CFG - Practical session 2

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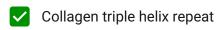
Trimming questions

By looking at the initial part of the alignment (alignment positions 70 to 163), you will see that there is a conserved region shared between some sequences.

Based on the InterProScan results, can you identify which matches (domain, repeat...) corresponds to this region?

Hint: To check the position of the aligned amino acid in the unaligned protein sequence look at the information displayed at the bottom left of the JalView software.

- [ ] None of them

- [ ] Non cytoplasmatic domain

- [x] Collagen triple helix repeat

How many sites have been trimmed in relation to the original alignment?

674

What could be the benefit from having trimmed a fraction of the alignment? Are there any potential drawbacks associated with this process?

☐ By trimming the alignment, there will be less informative sites, and this will always increase the computational time needed by the phylogenetic inference software to compute a phylogeny

☑ By trimming the alignment, we may have removed informative signal

☑ In general, we can expect alignment trimming to reduce computational time of the phylogenetic inference

☐ Trimming the alignment will always improve the accuracy of the phylogenetic inference

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