




ClustalLite : Alignement multiple heuristique par la méthode Clustal

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M2 Bio-informatique parcours biologie informatique

Développement

- <https://github.com/gnanalin/ClustalLite/tree/main>
- CONDA (v.24.7.1)  env_clustallite

Applications

Outil d'alignement
multiple

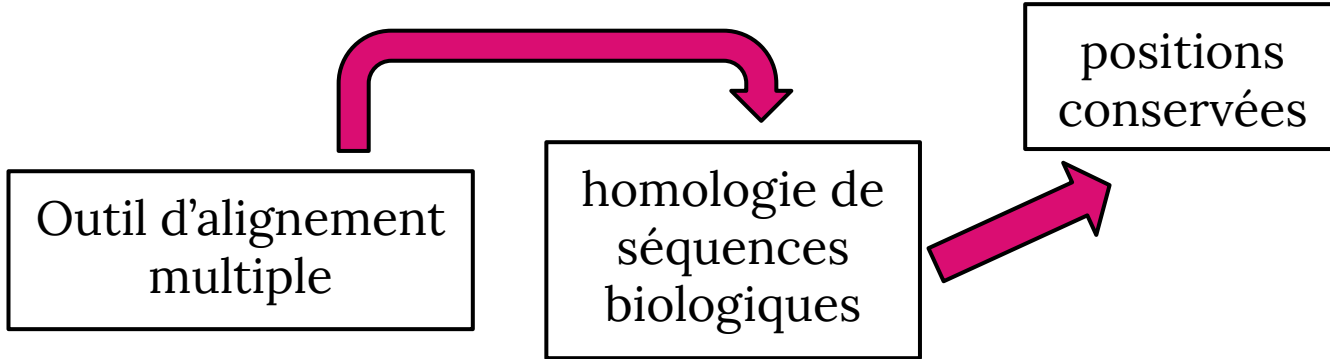
Applications



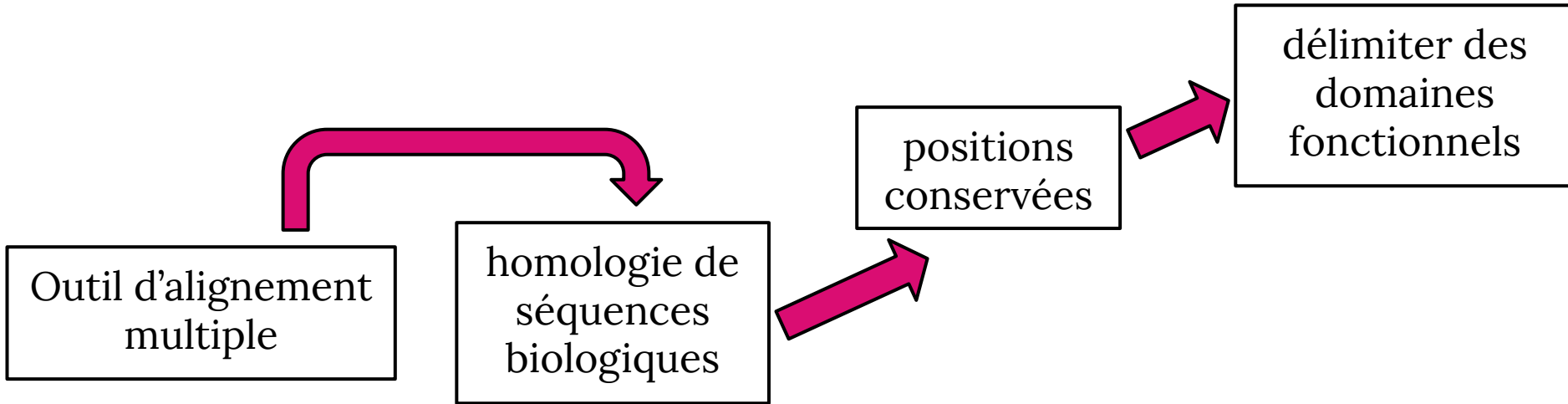
Outil d'alignement
multiple

homologie de
séquences
biologiques

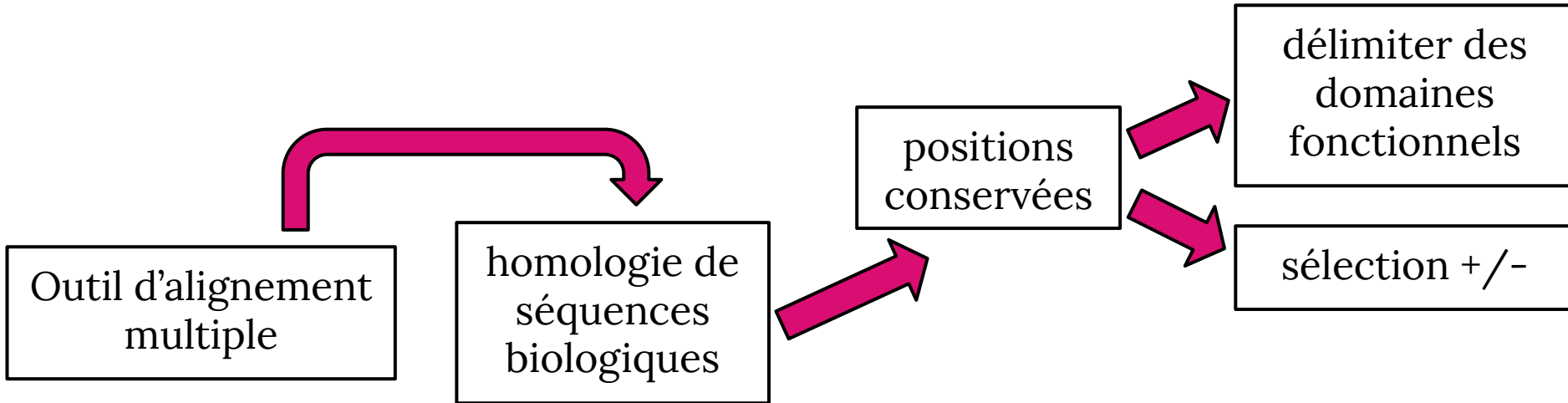
Applications



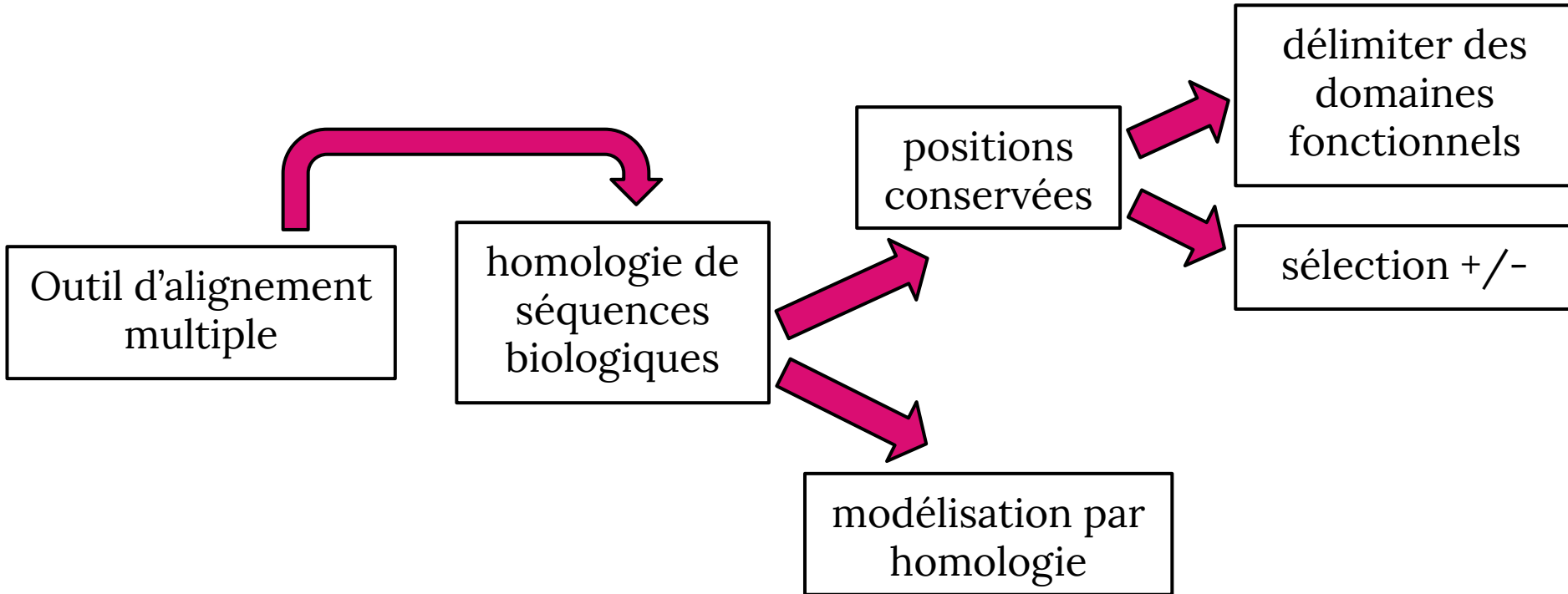
Applications



Applications

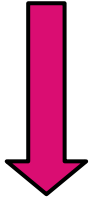


Applications



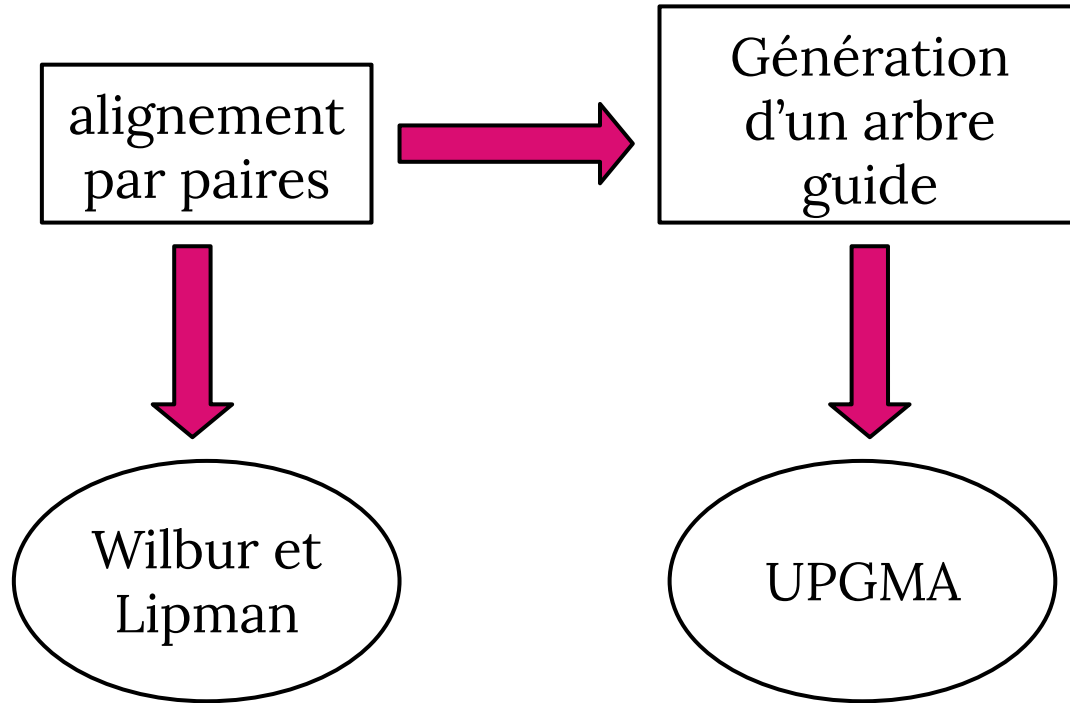
