

Ancestral state reconstruction

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Outline

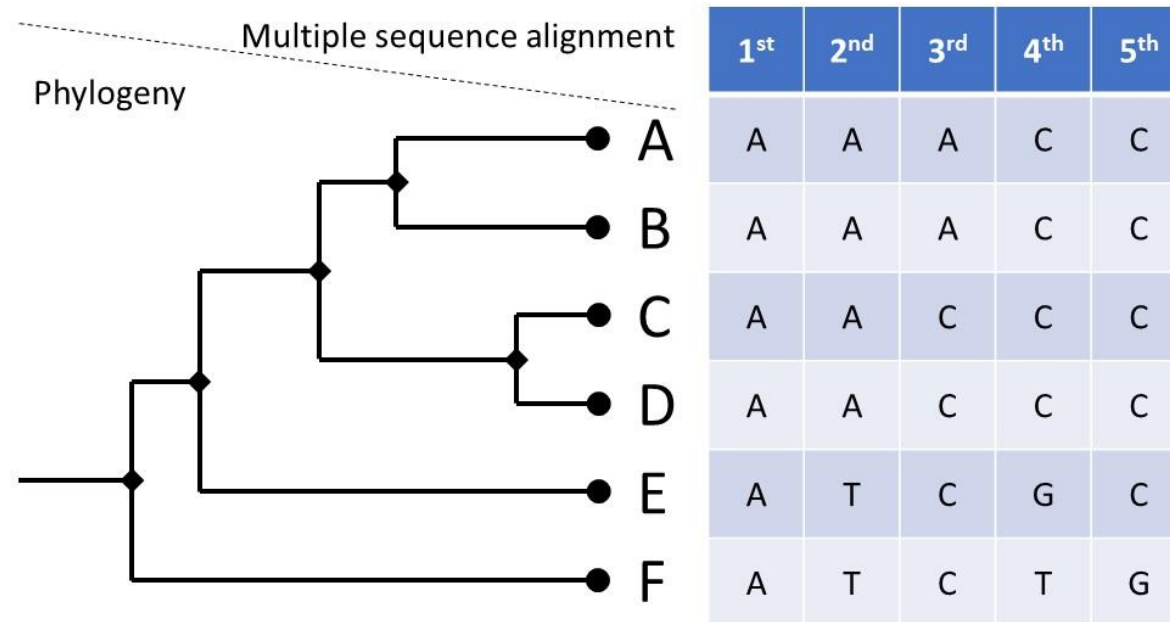
- What is ancestral state reconstruction?
- Applications of ancestral state reconstruction
- Ancestral state reconstruction in the context of systematics
- How to reconstruct ancestral state of nucleotide sequences?

What is ancestral state reconstruction?

What do organisms look like in the past?

What is ancestral state reconstruction?

- Extrapolation back in time from characteristics of individuals that you observe to their common ancestors

