# Parasite communities

# Community

 Heterotypic assemblage composed of individuals of different species which may actually interact
 i.e. communities of gill parasites in fish





# Hierarchical classification of parasite communities

#### Infracomunity

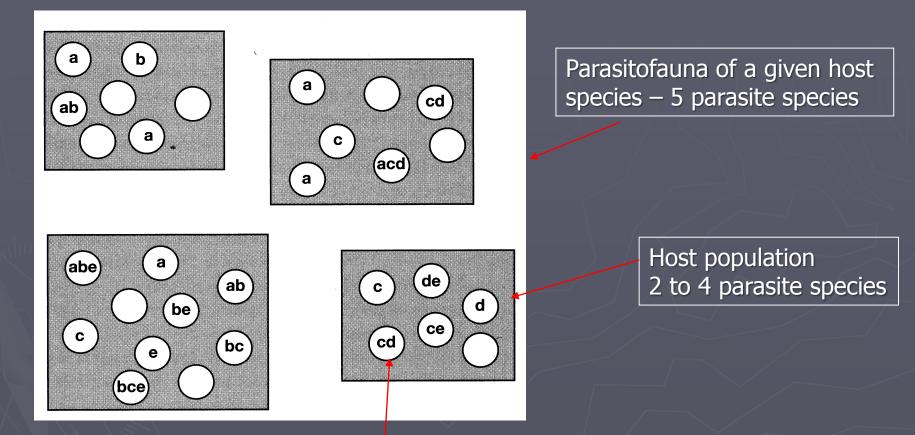
assemblage consisting of all parasites of different species in the same host individual

#### Metacommunity or component community

Assemblage consisting of all parasites of different species exploiting host population (in a given time and in a given space)

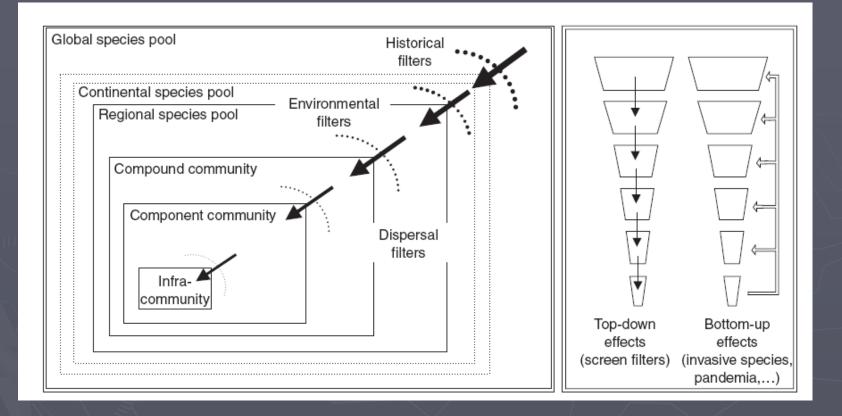
Supracommunity or compoud community assemblage composed of all metacommunities in a given ecosystem

# Hierarchical classification of parasite communities in a given host species



Host individual – 0 to 3 parasite species

# Hierarchical level of parasite communities



# Infracommunity

Number of parasite species

 Relative abundance (number of specimens of each parasite species)

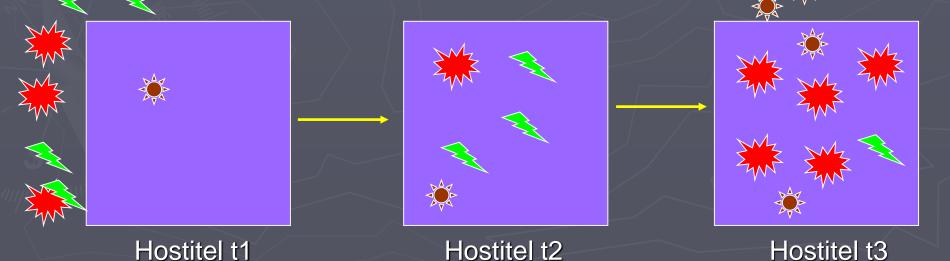
Dynamic system – mobility, natality, mortality
 Formation during ecological time, influence of infection and demographic processes
 Typically short-lived

# Infracommunity

Number of parasite species
 Relative abundance (number of specimens of each parasite species)

