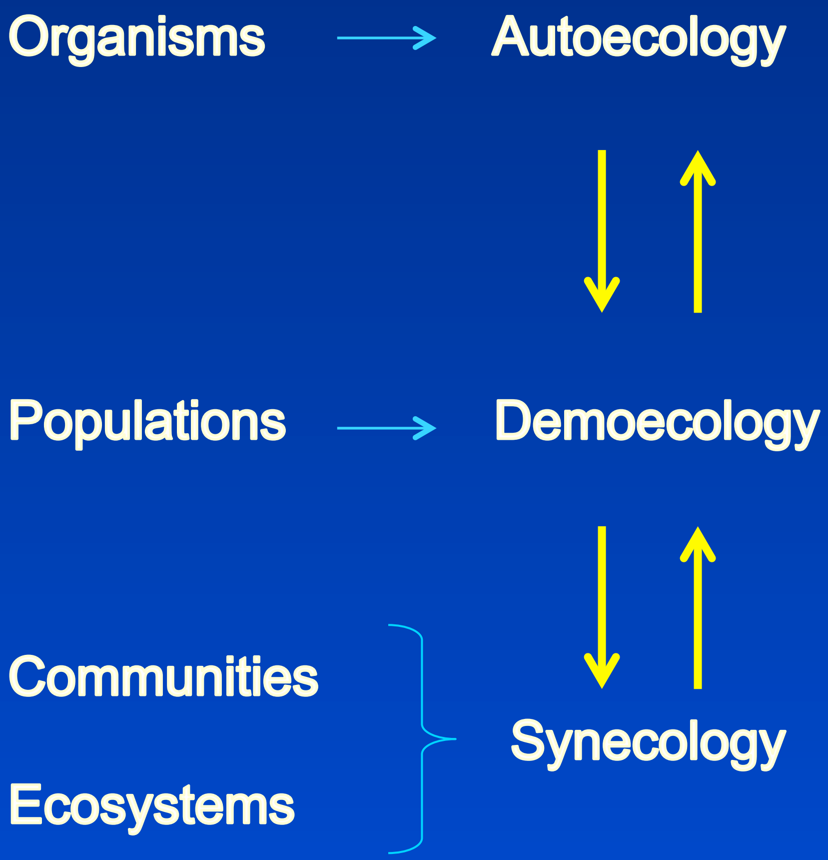
SYNECOLOGY

Community & Ecosystem Ecology

Guido Chelazzi 2017

Levels of integration in Ecology



Organisms → Autoecology

Populations → Demoecology

Communities
Ecosystems
Synecology

Community Ecology

- ✓ What is a BIOTIC COMMUNITY
- ✓ How do we get informations on the COMPOSITION and STRUCTURE of a biotic community
- ✓ Numerical tools for assessing the DIVERSITY of a community
- ✓ The vatiation of communities in time: SUCCESSIONS
- ✓ What is the rapport between the communities and the BIOMES
- ✓ What is and how we can describe a TROPHIC WEB
- ✓ What makes STABLE/UNSTABLE a trophic web
- ✓ How materials and energy circulate and flow within the trophic web and outside (BIOTIC-ABIOTIC relationships) →ECOSYSTEM

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Community Ecology

✓ General definition of a BIOTIC COMMUNITY

The whole set of population of different species living at the same TIME in the same portion of SPACE

✓ Two different views of the biotic community

A) Frederic Edward Clements (1874 –1945)

Community as an integrated group of populations of different species linked by functional relationships (predation, competition, mutualism etc.)

B) **Henry Allan Gleason** (1882–1975)

Comunity as an occasional set of populations of different species sharing autoecological prophile (niche similarity)

Community Ecology

- ✓ Descriptive (structuralistic) analysis

  Which species belong to the community
  What is their quantitative composition (abundance)

- ✓ Dynamic (storicistic-evolutionary) analysis

  How a community takes its structure
  How a community varies in time

- ✓ Functional analysis

  Which are the relationships between the different species
  How do they exchange matter and energy
  How do they compete/collaborate for extracting resources
  Which factors determine the stability/resilience to the community

Community structure: sampling

Community sampling

Community analysis is made within a selected area:

A. Objective boundaries (e.g. a lake, a grassland patch, a forest,a cultivated area etc.)

B. Subjective boundaries delimiting a study area (e.g. an administrative region) within a wider (natural) area

Community sampling

Random sampling

1.Select a particular area (objective or arbitrary)

2.Draw a “grid” or a “transect”

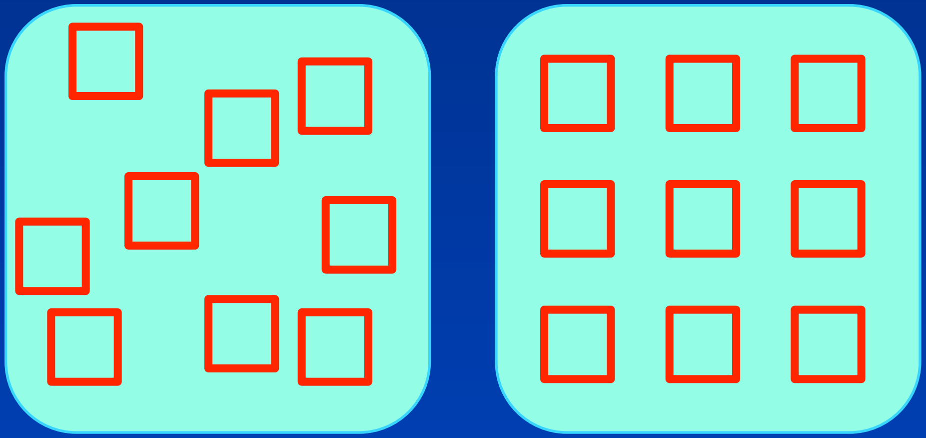
3.Select randomly a given number of sampling units

If the area is not homogeneous a stratified sampling is implemented:

Repeat (3) in the different subsystems
(e.g. grassland, forest etc.)

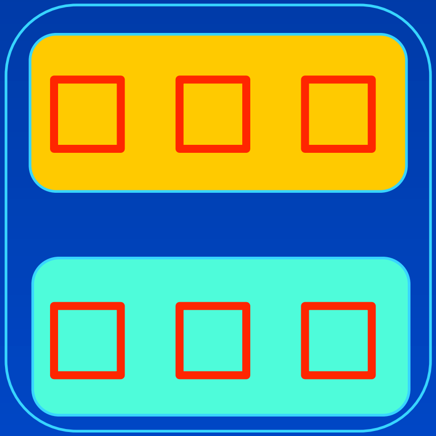
Community sampling

Homogeneous habitat structure
e.g. grassland



Random or uniform sampling

Heterogeneous habitat structure
e.g. grassland-forest



Stratified sampling

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Community study

In practice, most community analyses are made on a subset of species sampled in a selected area:

A) Taxonomic subsystem (assemblage): e.g. plant community, bird community, insect community etc.

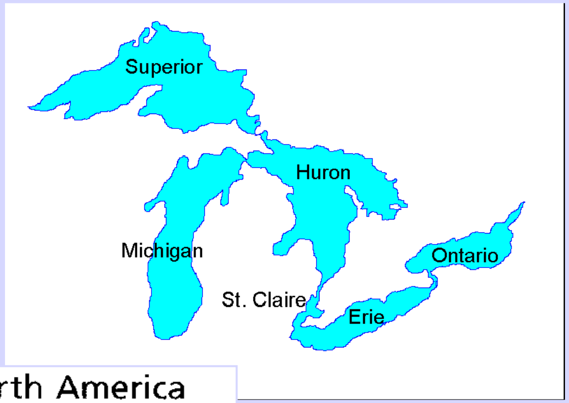
B) Functional subsystem (guild): e.g. primary producers, herbivores, predators, scavengers etc.

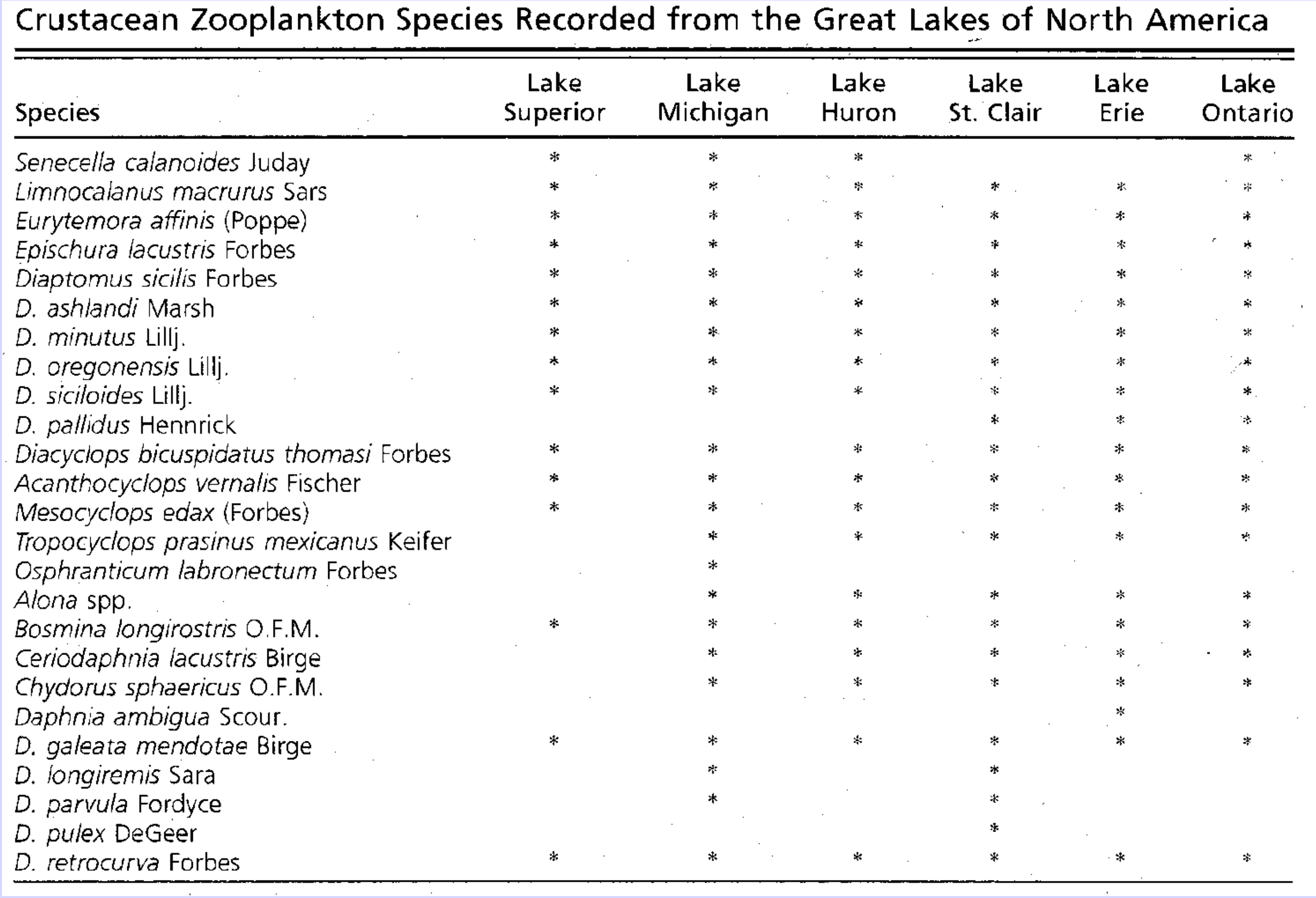
Or both: mammal predators, insect scavengers, insectivores birds etc.