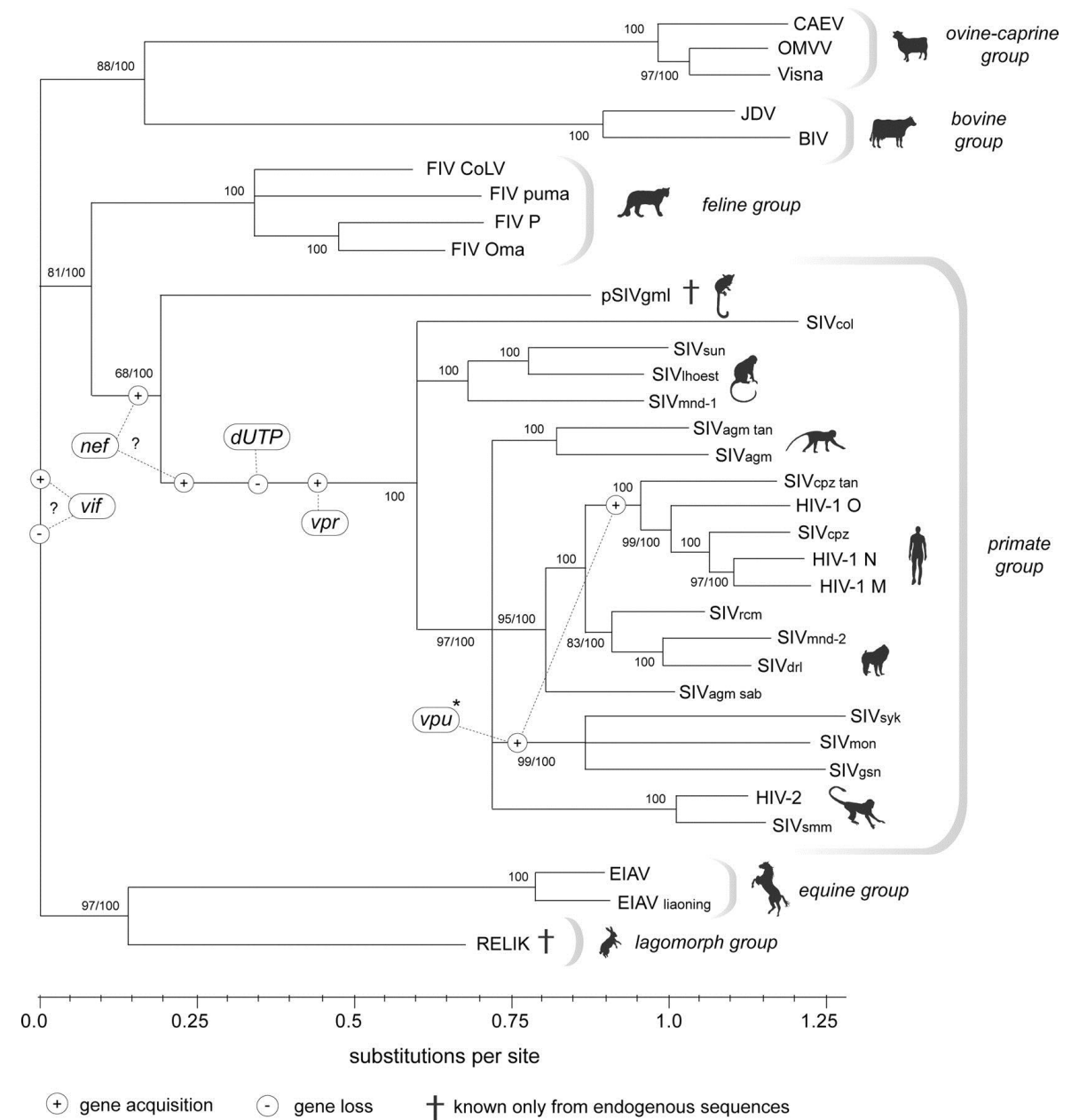


What did the MRCA of A and B look like for this 5 nucleotide positions?

What did the MRCA of A, B, and D look like for this 5 nucleotide positions?

