Oral: BQ4CY010 Programmation 3 et projet tuteuré



ClustalLite : Alignement multiple heuristique par la méthode Clustal

Stéphanie Gnanalingam

M2 Bio-informatique parcours biologie informatique

Développement

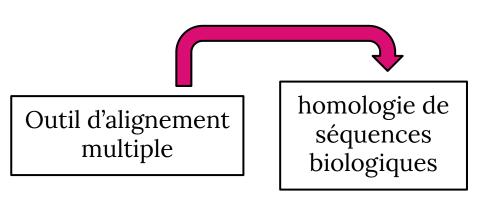
https://github.com/gnanalin/ClustalLite/tree/main

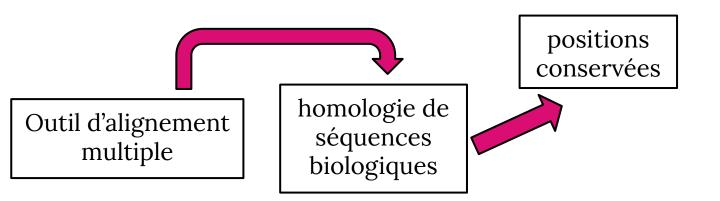
• CONDA (v.24.7.1)

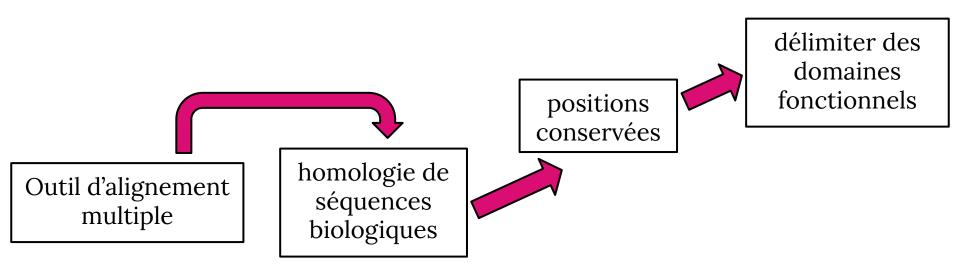


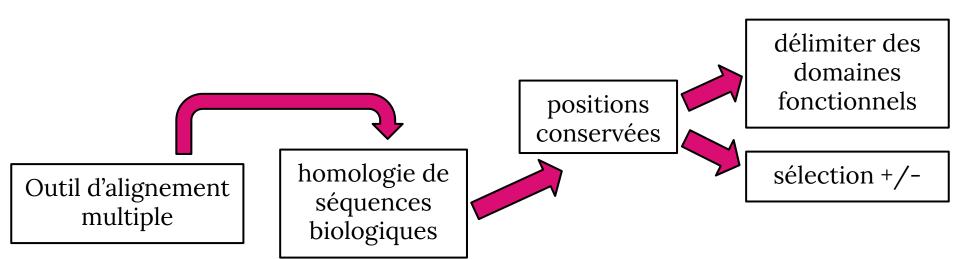
env_clustallite

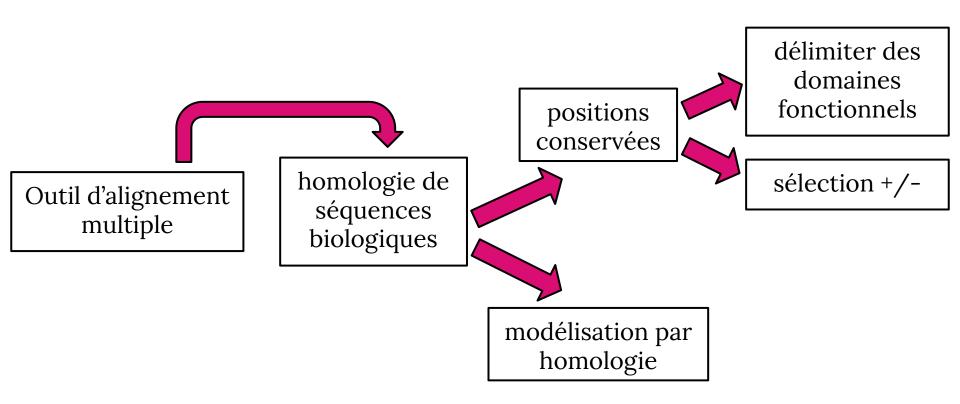
Outil d'alignement multiple







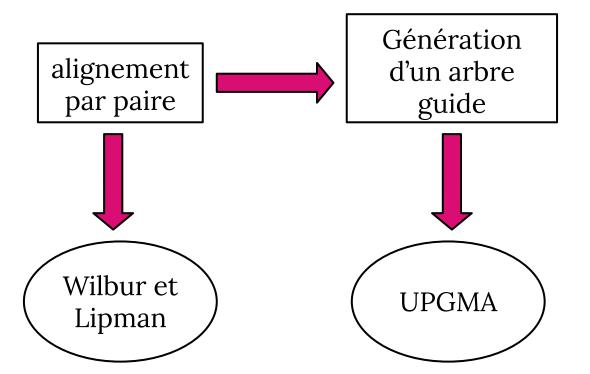




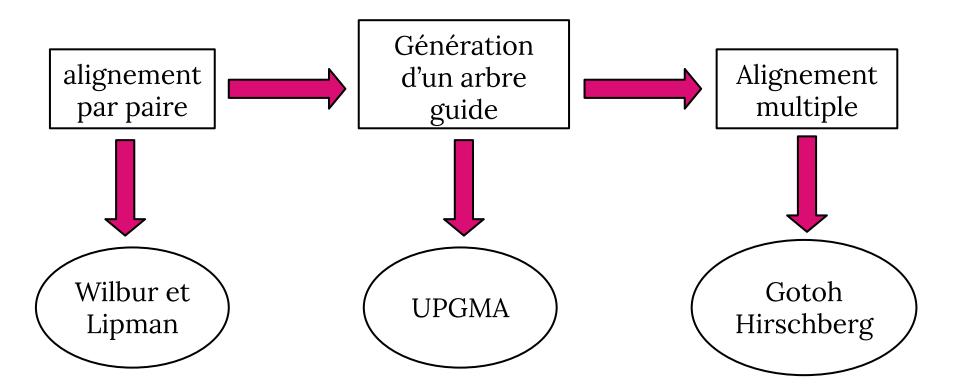
Étapes

alignement par paire Wilbur et Lipman

Étapes



Étapes

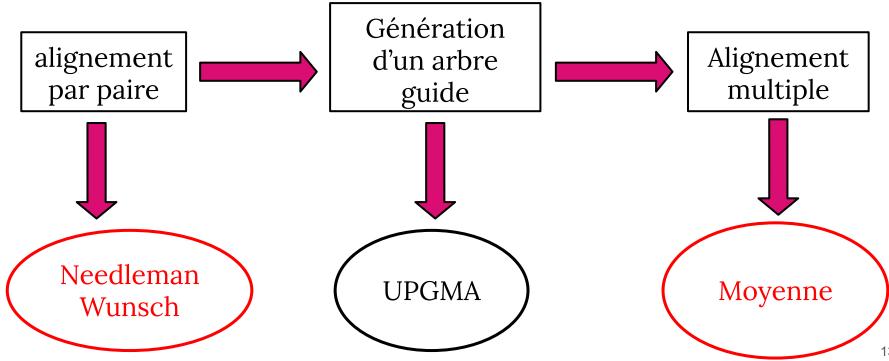


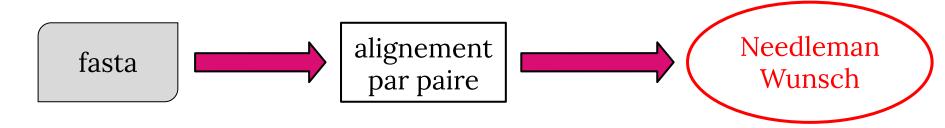
Objectif

• Réimplémenter une version simplifiée de Clustal

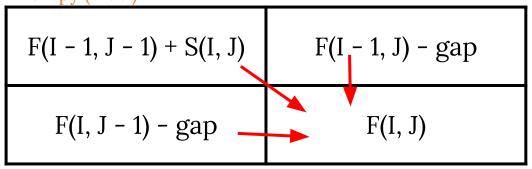
Objectif

• Réimplémenter une version simplifiée de Clustal

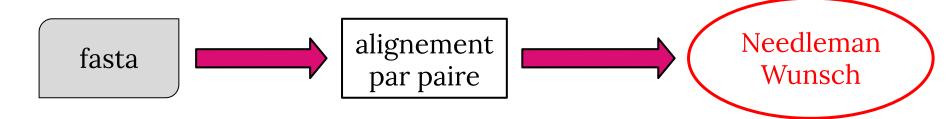




numpy (v2.1.1)



