SPECIES DISSIMILARITY

Distance matrix for species data:
the dissimilarity matrix

- instead of using the Pythagorean Theorem to calculate 'distances' between species, we use
  - <u>Bray-Curtis</u> or <u>Jaccard</u> indices for abundance data, or
  - <u>Jaccard</u> (`vegdist(x, binary = TRUE)`) for presence-absence data − this is called the <u>Sørensen</u> dissimilarity index
- instead of having columns with measurements of environmental variables we have species abundance or presence-absence data
- Dissimilarity = 1 - Similarity
  - dissimilarity: the indices go from 0 (sites are identical) to 1 (sites are completely dissimilar)
  - similarity: the indices go from 0 (sites are completely dissimilar) to 1 (sites are identical)
- many more dissimilarity indices in **vegan**; see `?vegdist` and `?betadiver`, and 'Koleff et al. (2003). Measuring β-diversity for presence–absence data. Journal of Animal Ecology, 72(3), 367-382'.
- Qualitative indices (e.g. applied to presence-absence data) give more weight to rare species because the weights assigned to rare and common species are the same (1 in both instances).
- Quantitative indices give more weight to common species, which have more numerical variation between plots and these 'weights' feature more strongly in the calculation of indices.

Distance matrices: some old, some new

- recap
  - <u>Euclidian distance</u> for environmental data
  - <u>Bray-Curtis</u> or <u>Jaccard</u> for species <u>abundances</u> (but also many others in `vegdist()`) and elsewhere
  - <u>Sørenson</u> for <u>presence-absence</u> (binary Bray-Curtis in **vegan**) species data

- ...also <u>Gower's distance</u> for <u>categorical</u> (factor; must be declared) data, i.e. use `daisy()` in the **cluster** package or `gowdis()` in the **FD** package
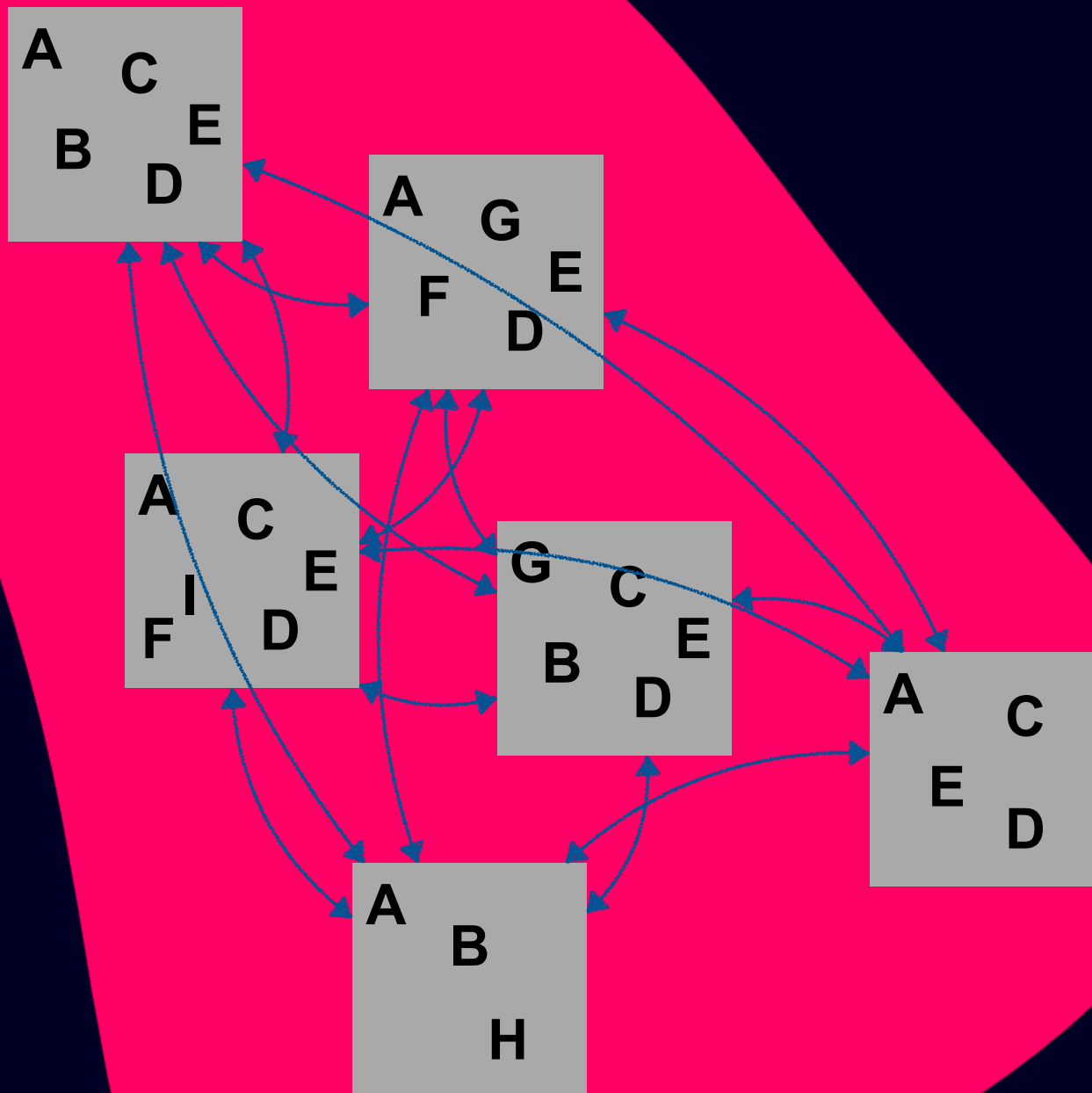
3. β-diversity based on pairwise comparisons
a)   Turnover β-diversity
b)   Nestedness-resultant β-diversity

Refer to Baselga (2010), especially to Figure 1, where the distinction between turnover and nestedness-resultant β-diversity is explained.

Calculating the two forms of β-diversity depends on two diversity indices, namely, the Sørensen pairwise dissimilarity and the Simpson pairwise dissimilarity. Again, refer to Baselga (2010) for details.

These equations are easy to understand and apply in practice for one pair of sampling units, but in the case here there are (6 × (6 - 1))/2 = 15 possible pairs, so it will become tedious very quickly.

In R, use the **BiodiversityR** package, and its `diversityresult()` function to do this automatically.

Baselga, A. (2010). Partitioning the turnover and nestedness components of beta diversity. Global ecology and biogeography, 19(1), 134–143.

Distance matrix for species data

- using the Doubs species data:

  ... look at the data

  ... would we use Bray-Curtis or Jaccard dissimilarities?

  ... apply the calculation

  ... explain the meaning of the results in broad terms

  ... examine it more closely: what general pattern comes out?

  ... plot this pattern (hint, it is best seen in the 1st column of the dissimilarity matrix)

  ... what explanation can you offer for this pattern?

  ... using the `decostand()` function, create presence/absence data, and apply the appropriate

  `vegdist()` function to obtain a suitable dissimilarity matrix