Presence sampling

Zooplancton community in the Great Lakes (North America)

Contingency table





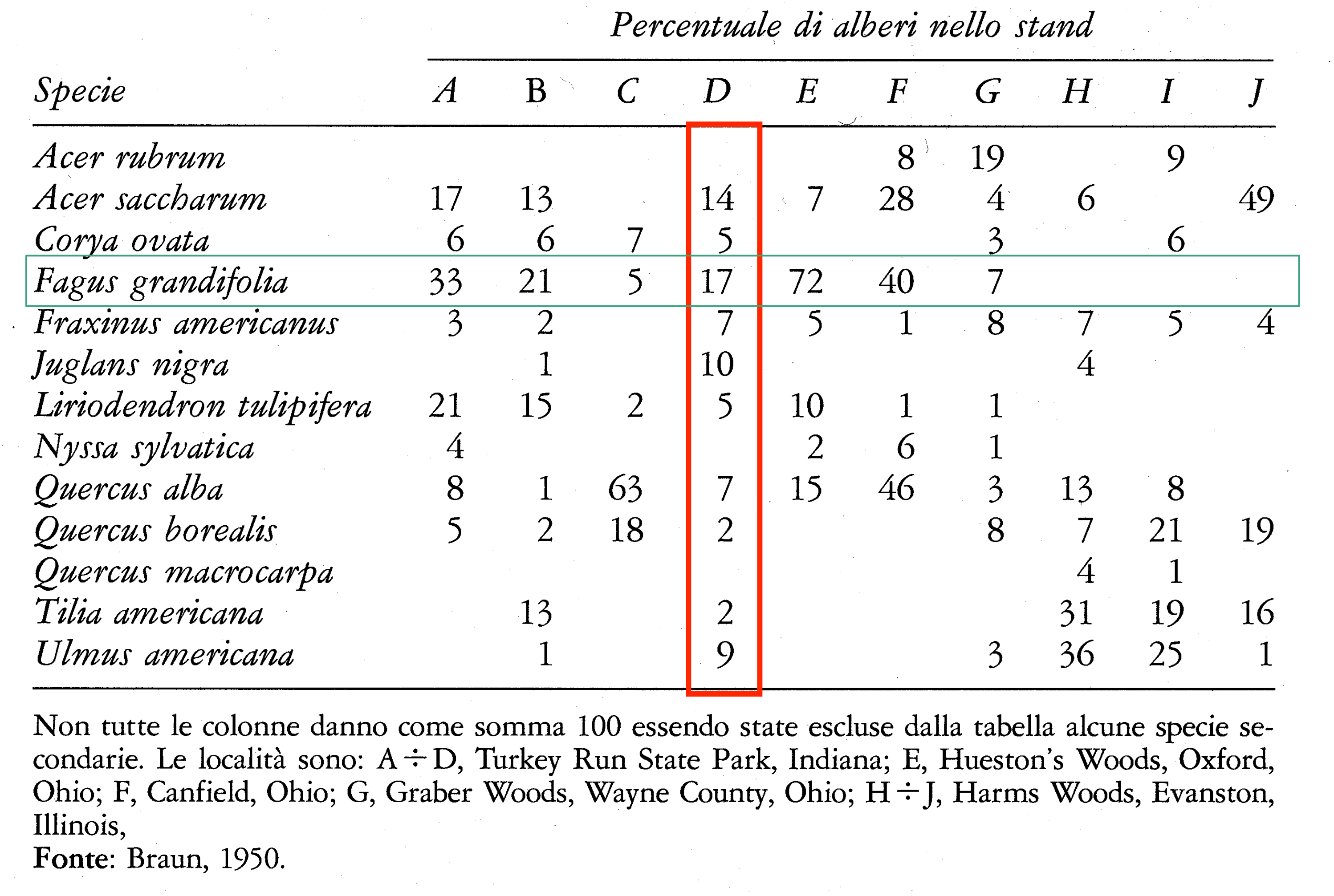
Crustacean Zooplankton Species Recorded from the Great Lakes of North America

Species	Lake Superior	Lake Michigan	Lake Huron	Lake St. Clair	Lake Erie	Lake Ontario
Senecella calanoides Juday	*	*	*			*
Limnocalanus macrurus Sars	*	*	*	*	*	*
Eurytemora affinis (Poppe)	*	*	*	*	*	*
Epischura lacustris Forbes	*	*	*	*	*	*
Diaptomus sicilis Forbes	*	*	*	*	*	*
D. ashlandi Marsh	*	*	*	*	*	*
D. minutus Lillj.	*	*	*	*	*	*
D. oregonensis Lillj.	*	*	*	*	*	*
D. siciloides Lillj.	*	*	*	*	*	*
D. pallidus Hennrick				*	*	*
Diacyclops bicuspidatus thomasi Forbes	*	*	*	*	*	*
Acanthocyclops vernalis Fischer	*	*	*	*	*	*
Mesocyclops edax (Forbes)	*	*	*	*	*	*
Tropocyclops prasinus mexicanus Keifer		*	*	*	*	*
Osphranticum labronectum Forbes		*				
Alona spp.		*	*	*	*	*
Bosmina longirostris O.F.M.	*	*	*	*	*	*
Ceriodaphnia lacustris Birge		*	*	*	*	*
Chydorus sphaericus O.F.M.		*	*	*	*	*
Daphnia ambigua Scour.					*	
D. galeata mendotae Birge	*	*	*	*	*	*
D. longiremis Sara		*		*		
D. parvula Fordyce		*		*		
D. pulex DeGeer				*		
D. retrocurva Forbes	*	*	*	*	*	*

Abundance sampling

Temperate forest community in the Western U.S.A.

Abundance matrix



	Percentuale di alberi nello stand									
Specie	*A*	B	*C*	*D*	*E*	*F*	*G*	*H*	*I*	*J*
Acer rubrum						8	19		9	
Acer saccharum	17	13		14	7	28	4	6		49
Corya ovata	6	6	7	5			3		6	
Fagus grandifolia	33	21	5	17	72	40	7			
Fraxinus americanus	3	2		7	5	1	8	7	5	4
Juglans nigra		1		10				4		
Liriodendron tulipifera	21	15	2	5	10	1	1			
Nyssa sylvatica	4				2	6	1			
Quercus alba	8	1	63	7	15	46	3	13	8	
Quercus borealis	5	2	18	2			8	7	21	19
Quercus macrocarpa								4	1	
Tilia americana		13		2				31	19	16
Ulmus americana		1		9			3	36	25	1

Non tutte le colonne danno come somma 100 essendo state escluse dalla tabella alcune specie secondarie. Le località sono: A ÷ D, Turkey Run State Park, Indiana; E, Hueston's Woods, Oxford, Ohio; F, Canfield, Ohio; G, Graber Woods, Wayne County, Ohio; H ÷ J, Harms Woods, Evanston, Illinois,

Fonte: Braun, 1950.

