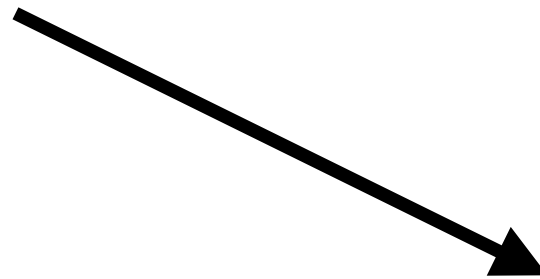


Multiple Sequence Alignment Introduction

Sequence Alignment

ACGTGGT

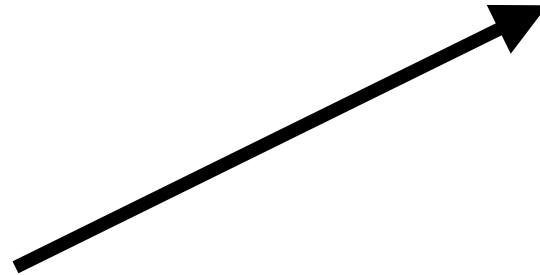


ACGTGGT

ACGTCGT



ACGTCGT



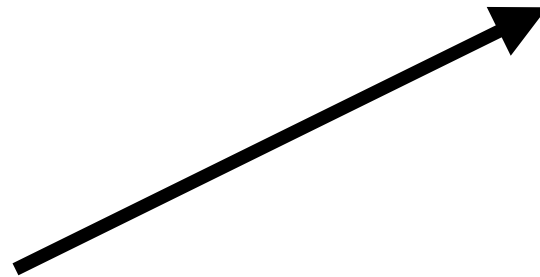
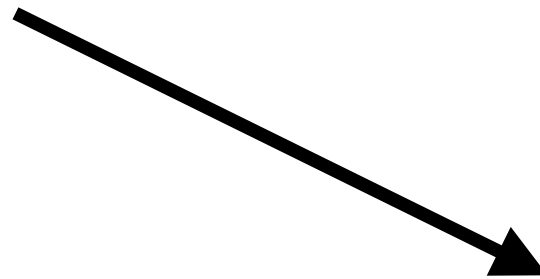
Sequence Alignment