- gap = 8
- S(I, J): BLOSUM62 pandas (v2.2.2)



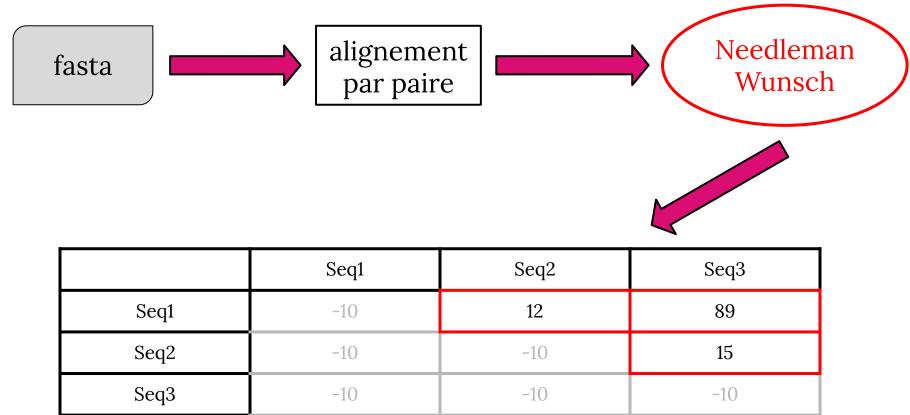
F(I - 1, J - 1) + S(I, J)	F(I - 1, J) - gap
F(I, J - 1) - gap	F(I, J)

1	1
2	0

0 : diagonale

1: gauche

2: haut

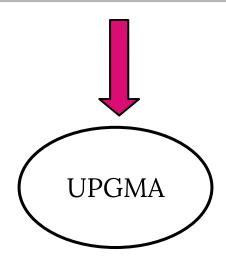


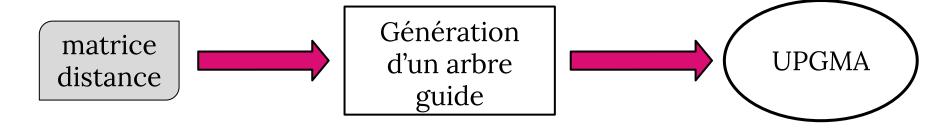
	Seq1	Seq2	Seq3
Seq1	-10	12	89
Seq2	-10	-10	15
Seq3	-10	-10	-10



 $matrice\ distances\ =\ 1\ -\ ((matrice\ scores\ -\ minimum)\ /\ maximum\ -\ minimum)$

	Seq1	Seq2	Seq3
Seq1	-10	1	0
Seq2	-10	-10	0.96
Seq3	-10	-10	-10





	Seq1	Seq2	Seq3
Seq1	-10	1	0
Seq2	-10	-10	0.96
Seq3	-10	-10	-10

	Seq1, Seq3	Seq2	
Seq1, Seq3	-10	0.98	
Seq2	-10	-10	

distance ((i, j), k) =
$$\frac{n_i * d_{ki} + n_k + d_{kj}}{n_i + n_j} <$$

	Seq1, Seq3	Seq2
Seq1, Seq3	-10	0.98
Seq2	-10	-10

distance ((i, j), k) =
$$\frac{n_i * d_{ki} + n_k + d_{kj}}{n_i + n_j}$$



Arbre guide : ((Seq1, Seq3), Seq2)



Alignement multiple



diagonale(F(i, j)) = F(i - 1, j - 1) + moyenne(cluster1(i), cluster2(j))

Arbre guide: ((Seq1, Seq3), Seq2)



Alignement multiple



diagonale(F(i, j)) = F(i - 1, j - 1) + moyenne(cluster1(i), cluster2(j))

Seq1: AWVED

Seq2: -TALD



diagonale = (S(A, R)-gap)/2

Seq3: REDAL

The file exists and is going to be parsed...

Here is the file's content :

Alpha-crystallinBchain: MDIAIHHPWIRRPFFPFHSPSRLFDQFFGEHLLESDLFPTSTSLSPFYLRPPSFLRAPSWFDTGLSEMRLEKDRFSVNLDVKHFSPEELKVKVLGDVIEVH
GKHEERQDEHGFISREFHRKYRIPADVDPLTITSSLSSDGVLTVNGPRKQVSGPERTIPITREEKPAVTAAPKK

Alpha-crystallinAchain: MDVTIQHPWFKRTLGPFYPSRLFDQFFGEGLFEYDLLPFLSSTISPYYRQSLFRTVLDSGISEVRSDRDKFVIFLDVKHFSPEDLTVKVQDDFVEIHGKHN ERODDHGYISREFHRRYRLPSNVDQSALSCSLSADGMLTFCGPKIQTGLDATHAERAIPVSREEKPTSAPSS

Heatshockproteinbeta-6: MEIPVPVQPSWLRRASAPLPGLSAPGRLFDQRFGEGLLEAELAALCPTTLAPYYLRAPSVALPVAQVPTDPGHFSVLLDVKHFSPEEIAVKVVGEHVEVHA
RHEERPDEHGFVAREFHRRYRLPPGVDPAAVTSALSPEGVLSIQAAPASAQAPPPAAAK

Heatshockproteinbeta-1: MTERRVPFSLLRGPSWDPFRDWYPHSRLFDQAFGLPRLPEEWSQWLGGSSWPGYVRPLPPAAIESPAVAAPAYSRALSRQLSSGVSEIRHTADRWRVSLDV
NHFAPDELTVKTKDGVVEITGKHEERQDEHGYISRCFTRKYTLPPGVDPTQVSSSLSPEGTLTVEAPMPKLATQSNEITIPVTFESRAQLGGPEAAKSDETAAK

Heatshockproteinbeta-2: MSGRSVPHAHPATAEYEFANPSRLGEQRFGEGLLPEEILTPTLYHGYYVRPRAAPAGEGSRAGASELRLSEGKFQAFLDVSHFTPDEVTVRTVDNLLEVSA RHPQRLDRHGFVSREFCRTYVLPADVDPWRVRAALSHDGILNLEAPRGGRHLDTEVNEVYISLLPAPPDPEEEEEAAIVEP

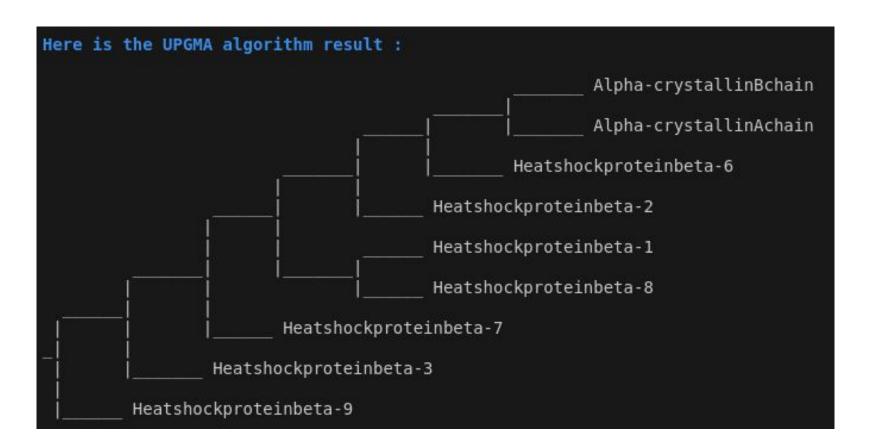
Heatshockproteinbeta-8: MADGQMPFSCHYPSRLRRDPFRDSPLSSRLLDDGFGMDPFPDDLTASWPDWALPRLSSAWPGTLRSGMVPRGPTATARFGVPAEGRTPPPFPGEPWKVCVN VHSFKPEELMVKTKDGYVEVSGKHEEKQQEGGIVSKNFTKKIQLPAEVDPVTVFASLSPEGLLIIEAPOVPPYSTFGESSFNNELPQDSQEVTCT

