

# Introduction to Bioinformatics for Computer Scientists

## Lecture 5

# Open Questions Molecular Biology

- Can RNA fold in several ways?

Yes, as the secondary structure is not only determined by the RNA sequence, but also by its environment → interaction with other RNA molecules.

- How is the start/stop of an exon recognized?

Short motifs/strings mark intron-exon boundaries. Usually introns start with a *GU* and end with an *AG*. However it seems to be more complicated and is not fully understood yet.

- Does DNA contain redundancy for error correction?

This is not entirely clear yet, although there is research pointing into this direction, see, for instance,

<http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0036644>

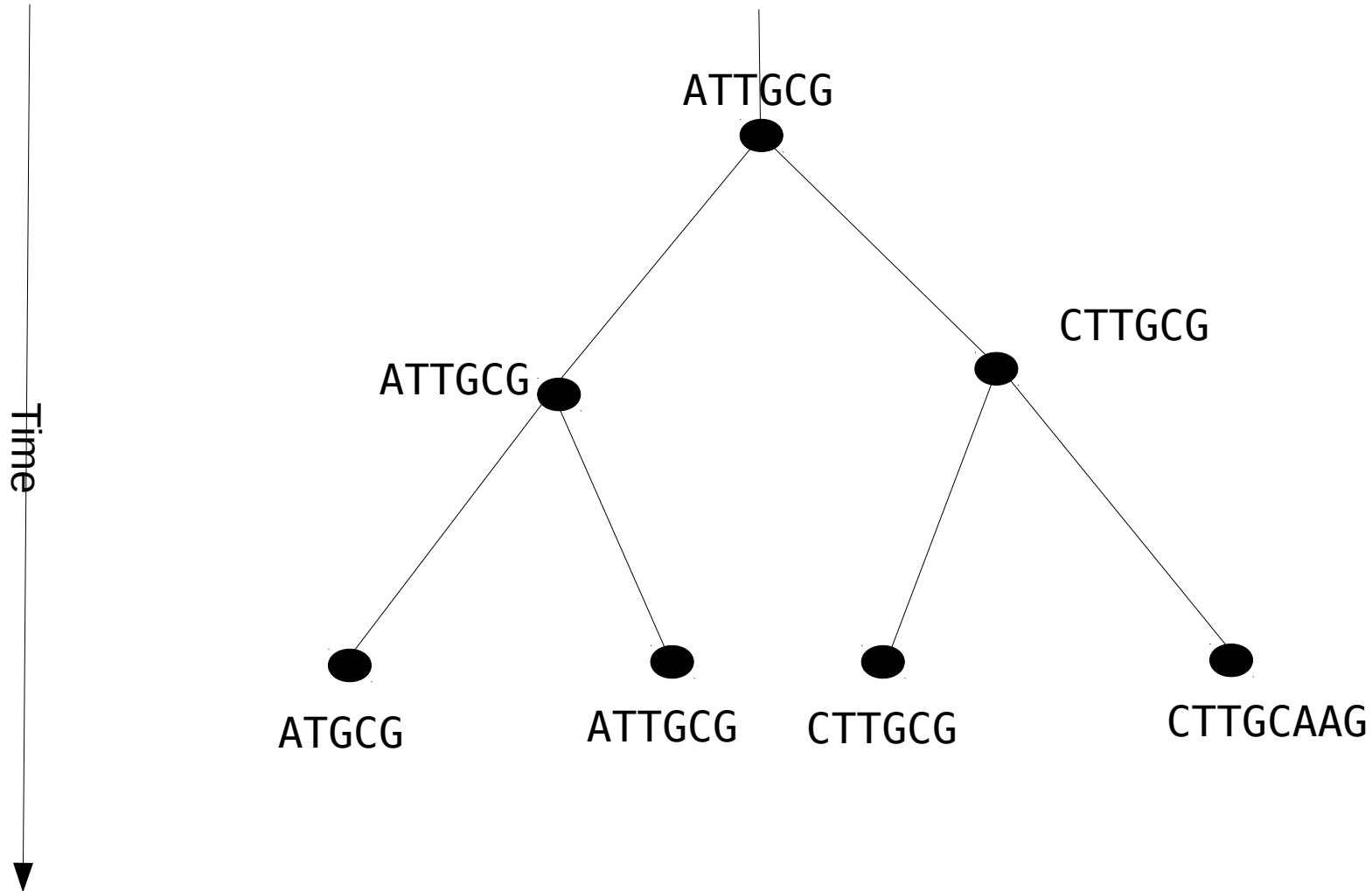
# Plan for next lectures

- Today: Multiple Sequence Alignment
- Lecture 6: Introduction to phylogenetics
- Lecture 7: Phylogenetic search algorithms
- Lecture 8 (Alexis): Statistical Models of Evolution I
- Lecture 9 (Alexis): Statistical Models of Evolution II

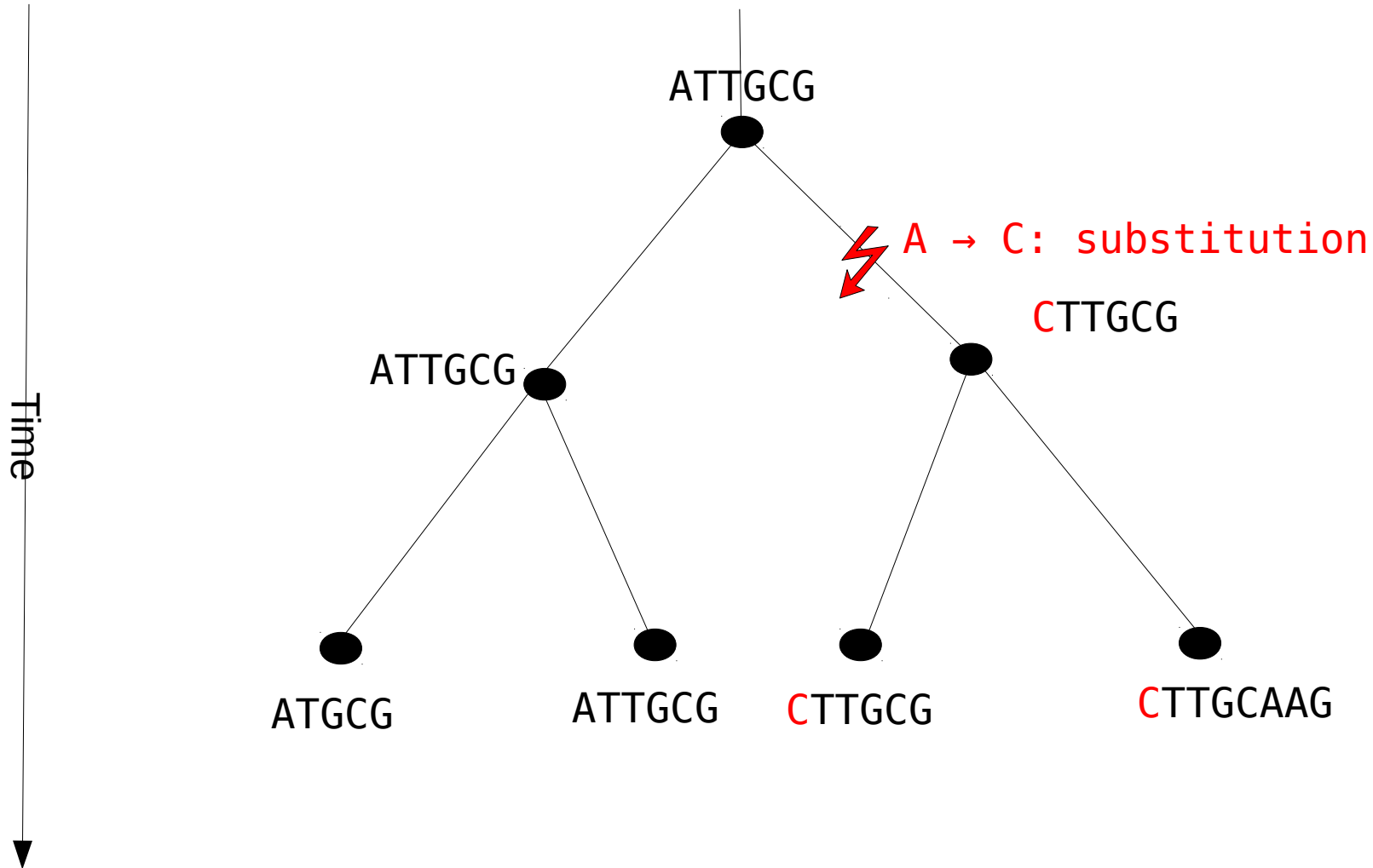
# Multiple Sequence Alignment

- What are we trying to reconstruct?