ACGTGGT

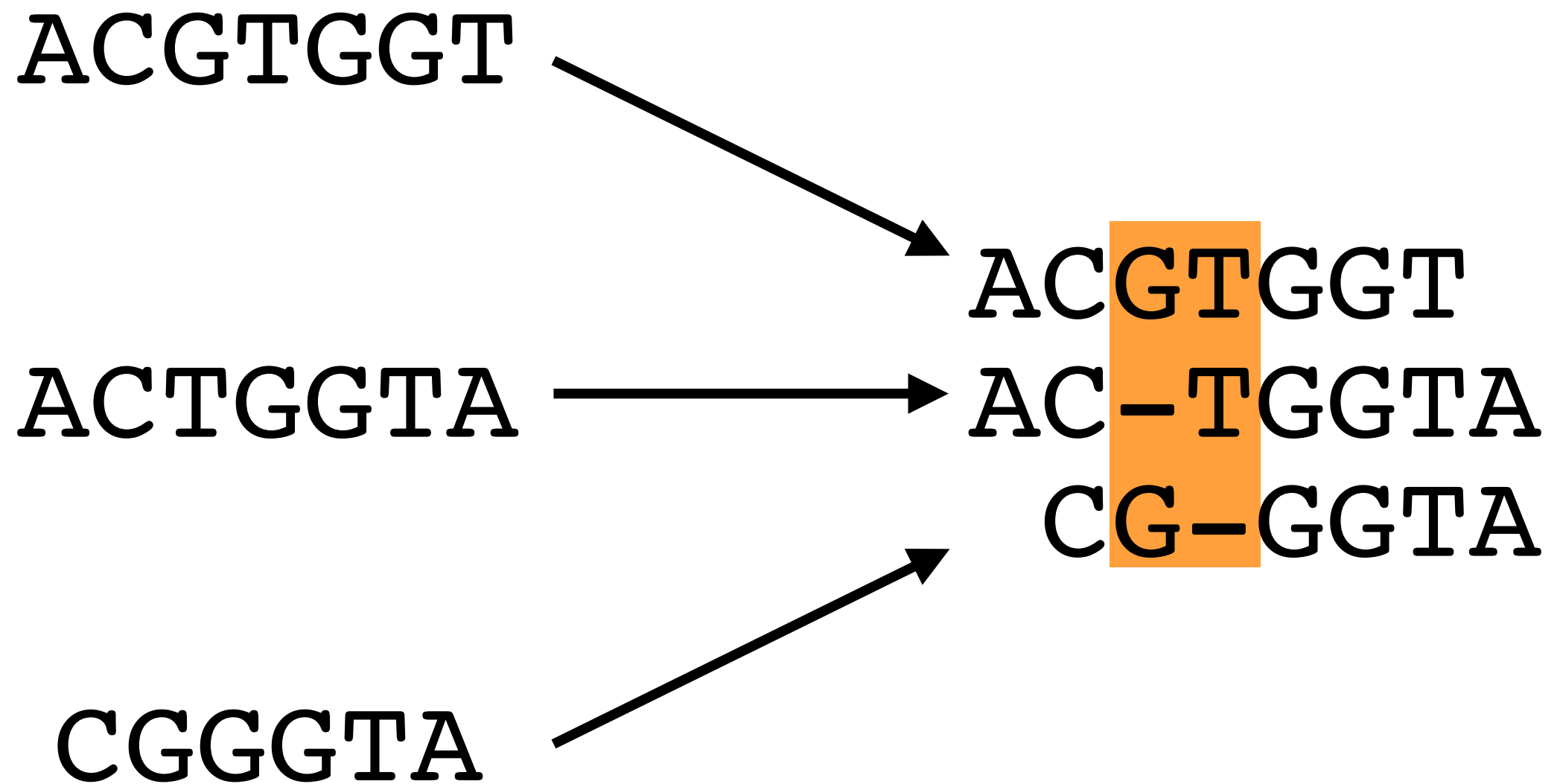
CGGGTA

ACGTGGT

CG-GGTA

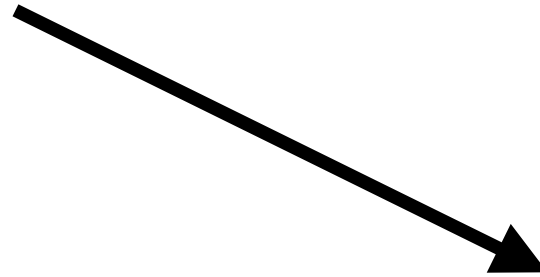


Multiple Sequence Alignment



Multiple Sequence Alignment

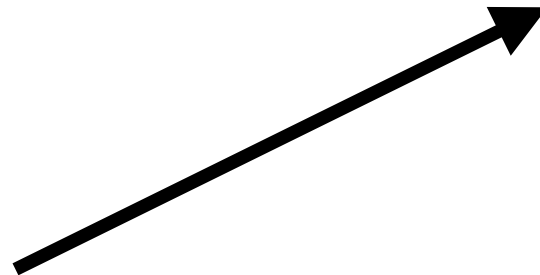
ACGTGGT



GCTGGACNC



TTCGACT



Multiple Sequence Alignment

Workshop on Molecular Evolution 2000

M	O	L	E	C	U	L	A	R	•	•	•	E	V	O	L	U	T	I	O	N
•	•	•	•	C	A	P	T	A	I	N	•	K	I	D	D	•	•	•	•	•
•	•	S	L	E	E	P	•	•	L	E	A	R	N	•	•	•	•	•	•	
•	•	•	•	•	C	H	O	O	S	E	•	T	W	O	•	•	•	•	•	