Étapes

alignement
par paires

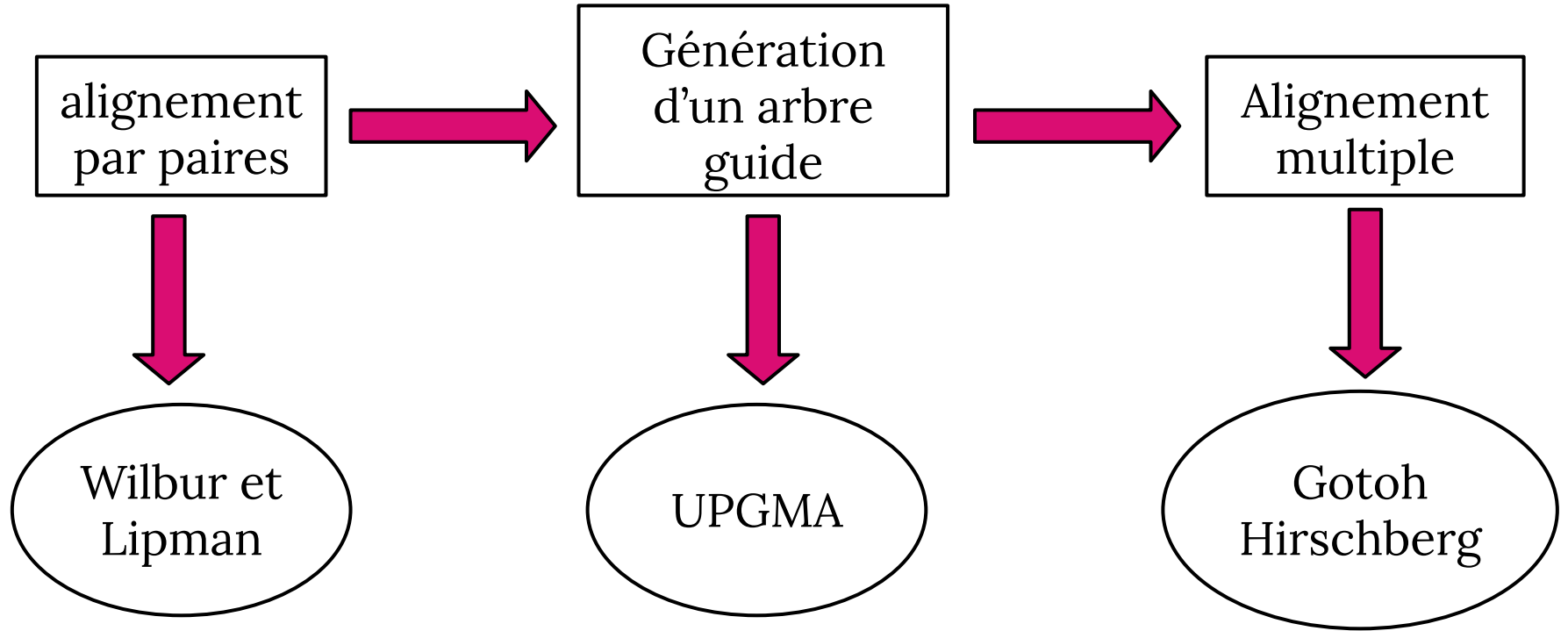


Wilbur et
Lipman

Étapes



Étapes

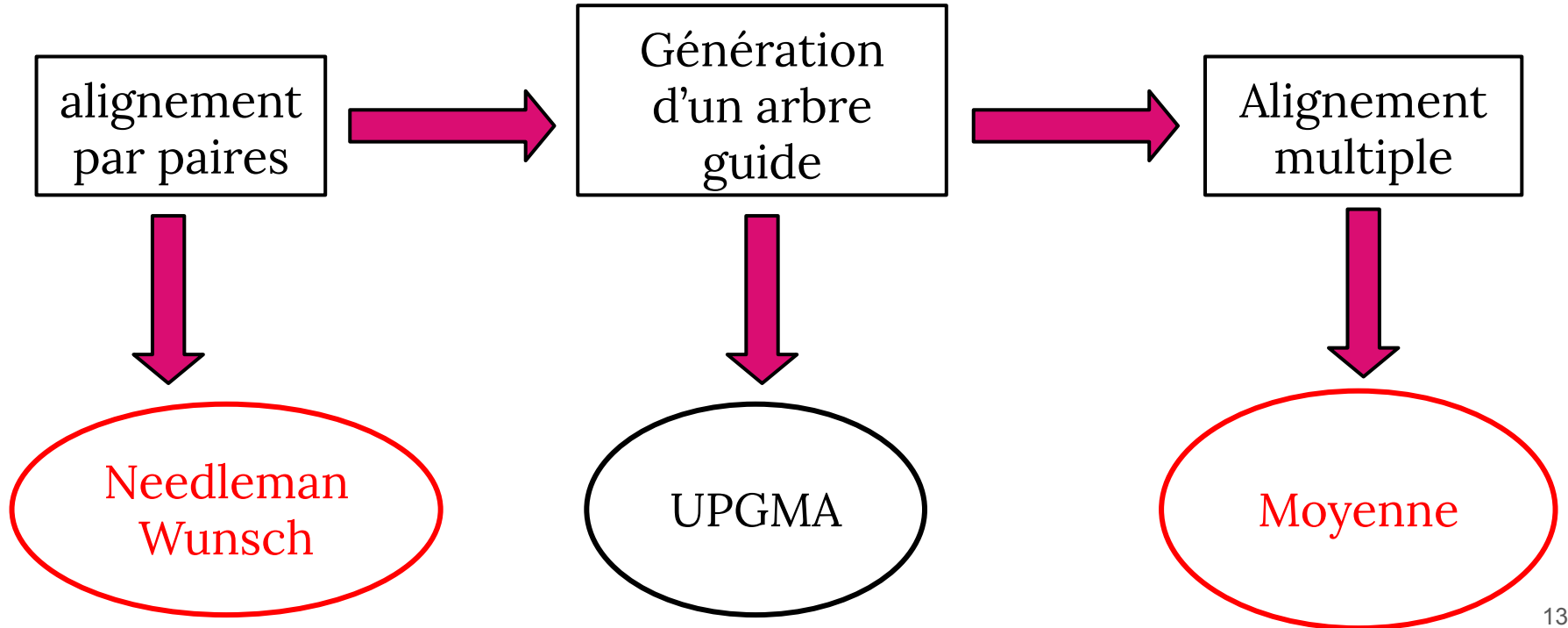


Objectif

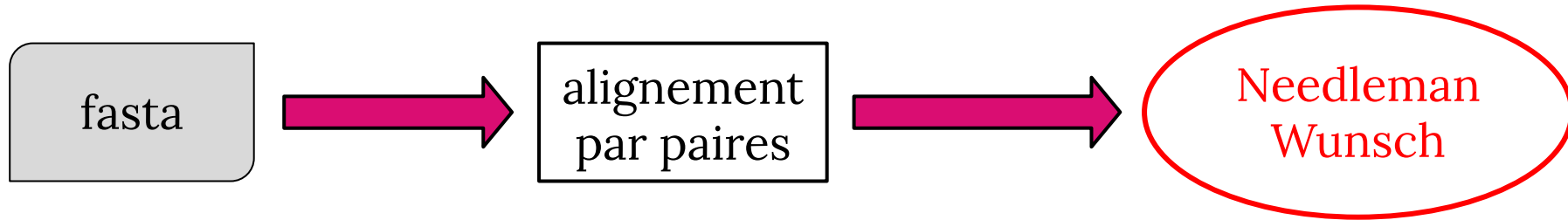
- *Réimplémenter une version simplifiée de Clustal*

Objectif

- Réimplémenter une version simplifiée de Clustal



Les algorithmes



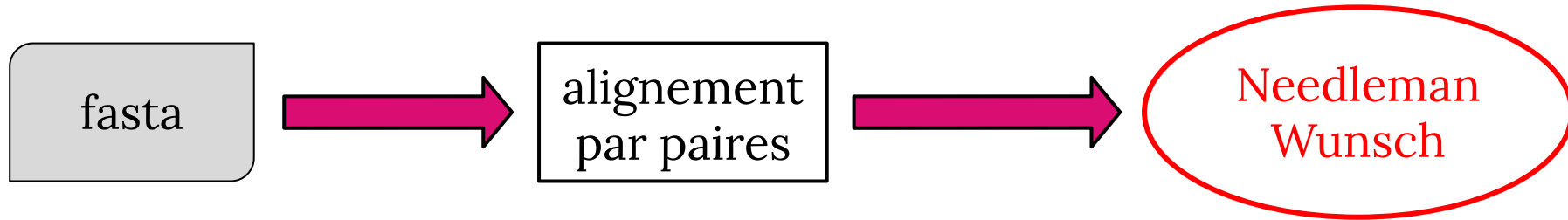
numpy (v2.1.1)

$F(I - 1, J - 1) + S(I, J)$	$F(I - 1, J) - \text{gap}$
$F(I, J - 1) - \text{gap}$	$F(I, J)$

Red arrows indicate dependencies: one from the top-left cell to the bottom-right cell, one from the top-right cell to the bottom-right cell, and one from the bottom-left cell to the bottom-right cell.