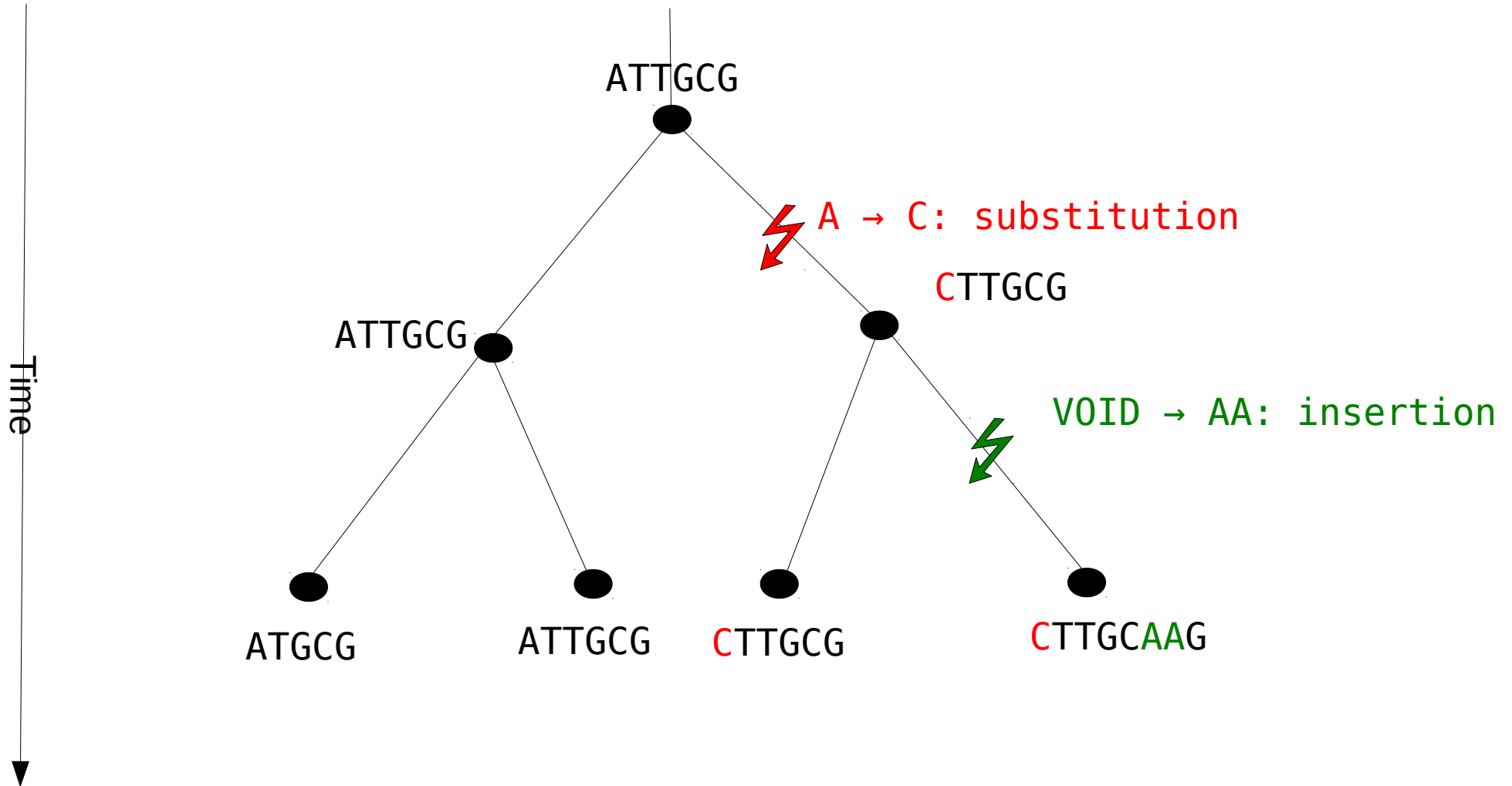
# Insertions, Deletions & Substitutions



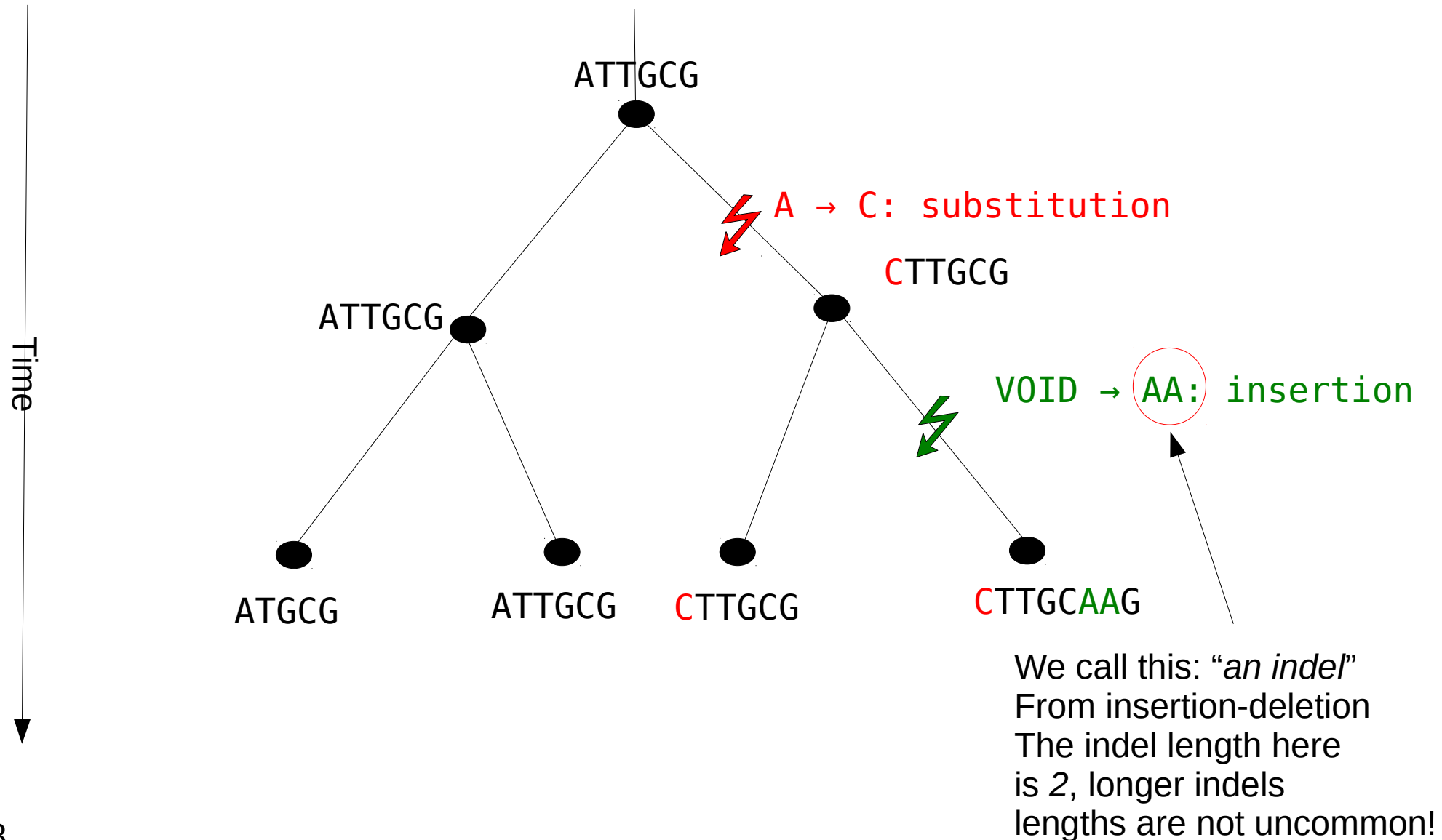
# Insertions, Deletions & Substitutions



# Insertions, Deletions & Substitutions

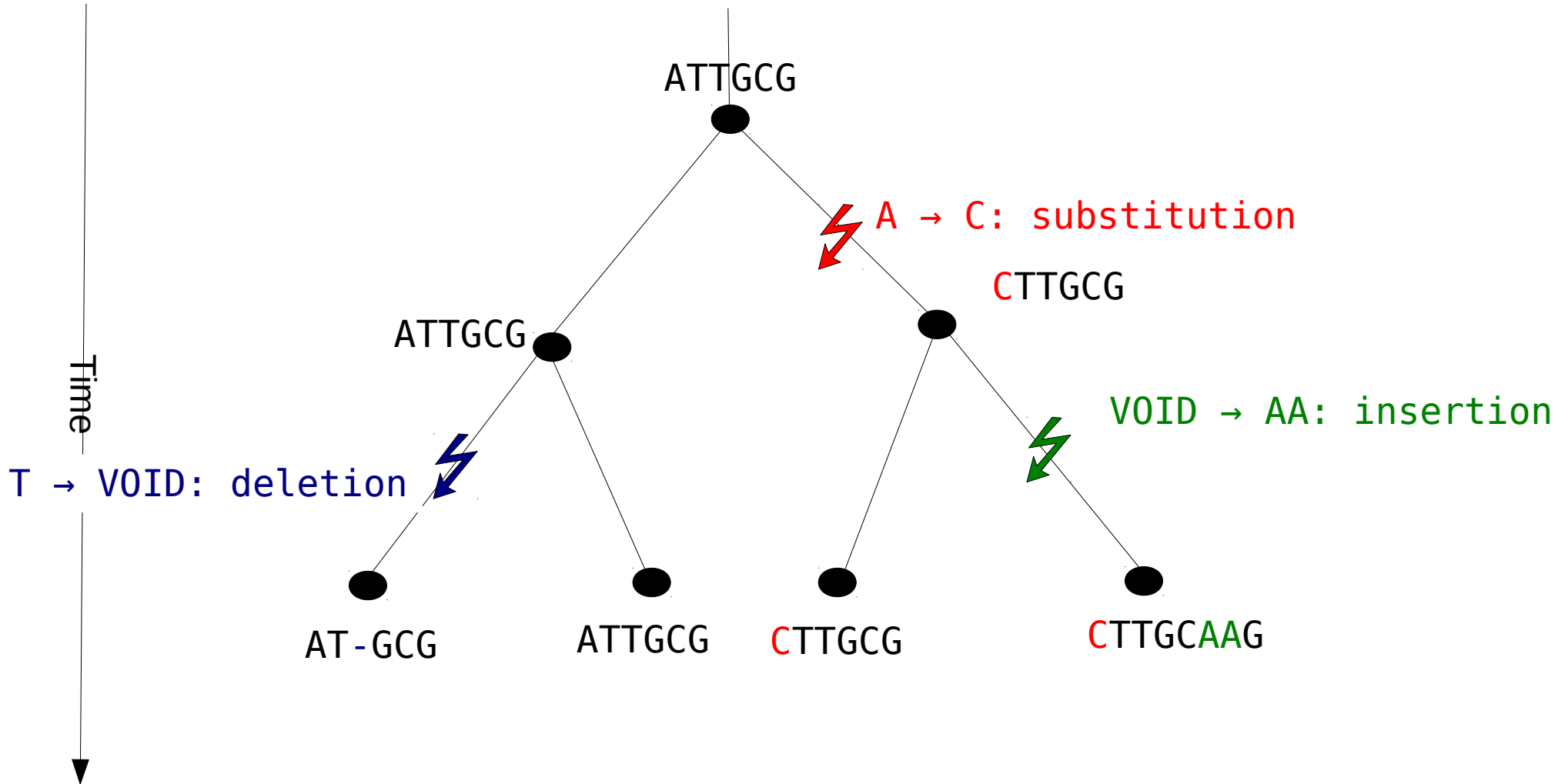


# Insertions, Deletions & Substitutions

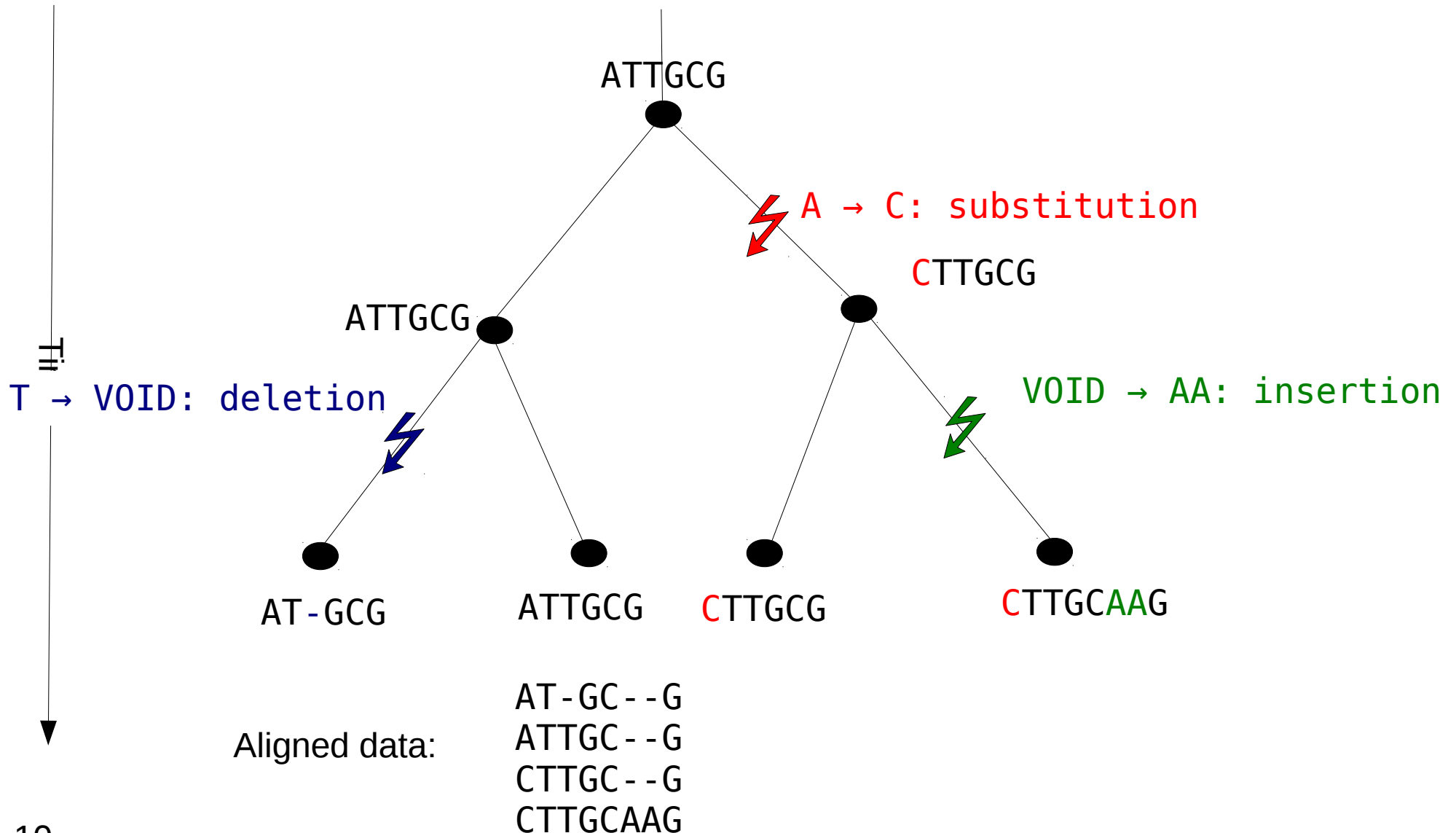




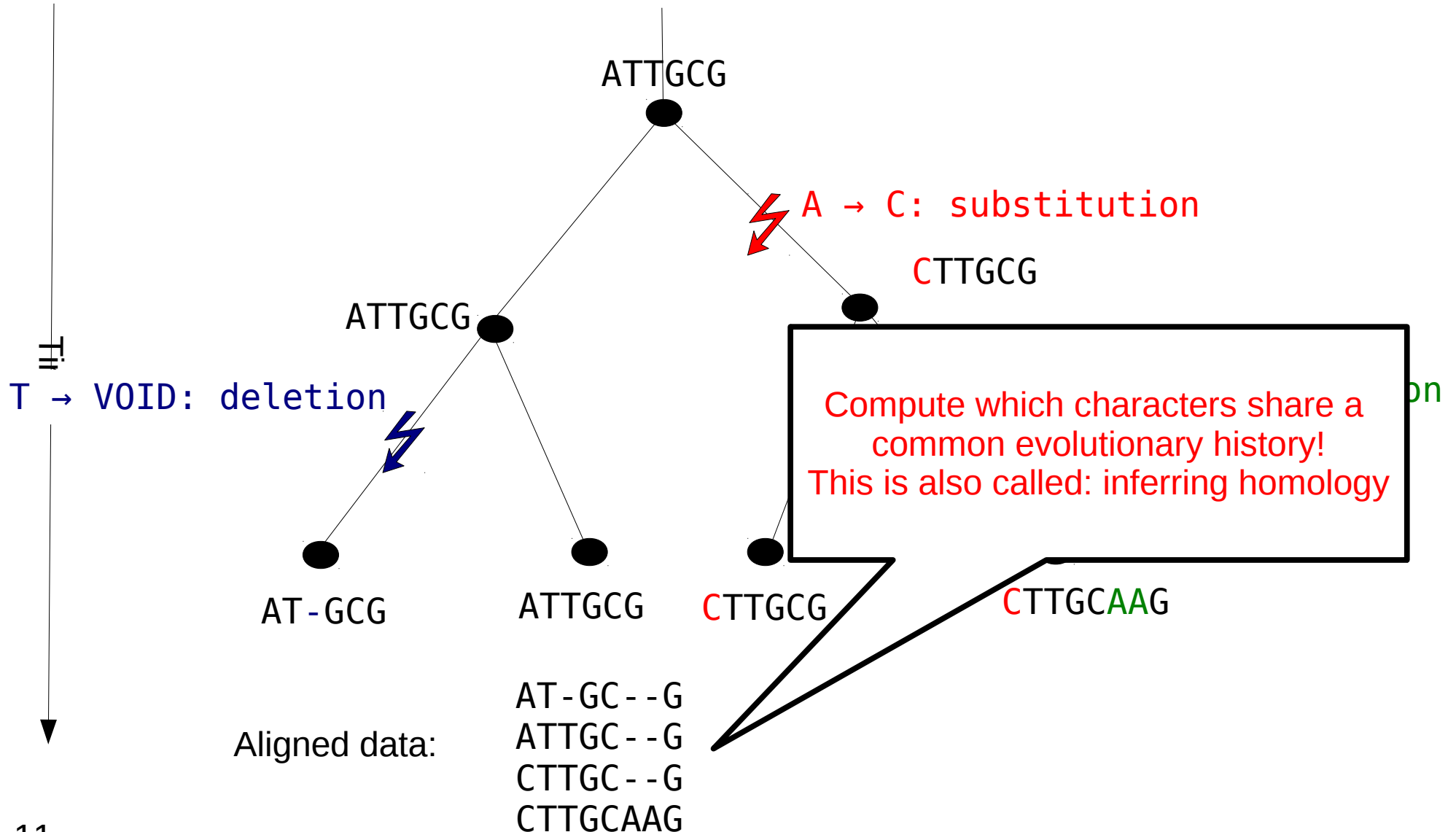
# Insertions, Deletions & Substitutions



# Insertions, Deletions & Substitutions



# Insertions, Deletions & Substitutions



# Multiple Sequence Alignment

- So far:
  - Comparing two sequences
  - Mapping a sequence/read to a reference genome
- What do we do when we want to compare more than two sequences at a time?
- Multiple Sequence Alignment (MSA)
- Open question: how do we assess the quality/accuracy of MSA algorithms?
  - nice review paper: “Who watches the watchmen?”  
<http://arxiv.org/abs/1211.2160>

# Why do we need MSAs?

- Input for phylogenetic reconstruction
- Discover important (conserved) parts of a *protein family*
- *Protein family* → group of evolutionarily related genes/proteins in different species with similar function/structure
- ***Family*** has a different meaning than in taxonomy!

# MSA

- Generalization of pair-wise sequence alignment problem
- Given  $n$  **orthologous** sequences  $s_1, \dots, s_n$  of different lengths, insert gaps “-” such that:
  - All sequences have the same length
  - Some criterion is optimized
  - *Corresponding (homologous) characters* in  $s_i$  and  $s_j$  are aligned to each other (in the same alignment column/site)
  - Columns/sites that entirely consist of gaps are **not** allowed

# MSA Terminology

s1	M	Q	P	I	L	L	L
s2	M	L	R	-	L	L	-
s3	M	K	-	I	L	L	L
s4	M	P	P	V	L	I	L



Alignment site/Alignment column

*Orthologous* sequences:

Sequences in different species that have evolved from the same **ancestral** gene

→ sequences that share a common evolutionary history

# MSA Terminology

*Homologous* characters:  
Characters that share a common  
evolutionary history

s1	M	Q	P	I	L	L	L
s2	M	L	R	-	L	L	-
s3	M	K	-	I	L	L	L
s4	M	P	P	V	L	I	L

Alignment site/Alignment column



# MSA Terminology

s1	M	Q	P	I	L	L	L
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s3	M	K	-	I	L	L	L
s4	M	P	P	V	L	I	L

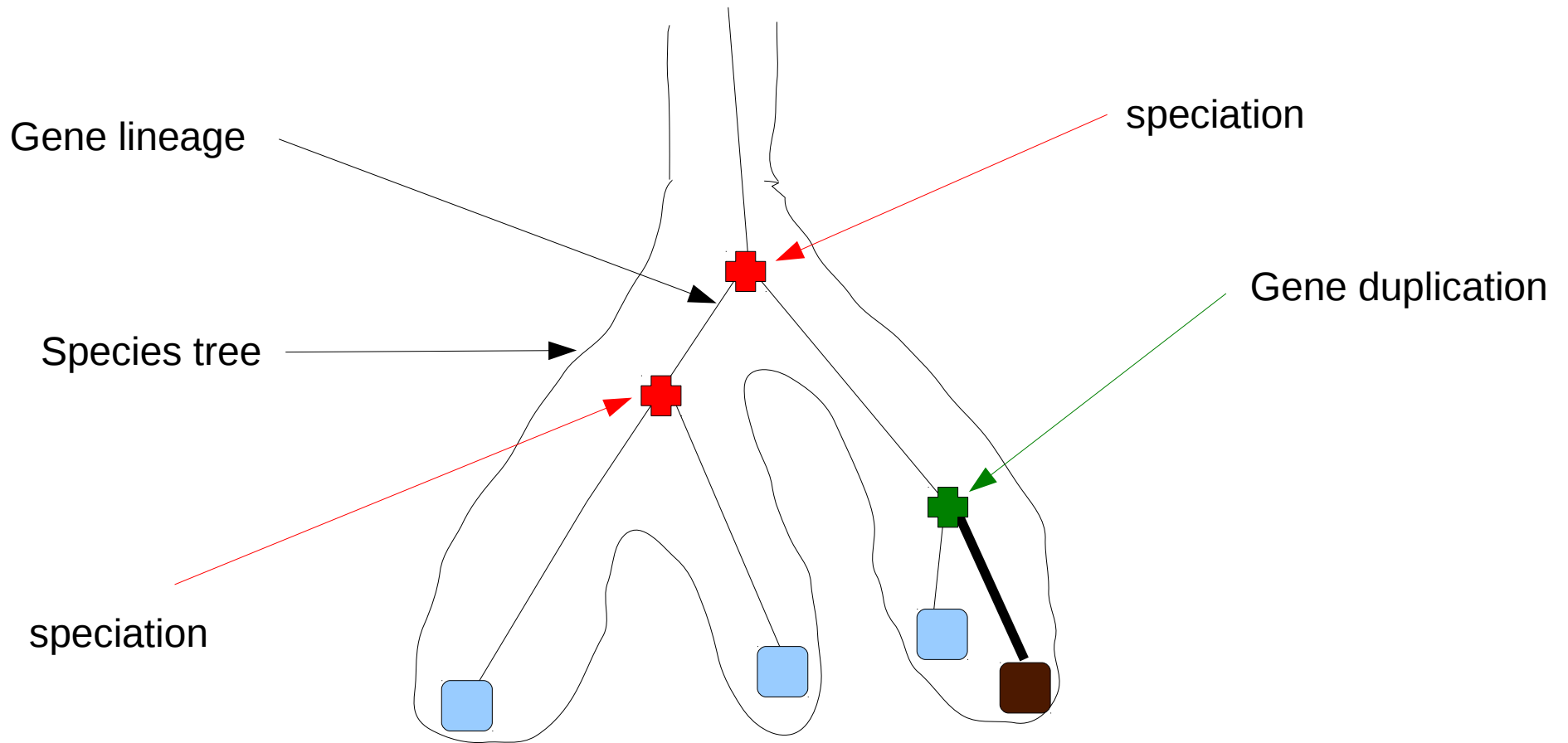
Alignment site/Alignment column

*Homologous* characters:  
Characters that share a common evolutionary history

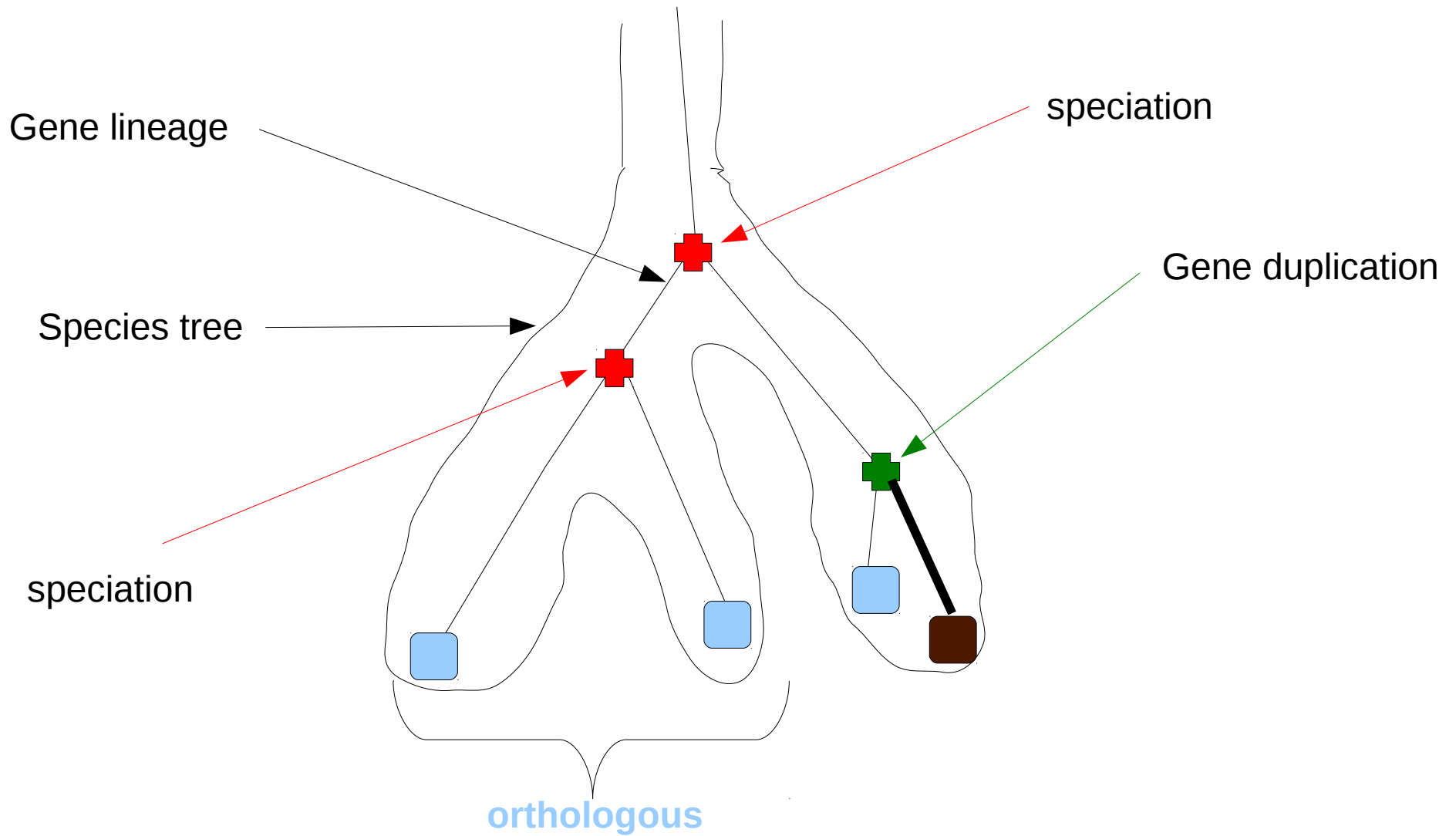
Note that, in this column the characters are similar (*analogous*), but this does not automatically induce homology!

