Cladistic approach (parsimonic analysis)

Hennig, W.

- 1950: Grundzüge einer Theorie der phylogenetischen Systematik. Deutsche Zentralverlag, Berlin.
- 1965: Phylogenetic systematics. *Annual Review of Entomology* 10: 97-116.
- 1966: Phylogenetic systematics. University of Illinois Press, Urbana.

Botaniccal cladistics:

- Koponen, T., 1968: Generic revision of Mniaceae Mitt. (Bryophyta). *Ann. Bot. Fenn.* 5: 117-151.
- Funk, V. & Stuessy, T. F. 1978: Cladistics for practicing plant taxonomist. *Syst. Bot.* 3: 159-178.
- Bremer, K. & Wantorp, H.- E. 1978: Phylogenetic systematics in botany. Taxon 27: 317-329.

A Y-Z, X-Y-Z monophyletic groups

B X-Y paraphyletic group

C X-Y polyphyletic group, parallelism

D X-Y polyphyletic group, convergence

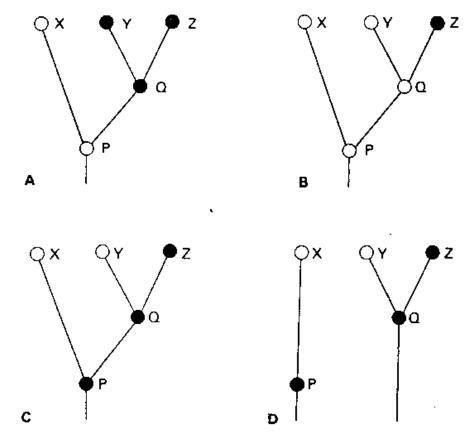
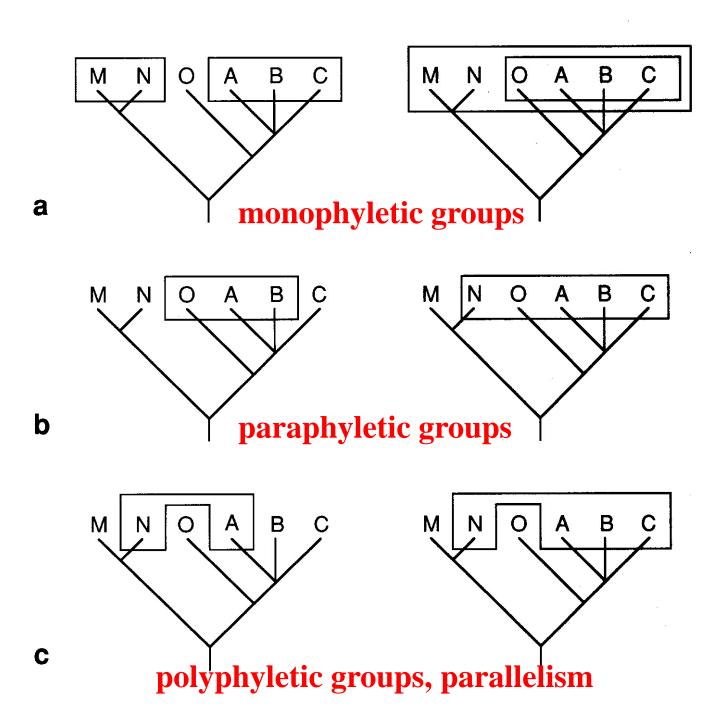


Fig. 2.6 Four diagrams showing different origins of three species (X, Y, Z) from the ancestral taxa P and Q in order to illustrate the concepts of monophyly, paraphyly, polyphyly, parallelism and convergence. The possession of one or other of two contrasting character-states by each of the five taxa is indicated by an open or closed circle respectively. A. Groups YZ and XYZ are both monophyletic; the similarity between Y and Z is a synapomorphy; the difference between X and YZ is due to divergence. B. Group XY is paraphyletic; group XYZ is monophyletic; the similarity between X and Y is a symplesiomorphy; the difference between Y and Z is due to divergence. C. Group XY is polyphyletic; group XYZ is monophyletic; the similarity between X and Y is a false synapomorphy caused by parallelism. D. Groups XY and XYZ are both polyphyletic; group YZ is monophyletic; the similarity between X and Y is a false synapomorphy caused by convergence.