Species diversity (biodiversity indices)

S = number of species present (in the sample)
P_i = fraction of individuals of the i-th species on the total

Simpson' index

$$D = \frac{1}{\sum_{i=1}^{S} P_i^2}$$

➡ $1 \le D \le S$

Evenness

$$E = \frac{D}{S}$$

➡ $0 \le E \le 1$

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Simpson’s index

Species	**N**	**Pi**	**Pi^2**		
A	20	0,20	0,04		
B	20	0,20	0,04		
C	20	0,20	0,04		
D	20	0,20	0,04		
E	20	0,20	0,04	**D**	**E**
Total	100	1,00	0,20	5,00	1,00

Species	**N**	**Pi**	**Pi^2**		
A	50	0,50	0,25		
B	50	0,50	0,25	**D**	**E**
Totale	100	1,00	0,50	2,00	1,00

A	96	0,96	0,92		
B	1	0,01	0,00		
C	1	0,01	0,00		
D	1	0,01	0,00		
E	1	0,01	0,00	**D**	**E**
Total	100	1,00	0,92	1,09	0,22

Species diversity (biodiversity indices)

Shannon-Wiener index

$$H = -\sum_{i=1}^{S} P_i \log P_i$$

$0 \leq H \leq \text{Log } S$

If S=1, H=0

If S>1, H → 0 if one species is strongly prelalent

H → Log S if species presence is balanced

Evenness

$$J = \frac{H}{H_{MAX}} = \frac{H}{\log S}$$

$0 \leq J \leq 1$

Comparison of communities (similarity)

1) Binary similarity

Starting from contingency tables or abundance matrices of two communities it is possible to compute a BS index

2) Multiple (hyerarchic) similarity

Starting from BS indices of a set of communities it is possible to draw a graph showing the hyerarchic similarity among those communities

Binary similarity (contingency table)

Species	CA	CB
S1	+	-
S2	-	+
S3	+	+
S4	+	-
S5	-	+
S6	+	+

a = present in CA and CB
b = only in *CA*
c = only in *CB*

Jaccard's index

$$J = \frac{a}{a+b+c}$$

J = 2/(2+2+2) = 0.33

Sørensen's index

$$S = \frac{2a}{2a+b+c}$$

S = 4/(4+2+2) = 0.50

Binary similarity (Abundance matrix)

Bray-Curtis index

$$D_{A,B} = 1 - \frac{\sum_{i=1}^{S} \left| P_{i,A} - P_{i,B} \right|}{\sum_{i=1}^{S} \left| P_{i,A} + P_{i,B} \right|}$$

$P_{i,A}$ = abundance of **i-th** species in location **A**
$P_{i,B}$ = abundance of **i-th species** in location **B**

Multiple similarity (abundance matrix)

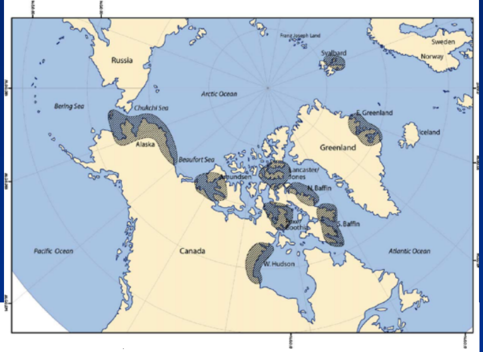
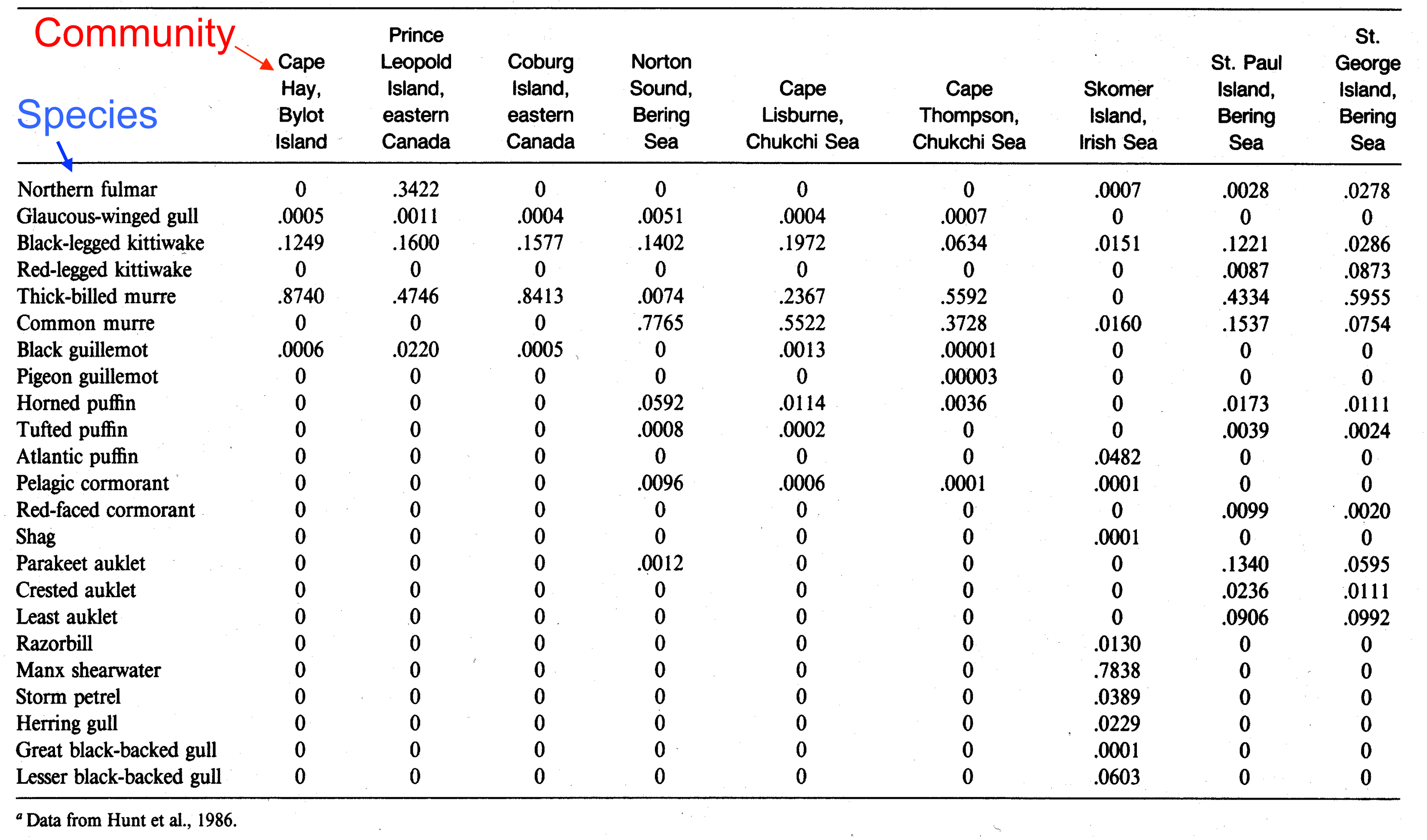


TABLE 9.5 RELATIVE ABUNDANCES (PROPORTIONS) OF 23 SPECIES OF SEABIRDS ON 9 COLONIES IN NORTHERN POLAR AND SUBPOLAR AREAS[a]



Community Species	Cape Hay, Bylot Island	Prince Leopold Island, eastern Canada	Coburg Island, eastern Canada	Norton Sound, Bering Sea	Cape Lisburne, Chukchi Sea	Cape Thompson, Chukchi Sea	Skomer Island, Irish Sea	St. Paul Island, Bering Sea	St. George Island, Bering Sea
Northern fulmar	0	.3422	0	0	0	0	.0007	.0028	.0278
Glaucous-winged gull	.0005	.0011	.0004	.0051	.0004	.0007	0	0	0
Black-legged kittiwake	.1249	.1600	.1577	.1402	.1972	.0634	.0151	.1221	.0286
Red-legged kittiwake	0	0	0	0	0	0	0	.0087	.0873
Thick-billed murre	.8740	.4746	.8413	.0074	.2367	.5592	0	.4334	.5955
Common murre	0	0	0	.7765	.5522	.3728	.0160	.1537	.0754
Black guillemot	.0006	.0220	.0005	0	.0013	.00001	0	0	0
Pigeon guillemot	0	0	0	0	0	.00003	0	0	0
Horned puffin	0	0	0	.0592	.0114	.0036	0	.0173	.0111
Tufted puffin	0	0	0	.0008	.0002	0	0	.0039	.0024
Atlantic puffin	0	0	0	0	0	0	.0482	0	0
Pelagic cormorant	0	0	0	.0096	.0006	.0001	.0001	0	0
Red-faced cormorant	0	0	0	0	0	0	0	.0099	.0020
Shag	0	0	0	0	0	0	.0001	0	0
Parakeet auklet	0	0	0	.0012	0	0	0	.1340	.0595
Crested auklet	0	0	0	0	0	0	0	.0236	.0111
Least auklet	0	0	0	0	0	0	0	.0906	.0992
Razorbill	0	0	0	0	0	0	.0130	0	0
Manx shearwater	0	0	0	0	0	0	.7838	0	0
Storm petrel	0	0	0	0	0	0	.0389	0	0
Herring gull	0	0	0	0	0	0	.0229	0	0
Great black-backed gull	0	0	0	0	0	0	.0001	0	0
Lesser black-backed gull	0	0	0	0	0	0	.0603	0	0

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[a] Data from Hunt et al., 1986.

Multiple similarity

Binary similarity matrix (Bray-Curtis)

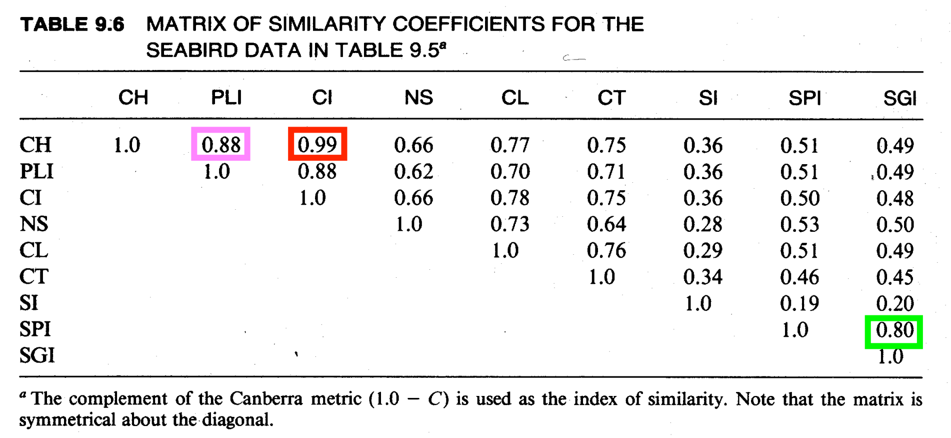
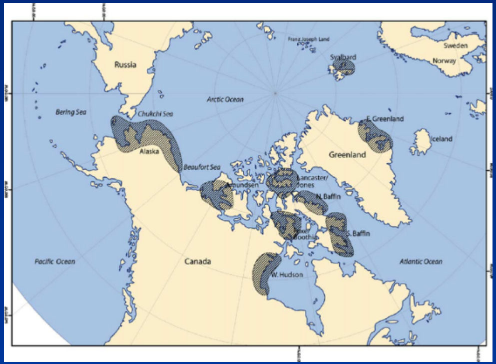


TABLE 9.6 MATRIX OF SIMILARITY COEFFICIENTS FOR THE SEABIRD DATA IN TABLE 9.5[a]

	CH	PLI	CI	NS	CL	CT	SI	SPI	SGI
CH	1.0	0.88	0.99	0.66	0.77	0.75	0.36	0.51	0.49
PLI		1.0	0.88	0.62	0.70	0.71	0.36	0.51	0.49
CI			1.0	0.66	0.78	0.75	0.36	0.50	0.48
NS				1.0	0.73	0.64	0.28	0.53	0.50
CL					1.0	0.76	0.29	0.51	0.49
CT						1.0	0.34	0.46	0.45
SI							1.0	0.19	0.20
SPI								1.0	0.80
SGI									1.0

[a] The complement of the Canberra metric (1.0 − *C*) is used as the index of similarity. Note that the matrix is symmetrical about the diagonal.