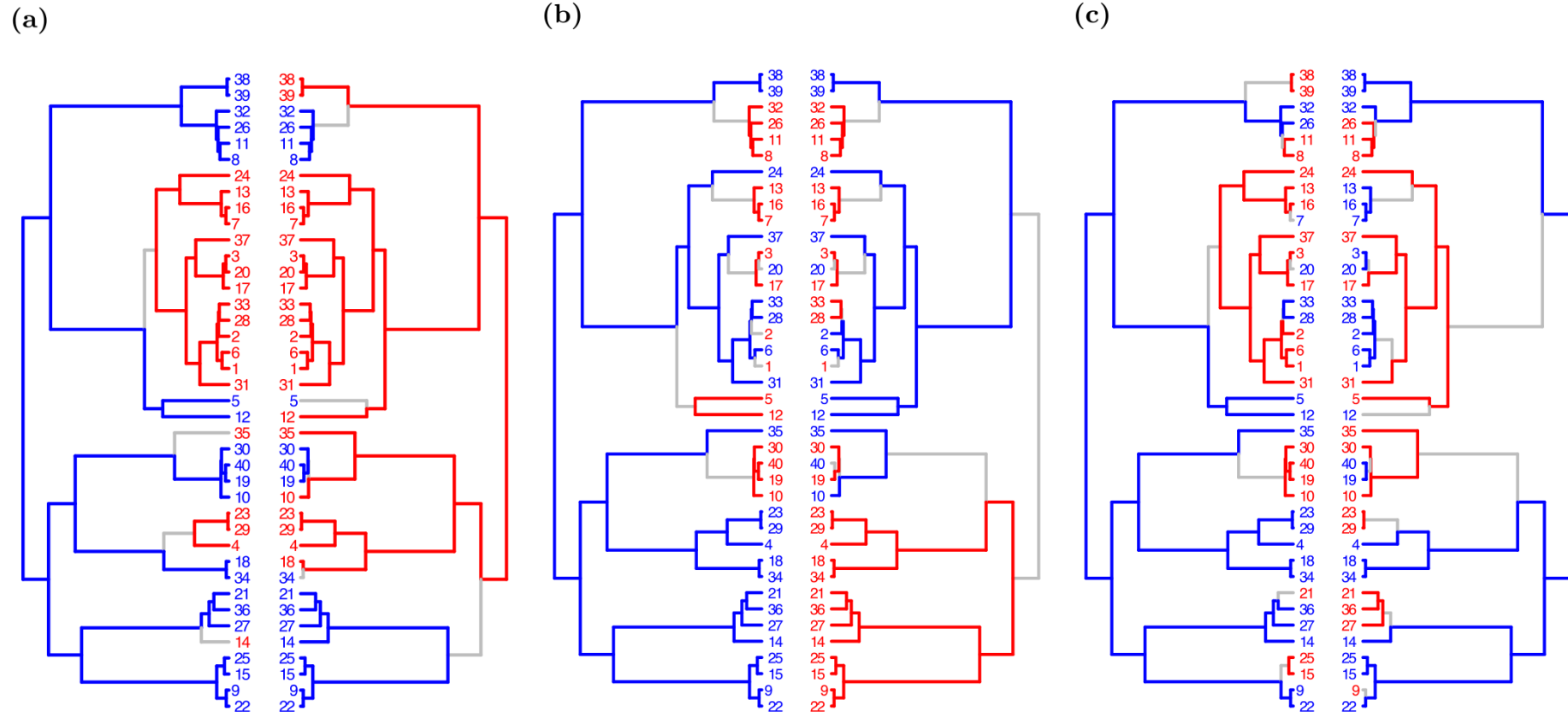
Applications of ancestral state reconstruction