They could be similar by chance or via Convergent evolution (see slides later-on)

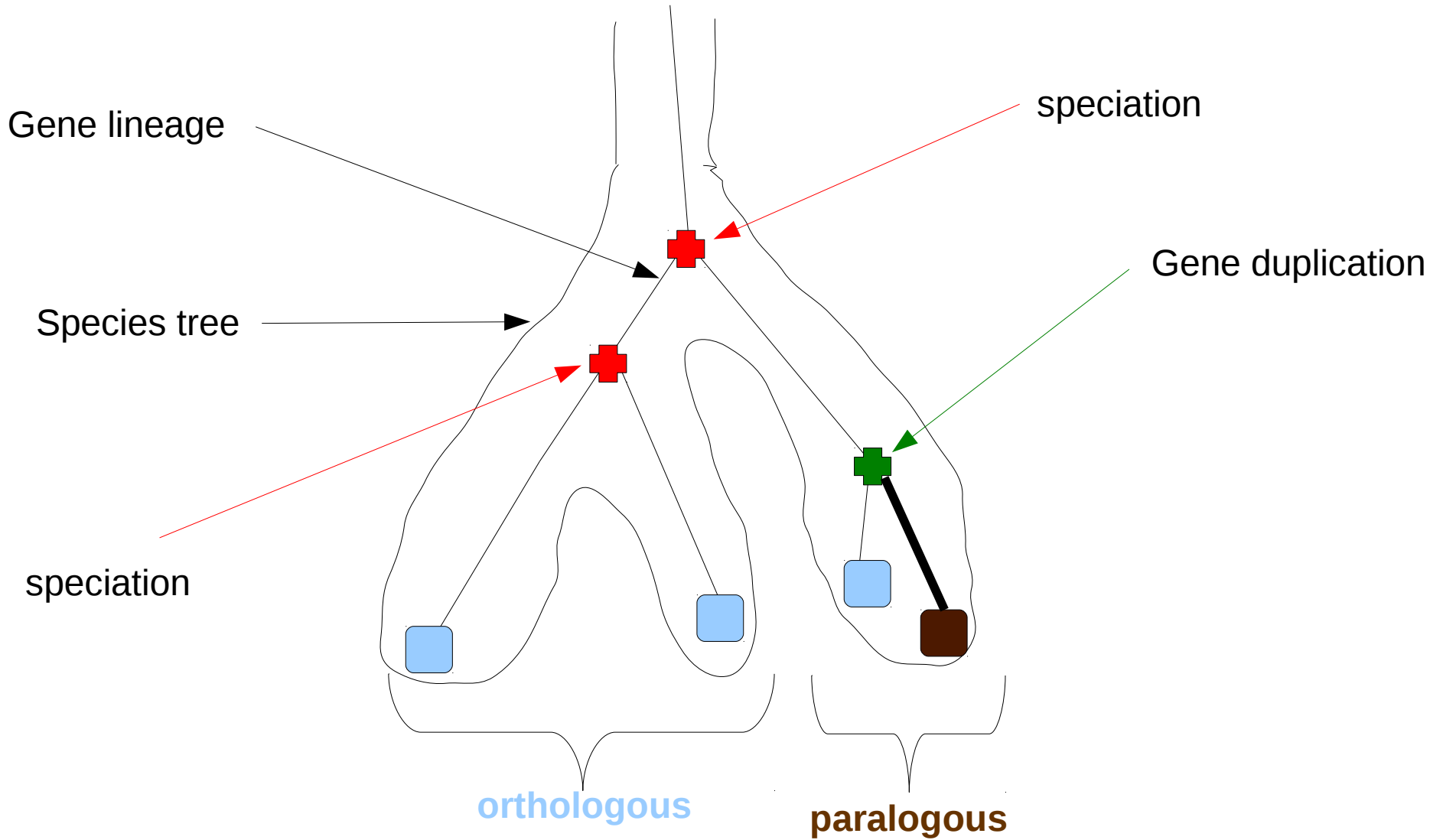
# Orthology



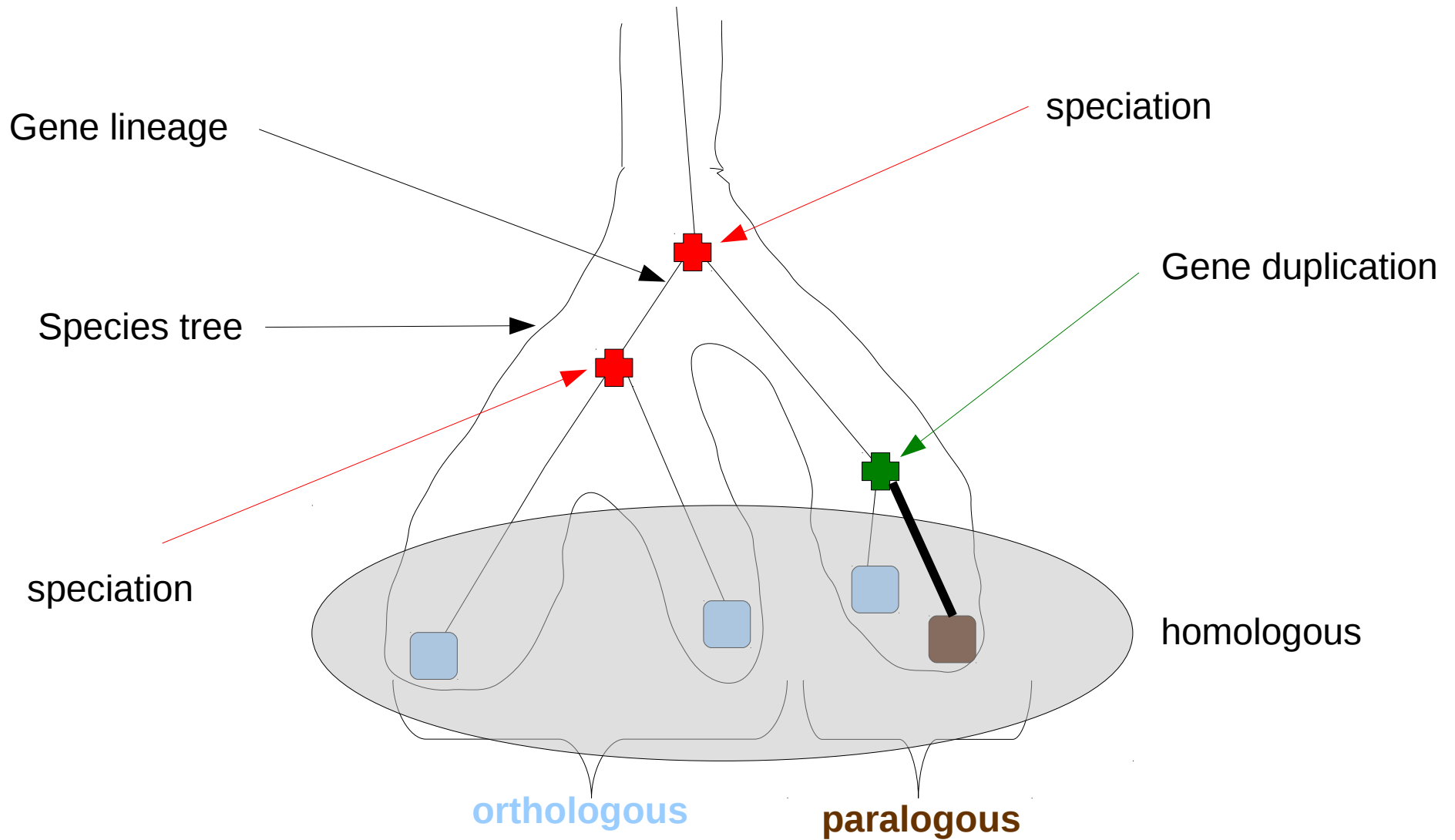
# Orthology



# Orthology



# Orthology

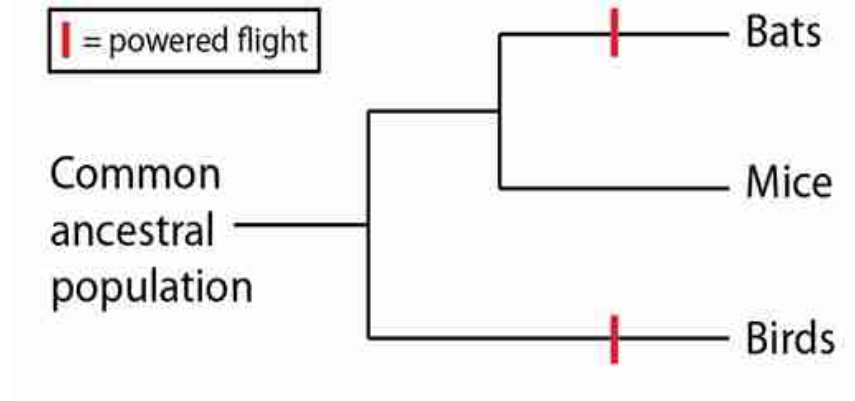
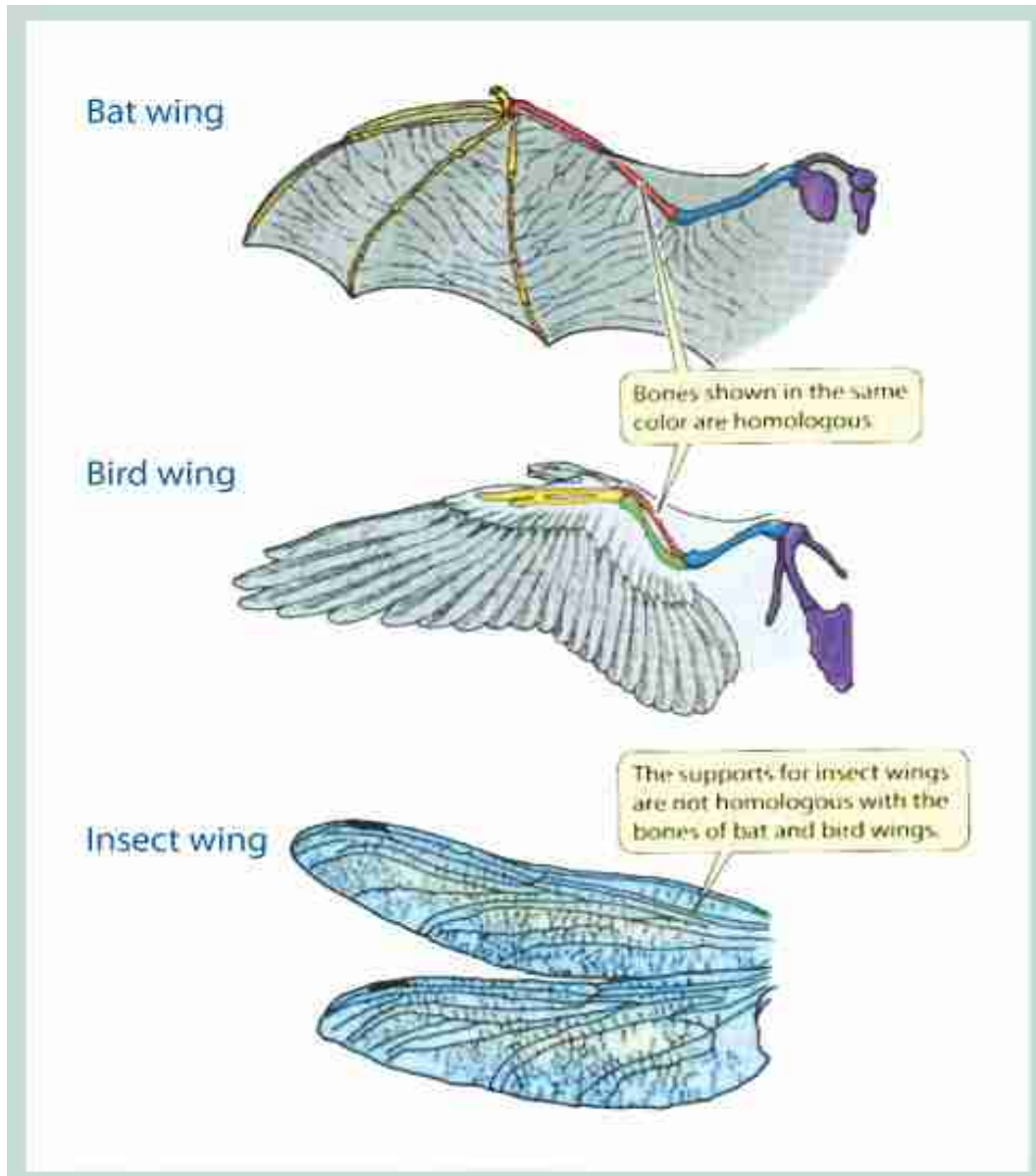


# Homology

- High sequence similarity does not automatically induce homology
  - Same sequence (gene function) can have evolved independently twice → convergent evolution
  - For short sequences: similar by chance



# Convergent Evolution



# Orthology Assignment

- Numerous methods available
- Will not be covered here → difficult problem
- Let's assume that we have a set of  $n$  orthologous sequences  $s_1, \dots, s_n$  and see how we can align them



# Alignment Criteria

- How do we define alignment quality?
- There are different criteria
  - The SP (sum of pairs) measure
  - Real data benchmarks
  - Curated alignments (based on protein structure)
  - Evolutionary measures
  - Simulations

# Alignment Criteria

- How do we define alignment quality?
- There are different criteria
  - **The SP (sum of pairs) measure**
  - Real data benchmarks
  - Curated alignments (based on protein structure)
  - Evolutionary measures
  - Simulations

# The SP measure

- SP: *sum-of-pairs* score
- Score each MSA site and then add up the scores over all sites
  - Penalize mismatches and gaps
  - Favor matches
  - The per-site score is defined as the sum of all pairwise scores between characters of a site

# SP an example

- $SP\text{-score}(l, -, l, V) =$   
 $p(l, -) + p(l, l) + p(l, V) + p(-, l) + p(-, V) + p(l, V)$
- Where  $p()$  is the penalty function and  $p(-, -) := 0$
- Given a MSA with  $n$  sequences and  $m$  sites we can thus compute the overall score as:

```
sp = 0;
```

```
for(i = 0; i < m; i++)
```

```
    sp += SP-score(sites[i]);
```

# An example

s1	A	A	G	A	A	-	A
s2	A	T	-	A	A	T	G
s3	C	T	G	-	G	-	G

Using the the edit distance for  $p()$  the score is:

$$2 + 2 + 2 + 2 + 2 + 2 + 2 = 14$$

Note that, we can also compute this as the sum of pair-wise edit distances between the aligned sequences:

$$e(s1,s2) + e(s1,s3) + e(s2,s3) = 4 + 5 + 5$$

Keep in mind that,  $p(-,-) := 0$

# The $SP$ measure

- Note that, this is only **one way** to quantify the quality of an alignment
- One can build alignment algorithms that optimize the  $SP$  measure
- However, alignments (MSAs) with larger  $SP$  scores may better represent the true evolutionary history of the characters!

# How can we extend pair-wise alignment to triple-wise alignment?

- Any ideas?
- What is the time and space complexity?

# SP-based optimization

- We can extend the dynamic programming approach for pair-wise sequence alignment to  $n$  sequences for calculating an *SP-optimal* MSA
- Assume that all  $n$  sequences have equal length  $m$ 
  - Storing the dynamic programming matrix requires  $O(m^n)$  space
  - And the lower bound for time is also  $O(m^n)$  because all  $m^n$  entries need to be computed → consider an example with  $n := 3$
- As you can imagine, computing the *SP-optimal* MSA is **NP-complete**



# SP-based MSA

- NP-complete
- Not granted that *SP* is the correct (biologically most plausible) criterion!
- Depends on -arbitrary- choice of scoring function  $p()$
- We need heuristics or approximation algorithms!
- We will have a look at some basic approaches now ...