Hyerarchical similarity dendrogram

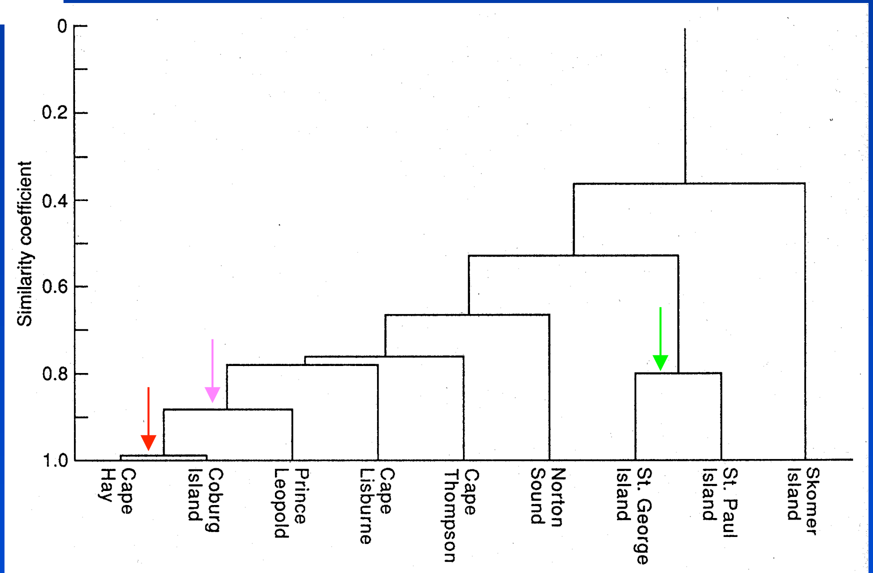
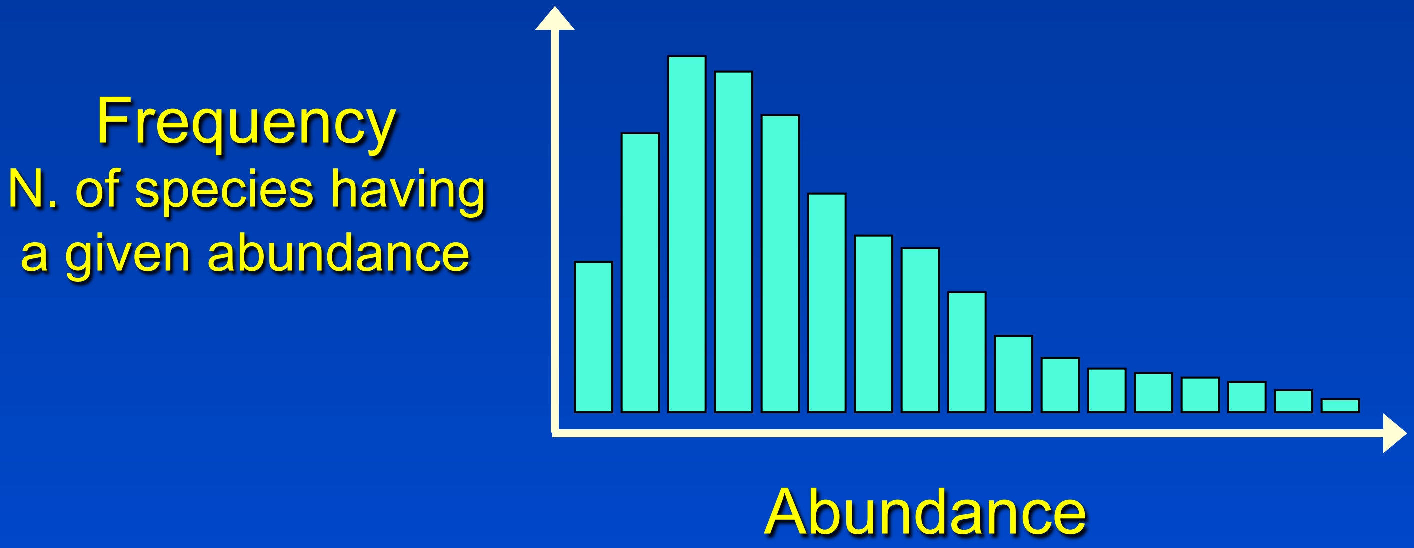


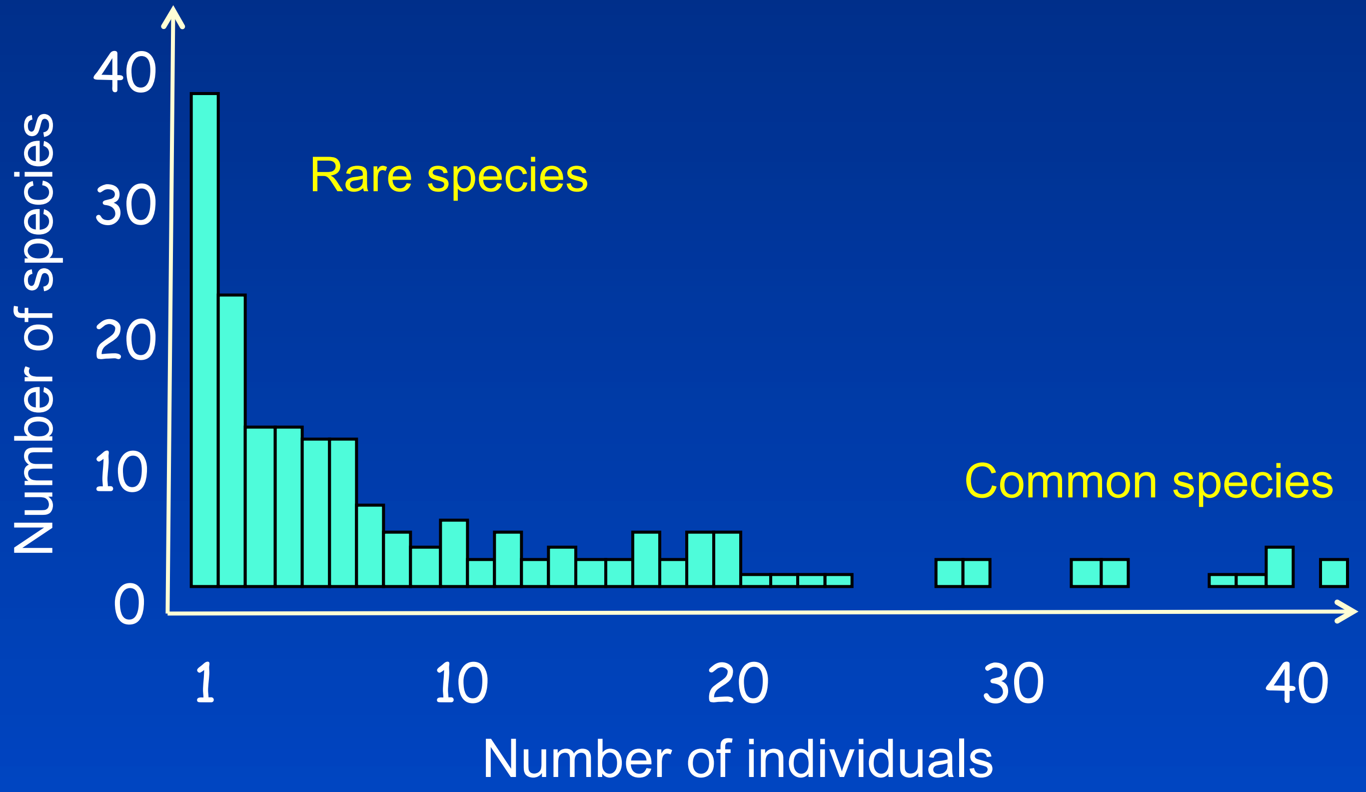
Figure 9.6 Tree diagram resulting from a single linkage cluster analysis of the data shown in Table 9.5 and analyzed in Box 9.4.

Community structure

Quantitative composition of the community i.e. the number of species having different abundance values (numbers of individuals or biomass, energy, coverage etc.)



