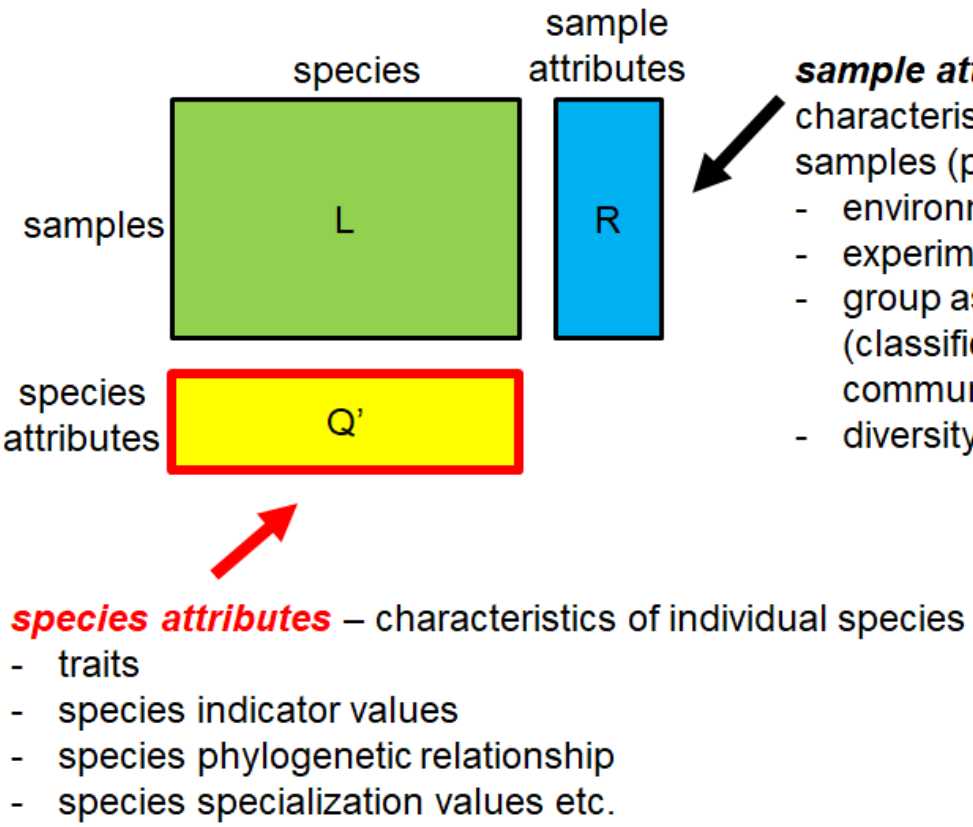
Analysis of species attributes

Needs to fix: Fix Me!

- link to the example with SLA and light availability
- link to the example about PCA on species attributes (needs to be done first),

Species attributes are measured or estimated characteristics of species. I could simply call them *traits*, but there is a much wider range of species characteristics than just traits (e.g. "Ellenberg-type" species indicator values, species specialisation values, or phylogenetic age). Analyses described in this section involve three data matrices: **R** –*sample attributes* (characteristics of individual samples/plots, like environmental variables, assignments to experimental treatments, diversity etc.), **L** – species composition data (presences absences of abundances of species in samples), and **Q** – *species attributes* (e.g. species traits or species ecological optima)(note that **R** and **Q** may be represented by only a single sample attribute or species attribute, respectively; then these are not matrices, but vectors).



A common ecological question which is being asked on such data is: how are species attributes related to sample attributes? (e.g. how do species functional traits relate to environmental variables?). There is no easy way how to connect species and sample attributes directly (for an obvious reason – species attributes are attributes of species, while sample attributes are attributes of samples/plots, and there is no straightforward match between species and samples), and the matrix of species composition here acts as a glue mediating such link.

There is a range of methods to solve such question, divided here into two categories:

1. Relating a single species attribute to a single sample attribute (e.g. specific leaf area (SLA) to availability of light as in the example Fix Me!): this can be done by relating community-weighted means of species attributes (CWM) to sample attributes (CWM approach), species niche centroids of sample attributes (SNC) to species attributes (SNC approach) or by relating all three matrices (R, L and Q) together using the fourth-corner problem.

2. Relating several species attributes to one or several sample attributes: this becomes an ordination problem, with CWM-RDA or RLQ methods available.

This list of methods is indeed not complete and other methods exist. Species attributes can also be analysed independently on the species composition and sample attributes, e.g. by applying PCA ordination on the matrix of standardised species attributes to explore their inter-correlation and main dimensions they represent (see example X Fix Me! in the PCA & tb-PCA (linear unconstrained ordination section).

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

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