# Star Alignment Approximation

- Pick a center sequence  $s_c$
- Align all remaining sequences to  $s_c$  using a pairwise sequence alignment algorithm
- “Once a gap, always a gap” strategy
  - gaps inserted into  $s_c$  can not be removed again
- $s_c$  can be picked by computing all  $O(n^2)$  [more precisely:  $(n^2 / 2) - n$ ] optimal pair-wise alignments and selecting *the* sequence that has the largest similarity to all other sequences

# Star Alignment

s1: ATTGCCATT

s2: ATGGCCATT

s3: ATCCAATTTT

s4: ATCTTCTT

s5: ACTGACC

# Star Alignment

s1: ATTGCCATT ← center sequence

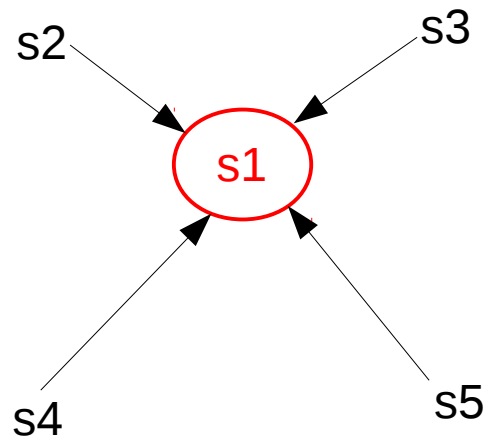
s2: ATGGCCATT

s3: ATCCAATTTT

s4: ATCTTCTT

s5: ACTGACC

# Star Alignment



# Star Alignment

s1: ATTGCCATT

s2: ATGGCCATT

s1: ATTGCCATT - -

s3: ATC-CAATTTT

s1: ATTGCCATT

s4: ATCTTC-TT

s1: ATTGCCATT

s5: ACTGACC - -

# Star Alignment

s1: ATTGCCATT

s2: ATGGCCATT

s1: ATTGCCATT--

← Gaps inserted

s3: ATC-CAATTTT

s1: ATTGCCATT--

← "Once a gap, always a gap"

s4: ATCTTC-TT--

s1: ATTGCCATT--

s5: ACTGACC----

# The Star Alignment

s1: **ATTGCCATT** - -

s2: ATGGCCATT - -

s3: ATC - CAATTTT

s4: ATCTTC - TT - -

s5: ACTGACC - - - -



# Another Example

s1: ATTGCCATT

s2: ATGGCCATT

s3: ATCCAATTTT

s4: ATCTTCTT

s5: ATTGCCGATT

# Another Example

s1: ATTGCCATT

s2: ATGGCCATT

s1: ATTGCCATT - -

s3: AT - CCAATTTT

s1: ATTGCCATT

s4: ATCTTC - TT

s1: ATTGCC - ATT

s5: ATTGCCGATT

# Another Example

s1: ATTGCCATT

s2: ATGGCCATT

s1: ATTGCCATT

s2: ATGGCCATT

s1: ATTGCCATT - -

s3: AT - CCAATTTT

s1: ATTGCCATT

s4: ATCTTC - TT

s1: ATTGCC - ATT

s5: ATTGCCGATT

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s1: ATTGCCATT

s2: ATGGCCATT

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s3: AT - CCAATTTT

s1: ATTGCCATT

s4: ATCTTC - TT

s1: ATTGCC - ATT

s5: ATTGCCGATT

s1: ATTGCCATT

s2: ATGGCCATT

s1: ATTGCCATT - -

s2: ATGGCCATT - -

s3: AT - CCAATTTT

# Another Example

s1: ATTGCCATT

s2: ATGGCCATT

s1: ATTGCCATT - -

s3: AT - CCAATTTT

s1: ATTGCCATT

s4: ATCTTC - TT

s1: ATTGCC - ATT

s5: ATTGCCGATT

s1: ATTGCCATT

s2: ATGGCCATT

s1: ATTGCCATT - -

s2: ATGGCCATT - -

s3: AT - CCAATTTT

s1: ATTGCCATT - -

s2: ATGGCCATT - -

s3: AT - CCAATTTT

s4: ATCTTC - TT - -

# Another Example

s1: ATTGCCATT

s2: ATGGCCATT

s1: ATTGCCATT - -

s3: AT - CCAATTTT

s1: ATTGCCATT

s4: ATCTTC - TT

s1: ATTGCC - ATT

s5: ATTGCCGATT

s1: ATTGCCATT

s2: ATGGCCATT

s1: ATTGCCATT - -

s2: ATGGCCATT - -

s3: AT - CCAATTTT

s1: ATTGCCATT - -

S2: ATGGCCATT - -

S3: AT - CCAATTTT

s4: ATCTTC - TT - -

s1: ATTGCC - ATT - -

S2: ATGGCC - ATT - -

S3: AT - CCA - ATTTT

s4: ATCTTC - - TT - -

s5: ATTGCCGATT - -

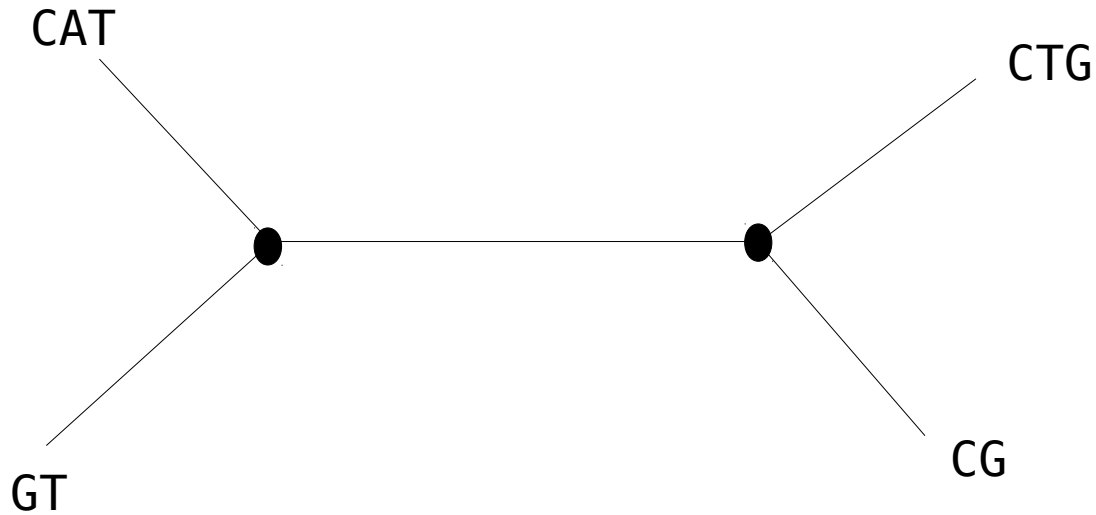
Shift right!

# Star Alignment Approximation

- Produces an MSA whose SP score is  $< 2 * optimum$
- Proof omitted
- Reference: D. Gusfield “Efficient methods for multiple sequence alignment with guaranteed error bounds”, *Bulletin of Mathematical Biology*, 1993.

# Tree Alignment

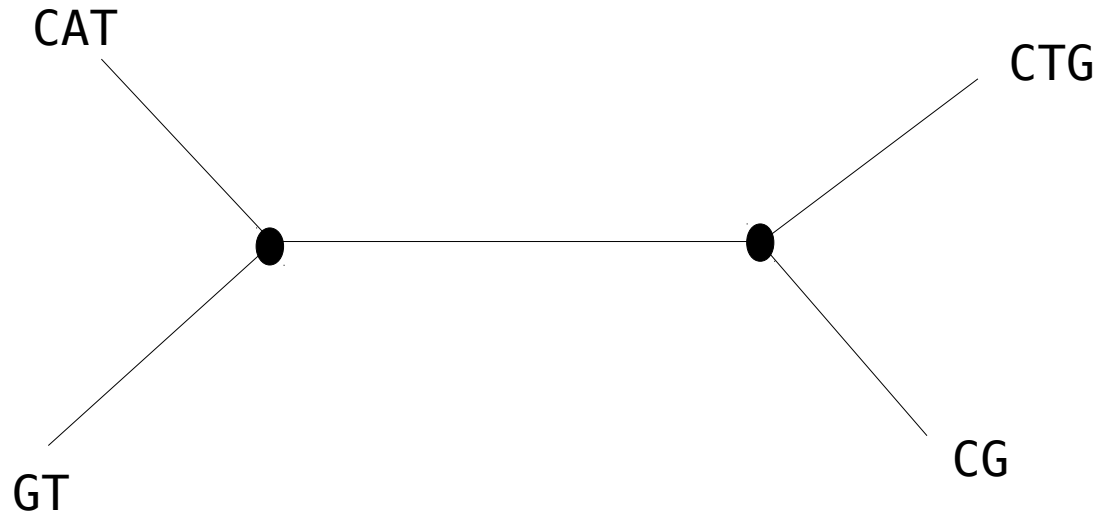
- If an evolutionary tree for the sequences is available





# Tree Alignment

- Find an assignment of sequences to the inner nodes such that the sum over the similarity scores on all branches is maximized

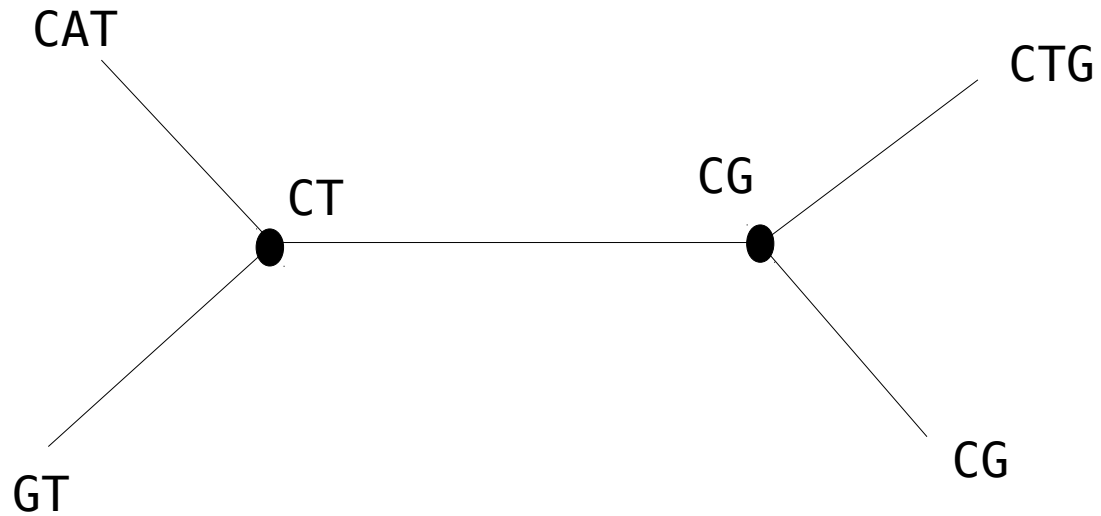


# Tree Alignment

$p(a,b) := 1$  if  $a = b$

$p(a,b) := 0$  if  $a \neq b$

$p(a,-) := -1$

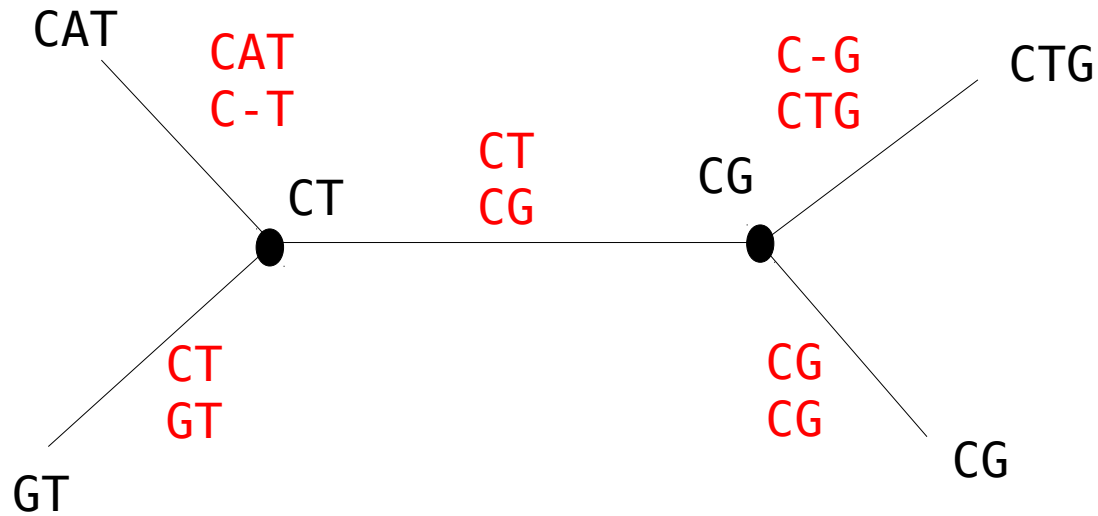


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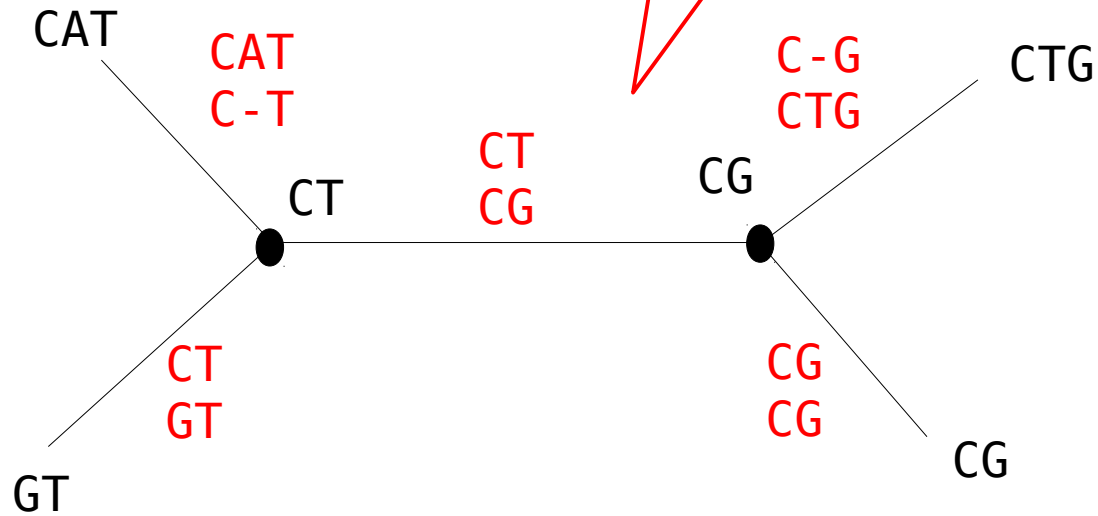


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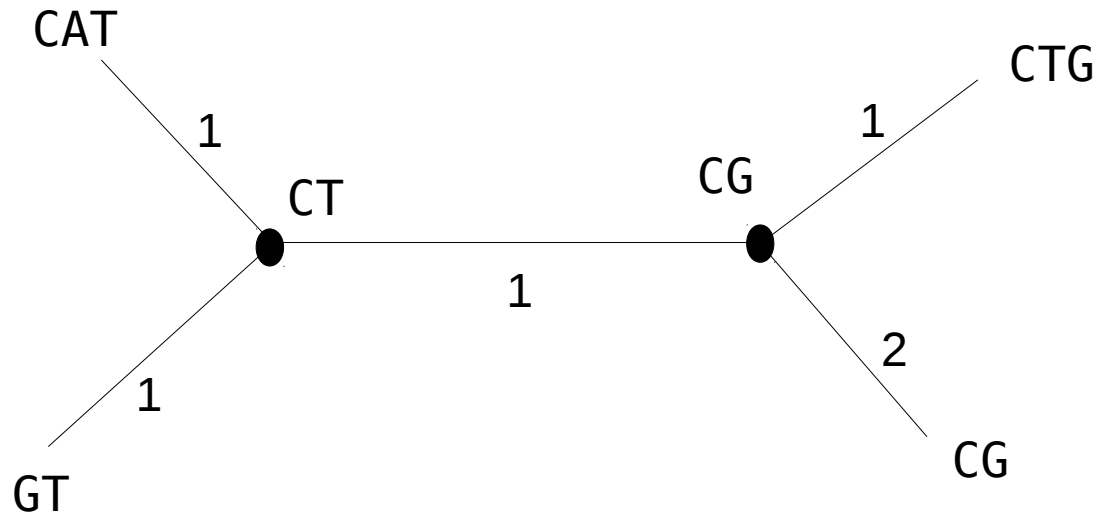
What is the score of this tree?