#### Dynamic system

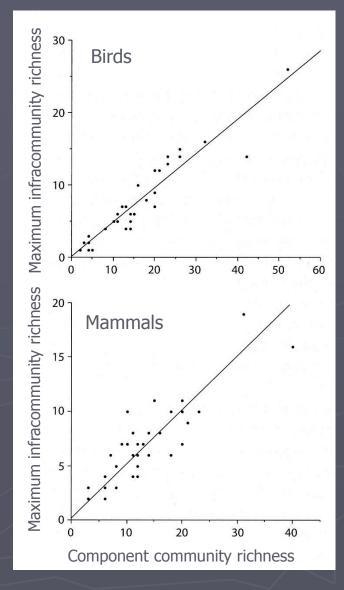
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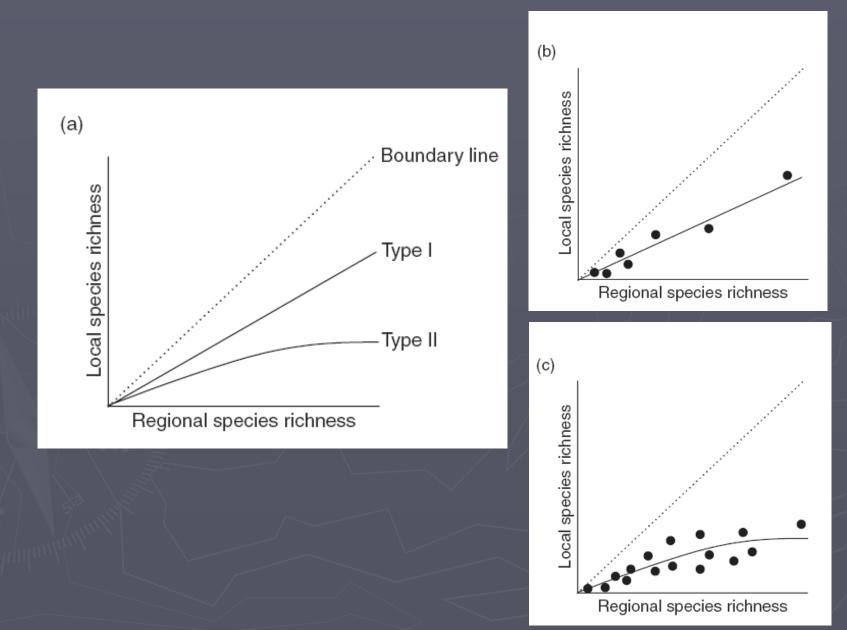
# Infracommunity

Maximum number of species in IC = number of species in MC This upper limit is not realized.

i.e. 31 intestinal helminthcommunities in birds37 intestinal helminthcommunities in mammals



# Saturation of communities



# Saturation of parasite infracommunities?

Kennedy & Guégan (1996) 64 metacommunities of intestinal helminths Can the saturation limit the number of species in helminth infracommunities?

maximum number of species in infracommunities = 3 number of species in metacommunities > 3 saturation of infracommunities – number of species in IC bellow the number of species in MC

very rare saturation of infracommunities by parasite species – vacant niches

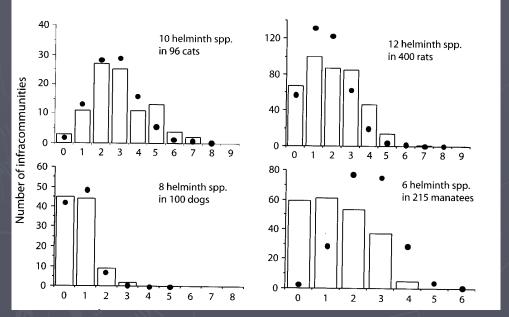
saturation by parasite biomass E.g. Helminth communities in 131 vertebrate species total biomass of intracommunity increased with host body size, large hosts = high biomass of parasites

Variability in the number of species in infracommunities of a given host population

- infracommunities with low number of species, infracommunities with high number of species

Number of species in infracommunities
 1. random distribution of parasite species on/in host
 2. affected by interactions (competitive exclusion) or colonization of one species is dependent on the other species

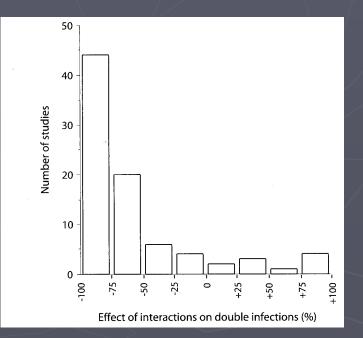
Frequency distribution of parasite species in infracommunities (species prevalence) – observed vs. predicted distribution by null model (Janovy et al., 1995)



