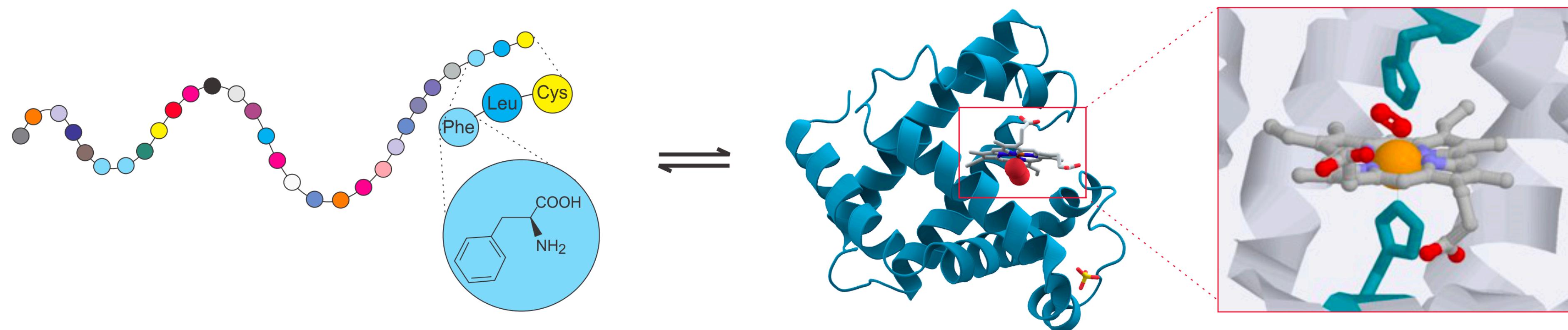
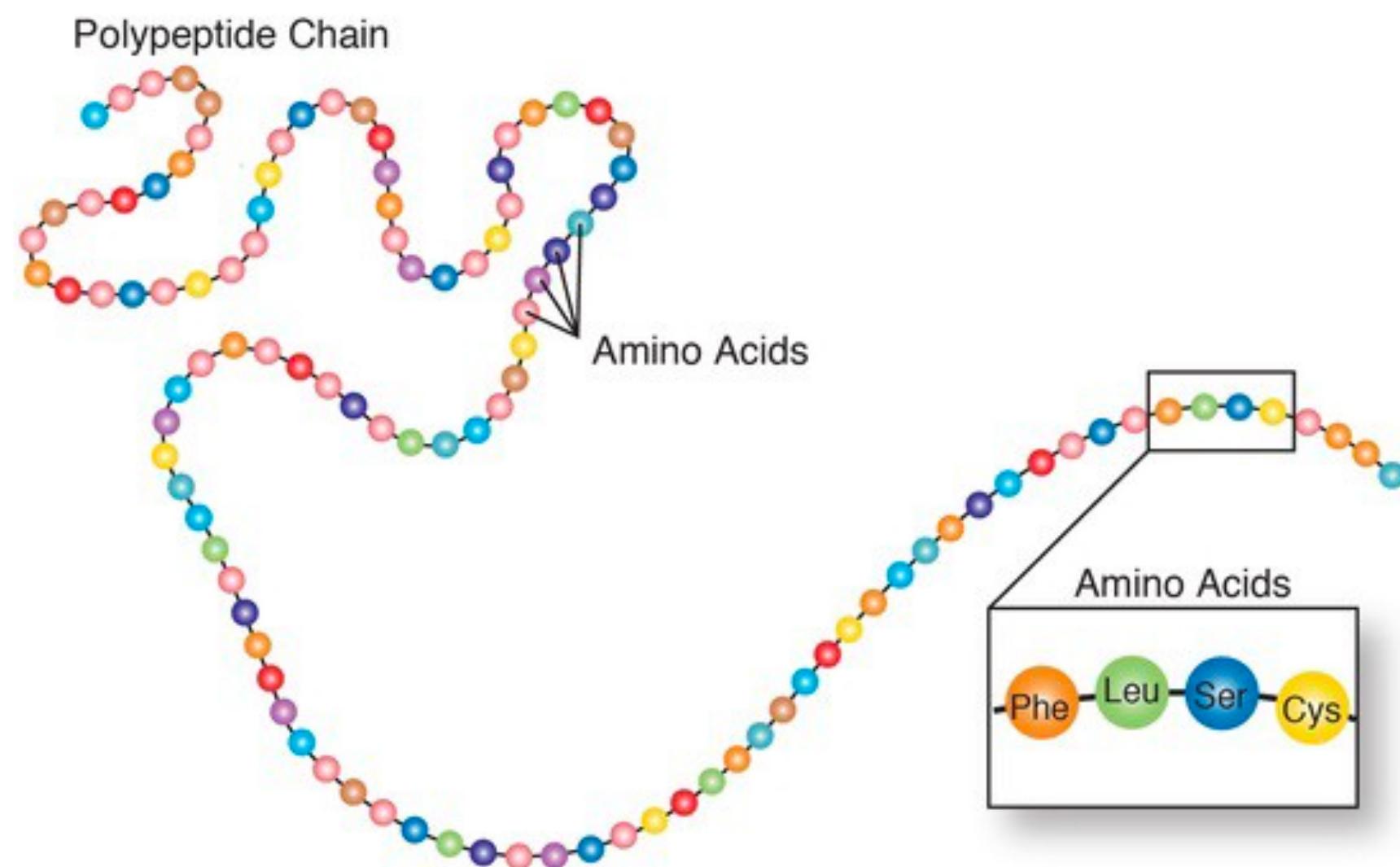
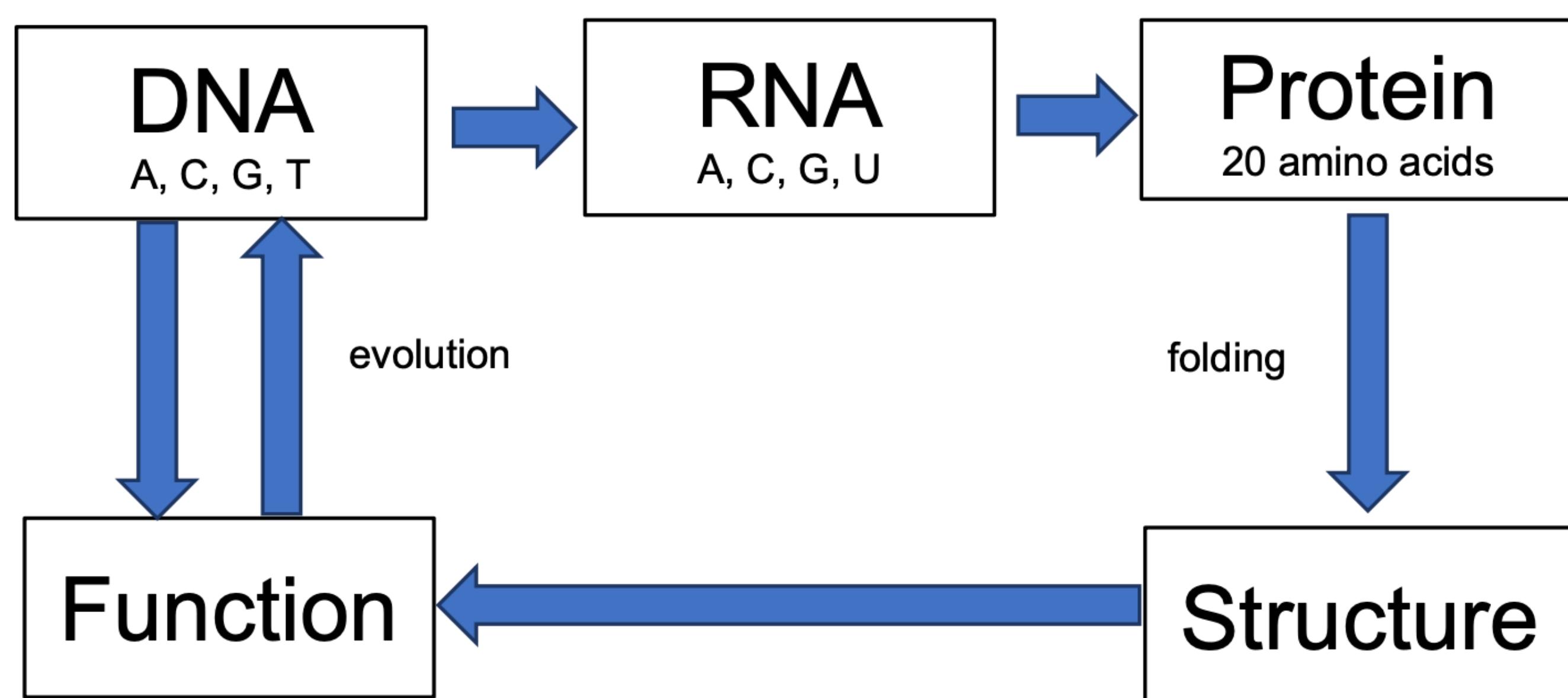