# Tree Alignment

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$p(a,-) := -1$

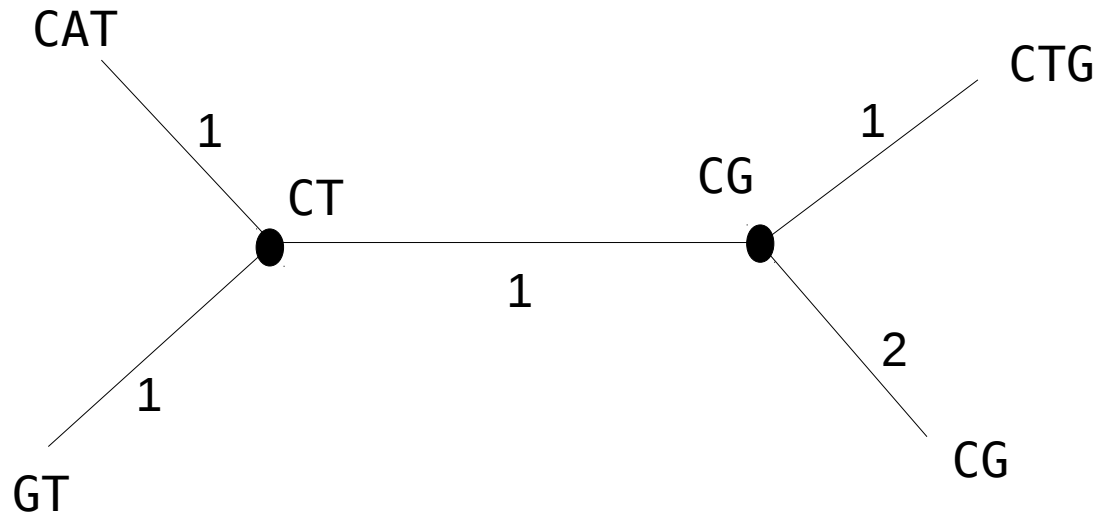


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$p(a,-) := -1$



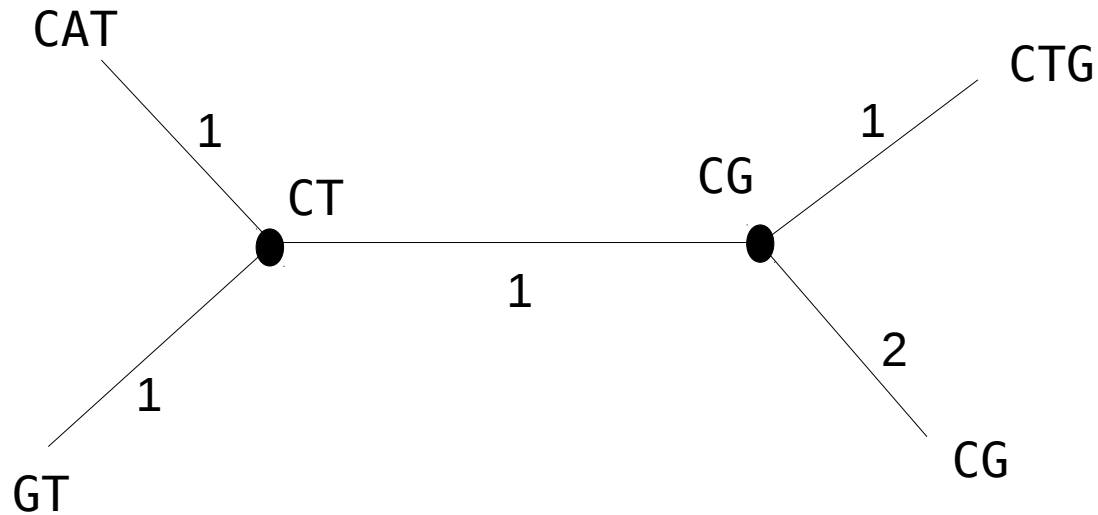
Overall score: 6 → maximize this score

# Tree Alignment

$p(a,b) := 1$  if  $a = b$

$p(a,b) := 0$  if  $a \neq b$

$p(a,-) := -1$



Overall score: 6 → maximize this score

This problem is NP-hard because we don't have the ancestral states

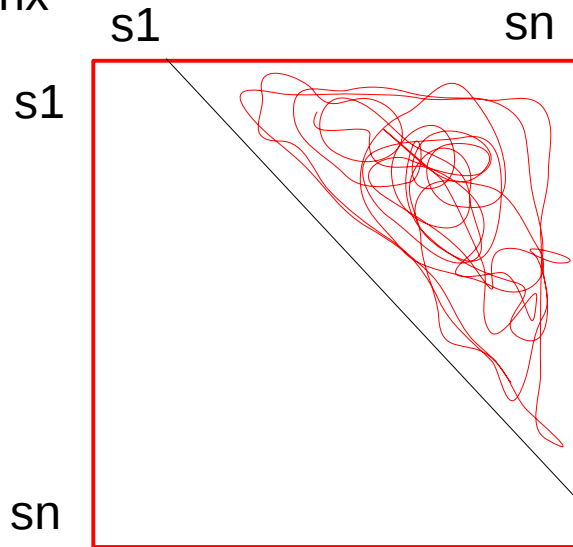
# Tree-Based Alignment

- Hen and egg problem
  - we need a MSA to build a tree
  - we need a tree to compute a MSA
  - if the alignment is wrong, the tree might be wrong
  - if the tree is wrong, the MSA might be wrong
- One idea
  - simultaneous inference of tree & alignment
  - very hard problem: trying to solve two generally NP-hard or NP-complete problems simultaneously



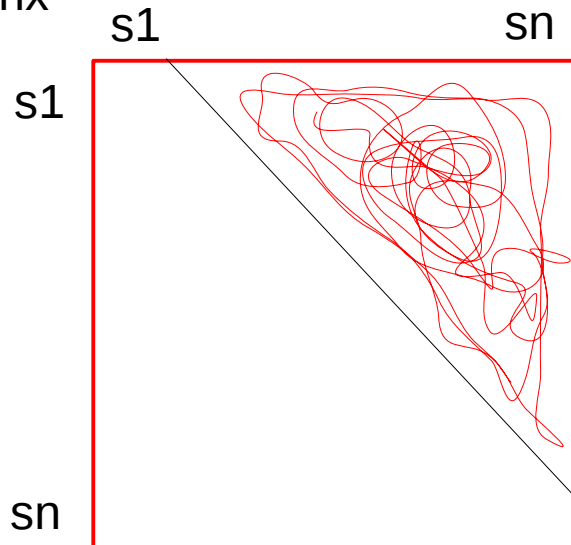
# Practical approaches

Build a pair-wise  
distance matrix



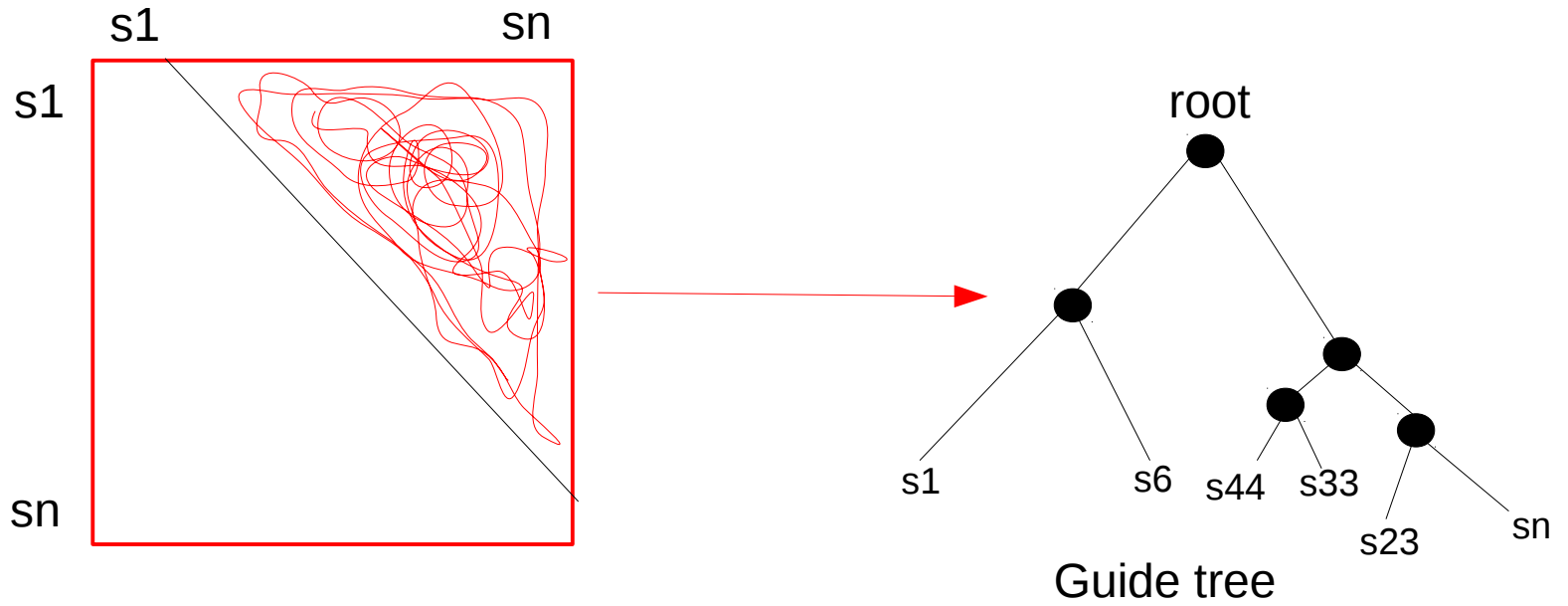
# Practical approaches

Build a pair-wise distance matrix

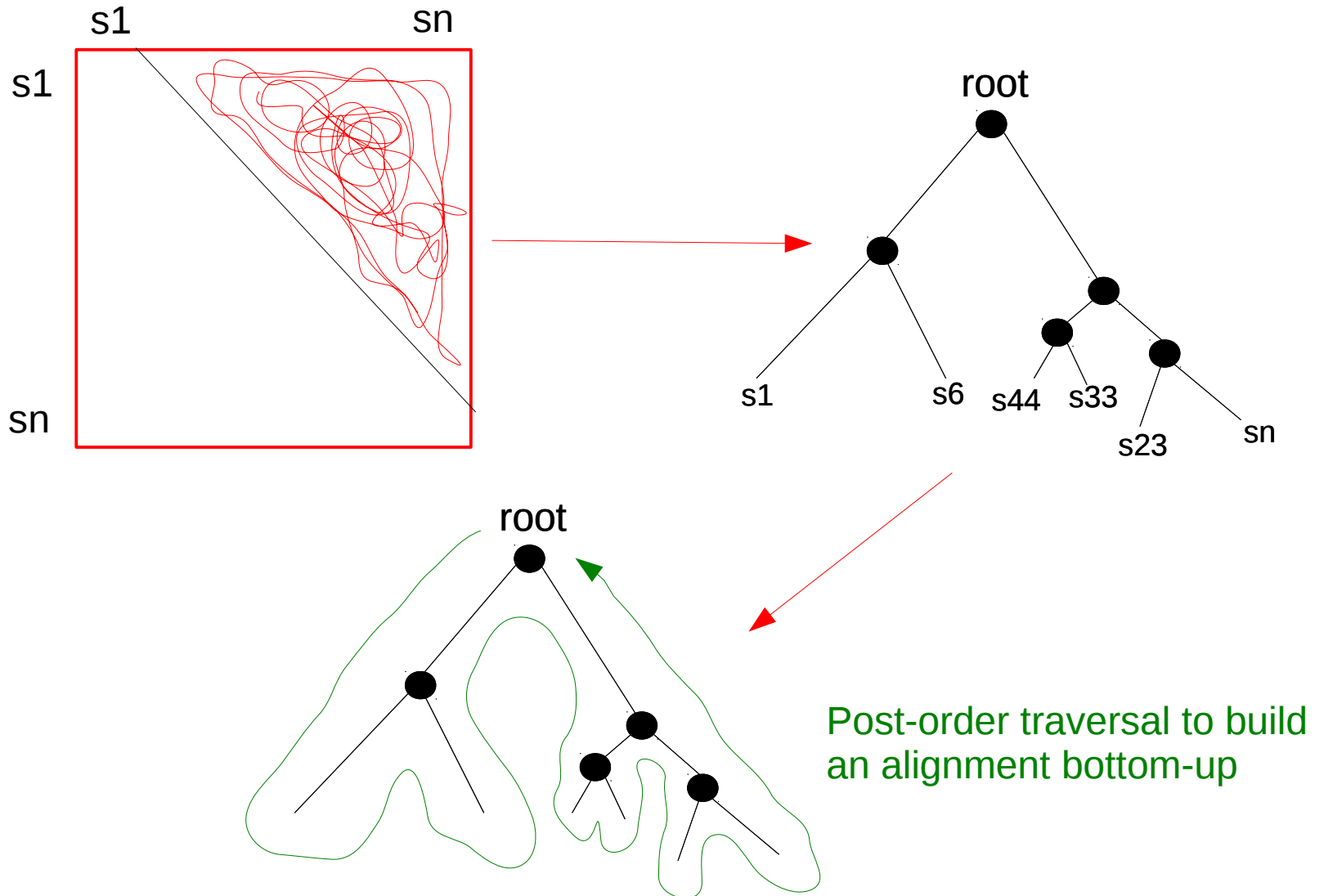


Computation of pair-wise distance matrix  
Using pair-wise alignment scores can be time and memory-intensive due to  $O(n^2)$  complexity  
One may use approximate distance methods based on *k-mers*  
(remember last lecture!)

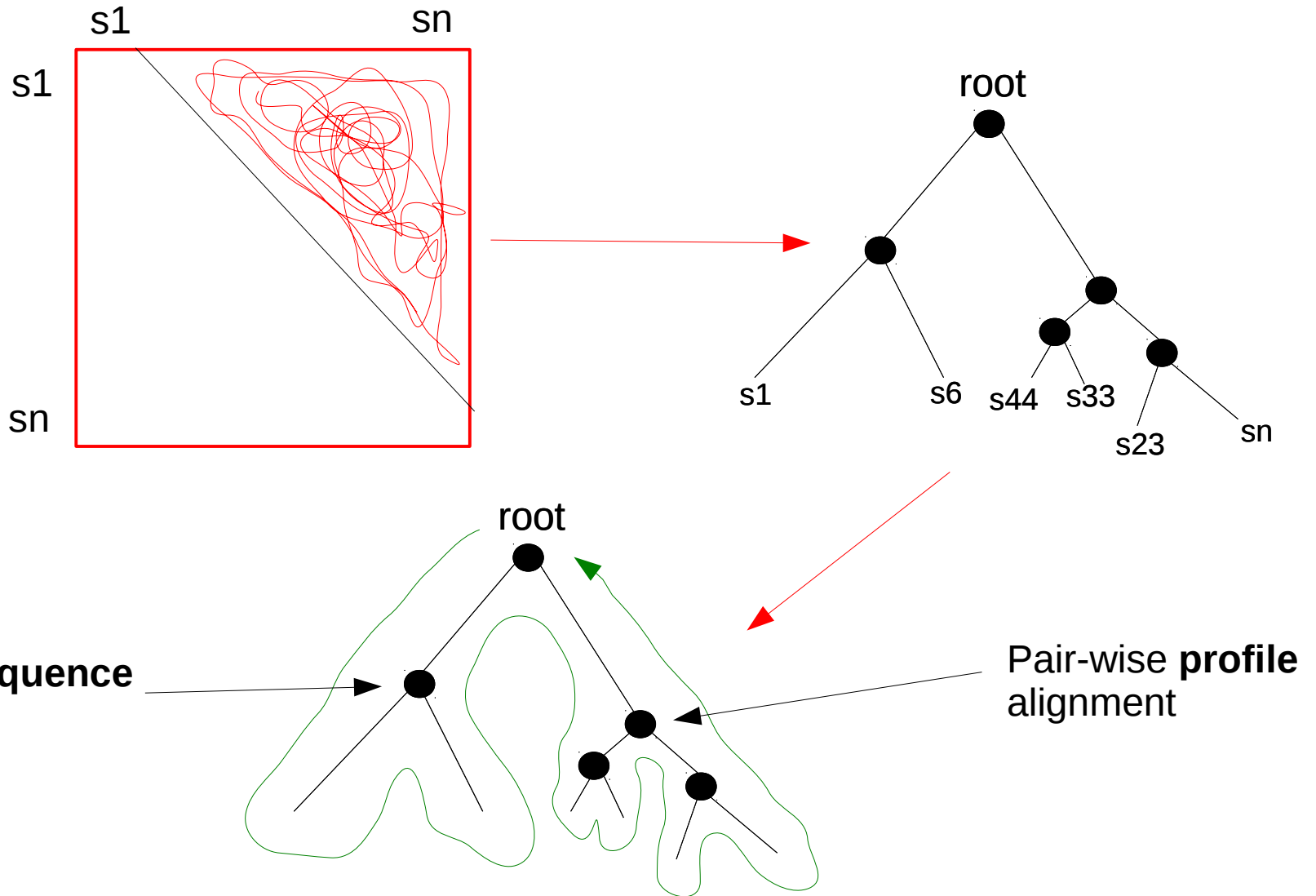
# Practical approaches



# Practical approaches



# Practical approaches



# Practical Approaches

- Guide-tree approach
- Compute all  $(n^2/2)-n$  pair-wise distances (alignments) between the  $n$  sequences
- Use these distances for hierarchical clustering
  - e.g. with the neighbor joining algorithm → we will see this later-on for tree building
- Use the distance-based tree to calculate pair-wise
  - Sequence-sequence
  - Sequence-profile
  - Profile-profile

... alignments bottom up toward the root via a post-order tree traversal
- Many widely-used MSA programs rely on this idea: e.g., **Clustal** family of tools, **T-COFFEE**

# Progressive MSA



AC



ATG



TCG



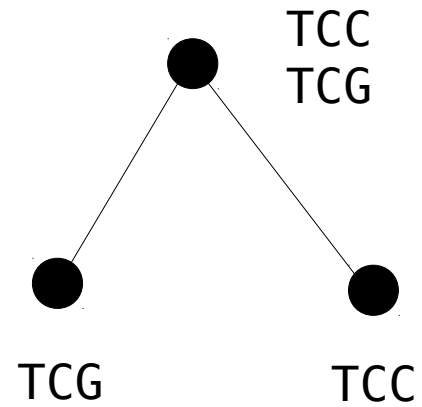
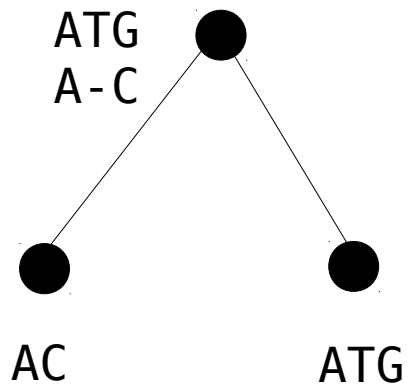
TCC