- 1. interactive community competitive exclusion
- 2. positive interactions using host by other parasite species is facilitated
- 3. heterogeneity among hosts in susceptibility to infection

4 metacommunities of gastrointestinal helminths in mammals

► Larval digeneans in intermediate hosts (snails)
 - very few infracommunities with more than 1 species
 → temporal and spatial heterogeneity in infection rate
 → relative effect of antagonistic interactions on frequency of infections between two larval digenean species



# Metacommunity

Longer-lived assemblages than any of their infracommunities

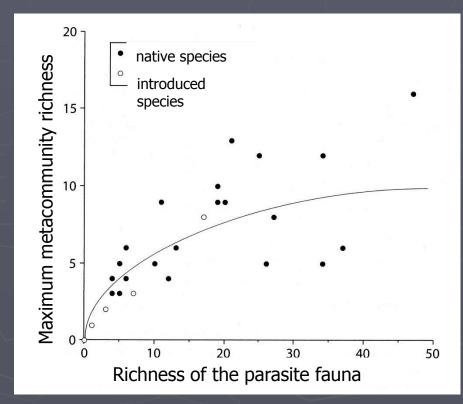
MC is formed over evolutionary time scales by invasion, speciation, extinction, colonization or host switches

Maximum number of parasite species in MC = the number of species in the parasite fauna

Often a saturation of the level of species below that of the parasite fauna

# Saturation of metacommunity

Ex. relationship between parasite species richness in MC and richness in the parasite fauna (helminth parasites of 32 freshwater fish species in UK published by Kennedy & Guégan, 1994)



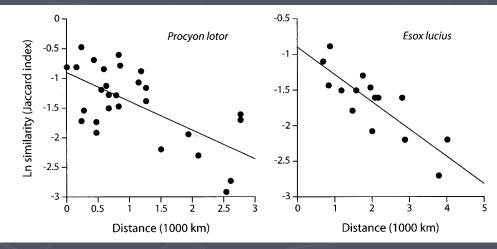
# Decay in metacommunities similarity with increasing distances

Geographical distances Climatic or environmental gradient Species-specific dispersion

# Similarity in parasite metacommunities

Contacts of host populations and exchange of parasites
 Physically isolated host populations – different parasite MC
 Geographical distances – good predictor of similarity in species composition (but this is not universal phenomenon)







# Similarity in parasite metacommunities: role of host

Dispersal capacity and migration – homogeneity of metacommunities in region

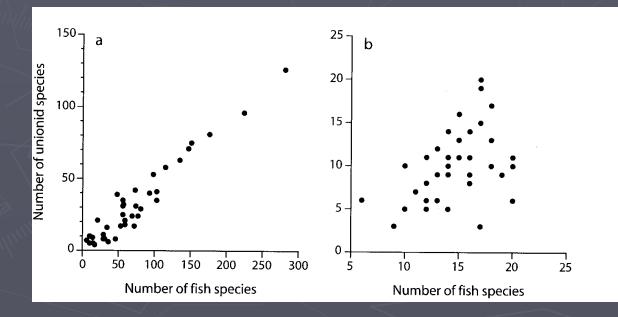
e.g. limited dispersal capacity of freshwater fish (fragmented freshwater habitats), no-limited dispersal capacity in open space in marine

Different food availabilities and preferences in different continents

## Diversity of metacommunities: role of host

► Higher host diversity → species-richer parasite metacommunities

Positive relationship between number of host species of a given taxon in a habitat and number of parasite species using this taxon



## Diversity of metacommunities: role of host

Time necessary for evolution of metacommunity

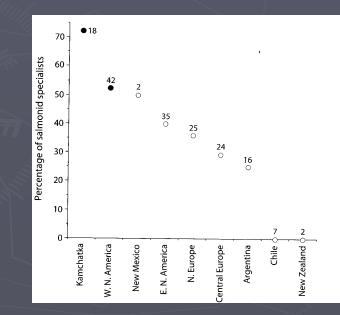
Translocation of host populations
 e.g. introduction of host species

