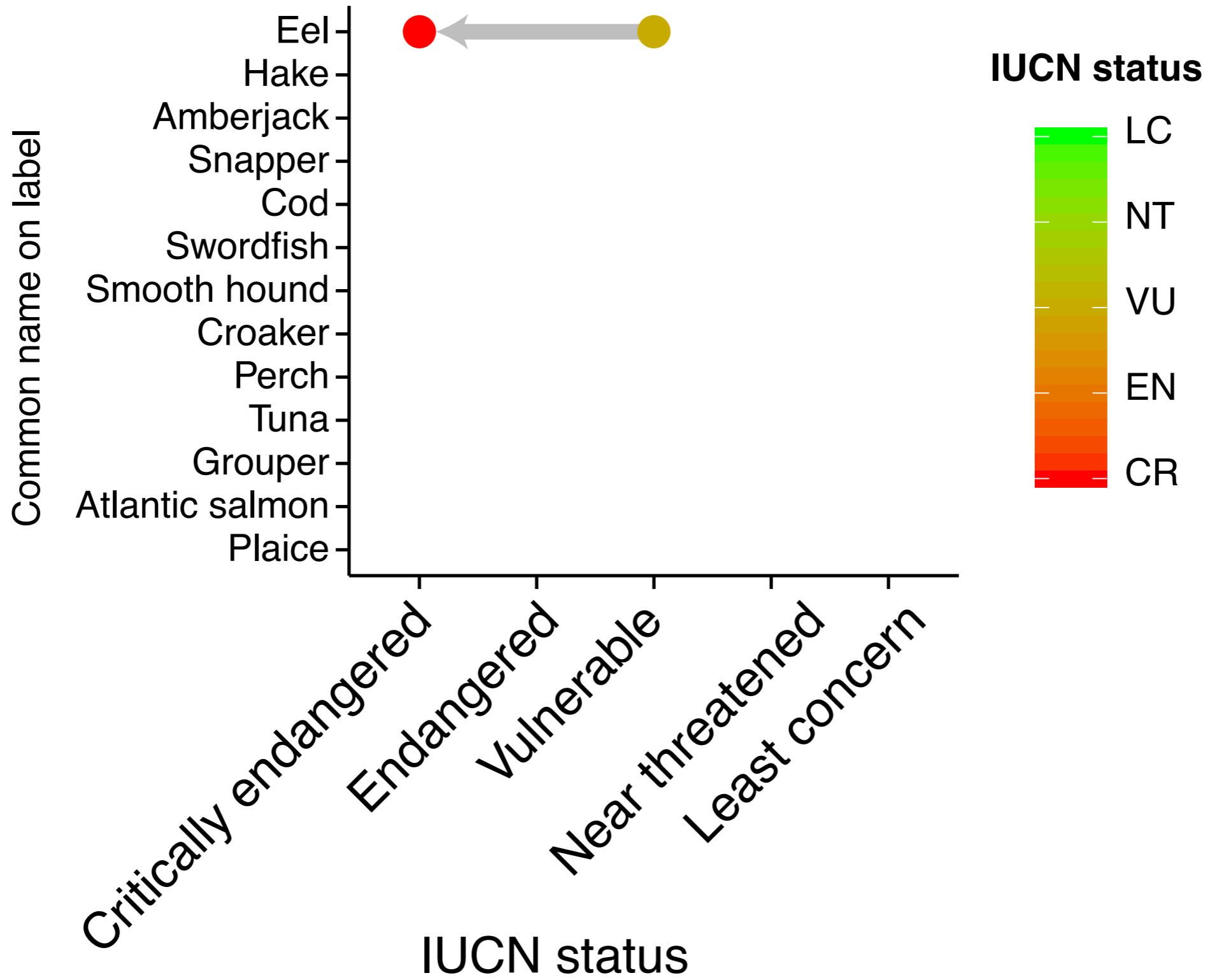


Seafood mislabeling



Are people being 'tricked' into eating less sustainable seafood?



