

AssaySpecificity

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Load data

Input data should have columns: Genus, Species, AP

```
data <- read.csv(file.choose())
group_by(data, Genus) %>% summarize(N = n(), MeanAP = mean(AP))
```

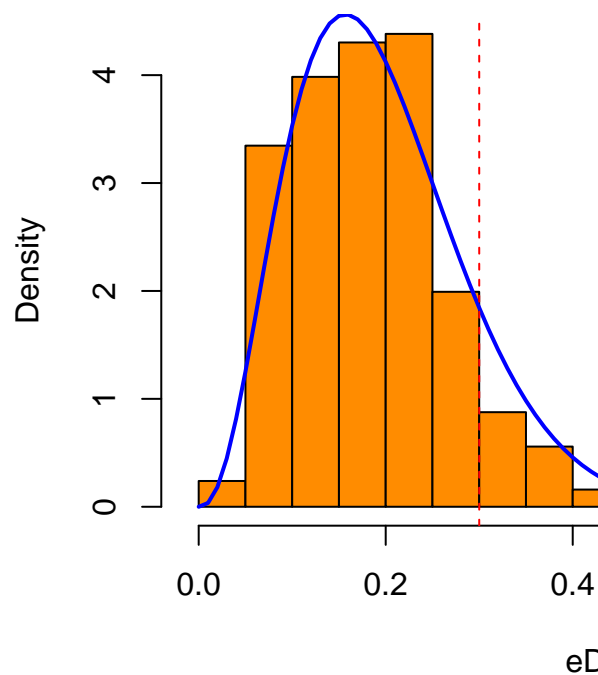
```
## # A tibble: 13 x 3
##   Genus      N MeanAP
##   <chr>    <int> <dbl>
## 1 Barbicambarus      2  0.115
## 2 Bouchardina        1  0.307
## 3 Cambarellus        8  0.168
## 4 Cambarus          72  0.154
## 5 Creaserinus        1  0.07
## 6 Fallicambarus      6  0.252
## 7 Faxonella          2  0.183
## 8 Faxonius          70  0.160
## 9 Hobbseus           6  0.229
## 10 Lacunicambarus    6  0.062
## 11 Orconectes         6  0.107
## 12 Procambarus      70  0.256
## 13 Troglocambarus    1  0.299
```

Estimate beta probability density function

```
beta
```

```
##      shape1      shape2
## 3.5774506 14.8532310
## ( 0.2167669) ( 0.9494730)
```

Histogram and inferred probability density function



Observed eDNA assignment probabilities are shown in the histogram.

Summary table

Table showing estimated probability of an unsampled confamilial exceeding an assignment probability threshold of 0.30 (first row) or 0.50 (second row) using probability density functions.

##	Estimate
## 0.30 threshold	0.128
## 0.50 threshold	0.003