What is phylogenetics tree

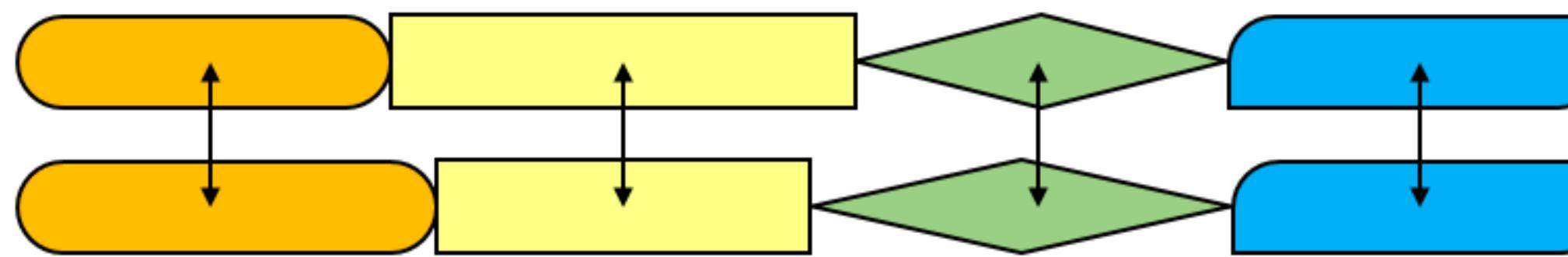
Chapter 1 - A introduction to bioinformatics