Heatshockproteinbeta-3: MAKIILRHLIEIPVRYQEEFEARGLEDCRLDHALYALPGPTIVDLRKTRAAQSPPVDSAAETPPREGKSHFQILLDVVQFLPEDIIIQTFEGWLLIKAQHG
TRMDEHGFISRSFTRQYKLPDGVEIKDLSAVLCHDGILVVEVKDPVGTK

Heatshockproteinbeta-7: MSHRTSSTFRAERSFHSSSSSSSSSSSSSSSSARALPAQDPPMEKALSMFSDDFGSFMRPHSEPLAFPARPGGAGNIKTLGDAYEFAVDVRDFSPEDIIVTTS
NNHIEVRAEKLAADGTVMNTFAHKCQLPEDVDPTSVTSALREDGSLTIRARRHPHTEHVQQTFRTEIKI

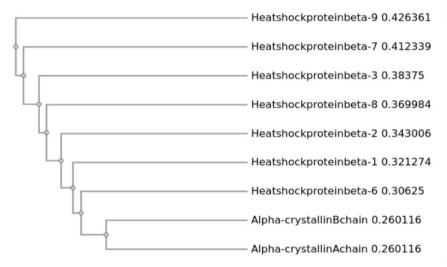
Heatshockproteinbeta-9: MQRVGNTFSNESRVASRCPSVGLAERNRVATMPVRLLRDSPAAQEDNDHARDGFQMKLDAHGFAPEELVVQVDGQWLMVTGQQQLDVRDPERVSYRMSQKV HRKMLPSNLSPTAMTCCLTPSGQLWVRGQCVALALPEAQTGPSPRLGSLGSKASNLTR

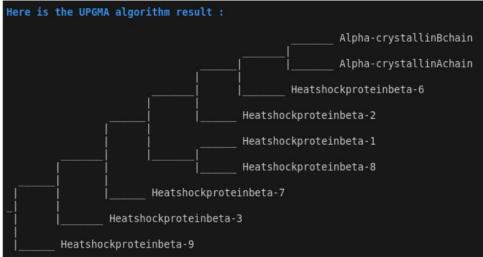
```
Here are the Needleman-Wunsch alignements :
Alpha-crystallinBchain: MDIAIHHPWIRRPFFPFHSPSRLFDQFFGEHLLESDLFP-TSTSLSPFYLRPPSFLRAPS
Alpha-crystallinAchain: MDVTIQHPWFKRTLGPFY-PSRLFDQFFGEGLFEYDLLPFLSSTISPYY-R-QSLFR--T
Alpha-crystallinBchain: WFDTGLSEMRLEKDRFSVNLDVKHFSPEELKVKVLGDVIEVHGKHEERQDEHGFISREFH
Alpha-crystallinAchain: VLDSGISEVRSDRDKFVIFLDVKHFSPEDLTVKVQDDFVEIHGKHNERQDDHGYISREFH
Alpha-crystallinBchain: RKYRIPADVDPLTITSSLSSDGVLTVNGPRKQ--VSG--PERTIPITREEKPAVTAAPKK
Alpha-crystallinAchain: RRYRLPSNVDQSALSCSLSADGMLTFCGPKIQTGLDATHAERAIPVSREEKP--TSAPSS
 Alignement score: 466
Alpha-crystallinBchain: MDIAIH-HP-WIRR-PF-FP-FHSPSRLFDQFFGEHLLESDLFPTSTSLSPFYLRPPSFL
Heatshockproteinbeta-6: MEIPVPVQPSWLRRASAPLPGLSAPGRLFDQRFGEGLLEAEL---A-ALCPTTL-APYYL
Alpha-crystallinBchain: RAPSWFDTGLSEMRLEKDRFSVNLDVKHFSPEELKVKVLGDVIEVHGKHEERQDEHGFIS
Heatshockproteinbeta-6: RAPS-VALPVAQVPTDPGHFSVLLDVKHFSPEEIAVKVVGEHVEVHARHEERPDEHGFVA
Alpha-crystallinBchain: REFHRKYRIPADVDPLTITSSLSSDGVLTVNGPRKQVSGPERTIPITREEKPAVTAAPKK
Heatshockproteinbeta-6: REFHRRYRLPPGVDPAAVTSALSPEGVLSI----Q-AAP-AS---AQAPPPA--AA--K
 Alignement score: 254
```