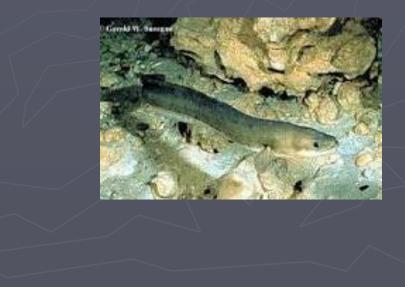
- initial stage species-poor metacommunties
- increasing diversity in time host switching between sympatric hosts, migration of new parasitized specimens of host

# Diversity of metacommunities: role of host

Composition of metacommunities in relation to host specificity

- e.g. Anguilla rostrata metacommunities with mainly specialists on the Atlantic coast, and mainly generalits in the continents
- in geographical space the number of species in parasitofauna increases, relative number of specialists decreases





# Similarity in parasite metacommunities: role of parasite

- Colonization and dispersion of some parasites associated with life cycle (IH, DH, parathenic hosts)
- allogenic parasites used birds as a DH homogenous and predicted metacommunities
- autogenic parasites used strictly water organisms, different metacommunities

e.g. Coregonus lavaretus – helminth metacommunities

- share allogenetic species

- differ in autogenic species depending on the distances between lakes



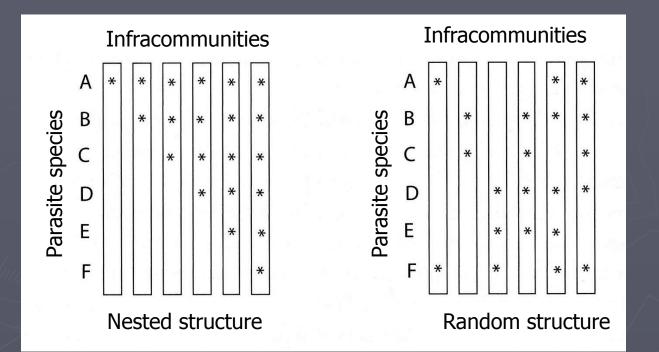
# Nested structure of parasite infracommunities

Nonrandom distribution of species richness among infracommunities

 Type of hierarchical structure of communities in fragmented habitats (firstly described for mammal communities in islands)

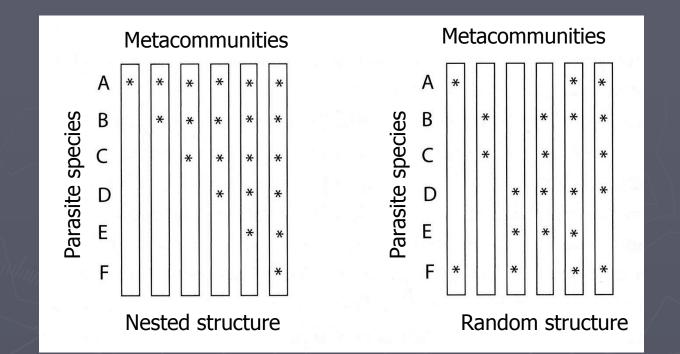
Host = fragmented habitat – nonrandom distribution of parasite species among IC i.e. within MC

# Nested structure of parasite infracommunities



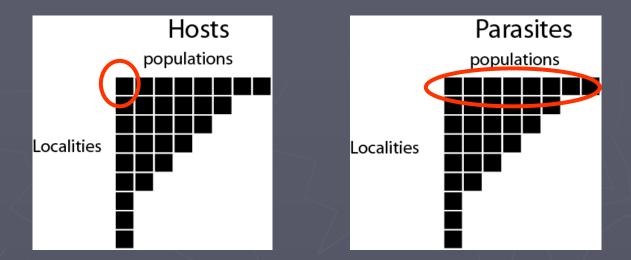
Two hypothetical distributions of parasite species among the infracommunities Each parasite species of a species poorer infracommunity is the subset of species-richer infracommunity

# Nestedness in parasite metacommunities

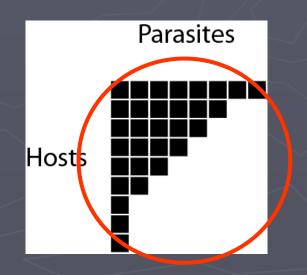


Each parasite species of a species-poorer locality (host population) is the subset of species-richer locality (host population)