Marine Biological Laboratory, Woods Hole, MA

Scoring schemes

Match: +1 / Mismatch: -1 / Indel: -1

SLEEP--LEARN-
---CHOOSE-TWO

Scoring schemes

Match: +1 / Mismatch: -1 / Indel: -1

SLEEP--LEARN--
--CHOOSE-TWO

-1

Total: -1

Scoring schemes

Match: +1 / Mismatch: -1 / Indel: -1

SLEEP--LEARN--
--CHOOSE-TWO
-1

Total: -2

Scoring schemes

Match: +1 / Mismatch: -1 / Indel: -1

SLEEP--LEARN--
--CHOOSE-TWO
-1

Total: -3

Scoring schemes

Match: +1 / Mismatch: -1 / Indel: -1

SLEEP--LEARN-
---CHOOSE-TWO
-1

Total: -4

Scoring schemes

Match: +1 / Mismatch: -1 / Indel: -1

SLEEP--LEARN--
---CHOOSE-TWO

-1

Total: -5

Scoring schemes

Match: +1 / Mismatch: -1 / Indel: -1

SLEEP--LEARN--
---CHOOSE--TWO
 -1

Total: -6

Scoring schemes

Match: +1 / Mismatch: -1 / Indel: -1

SLEEP--LEARN--
---CHOOSE--TWO

-1

Total: -7

Scoring schemes

Match: +1 / Mismatch: -1 / Indel: -1

SLEEP--LEARN--
---CHOOSE--TWO

-1

Total: -8

Scoring schemes

Match: +1 / Mismatch: -1 / Indel: -1

SLEEP--LEARN--
---CHOOSE-TWO

+1

Total: -7

Scoring schemes

Match: +1 / Mismatch: -1 / Indel: -1

SLEEP--LEARN--
---CHOOSE--TWO

-1

Total: -8

Scoring schemes

Match: +1 / Mismatch: -1 / Indel: -1

SLEEP--LEARN--
---CHOOSE-TWO
-1

Total: -9

Scoring schemes

Match: +1 / Mismatch: -1 / Indel: -1

SLEEP--LEARN--
---CHOOSE-TWO
-1

Total: -10

Scoring schemes

Match: +1 / Mismatch: -1 / Indel: -1

SLEEP--LEARN--
---CHOOSE-TWO

-1

Total: -11

Gap opening / extension

Match: +1 / Mismatch: -1 / Gap opening: -1 / Gap extension: -0.5

SLEEP--LEARN--
---CHOOSE-TWO

Gap opening / extension

Match: +1 / Mismatch: -1 / Gap opening: -1 / Gap extension: -0.5

SLEEP--LEARN--
--CHOOSE-TWO

-1

Total: -1

Gap opening / extension

Match: +1 / Mismatch: -1 / Gap opening: -1 / Gap extension: -0.5

SLEEP--LEARN--
--CHOOSE-TWO
-0.5

Total: -1.5

Gap opening / extension

Match: +1 / Mismatch: -1 / Gap opening: -1 / Gap extension: -0.5

SLEEP--LEARN--
--CHOOSE-TWO
-0.5

Total: -2

Gap opening / extension

Match: +1 / Mismatch: -1 / Gap opening: -1 / Gap extension: -0.5

SLEEP--LEARN--
---CHOOSE-TWO
-1

Total: -3

Gap opening / extension

Match: +1 / Mismatch: -1 / Gap opening: -1 / Gap extension: -0.5

SLEEP--LEARN--
---CHOOSE-TWO
-1

Total: -4

Gap opening / extension

Match: +1 / Mismatch: -1 / Gap opening: -1 / Gap extension: -0.5

SLEEP--LEARN--
---CHOOSE--TWO
 -1

Total: -5

Gap opening / extension

Match: +1 / Mismatch: -1 / Gap opening: -1 / Gap extension: -0.5

SLEEP--LEARN--
---CHOOSE--TWO

-0.5

Total: -5.5

Gap opening / extension

Match: +1 / Mismatch: -1 / Gap opening: -1 / Gap extension: -0.5

SLEEP--LEARN--
---CHOOSE-TWO
-1

Total: -6.5

Gap opening / extension

Match: +1 / Mismatch: -1 / Gap opening: -1 / Gap extension: -0.5

SLEEP--LEARN--
---CHOOSE-TWO
+1

Total: -5.5

Gap opening / extension

Match: +1 / Mismatch: -1 / Gap opening: -1 / Gap extension: -0.5

SLEEP--LEARN--
---CHOOSE-TWO
-1

Total: -6.5

Gap opening / extension

Match: +1 / Mismatch: -1 / Gap opening: -1 / Gap extension: -0.5

SLEEP--LEARN--
---CHOOSE-TWO
-1

Total: -7.5

Gap opening / extension

Match: +1 / Mismatch: -1 / Gap opening: -1 / Gap extension: -0.5

SLEEP--LEARN--
---CHOOSE-TWO
-1

Total: -8.5

Gap opening / extension

Match: +1 / Mismatch: -1 / Gap opening: -1 / Gap extension: -0.5

SLEEP--LEARN--
---CHOOSE-TWO

-1

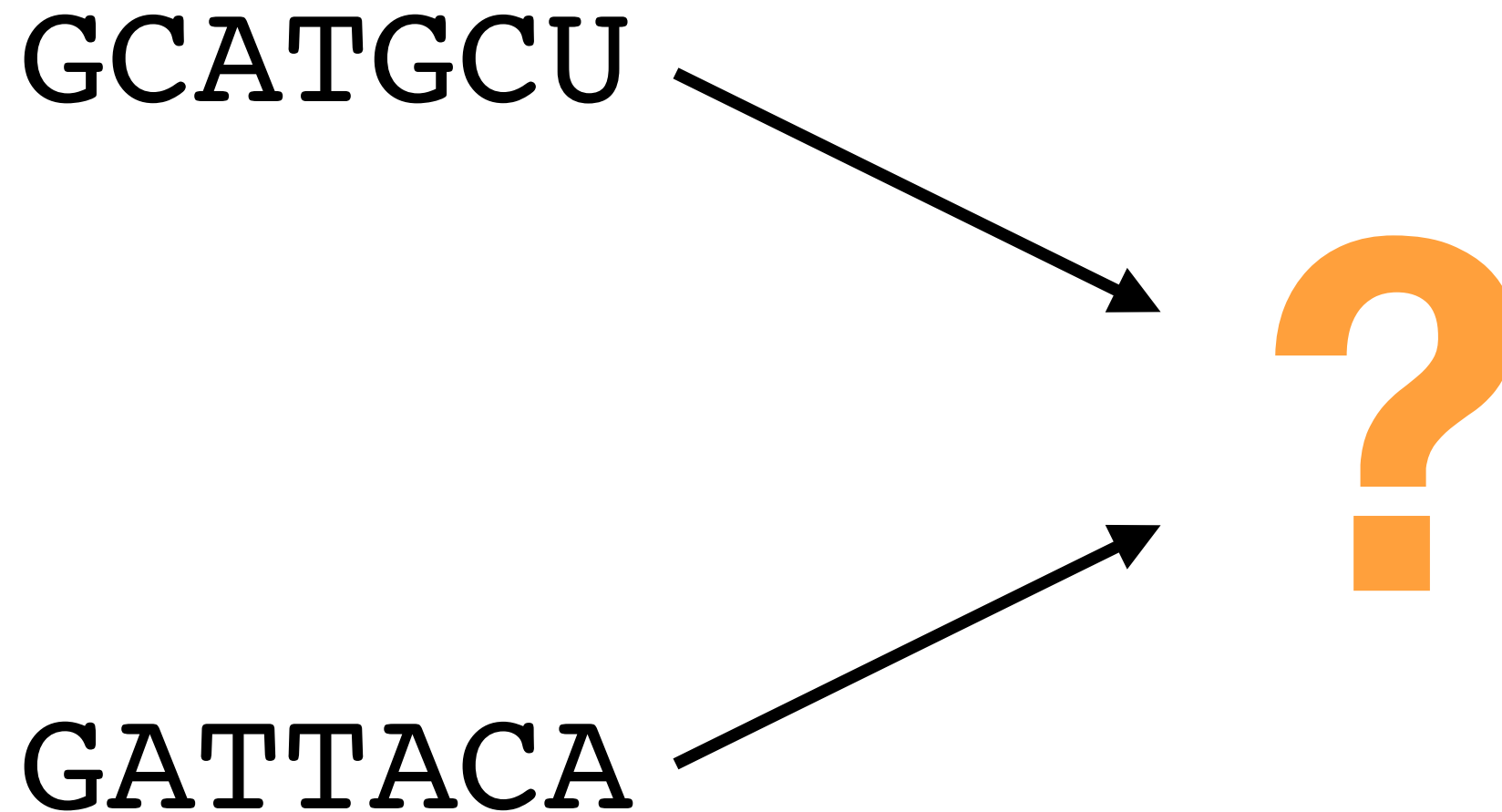
Total: -9.5

Match / Mismatch: Blossum 62

BLOcks SUBstitution Matrix																				
C	9																			
S	-1	4																		
T	-1	1	5																	
P	-3	-1	-1	7																
A	0	1	0	-1	4															
G	-3	0	-2	-2	0	6														
N	-3	1	0	-2	-2	0	6													
D	-3	0	-1	-1	-2	-1	1	6												
E	-4	0	-1	-1	-1	-2	0	2	5											
Q	-3	0	-1	-1	-1	-2	0	0	2	5										
H	-3	-1	-2	-2	-2	-2	1	-1	0	0	8									
R	-3	-1	-1	-2	-1	-2	0	-2	0	1	0	5								
K	-3	0	-1	-1	-1	-2	0	-1	1	1	-1	2	5							
M	-1	-1	-1	-2	-1	-3	-2	-3	-2	0	-2	-1	-1	5						
I	-1	-2	-1	-3	-1	-4	-3	-3	-3	-3	-3	-3	-3	1	4					
L	-1	-2	-1	-3	-1	-4	-3	-4	-3	-2	-3	-2	-2	2	2	4				
V	-1	-2	0	-2	0	-3	-3	-3	-2	-2	-3	-3	-2	1	3	1	4			
F	-2	-2	-2	-4	-2	-3	-3	-3	-3	-3	-1	-3	-3	0	0	0	-1	6		
Y	-2	-2	-2	-3	-2	-3	-2	-3	-2	-1	2	-2	-2	-1	-1	-1	-1	3	7	
W	-2	-3	-2	-4	-3	-2	-4	-4	-3	-2	-2	-3	-3	-1	-3	-2	-3	1	2	11
	C	S	T	P	A	G	N	D	E	Q	H	R	K	M	I	L	V	F	Y	W

Needleman-Wunsch algorithm

Global alignments



Needleman-Wunsch algorithm

Global alignments

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

Needleman-Wunsch algorithm

Global alignments (match: +1, mismatch: -1, indel: -1)

		G	C	A	T	G	C	T	
		0	-1	-2	-3	-4	-5	-6	-7
G		-1							
A		-2							
T		-3							
T		-4							
A		-5							
C		-6							
A		-7							

Needleman-Wunsch algorithm

Global alignments (match: +1, mismatch: -1, indel: -1)

		G	C	A	T	G	C	T	
		0	-1	-2	-3	-4	-5	-6	-7
G		-1							
A		-2							
T		-3							
T		-4							
A		-5							
C		-6							
A		-7							

Needleman-Wunsch algorithm

Global alignments (match: +1, mismatch: -1, indel: -1)

