

AllelicRichRaref: User Manual

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AllelicRichRaref is a function written for the platform R (R Core Team, 2016). It calculates the mean allelic richness using rarefaction for different sample sizes, without loci, alleles or individuals size limitation. To estimate allelic richness, it was used the formula:

$$R_{ik} = \sum_k (1 - P_{ik})$$

where $\binom{N_i - N_{ik}}{g} / \binom{N_i}{g}$

is the probability that allele k does not occur in a sample of g genes chosen as reference. N_{ik} is the number of alleles k in the sample of size N_i (Foulley & Ollivier, 2006).

This user manual is suitable for people with no or limited experience with R. It is a complement to the comments already provided in the file AllelicRichRaref.R which contains the code of the function. You can download the function from <https://github.com/KChavez-Congrains/AllelicRichRaref>.

1st step: To prepare the input file:

You need to create a file containing the genotypes of each individual:

- i. the input file does not need to contain the individuals' identifiers;
- ii. two columns per locus are need: One for each allele; alleles must be coded as numeric values; for missing data, use NA;
- iii. the first row may or may not contain the column names (see the test files deposited in <https://github.com/KChavez-Congrains/AllelicRichRaref>).

2nd step: To import the input file in R:

Open R, and use the command `read.table(file.choose(),header=T)` if your input file has a header or `read.table(file.choose(),header=F)` if doesn't have it, then these will open a Choose File window. Ex:

```
test <- read.table(file.choose(),header=T)           #choose the file testfile1.txt
```

```
test <- read.table(file.choose(),header=F)           #choose the file testfile2.txt
```

3rd step: To load the AllelicRichRaref function:

Open the file AllelicRichRaref.R (>>File>>Open File) or copy and paste all the text containing the code of the function in the R window. Then, select all the code and run it by pressing the Ctrl+R button combination; if you are using RStudio press the Ctrl+Enter combination or click in the Run icon.

4th step: To calculate the Allelic Richness:

To run the function `AllelicRichRaref`, you should simply specify the name of the object containing the input file information. Run the command `AllelicRichRaref(name_object)`. Ex:

`AllelicRichRaref(test)`

It will print a data frame with the result:

```
> AllelicRichRaref(test)
  sampleSize allelicrich
1           1    1.783333
2           2    2.346164
3           3    2.782130
4           4    3.127499
5           5    3.406167
6           6    3.634556
7           7    3.824299
8           8    3.983837
9           9    4.119419
10          10    4.235757
11          11    4.336462
12          12    4.424339
13          13    4.501601
14          14    4.570011
15          15    4.630987
16          16    4.685683
17          17    4.735045
18          18    4.779852
19          19    4.820753
20          20    4.858286
```

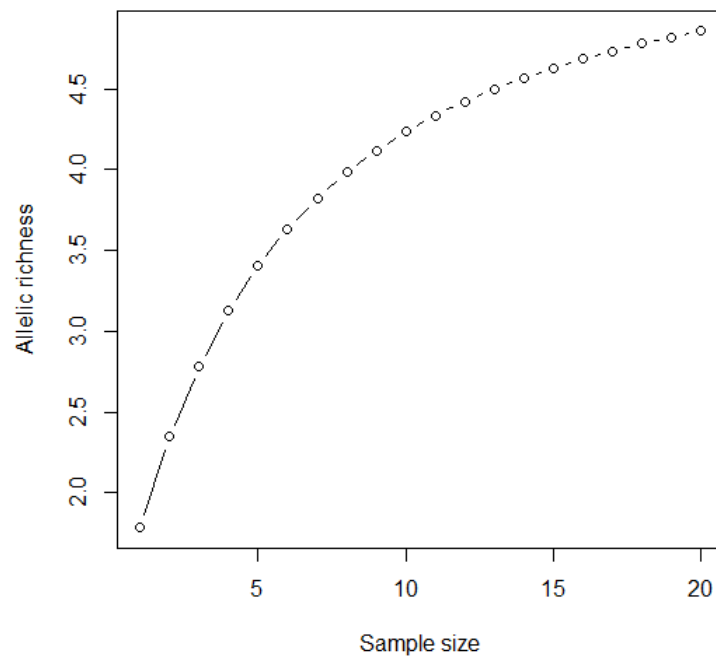
The result can be saved as an object, for that you can use the command:

`TEST <- AllelicRichRaref(test)`

5th step: To plot the result – extra step:

To obtain a graph you can use the `plot` function or the `ggplot2` package. Ex:

`plot(TEST$SampleSize,TEST$allelicrich, type = "b", ylab = "Allelic richness", xlab = "Sample size")`



```
install.packages("ggplot2")
```

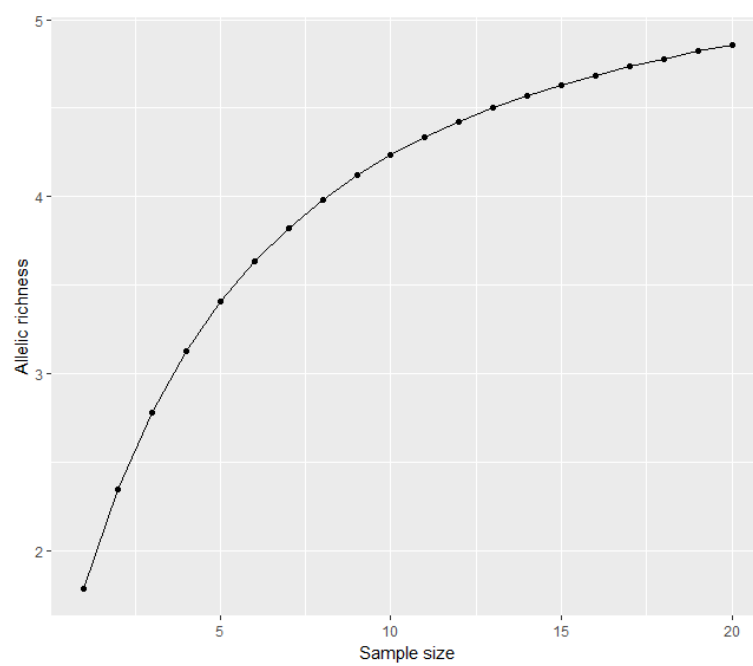
```
library(ggplot2)
```

```
ggplot(TEST, aes(x=G, y=allelicrich)) +
```

```
  geom_point() +
```

```
  geom_line() +
```

```
  labs(x="Sample size", y="Allelic richness")
```



Foulley, J. L., & Ollivier, L. (2006). Estimating allelic richness and its diversity. *Livestock Science*, 101(1), 150-158.

R Core Team (2016). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL <https://www.R-project.org/>.