- $\text{gap} = 8$
- $S(I, J)$: BLOSUM62
pandas (v2.2.2)

Les algorithmes



$F(I - 1, J - 1) + S(I, J)$	$F(I - 1, J) - \text{gap}$
$F(I, J - 1) - \text{gap}$	$F(I, J)$

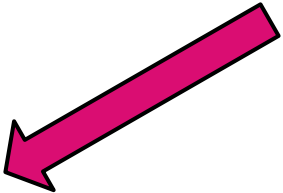
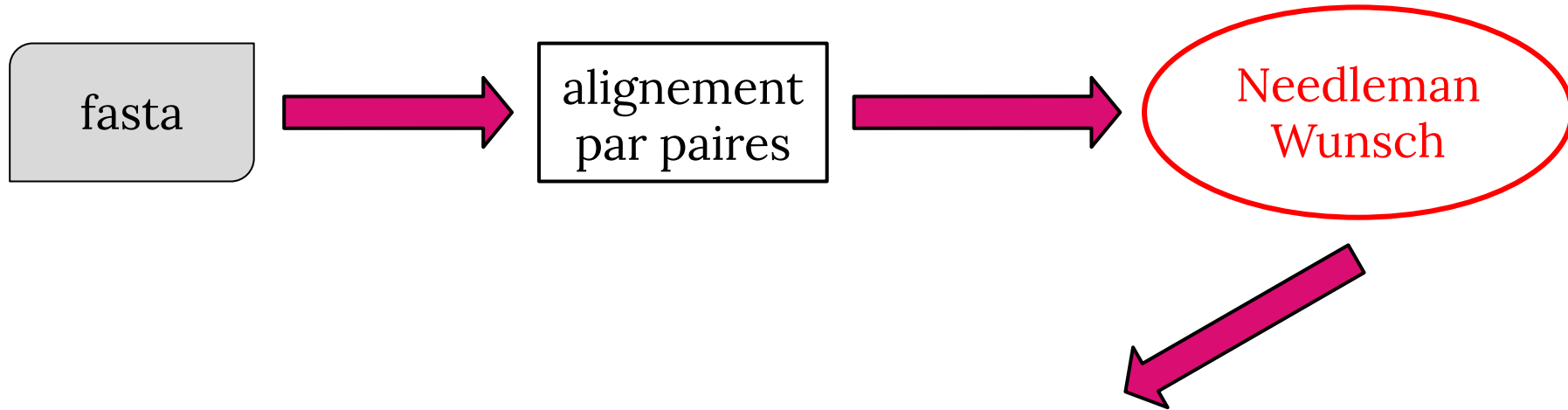
1	1
2	0

0 : diagonale

1: gauche

2: haut

Les algorithmes



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

Les algorithmes

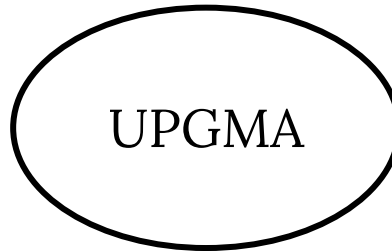
	Seq1	Seq2	Seq3
Seq1	-10	12	89
Seq2	-10	-10	15
Seq3	-10	-10	-10



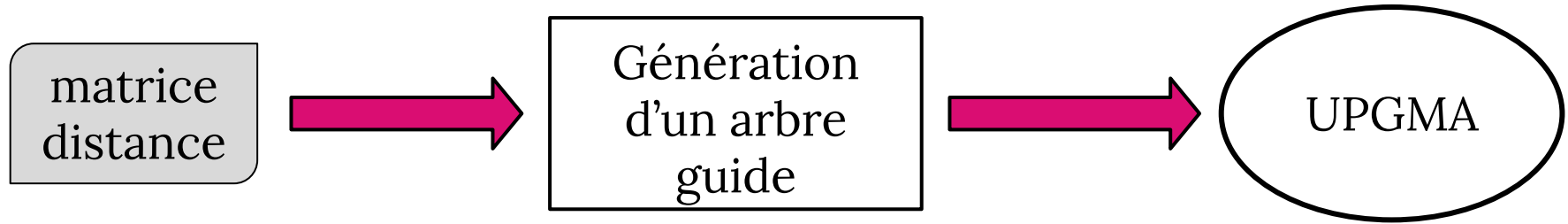
$$\text{matrice distances} = 1 - ((\text{matrice scores} - \text{minimum}) / \text{maximum} - \text{minimum})$$

Les algorithmes

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



Les algorithmes

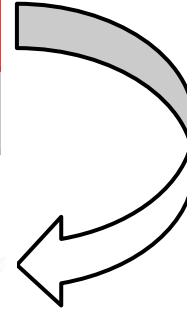


	Seq1	Seq2	Seq3
Seq1	-10	1	0
Seq2	-10	-10	0.96
Seq3	-10	-10	-10

Les algorithmes

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

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



Les algorithmes

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

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

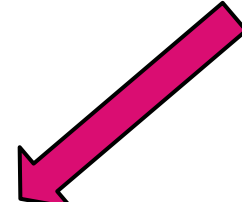
Arbre guide : ((Seq1, Seq3), Seq2)

Les algorithmes

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



Alignement multiple



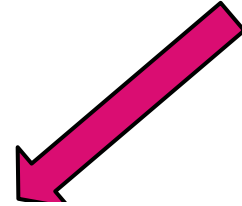
$$\textit{diagonale}(F(i, j)) = F(i - 1, j - 1) + \textit{moyenne}(\textit{cluster1}(i), \textit{cluster2}(j))$$

Les algorithmes

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



Alignement multiple



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

Seq1 : **A**WVED

Seq2 : -TALD

Seq3 : **R**EDAL



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

Résultats

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

Here is the file's content :

Alpha-crystallinBchain: MDIAIHHWPWIRRPFFPFHSPSRLFDQFFGEHLLESDFPTSTSLSPFYLRPPSFLRAPSWFDTGLSEMRLEKDRFSVNLVDVKHFSPEELKVKVLGDVIEVHGKHEERQDEHGFISREFHRRYRIPADVDPDLTITSSLSDDGLTVNGPRKQVSGPERTIPITREEKPAVTAAPKK

Alpha-crystallinAchain: MDVTIQHPWFKRTLGPFPYSRLFDQFFGEGLFEYDLLPFLSSTISPYRQSLFRTVLDSGISEVRSRDKFVIFLDVKHFSPEDLTVKVQDDFVEIHGKHNERQDDHGYISREFHRRYRLPSNVDQSALSCSLSADGMLTFCGPKIQTGLDATHAERAIPVSREEKPTSAPSS

Heatshockproteinbeta-6: MEIPVPVQPSWLRRASAPLPGLSAPGRLFDQRFGEGLLEAELAALCPTTLAPYYLRAPSVALPVAQVPTDPGHFSVLLDVKHFSPEEIAVKVGEHVEVHA RHEERPDEHGFVAREFHRRYRLPPGVDPAAVTSALSPEGVLSIQAAPASQAAPPPAAAK

Heatshockproteinbeta-1: MTERRVPFSLLRGPSWDPFRDWYPHSRLFDQAFGLPRLPEEWSQWLGGSSWPGYVRPLPPAAIESPAVAAPAYSRLSRQLSSGVSEIRHTADRWVSLDV NHFAPDELTVKTKDGVVEITGKHEERQDEHGYISRCFTRKYTLPPGVDPTQVSSSLSPGTLTVEAPMPKLATQSNEITIPVTESRAQLGGPEAAKSDETAAK

Heatshockproteinbeta-2: MSGRSVPHAHPATAEYEFANPSRLGEQRFGEGLLPEEILTPTLYHGYVVRPRAAPAGEGSRAGASELRLSEGKFQAFLDVSHFTPDEVTVRTVDNLLVSA RHPQRLDRHGFVSREFCRITYLPADVDPWRVRAALSHDGILNLEAPRGGRHLDTEVNEVYISLLPAPPDPEEEEEAAIVEP

Heatshockproteinbeta-8: MADGQMPFSCHYPSRLRRDPFRDPSLSSRLDDGFGMDPFPDDLTA SWPDWALPRLSSAWPGTLRSGMVPRGPTATARFGVPAEGRTPPPPFGEPWKVCVN VHSFKPEELMVKTKDGYVEVSGKHEEKQEGGIVSKNFTKKIQLPAEVDPVTVFASLSPEGLLIIEAPQVPPYSTFGESSFNNELPQDSQEVTC

Heatshockproteinbeta-3: MAKIILRHLIEIPVRYQEEFEARGLEDCLRDHALYALPGPTIVDLRKTRAAQSPPVDSAAETPPREGKSHFQILLDVVQFLPEDIIIQTFEGWLLIKAQHGT RMDEHGFISRSFTRQYKLPDGV EIKDLSAVLCHDGILVVEVKDPVGTK

Heatshockproteinbeta-7: MSHRTSSTFRAERSFHSSSSSSSSSTSSASRALPAQDPPMEKALSMFSDDFGSFM RPHEPLAFPARPGGAGNIKTLGDAYEFAVDVRDFSPEDIIVTTS NNHIEVRAEKLAADGTMNTFAHKCQLPEDVDPTSVTSALREDGSLTIRARRHPHTEHVQQTFRTEIKI

Heatshockproteinbeta-9: MQRVGNTFSNESRVASRCPVGLAERNRVATMPVRLLRDSPAAQEDNDHARDGFQMKLDAHGFAPEELVVQVDGQWLMVTGQQQLDVRDPERVSYRMSQKVR HKMLPSNLSPTAMTCCLTPSGQLWVRGQCVALALPEAQTGPSRLGSLGSKASNLTR

Résultats

Here are the Needleman-Wunsch alignments :

Alpha-crystallinBchain: MDIAIHPWIRRPFFPFHSPSRLFDQFFGEHLLESDFP-TSTSLSPFYLRPPSFLRAPS

Alpha-crystallinAchain: MDVTIQHPWFKRTLGPFFY-PSRLFDQFFGEGLFEYDLLPFLSSTISPYR-R-QSLFR--T

Alpha-crystallinBchain: WFDTGLSEMRLEKDRFSVNLDVKHFSPEELKVVLGDVIEVHGKHEERQDEHGFISREFH

Alpha-crystallinAchain: VLDSGISEVRSDRDKFVIFLDVKHFSPEDLTVKVQDDFVEIHGKHNERQDDHGYISREFH

Alpha-crystallinBchain: RKYRIPADVDPLTITSSLSSDGVLTVNGPRKQ--VSG--PERTIPITREEKPAVTAAPKK

Alpha-crystallinAchain: RRYRLPSNVDQSALSCSLSADGMLTFCGPKIQTGLDATHAERAIPVSREEKP--TSAPSS

Alignement score : 466

Alpha-crystallinBchain: MDIAIH-HP-WIRR-PF-FP-FHSPSRLFDQFFGEHLLESDFPTSTSLSPFYLRPPSFL

Heatshockproteinbeta-6: MEIPVPVQPSWLRRASAPLPGLSAPGRLFDQRFGEGLLEAEL--A-ALCPTTL-APYYL

Alpha-crystallinBchain: RAPSWFDTGLSEMRLEKDRFSVNLDVKHFSPEELKVVLGDVIEVHGKHEERQDEHGFIS

Heatshockproteinbeta-6: RAPS-VALPVAQVPTDPGHFSVLLDVKHFSPEEIAVKVVEHVEVHARHEERPDEHGFVA

