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```

hp.abund <- read.delim
('https://raw.githubusercontent.com/zdealveindy/anadat-r/master/data/hp.abun
d.txt')
hp.incid <- read.delim
('https://raw.githubusercontent.com/zdealveindy/anadat-r/master/data/hp.inci
d.txt')
hp.elev <- read.delim
('https://raw.githubusercontent.com/zdealveindy/anadat-r/master/data/hp.elev
.txt', row.names = 1)
head (hp.abund)

# We will use package iNEXT (interpolation-extrapolation) developed by the
lab of prof. Anne Chao (Tsinghua University, Hsinchu;
http://chao.stat.nthu.edu.tw/wordpress/software_download/inext-online/)
# install.packages ('iNEXT')
library (iNEXT)

DataInfo (hp.abund, datatype = 'abundance')
DataInfo (hp.incid, datatype = 'incidence')

D_abund <- iNEXT (hp.abund, datatype = 'abundance')
plot (D_abund)

D_abund_232 <- iNEXT (hp.abund, datatype = 'abundance', endpoint = 232)
plot (D_abund_232)

est_D_abund <- estimatedD (hp.abund, datatype = 'abundance', conf = NULL)
est_D_abund

D_individuals <- est_D_abund$q = 0`

plot (D_abund, type = 3)
plot (D_abund, type = 3, xlim = c(.95, 1))

est_D_abund_coverage <- estimatedD (hp.abund, datatype = 'abundance', base =
'coverage', conf = NULL)
est_D_abund_coverage
D_coverage <- est_D_abund_coverage$q = 0`
D_area <- DataInfo (hp.abund, datatype = 'abundance')$S.obs

D_est <- cbind (D_area, D_individuals, D_coverage)
rownames (D_est) <- D_area <- DataInfo (hp.abund, datatype =
'abundance')$site

barplot ( (D_est), beside = T, legend.text = T, col = heat.colors (7), xlab
= 'Sample standardisation', ylab = 'Species richness', names.arg = c('sample
area', '# of individuals', 'sample coverage'))

matplot (scale (D_est), type = 'b', axes = F, xlab = 'Locality', ylab =

```

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'Standardized species richness')
axis (1, at = 1:7, labels = rownames (D_est))
axis (2)
box ()
legend ('topright', title = 'Diversity standardised by:', legend = c('sample
area', '# individuals', 'sample coverage'), pch = as.character (1:3), col =
1:3, lty = 1:3)

# The function iNEXT calculates rarefaction curves (can even extrapolate it
beyond the observed number of samples/individuals)
D_incid <- iNEXT (hp.incid, datatype = 'incidence_freq') # this is for
incidence-based data in hp.incid
plot (D_incid)

D_abund <- iNEXT (hp.abund, datatype = 'abundance', endpoint = 464) # and
this for abundance-based data for hp.abund
D_abund$DataInfo
plot (D_abund)

D_abund_est <- estimatedD (hp.abund, datatype = 'abundance', conf = NULL) #
function estimatedD returns estimated diversities from given dataset (in the
default setting, the estimate is done to the lowest number of
samples/individuals in the dataset, here 232 individuals as in locality FT)
plot (D_abund_est[D_abund_est$order == 0, 'qD'] ~ elev$Elevation) # draw
pattern of diversity along elevation

# calculate rarefaction for completeness/coverage
D_abund <- iNEXT (hp.abund, datatype = 'abundance')
plot (D_abund, type = 2, ylim = c(0.95, 1))
plot (D_abund, type = 3)
abline (v = 0.9658)

D_abund_est_coverage <- estimatedD (hp.abund, datatype = 'abundance', base =
'coverage', conf = NULL)
D_abund_est_coverage

D_area <- D_abund$DataInfo$S.obs
D_indi <- D_abund_est$q = 0`
D_cove <- D_abund_est_coverage$q = 0`

Div <- cbind (D_area, D_indi, D_cove)
rownames (Div) <- D_abund$DataInfo$site
Div
matplot (t(scale (Div)), type = 'b')

```

From:

<https://anadat-r.davidzeleny.net/> - **Analysis of community ecology data in R**

Permanent link:

[https://anadat-r.davidzeleny.net/doku.php/en:rarefaction\\_examples\\_rscript](https://anadat-r.davidzeleny.net/doku.php/en:rarefaction_examples_rscript)

Last update: **2018/06/08 12:14**