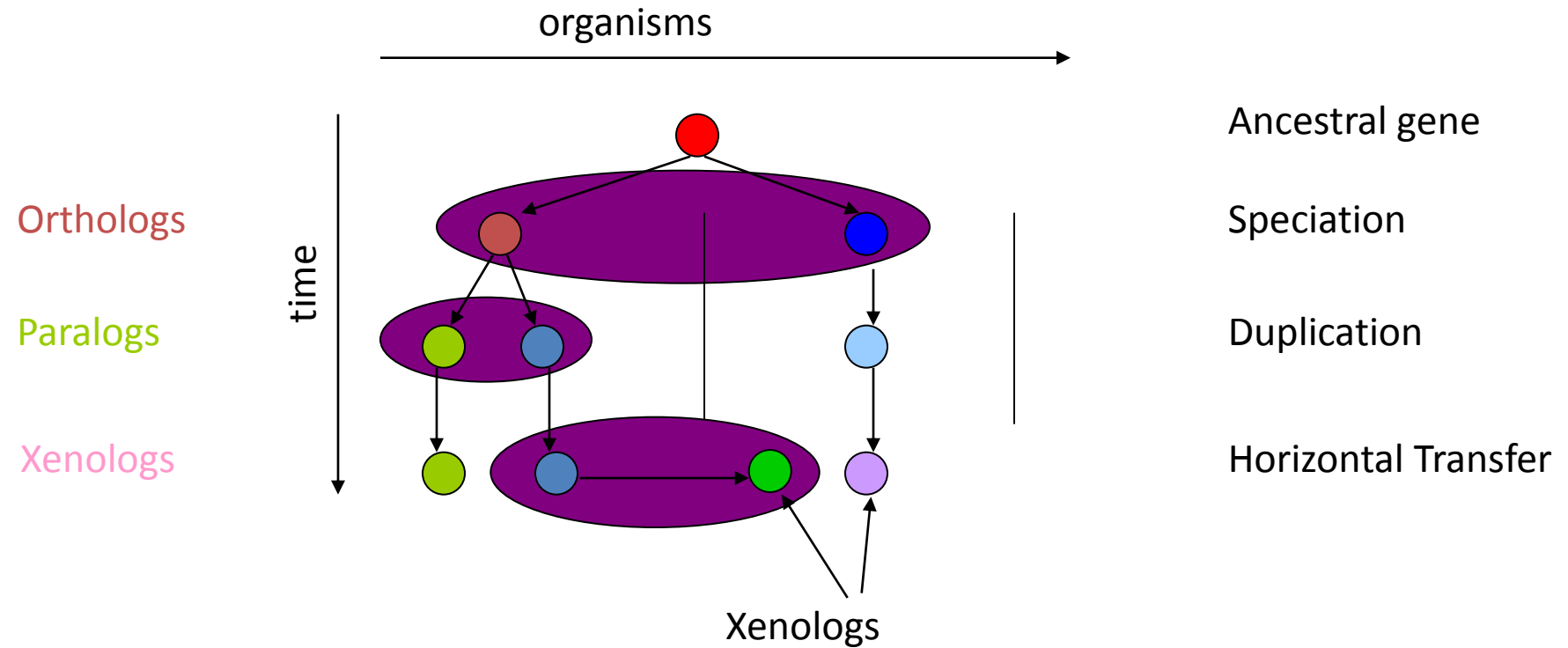


Tutorial No. 9

Evolution by Horizontal Transfer

Xenologs arise by horizontal transfer



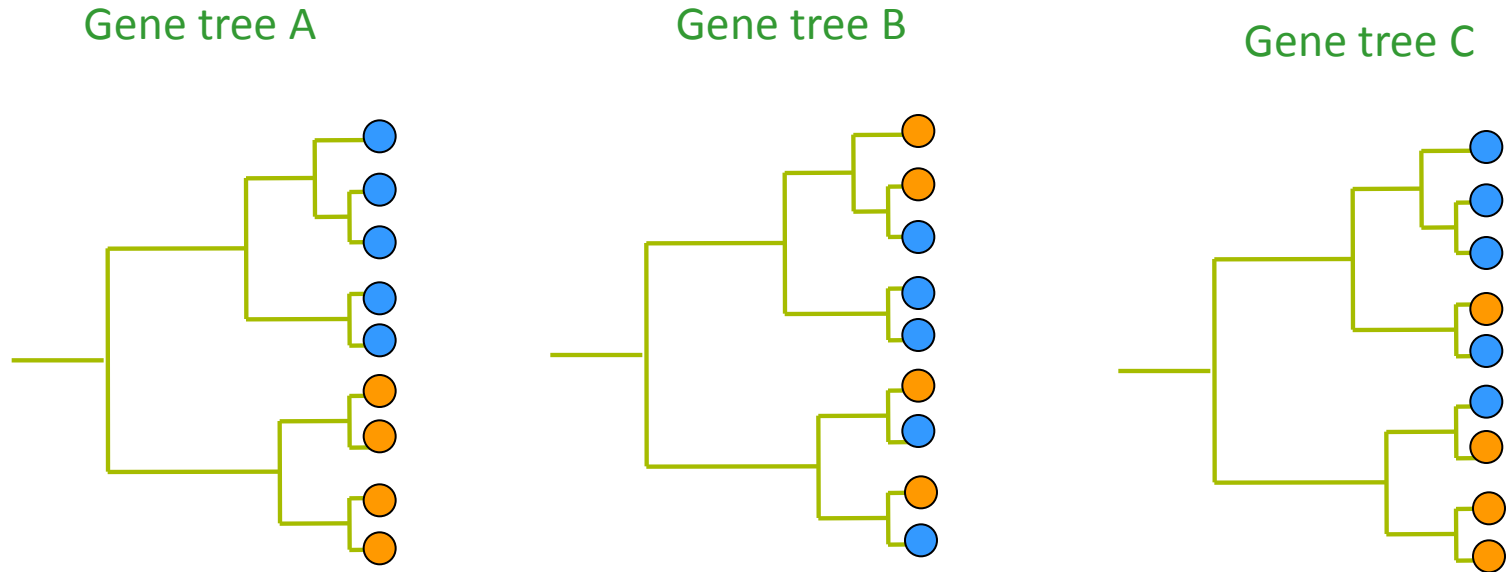
Xenologs – homologs related by horizontal transfer

Orthologs – homologs related by speciation

Paralogs – homologs related by duplication

The problem: different molecules can yield different trees AND may still be telling the truth