		G	C	A	T	G	C	T	
		0	-1	-2	-3	-4	-5	-6	-7
G	-1	?							
A	-2								
T	-3								
T	-4								
A	-5								
C	-6								
A	-7								

Needleman-Wunsch algorithm

Global alignments (match: +1, mismatch: -1, indel: -1)

		G	C	A	T	G	C	T	
		0	-1	-2	-3	-4	-5	-6	-7
G		↑ -1	-2						
A		-2							
T		-3							
T		-4							
A		-5							
C		-6							
A		-7							

Needleman-Wunsch algorithm

Global alignments (match: +1, mismatch: -1, indel: -1)

		G	C	A	T	G	C	T
G	0	-1	-2	-3	-4	-5	-6	-7
A	-1	1						
T	-2							
T	-3							
A	-4							
C	-5							
A	-6							
	-7							

Needleman-Wunsch algorithm

Global alignments (match: +1, mismatch: -1, indel: -1)

		G	C	A	T	G	C	T	
		0	-1	-2	-3	-4	-5	-6	-7
G		-1	-2						
A		-2							
T		-3							
T		-4							
A		-5							
C		-6							
A		-7							

Needleman-Wunsch algorithm

Global alignments (match: +1, mismatch: -1, indel: -1)

		G	C	A	T	G	C	T	
		0	-1	-2	-3	-4	-5	-6	-7
G		-1	1						
A		-2							
T		-3							
T		-4							
A		-5							
C		-6							
A		-7							

Needleman-Wunsch algorithm

Global alignments (match: +1, mismatch: -1, indel: -1)

		G	C	A	T	G	C	T	
		0	-1	-2	-3	-4	-5	-6	-7
G		-1	1	?					
A		-2							
T		-3							
T		-4							
A		-5							
C		-6							
A		-7							

Needleman-Wunsch algorithm

Global alignments (match: +1, mismatch: -1, indel: -1)

		G	C	A	T	G	C	T	
		0	-1	-2	-3	-4	-5	-6	-7
G		-1	1	0					
A		-2							
T		-3							
T		-4							
A		-5							
C		-6							
A		-7							

Needleman-Wunsch algorithm

Global alignments (match: +1, mismatch: -1, indel: -1)

		G	C	A	T	G	C	T	
		0	-1	-2	-3	-4	-5	-6	-7
G		-1	1	-2					
A		-2							
T		-3							
T		-4							
A		-5							
C		-6							
A		-7							

Needleman-Wunsch algorithm

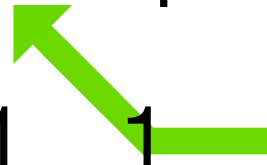
Global alignments (match: +1, mismatch: -1, indel: -1)

		G	C	A	T	G	C	T
G	0	-1	-2	-3	-4	-5	-6	-7
A	-1	1	-3					
T	-2							
T	-3							
A	-4							
C	-5							
A	-6							
	-7							

Needleman-Wunsch algorithm

Global alignments (match: +1, mismatch: -1, indel: -1)

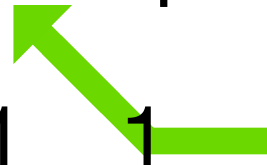
		G	C	A	T	G	C	T	
		0	-1	-2	-3	-4	-5	-6	-7
G		-1	1	0					
A		-2							
T		-3							
T		-4							
A		-5							
C		-6							
A		-7							



Needleman-Wunsch algorithm

Global alignments (match: +1, mismatch: -1, indel: -1)

		G	C	A	T	G	C	T	
		0	-1	-2	-3	-4	-5	-6	-7
G		-1	1	0	?	?	?	?	?
A		-2	?	?	?	?	?	?	?
T		-3	?	?	?	?	?	?	?
T		-4	?	?	?	?	?	?	?
A		-5	?	?	?	?	?	?	?
C		-6	?	?	?	?	?	?	?
A		-7	?	?	?	?	?	?	?



Needleman-Wunsch algorithm

Global alignments (match: +1, mismatch: -1, indel: -1)

		G	C	A	T	G	C	T	
		0	-1	-2	-3	-4	-5	-6	-7
G		-1	1	0	-1	-2	-3	-4	-5
A		-2	0	0	1	0	-1	-2	-3
T		-3	-1	-1	0	2	1	0	-1
T		-4	-2	-2	-1	1	1	0	-1
A		-5	-3	-3	-1	0	0	0	1
C		-6	-4	-2	-2	-1	-1	1	0
A		-7	-5	-3	-1	-2	-2	0	0

Needleman-Wunsch algorithm

Global alignments (match: +1, mismatch: -1, indel: -1)

		G	C	A	T	G	C	T
	0	-1	-2	-3	-4	-5	-6	-7
G	-1	1	0	-1	-2	-3	-4	-5
A	-2	0	0	1	0	-1	-2	-3
T	-3	-1	-1	0	2	1	0	-1
T	-4	-2	-2	-1	1	1	0	-1
A	-5	-3	-3	-1	0	0	0	1
C	-6	-4	-2	-2	-1	-1	1	0
A	-7	-5	-3	-1	-2	-2	0	0

GCATG-CT
G-ATTACA

Needleman-Wunsch algorithm

Global alignments (match: +1, mismatch: -1, indel: -1)

		G	C	A	T	G	C	T
	0	-1	-2	-3	-4	-5	-6	-7
G	-1	1	0	-1	-2	-3	-4	-5
A	-2	0	0	1	0	-1	-2	-3
T	-3	-1	-1	0	2	1	0	-1
T	-4	-2	-2	-1	1	1	0	-1
A	-5	-3	-3	-1	0	0	0	1
C	-6	-4	-2	-2	-1	-1	1	0
A	-7	-5	-3	-1	-2	-2	0	0

GCATG-CT
G-ATTACA

GCAT-GCT
G-ATTACA

Smith-Waterman algorithm

Local alignments (match: +1, mismatch: -1, indel: -1)

		G	C	A	T	G	C	T
		0	0	0	0	0	0	0
G	0	Maximum of: - 0 - upper left value +1 (if match) - upper left value -1 (if mismatch) - max (value to left minus distance to it) - max (value above minus distance to it)						
A	0							
T	0							
T	0							
A	0							
C	0							
A	0							

- Maximum of:
- 0
 - upper left value +1 (if match)
 - upper left value -1 (if mismatch)
 - max (value to left minus distance to it)
 - max (value above minus distance to it)