Ancestral (primitive) state of character

Plesiomorphy Symplesiomorphy

Descendant (advanced) state of character

Apomorphy Autapomorphy Synapomorphy

Homoplasy = convergency + parallelism

A taxon is a group of organisms that is given a name

Category, rank

(You should not confuse the rank of a taxon with its reality as a group)

A grade is an artificial taxon. Grade taxa are frequently paraphyletic and sometimes polyphyletic but are supposed to represent some level of evolutionary progress, level of organization, or level of adaptation (e.g., Reptilia or Vermes).

Relationship – genealogical relationship, purely phenetic relation is explicitly excluded

Ingroup – studied group

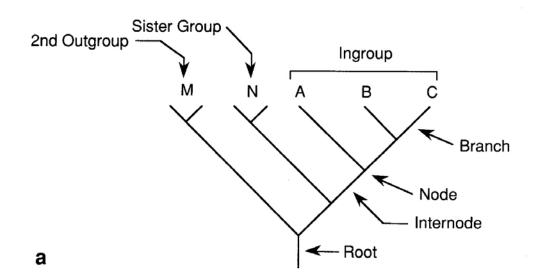
Sister group

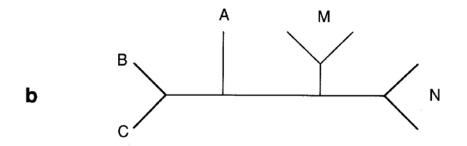
Outgroup

Character polarization

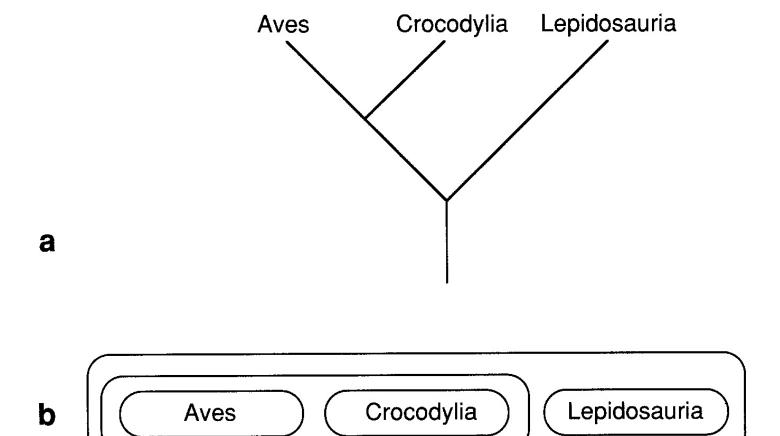
Outgroup comparison

Node – speciation event, origin of species





Tree is rooted or unrooted



Venn diagram

Either

Character - character states

Or

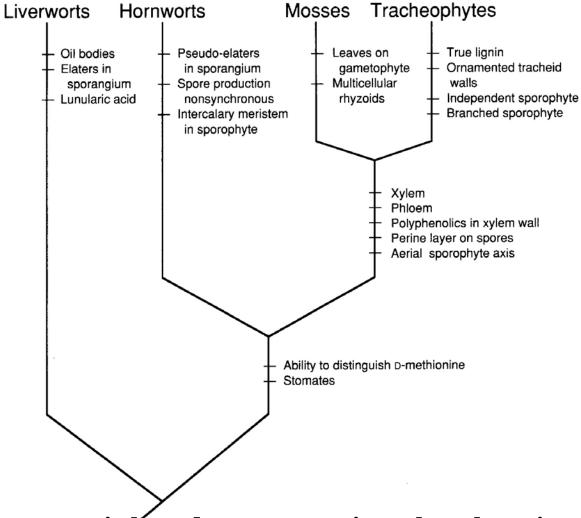
Transformation series - characters

Plesiomorphic – apomorphic character states (convention: 0 ancestral/primitive state, 1 descendant/advanced state)

Characters/character states – ordered / unordered

Character polarization – based on *a priori* arguments

Character optimization - consists of *a posteriori* arguments as to how particular characters should be polarized given a particular tree topology