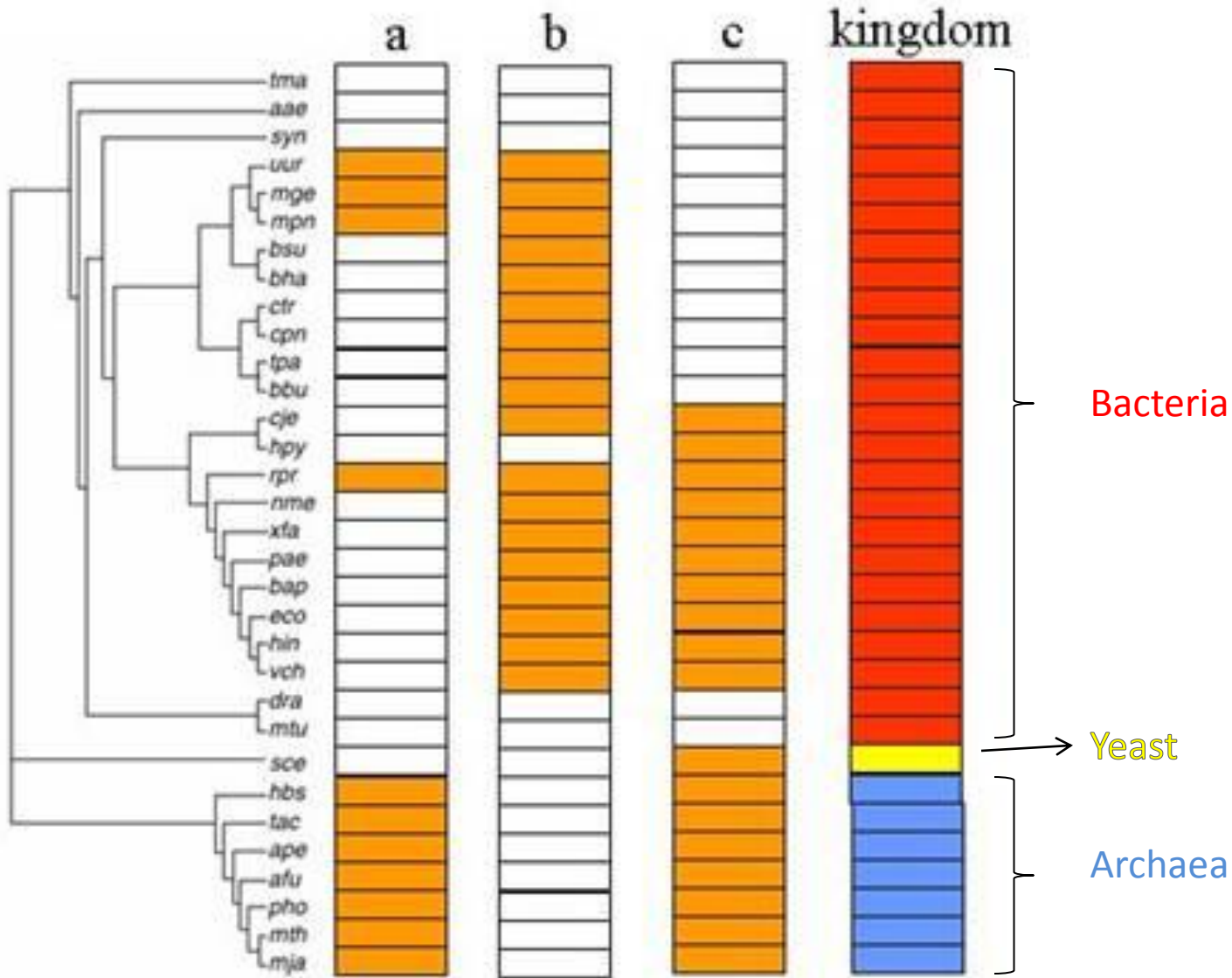
Even the sacred of sacreds of phylogenetic taxonomy can be violated:



● Archaea
● Bacteria

Kingdoms are not monophyletic in gene tree B and C

Problem 1 – Gene loss versus gene transfer



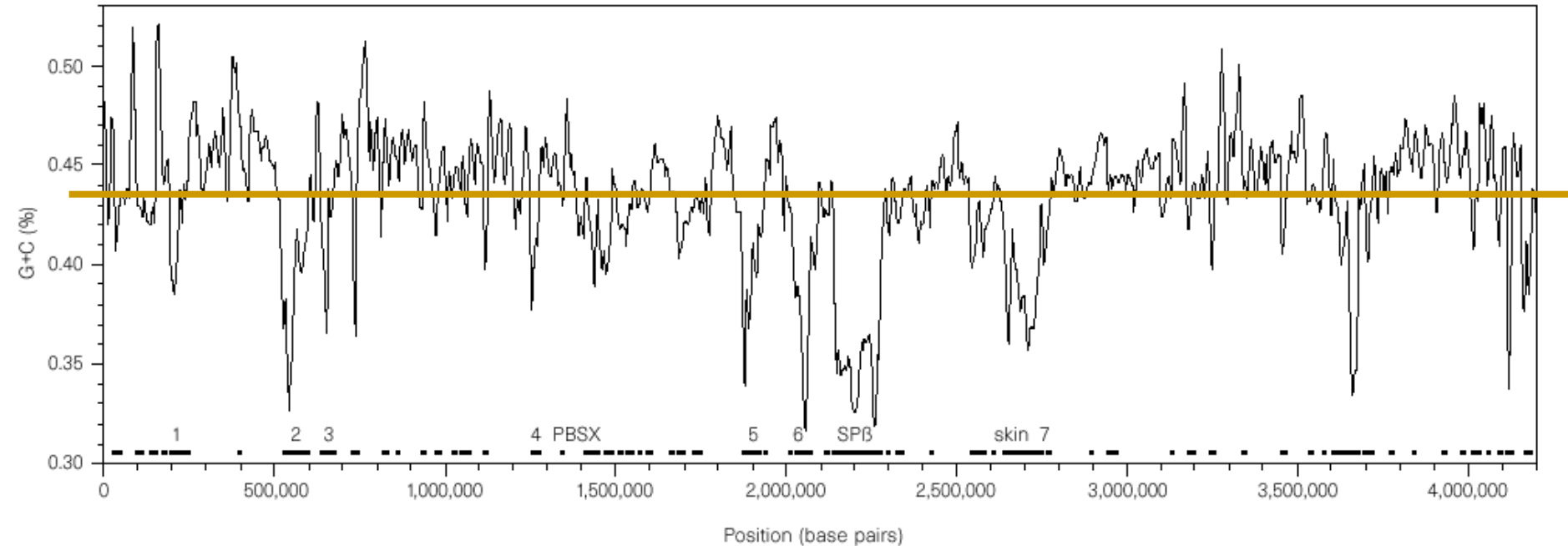
Problem 2: *Anomalous DNA composition.* Why does the method of anomalous DNA composition fail to identify ancient transfers?

Horizontally transferred genes use the genetic code differently

Codon usage bias in *B. subtilis* genes.

AA*	Codon† tRNA genes	Gene class§			
		All	I	II	III
Phe	UUU •	68.7	69.5	36.1	74.9
	UUC B, D, Y	31.3	30.5	63.9	25.1
Thr	ACU •	17.3	13.8	35.0	33.4
	ACC I	15.8	17.0	4.0	12.6
	ACA B, D, J, SL1	41.1	40.7	46.5	41.6
	ACG •	25.8	28.5	14.5	12.4
Asn	AAU •	57.1	56.7	29.5	69.7
	AAC B, D, I, S	42.9	43.3	70.6	30.3
Lys	AAA B, J, S, Y	70.4	69.3	83.2	72.8
	AAG •	29.6	30.7	16.8	27.2

Most genes have roughly the same GC content within a genome



- Distribution of A + T-rich islands along the chromosome of *B. subtilis*.
- Location of genes from **class 3** according to codon usage analysis is indicated by dots at the bottom of the graph.
- Known prophages (PBSX, SPb and skin) are indicated by their names, and prophage-like elements are numbered from 1 to 7.

Problem 3: *Evolutionary scenarios.* Explain how in light of horizontal transfer the following two sentences are incorrect:

- Any two homologs within the same genome are paralogs.
- If a gene is universal, i.e. exists in all genomes like a ribosomal gene, it is expected to yield a tree free from horizontal transfers because a transfer of a redundant gene would not be useful.

Detecting Horizontal Transfers

1. Unexpected ranking of sequence similarity among homologs
2. Unexpected phylogenetic tree topology
3. Unusual phyletic pattern
4. Conservation of gene order
5. Anomalous DNA composition

“All criteria for identifying probable horizontal gene transfer, or more precisely acquisition of foreign genes by a particular genome, inevitably rely on some unusual feature(s) of subsets of genes that distinguishes them from the bulk of genes in the genome.” Koonin et al. 2001

- Direct proofs are unavailable
- Indications of horizontal transfers remain probabilistic

Problem 4 (2 points): We will be using the unicellular version of the [COG database](#)