# Progressive MSA

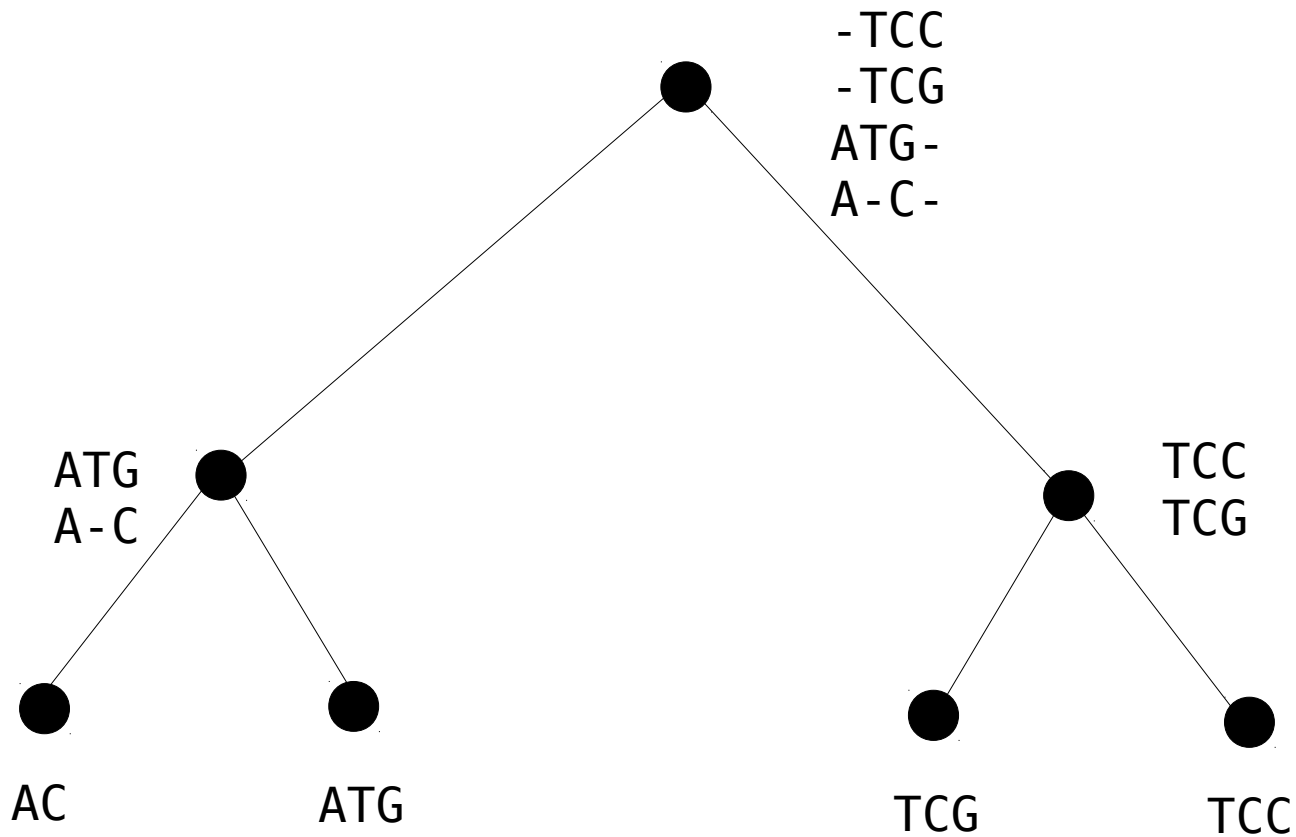




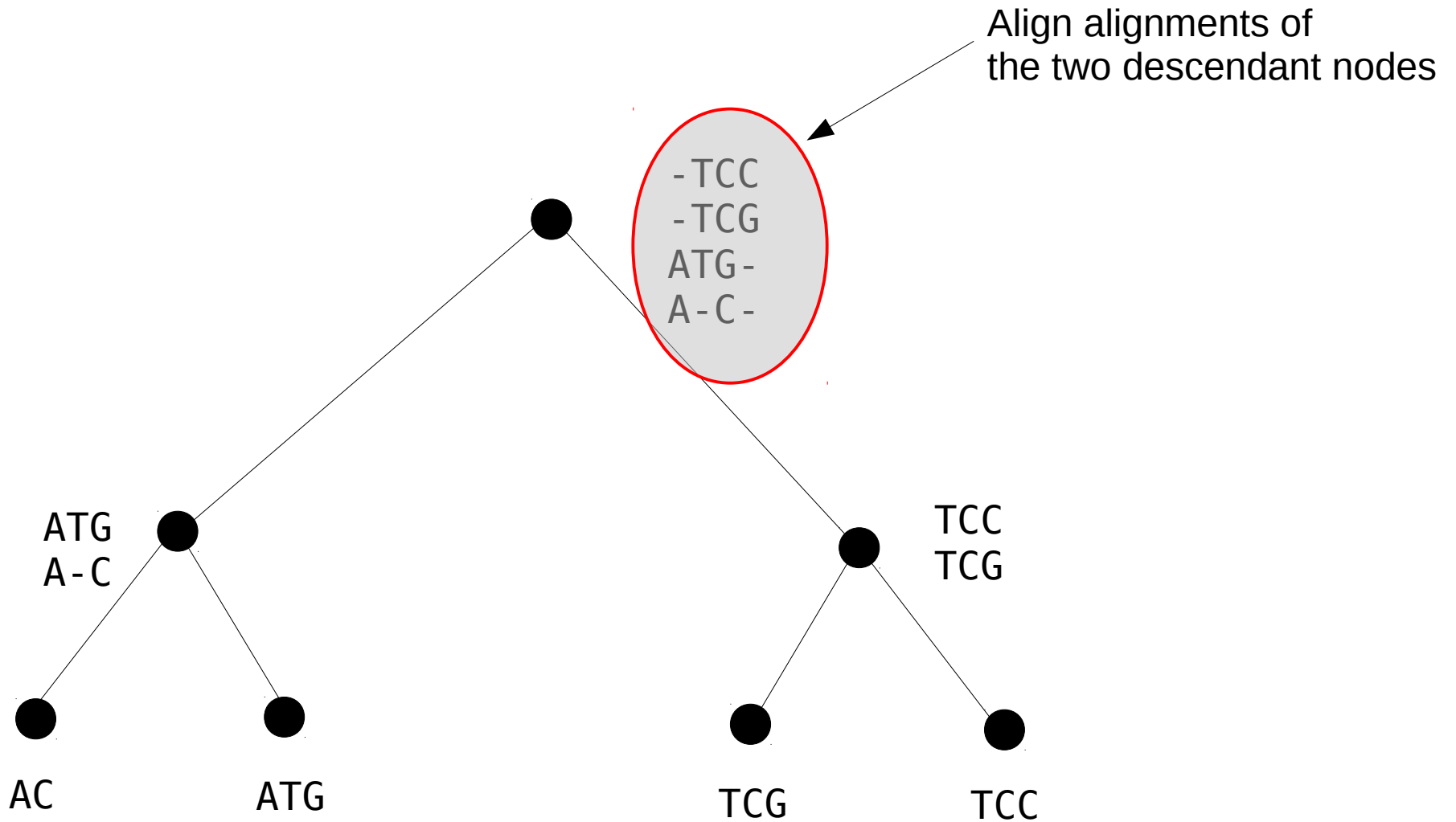
# Progressive MSA



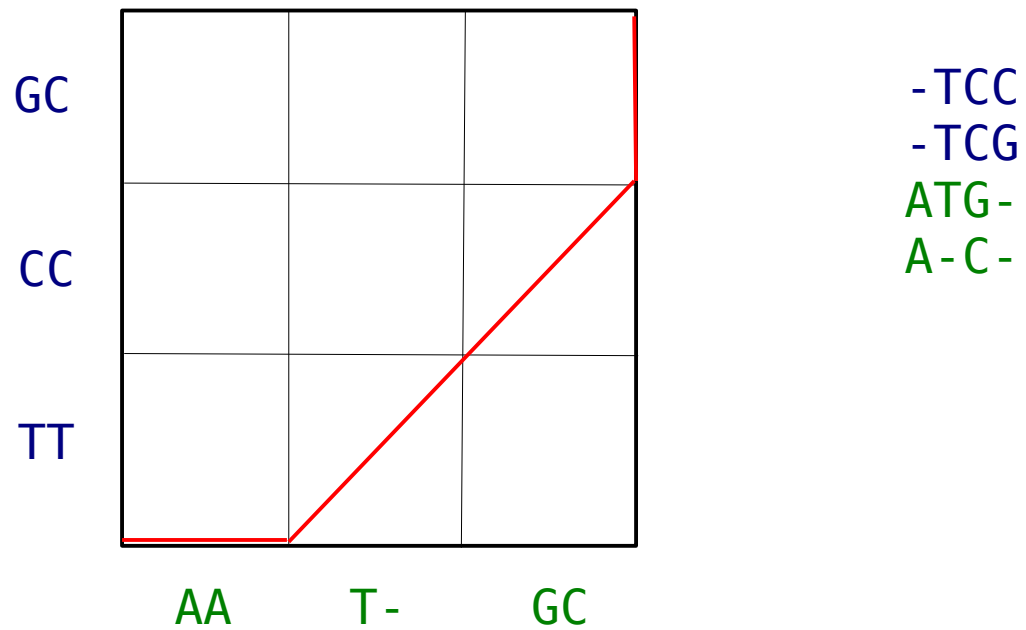
# Progressive MSA



# Progressive MSA

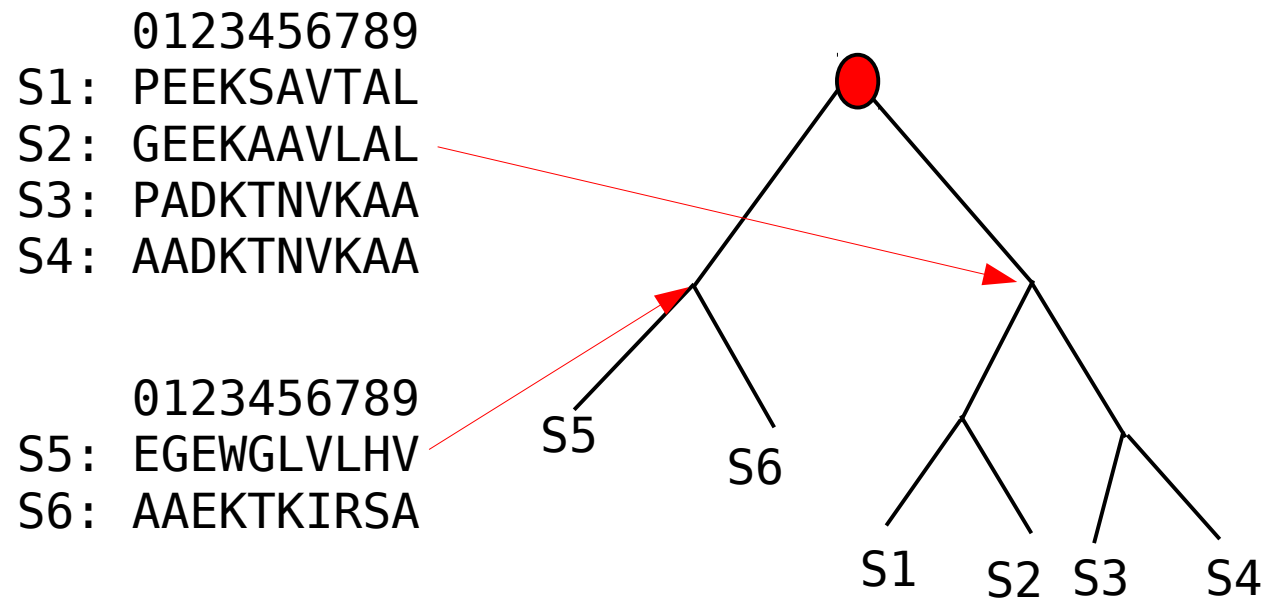


# Profile Alignment



# Profile Alignment

- Generalization of pair-wise sequence alignment to pair-wise profile alignment
- Average over all possibilities

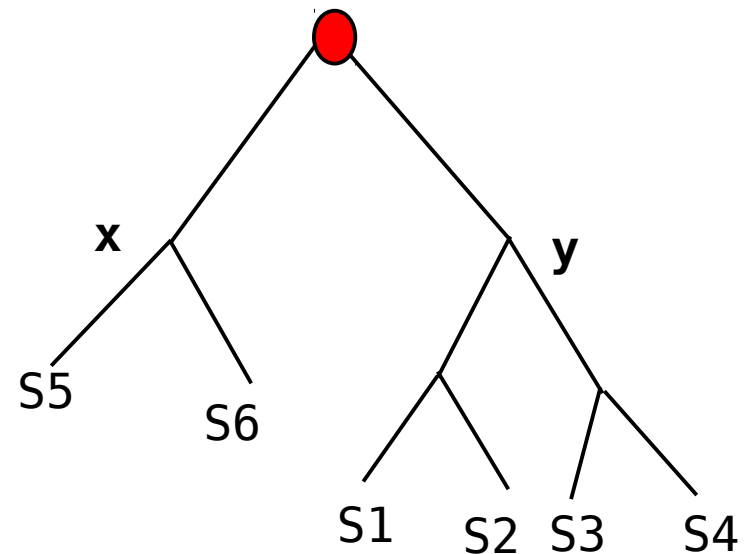


# Profile Alignment

- Generalization of pair-wise sequence alignment to pair-wise profile alignment
- Average over all possibilities

0123456789  
S1: PEEKSAVTAL  
S2: GEEKA AVLAL  
S3: PADKTNVKAA  
S4: AADKTNVKAA

0123456789  
S5: EGEWGLVLHV  
S6: AAEKTKIRSA



Compute score between position 6 of **x** and position 7 of **y**

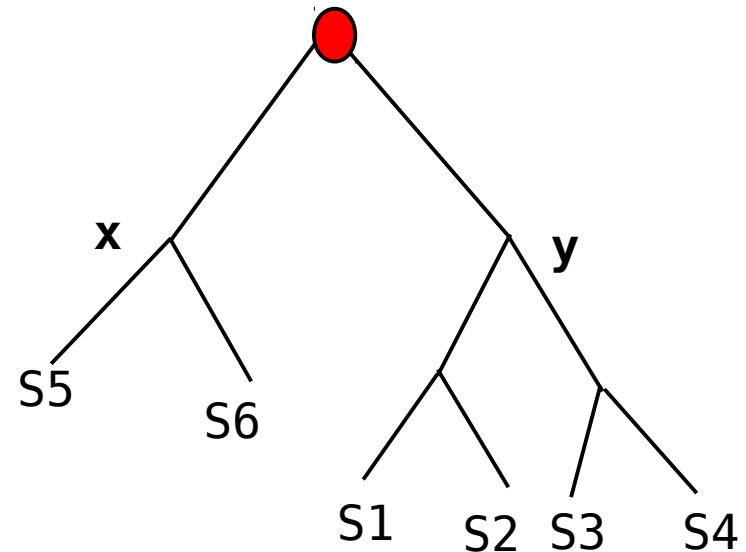
# Profile Alignment

- Generalization of pair-wise sequence alignment to pair-wise profile alignment
- Average over all possibilities

	0	1	2	3	4	5	6	7	8	9
S1:	P	E	E	K	S	A	V	T	A	L
S2:	G	E	E	K	A	A	V	L	A	L
S3:	P	A	D	K	T	N	V	K	A	A
S4:	A	A	D	K	T	N	V	K	A	A

	0	1	2	3	4	5	6	7	8	9
S5:	E	G	E	W	G	L	V	L	H	V
S6:	A	A	E	K	T	K	I	R	S	A



Weighted average over all 8 (2 \* 4) possibilities:

Score:  $1/8 * [p(T,V) + p(T,I) + p(L, V) + p(L, I) + p(K,V) + p(K,I) + p(K,V) + p(K,I)]$

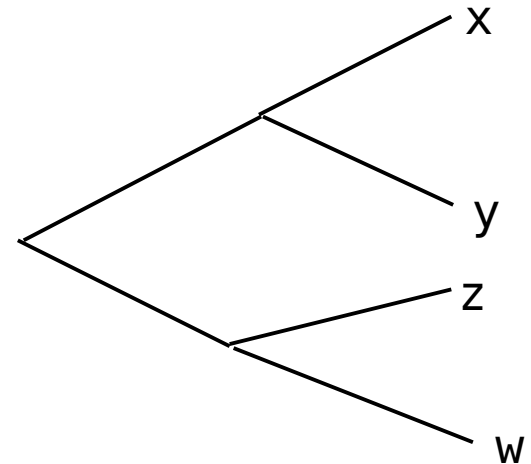
# Problems with progressive MSA

- Initial pair-wise alignments are “frozen”
- Can't be corrected when new evidence emerges

x: GAAGTT  
y: GAC-**TT** → frozen by initial alignment

z: GAA**CTG**  
w: GTA**CTG** } y: GA-**CTT**

should be flipped

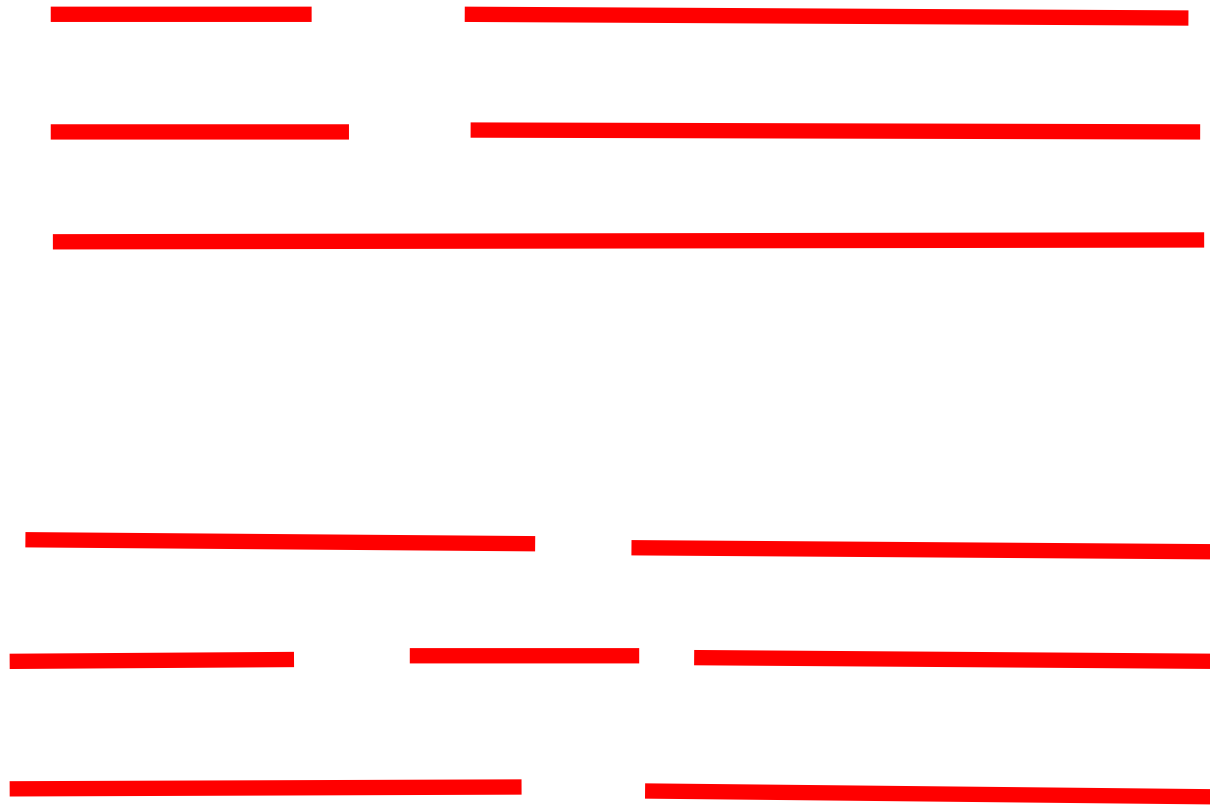
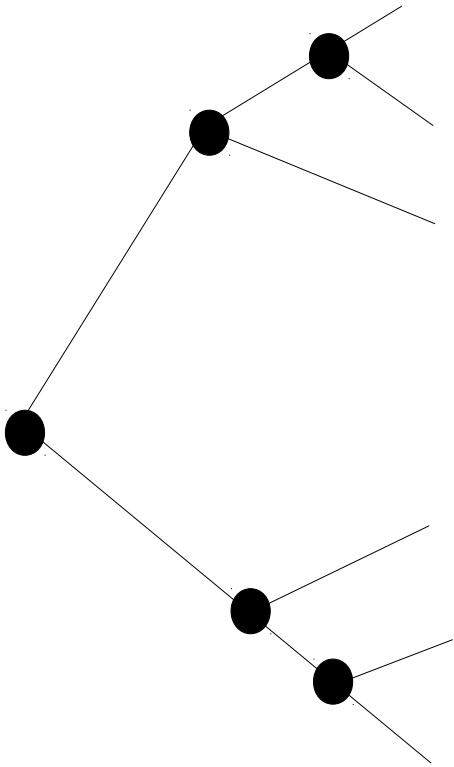