# Nestedness in different hierarchical level of organization of parasite communities

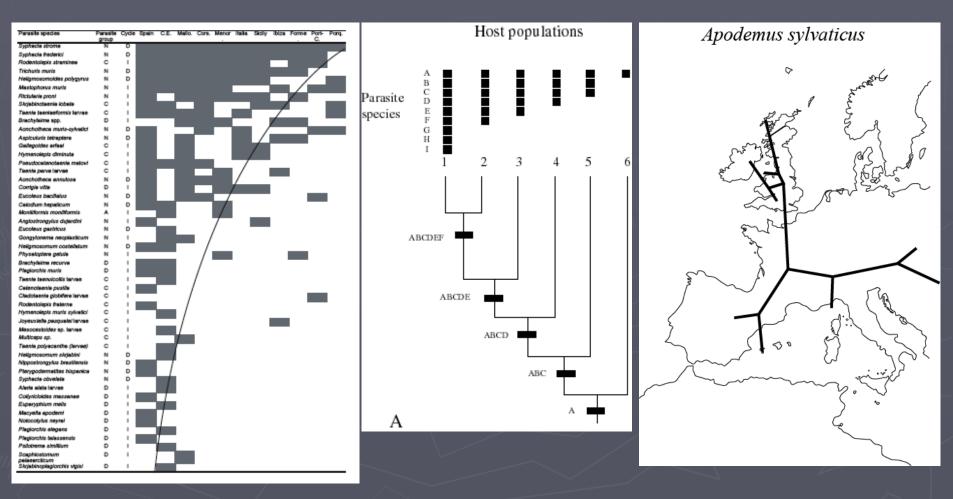


#### from local to regional level

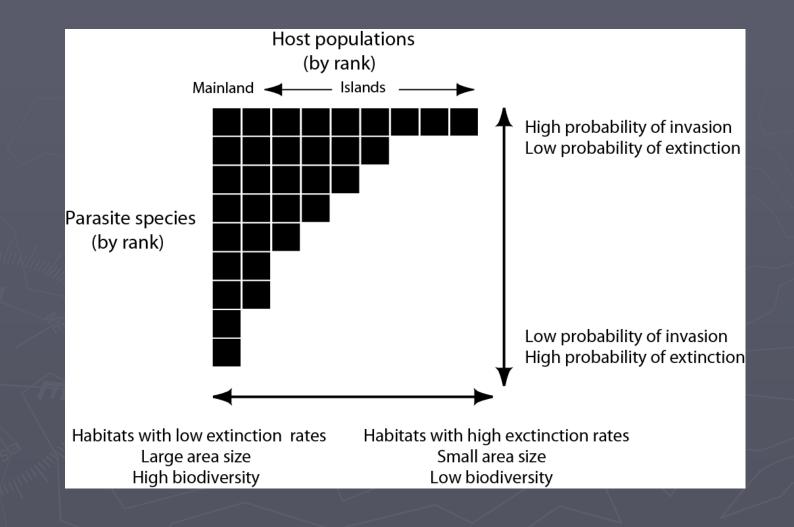


# Nestedness of metacommunities and phylography

Ex. Helminths in Apodemus sylvaticus



# Nestedness in metacommunities



# Which processes generate the nested pattern?

Free living species – different extinction, colonization and dispersion

#### Parasites

- different transmission, host heterogeneity generates different extinction and colonization of parasites
- heterogeneity in host size, small host  $\rightarrow$  big host
  - competition different opinions (increase/descrease/no effect)
  - association to host specificity

e.g. *Gyrodactylus* in freshwater cyprinids (high nestednesss in the communities with dominant position of specialists)



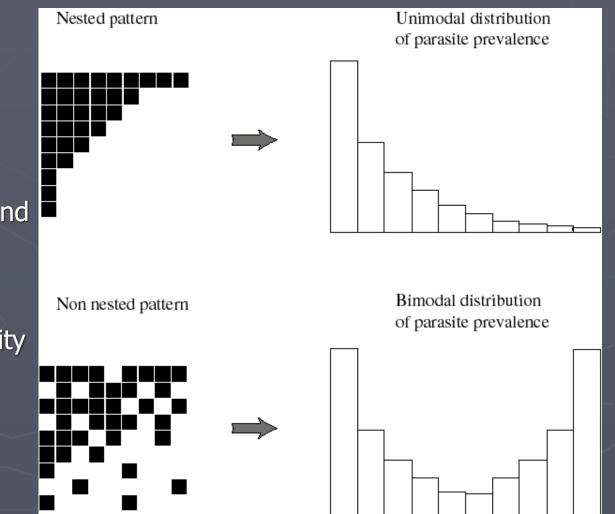




# Which processes generate nestedness?

Nestedness – result of epidemiological processes (Morand et al., 2002)