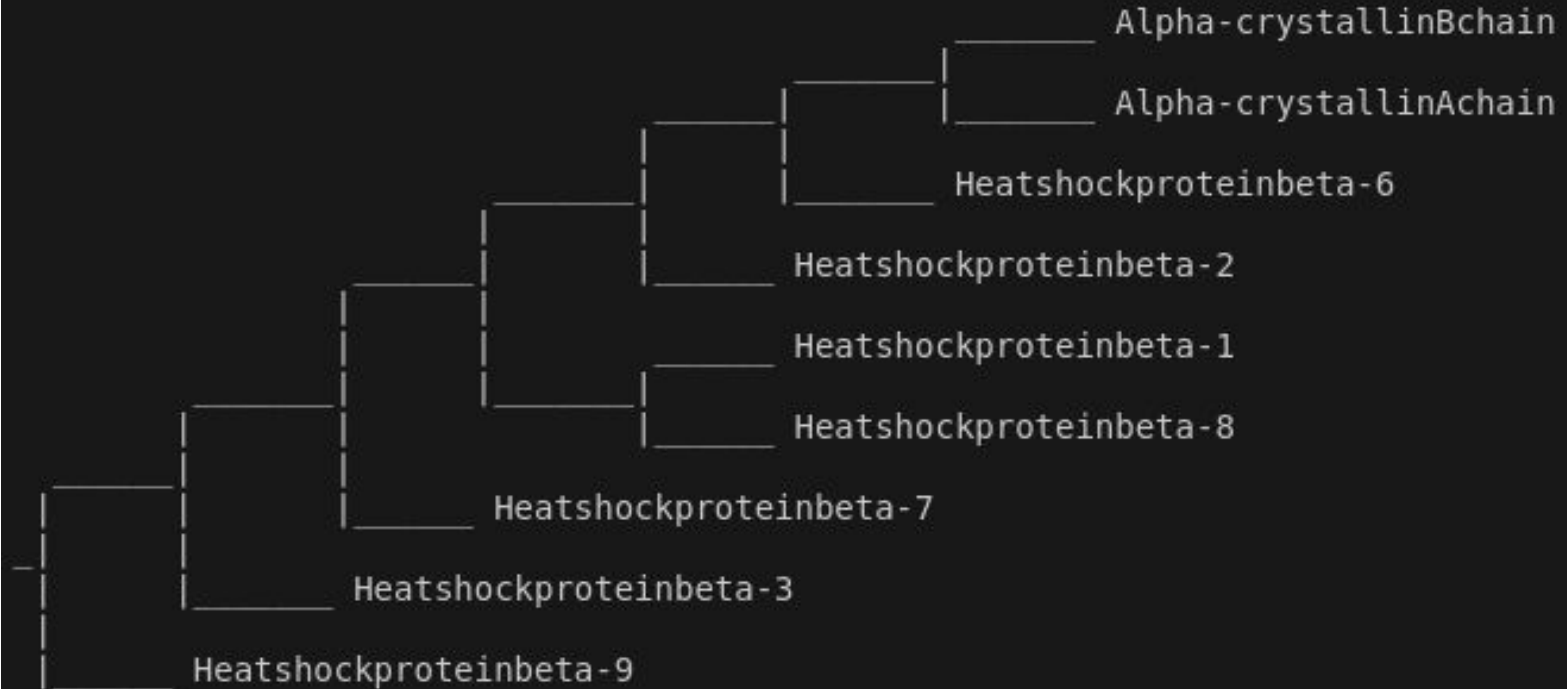
Alpha-crystallinBchain: REFHRKYRIPADVDPLTITSSLSSDGVLTVNGPRKQVSGPERTIPITREEKPAVTAAPKK

Heatshockproteinbeta-6: REFHRRYRLPPGVDPAAVTSALSPEGVLSI-----Q-AAP-AS---AQAPPPA--AA--K

Alignement score : 254

Résultats

Here is the UPGMA algorithm result :



Résultats

Here is the multiple alignment result :

```
Alpha-crystallinBchain: M-DIAIH-HP-WIRR-PFFPF--HS-PSRLFDQFFGEHLLES-D-LFP-TSTSLSPFYLRP--P----S-F
Alpha-crystallinAchain: M-DVTIQ-HP-WFKR-TLGP--Y--PSRLFDQFFGEGLFEYD-LLPFLSSTISPY--R---Q----S-L
Heatshockproteinbeta-6: M-EIPVPVQPSWLR--ASAPLPGLSAPGRLFDQRFGEGLLEAE-LAALCPTTLAPYYLRA--P----S--
Heatshockproteinbeta-2: M-S-GRS-VP-HAHP-ATAEYE-FANPSRLGEQRFGEGLLEE-IL--TPTLYHGYVVR--P----R-A
Heatshockproteinbeta-1: MTERRVPFSL-LRGP-SWDPRDWYPHSRLFDQAFGLPRLPEE-WSQWLGSSWPGYVRPLPPAAIESPA
Heatshockproteinbeta-8: MADGQMPFSCHYPSRLRRDPFRDSPLSRLDDGFGMDPFPDDLTAW-PDWALP-RLSSAWPGTLRSGM
Heatshockproteinbeta-7: M-SHRTS-ST-F--R-AERSFHSSSSSSSSSTSSSASRALPAQ-DPP-MEKALSMFSDDF--G----S-F
Heatshockproteinbeta-3: M-A-KI--I--LRHL-IEIPVR-Y--QEEFEARGLEDCLRDHA-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-GLSEMRLEKDRFSVNLVDVKHFSPEELKVKVLGDVIEVHGKHE-E-RQDEH-GF-
Alpha-crystallinAchain: FR---T-V-LD--S-GISEVRSRDKFVIFLDVKHFSPELTVKVQDDFVEIHGKH--E-RQDDH-GY-
Heatshockproteinbeta-6: V----A---L---P--VAQVPTDPGHFSVLLDVKHFSPEEIAVKVGEHVEVHARHE-E-RPDEH-GF-
Heatshockproteinbeta-2: APAG--E-G-SR--A-GASELRLSEGKFAQLDVSHFTPDEVTVRTVDNLEVSARHP-Q-RLDRH-GF-
Heatshockproteinbeta-1: VAAPAYSRLSRQLSSGVSEIRHTADRWRVSLDVNHFADELTVKTKDGVVEITGKHE-E-RQDEH-GY-
Heatshockproteinbeta-8: VPRGPTATARFGVPAEGRTPPFPPEGPWKVCNVVHSFKPEELMVKTKDGYEVVSGKHE-E-KQQEG-GI-
Heatshockproteinbeta-7: MRPHSEPLA-FPARPGGAGNIKTLDGAYEFAVDVDRFSPEDIIVTTSNNHIEVRA---E-KLAAD-GT-
Heatshockproteinbeta-3: AQSP--P-V-DS--A-AETPPREGKSHFQILLDVVQFLPEDIIITQFEGWLLIKAQH-G-T-RMDEH-GF-
Heatshockproteinbeta-9: LR-D--S---P--A-AQENDNHARDGFMKLDAGHFAPEELVVQVDGQWLMVTGQQQLDVRDPERVSYR
```

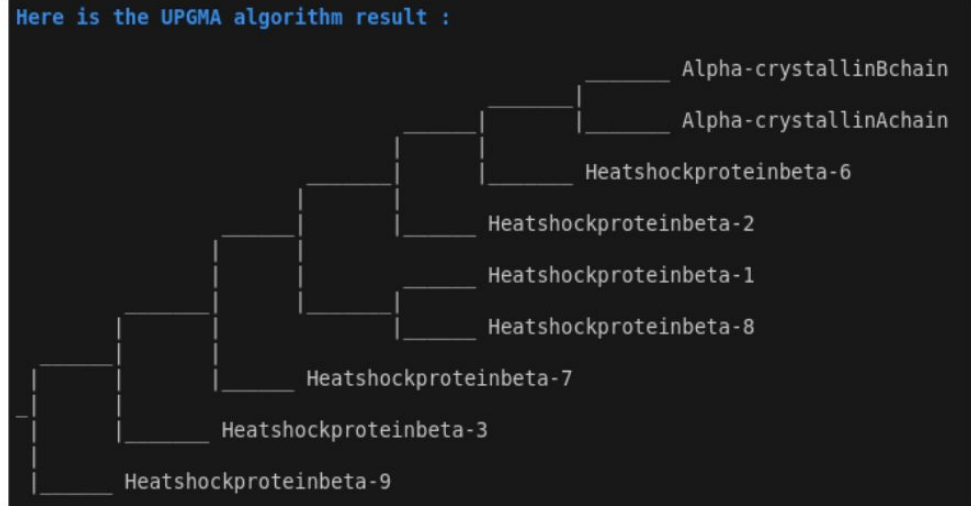
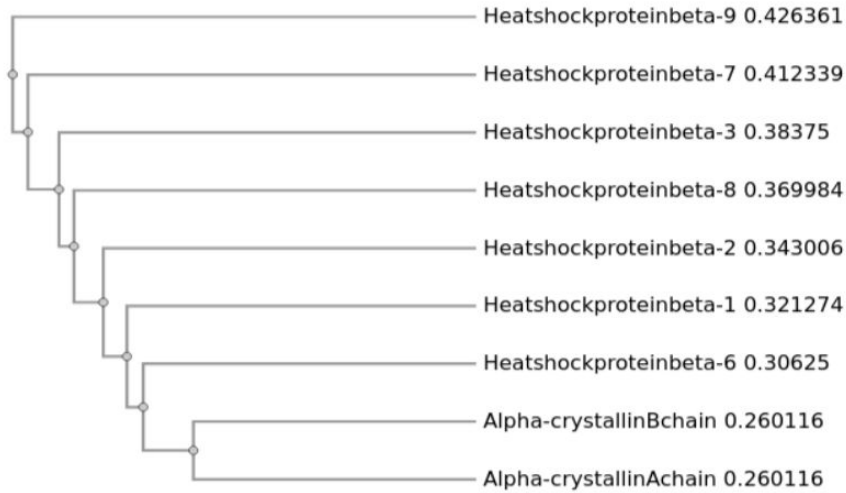
```
Alpha-crystallinBchain: ISREFHRKYRIPADVPLTITSSSSDGLTVNGPRKQ--VSG--PE-R-T-IPITR-EE-KPAV-TAA-
Alpha-crystallinAchain: ISREFHRRYRLPSNVDSALSCSLSDAGMLTFCGPKIQTGLDATHAE-R-A-IPVSR-EE-KP---TSA-
Heatshockproteinbeta-6: VAREFHRRYRLPPGVDPAAVTSALSPEGVLSI-----Q---A-----A--PASA-QA-PP---PAA-
Heatshockproteinbeta-2: VSREFCRTYVLPADVDPWRVRAALSHDGILNLEAPRGGRHLDTEVNEVYISLLPAPP-DP-EEEE-EAAI
Heatshockproteinbeta-1: ISRCFTRKYTLPPGVDPQTQVSSSLSPGTLTVEAP-MP-KLATQSNITIPVTTFESRAQLGGPEAAKSDE
Heatshockproteinbeta-8: VSKNFTKKIQLPAEVDVPTVFASLSPEGLLIEAPQVP-PYST-FGE-S---SF-NN-EL--PQ--DSQE
Heatshockproteinbeta-7: VMNTHFAHKCQLPEDVDPTSVTSALREDGSLTIRARRHP-H--T---E-H---V---Q-QT--F--RTE-
Heatshockproteinbeta-3: ISRSFTRQYKLPDGVIEIKDLSAVLCHDGILVV-----E-----V---K-D---P---VG-
Heatshockproteinbeta-9: MSQKVHRKM-LPSNLSPTAMTCLTPSGQLWVRGQCVA--LAL--PEAQ-T-GPSRLGS-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
```