- It is an important application of phylogenetics



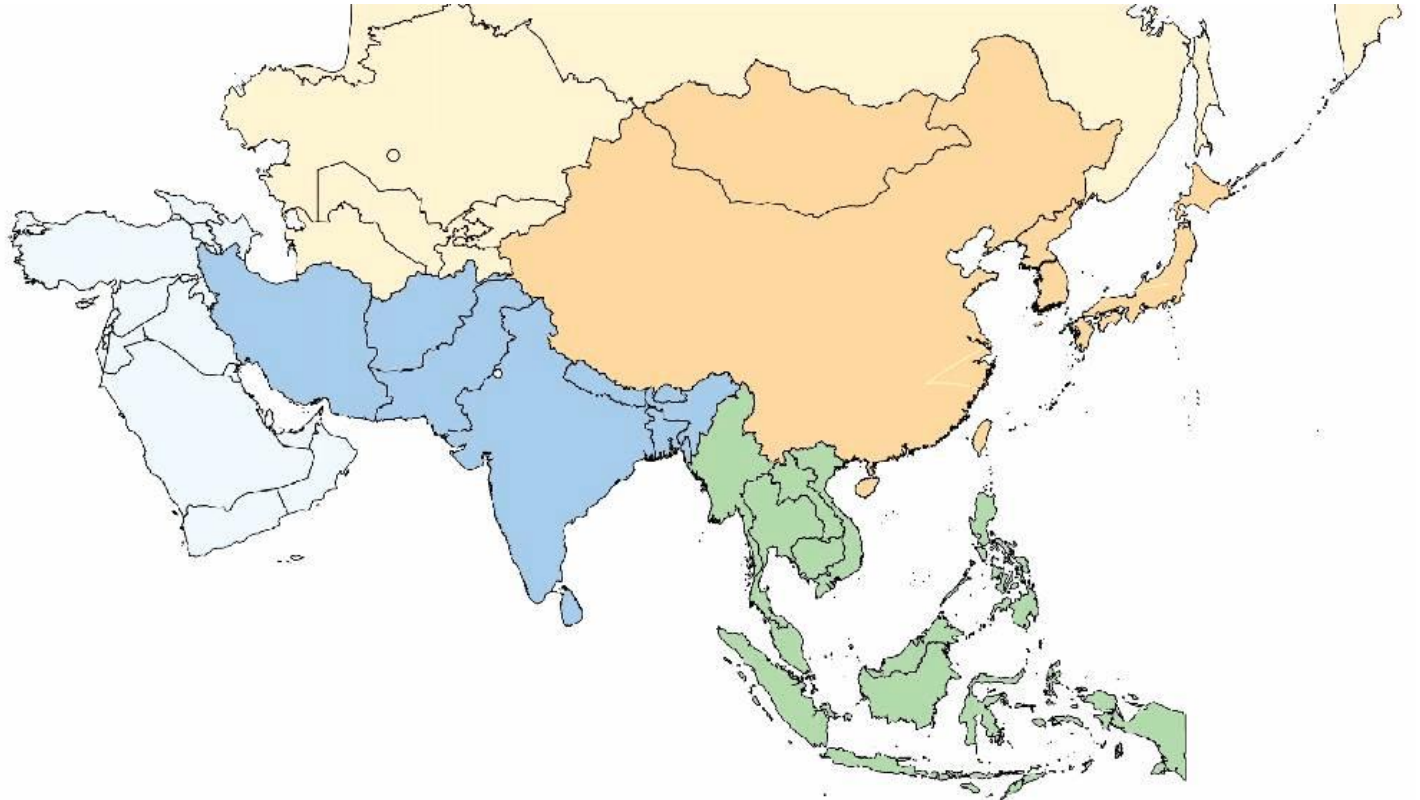