Link between nestedness and parasite prevalence – consequences of different parasite colonization and extinction linked with natality and mortality



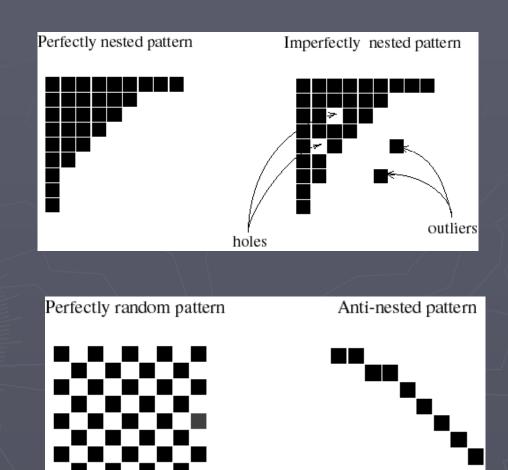
### Nestedness vs. antinestedness

Nested structure = one extreme case of hierarchical structure of parasite communities

Alternative antinested structure – parasite species present in species-poor communities are never present in species rich communities (some parasite communities of fish)

Biological interpretation unclear

# Nestedness vs. antinestedness



# Basics of data processing of parasitic communities

Number of parasite species in communities

|           | Community A                  | Community B |
|-----------|------------------------------|-------------|
| Species 1 | $\diamond \diamond \diamond$ |             |
| Species 2 | <b>**</b>                    | ♠♠          |
| Species 3 | <b>***</b>                   | *****       |

Analyses of diversity of parasite communities index of diversity – Shannon index diversity Brillouin index diversity

# Shannon index diversity

it assumes a random selection of individuals from a theoretically unlimited number and the presence of all species of community in the sample

to analyze diversity of parasite metacommunities

$$H' = -\sum p_i \ln p_i - \frac{S-1}{N} + \frac{1-\sum p_i^{-1}}{12N^2} + \frac{\sum (p_i^{-1} - p_i^{-2})}{12N^3} \qquad p_i = \frac{n_i}{N}$$

where S is the total number of species, pi is the proportion of individuals of the i-th species, N is the total number individuals, ni is the number of individuals of the i-th species

variability in Shannon diverzity

$$VarH' = \frac{\sum p_i (\ln p_i)^2 - (\sum p_i \ln p_i)^2}{N} + \frac{S - 1}{2N^2}$$

# Shannon index diverzity

The difference between the Shannon index values for the two communities can be compared using a t-test

$$t = \frac{H_{1} - H_{2}}{(VarH_{1} + VarH_{2})^{\frac{1}{2}}} \qquad \qquad df = \frac{(VarH_{1} + VarH_{2})^{2}}{\frac{(VarH_{1})^{2}}{N_{1}} + \frac{(VarH_{2})^{2}}{N_{2}}}$$

The maximum value of the Shannon index for a given community = In S = Shannon index at identical species frequency in the community

# Indexes of diversity

Equitability = evenness - the relative value of the diversity depleted by a given community in relation to a community with the same number of species

$$E = \frac{H'}{H_{\text{max}}} = \frac{H'}{\ln S}$$

#### Brillouin index of diverzity

- in case it is not possible to ensure random sampling or the sample contains all members
- describes only the sampled part of the community
- for the study of parasite infracommunities

 $HB = \frac{\ln N! - \sum \ln n_i!}{N}$ 

 $n_i$  – number of specimens of *i*-th species N – total number of specimens

# Indexes of dominance

the most important is the number of the most common species

- Simpson index of dominance
  - strongly dependent on the most numerous species in the community, less sensitive to rare species

 with increasing value, dominance increases and equitability of community decreases, often uses its inverse or subtraction from one

$$D = \sum \left( \frac{n_i(n_i - 1)}{N(N - 1)} \right)$$

 $n_i$  – number of specimens of *i*-th species N – total number of specimens

# Indexes of dominance

#### Berger-Parker index

expresses the relative importance of the most numerous species

- its inverse value is often used

- is independent of the number of species but is affected by the sample size

$$d = \frac{N_{\max}}{N}$$

 $N_{max}$  - number of specimens of the most numerous species N - total number of specimens