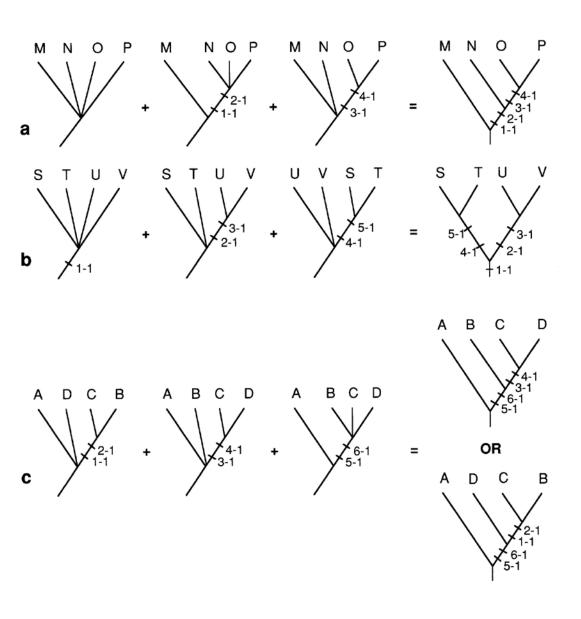


Phylogenetic system is based on expectation, that there is only one unique genealogical history of all organisms.

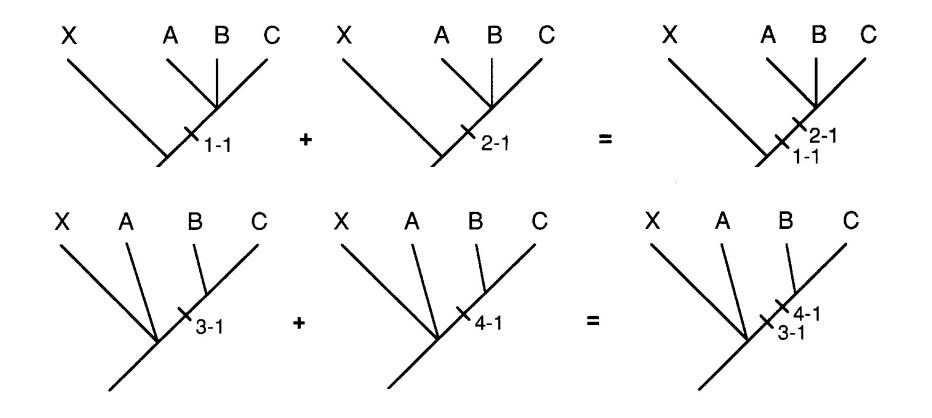
Because characters are properties of organisms, they must be placed on the tree, that represents this history. Hennig's auxiliary principle - Never assume convergence or parallel evolution, always assume homology in the absence of contrary evidence.

Grouping rule - Synapomorphies are evidence for common ancestry relationships, whereas symplesiomorphies, convergences, and parallelisms are useless in providing evidence of common ancestry.

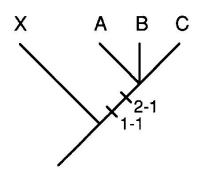
Inclusion/exclusion rule - The information from two transformation series can be combined into a single hypothesis of relationship if that information allows for the complete inclusion or the complete exclusion of groups that were formed by the separate transformation series. Overlap of groupings leads to the generation of two or more hypotheses of relationship because the information cannot be directly combined into a single hypothesis.

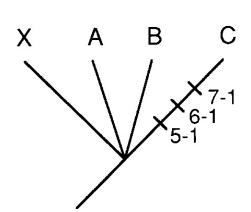


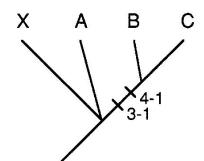
Taxon	Transformation series							
	1	2	3	4	5	6	7	
X (outgroup)	0	0	0	0	0	0	0	
A	1	1	0	0	0	0	0	
В	1	1	1	1	0	O	0	
C	1	1	1	1	1	1	1	

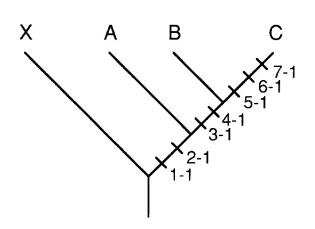


	Transformation series							
Taxon	1	2	3	4	5	6	7	
X (outgroup)	0	0	0	0	0	0	0	
A	1	1	0	0	0	0	0	
В	1	1	1	1	0	0	0	
C	1	1	1	1	1	1	1	