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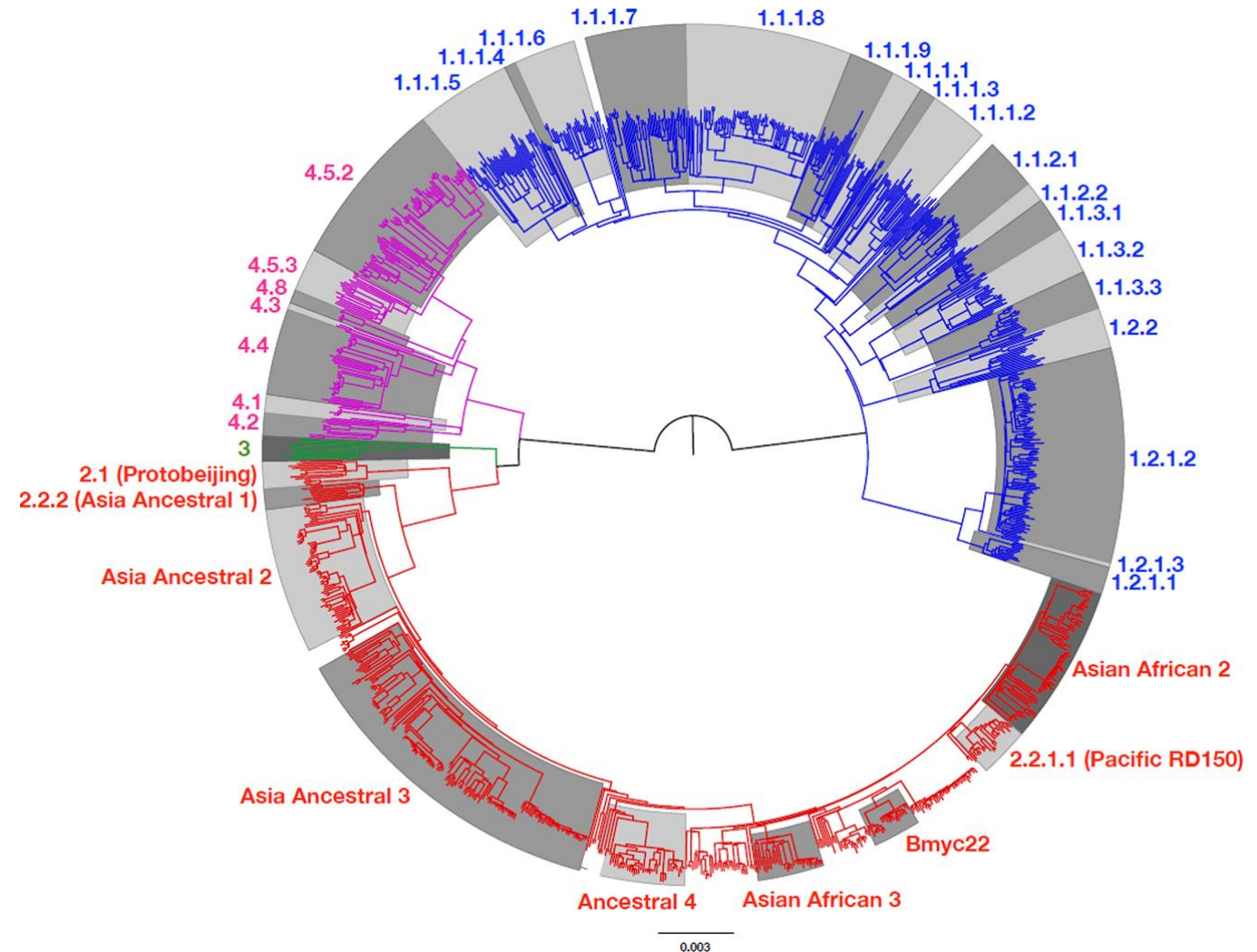