Xinchun Ran

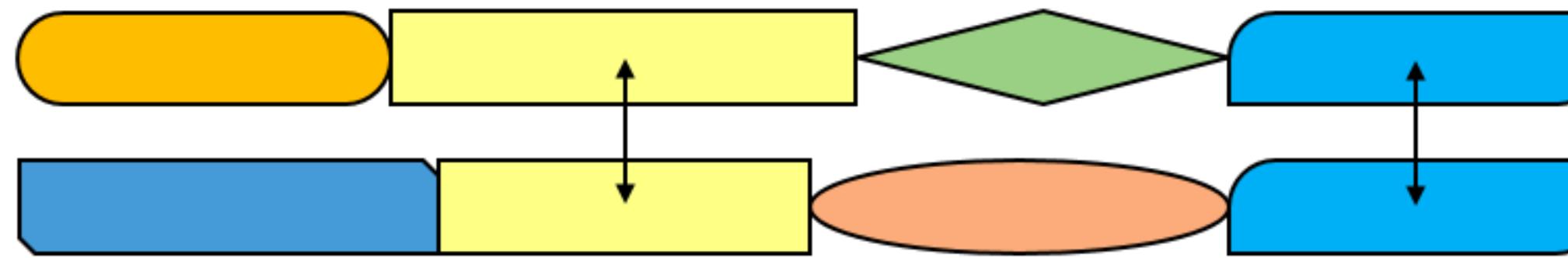
Basics protein sequences



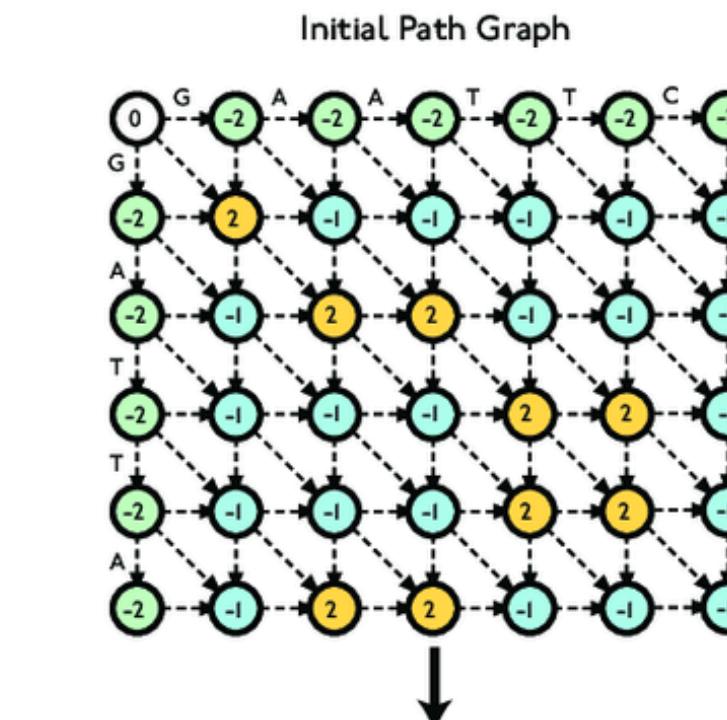
Basics protein sequences - similarity



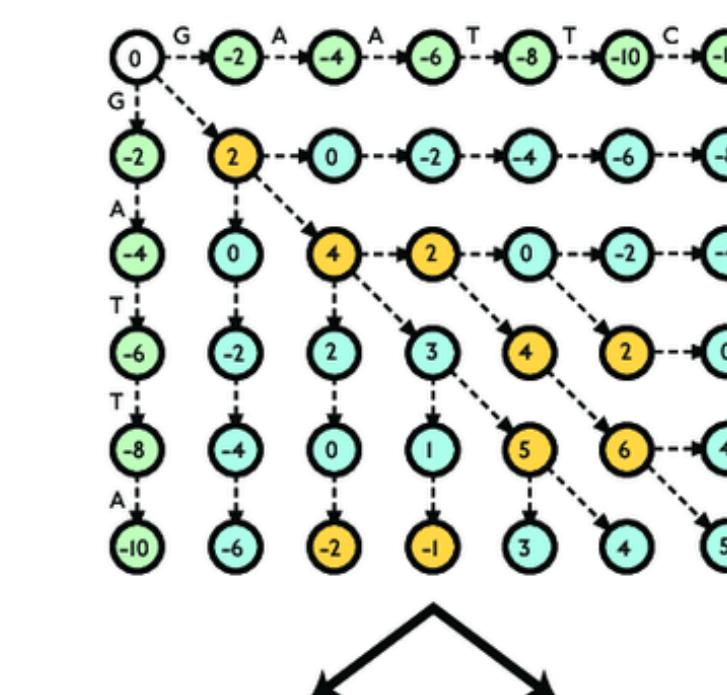
Global Alignment



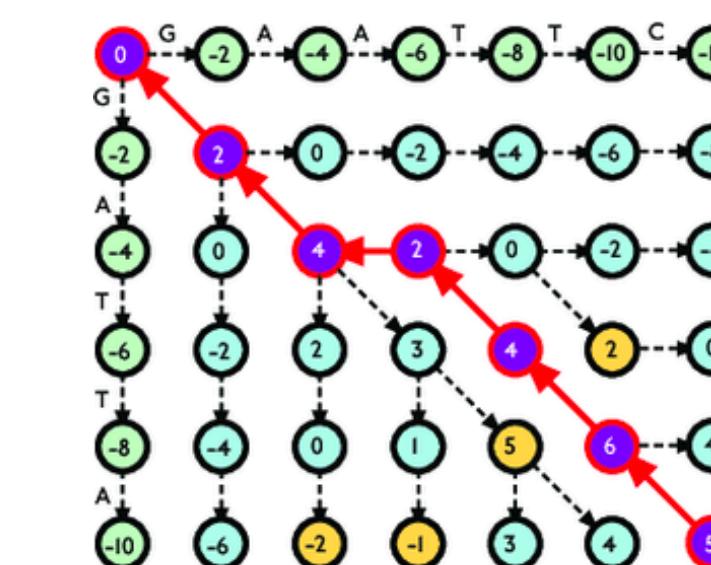
Local Alignment



After Dynamic Programming Pass



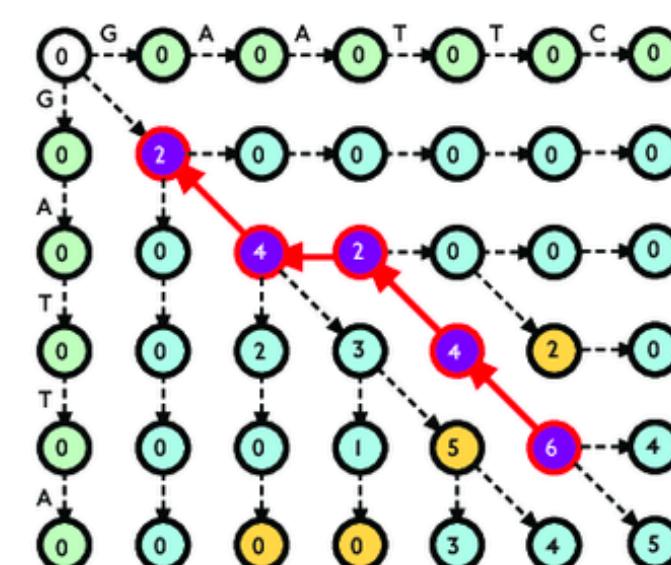
Needleman-Wunsch Optimal Global Path



Global Alignment (Score=5)

GAATTC
GA-TTA

Smith-Waterman Optimal Local Path



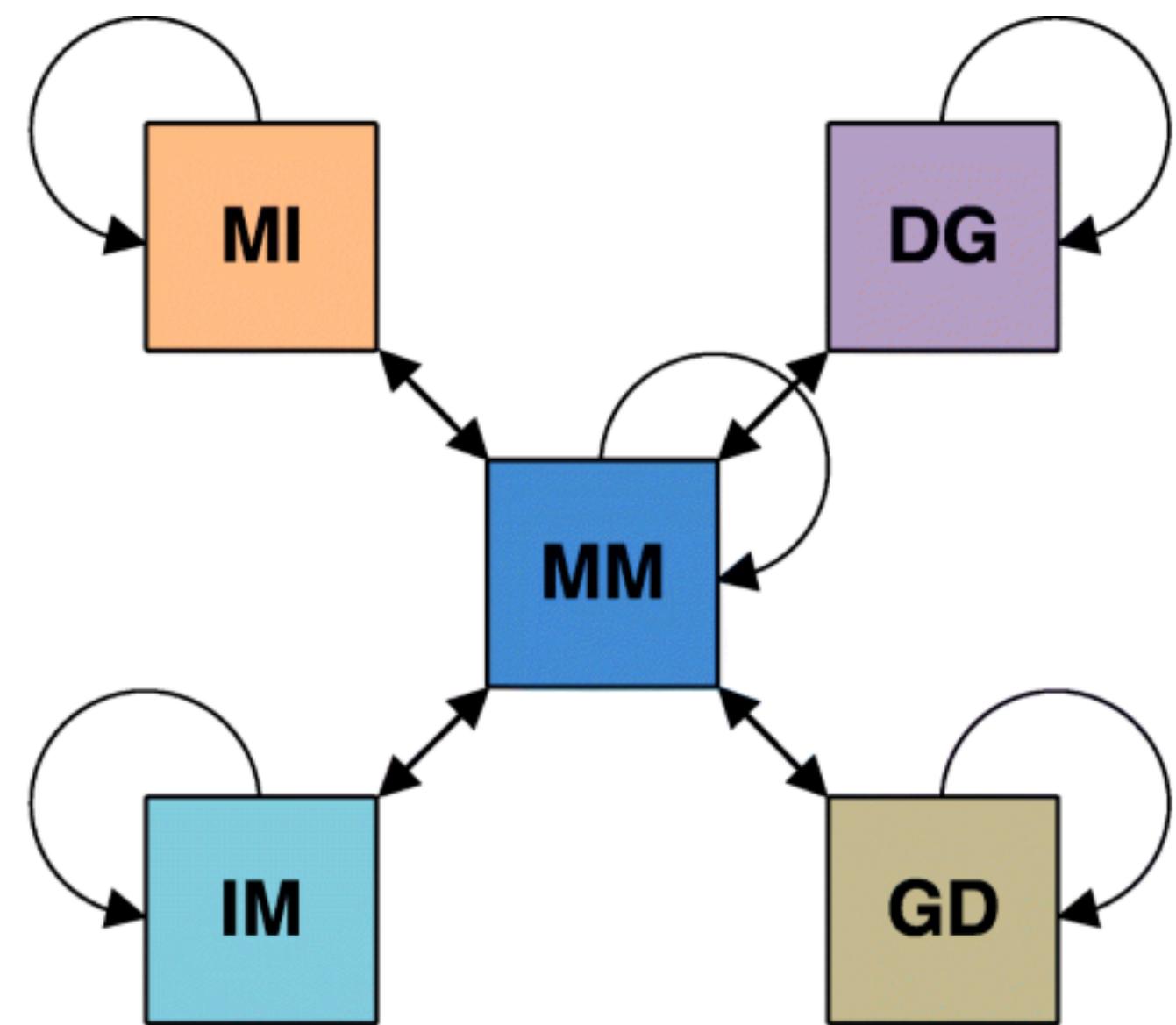
Local Alignment (Score=6)

