

ProCKSI - Support #112

MaxCMO

06/25/2018 08:42 PM - Anonymous

Status:	New	Estimated time:	0.00 hour
Priority:	Normal		
Assignee:			
Category:			
Target version:			
Resolution:			
Description			
<p>Hi I recently ran an ProCKSI experiment and have been slowly digesting the results.</p> <p>I came across a result in MaxCMO that is difficult to understand.</p> <p>I'm comparing a family of proteins with a similar fold. One particular pdb 5ue8 chain A and B were compared using MaxCMO. This is the same protein and structure just a different chain. MaxCMO does not align these proteins correctly and states there is 5% sequence identity between these proteins. 5ue8 A and B are identical proteins with several residues in one chain not represented in the other chain.</p> <p>Is this a flaw in how MaxCMO aligns 5ue8-A against 5ue8-B?</p> <p>I would very much appreciate your advice on how i should interpret these results.</p> <p>here is the link to the page " http://www.procksi.net/data/5580955b2e2df751d1f90557e8e84d11/MaxCMO/0_1/0_1.al "</p> <p>Could you also extend the time limit on the expiration of these results as it is taking me a long time to fully understand the results .</p> <p>Declan</p>			

History

#1 - 06/25/2018 09:54 PM - Paweł Widera

The methods used by ProCKSI compare protein structures, not sequences. Max-CMO in particular, maximises the number of overlaps between **contacts** (with default settings: pairs of C-alpha atoms not farther from each other than 0.75nm). The alignment is structural, not sequence-driven. This is why you should look at the **overlap value** or **number of alignments** in the results, rather than the sequence identity. This is what the distance matrices in the Results Manager show:

http://www.procksi.net/data/5580955b2e2df751d1f90557e8e84d11/MaxCMO/results_MaxCMO.html

You can download all the results to your computer before the experiment expires. We are unable to store it long term, sorry.