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Diversity analysis

Plan: Divide the chapter into alpha+gamma diversity section and beta diversity section. One option - use Jurasinsky et al 2009 schema and talk about inventory, differentiation and proportional diversity (inventory = alpha and gamma, differentiation = based on dissimilarity measures, incl. variation within compositional matrix and length of DCA axis; proportional - gamma vs alpha, additive vs multiplicative, using Hill's numbers for it etc.) Other option is to divide the whole topic into several chapters:

1. alpha diversity (inventory diversity)
2. includes species richness, Shannon entropy, Simpson concentration index, Hill's numbers, effective number of species

- rarefaction and accumulation curves, estimates of unseen species - beta diversity

1. differentiation diversity - Legendre's approach, incl. LCBD, mean of pairwise dissimilarity indices, multisite dissimilarity indices
2. proportional diversity - Whittaker's beta, beta based on Hill's numbers, Chao's beta diversity (beta differentiation)

Rarefaction and accumulation curves

Dictionary of terms:

- **Rarefaction curves** answers the question "what would be the number of species in community if we sampled less individuals/samples", while accumulation curves shows whether we sampled enough (the curve flattens to asymptote) or we haven't (curve still steeply climbing up).
- **Accumulation curve** can be extrapolated to get hypothetical richness of larger sample or species pool, while rarefaction curve is basically an interpolation.
- **Individual-** vs **sample- (incidence)** based data: while individual-based data represent vector with number of individuals recorded for each species in single representative sample of the community, sample-based data consist of a set of sampling units (plots, traps, quadrats, transects), where incidence (presence) of species is recorded for each sampling unit.

packages dealing with rarefaction/accumulation curves: vegan, rich, iNEXT,

> **R functions**
>
> - **specaccum** (library vegan) - calculates accumulation curve on the community data matrix (one curve per matrix); plot draws the result (optionally with confidence interval).
> - **rarecurve** (library vegan) - draws rarefaction curves (each row of the matrix is one curve), without confidence intervals.
> - **rarefy** (library vegan)
> - **rarc** (library rich)
> - **iNEXT** (library iNEXT)

```
beetles <- read.delim
('http://www.davidzeleny.net/anadat-r/data-download/carabid-beetles-boreal-f
orest.txt', row.names = 1)

rarecurve (t(beetles))

# draw rarefaction curve with confidence intervals

rarecurve.ci <- function (x, step.ci = 1)
{
rar.temp <- apply (com, 1, FUN = function (x) rarefy (x, se = T, sample =
1:sum (x)))
plot.new ()
plot.window (xlim = c(1, max (rowSums (com))), ylim = c(1, max (rowSums (com
> 0)) ))
box ()
axis (1)
axis (2)
for (i in seq (1, length (rar.temp)))
    {
    y <- rar.temp[[i]]
    points (y[1,], type = 'l', col = i)
    col.ci <- rgb(red = col2rgb (i)[1,], green = col2rgb (i)[2,], blue =
col2rgb (i)[3,], alpha = 100, max = 255)
    for (x.coord in seq (1, length (y[2,]), by = step.ci))
        lines (x = c(x.coord, x.coord), y = c(y[1, x.coord] + 1.95*y[2,
x.coord], y[1, x.coord] - 1.95*y[2, x.coord]),
        col = col.ci)
    }
}

rarecurve.ci (t(beetles))
```

iNext package of Chao et al. 2014, maintained by Hsieh T.C. (謝宗震), offers drawing of rarefaction curves with intra- and extrapolation options and confidence intervals. Additionally to rarefied species richness (of Hill numbers 1, 2 and 3) it also calculates sample completeness (coverage) and allows to standardise samples by completenes. More details in this blog post.

References

- Chao A., Gotelli N.J., Hsieh T.C., Sander E.L., Ma K.H., Colwell R.K. & Ellison A.M. (2014): Rarefaction and extrapolation with Hill numbers: a framework for sampling and estimation in species diversity studies. *Ecological Monographs*, 84: 45-67.

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https://anadat-r.davidzeleny.net/doku.php/en:alpha_beta_diversity?rev=1466875169

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