GAATTC
GA-TT

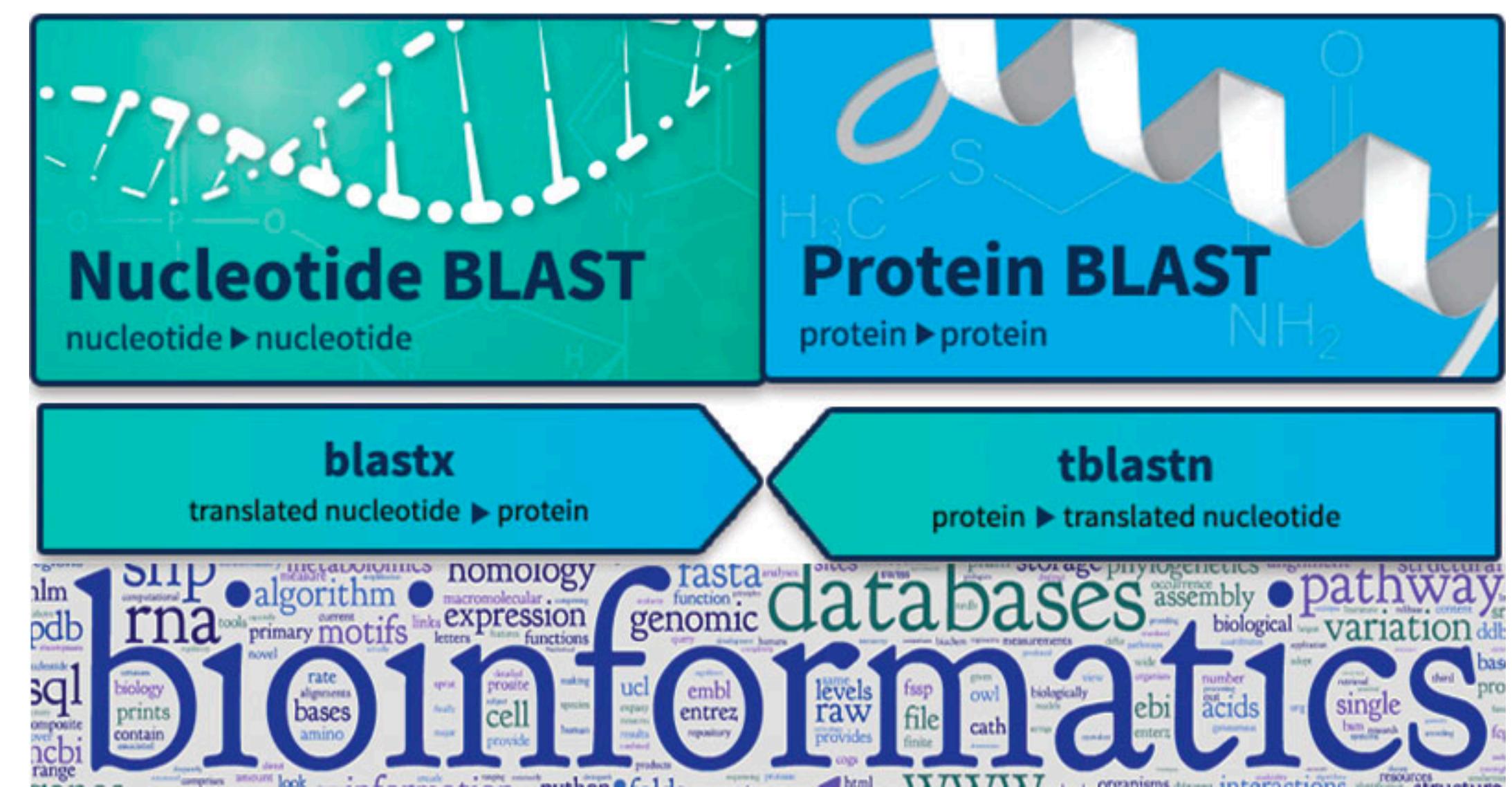


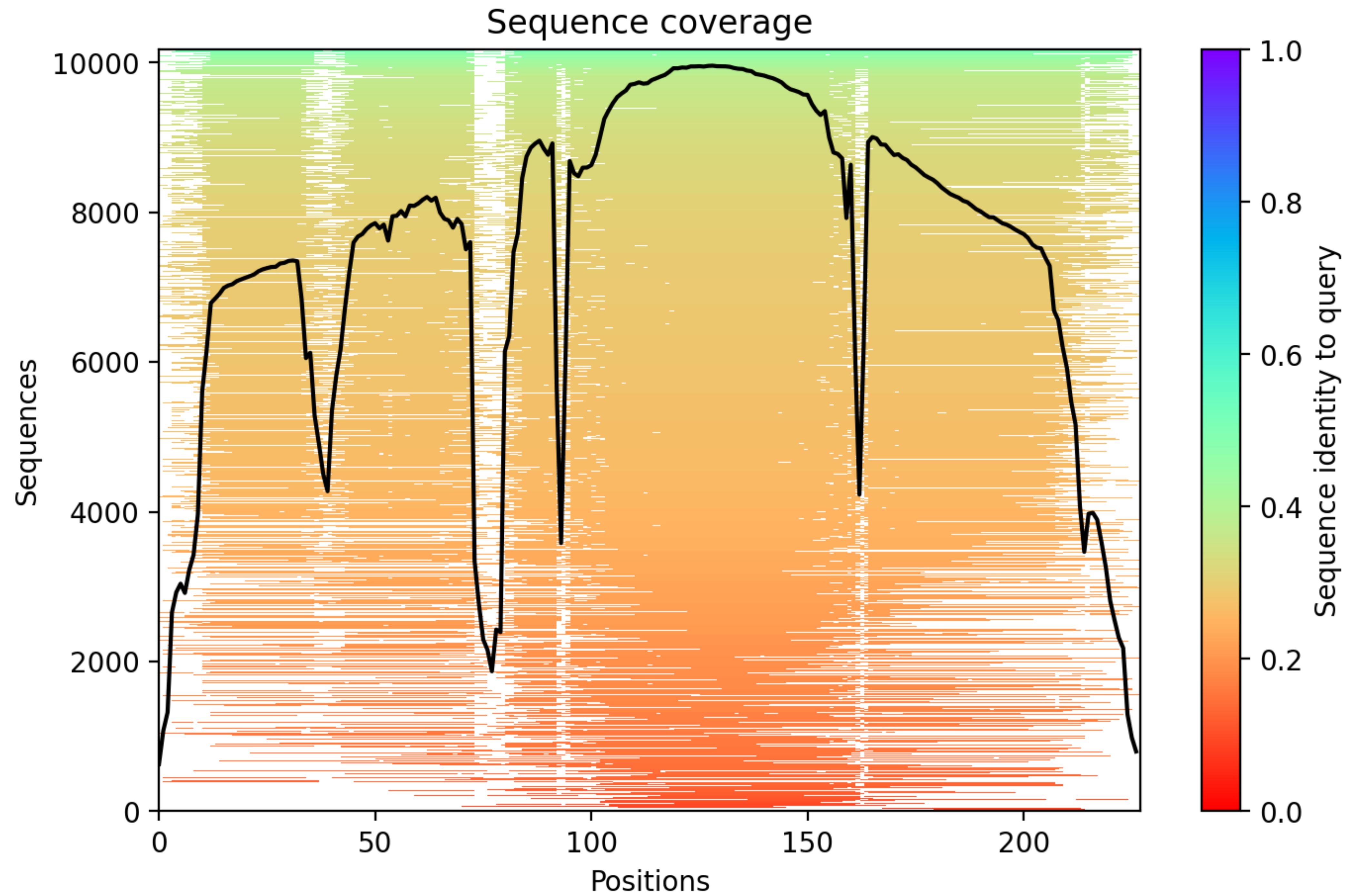
HMMER

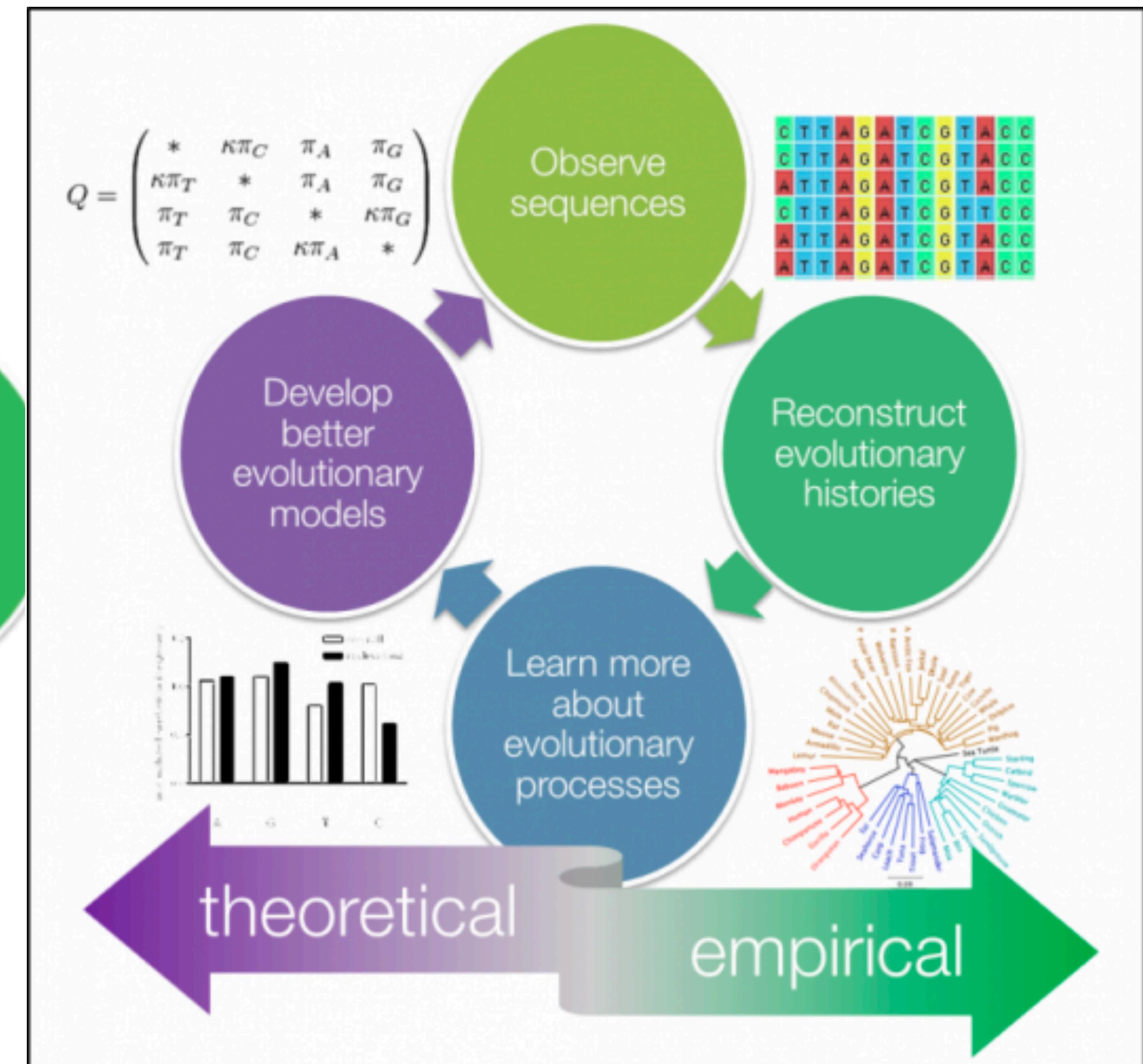
Biosequence analysis

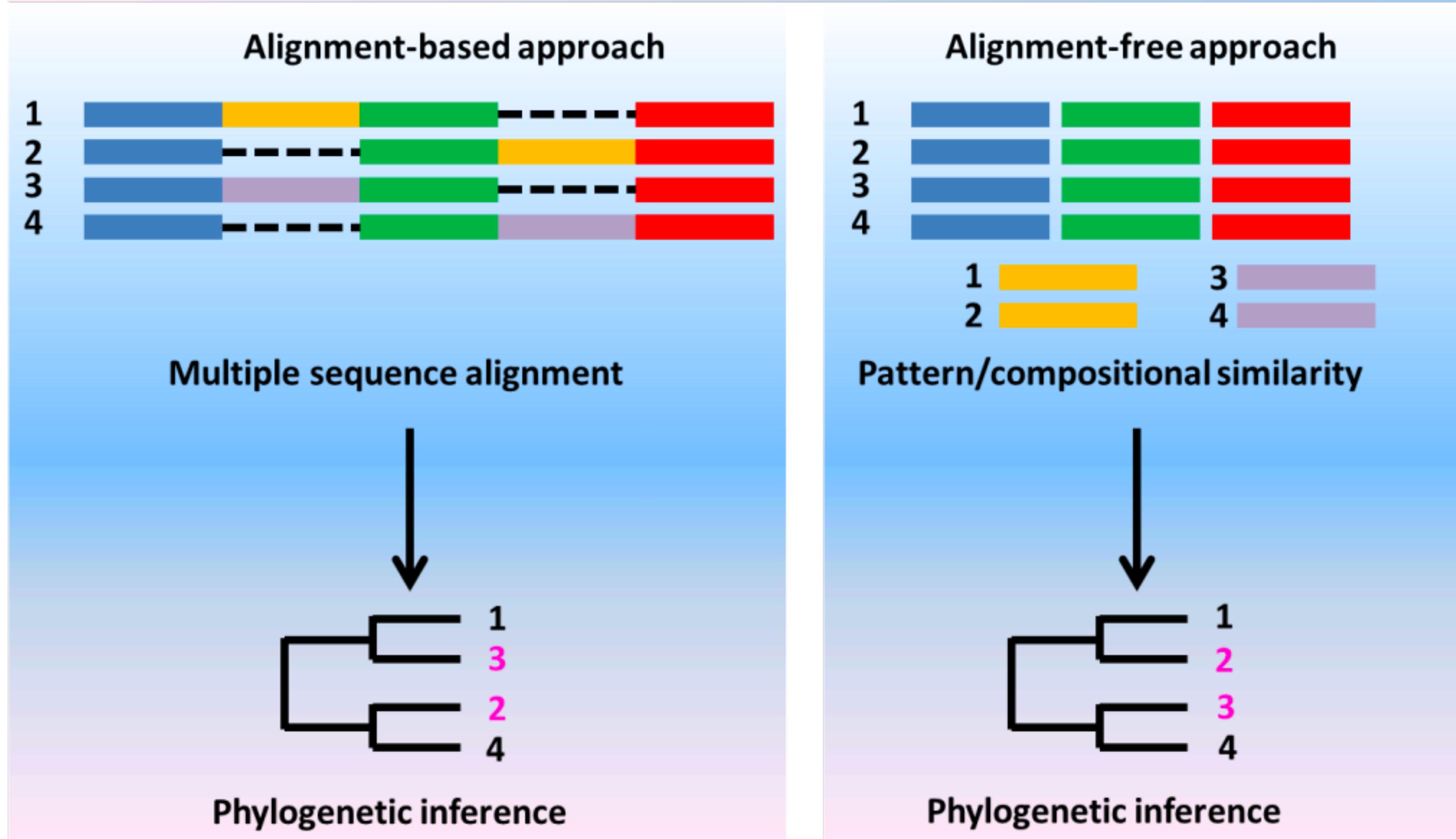


cell-off	MI	DG	IM	GD	MM	MM	MM
7	6	5	4	3	2	1	0

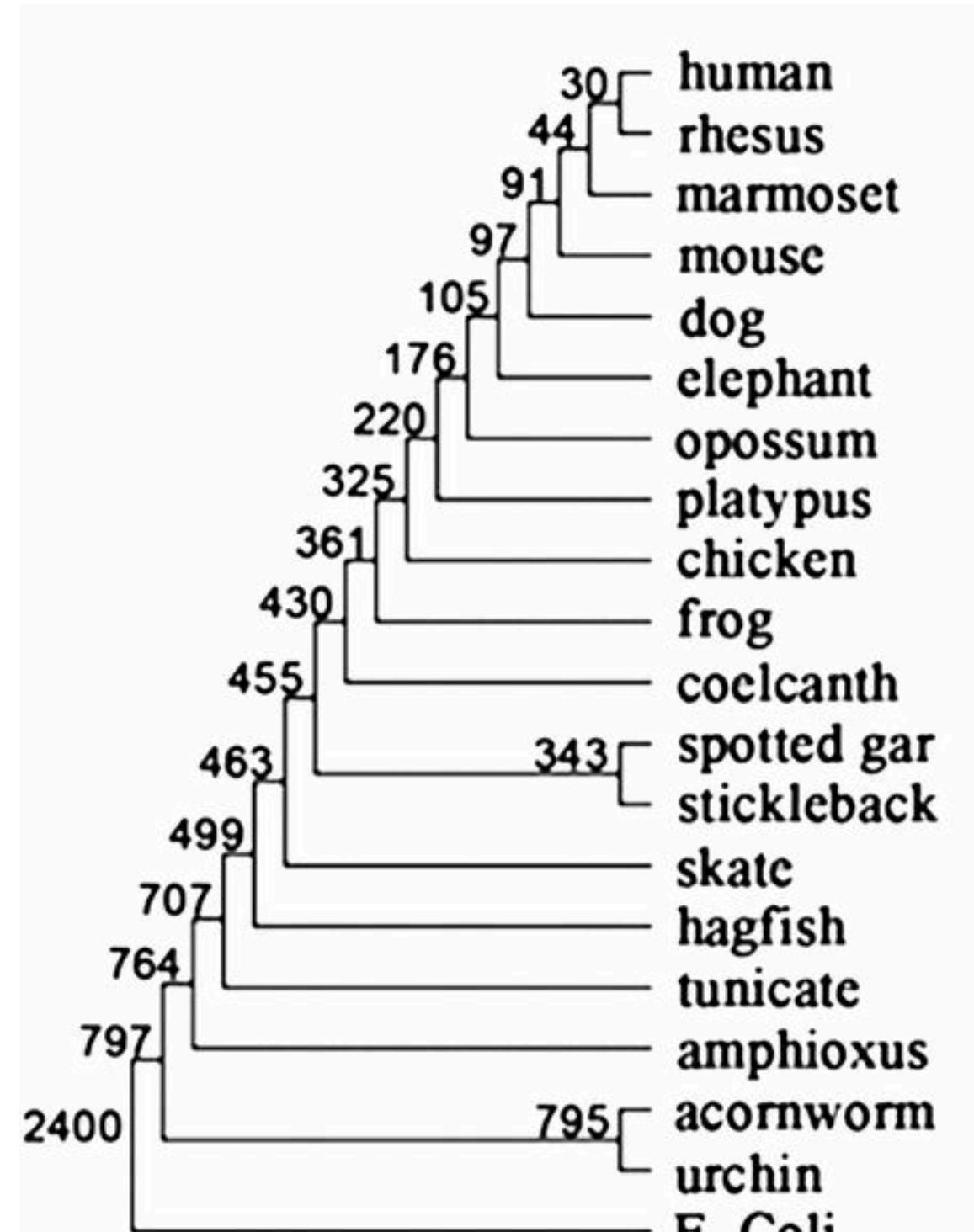






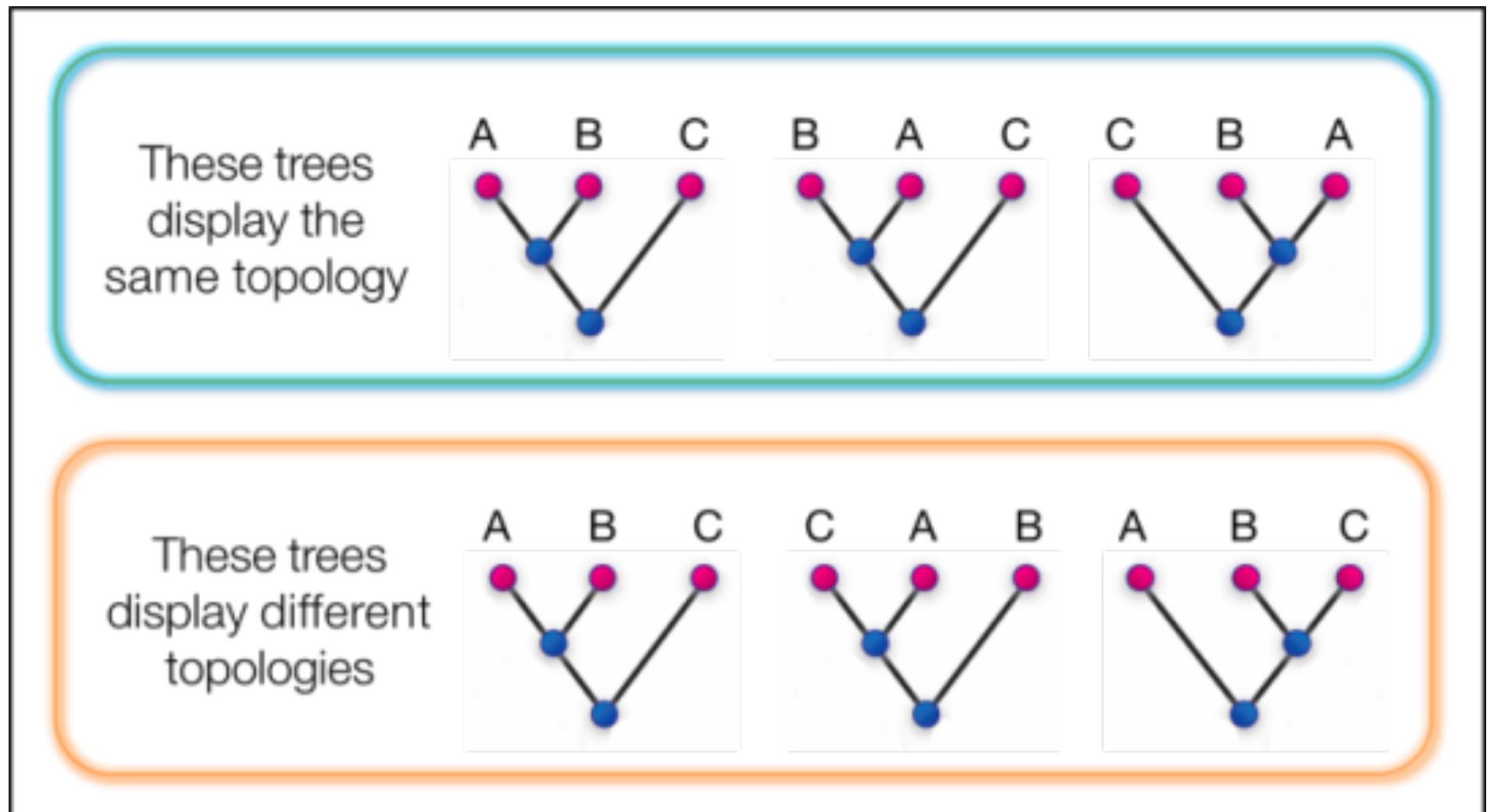


- Topology
- Branches
- Nodes
 - Tips
 - Internal nodes
 - Root
- Confidence