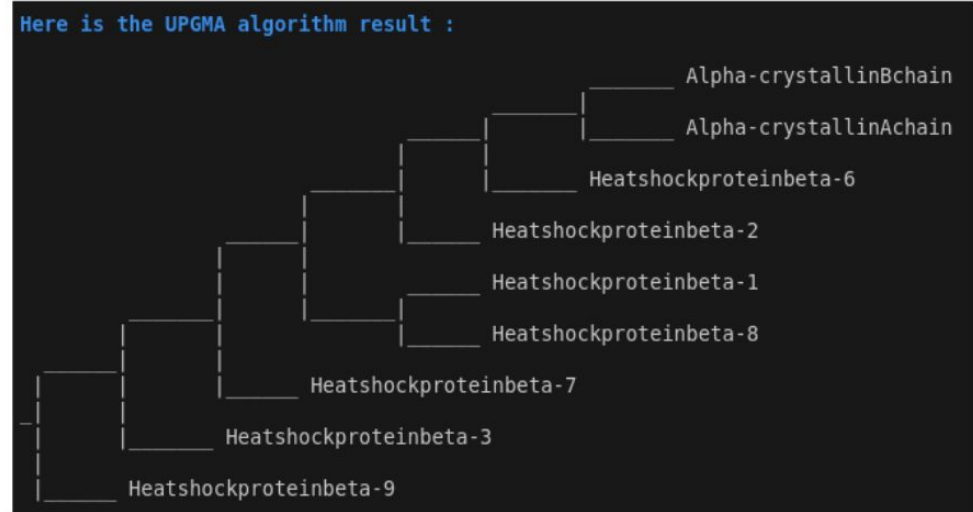
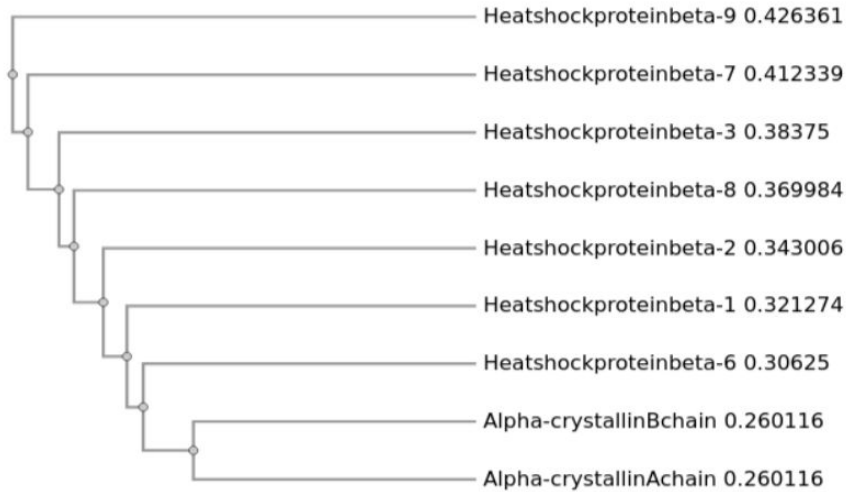
Résultats

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

Résultats : Comparaison

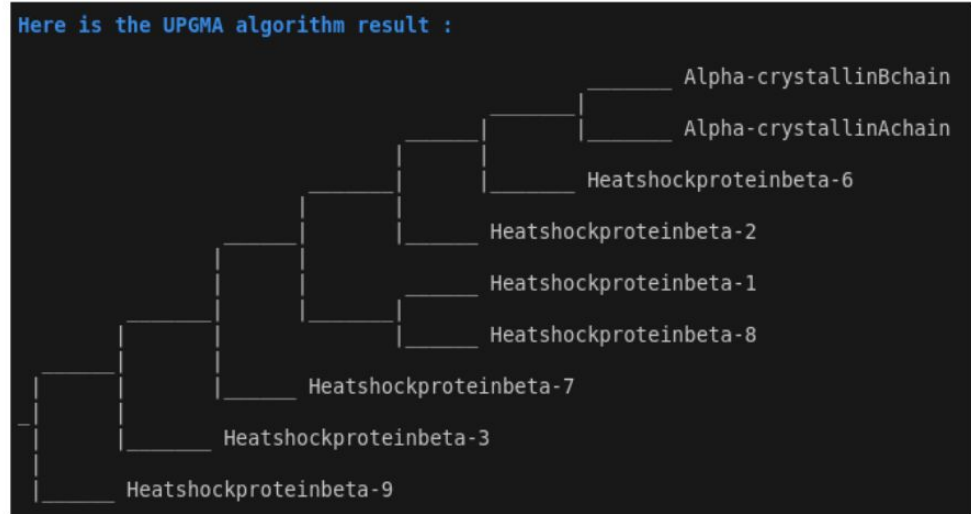
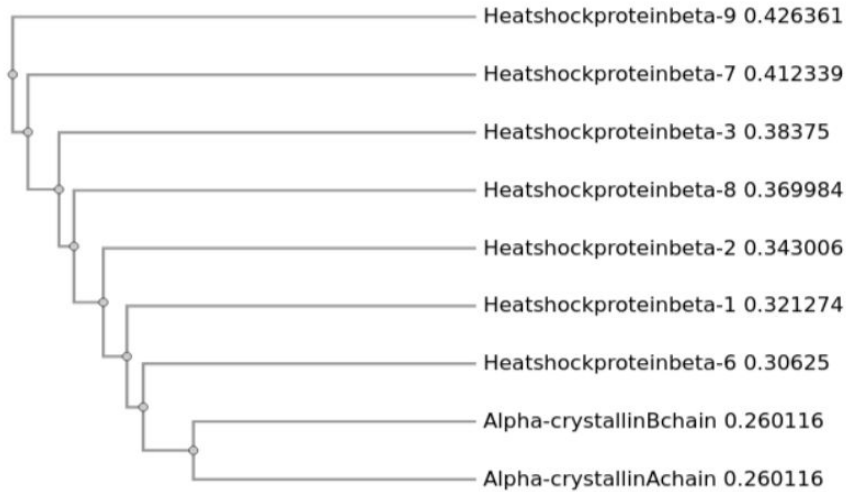


Résultats : Comparaison



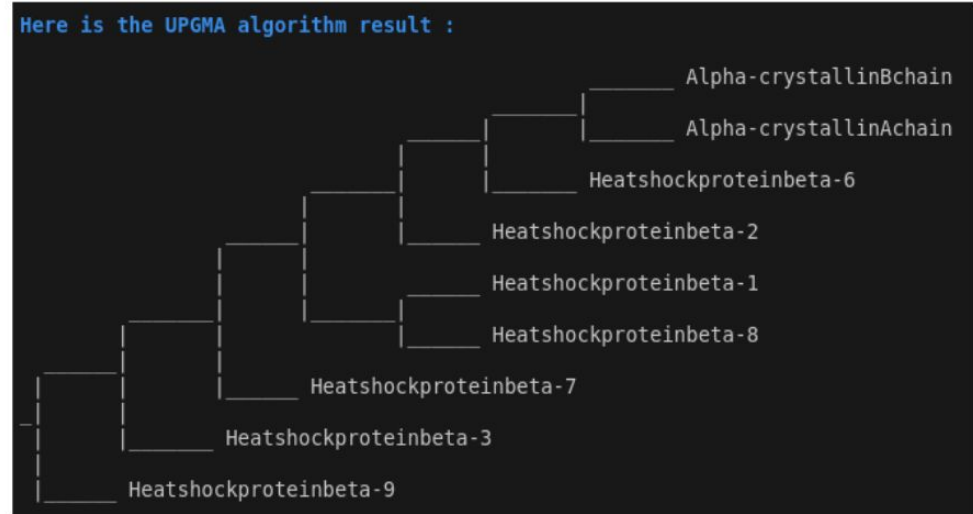
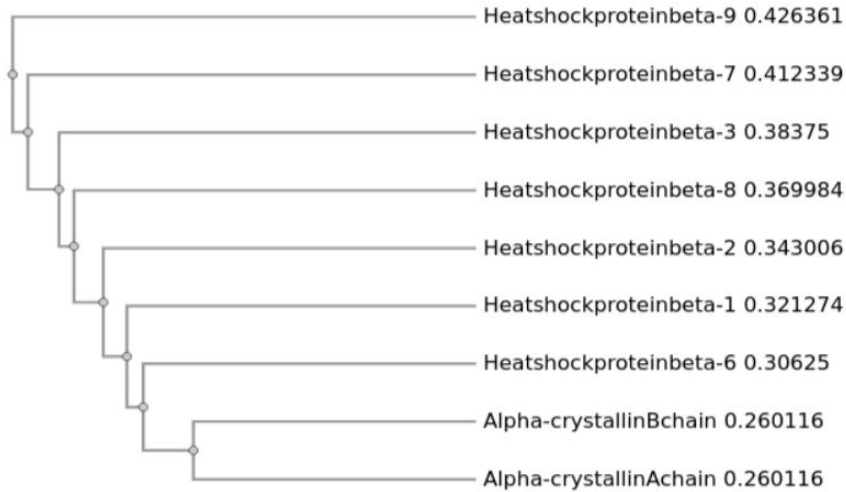
- Needleman-Wunsch VS Wilbur et Lipman