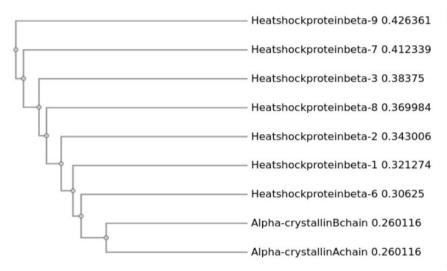


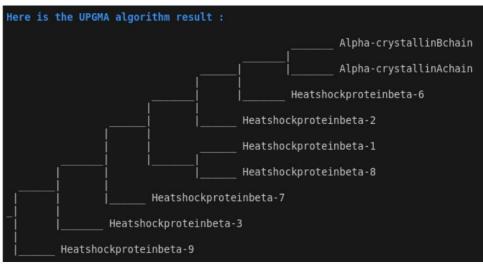
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Here is the multiple alignment result :
Alpha-crystallinBchain: M-DIAIH-HP-WIRR-PFFPF--HS-PSRLFDOFFGEHLLESD-LFP-TSTSLSPFYLRP--P----S-F
Alpha-crystallinAchain: M-DVTIO-HP-WFKR-TLGPF--Y--PSRLFDOFFGEGLFEYD-LLPFLSSTISPYY-R---O----S-L
Heatshockproteinbeta-6: M-EIPVPVQPSWLRR-ASAPLPGLSAPGRLFDQRFGEGLLEAE-LAALCPTTLAPYYLRA--P----S--
Heatshockproteinbeta-2: M-S-GRS-VP-HAHP-ATAEYE-FANPSRLGEORFGEGLLPEE-IL--TPTLYHGYYVR---P----R-A
Heatshockproteinbeta-1: MTERRVPFSL-LRGP-SWDPFRDWYPHSRLFDOAFGLPRLPEE-WSOWLGGSSWPGYVRPLPPAAIESPA
Heatshockproteinbeta-8: MADGQMPFSCHYPSRLRRDPFRDSPLSSRLLDDGFGMDPFPDDLTASW-PDWALP-RLSSAWPGTLRSGM
Heatshockproteinbeta-7: M-SHRTS-ST-F--R-AERSFHSSSSSSSSSSSSSSSASRALPAQ-DPP-MEKALSMFSDDF--G----S-F
Heatshockproteinbeta-3: M-A-KI--I--LRHL-IEIPVR-Y--QEEFEARGLEDCRLDHA-LYA-LPGPTIV-DLRK--T----R-A
Heatshockproteinbeta-9: M-O-RVG-NT-FSNE-SR--V-----ASRC-PS-VG--LAERN--R--VAT-M-P--VR------L
Alpha-crystallinBchain: LRAP--S-W-FD--T-GLSEMRLEKDRFSVNLDVKHFSPEELKVKVLGDVIEVHGKHE-E-RODEH-GF-
Alpha-crystallinAchain: FR----T-V-LD--S-GISEVRSDRDKFVIFLDVKHFSPEDLTVKVODDFVEIHGKHN-E-RODDH-GY-
Heatshockproteinbeta-6: V-----A---L---P--VAQVPTDPGHFSVLLDVKHFSPEEIAVKVVGEHVEVHARHE-E-RPDEH-GF-
Heatshockproteinbeta-2: APAG--E-G-SR--A-GASELRLSEGKFQAFLDVSHFTPDEVTVRTVDNLLEVSARHP-Q-RLDRH-GF-
Heatshockproteinbeta-1: VAAPAYSRALSRQLSSGVSEIRHTADRWRVSLDVNHFAPDELTVKTKDGVVEITGKHE-E-RQDEH-GY-
Heatshockproteinbeta-8: VPRGPTATARFGVPAEGRTPPPFPGEPWKVCVNVHSFKPEELMVKTKDGYVEVSGKHE-E-KO0EG-GI-
Heatshockproteinbeta-7: MRPHSEPLA-FPARPGGAGNIKTLGDAYEFAVDVRDFSPEDIIVTTSNNHIEVRA----E-KLAAD-GT-
Heatshockproteinbeta-3: AQSP--P-V-DS--A-AETPPREGKSHFQILLDVVQFLPEDIIIQTFEGWLLIKAQHG-T-RMDEH-GF-
Heatshockproteinbeta-9: LR-D--S----P--A-AQEDNDHARDGFQMKLDAHGFAPEELVVQVDGQWLMVTGQQQLDVRDPERVSYR
Alpha-crystallinBchain: ISREFHRKYRIPADVDPLTITSSLSSDGVLTVNGPRKQ--VSG--PE-R-T-IPITR-EE-KPAV-TAA-
Alpha-crystallinAchain: ISREFHRRYRLPSNVDQSALSCSLSADGMLTFCGPKIQTGLDATHAE-R-A-IPVSR-EE-KP---TSA-
Heatshockproteinbeta-6: VAREFHRRYRLPPGVDPAAVTSALSPEGVLSI-----0----A----A--PASA-OA-PP---PAA-
Heatshockproteinbeta-2: VSREFCRTYVLPADVDPWRVRAALSHDGILNLEAPRGGRHLDTEVNEVYISLLPAPP-DP-EEEE-EAAI
Heatshockproteinbeta-1: ISRCFTRKYTLPPGVDPTQVSSSLSPEGTLTVEAP-MP-KLATQSNEITIPVTFESRAQLGGPEAAKSDE
Heatshockproteinbeta-8: VSKNFTKKIQLPAEVDPVTVFASLSPEGLLIIEAPQVP-PYST-FGE-S---SF-NN-EL--PQ--DSQE
Heatshockproteinbeta-7: VMNTFAHKCOLPEDVDPTSVTSALREDGSLTIRARRHP-H--T---E-H---V---O-OT--F---RTE-
Heatshockproteinbeta-3: ISRSFTROYKLPDGVEIKDLSAVLCHDGILVV-----E----V--K-D---P----VG-
Heatshockproteinbeta-9: MSQKVHRKM-LPSNLSPTAMTCCLTPSGQLWVRGQCVA--LAL--PEAQ-T-GPSPRLGS-LGS--KASN
Alpha-crystallinBchain: PK-K
Alpha-crystallinAchain: PS-S
Heatshockproteinbeta-6: -A-K
Heatshockproteinbeta-2: VE-P
Heatshockproteinbeta-1: TAAK
Heatshockproteinbeta-8: VTCT
Heatshockproteinbeta-7: IK-I
Heatshockproteinbeta-3: -T-K
Heatshockproteinbeta-9: LT-R
```

9 séquences : COMPLEXITÉ EN TEMPS DE O(n²)		
175 acides aminés	14 secondes	
355 acides aminés	37 secondes	
860 acides aminés	2 minutes 19 secondes	

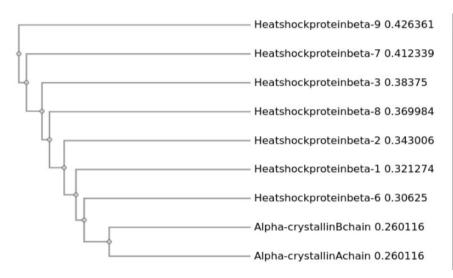


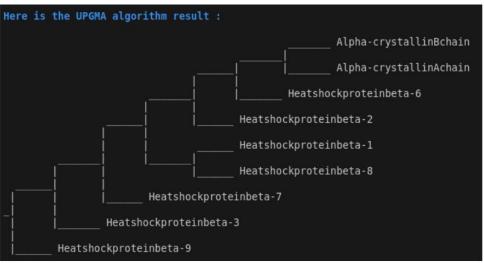




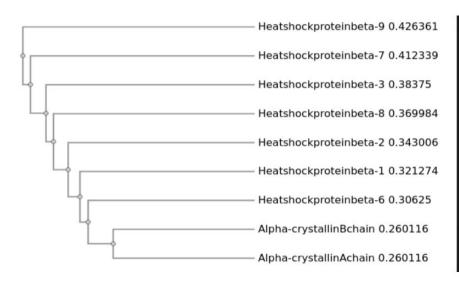


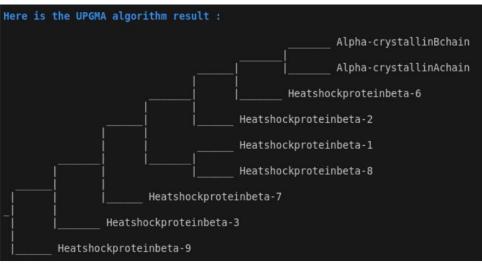
Needleman-Wunsch VS Wilbur et Lipman





- Needleman-Wunsch VS Wilbur et Lipman
- pénalité de gap constante





- Needleman-Wunsch VS Wilbur et Lipman
- pénalité de gap constante
- plusieurs méthodes de clusterisation (mBed, k-means, UPGMA)

CLUSTAL O(1.2.4) MULTIPLE SEQUENCE ALIGNMENT -----VASR 17 HEATSHOCKPROTEINBETA-9 HEATSHOCKPROTEINBETA-7 MSHRT-----SSTF----RAERSFHSSSSSSSSSSSSSSSSASRALPAODPPMEKALS--46 HEATSHOCKPROTEINBETA-3 MAKIILRHLI------EIPVRYO---EEF------EARGLEDCRL---30 HEATSHOCKPROTEINBETA-8 MADGQMPFSCHYP-SRL--RRDPFRDSPLSSRLL---DDG------FGMDPFPDDLTAS 47 HEATSHOCKPROTEINBETA-2 MSGRSVPHAHP-----ATAEYEFANPSRLG---EOR-----FGEGLLPEETLT-40 HEATSHOCKPROTEINBETA-1 MTERRYPESLLRGPSW-----DPFRDWYPHSRLF---DOA------FGLPRLPEEWSOW 45 HEATSHOCKPROTEINBETA-6 -----MEIPVPVOPSWLRRASAPLPGLSAPGRLF---DOR------FGEGLLEAELAAL 45 ALPHA-CRYSTALLINBCHAIN -----FGEHLLESDLFPT 40 -----FGEGLFEYDLLPF 39 ALPHA-CRYSTALLINACHAIN HEATSHOCKPROTEINBETA-9 CPS-----VGLAERNRVAT------MPV---RLLRDSPAA0EDNDHARDGFOMK 57 -----LAFPARPGGAGNIKTLGDAYEFA 85 HEATSHOCKPROTEINBETA-7 HEATSHOCKPROTEINBETA-3 -----DHALYALPGPT--IVDLR---KTRAAQSPPVDSAAETPPREGKSHFQIL 74 WPDWALPRLSSAWPGTLRSGMVPR------GPTA-TARFGVPAEGRTPPPFPGEPWKVC 99 HEATSHOCKPROTEINBETA-8 -P-----TLYHGYYVRPRAAP------AGEGSRAGASELRLSEGKFOAF 77 HEATSHOCKPROTEINBETA-2 HEATSHOCKPROTEINBETA-1 LG-----GSSWPGYVRPLPPAAIESPAVAAPAYSRALSROLSSGVSEIRHTADRWRVS 98 CP-----TTLAPYYLRA------PSV------ALPVAOVPTDPGHFSVL 77 HEATSHOCKPROTEINBETA-6 ALPHA-CRYSTALLINBCHAIN ST-----PSFLR-APSWFDTGLSEMRLEKDRFSVN 78 ALPHA-CRYSTALLINACHAIN LS-----STISPYY-RO------SLF----RTVLDSGISEVRSDRDKFVIF 74 HEATSHOCKPROTEINBETA-9 LDAHGFAPEELVVQVDGQWLMVTGQQQLDVRDPERVSYRMSQKVHRKMLPSNLSPTAMTC 117 VDVRDFSPEDIIVTTSNNHIEVRA---EKLAADG---TVMNTFAHKCOLPEDVDPTSVTS 139 HEATSHOCKPROTEINBETA-7 HEATSHOCKPROTEINBETA-3 LDVVOFLPEDIIIOTFEGWLLIKAOHGTRMDEHG---FISRSFTROYKLPDGVEIKDLSA 131 HEATSHOCKPROTEINBETA-8 VNVHSFKPEELMVKTKDGYVEVSGKHEEKQQEGG---IVSKNFTKKIQLPAEVDPVTVFA 156 HEATSHOCKPROTEINBETA-2 LDVSHFTPDEVTVRTVDNLLEVSARHPORLDRHG---FVSREFCRTYVLPADVDPWRVRA 134 HEATSHOCKPROTEINBETA-1 LDVNHFAPDELTVKTKDGVVEITGKHEERODEHG---YISRCFTRKYTLPPGVDPTOVSS 155 LDVKHFSPEEIAVKVVGEHVEVHARHEERPDEHG---FVAREFHRRYRLPPGVDPAAVTS 134 HEATSHOCKPROTEINBETA-6 ALPHA-CRYSTALLINBCHAIN LDVKHFSPEELKVKVLGDVIEVHGKHEERQDEHG---FISREFHRKYRIPADVDPLTITS 135 ALPHA-CRYSTALLINACHAIN LDVKHFSPEDLTVKVODDFVEIHGKHNERODDHG---YISREFHRRYRLPSNVDOSALSC 131 ::. * *::: : . : : . : :* :. : . HEATSHOCKPROTEINBETA-9 CLTPSGQLWVRGQCVALALPEAQTGP------SPRLGSLGSKASNLTR----- 159 HEATSHOCKPROTEINBETA-7 ALREDGSLTIRARRHPHTEHVQQ-TFRTEIKI-----HEATSHOCKPROTEINBETA-3 VLCHDGILVVEVKDPVGTK------HEATSHOCKPROTEINBETA-8 SLSPEGLLIIEAPOVPPYSTFGESSFNNELPODSOE------VTCT---- 196 HEATSHOCKPROTEINBETA-2 ALSHDGTLNLEAPRGGRHLDTEVN--EVYTSLLPA-----PPDPEEEEEAATVEP HEATSHOCKPROTEINBETA-1 SLSPEGTLTVEAPMPKLAT--QSN--EITIPVTFESRAQLGGPEAAKSDETAAK--- 205 HEATSHOCKPROTEINBETA-6 ALSPEGVLSTOAAPASAOAPPPAA -- AK------ALPHA-CRYSTALLINBCHAIN SLSSDGVLTVNGPRKOV----SGP--ERTIPITREEKPAVTAAPKK------ 175 ALPHA-CRYSTALLINACHAIN SLSADGMLTFCGPKIOTGLDATHA--ERAIPVSREEKPTSAPSS------ 173 * .* * .