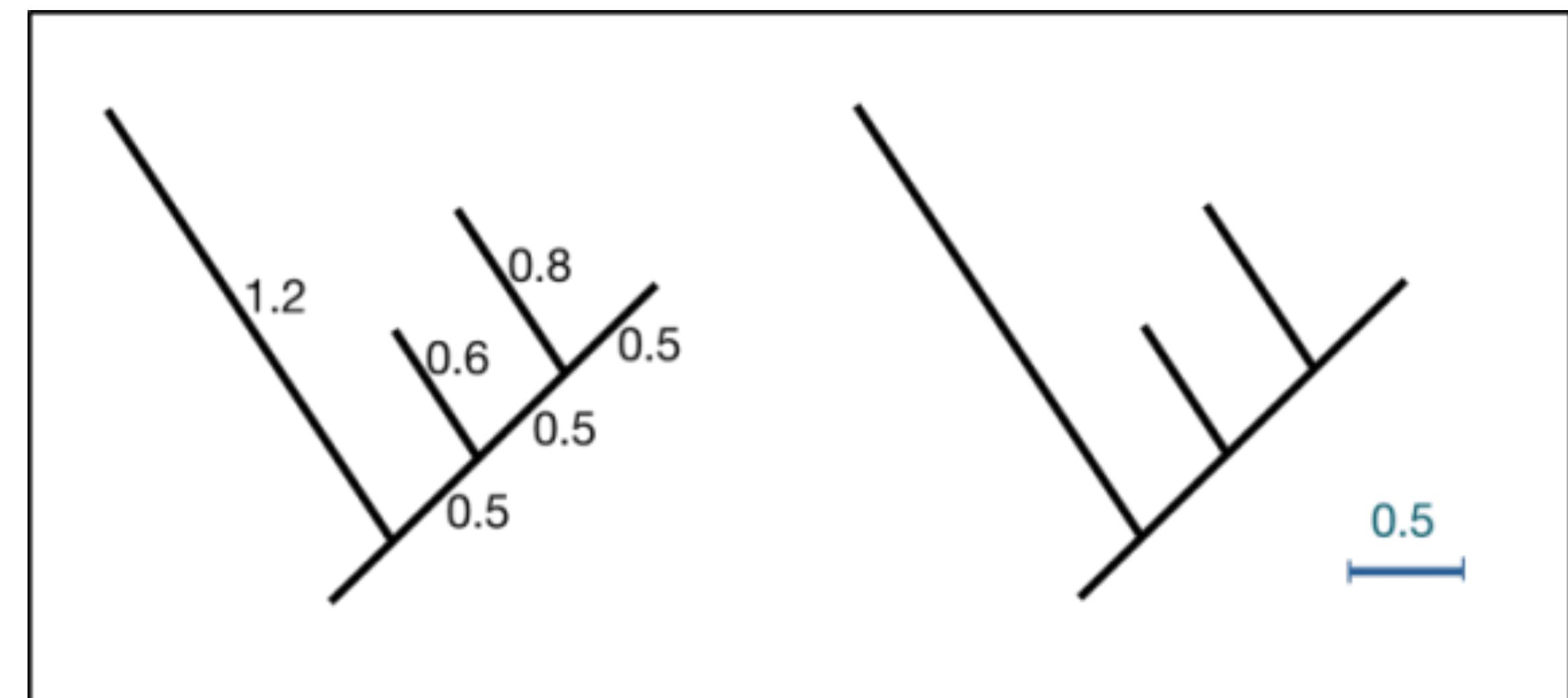


	24	30 32	62	71	
homSap	PWPPLR--NEFRYFQRMTTSSVEGKQNLVIMGKKTWFSIPEKNRPLKGR				
macMul	PWPPLR--NEFRYFQRMTTSSVEGKQNLVIMGKKTWFSIPEKNRPLKGR				
calJac	PWPPLR--NEFRYFQRMTTSSVEDKQNLVIMGRKTWFSIPEKNRPLKDR				
musMus	PWPPLR--NEWKYFQRMTTSSVEGKQNLVIMGRKTWFSIPEKNRPLKDR				
canFam	PWPPLR--NEFKYFQRMTTNSSVEGKQNLVIMGRKTWFSIPEKNRPLKDR				
loxAfr	PWPPLR--NEFKYFQRMTTSSVEGKQNLVIMGRKTWFSIPEKNRPLKDR				