Smith-Waterman algorithm

Local alignments (match: +1, mismatch: -1, indel: -1)

		G	C	A	T	G	C	T
G	0	0	0	0	0	0	0	0
A	0	1	0	0	0	1	0	0
T	0	0	0	1	0	0	0	0
T	0	0	0	0	2	1	0	1
A	0	0	0	0	1	1	0	1
C	0	0	0	1	0	0	0	0
A	0	0	1	0	0	0	1	0
A	0	0	0	2	1	0	0	0

Smith-Waterman algorithm

Local alignments (match: +1, mismatch: -1, indel: -1)

		G	C	A	T	G	C	T	
		0	0	0	0	0	0	0	
G		0	1	0	0	1	0	0	
A		0	0	0	1	0	0	0	AT
T		0	0	0	0	2	1	1	AT
T		0	0	0	0	1	1	1	
A		0	0	0	1	0	0	0	
C		0	0	1	0	0	1	0	CA
A		0	0	0	2	1	0	0	CA

Benchmarks: SP score

Proportion of correctly aligned sequence pairs

	ClustalW	MAFFT	MUSCLE	Probalign	Probcons	T-Coffee
set 1	0.415	0.538	0.465	0.571	0.547	0.549
set 2	0.799	0.863	0.845	0.883	0.875	0.874
set 3	0.769	0.846	0.820	0.846	0.834	0.833
set 4	0.638	0.769	0.717	0.756	0.751	0.739
set 5	0.637	0.774	0.702	0.766	0.766	0.763

Benchmarks: Execution time

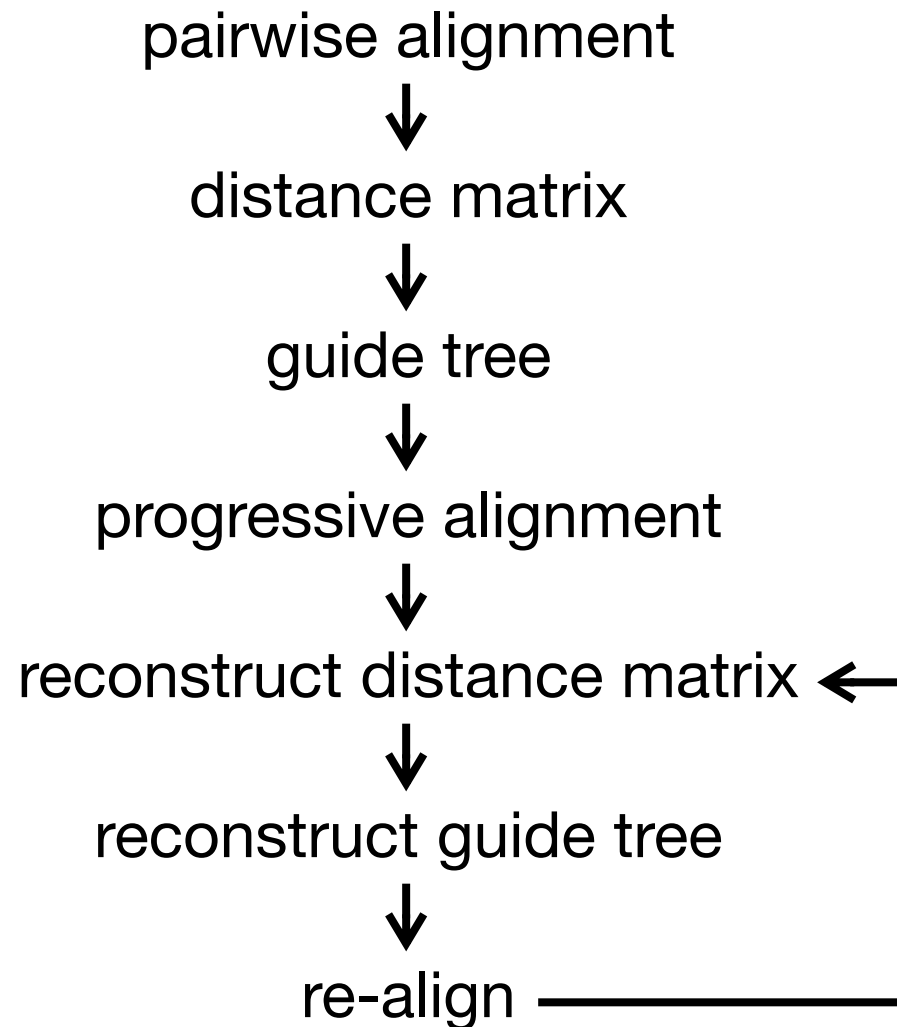
	ClustalW	MAFFT	MUSCLE	Probalign	Probcons	T-Coffee
set 1	7 sec	27 sec	24 sec	42 sec	68 sec	86 sec
set 2	26 sec	46 sec	32 sec	193 sec	243 sec	298 sec
set 3	335 sec	591 sec	259 sec	4171 sec	5170 sec	-
set 4	417 sec	585 sec	266 sec	6040 sec	8143 sec	-
set 5	90 sec	298 sec	133 sec	1370 sec	1813 sec	3805 sec

MAFFT

Multiple Alignment using Fast Fourier Transform

nucleotides are converted to four-dimensional vectors

iterative refinement



MAFFT

```
m_matschiner — bash — 80x26
ceesbob:~ m_matschiner$ mafft --help

-----
MAFFT v7.213 (2014/12/05)
http://mafft.cbrc.jp/alignment/software/
MBE 30:772-780 (2013), NAR 30:3059-3066 (2002)
-----

High speed:
% mafft in > out
% mafft --retree 1 in > out (fast)

High accuracy (for <~200 sequences x <~2,000 aa/nt):
% mafft --maxiterate 1000 --localpair in > out (% linsi in > out is also ok)
% mafft --maxiterate 1000 --genafpair in > out (% einsl in > out)
% mafft --maxiterate 1000 --globalpair in > out (% ginsi in > out)

If unsure which option to use:
% mafft --auto in > out

--op # :          Gap opening penalty, default: 1.53
--ep # :          Offset (works like gap extension penalty), default: 0.0
--maxiterate # :  Maximum number of iterative refinement, default: 0
--clustalout :     Output: clustal format, default: fasta
--reorder :       Outorder: aligned, default: input order
--quiet :         Do not report progress
--thread # :      Number of threads (if unsure, --thread -1)
```