Alpha-crystallinBchain: M-DIAIH-HP-WIRR-PFFPF--HS-PSRLFDOFFGEHLLESD-LFP-TSTSLSPFYLRP--P---S-F Alpha-crystallinAchain: M-DVTIQ-HP-WFKR-TLGPF--Y--PSRLFDQFFGEGLFEYD-LLPFLSSTISPYY-R---Q----S-L Heatshockproteinbeta-6: M-EIPVPVQPSWLRR-ASAPLPGLSAPGRLFDQRFGEGLLEAE-LAALCPTTLAPYYLRA--P----S--Heatshockproteinbeta-2: M-S-GRS-VP-HAHP-ATAEYE-FANPSRLGEQRFGEGLLPEE-IL--TPTLYHGYYVR---P----R-A Heatshockproteinbeta-1: MTERRVPFSL-LRGP-SWDPFRDWYPHSRLFDQAFGLPRLPEE-WSQWLGGSSWPGYVRPLPPAAIESPA Heatshockproteinbeta-8: MADGOMPFSCHYPSRLRRDPFRDSPLSSRLLDDGFGMDPFPDDLTASW-PDWALP-RLSSAWPGTLRSGM Heatshockproteinbeta-7: M-SHRTS-ST-F--R-AERSFHSSSSSSSSSSSSSSASRALPAQ-DPP-MEKALSMFSDDF--G----S-F Heatshockproteinbeta-3: M-A-KI--I--LRHL-IEIPVR-Y--OEEFEARGLEDCRLDHA-LYA-LPGPTIV-DLRK--T----R-A Heatshockproteinbeta-9: M-Q-RVG-NT-FSNE-SR--V----ASRC-PS-VG--LAERN--R--VAT-M-P--VR------L Alpha-crystallinBchain: LRAP--S-W-FD--T-GLSEMRLEKDRFSVNLDVKHFSPEELKVKVLGDVIEVHGKHE-E-RQDEH-GF-Alpha-crystallinAchain: FR----T-V-LD--S-GISEVRSDRDKFVIFLDVKHFSPEDLTVKVODDFVEIHGKHN-E-RODDH-GY-Heatshockproteinbeta-6: V-----A---L---P--VAQVPTDPGHFSVLLDVKHFSPEEIAVKVVGEHVEVHARHE<u>-E-RPDEH-</u>GF-Heatshockproteinbeta-2: APAG--E-G-SR--A-GASELRLSEGKF0AFLDVSHFTPDEVTVRTVDNLLEVSARHP-0-RLDRH-GF-Heatshockproteinbeta-1: VAAPAYSRALSRQLSSGVSEIRHTADRWRVSLDVNHFAPDELTVKTKDGVVEITGKHE-E-RQDEH-GY-Heatshockproteinbeta-8: VPRGPTATARFGVPAEGRTPPPFPGEPWKVCVNVHSFKPEELMVKTKDGYVEVSGKHE-E-KQQEG-GI-Heatshockproteinbeta-7: MRPHSEPLA-FPARPGGAGNIKTLGDAYEFAVDVRDFSPEDIIVTTSNNHIEVRA----E-KLAAD-GT-Heatshockproteinbeta-3: AQSP--P-V-DS--A-AETPPREGKSHFQILLDVVQFLPEDIIIQTFEGWLLIKAQHG-T-RMDEH-GF-Heatshockproteinbeta-9: LR-D--S----P--A-AQEDNDHARDGFQMKLDAHGFAPEELVVQVDGQWLMVTGQQQLDVRDPERVSYR Alpha-crystallinBchain: ISREFHRKYRIPADVDPLTITSSLSSDGVLTVNGPRKQ--VSG--PE-R-T-IPITR-EE-KPAV-TAA-Alpha-crystallinAchain: ISREFHRRYRLPSNVDQSALSCSLSADGMLTFCGPKIQTGLDATHAE-R-A-IPVSR-EE-KP---TSA-Heatshockproteinbeta-6: VAREFHRRYRLPPGVDPAAVTSALSPEGVLSI-----Q----A-----A--PASA-QA-PP---PAA-Heatshockproteinbeta-2: VSREFCRTYVLPADVDPWRVRAALSHDGILNLEAPRGGRHLDTEVN<u>EVYISLLPAPP-DP-EEEE-EAAI</u> Heatshockproteinbeta-1: ISRCFTRKYTLPPGVDPTOVSSSLSPEGTLTVEAP-MP-KLATOSNEITIPVTFESRAOLGGPEAAKSDE Heatshockproteinbeta-8: VSKNFTKKIQLPAEVDPVTVFASLSPEGLLIIEAPQVP-PYST-FGE-S---SF-NN-EL--PQ--DSQE Heatshockproteinbeta-7: VMNTFAHKCQLPEDVDPTSVTSALREDGSLTIRARRHP-H--T---E-H---V---Q-QT--F---RTE-Heatshockproteinbeta-3: ISRSFTROYKLPDGVEIKDLSAVLCHDGILVV------E-----E-----V---K-D---P----VG-Heatshockproteinbeta-9: MSQKVHRKM-LPSNLSPTAMTCCLTPSGQLWVRGQCVA--LAL--PEAQ-T-GPSPRLGS-LGS--KASN Alpha-crystallinBchain: PK-K Alpha-crystallinAchain: PS-S Heatshockproteinbeta-6: -A-K Heatshockproteinbeta-2: VE-P Heatshockproteinbeta-1: TAAK Heatshockproteinbeta-8: VTCT leatshockproteinbeta-7: IK-I Heatshockproteinbeta-3: -T-K leatshockproteinbeta-9: LT-R



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CLUSTAL O(1.2.4) MULTIPLE SEQUENCE ALIGNMENT
                                                                                        Alpha-crystallinBchain:
                                                                                                                  M.DIAIH-HP-WIRR-PFFPF--HS-PSRLFDOFFGEHLLESD-LFP-TSTSLSPFYLRP--P---S-F
                                                                                                                  M.DVTIQ-HP-WFKR-TLGPF--Y--PSRLFDQFFGEGLFEYD-LLPFLSSTISPYY-R---Q----S-L
                                                                                         Alpha-crystallinAchain:
                                                                                         Heatshockproteinbeta-6:
                                                                                                                  M-EIPVPVQPSWLRR-ASAPLPGLSAPGRLFDQRFGEGLLEAE-LAALCPTTLAPYYLRA--P----S--
                                                                                 17
HEATSHOCKPROTEINBETA-9
                       -----VASR
                                                                                         Heatshockproteinbeta-2:
                                                                                                                  M-S-GRS-VP-HAHP-ATAEYE-FANPSRLGEORFGEGLLPEE-IL--TPTLYHGYYVR---P----R-A
HEATSHOCKPROTEINBETA-7
                       MSHRT-----SSTF----RAERSFHSSSSSSSSSSSSSSSSASRALPAODPPMEKALS--
                                                                                 46
                                                                                         Heatshockproteinbeta-1:
                                                                                                                  MTERRVPFSL-LRGP-SWDPFRDWYPHSRLFDQAFGLPRLPEE-WSQWLGGSSWPGYVRPLPPAAIESPA
HEATSHOCKPROTEINBETA-3
                       MAKIILRHLI-----EIPVRYO---EEF-----EARGLEDCRL---
                                                                                 30
                                                                                         leatshockproteinbeta-8:
                                                                                                                  MADGOMPFSCHYPSRLRRDPFRDSPLSSRLLDDGFGMDPFPDDLTASW-PDWALP-RLSSAWPGTLRSGM
HEATSHOCKPROTEINBETA-8
                       MADGOMPFSCHYP-SRL--RRDPFRDSPLSSRLL---DDG------FGMDPFPDDLTAS
                                                                                 47
                                                                                         Heatshockproteinbeta-7:
                                                                                                                  M-SHRTS-ST-F--R-AERSFHSSSSSSSSSSSSSSASRALPAQ-DPP-MEKALSMFSDDF--G---S-F
HEATSHOCKPROTEINBETA-2
                       MSGRSVPHAHP-----ATAEYEFANPSRLG---EOR-----FGEGLLPEETLT-
                                                                                 40
HEATSHOCKPROTEINBETA-1
                       MTERRYPESLLRGPSW-----DPFRDWYPHSRLF---DOA------FGLPRLPEEWSOW
                                                                                 45
                                                                                         deatshockproteinbeta-3: M.A-KI--I--LRHL-IEIPVR-Y--OEEFEARGLEDCRLDHA-LYA-LPGPTIV-DLRK--T----R-A
HEATSHOCKPROTEINBETA-6
                       -----MEIPVPVOPSWLRRASAPLPGLSAPGRLF---DOR------FGEGLLEAELAAL