monDom	PWPPLR--NEFKYFQKMTTPSVEGKQNLVIMGKKTWFSIPEKCRPLKDR				
ornAna	PWPALR--NEFRYFQKMTTPPTVKGKQNLVIMGKKTWFSIPEKSRLPKDR				
galGal	PWPPLR--NEYKYFQRMTSTSHVEGKQNAVIMGKKTWFSIPEKNRPLKDR				
xenTro	PWPPLR--NEFKHFQRLTMTPTVEDKKNVVIIGRKTWFSIPEKNRPLKER				
lacCha	PWHPKRLSNEFRYFQKMTTPPTVEGKQNVVIIGRKTWFSIPEKNRPLKGR				
lepOcu	PWHPKRLSNEFKYFQKMTTPPTLEGQQNAVIMGRKTWFSIPERNRPLKRN				
gasAcu	PWHPLRLSNEFKHFRRTATASVKDKQNVVIIGRKTWFSIPEKNRPLNNR				
leuEri	PWHPIRLSKEFKHFQRMSTPSVEGKCNAVIMGRKTWHSIPEKNRPLKRN				
eptBur	PWHSKSLVKEMKHTRLTSAAA-EGKQNAVVMGRKTWESIPEKFRPLRN				
cioInt	PW---RLPKEMKYFKRITTGEVEEGRRNAIIIGRKTWESIPKSFKPLKDR				
braFlo	PW---TLRGDMKFFSRLTSGTEEAGKQNAVVMGRKTWFSIPDRFRPLPKR				
sacKow	PW---RLRKEMSFTKVTSSETKEDGKQNAVVMGRKTWFSIPEKYRPLAGR				
strPur	PW---RLRQEEMAYFERLTKTAQMEGMKNAVIMGRKTWDSIPEKFRPLKDR				
escCol	PW---NLPADLAWFKRNTLN-----KPVIMGRHTWESI---GRPLPGR				