Hollow curve distribution



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Hollow curve distribution = logarithmic series

$$\alpha \cdot x, \frac{\alpha \cdot x^2}{2}, \frac{\alpha \cdot x^3}{3}, \ldots, \boxed{\frac{\alpha \cdot x^n}{n}}$$

N. of species represented by 1 organism each

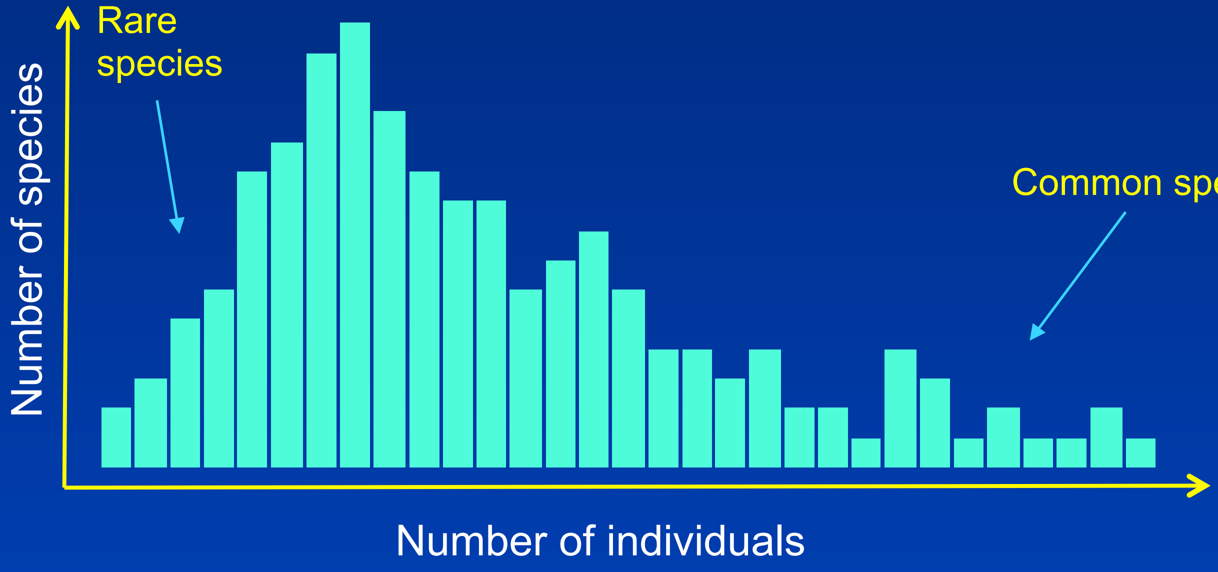
N. of species represented by 2 organisms each

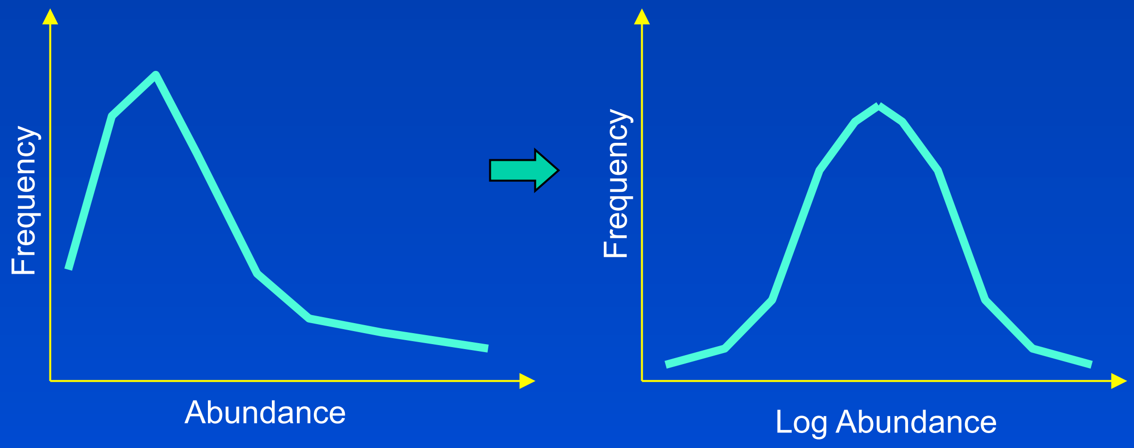
N. of species represented by 3 organism each

N. of species represented by n organisms each

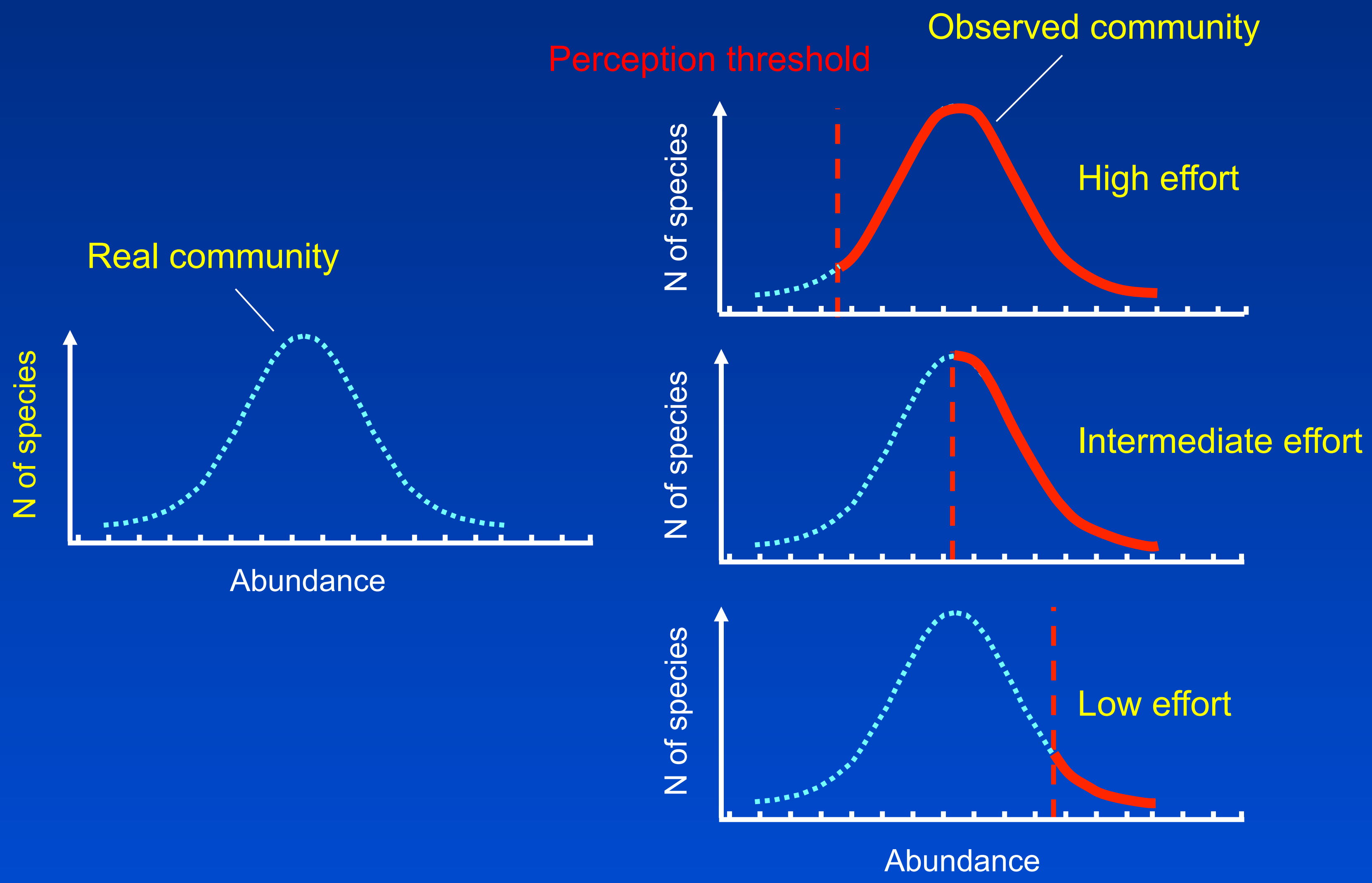
x is a positive constant ($0 \leq x \leq 1$)
α Fisher's parameter giving a specific shape to the function

Log-normal distribution





Log-normal distribution (deformation)