                                                                                 45
                                                                                         Heatshockproteinbeta-9: M·Q-RVG-NT-FSNE-SR--V-----ASRC-PS-VG--LAERN--R--VAT-M-P--VR------L
ALPHA-CRYSTALLINBCHAIN
                       -----FGEHLLESDLFPT
                                                                                 40
                       -----FGEGLFEYDLLPF
                                                                                 39
ALPHA-CRYSTALLINACHAIN
                                                                                        Alpha-crystallinBchain: LRAP--S-W-FD--T-GLSEMRLEKDRF: VNLDVKHFSPEELKVKVLGDVIEVHGKHE E
                                                                                        Alpha-crystallinAchain: FR----T-V-LD--S-GISEVRSDRDKFVIFLDVKHFSPECLTVKVODDFVEIHGKHN
HEATSHOCKPROTEINBETA-9
                       CPS-----VGLAERNRVAT------MPV---RLLRDSPAA0EDNDHARDGFOMK
                                                                                 57
                                                                                         Heatshockproteinbeta-6: V-----A---L---P--VAQVPTDPGHF:VLLDVKHFSPETIAVKVVGEHVEVHARHE
                       -----LAFPARPGGAGNIKTLGDAYEFA
                                                                                 85
HEATSHOCKPROTEINBETA-7
                                                                                         Heatshockproteinbeta-2: APAG--E-G-SR--A-GASELRLSEGKF<mark>GAFLDVSHFTFDC</mark>VTVRTVDNLLEVSARHP
HEATSHOCKPROTEINBETA-3
                       -----DHALYALPGPT--IVDLR---KTRAAOSPPVDSAAETPPREGKSHFOIL
                                                                                 74
                                                                                         Heatshockproteinbeta-1: VAAPAYSRALSRQLSSGVSEIRHTADRWRVSLDVNHFAPDELTVKTKDGVVEITGKHE
                       WPDWALPRLSSAWPGTLRSGMVPR------GPTA-TARFGVPAEGRTPPPFPGEPWKVC
                                                                                 99
HEATSHOCKPROTEINBETA-8
                                                                                         Heatshockproteinbeta-8: VPRGPTATARFGVPAEGRTPPPFPGEPWKVCVNVHSFKPEELMVKTKDGYVEVSGKHE
                                                                                 77
HEATSHOCKPROTEINBETA-2
                       -P-----TLYHGYYVRPRAAP------AGEGSRAGASELRLSEGKFOAF
                                                                                         Heatshockproteinbeta-7: MRPHSEPLA-FPARPGGAGNIKTLGDAYEFAVDVRDFSPEDIIVTTSNNHIEVRA---
HEATSHOCKPROTEINBETA-1
                       LG-----GSSWPGYVRPLPPAAIESPAVAAPAYSRALSROLSSGVSEIRHTADRWRVS
                                                                                 98
                                                                                         Heatshockproteinbeta-3: AQSP--P-V-DS--A-AETPPREGKSHFQILLDVVQFLPEDIIIQTFEGWLLIKAQHG
                       CP-----TTLAPYYLRA------PSV------ALPVAOVPTDPGHFSVL
                                                                                 77
HEATSHOCKPROTEINBETA-6
                                                                                         Heatshockproteinbeta-9: LR-D--S----P--A-AQEDNDHARDGFQMKLDAHGFAPEELVVQVDGQWLMVTGQQQ<mark>.D</mark>/RDPERVSYR
ALPHA-CRYSTALLINBCHAIN
                       ST-----PSFLR-APSWFDTGLSEMRLEKDRFSVN
                                                                                 78
ALPHA-CRYSTALLINACHAIN
                       LS-----STISPYY-RO------SLF----RTVLDSGISEVRSDRDKFVIF
                                                                                 74
                                                                                        Alpha-crystallinBchain:
                                                                                                                  ISREFHRKYRIPADVDPLTITSSLSSDGVLTVNGPRKQ--VSG--PE-R-T-IPITR-EE-KPAV-TAA-
HEATSHOCKPROTEINBETA-9
                       LDAHGFAPEELVVQVDGQWLMVTGQQQLDVRDPERVSYRMSQKVHRKMLPSNLSPTAMTC
                                                                                 117
                                                                                        Alpha-crystallinAchain:
                                                                                                                  ISREFHRRYRLPSNVDOSALSCSLSADGMLTF GPKIOTGLDATHAE-R-A-IPVSR-EE-KP---TSA-
                       VDVRDFSPEDIIVTTSNNHIEVRA---EKLAADG---TVMNTFAHKCOLPEDVDPTSVTS
                                                                                 139
HEATSHOCKPROTEINBETA-7
                                                                                         leatshockproteinbeta-6: VAREFHRRYRLPPGVDPAAVTSALSPEGVLSI-----Q----A-----A--PASA-QA-PP---PAA-
                       LDVVOFLPEDIIIOTFEGWLLIKAOHGTRMDEHG---FISRSFTROYKLPDGVEIKDLSA
                                                                                 131
HEATSHOCKPROTEINBETA-3
                                                                                         leatshockproteinbeta-2:
                                                                                                                  VSREFCRTYVLPADVDPWRVRAALSHDGILNLEAPRGGRHLDTEVNEVYISLLPAPP-DP-EEEE-EAAI
                       VNVHSFKPEELMVKTKDGYVEVSGKHEEKQQEGG---IVSKNFTKKIQLPAEVDPVTVFA
                                                                                 156
HEATSHOCKPROTEINBETA-8
                                                                                         Heatshockproteinbeta-1: ISRCFTRKYTLPPGVDPTOVSSSLSPEGTLTVEAP-MP-KLATOSNEITIPVTFESRAOLGGPEAAKSDE
HEATSHOCKPROTEINBETA-2
                       LDVSHFTPDEVTVRTVDNLLEVSARHPORLDRHG---FVSREFCRTYVLPADVDPWRVRA
                                                                                 134
                                                                                         Heatshockproteinbeta-8:
                                                                                                                  VSKNFTKKIQLPAEVDPVTVFASLSPEGLLII APQVP-PYST-FGE-S---SF-NN-EL--PQ--DSQE
HEATSHOCKPROTEINBETA-1
                       LDVNHFAPDELTVKTKDGVVEITGKHEERODEHG---YISRCFTRKYTLPPGVDPTOVSS