Ancestral state reconstruction in the context of systematics

Making SNP barcodes

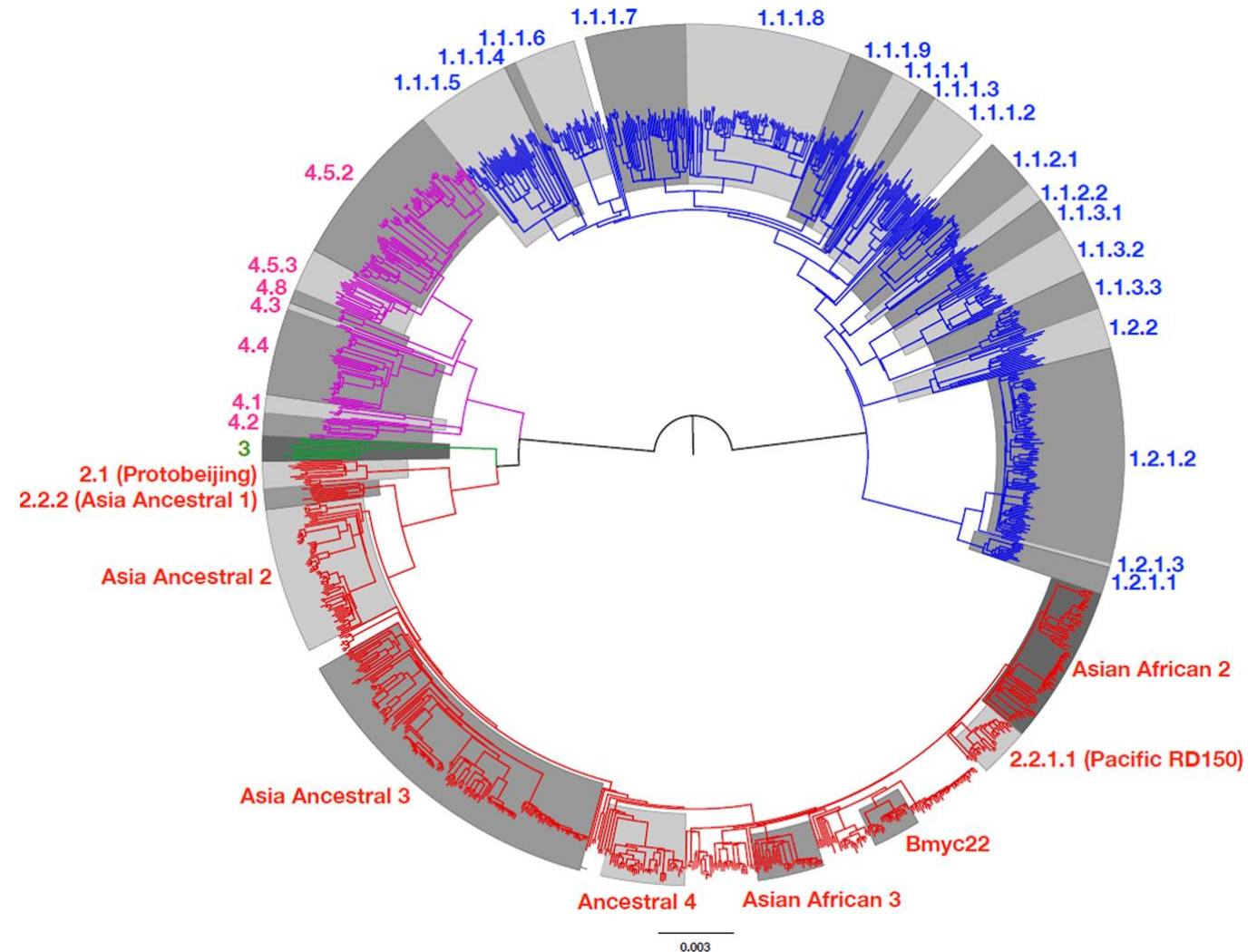
Ancestral state reconstruction in the context of systematics

