



University
of Glasgow

Sequence alignments

Martha Luka

**WORLD
CHANGING
GLASGOW**

**A WORLD
TOP 100
UNIVERSITY**



Alignment

- Sequence alignment is a way of arranging the sequences to identify regions of similarity
 - May be a consequence of functional, structural, or evolutionary relationships between the sequences
- Sequence alignments can be pairwise:
 - only between two sequences
 - BLAST, DIAMOND
- Or multiple sequence alignments:
 - between more than one homologous sequences
 - **MAFFT**, Clustal, MUSCLE, T-Coffee, Kalign
 - **(this is what we're going to focus on here)**



Alignment

- We can try to see how sequences compare to each other:

A	T	C	G	A	T	C	G	
A	T	C	G	A	T	G	G	
A	T	C	G	A	T	C	C	G

A	T	C	G	A	T	C	-	G
A	T	C	G	A	T	G	-	G
A	T	C	G	A	T	C	C	G

- It can be more accurate to do this by eye, as algorithms can make mistakes!
 - **BUT** this quickly becomes very difficult with lots of long sequences
- Instead, we use algorithms and then check by eye to make sure it looks sensible!



Alignment

- Building a tree first requires an alignment
- Need to be able to see the unbroken history of each nucleotide to determine changes over time and relatedness of sequences
 - This can be an issue when indels have occurred
- Need an algorithm to determine the least costly alignment

SpA	ATGCAGGTA
SPB	ATGCTGCTA
SpC	ATGCAGCTC
SpD	TAGCAGGAC



Phylogenetic Analysis Steps

- 1) Collect homologous sequences
- 2) Conduct multiple alignment
- 3) Fit an appropriate substitution model
- 4) Estimate tree(s) under that model
- 5) Test the reliability of the estimated tree(s)
- 6) Interpret and apply the phylogenetic tree
- 7) Potentially repeat steps 4-6 using different tree building methods and/or additional data



Phylogenetic Analysis Steps

- 1) Collect homologous sequences
- 2) Conduct multiple alignment
- 3) Fit an appropriate substitution model
- 4) Estimate tree(s) under that model
- 5) Test the reliability of the estimated tree(s)
- 6) Interpret and apply the phylogenetic tree
- 7) Potentially repeat steps 4-6 using different tree building methods and/or additional data



University
of Glasgow

On to phylogenetics!

#UofGWorldChangers



@UofGlasgow

@ThatKatC