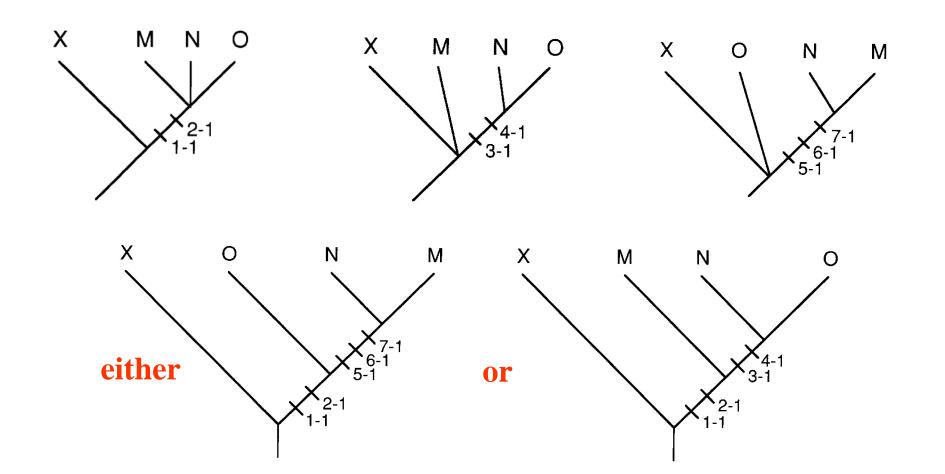


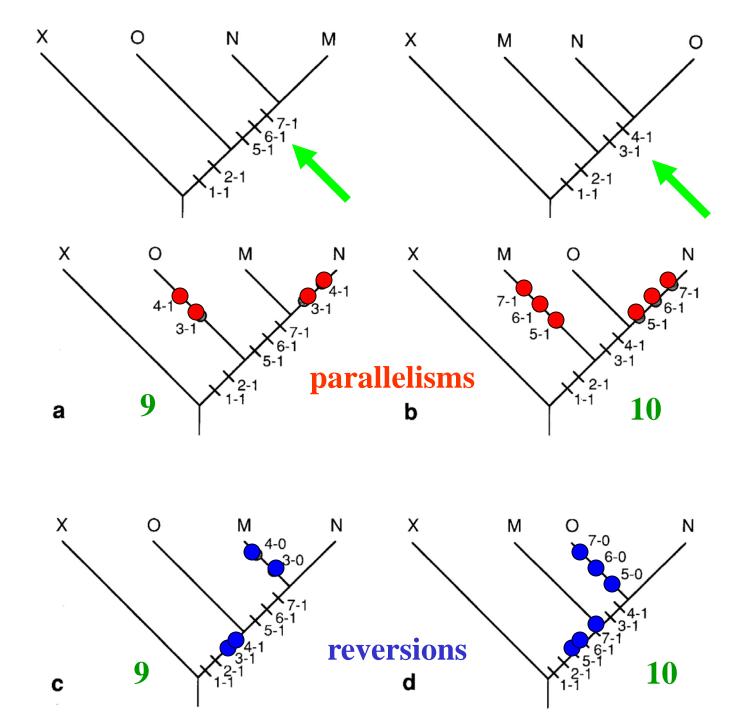




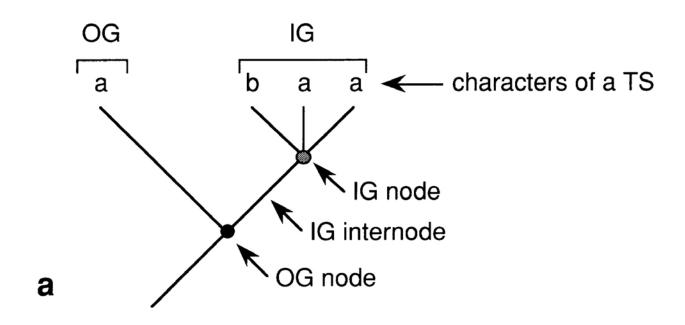


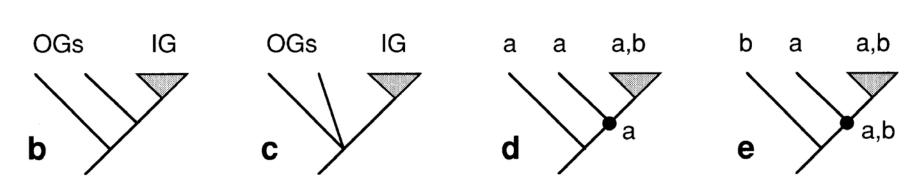
	Transformation series							
Taxon	1	2	3	4	5	6	7	
X (outgroup)	0	0	0	0	0	0	0	
M	1	1	0	0	1	1	1	
N	1	1	1	1	1	1	1	
O	1	1	1	1	0	0	0	