Résultats : Comparaison



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

Résultats : Comparaison



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

Résultats : Comparaison

CLUSTAL O(1.2.4) MULTIPLE SEQUENCE ALIGNMENT

HEATSHOCKPROTEINBETA-9	-----MQ-----RVNGTFSNEIR-----VASR	17
HEATSHOCKPROTEINBETA-7	MSHRT-----SSTF-----RAERFSHSSSSSSSSSSSSASRALPAQDPPEKALKS	46
HEATSHOCKPROTEINBETA-3	MAKIIILRLK-----EETPVRVQ-----EEF-----EARGLEDPCDL	30
HEATSHOCKPROTEINBETA-8	MADGQMFSSCHYP-SRL--RRDPFRDPSLSSRL--DDG-----FGMDPPDRLTAS	47
HEATSHOCKPROTEINBETA-2	MSGRSVPAHP-----ATAEYEFANPSRLG--EQK-----FGGLPEELIT-	40
HEATSHOCKPROTEINBETA-1	MTRRVRFVSLGRPSW--PDFRWYPSHSLRF--DQA-----FGLPRLPESSQW	45
HEATSHOCKPROTEINBETA-6	-----MEIVPVPVQSLRRASAPLGLSAPGRFL--DQR-----FGHGLEAEALAL	45
ALPHA-CRYSTALLINBCHAIN	-----MDIAIHPWTRRPFPP--FHSPSRLF--DQF-----FGHGLESLDPLP	40
ALPHA-CRYSTALLINBCHAIN	-----MDVIQHPFKRTLGF--F-YPSRLF--DQF-----FGHGFEDYLLPF	39

HEATSHOCKPROTEINBETA-9	CPS-	-VGLAEINRVAT-	MPV-	-LLRLDPAAQEGDNHARDGQFMK	57
HEATSHOCKPROTEINBETA-7	-	MPDQFGFSNRPHSV-	-	LAPFAAPGAGNIGITLGDAYEFA	85
HEATSHOCKPROTEINBETA-3	-	DHALYALPGPT-	TVDLR-	-KTRAAGSPVPYGSAAETPPREGKSHFOIL	94
HEATSHOCKPROTEINBETA-8	WPDWALPRLSSAMPTGLRSGMVRP-	-	GPTA-	TARFVGPAEGRTPPPFPGEKWKV	79
HEATSHOCKPROTEINBETA-2	-P-	TLHYGVYVPRPAAP-	-	AGEGRGASGLSELRGQFAF	77
HEATSHOCKPROTEINBETA-1	LG-	GSSNPQGVYRPLPAATESPAVAAYASRLS	QSLSGVSEIRTHADNRMVS	98	
HEATSHOCKPROTEINBETA-6	CP-	TTLAPPLYLA-	PSV-	ALPVAQVPTDPGHSLV	98
ALPHA-CRYSTALLINBCHAIN	ST-	SLSPFYLR-RP-	PSFLR-	APSWITGISEMRLEKRGKVF	78
ALPHA-CRYSTALLINACHAIN	LS-	STISPY-RQ-	SLF-	RTVLDSGISEVRSRDKQFVTF	78

HEATSHOCKPROTEINBETA-9 LDAGHFAPEELVVQVGDGVVQDGLVDVPRPVSRYKQVHKMLPSLTAMTC 117
HEATSHOCKPROTEINBETA-7 DVDRFDSPEDIIIVTSGMNIIEVRA---EKKLADE---TVNMTFAKQCLPDDVTS 139
HEATSHOCKPROTEINBETA-3 LDVVQFLPEDIITQFEGWLLIKAQHGRMDEHG---FISRSFTRQYKLPDGVKIDLSA 139
HEATSHOCKPROTEINBETA-8 VNVHSPKPEELWKLWQGVVEVSGHEEKQEGEG---IVSKNFKTIQLPADVDVPVTFVA 156
HEATSHOCKPROTEINBETA-2 LDVSHFTPDQVTVRTVDNLLVFSARHPQDLRHHG---FVFSREFCTRYVLPADVDPMWIRA 156
HEATSHOCKPROTEINBETA-1 LDVNHFAPELDTYKTDGNGVHGHKEERQDEHG---YISRCFTKYTLPDGVQTVSS 158
HEATSHOCKPROTEINBETA-6 LDVNHFSPEETAIVKVGVEHVHGAHEERPDHG---FVAFERHRRYRLPGVDPAVTS 139
ALPHA-CRYSTALLINBCHAIN LDVKHFSPEELKVKVLGDVIEVHGHEERQDEHG---FISREFHRRYKIPADVDPLITS 139
ALPHA-CRYSTALLINACHAIN LDVKHFSPEDLTVKVGQDFDIEVHGKNERQDDHG---YISREFHRRYRLPSNVQSQALSC 131

HEATSHOCKPROTEINBETA-9	CLTPSGQLVMVRGQVICALPEAQGTG-----SPRLGSLGSKASNLTR----	159
HEATSHOCKPROTEINBETA-7	ALRDGSLDITLRAARPHHTHVHQVQ-TRFEIKI-----	170
HEATSHOCKPROTEINBETA-3	VLCHDGLLVVEVDQPVGTG-----	150
HEATSHOCKPROTEINBETA-8	SLSPGELLIIAEPQVPSYTFGESSFNNELPDQDSQE-----VTCT-----	196
HEATSHOCKPROTEINBETA-2	ALSHDGLNLVQAGRGHGLDTEVN--EYVTSLLPA-----PPDPEEEEEAAIVP	182
HEATSHOCKPROTEINBETA-1	SLSPGTLTVAAEPMKPLAT--QSN-EITTPVTFESRQLQGPEAAKSDEATAAK--	205
HEATSHOCKPROTEINBETA-6	ALSPGVLTVQAPASQAAPPPA--AK-----	160
ALPHA-CRYSTALLINBCHAIN	SLSDGVLTVGPGPKIVQV---SGP-ERTPTITREKPAVTAAPKK-----	175
ALPHA-CRYSTALLINBCHAIN	SLSADGMLTFCGPKITQGLDGLA--ERATIPVREKPTSPAPSS-----	173

Alpha-crystallinBchain: :DIATH-HP-WIRR-PFFPF--HS-PSRLFDQFFGEGHLLSE-D-LFP-TSTSLSPFYLRP--P----S-F
Alpha-crystallinAchain: M-DVTIQ-HP-WFKR-TGLPF--Y--PSRLFDQFFGEGGLEED-LLPFLSSSTISPYLR--Q----S-F
Heatshockproteinbeta-6: M-EIYPVPQSVLWRR-ASAPGLPSAGRLFDQRFGEFLYE-LAALCPPTLAPYYLR--P----S--
Heatshockproteinbeta-2: M-S-GRS-VF-HAMP-ATAEY-FANPSRLGEQRFEGGLPEE-IL--TPTLYGGYYVR--P----R-A
Heatshockproteinbeta-1: MTERRVQFSL-LRGP-SWDPFRDWPHSRLFDQAQFLRLPCE-WSQWLGSSWGPGVYRPLPPAAIESPA
Heatshockproteinbeta-8: MADGQVFFSCHYSRLRRDPFRDPSLLSLDDGFMGFPDDLTAS-PDWALP-LSSAAGPTLRSGM
Heatshockproteinbeta-7: M-SHRTS-ST-F--R-AERSFHSVSSSSSSSSSSSSAALPAQ-DPP-MEKALSMFSDDF--G----S-F
Heatshockproteinbeta-3: M-A-KI-I--LRHL-TEIYPR-Y---QEFEAGLEDRLDHA-LYA-LPGPTIV-DLRK-T----R-A
Heatshockproteinbeta-9: M-Q-RVG-NT-FSNE-SR-V---ASRC-PS-VG-LAERN-R-VAT-M-P-VR-----

Alpha-crystallinBchain: LRAP--S-W-FD--T-GLSEMRLEKDRFSVNLDVKKHFSPEELKVKVLGDVIEVHGKHE-E-RQDEH-GF-
Alpha-crystallinAchain: FR---T-V-LD--S-GISEVSRDQDKFVFLDVKKHFSPEELTKVQVDDFVEIHGKHE-E-RQDDH-GY-
Heatshockproteinbeta-6: V-----A--L--P--VAQSPDTPGHSFVLNLDVKKHFSPEELIAVVVGVGVHEVHKKH-E-RPDEH-GF-
Heatshockproteinbeta-2: APAG--E-G-SR--A-GASELRLSEGKQFAFLDVDSHFTPDVEVTVRTVDNLLVEVSARHP-Q-RLDRH-GF-
Heatshockproteinbeta-1: VAAPAYSRAISRQLSSVSEIRHDAWRKVSVDVNHFPADLETKTKDGVLETSKHE-E-E-RQDEH-GY-
Heatshockproteinbeta-8: VPRGTATARGFVPAEGRTPPPFPFGEKMKCVNHHSPKPEELMKTKDGVVEVSGKHE-E-QQEG-GF-
Heatshockproteinbeta-7: MRPHSEPLA-FPARPGGAGNIKTLGDAYEFQAVLDVDFSPEDIIVTSSNNHLEKRA---E-KLAAD-GT-
Heatshockproteinbeta-4: AQPSP--P-V-DS--A-AETPPREGKSHFQLVDVDFPELIIITTFEGWLLIVRA---E-RMDEH-GF-
Heatshockproteinbeta-9: LR-D-S--S---P--A-AEQNDHARDGFQMKLDAHGAPPELVQVQDQGLVMTGQQLDVRDPERVSY-

Alpha-crystallinBchain: ISREFHRRKYRIPADVPLTITSSSSDGLVTVNGPRKQ--VSG--PE-R-T-IPITR-EE-KPAV-TAA-
Alpha-crystallinAchain: VREFHRRYRLPPGVNDQSLASCSLSADGMLTFCGPKITQGLDATHAE-R-A-IPVSR-EE-KP--TSA-
Heatshockproteinbeta-6: VAREFHRRYRLPPGVNDQSPAAVTSQSGELSI---Q---Q---A---PASA-QA-PP---PAA-
Heatshockproteinbeta-2: VSRECFTRVYLPADVDPWRVRAALSHDGLNLNEAPGRGRHLDTEVNEVYSLLPAP-PP-EEEE-EAAI-
Heatshockproteinbeta-1: ISRCFTRYKTLPPGVDPDTQVSSLSPEGTITLVEAP-MP-KLATQSNIEITPVTFESPAQLGGPEAAKSDE-
Heatshockproteinbeta-8: VSKNFTKKYQLPAEVDPTVTFVSSPEGLLIEAPQP-PYST-FGE-S--SF-NN-LD-PQ--DSQE-
Heatshockproteinbeta-7: VMNFTAHKQCLPEVDPTSVTSALREDGSLTIRARRHP-H-T--E-H--V--Q-Q-T-F--RTE-
Heatshockproteinbeta-9: ISRSFTRQYKLPDGVGEIKLISAVLCHDGLTV---E---E---V--K-D--P--V--VG-
Heatshockproteinbeta-3: MSQKHVRKM-LPSNLSPANTCCLTPSGOLWVRGQCA--LAL-PEAQ-T-GPSPLRGS-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