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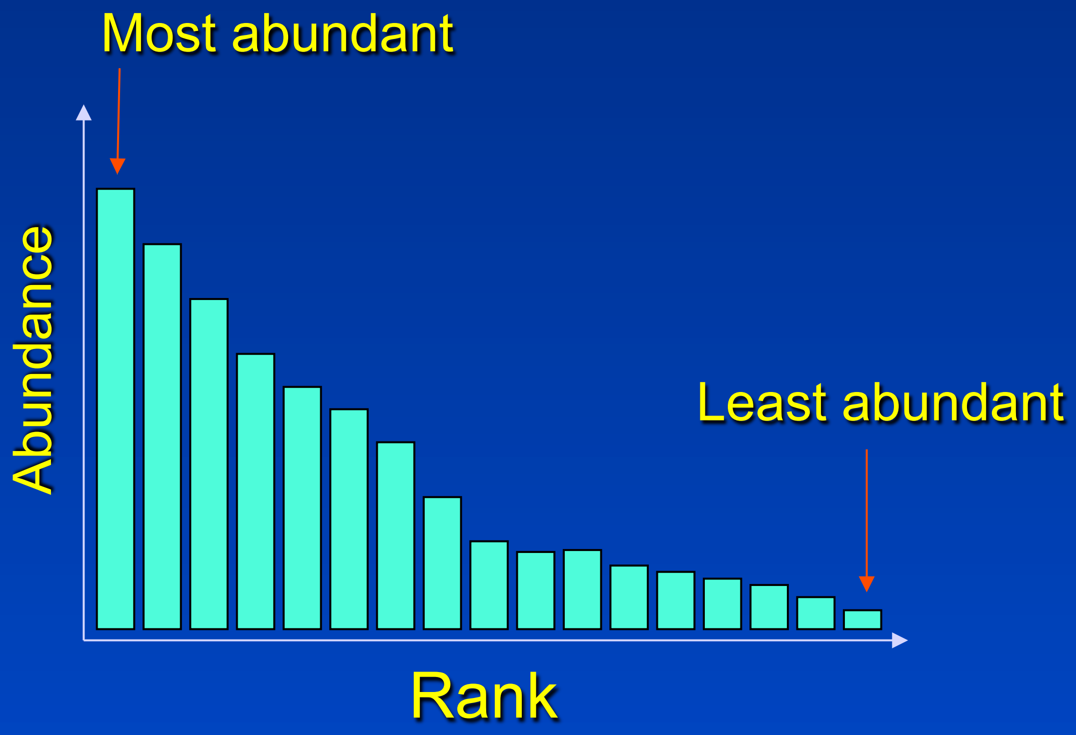
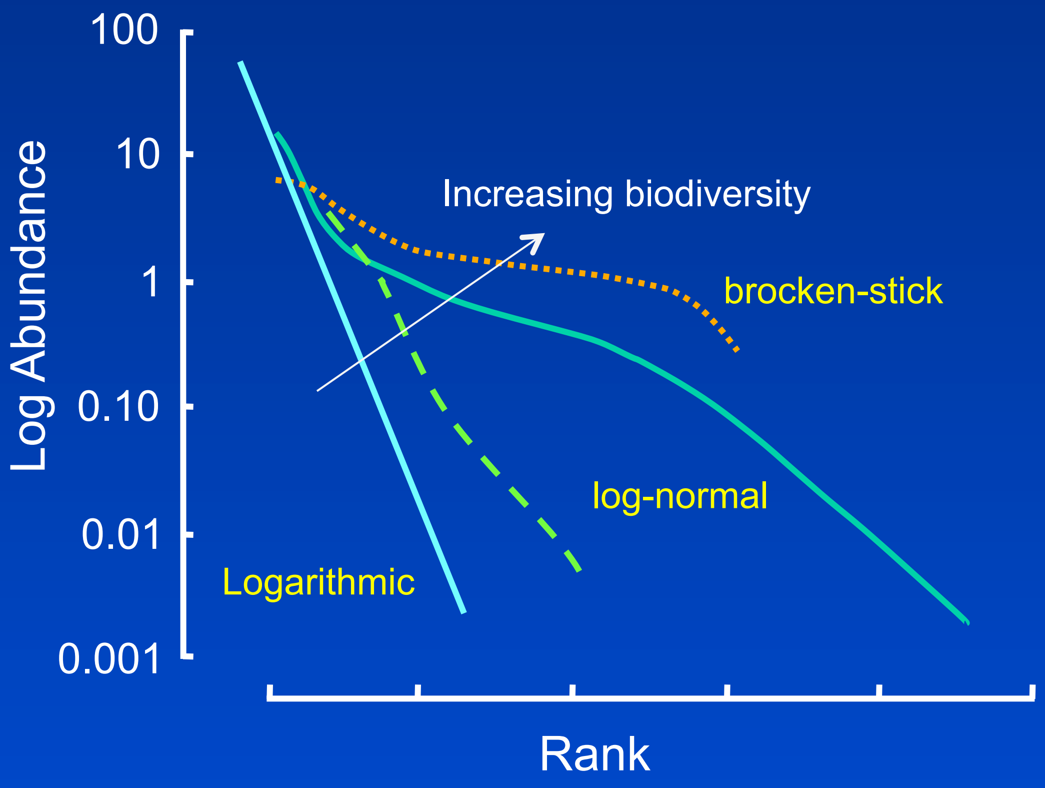
Abundance ranking



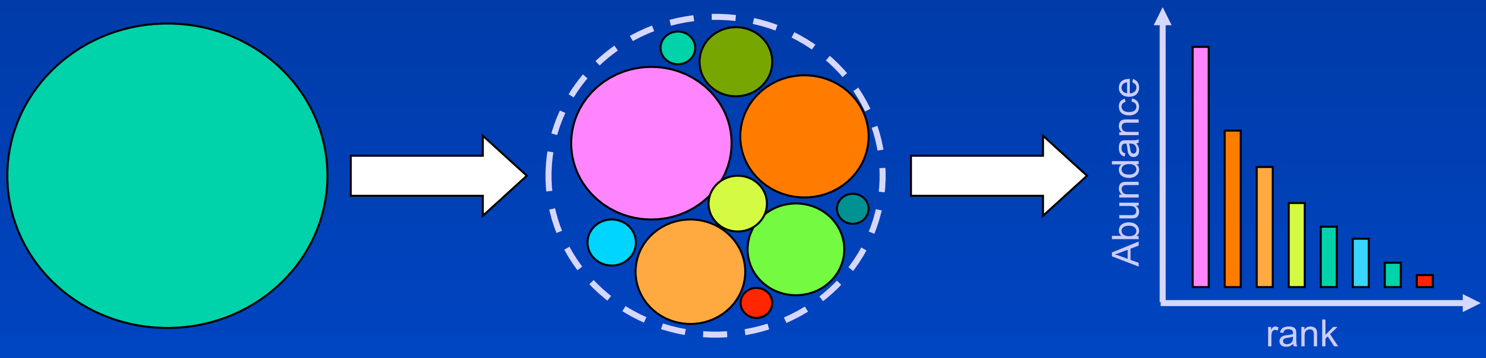
Abundance ranking



Community structure

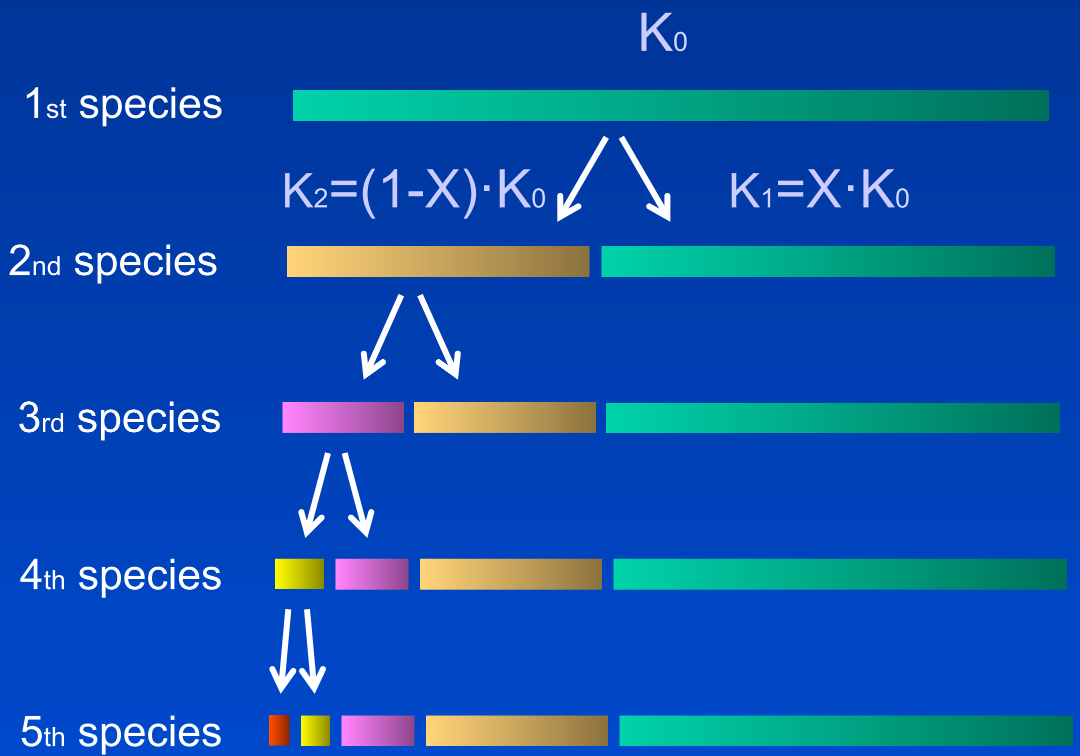
One determinant of community (guild) structure is the competition for the resources among the different species

Available pool of resources　　Resource partitioning　　Relative abundance



Logarithmic distribution

Hyerarchic resource appropriation (X : apportionment ratio)



K_0

1st species

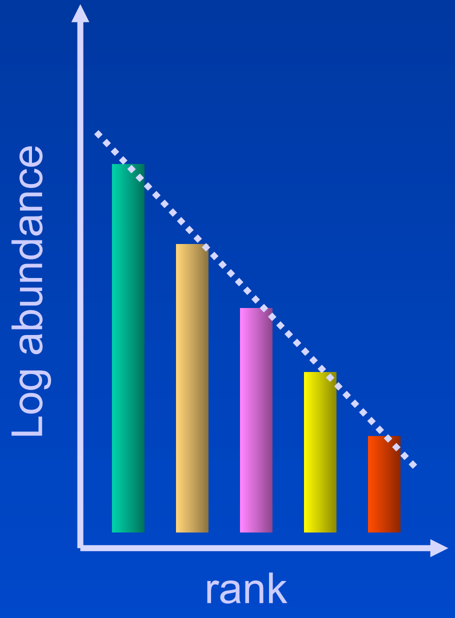
$K_2=(1-X)\cdot K_0$ $K_1=X\cdot K_0$

2nd species

3rd species

4th species

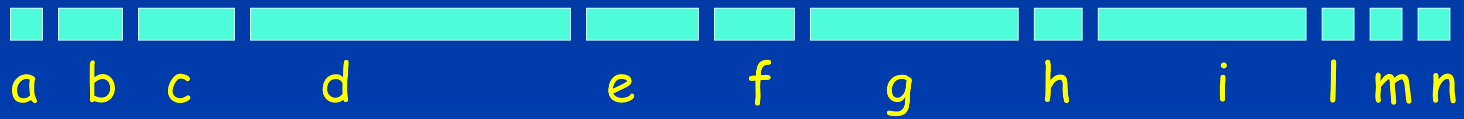
5th species



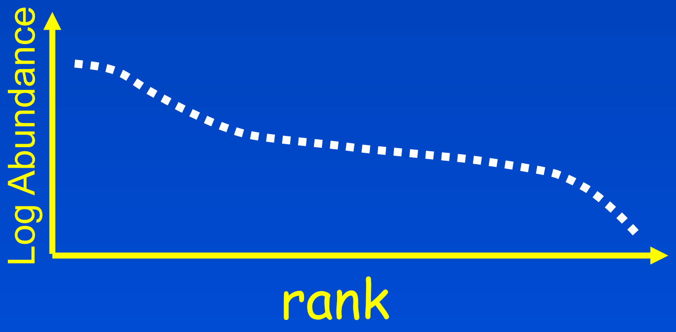
Brocken stick distribution

Available stock of resources

Random partitioning among the species



Community (guild) structure



Community dynamics

Communities are not static systems: they change in time

Variation of the community composition/structure in time is called SUCCESSION

The therm does not necessarily imply an ordered, directional change

Some successions are chaotic variations in time of the community structure

In other cases the succession follows a circular (cyclic) pattern

Succesions' drivers

Variations in the community's strucure are driven by different classed of "internal" and "external" drivers