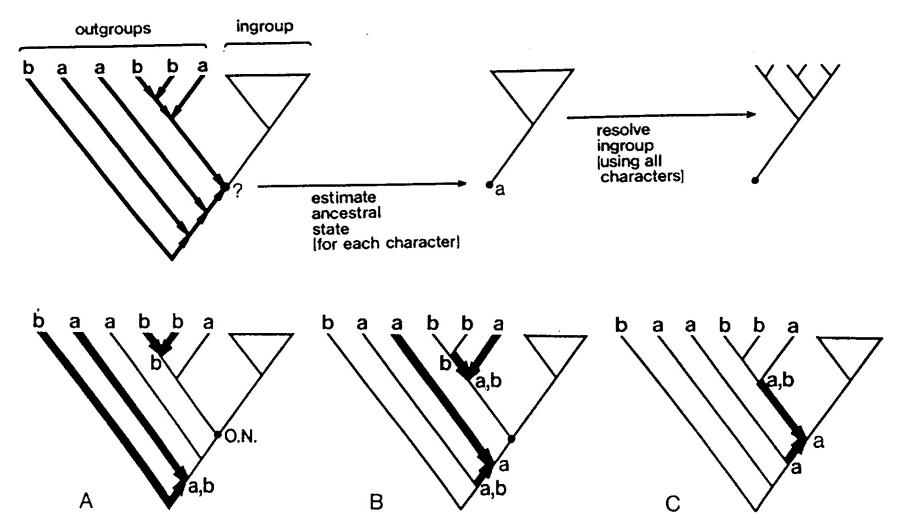
Outgroup comparison

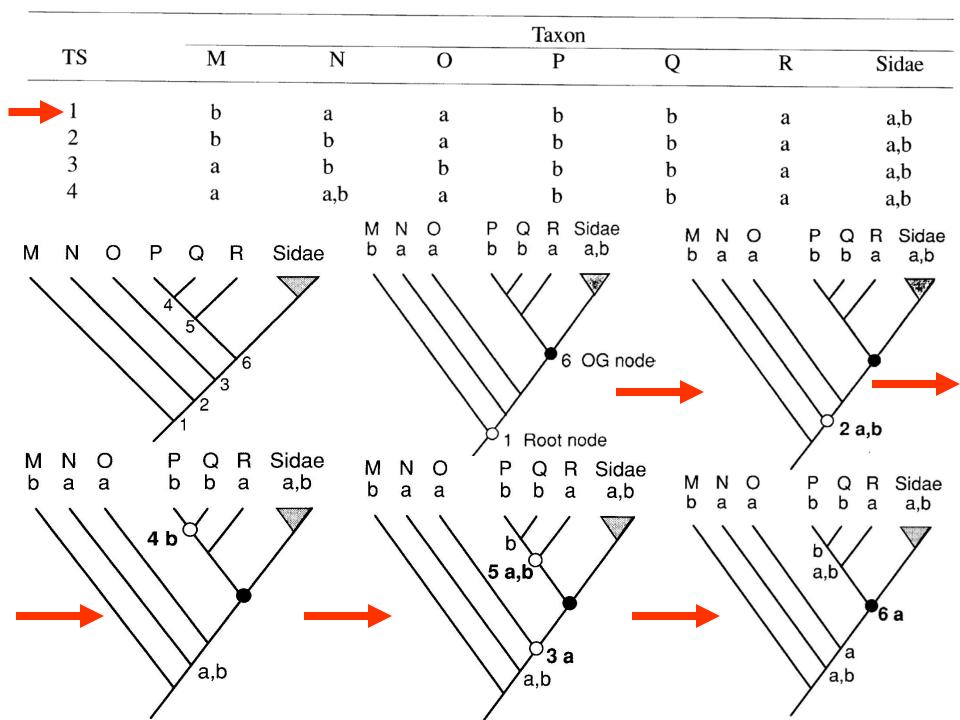




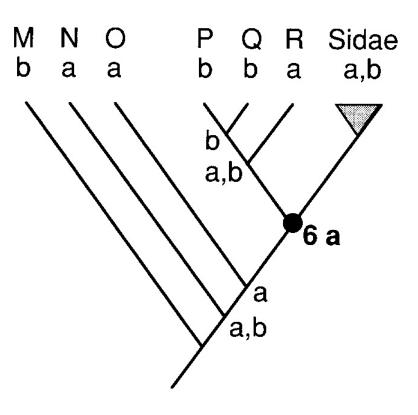
Outgroup comparison - higher amount of outgroups