Résultats : Comparaison

CLUSTAL O(1.2.4) MULTIPLE SEQUENCE ALIGNMENT

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HEATSHOCKPROTEINBETA-9  -----MQ-----RVGNTFSNEIR-----VASR      17
HEATSHOCKPROTEINBETA-7  MSHRT-----SSTF-----RAERSFHSSSSSSSTSSASRALPAQDPPEKALS--      46
HEATSHOCKPROTEINBETA-3  MAKILRLHL-----ETPRVQ-----EEF-----EARGLEDCRL--      38
HEATSHOCKPROTEINBETA-8  MADGQMPFSCHYP-SRL-----RRDPFRDPSLSRL-----DDG-----FGMDPFDOLTAS      47
HEATSHOCKPROTEINBETA-2  MSGRSVPHAHP-----ATAEYEFANPRDG-----EQR-----FGEGGLEPEILIT-      40
HEATSHOCKPROTEINBETA-1  MTERRVPFSLRRGSPW-----DPFRDWPYHRRF-----DQA-----FGLPRLPEEWSQW      45
HEATSHOCKPROTEINBETA-6  -----MEIPVPVQPSWLRASAPLPLGLSAPRRF-----DQR-----FGGLELAELAAL      45
ALPHA-CRYSTALLINBCHAIN  -----MDIAIHPWIRRRPFPP-----FHSPPRRF-----DQF-----FGHELESOLFPT      48
ALPHA-CRYSTALLINACHAIN  -----MDVTIQHWPKRTLGP-----F-YPRRRF-----DQF-----FGGLEFEYDLPF      39
  
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HEATSHOCKPROTEINBETA-9  CPS-----VGLAERNRVAT-----MPV-----RLRLDSPAQQEDNDHARDGFMK      57
HEATSHOCKPROTEINBETA-7  -----MFSDDFGSFMRPHSEP-----LAFPARPGGAGNIKTLGDAYEFA      85
HEATSHOCKPROTEINBETA-3  -----DHALYALPGPT-----IVDLR-----KTRAAQSPVVDAAETPPREGKSHFQIL      74
HEATSHOCKPROTEINBETA-8  WPDNALRLSSAMPTLRSGMVRP-----GPTA-TARFQVPAEGRTPPPFGPEKQVC      99
HEATSHOCKPROTEINBETA-2  -P-----TLYHGYYVPRPAAP-----AGEGSRAGASRLSEKGFQAF      77
HEATSHOCKPROTEINBETA-1  LG-----GSSMPGYRPLPAAAEISPAVAAPAYSRLSRQLSSGVSEIRHTADMRVRS      98
HEATSHOCKPROTEINBETA-6  CP-----TTLAPYYLR-----PSV-----ALPVAQVTPDGHFSVL      77
ALPHA-CRYSTALLINBCHAIN  ST-----SLSPFLY-RR-----PSFLR-APSWIFDGLSEMRLEKDFSVN      78
ALPHA-CRYSTALLINACHAIN  LS-----STISPIY-RQ-----SLF-----RTVDSGISEVRSRDRKQVIF      74
  
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HEATSHOCKPROTEINBETA-9  .DAHGFAPEELVVQVQDGLMVTGQQQLDVRDPEVSYVMSQKVHRKMLPSLSPMTATC      117
HEATSHOCKPROTEINBETA-7  VVDRDQSPEDIIVTTSNNHIEVRA-----EKLAADG-----TMMTFFAHKCQLPEDVPTSVTS      139
HEATSHOCKPROTEINBETA-3  .DVVQFLPEDIIQTTFEGWLLIKAQHGTRDEHG-----FSSRSFTQYKLPDGVIEIKDLSA      131
HEATSHOCKPROTEINBETA-8  VNVHSFKPEELMWKTDGVEVSGVSGHKEEKQEGG-----IVSKNFTKKIQLPAEVDVPTVFA      156
HEATSHOCKPROTEINBETA-2  .DVSHFTPDEVTVRTVDNLLVESARHPQLDRHG-----FSSREFCRTYVLPADVDPWRVRA      134
HEATSHOCKPROTEINBETA-1  .DVNHFAPELTVKTKDGVVEITGKHEERQDEHG-----VYSRCFTKYTLPPGVDPTQVSS      155
HEATSHOCKPROTEINBETA-6  .DVKHFSPEEIAVKVVEGVHVEHARHEERDQHG-----FPAREFHRRYRLPPGVDPAVTS      145
ALPHA-CRYSTALLINBCHAIN  .DVKHFSPEELKVYKLVGVIEVHGKHEERQDEHG-----FSSREFHRRYRIPADVDPILTITS      135
ALPHA-CRYSTALLINACHAIN  .DVKHFSPEELTVKVQDDFVEIHGKHNERQDQHG-----YYSREFHRRYRLPSNDQSQALS      131
  
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HEATSHOCKPROTEINBETA-9  CLTPSGQLWVRGQCVALLPEAQGTG-----SPRLGSLGSKASNLTR-----      159
HEATSHOCKPROTEINBETA-7  ALREDGSLTIRARRHPHTEHVQQTFRTEIKI-----      170
HEATSHOCKPROTEINBETA-3  VLCHDGLVVEVQDPVGTG-----      150
HEATSHOCKPROTEINBETA-8  SLSPEGLLIEAPQVPPYSTFGGESSNNELPQDSQE-----VTCT-----      196
HEATSHOCKPROTEINBETA-2  ALSHDGILNLEAPRGGRHLDETVN-----EYISLLPA-----PPDPEEEEEAAIVP      182
HEATSHOCKPROTEINBETA-1  SLSPEGLTVEAPMKLAT--QSN--EITIPVTFESRAQLGGPEAAKSDETAAK--      205
HEATSHOCKPROTEINBETA-6  ALSPEGVLISQAAPASQAAPPA--AK--      160
ALPHA-CRYSTALLINBCHAIN  SLSSDGVLTVNGPRKQV-----SGP--ERTIPITREKPAVTAAPK--      175
ALPHA-CRYSTALLINACHAIN  SLSADGMLTFCGPKIQTLGDATHA--ERAIPVSREEKPTAPS--      173
  
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Alpha-crystallinBchain: M-DIAIH-HP-WIRR-PFFPF--HS-PRLFDQFFGHELLSLED-LFP-TSTLSLSPFYLRP--P---S-F
Alpha-crystallinAchain: M-DVTIQ-HP-WFKR-TLGP--Y--PRLFDQFFGEGLEFYD-LLPFLSSSTISPIY-R---Q---S-L
Heatshockproteinbeta-6: M-EIPVPVQPSWLR--ASAPLPLGLSAPRLFDQRFEGGLEAE--LAALCPPTLAPYYLR--P---S-S-
Heatshockproteinbeta-2: M-S-GRS-V-PAHPR-ATAEYF-FANPRLGEORFEGGLEPPE-IL--TPTLYHGYYVR--P---R-A
Heatshockproteinbeta-1: MTERRVPFSL-LRGP-SWDPRDWPYHRLFDQAFGLPRLPEE-WSQWLGGSSWPGYVRPLPPAAIESPA
Heatshockproteinbeta-8: MADGQMPFSCHYPSRLRRDPFRDPSLSRLLDGFGMDPFPDDL TASW-PDWALP-RLSSAWPGTLRSGM
Heatshockproteinbeta-7: M-SHRTS-ST-F--R-AERSFHSSSSSSSSSTSSASRALPAQ-DPP-MEKALSMFSDDF--G---S-F
Heatshockproteinbeta-3: M-A-KI--I--LRHL-IEIPVR-Y--QEEFEARGLEDCLRDHA-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-GLSEMRLEKDRFS/NLDVKHFSPEELKVKVLGDVIEVHGKHE-E-RQDEH-GF-
Alpha-crystallinAchain: FR---T-V-LD--S-GISEVRSRDRKDFV/LDVKHFSPEELTVKVQDDFVIEHGKHN-E-RQDDH-GY-
Heatshockproteinbeta-6: V-----A--L--P--VAQVPTDPGHFS/LDVKHFSPEEIAVKVVEGVHARHE-E-RPDEH-GF-
Heatshockproteinbeta-2: APAG--E-G-SR--A-GASELRLSEGKFAVLDVSHFTPDEVTVRTVDNLLVESARHP-Q-LDRH-GF-
Heatshockproteinbeta-1: VAAPAYSRLSRQLSSGVSEIRHTADRWRLVDVNHFAPELTVKTKDGVVEITGKHE-E-RQDEH-GY-
Heatshockproteinbeta-8: VPRGPTATARFGVPAEGRTPPPPFGPEKWK/CNVHFSKPEELMWKTDGVEVSGKHE-E-KQDEH-GI-
Heatshockproteinbeta-7: MRPHSEPLA-FPARPGGAGNIKTLGDAYEFAVDVDRDQSPEDIIVTTSNNHIEVRA---E-KLAAD-GT-
Heatshockproteinbeta-3: AQSP--P-V-DS--A-AETPPREGKSHFQ/LLDVVQFLPEDIITQTFEGWLLIKAQHG-T-RMDEH-GF-
Heatshockproteinbeta-9: LR-D--S---P--A-AQEDNDHARDGFMK/LDAHGFAPEELVVQVQDGLMVTGQQQLDVRDPERVSYR
  
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Alpha-crystallinBchain: ISREFHRRYRIPADVDPILTITS/LSSDGVLTVNGPRKQ--VSG--PE-R-T-IPITR-EE-KPAV-TAA-
Alpha-crystallinAchain: ISREFHRRYRLPSNDQSQALSGLSADGMLTFCGPKIQTLGDATHAE-R-A-IPVSR-EE-KP--TSA-
Heatshockproteinbeta-6: VAREFHRRYRLPPGVDPAVTS/LSPEGVLSI-----Q-----A-----A-PASA-QA-PP--PAA-
Heatshockproteinbeta-2: VSREFCRTYVLPADVDPWRVRA/LSHDGILNLEAPRGGRHLDETVNEVYISLLPAPP-DP-EEEE-EAAI-
Heatshockproteinbeta-1: ISRCFTKRYKTLPPGVDPTQVSS/LSPEGLTVEAP-MP-KLATQSNIEITPVTFESRAQLGGPEAAKSDE
Heatshockproteinbeta-8: VSKNFTKILQPAEVDVPTVFA/LSPEGLLIEAPQV-PYST-FGE-S---SF-NN-EL--PQ--DSQE
Heatshockproteinbeta-7: VMNFTFAHKCQLPEDVPTSVTS/LREDGSLTIRARRHP-H--T---E-H---V---Q-QT--F---RTE-
Heatshockproteinbeta-3: ISRSFTQYKLPDGVIEIKDLSA/LCHDGLLV-----E-----V---K-D---P---VG-
Heatshockproteinbeta-9: MSQKVHRKM-LPSNLSPMTATC/CLTPSGQLWVRGQCV--LAL--PEAQ-T-GPSRLGS-LGS--KASN
  
```

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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
  