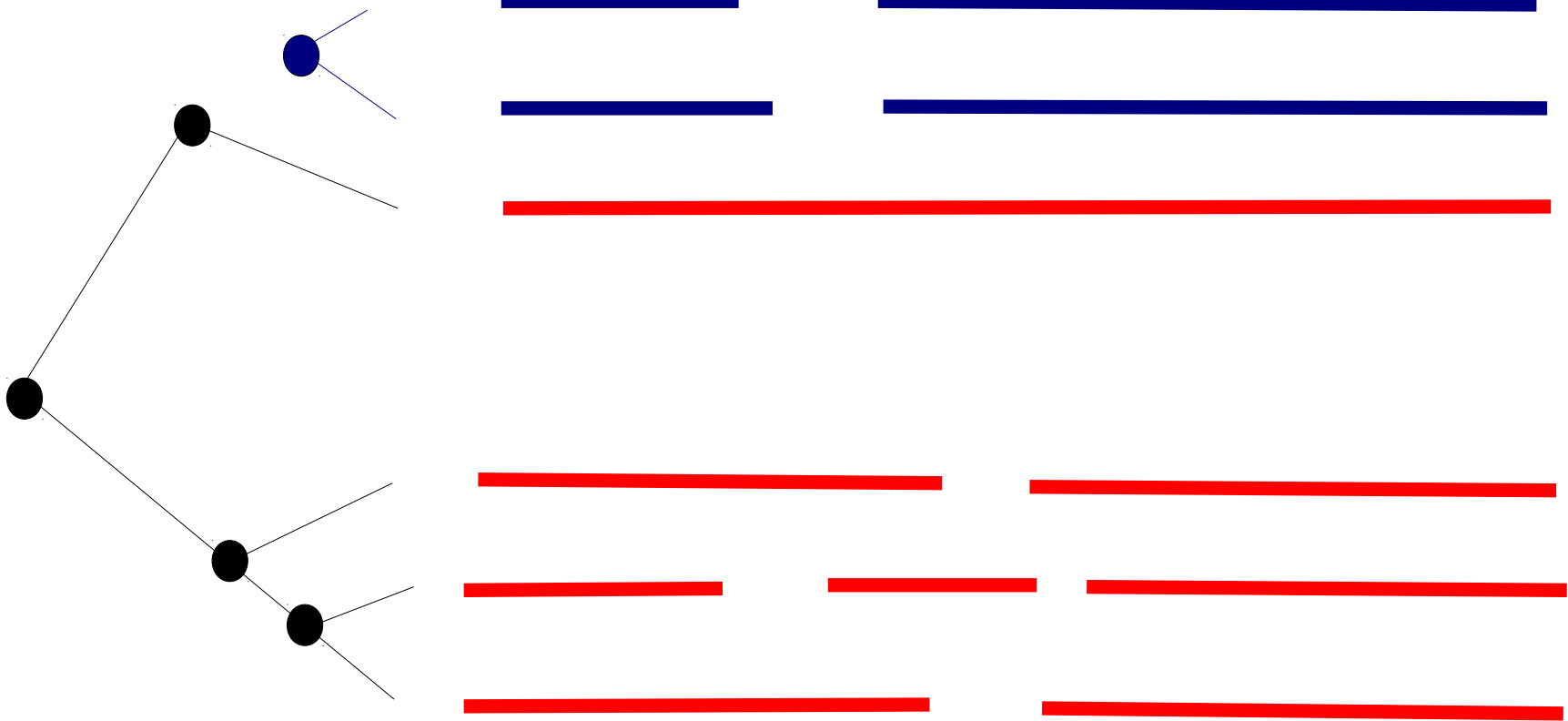
# Iterative Progressive MSA

- e.g. MUSCLE, PRRP, MAFFT
- Execute progressive MSA several times to refine the alignment

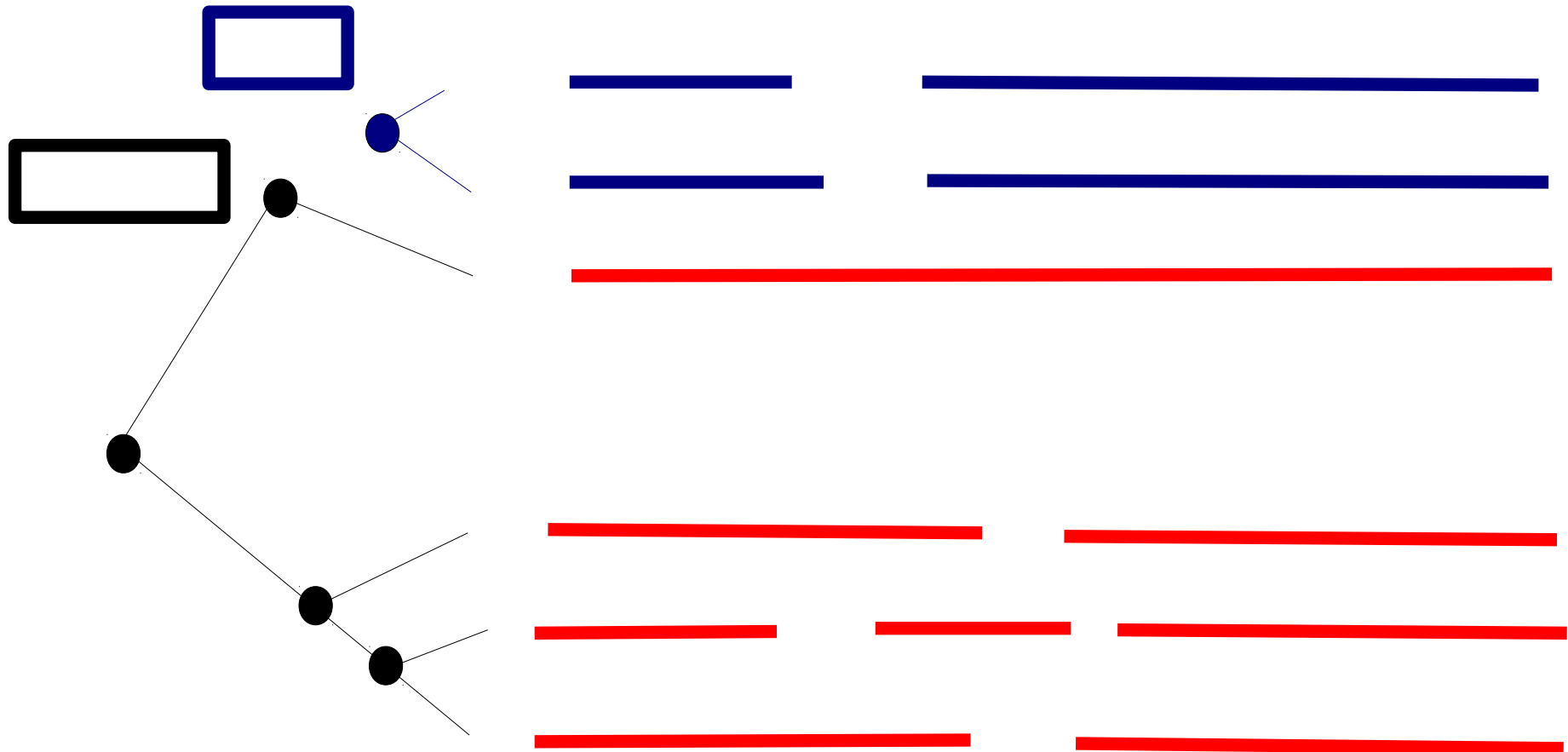
# MUSCLE Re-Finement



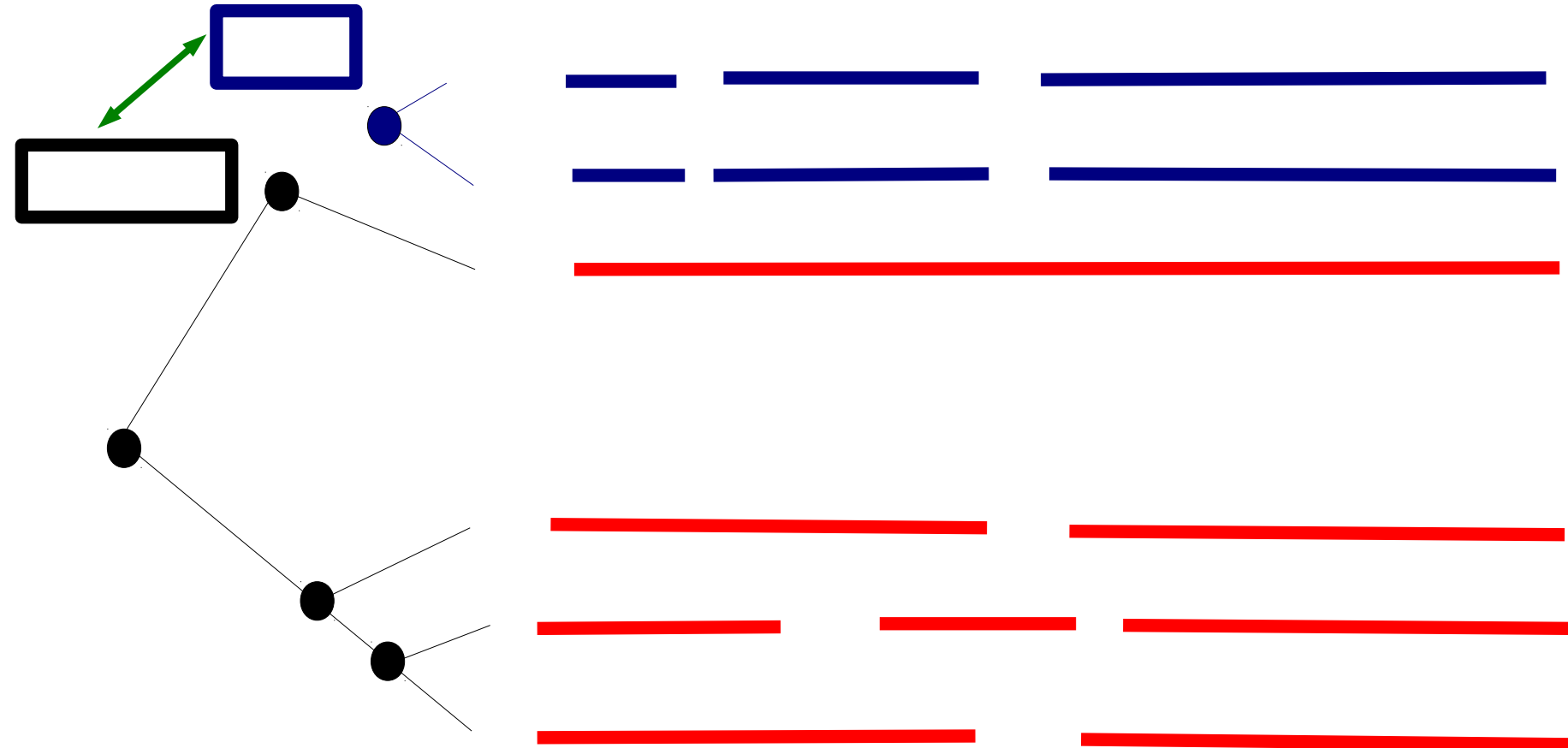
# MUSCLE Re-Finement



# MUSCLE Re-Finement



# MUSCLE Re-Finement



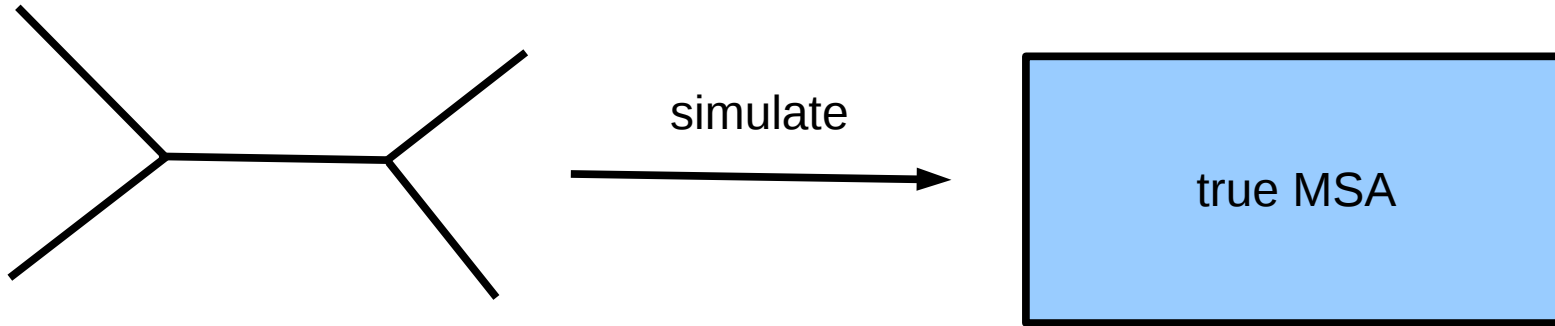
# Motif-based approaches

- Find a small motif (substring) common to all sequences
- Called: anchor, block, region, q-gram *etc*
- If motif is found → shift sequences such that the motifs are “in alignment”
- Then, align regions around these motifs using for instance progressive alignment

# Benchmarking MSAs

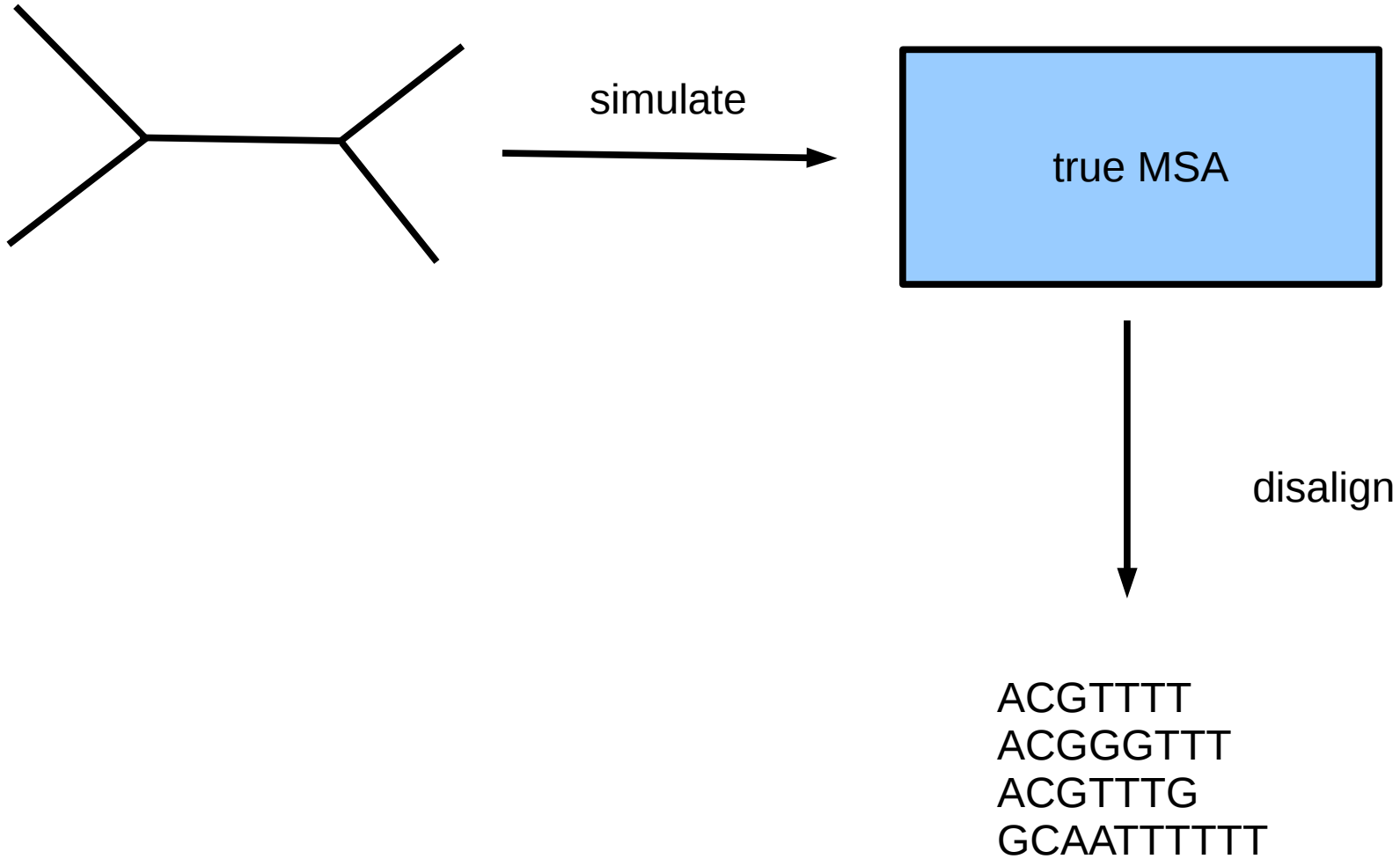
- MSA benchmarks → mostly structural protein data that has been manually aligned to reflect the protein structure
  - Databases: BALiBASE 2.0, OXBench, PREFAB, etc
- Simulation
  - focus on alignment
  - focus on phylogeny