MAFFT

Needleman-Wunsch

```
m_matschiner — bash — 80x26
ceesbob:~ m_matschiner$ mafft --help

-----
MAFFT v7.213 (2014/12/05)
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% mafft --maxiterate 1000 --genafpair in > out (% einsl in > out)
% mafft --maxiterate 1000 --globalpair in > out (% ginsi in > out)

If unsure which option to use:
% mafft --auto in > out

--op # :          Gap opening penalty, default: 1.53
--ep # :          Offset (works like gap extension penalty), default: 0.0
--maxiterate # :  Maximum number of iterative refinement, default: 0
--clustalout :     Output: clustal format, default: fasta
--reorder :       Outorder: aligned, default: input order
--quiet :         Do not report progress
--thread # :      Number of threads (if unsure, --thread -1)
```

MAFFT

Smith-Waterman

```
m_matschiner — bash — 80x26

ceesbob:~ m_matschiner$ mafft --help

-----
MAFFT v7.213 (2014/12/05)
http://mafft.cbrc.jp/alignment/software/
MBE 30:772-780 (2013), NAR 30:3059-3066 (2002)
-----

High speed:
% mafft in > out
% mafft --retree 1 in > out (fast)

High accuracy (for <~200 sequences x <~2,000 aa/nt):
% mafft --maxiterate 1000 --localpair in > out (% linsi in > out is also ok)
% mafft --maxiterate 1000 --genafpair in > out (% einsl in > out)
% mafft --maxiterate 1000 --globalpair in > out (% ginsi in > out)

If unsure which option to use:
% mafft --auto in > out

--op # :          Gap opening penalty, default: 1.53
--ep # :          Offset (works like gap extension penalty), default: 0.0
--maxiterate # :  Maximum number of iterative refinement, default: 0
--clustalout :     Output: clustal format, default: fasta
--reorder :        Outorder: aligned, default: input order
--quiet :          Do not report progress
--thread # :       Number of threads (if unsure, --thread -1)
```


MAFFT

Gap openings

```
m_matschiner — bash — 80x26

ceesbob:~ m_matschiner$ mafft --help

-----
MAFFT v7.213 (2014/12/05)
http://mafft.cbrc.jp/alignment/software/
MBE 30:772-780 (2013), NAR 30:3059-3066 (2002)
-----

High speed:
% mafft in > out
% mafft --retree 1 in > out (fast)

High accuracy (for <~200 sequences x <~2,000 aa/nt):
% mafft --maxiterate 1000 --localpair in > out (% linsi in > out is also ok)
% mafft --maxiterate 1000 --genafpair in > out (% einsl in > out)
% mafft --maxiterate 1000 --globalpair in > out (% ginsi in > out)

If unsure which option to use:
% mafft --auto in > out

--op # :          Gap opening penalty, default: 1.53
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--maxiterate # :  Maximum number of iterative refinement, default: 0
--clustalout :     Output: clustal format, default: fasta
--reorder :       Outorder: aligned, default: input order
--quiet :         Do not report progress
--thread # :      Number of threads (if unsure, --thread -1)
```

MAFFT

Gap extensions

```
m_matschiner — bash — 80x26

ceesbob:~ m_matschiner$ mafft --help

-----
MAFFT v7.213 (2014/12/05)
http://mafft.cbrc.jp/alignment/software/
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--reorder :       Outorder: aligned, default: input order
--quiet :         Do not report progress
--thread # :      Number of threads (if unsure, --thread -1)
```


MAFFT

no idea

```
m_matschiner — bash — 80x26
ceesbob:~ m_matschiner$ mafft --help

-----
MAFFT v7.213 (2014/12/05)
http://mafft.cbrc.jp/alignment/software/
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--reorder :      Outorder: aligned, default: input order
--quiet :        Do not report progress
--thread # :     Number of threads (if unsure, --thread -1)
```

MAFFT

default

```
m_matschiner — bash — 80x26
ceesbob:~ m_matschiner$ mafft --help

-----
MAFFT v7.213 (2014/12/05)
http://mafft.cbrc.jp/alignment/software/
MBE 30:772-780 (2013), NAR 30:3059-3066 (2002)
-----

High speed:
% mafft in > out
% mafft --retree 1 in > out (fast)

High accuracy (for <~200 sequences x <~2,000 aa/nt):
% mafft --maxiterate 1000 --localpair in > out (% linsi in > out is also ok)
% mafft --maxiterate 1000 --genafpair in > out (% einsl in > out)
% mafft --maxiterate 1000 --globalpair in > out (% ginsi in > out)

If unsure which option to use:
% mafft --auto in > out

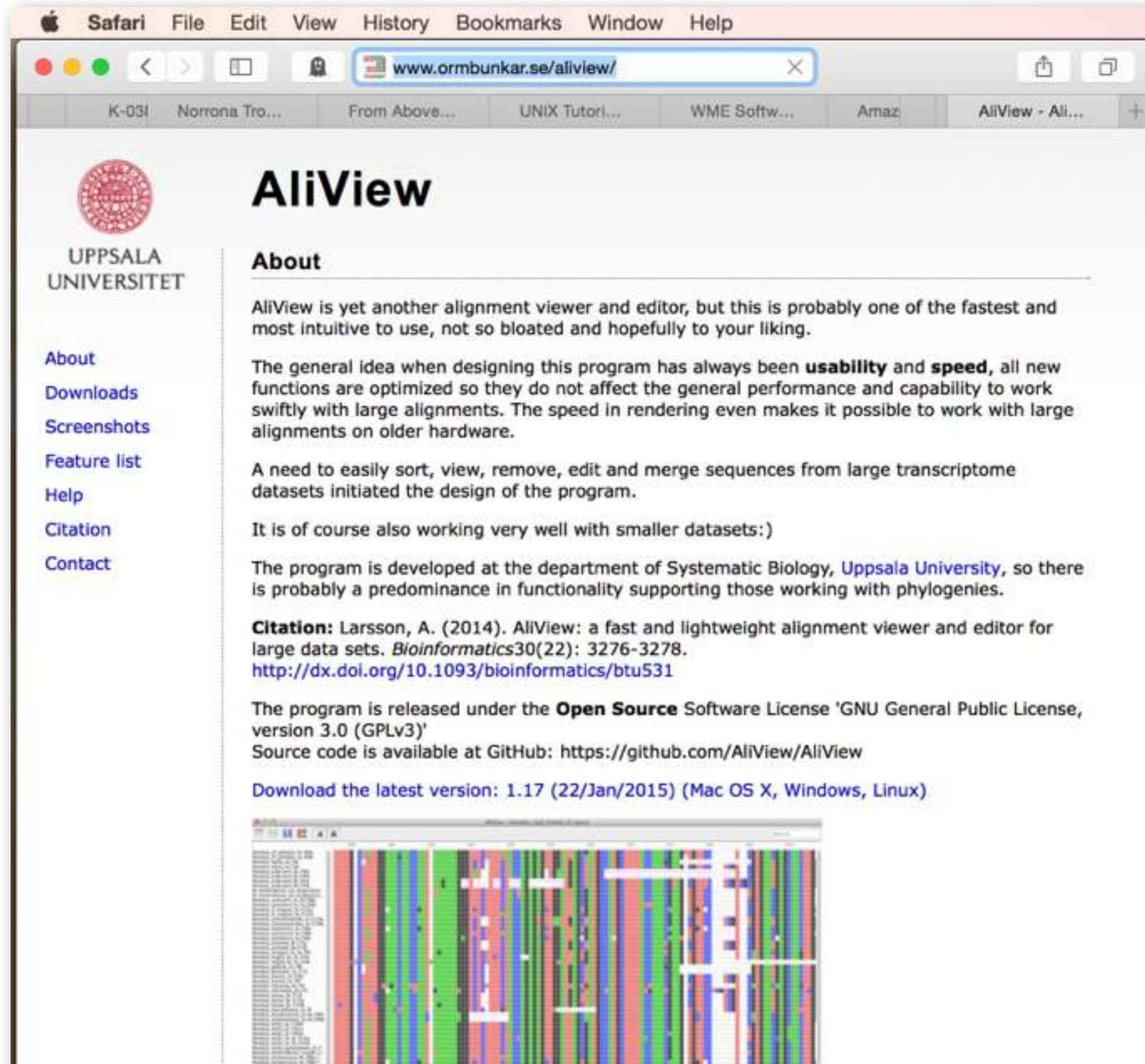
--op # :          Gap opening penalty, default: 1.53
--ep # :          Offset (works like gap extension penalty), default: 0.0
--maxiterate # :  Maximum number of iterative refinement, default: 0
--clustalout :     Output: clustal format, default: fasta
--reorder :       Outorder: aligned, default: input order
--quiet :         Do not report progress
--thread # :      Number of threads (if unsure, --thread -1)
```