- **Biological systematics** is the study that deals with **systematic arrangement of organisms**
- **Evolutionary taxonomy**

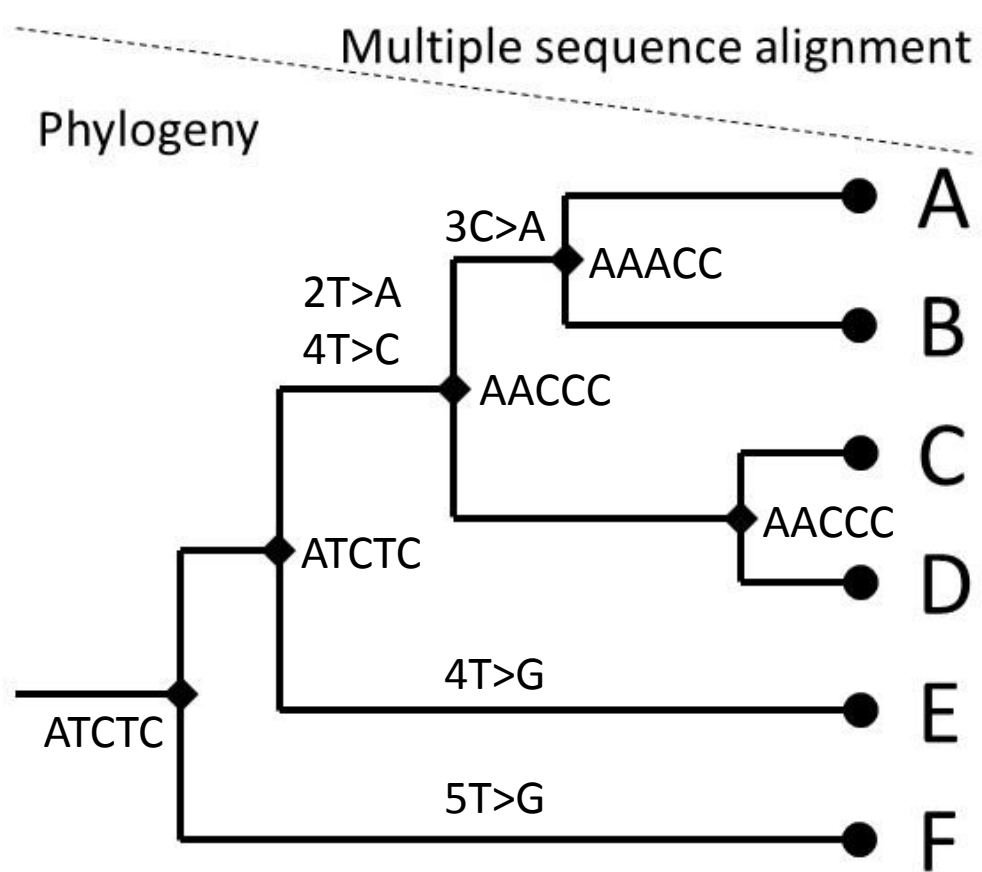


Ancestral state reconstruction in the context of systematics

- Now that we have organised organisms into groups based on their evolutionary history,...
- ...what are the unique features of each group, i.e. what are their identification keys?



Ancestral state reconstruction in the context of systematics

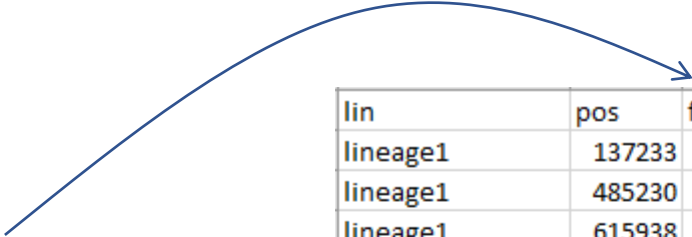


1 st	2 nd	3 rd	4 th	5 th
A	A	A	C	C
A	A	A	C	C
A	A	C	C	C
A	A	C	C	C
A	T	C	G	C
A	T	C	T	G

What are the changes specific to the clade of A, B, C and D?

Ancestral state reconstruction in the context of systematics

- **SNP barcode** is a set of clade-specific SNPs that are shared by all, or most, of the organisms in that clade, and do not present in any other organisms, or only a few, that are outside the clade



lin	pos	fst	gene_pos	ref_nt	alt_nt	cod_num	ref_cod	alt_cod	ref_aa	alt_aa	rv	gene	tags	genefunc	essential
lineage1	137233	1	945	C	T	315	GCC	GCT	A	A	Rv0112	gca	syn	cell wall a	essential
lineage1	485230	1	1254	C	T	418	CAC	CAT	H	H	Rv0404	fadD30	syn	lipid meta	essential
lineage1	615938	1	1104	G	A	368	GAG	GAA	E	E	Rv0524	hemL	syn	intermedi	essential
lineage1	649345	1	810	C	T	270	GCC	GCT	A	A	Rv0557	mgtA	syn	lipid meta	essential
lineage1	811492	1	120	C	G	40	GTC	GTG	V	V	Rv0714	rplN	syn	informati	essential
lineage1	865761	1	1176	C	T	392	CAC	CAT	H	H	Rv0772	purD	syn	intermedi	essential
lineage1	1119739	1	201	C	T	67	CTG	CTA	L	L	Rv1002c	.	syn	cell wall a	essential
lineage1	1320508	1	474	G	A	158	GTG	GTA	V	V	Rv1182	papA3	syn	lipid meta	essential
lineage1	1590555	1	159	C	T	53	ACC	ACT	T	T	Rv1415	ribA2	syn	intermedi	essential
lineage1	2696977	1	738	G	C	246	GCC	GCG	A	A	Rv2400c	subI	syn	cell wall a	essential
lineage1	3274545	1	474	G	A	158	CTG	CTA	L	L	Rv2938	drnC	syn	cell wall a	essential
lineage1	3424462	1	966	C	T	322	CTG	CTA	L	L	Rv3061c	fadE22	syn	lipid meta	essential
lineage1	3913737	1	798	G	A	266	GCC	GCT	A	A	Rv3495c	lprN	syn	cell wall a	essential
lineage1	3920109	1	753	G	T	251	ATC	ATA	I	I	Rv3501c	yrbE4A	syn	virulence,	essential
lineage1	3984926	1	520	G	A	174	CTG	TTG	L	L	Rv3545c	cyp125	syn	intermedi	essential

0 = two populations are genetically identical

1 = two populations have maximum genetic diversity

How to reconstruct ancestral state of nucleotide sequences?