✓ Interval drivers are those processes generated by the dynamic interactions among the species of the community (i.e. competition. mutualism, predation)
This case is defined as AUTOGENIC succession

✓ External drivers are those processes generated by the variation in time of environmental parameters such as climate or human impact.
This case is defined as ALLOGENIC succession

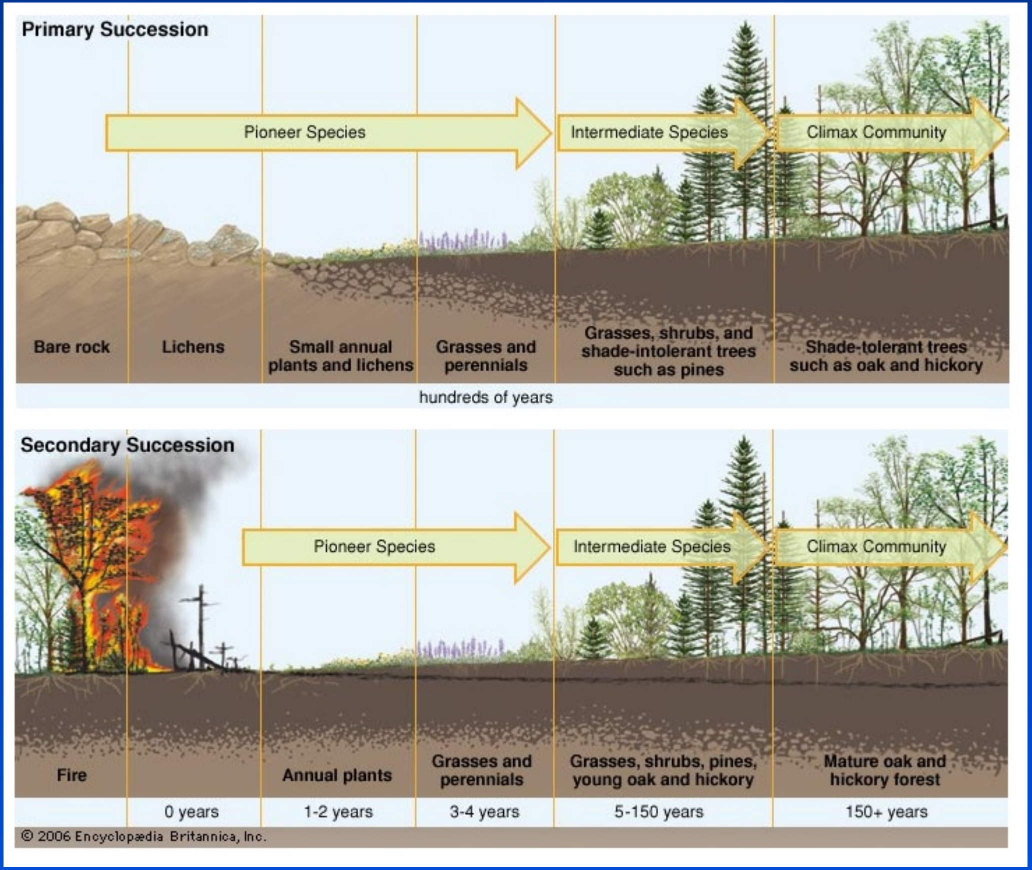
Real successions are often driven by complex blends of internal and external factors

Successions' analysis

Direct inference - Repeated sampling in a given area since a time zero (after colonization of a bare environment or a perturbation)

Opening of a new habitat or heavy disturb:
Primary succession

Low intensity disturb:
Secondary succession



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Primary succession

Glacier retreat

Bare rocks

Pioneer vegetation

Mature forest

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Secondary succession

Farmland abandonment

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Society for Ecological Restoration International

Old Fields

DYNAMICS AND RESTORATION OF ABANDONED FARMLAND

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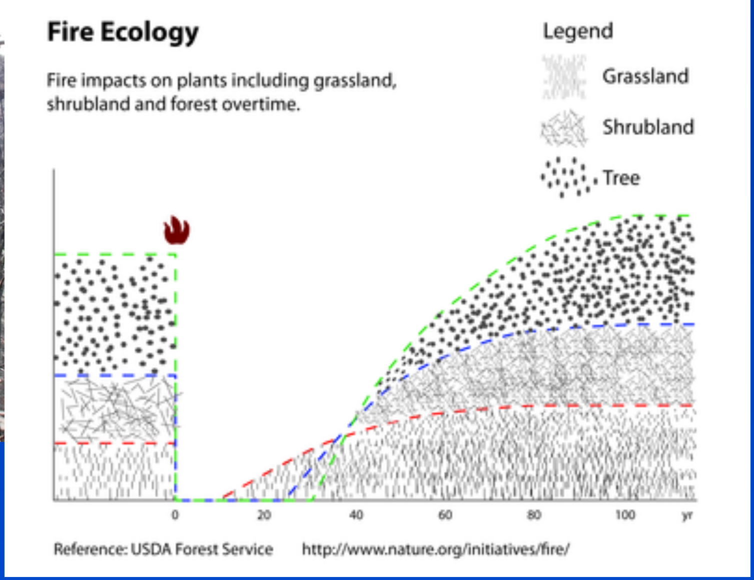
Secondary succession

Wildfires



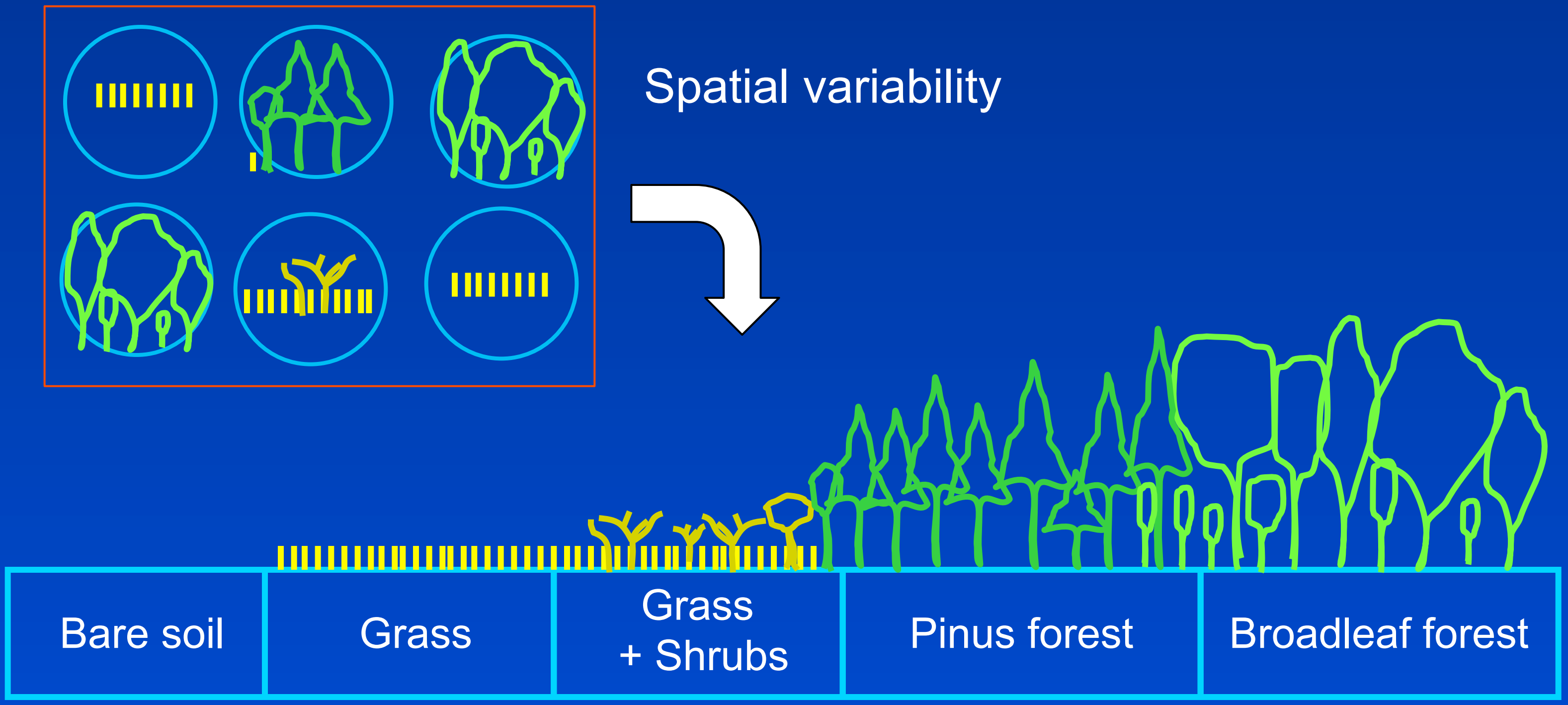
Fire Ecology

Fire impacts on plants including grassland, shrubland and forest overtime.