                                                                                 155
                                                                                         Heatshockproteinbeta-7:
                                                                                                                  VMNTFAHKCQLPEDVDPTSVTSALREDGSLTIRARRHP-H--T---E-H---V---Q-QT--F---RTE-
                       LDVKHFSPEEIAVKVVGEHVEVHARHEERPDEHG---FVAREFHRRYRLPPGVDPAAVTS
                                                                                 134
HEATSHOCKPROTEINBETA-6
                                                                                         Heatshockproteinbeta-3:
                                                                                                                  ISRSFTROYKLPDGVEIKDLSAVLCHDGILVV.------E-----E----V---K-D---P----VG-
ALPHA-CRYSTALLINBCHAIN
                       LDVKHFSPEELKVKVLGDVIEVHGKHEERQDEHG---FISREFHRKYRIPADVDPLTITS
                                                                                 135
                                                                                         Heatshockproteinbeta-9:
                                                                                                                  MSQKVHRKM-LPSNLSPTAMTCCLTPSGQLWVRGQCVA--LAL--PEAQ-T-GPSPRLGS-LGS--KASN
ALPHA-CRYSTALLINACHAIN
                       LDVKHFSPEDLTVKVODDFVEIHGKHNERODDHG---YISREFHRRYRLPSNVDOSALSC
                                                                                 131
                       ::. * *::: : . : : .
                                                             : :* :. : .
                                                                                        Alpha-crystallinBchain: PK-K
HEATSHOCKPROTEINBETA-9
                       CLTPSGOLWVRGOCVALALPEAOTGP-----SPRLGSLGSKASNLTR---- 159
                                                                                        Alpha-crystallinAchain: PS-S
HEATSHOCKPROTEINBETA-7
                       ALREDGSLTIRARRHPHTEHVQQ-TFRTEIKI-----
HEATSHOCKPROTEINBETA-3
                                                                                         Heatshockproteinbeta-6: -A-K
HEATSHOCKPROTEINBETA-8
                       SLSPEGLLIIEAPOVPPYSTFGESSFNNELPODS0E------VTCT----
                                                                                         Heatshockproteinbeta-2: VE-P
HEATSHOCKPROTEINBETA-2
                       ALSHDGTLNLEAPRGGRHLDTEVN--EVYTSLLPA-----PPDPEEEEEAATVEP
                                                                                         deatshockproteinbeta-1: TAAK
HEATSHOCKPROTEINBETA-1
                       SLSPEGTLTVEAPMPKLAT--QSN--EITIPVTFESRAQLGGPEAAKSDETAAK---
                                                                                         Heatshockproteinbeta-8: VTCT
HEATSHOCKPROTEINBETA-6
                       ALSPEGVLSTOAAPASAOAPPPAA--AK------
                                                                                         eatshockproteinbeta-7: IK-I
ALPHA-CRYSTALLINBCHAIN
                       SLSSDGVLTVNGPRKOV----SGP--ERTIPITREEKPAVTAAPKK------
                                                                                         Heatshockproteinbeta-3: -T-K
                       SLSADGMLTFCGPKIOTGLDATHA--ERAIPVSREEKPTSAPSS-----
ALPHA-CRYSTALLINACHAIN
                                                                                         leatshockproteinbeta-9: LT-R
                        * .* * .
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- RODEH - GF

- RLDRH - GF -

E-KOOEG-GI-

E-KLAAD-GT

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CLUSTAL 0(1.2.4) MULTIPLE SEQUENCE ALIGNMENT
                                                                                      lpha-crystallinBchain: M.DIAIH-HP-WIRR-PFFPF--HS-PSRLFDOFFGEHLLESD-LFP-TSTSLSPFYLRP--P----S-F
                                                                                      lpha-crystallinAchain: M.DVTIQ-HP-WFKR-TLGPF--Y--PSRLFDQFFGEGLFEYD-LLPFLSSTISPYY-R---Q----S-L
                                                                                     Heatshockproteinbeta-6: M·EIPVPVQPSWLRR-ASAPLPGLSAPGRLFDQRFGEGLLEAE-LAALCPTTLAPYYLRA--P----S-
HEATSHOCKPROTEINBETA-9 ------WO--RVGNTFSNESR-------VASR
HEATSHOCKPROTEINBETA-7 MSHRT-----SSTF---RAERSFHSSSSSSSSSSSSSSSSASRALPAODPPMEKALS--
                                                                                     leatshockproteinbeta-2: M⋅S-GRS-VP-HAHP-ATAEYE-FANPSRLGEORFGEGLLPEE-IL--TPTLYHGYYVR---P---R-A
                                                                                      eatshockproteinbeta-1: MCERRVPFSL-LRGP-SWDPFRDWYPHSRLFD0AFGLPRLPEE-WSOWLGGSSWPGYVRPLPPAAIESPA
                     MAKIILRHLI-----EIPVRYQ---EEF-----EARGLEDCRL---
HEATSHOCKPROTEINBETA-3
                                                                                      leatshockproteinbeta-8: MADGOMPESCHYPSRLRRDPERDSPLSSRLLDDGEGMDPEPDDLTASW-PDWALP-RLSSAWPGTLRSGM
HEATSHOCKPROTEINBETA-8 MADGOMPFSCHYP-SRL--RDPFRDSPLSSRLL---DDG------FGMDPFPDDLTAS
                                                                                      leatshockproteinbeta-7: M·SHRTS-ST-F--R-AERSFHSSSSSSSSSSSSSASRALPAQ-DPP-MEKALSMFSDDF--G---S-F
HEATSHOCKPROTEINBETA-2 MSGRSVPHAHP------ATAEYEFANPSRLG---EOR------FGEGLLPEEILT-
                                                                                      leatshockproteinbeta-3: M·A-KI--I--LRHL-IEIPVR-Y--OEEFEARGLEDCRLDHA-LYA-LPGPTIV-DLRK--T----R-A
HEATSHOCKPROTETNRETA-1 MTERRYPESI L RGPSW-----DPERDWYPHSRI E---D0A-------EGI PRI PEENSOW
HEATSHOCKPROTEINBETA-6 -----MEIPVPVQPSWLRRASAPLPGLSAPGRLF---DQR-------FGEGLLEAELAAL
                                                                                      leatshockproteinbeta-9: M-Q-RVG-NT-FSNE-SR--V----ASRC-PS-VG--LAERN--R<u>--VAT-M-P--VR------</u>
ALPHA-CRYSTALLINBCHAIN ------FGEHLLESDLFPT
ALPHA-CRYSTALLINACHAIN ------FGEGLFEYDLLPF
                                                                                    Alpha-crystallinBchain: LRAP--S-W-FD--T-GLSEMRLEKDRF VNLDVKHFSPEELKVKVLGDVIEVHGKHE E RODEH-GF-
                                                                                      lpha-crystallinAchain: FR----T-V-LD--S-GISEVRSDRDKF/IFLDVKHFSPELLTVKVQDDFVEIHGKHN <mark>E-</mark>RQDDF-GY