MAFFT

that's it.

AliView

<http://www.ormbunkar.se/aliview/>



The screenshot shows a Safari browser window with the address bar displaying www.ormbunkar.se/aliview/. The website has a header with the Uppsala University logo and the title "AliView". A left sidebar contains navigation links: "About", "Downloads", "Screenshots", "Feature list", "Help", "Citation", and "Contact". The main content area is titled "About" and contains the following text:

AliView is yet another alignment viewer and editor, but this is probably one of the fastest and most intuitive to use, not so bloated and hopefully to your liking.

The general idea when designing this program has always been **usability** and **speed**, all new functions are optimized so they do not affect the general performance and capability to work swiftly with large alignments. The speed in rendering even makes it possible to work with large alignments on older hardware.

A need to easily sort, view, remove, edit and merge sequences from large transcriptome datasets initiated the design of the program.

It is of course also working very well with smaller datasets:)

The program is developed at the department of Systematic Biology, [Uppsala University](http://www.uppsala.se), so there is probably a predominance in functionality supporting those working with phylogenies.

Citation: Larsson, A. (2014). AliView: a fast and lightweight alignment viewer and editor for large data sets. *Bioinformatics*30(22): 3276-3278.
<http://dx.doi.org/10.1093/bioinformatics/btu531>

The program is released under the **Open Source** Software License 'GNU General Public License, version 3.0 (GPLv3)'
Source code is available at GitHub: <https://github.com/AliView/AliView>

[Download the latest version: 1.17 \(22/Jan/2015\) \(Mac OS X, Windows, Linux\)](#)

At the bottom of the page, there is a small thumbnail image showing a screenshot of the AliView software interface, which displays a multiple sequence alignment with various colored bars representing different sequences.