Reference: USDA Forest Service http://www.nature.org/initiatives/fire/

Successions’ analysis

Indirect inference – Patches of habitat with different composition (e.g. vegetation) interpreted as developmental stages of a temporal process (chronoseries)



Spatial variability

Bare soil

Grass

Grass
+ Shrubs

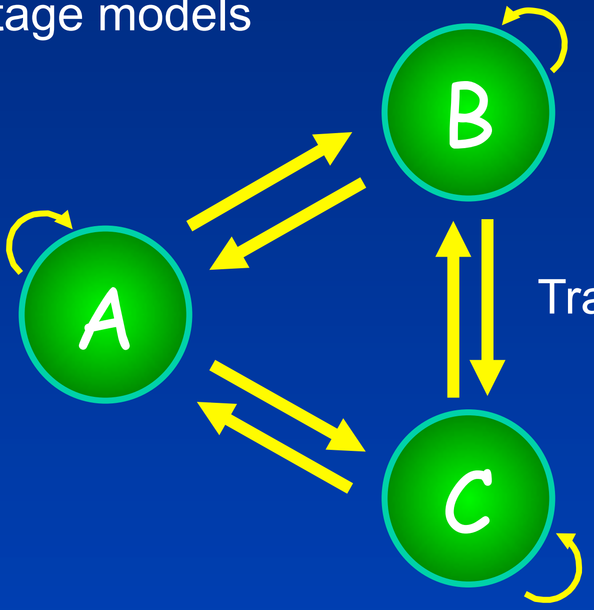
Pinus forest

Broadleaf forest

Temporal variation

Community dynamics

Predictive stage models



A = Pioneer stage
B = Intermediate stage
C = Mature stage

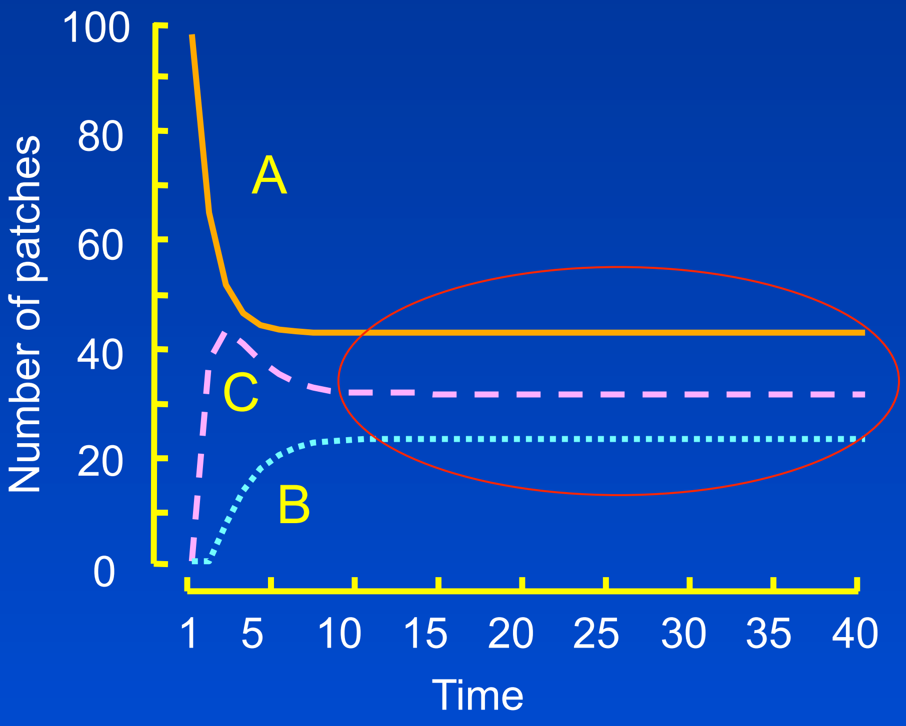
Variation probability (transition matrix)

		Present (t)		
Future (t+1)		A	B	C
	A	p_{AA}	p_{BA}	p_{CA}
	B	p_{AB}	p_{BB}	p_{CA}
	C	p_{AC}	p_{BC}	p_{CC}

Community dynamics

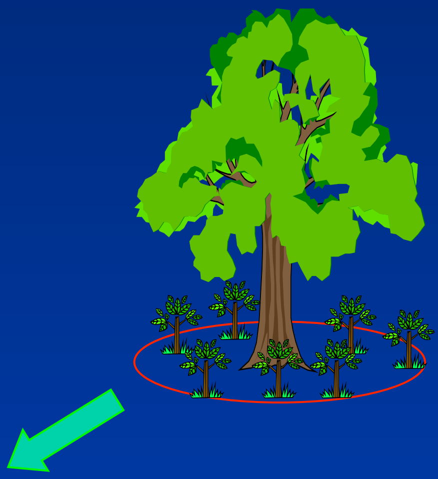
Predictive stage models

Stage (patch) models of community dynamics predict that given a set of transition coefficients, the community structure converges in time toward a defined, stable arrangement (climax)



Community dynamics

Individual substitution models
(Horn models)



Transition matrix obtained by counting the number of saplings of the different species within the "pertinence area" of adult trees of each species

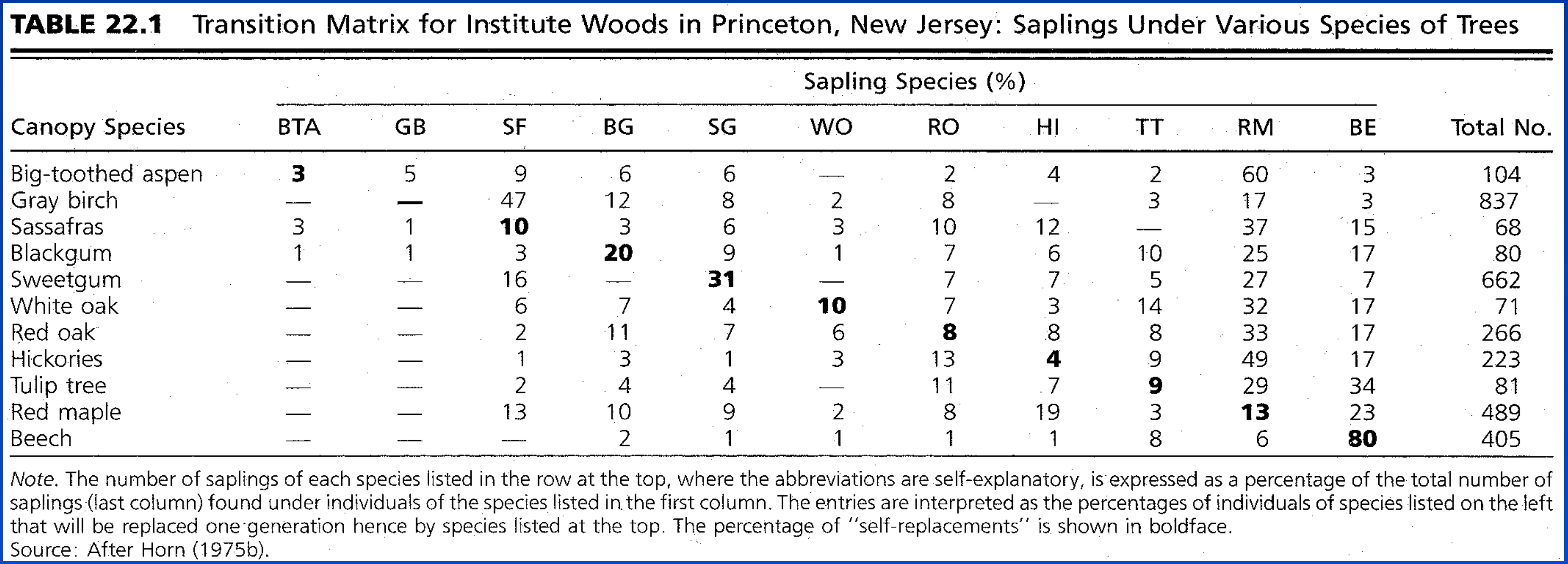


TABLE 22.1 Transition Matrix for Institute Woods in Princeton, New Jersey: Saplings Under Various Species of Trees

	Sapling Species (%)											
Canopy Species	BTA	GB	SF	BG	SG	WO	RO	HI	TT	RM	BE	Total No.
Big-toothed aspen	**3**	5	9	6	6	—	2	4	2	60	3	104
Gray birch	—	**—**	47	12	8	2	8	—	3	17	3	837
Sassafras	3	1	**10**	3	6	3	10	12	—	37	15	68
Blackgum	1	1	3	**20**	9	1	7	6	10	25	17	80
Sweetgum	—	—	16	—	**31**	—	7	7	5	27	7	662
White oak	—	—	6	7	4	**10**	7	3	14	32	17	71
Red oak	—	—	2	11	7	6	**8**	8	8	33	17	266
Hickories	—	—	1	3	1	3	13	**4**	9	49	17	223
Tulip tree	—	—	2	4	4	—	11	7	**9**	29	34	81
Red maple	—	—	13	10	9	2	8	19	3	**13**	23	489
Beech	—	—	—	2	1	1	1	1	8	6	**80**	405

Note. The number of saplings of each species listed in the row at the top, where the abbreviations are self-explanatory, is expressed as a percentage of the total number of saplings (last column) found under individuals of the species listed in the first column. The entries are interpreted as the percentages of individuals of species listed on the left that will be replaced one generation hence by species listed at the top. The percentage of "self-replacements" is shown in boldface.
Source: After Horn (1975b).

Community dynamics

Individual substitution models
(Horn models)