HEATSHOCKPROTEINBETA-9 CPS------VGLAERNRVAT------MPV---RLLRDSPAAOEDNDHARDGFOMK
                                                                                      eatshockproteinbeta-6: V-----A---L---P--VAQVPTDPGHF;VLLDVKHFSPE(IAVKVVGEHVEVHARHE_E-RPDEH-GF-
                     ----- NESDDEGSEMOPHSEP------ AFPARPGGAGNTKTI GDAYEFA
                                                                                     HEATSHOCKPROTETNBETA-7
HEATSHOCKPROTEINBETA-3 ------DHALYALPGPT--IVDLR---KTRAAOSPPVDSAAETPPREGKSHFOIL
                                                                                      eatshockproteinbeta-1: VAAPAYSRALSROLSSGVSEIRHTADRWRVSLDVNHFAPDELTVKTKDGVVEITGKHE
HEATSHOCKPROTEINBETA-8 WPDWALPRLSSAWPGTLRSGMVPR------GPTA-TARFGVPAEGRTPPPFPGEPWKVC
                                                                                      leatshockproteinbeta-8: VPRGPTATARFGVPAEGRTPPPFPGEPWKVCVNVHSFKPEELMVKTKDGYVEVSGKHE E-KQQEG-GI
HEATSHOCKPROTETNRETA-2 -P----TI YHGYYVRPPAAP------AGEGSRAGASEI RI SEGKEDAE
                                                                                      eatshockproteinbeta-7: MRPHSEPLA-FPARPGGAGNIKTLGDAYEFAVDVRDFSPEDIIVTTSNNHIEVRA----E-KLAAD-GT
HEATSHOCKPROTEINBETA-1 LG------GSSWPGYVRPLPPAAIESPAVAAPAYSRALSRQLSSGVSEIRHTADRWRVS
HEATSHOCKPROTETINETA-6 CP----TTLAPYYLRA-----PSV-----ALPVAOVPTOPGHESVL
                                                                                      eatshockproteinbeta-3: AOSP--P-V-DS--A-AETPPREGKSHFOILLDVVOFLPEDIIIOTFEGWLLIKAOHG
ALPHA-CRYSTALLINBCHAIN ST-----SLSPFYL-RP------PSFLR-APSWFDTGLSEMRLEKDRFSVN
                                                                                      leatshockproteinbeta-9: LR-D--S----P--A-AOEDNDHARDGFOMKLDAHGFAPEELVVOVDGOWLMVTGOOO D VRDPERVSYF
ALPHA-CRYSTALLINACHAIN LS-----STISPYY-RQ------SLF----RTVLDSGISEVRSDRDKFVIF
                                                                                      lpha-crystallinBchain: ISREFHRKYRIPADVDPLTITSSLSSDGVLTV GPRKO--VSG--PE-R-T-IPITR-EE-KPAV-TAA
HEATSHOCKPROTEINBETA-9 LDAHGFAPEELVVQVDGQWLMVTGQQQLDVRDPERVSYRMSQKVHRKMLPSNLSPTAMTC
                                                                                      lpha-crystallinAchain: ISREFHRRYRLPSNVDQSALSCSLSADGMLTF:GPKIQTGLDATHAE-R-A-IPVSR-EE-KP---TSA
HEATSHOCKPROTEINBETA-7 VDVRDFSPEDIIVTTSNNHIEVRA---EKLAADG---TVMNTFAHKCOLPEDVDPTSVTS
                                                                                      eatshockproteinbeta-6: VAREFHRRYRLPPGVDPAAVTSALSPEGVLSI ----Q---A-----A--PASA-QA-PP---PAA
HEATSHOCKPROTEINBETA-3 LDVVOFLPEDIIIOTFEGWLLIKAOHGTRMDEHG---FISRSFTROYKLPDGVEIKDLSA
                                                                                      eatshockproteinbeta-2: VSREFCRTYVLPADVDPWRVRAALSHDGILNLEAPRGGRHLDTEVNEVYISLLPAPP-DP-EEEE-EAAI
HEATSHOCKPROTEINBETA-8 VNVHSFKPEELMVKTKDGYVEVSGKHEEKODEGG---IVSKNFTKKIOLPAEVDPVTVFA
                                                                                      eatshockproteinbeta-1: ISRCFTRKYTLPPGVDPTOVSSSLSPEGTLTVEAP-MP-KLATOSNEITIPVTFESRAOLGGPEAAKSDE
HEATSHOCKPROTEINBETA-2
                     LDVSHFTPDEVTVRTVDNLLEVSARHPQRLDRHG---FVSREFCRTYVLPADVDPWRVRA
                                                                                      |eatshockproteinbeta-8:| VSKNFTKKIQLPAEVDPVTVFASLSPEGLLII<mark>=</mark>APQVP-PYST-FGE-S---SF-NN-EL--PQ--DSQE
HEATSHOCKPROTETNBETA-1
                     LDVNHFAPDELTVKTKDGVVEITGKHEERODEHG---YISRCFTRKYTLPPGVDPTQVSS
                                                                                      leatshockproteinbeta-7: VMNTFAHKCQLPEDVDPTSVTSALREDGSLTIRARRHP-H--T---E-H---V---Q-QT--F---RTE
HEATSHOCKPROTETNRETA-6 LOVKHESPEETAVKVVGEHVEVHARHEERPDEHG---EVAREEHRRYRI PPGVDPAAVTS
                                                                                      leatshockproteinbeta-3: ISRSFTRQYKLPDGVEIKDLSAVLCHDGILVV.-------E-----V---K-D---P----VG
ALPHA-CRYSTALLINGCHAIN LOVKHESPEELKVKVLGDVTEVHGKHEERODEHG---FISREEHRKYRIPADVDPLTITS
                                                                                    Heatshockproteinbeta-9: MSOKVHRKM-LPSNLSPTAMTCCLTPSGOLWV RGOCVA--LAL--PEAO-T-GPSPRLGS-LGS--KASN
ALPHA-CRYSTALLINACHAIN LDVKHFSPEDLTVKVODDFVEIHGKHNERODDHG---YISREFHRRYRLPSNVDOSALSC
HEATSHOCKPROTEINBETA-9 CLTPSGOLWYRGOCVALALPEAOTGP-----SPRLGSLGSKASNLTR---- 159
                                                                                    Alpha-crystallinBchain: PK-K
                     ALREDGSLTIRARRHPHTEHVQQ-TFRTEIKI----- 170
HEATSHOCKPROTEINBETA-7
                                                                                    Alpha-crystallinAchain: PS-S
HEATSHOCKPROTEINBETA-3 VLCHDGILVVEVKDPVGTK------ 150
                                                                                     Heatshockproteinbeta-6: -A-K
HEATSHOCKPROTEINBETA-8 SLSPEGLLIIEAPOVPPYSTFGESSFNNELPODSOE-------VTCT---- 196
                                                                                     łeatshockproteinbeta-2: VE-P
HEATSHOCKPROTEINBETA-2 ALSHDGILNLEAPRGGRHLDTEVN--EVYISLLPA------PPDPEEEEEAAIVEP 182
                                                                                     Heatshockproteinbeta-1: TAAK
HEATSHOCKPROTEINBETA-1 SLSPEGTLTVEAPMPKLAT--QSN--EITIPVTFESRAQLGGPEAAKSDETAAK--- 205
                                                                                     Heatshockproteinbeta-8: VTCT
HEATSHOCKPROTEINBETA-6 ALSPEGVLSIOAAPASAOAPPPAA--AK-----------------160
                                                                                     Heatshockproteinbeta-7: IK-I
ALPHA-CRYSTALLINBCHAIN SLSSDGVLTVNGPRKQV----SGP--ERTIPITREEKPAVTAAPKK------ 175
                                                                                     leatshockproteinbeta-3: -T-K
ALPHA-CRYSTALLINACHAIN SLSADGMLTFCGPKIQTGLDATHA--ERAIPVSREEKPTSAPSS------ 173
                                                                                      leatshockproteinbeta-9: LT-R
```

Arbre guide différent



- Arbre guide différent
- Modèle de Markov caché



- Arbre guide différent
- Modèle de Markov caché
- pénalité de gap constante

Conclusion



• Trois étapes implémentées

Conclusion



• Trois étapes implémentées



Complexité temporelle

Conclusion



• Trois étapes implémentées



Complexité temporelle



Des résultats satisfaisants