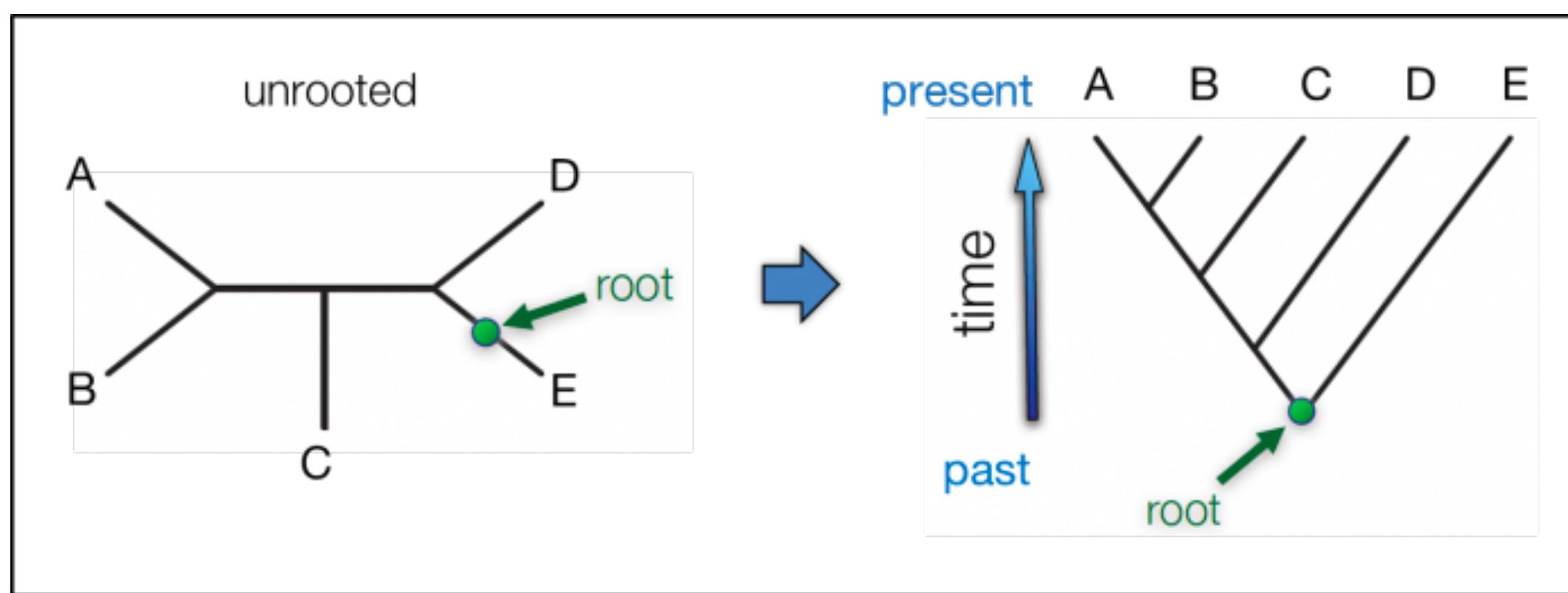
Topology



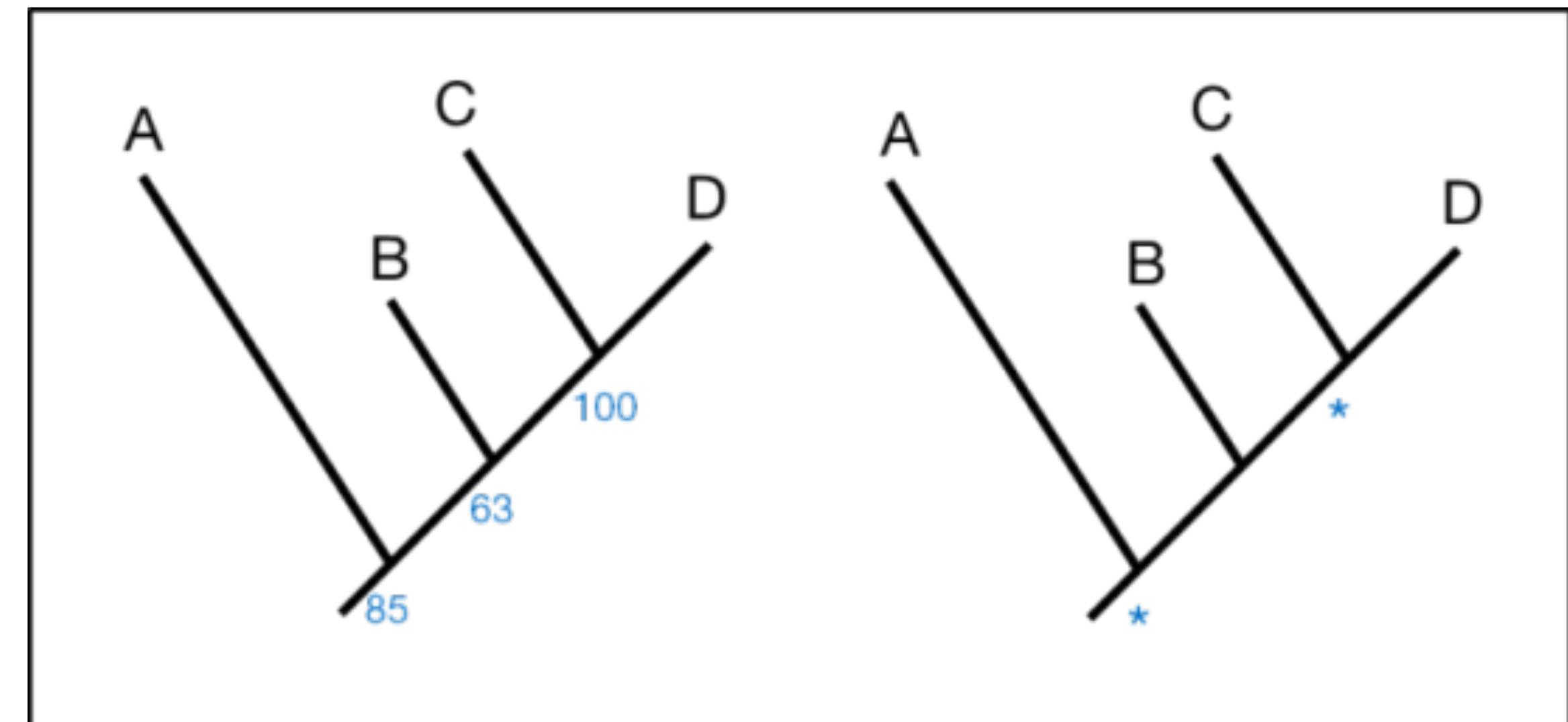
Branches

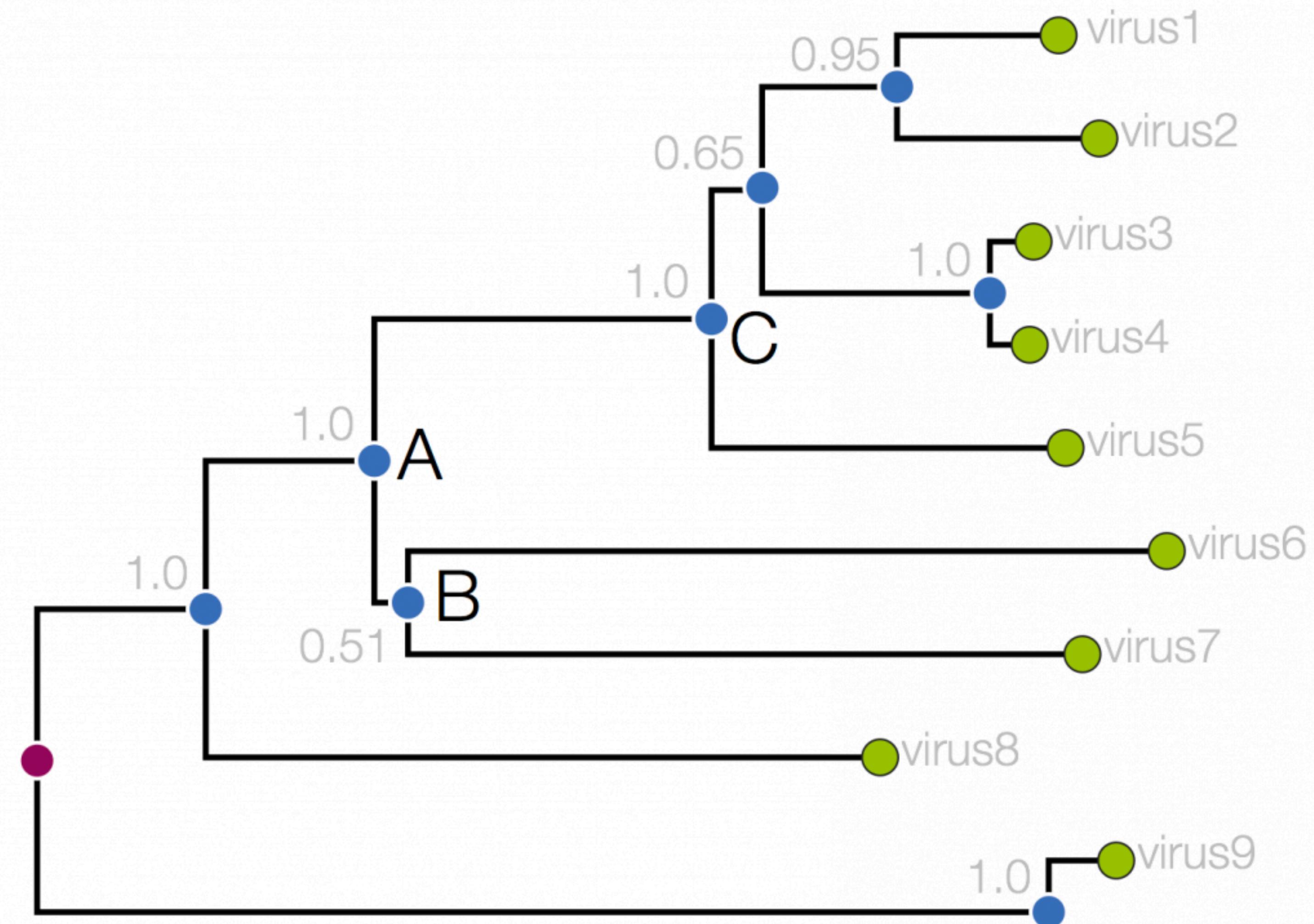


Roots



Confidence





0.07