```


Résultats : Comparaison

CLUSTAL O(1.2.4) MULTIPLE SEQUENCE ALIGNMENT

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HEATSHOCKPROTEINBETA-9      -----MQ-----RVGNTFSNESR-----VASR      17
HEATSHOCKPROTEINBETA-7      MSHRT-----SSTF-----RAERSFHSSSSSSSSSSSSASRALPAQDPPEKALS--      46
HEATSHOCKPROTEINBETA-3      MAKILRLHL-----ETPVRYQ-----EFGLEEDCRLL-----      38
HEATSHOCKPROTEINBETA-8      MADGQMPFSCHYP-SRL-----RRDPFRDPLSSRL-----DQG-----FGMDPPFDLTAS      47
HEATSHOCKPROTEINBETA-2      MSGRSVPHAHP-----ATAEYEFANPSRLG-----EQR-----FGEGGLEPEILIT      48
HEATSHOCKPROTEINBETA-1      MTERRVPFSLLRGPSW-----DPFRDWPYHSRLF-----DQA-----FGLPRLPEEWSQW      45
HEATSHOCKPROTEINBETA-6      -----MEIPVPVQPSWLRASAPLGLSAPGRLF-----DQR-----FGEGLLEAELAAL      46
ALPHA-CRYSTALLINBCHAIN      -----MDIAIHPWIRRRPFPP-----FHSPSRLF-----DQF-----FGEHLESDLPFT      48
ALPHA-CRYSTALLINCHAIN      -----MDVTIQHWPFKRTLGP-----F-YPSRLF-----DQF-----FGEGLFEYDLPF      39
  
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HEATSHOCKPROTEINBETA-9      CPS-----VGLAERNRVAT-----MPV-----RLRLDSPAQQEDNDHARDGFMK      57
HEATSHOCKPROTEINBETA-7      -----MFSDDFGSFMRPHSEP-----LAFPARPGGAGNIKTLGDAYEFA      85
HEATSHOCKPROTEINBETA-3      -----DHALYALPGPT-----IDVLR-----KTRAAQSPVVDAAETPPREGKSHFQIL      74
HEATSHOCKPROTEINBETA-8      WPDNALRLSSAMGPTLRSGMVRP-----GPTA-TARFGVPAAGTSPPPFGPEKQVC      99
HEATSHOCKPROTEINBETA-2      -P-----TLYHGYYVPPRAAP-----AGEGSRAGASRLSEGKFAF      97
HEATSHOCKPROTEINBETA-1      LG-----GSSMPGYRPLPAAAEISPAVAAPAYSRLSRQLSSGVSEIRHTADRMVR      98
HEATSHOCKPROTEINBETA-6      CP-----TTLAPYYLR-----PSV-----ALPVAQVTPDGHFSVL      77
ALPHA-CRYSTALLINBCHAIN      ST-----SLSPFL-RR-----PSFLR-APSWHFLDSEMRLEKQFVSN      78
ALPHA-CRYSTALLINCHAIN      LS-----STISPHY-RQ-----SLF-----RTVDSGISEVSRDRDKVFIF      74
  
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HEATSHOCKPROTEINBETA-9      LDAHGFAPEELVVQDQGLMVTGQQQLDVRDPERVSYRMSQVKHRLMPLSMLPTAMTC      117
HEATSHOCKPROTEINBETA-7      VDVRDQSPEDIIVTTSNNHIEVRA-----EKLAADG-----TVMNTFAHKCOLPEDVPTSVTS      139
HEATSHOCKPROTEINBETA-3      LDVVQFLPEDIIQTFFEGMLLKAQHGTRDMEHG-----FISRSFTRQYKLPDGEIKDLSA      131
HEATSHOCKPROTEINBETA-8      VNVHSFKPEELMWKTDGQVSEVSGKHEEQDEGG-----IVSKNFTKKIQLPAEDVPVTVFA      156
HEATSHOCKPROTEINBETA-2      LDVSHFTPDEVTVRTVDNLLSEARSHPQRLDRHG-----FVSRFCRTQYVLPADVDPNVRRA      134
HEATSHOCKPROTEINBETA-1      LDVNHFADELTVKTKDGVVEITGKHEERQDEHG-----YISRCFTKTYLTPGVDPTQVSS      155
HEATSHOCKPROTEINBETA-6      LDVKHFSPEEIAVKVVGHEVHARHEPDEHG-----FVAREFHRRYRLPGVDPAVTS      146
ALPHA-CRYSTALLINBCHAIN      LDVKHFSPEELKVKVGLGVIEVHGKHEERQDEHG-----FISREFHRRYRIPADVDPLTIS      135
ALPHA-CRYSTALLINCHAIN      LDVKHFSPEDLTKVKQDDFVIEVHGKHEERQDHHG-----YISREFHRRYRLPSNDQASAL      131
  
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HEATSHOCKPROTEINBETA-9      CLTPSGQLWVRGQCVALLPEAQGTG-----SPRLGSLGSKASNLTR-----      159
HEATSHOCKPROTEINBETA-7      ALREDGSLTIARRHPHTEHVQQTFRTEIKI-----      170
HEATSHOCKPROTEINBETA-3      VLCHDGLVVEVQDPVGTG-----      150
HEATSHOCKPROTEINBETA-8      SLSPEGLLIEAPQVPVPTGFGESSFNELPQDSQE-----VTCT-----      196
HEATSHOCKPROTEINBETA-2      ALSHOGILNLEAPRGGRHLDETVN-----EYISLLPA-----PPDPEEEEEAAIVP      182
HEATSHOCKPROTEINBETA-1      SLSPEGTLVEAPMKLAT-----QSN-----EITPVTFSRAQLGGPEAAKSDETAAM-----      205
HEATSHOCKPROTEINBETA-6      ALSPEGVLSIQAAPASQAAPPAA-----AIK-----      160
ALPHA-CRYSTALLINBCHAIN      SLSSDGVLTVNGPRKQV-----SGP-----ERTIPITREKPAVTAAPK-----      175
ALPHA-CRYSTALLINCHAIN      SLSADGMLTFCGPKIQTGLDATHA-----ERAPIVSREKPKTAPSS-----      173
  
```

```

Alpha-crystallinBchain: M-DIAIH-HP-WIRR-PFFPF--HS-PSRLFDQFFGEGHLLSD-LFP-TSTLSLSPFYLRP--P---S-F
Alpha-crystallinAchain: M-DVTIQ-HP-WFKR-TLGP--Y--PSRLFDQFFGEGLEFYD-LLPFLSSSTISPHY-R---Q---S-L
Heatshockproteinbeta-6: M-EIPVPVQPSWLR--ASAPLPLGSAPGRLDQRFEGGELLEAE-LAALCPTTLAPYYLR--P---S--
Heatshockproteinbeta-2: M-S-GRS-V-HP--ATAEYF-FANPSRLGEORFEGGELLPEE-IL--TPTLYHGYVVR--P---R-A
Heatshockproteinbeta-1: MTERRVPFSL-LRGP-SWDPRDWPYHSRLFDQAFGLPRLPEE-WSQWLGSSWPGVYRPLPPAAIESPA
Heatshockproteinbeta-8: MADGQMPFSCHYPSRLRRDPFRDPLSSRLLDGFGMDPPDDLTASW-PDWALP-RLSSAWPGTLRSGM
Heatshockproteinbeta-7: M-SHRTS-ST-F--R-AERSFHSSSSSSSSSSSSASRALPAQ-DPP-MEKALSMFSDDF--G---S-F
Heatshockproteinbeta-3: M-A-KI--I--LRHL-IEIPVR-Y--QEEFEARGLEDCLRDHA-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-GLSEMRLEKDRF--VNLDVKHFSPEELKVKVLGDVIEVHGKHE--RQDEH-GF-
Alpha-crystallinAchain: FR---T-V-LD--S-GISEVSRDRDKF--IFLDVKHFSPEELTKVKQDDFVEIHGKHN--EQDDH-GY-
Heatshockproteinbeta-6: V-----A--L--P--VAQVPTDPGHF--VNLDVKHFSPEEIAVKVVGHEVHARHE--RPDEH-GF-
Heatshockproteinbeta-2: APAG--E-G-SR--A-GASELRLSEGKFAF--LDVSHFTPDEVTVRTVDNLLVESARHP--QLDRH-GF-
Heatshockproteinbeta-1: VAAPAYSRLSRQLSSGVSEIRHTADRMVSLDVNHFADELTVKTKDGVVEITGKHE--RQDDH-GY-
Heatshockproteinbeta-8: VPRGPTATARFGVPAEGRTPPPPFGPEKVKCVNVHFSKPEELMVKTKDGVVEVSGKHE--EQQEG-GI-
Heatshockproteinbeta-7: MRPHSEPLA-FPARPGGAGNIKTLGDAYEFAVDVRDPSPEIDIIVTTSNNHIEVRA---E-KLAAD-GT-
Heatshockproteinbeta-3: AQSP--P-V-DS--A-AETPPREGKSHFQILLDVVQFLPEDIITQTFEGWLLKAQHG-T-RMDEH-GF-
Heatshockproteinbeta-9: LR-D--S---P--A-AQEDNDHARDGFMKLDHAGFAPEELVVQDQGLMVTGQQQLDVRDPERVSYR
  
```

```

Alpha-crystallinBchain: ISREFHRRKYRIPADVDPDLTITSSSLSSDGLTVVGRPKQ--VSG--PE-R-T-IPITR-EE-KPAV-TAA-
Alpha-crystallinAchain: ISREFHRRYRLPSNVQDSALSCSLADGMLTFCGPKIQTGLDATHAE-R-A-IPVSR-EE-KP--TSA-
Heatshockproteinbeta-6: VAREFHRRYRLPGVDPAVTSALSPEGVLSI-----Q-----A-----A-PASA-QA-PP--PAA-
Heatshockproteinbeta-2: VSREFCRTYVLPADVDPNVRRAALSHDGLNLEAPRGGRHLDETVNEVYISLLPAPP-DP-EEEE-EAAI
Heatshockproteinbeta-1: ISRCFTRKYTLPGVDPTQVSSSLPEGLTVLEAP-MP-KLATQSNIEITPVTFSRAQLGGPEAAKSDE
Heatshockproteinbeta-8: VSKNFTKILQPAEDVPVTVFASLSPEGLLIEAPQVP-PYST-FGE-S--SF--NN-EL--PQ--DSQE
Heatshockproteinbeta-7: VMNTFAHKQLPEDVPTSVTSALREDGSLTIARRHP-H--T---E-H---V---Q-QT--F---RTE-
Heatshockproteinbeta-3: ISRSFTRQYKLPDGEIKDLSAVLCHDGLLVV-----E-----V---K-D---P---V-G-
Heatshockproteinbeta-9: MSQKVHRKM-LPSNLSPMTAMTCLTPSGQLWVRGQCV--LAL--PEAQ-T-GPSRLGS-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
  
```

[illegible]

- 36

[illegible]

- 37

[illegible]

- 38

Conclusion



- Trois étapes implémentées

Conclusion



- Trois étapes implémentées



- Complexité temporelle

Conclusion



- Trois étapes implémentées



- Complexité temporelle



- Des résultats satisfaisants