AliView

Interface



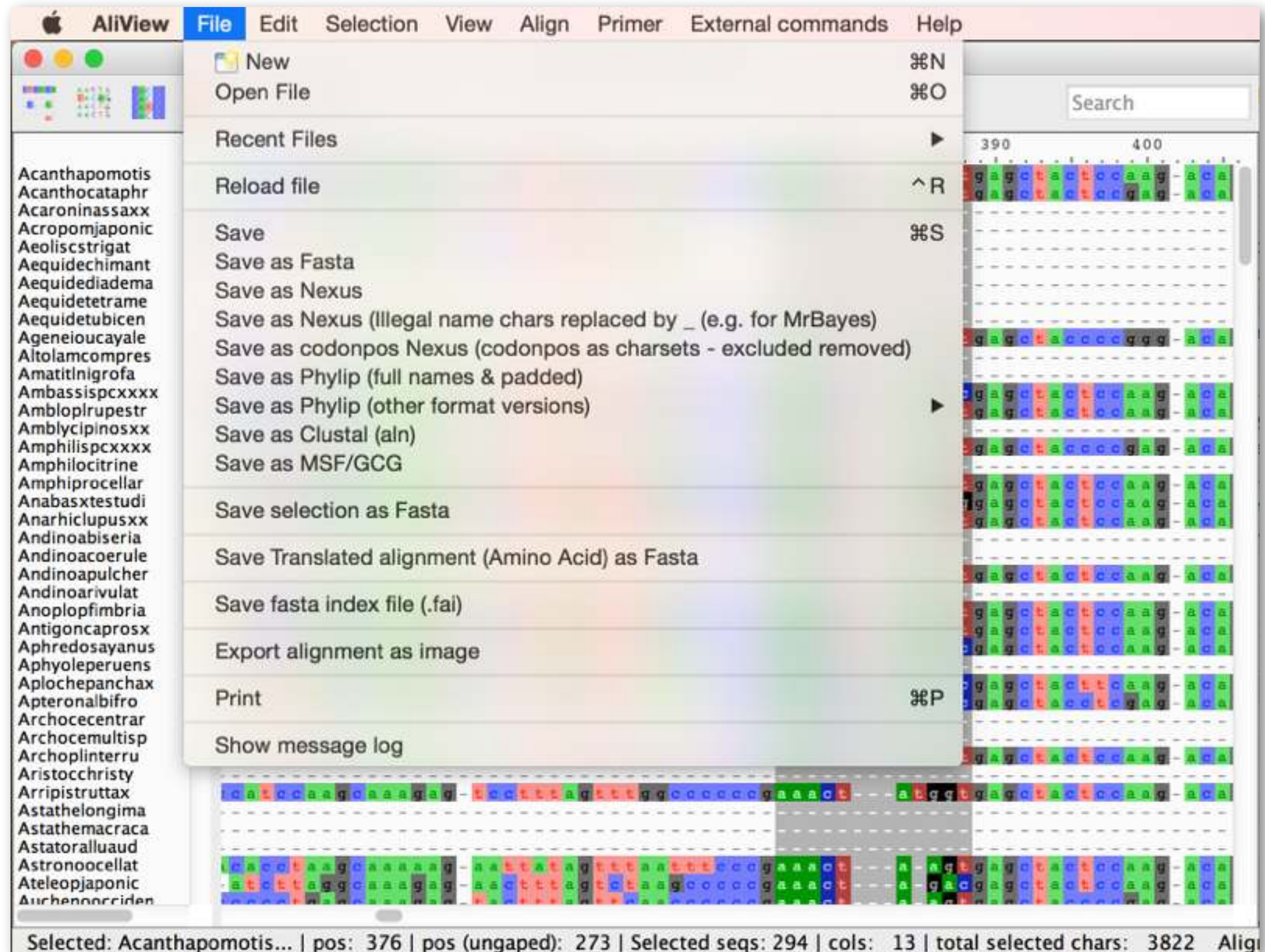
AliView

Site selection



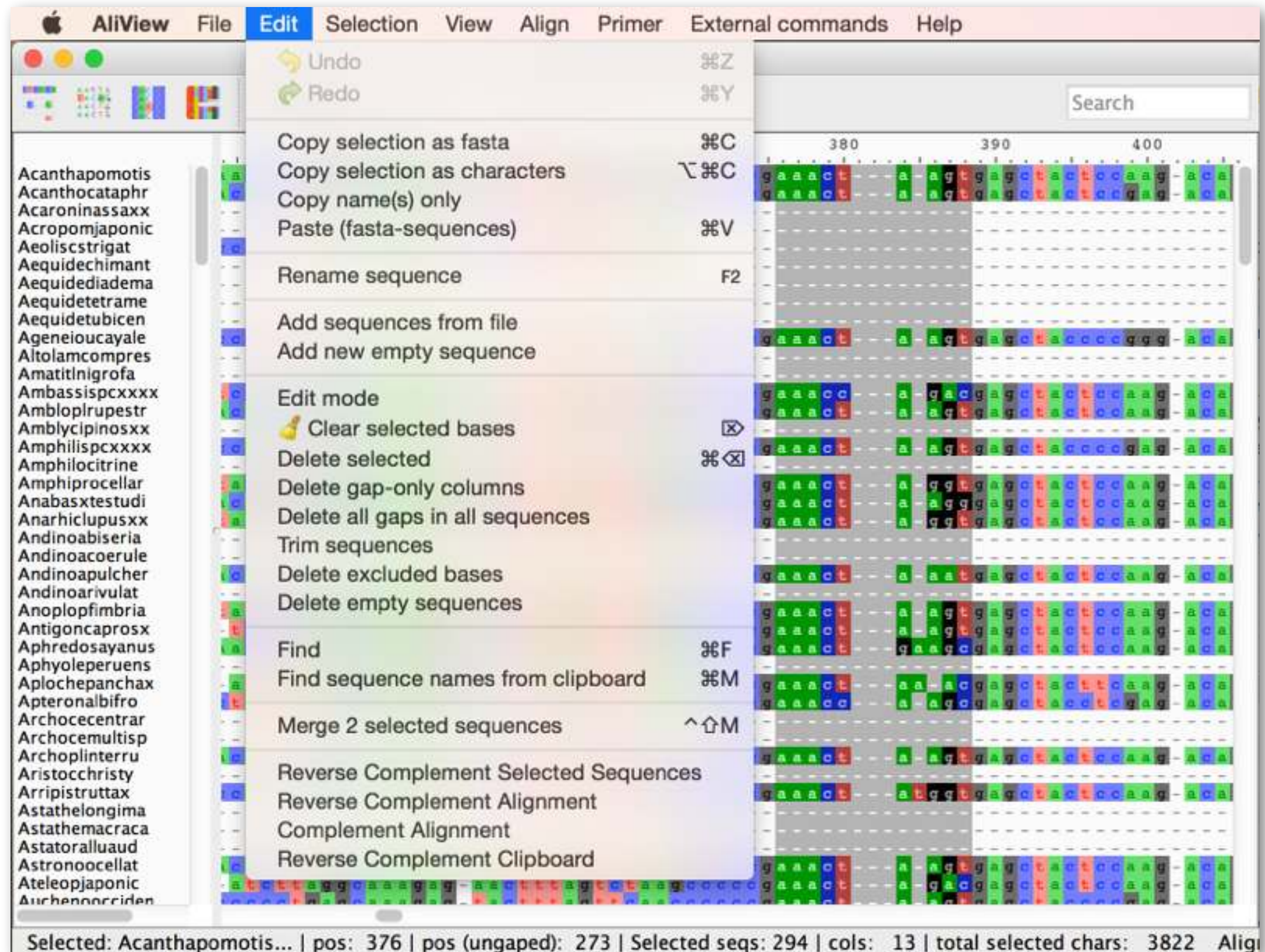
AliView

File menu



AliView

Edit menu



AliView

Selection menu



AliView

View menu



AliView

View menu



Multiple Sequence Alignment Exercise

<http://evomics.org/learning/bioinformatics/multiple-sequence-alignment-ami-version/>

The screenshot shows a Safari browser window displaying the website evomics.org. The page title is "Evolution and Genomics". The navigation menu includes Home, Workshops, Learning, Resources, People, and Apply. The main heading is "Multiple Sequence Alignment (AMI version)". Below this, a breadcrumb trail reads: "You are here: Home > Learning > Bioinformatics > Multiple Sequence Alignment (AMI version)".

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- [Exercise 3: Alignment and visualization of protein-coding sequences](#)
- [Exercise 4: Codon-based manual alignment curation](#)
- [Exercise 5: Adding further sequences to the alignment](#)

Lecture notes

[Multiple Sequence Alignment Introduction](#)

Expected learning outcomes

The objective of this activity is to become familiar with multiple sequence alignment options and the visualization and editing of alignments, both manually and in an automated fashion, and with both

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