# Simulation

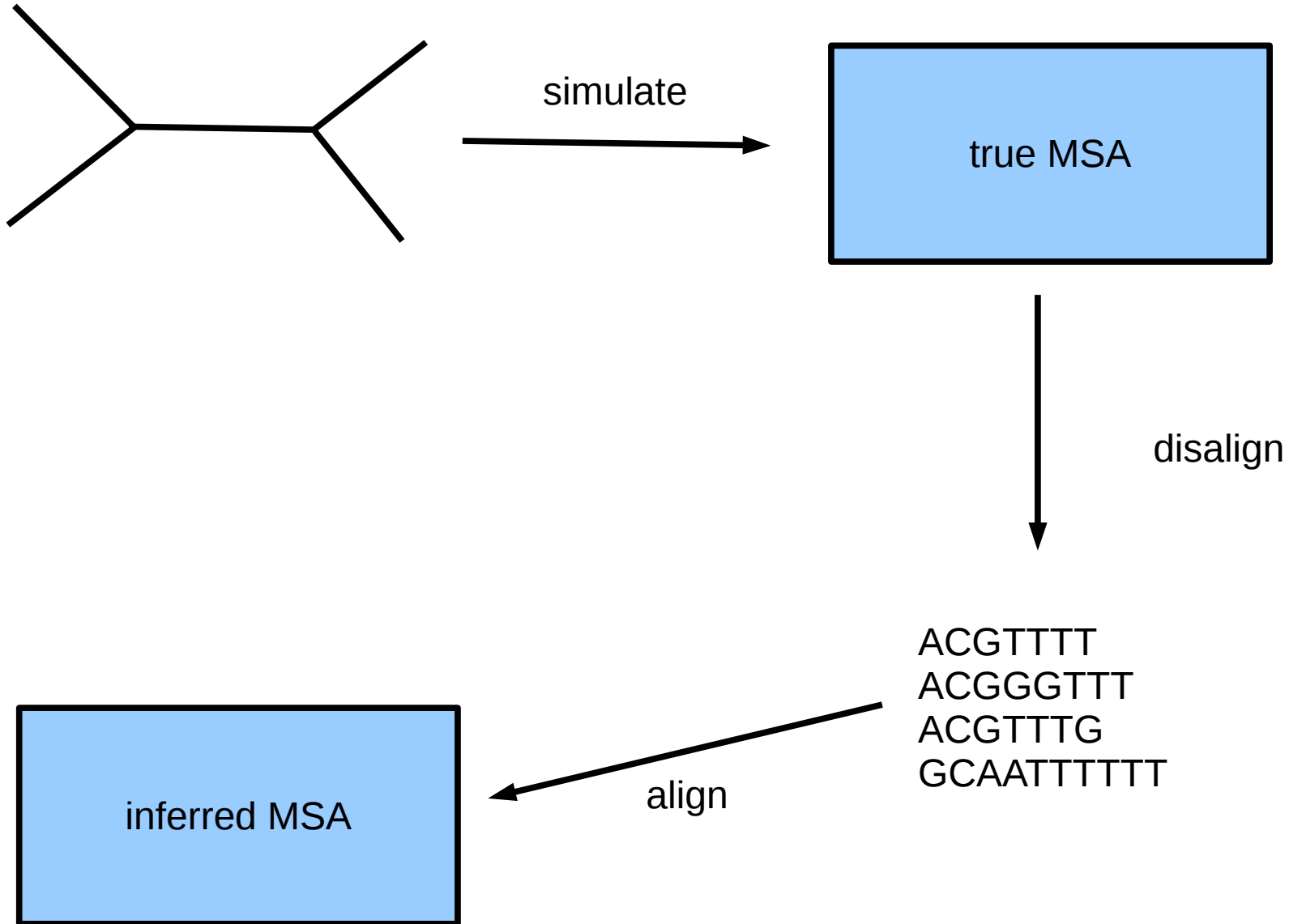




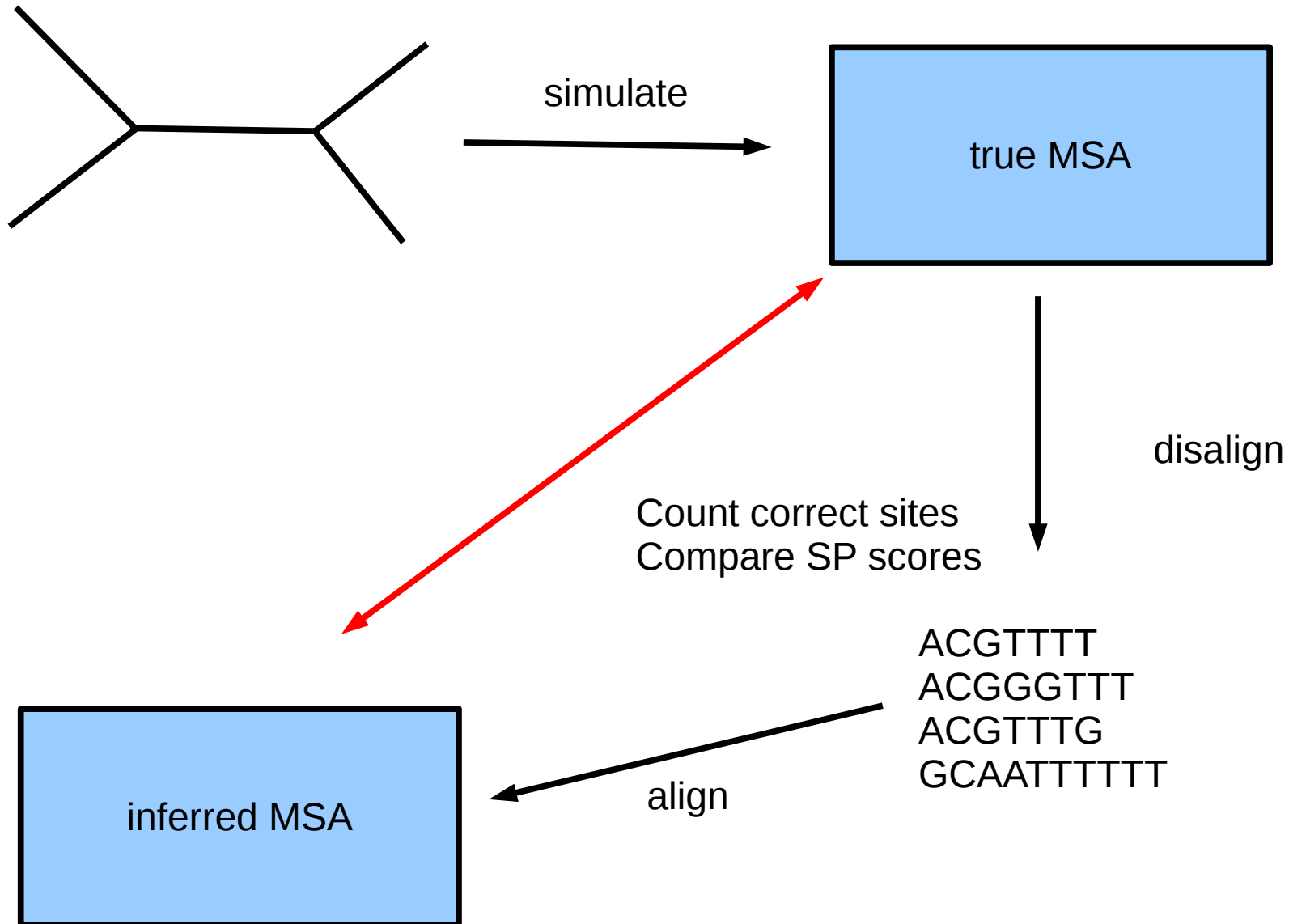
# Simulation



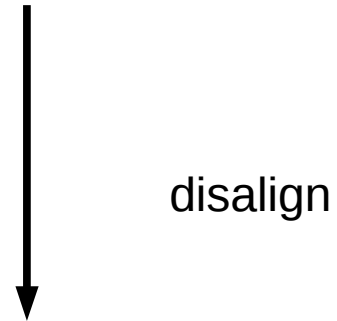
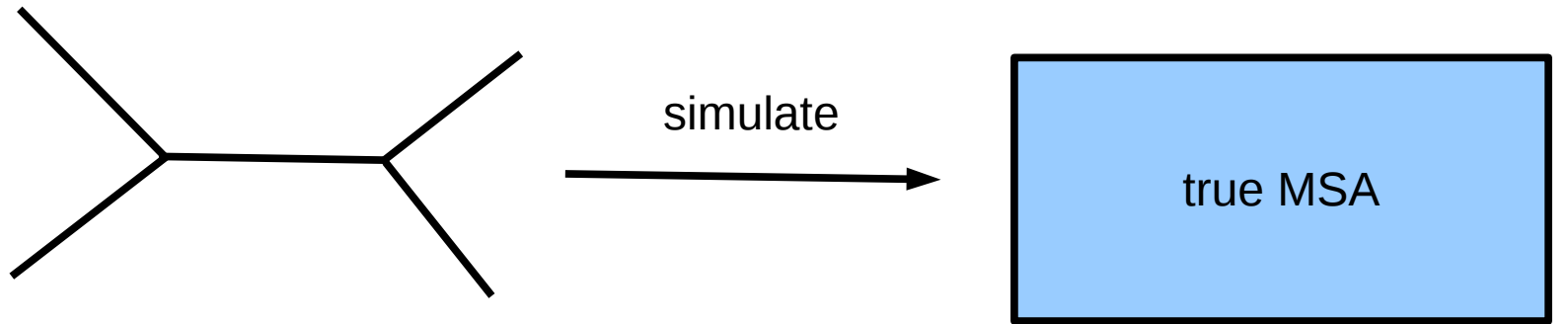
# Simulation



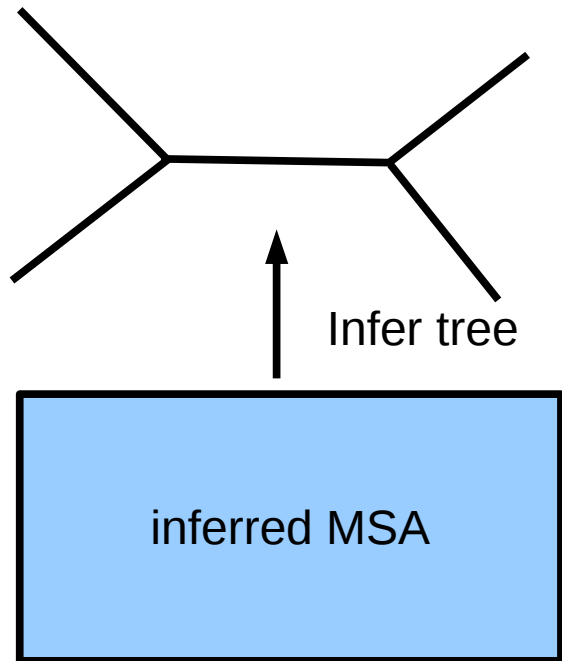
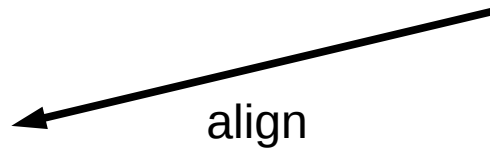
# Simulation



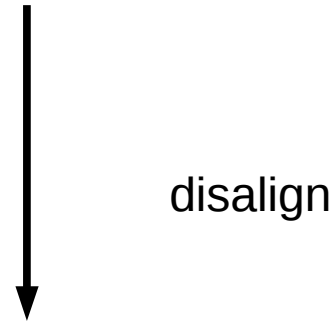
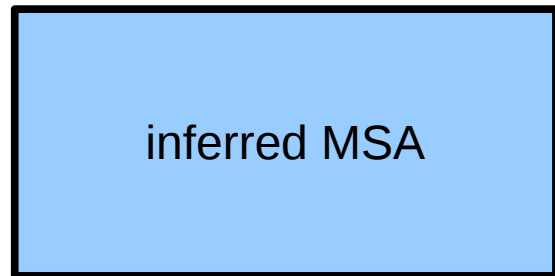
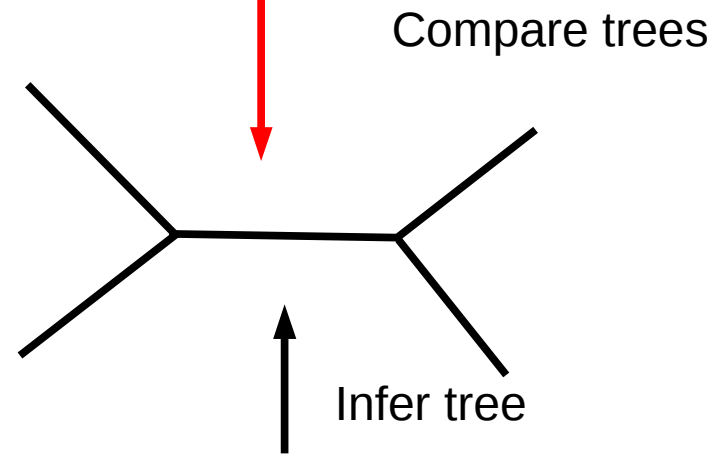
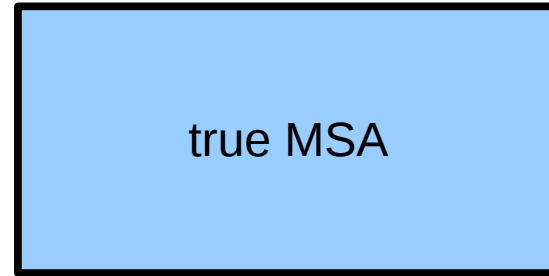
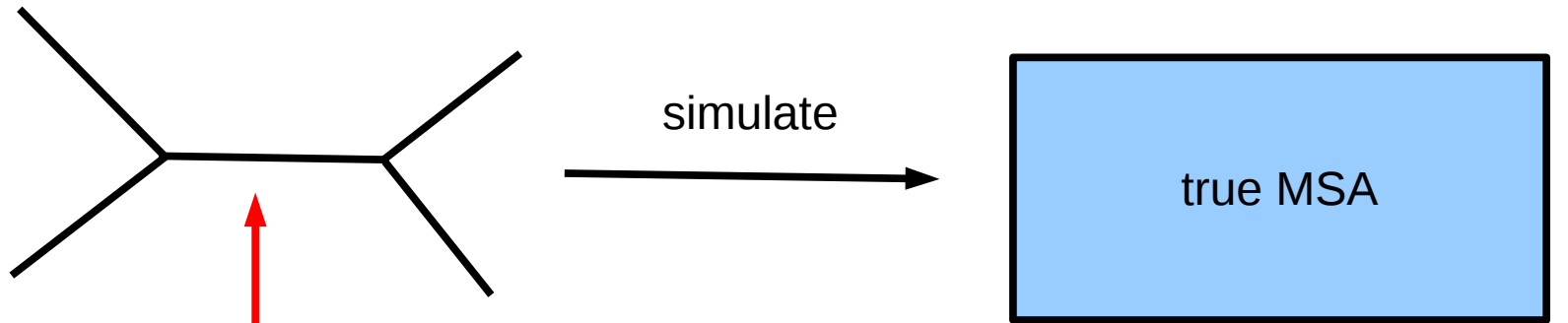
# Simulation



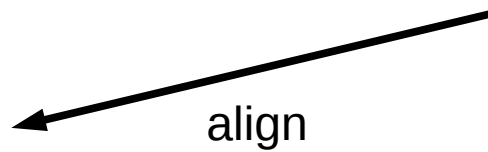
```
ACGTTTT  
ACGGGTTT  
ACGTTTG  
GCAATTTTTT
```



# Simulation



```
ACGTTTT  
ACGGGTTT  
ACGTTTG  
GCAATTTTTT
```



# Summary

- MSA is generally difficult due to lack of objective criteria
- MSA as defined per SP score is NP-complete
- Tree-alignment MSA is also NP-complete
- There exist heuristics with performance guarantees
- However, practical approaches use ad hoc heuristics that typically perform better
- Classes of algorithms
  - Progressive MSA
  - Progressive iterative MSA
  - Motif-based approaches
  - Statistical MSA (not covered)
  - Phylogeny-aware MSA (not covered)
  - Simultaneous MSA & tree inference (not covered)