# Similarity of communities

#### Association coefficients

dependence coefficients (0 – no dependence)

- similarity coefficients (maximum value identical communities, minimum value – completely different communities)
- distances coefficients (distances between communities increase with the value of coefficient)

Types of data: binary data (presence – absence) quantitative data (abundance)

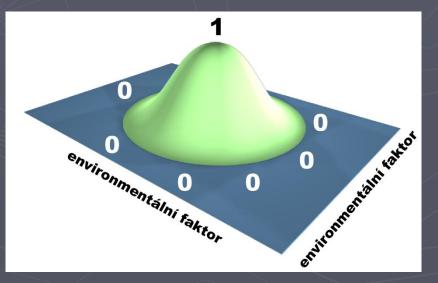
Numerical Ecology Legendre & Legendre (1998)

# Similarity of communities

asymmetric coefficients - zero values are evaluated differently than other values

symmetric coefficients - zero values for two objects are evaluated in the same way as other values for pairs of communities

problem of evaluation of double absence of species



# Qualitative similarity of communities

#### Association matrix – binary data

|             |   | Community 1 |                     |     |
|-------------|---|-------------|---------------------|-----|
|             |   | 1           | 0                   |     |
| Community A | 1 | a           | b                   | a+b |
|             | 0 | С           | d                   | c+d |
|             |   |             | •                   | -   |
|             |   | a+c         | <b>b</b> + <b>d</b> |     |

a - number of parasites present in two communities (in two localities)
d - number of absences of parasites in two communities (in two localities)
b - presence of parasites at the first locality, absence at the second locality
c - absence of parasites at the first locality, presence at the second locality

# Qualitative similarity of communities

#### Jaccard coefficient - asymmetric binary coefficient

 $S(x_1, x_2) = \frac{a}{a+b+c}$ 

a, b, c have the same weight

#### Sørensen coefficient

$$S(x_1, x_2) = \frac{2a}{2a+b+c}$$

where the presence of the species is more informative than the absence

# Quantitative similarity of communities

#### Symmetric coefficient

|                                     | Abundance of parasites |                         |  |  |   |  |  |  |  |  |
|-------------------------------------|------------------------|-------------------------|--|--|---|--|--|--|--|--|
| 9                                   | 3                      | 7                       | 3  | 4  | 9   | 5  | 4  | 0  | 6  |  |
| 2                                   | 3                      | 2                       | 1  | 2  | 9   | 3  | 2  | 0  | 6  |  |
| 0                                   | 1                      | 0                       | 0  | 0  | 1   | 0  | 0  | 1  | 1  |  |
| S(a, b) = congruence/p = 4/10 = 0.4 |                        |                         |  |  |   |  |  |  |  |  |
| Abundance of parasites aN bN jN     |                        |                         |  |  |   |  | jΝ   |  |  |  |
|                                     | 2<br>0                 | 2 3<br>0 1<br>/p = 4/10 | $\begin{array}{cccc} 2 & 3 & 2 \\ 0 & 1 & 0 \\ /p = 4/10 = 0.4 \\ \end{array}$ | 9  3  7  3 $2  3  2  1$ $0  1  0  0$ $/p = 4/10 = 0.4$ | 9  3  7  3  4 $2  3  2  1  2$ $0  1  0  0  0$ $/p = 4/10 = 0.4$ | $\begin{array}{cccccccccccccccccccccccccccccccccccc$ | $\begin{array}{cccccccccccccccccccccccccccccccccccc$ | $\begin{array}{cccccccccccccccccccccccccccccccccccc$ | $\begin{array}{cccccccccccccccccccccccccccccccccccc$ | $\begin{array}{cccccccccccccccccccccccccccccccccccc$ |

| Community a | 7 | 3 | 0 | 5 | 0 | 1 | 16 |    |    |
|-------------|---|---|---|---|---|---|----|----|----|
| Community b | 2 | 4 | 7 | 6 | 0 | 3 |    | 22 |    |
| Minimum     | 2 | 3 | 0 | 5 | 0 | 1 |    |    | 11 |

$$S(x_1, x_2) = \frac{2jN}{(aN+bN)}$$

where *aN* and *bN* are the total numbers of individuals in the community "a" or "b" <u>*jN* the sum is always</u> the lowest of the abundances of the

species found in one of the communities