Maximum likelihood methods of ancestral state reconstruction

Ancestral state reconstruction method - Maximum likelihood

- Maximum likelihood methods of ancestral state reconstruction attempt to ...

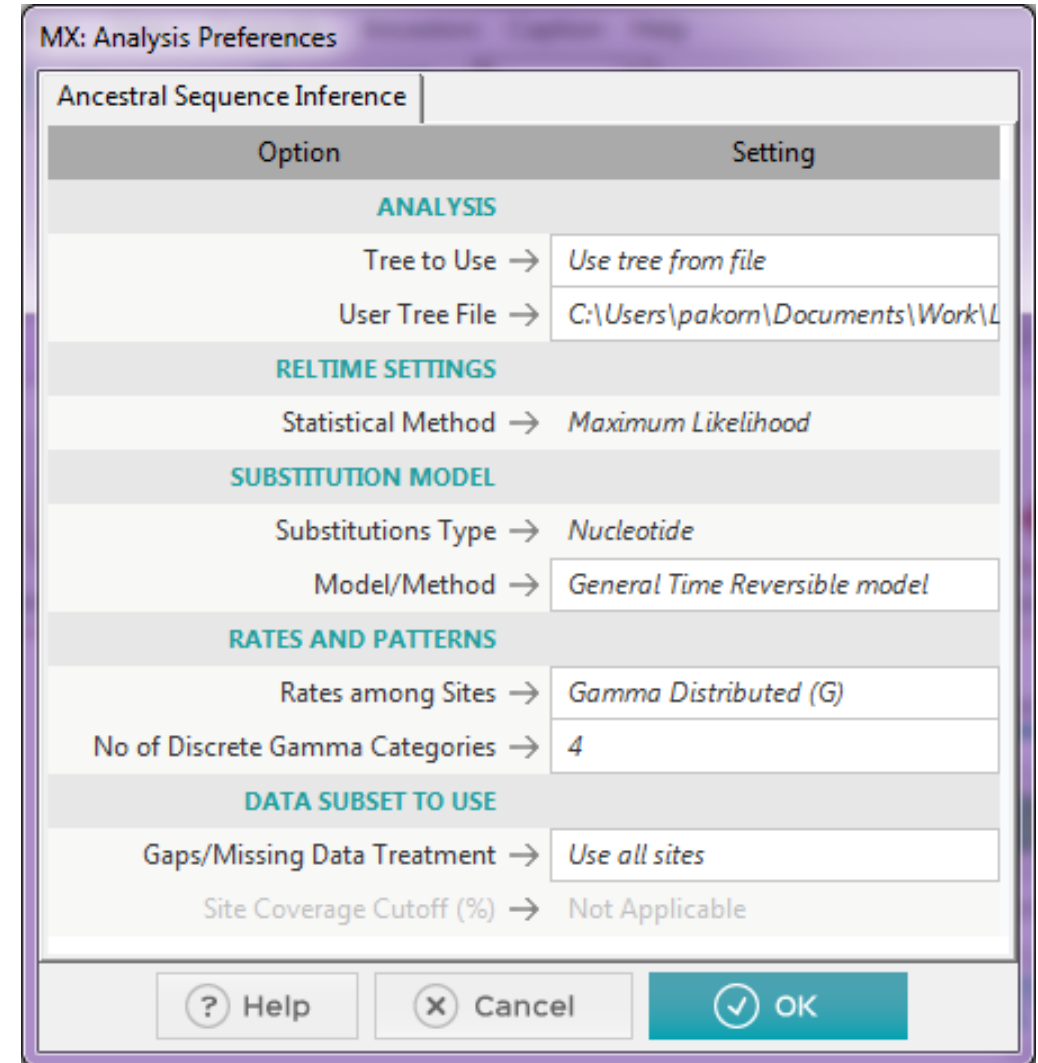
“

find character states at internal nodes that maximize the probability of the data (the observed character states) given the hypothesis (a model of evolution and a phylogeny relating the observed sequences or taxa)

”

Ancestral state reconstruction method - Maximum likelihood

- You can use MEGA to do this for you!
- You just need to give the program a tree and the MSA!



Ancestral state reconstruction method - Maximum likelihood

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