taxize use #1: get family names from genus names

```
##      X      Genus      Prob
## 1  1 Acanthocybium 1.0000000
## 2  2      Acipenser 0.8235294
## 3 13      Arapaima 0.0000000
## 4 14      Argyrops 0.0000000
## 5 15  Argirosomus 0.7411765
## 6 16  Argyrozona 0.1666667
```

This is what the data look like, a list of probabilities of mislabeling, by genus. Use `taxize` to get the family name for each of these genera:

```
library(dplyr)
library(taxize)

mislabeled.by.fam <- mislabeled.by.genus[1:10,] %>% # subsample bc whole dataset is time-consuming
  mutate(fam = tax_name(query = as.character(Genus),
                        get = "family",
                        db = "itis")$family)

head(mislabeled.by.fam)
```

```
##      X      Genus      Prob      fam
## 1  1 Acanthocybium 1.0000000  Scombridae
## 2  2      Acipenser 0.8235294  Acipenseridae
## 3 13      Arapaima 0.0000000  Osteoglossidae
## 4 14      Argyrops 0.0000000   Sparidae
## 5 15  Argirosomus 0.7411765  Sciaenidae
## 6 16  Argyrozona 0.1666667   Sparidae
```

taxize use #1: get family names from genus names

```
##      X      Genus      Prob
## 1  1 Acanthocybium 1.0000000
## 2  2      Acipenser 0.8235294
## 3 13      Arapaima 0.0000000
## 4 14      Argyrops 0.0000000
## 5 15  Argirosomus 0.7411765
## 6 16  Argyrozona 0.1666667
```

This is what the data look like, a list of probabilities of mislabeling, by genus. Use `taxize` to get the family name for each of these genera:

```
library(dplyr)
library(taxize)

mislabeled.by.fam <- mislabeled.by.genus[1:10,] %>% # subsample bc whole dataset is time-consuming
  mutate(fam = tax_name(query = as.character(Genus),
                        get = "family",
                        db = "itis")$family)

head(mislabeled.by.fam)
```

```
##      X      Genus      Prob      fam
## 1  1 Acanthocybium 1.0000000  Scombridae
## 2  2      Acipenser 0.8235294  Acipenseridae
## 3 13      Arapaima 0.0000000  Osteoglossidae
## 4 14      Argyrops 0.0000000   Sparidae
## 5 15  Argirosomus 0.7411765  Sciaenidae
## 6 16  Argyrozona 0.1666667   Sparidae
```

taxize use #2: go through species names and extract IUCN status

```
source("IUCN_API.R")
rawdata <- read.csv("RawDataExample.csv")
head(rawdata)
```

```
spps <- data.frame(species = unique(c(as.character(rawdata$Sci.labels),
                                     as.character(rawdata$Sci.actuals))),
                  IUCNstatus = NA)

for(i in 1:nrow(spps)){
  s <- try(iucn_summary(as.character(spps$species[i]),key=IUCN_key))
  spps[i, 'IUCNstatus'] <- iucn_status(s)
}

head(spps)
```

```
##           species IUCNstatus
## 1   Arapaima gigas          DD
## 2 Brachyplatystoma rousseauxii  LC
## 3   Argyrops spinifer          LC
## 4   Cheimerius nufar          DD
## 5   Anabas testudineus         DD
## 6   Clarias fuscus           LC
```

taxize use #2: go through species names and extract IUCN status

```
source("IUCN_API.R")
rawdata <- read.csv("RawDataExample.csv")
head(rawdata)
```

```
spps <- data.frame(species = unique(c(as.character(rawdata$Sci.labels),
                                     as.character(rawdata$Sci.actuals))),
                  IUCNstatus = NA)

for(i in 1:nrow(spps)){
  s <- try(iucn_summary(as.character(spps$species[i]),key=IUCN_key))
  spps[i, 'IUCNstatus'] <- iucn_status(s)
}

head(spps)
```

```
##           species IUCNstatus
## 1   Arapaima gigas          DD
## 2 Brachyplatystoma rousseauxii LC
## 3   Argyrops spinifer        LC
## 4   Cheimerius nufar         DD
## 5   Anabas testudineus       DD
## 6   Clarias fuscus          LC
```