a - decisive character polarityab - equivocal character polarity



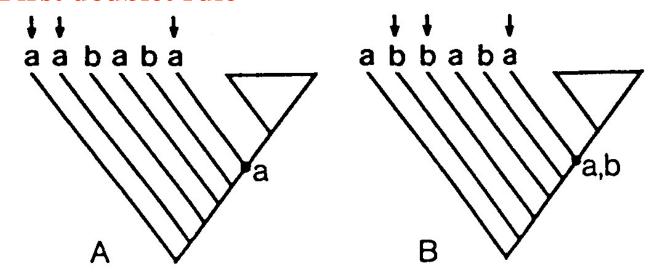


	Taxon								
TS	M	N	O	P	Q	R	Sidae		
1	b	a	a	b	b	a	a.b		
2	b	b	a	b	b	a	a,b		
3	a	b	b	b	b	a	a,b		
4	a	a,b	a	b	b	a	a,b		

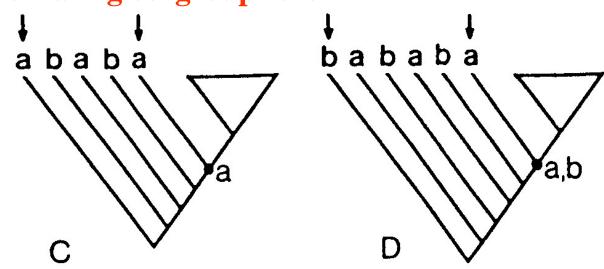


Taxa Characters

First doublet rule

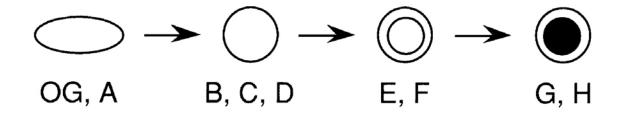


Alternating outgroup rule



Character/character states coding

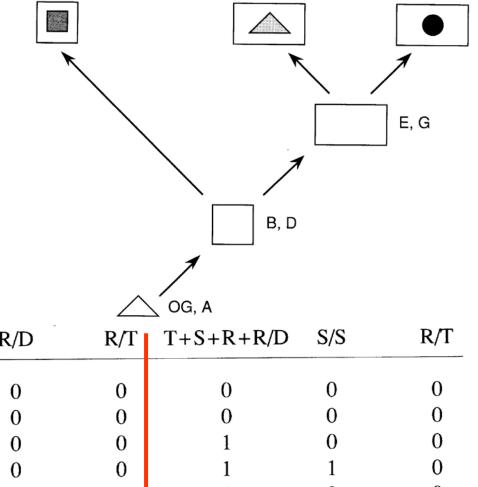
linear transformation series/characters



Taxon		1	Additive binary codir	ng*
	Linear coding	C + C/C + C/D	C/C + C/D	C/D
OG	0	0	0	0
A	0	0	0	0
В	1	1	0	0
C	1	1	0	0
D	1	1	0	0
E	2	1	1	0
F	2	1	1	0
G	3	1	1	1
Н	3	1	1	1

Character/character states coding

branchedtransformationseries/characters



Taxon	All except T	S/S	R+	R/D	R/T	T+S+R+R/D	S/S	R/T
OG	0	0	0	0	0	0	0	0
A	0	0	0	0	0	0	0	0
В	1	0	0	0	0	1	0	0
C	1	1	0	0	0	1	1	0
D	1	0	0	0	0	1	0	0
E	1	0	1	0	0	2	0	0
F	1	0	1	0	1	2	0	1
G	1	0	1	0	0	2	0	0
Н	1	0	1	1	0	3	0	0

neaditívne binárne

zmiešané

Н