

Θαλάσσια Μικροβιολογία

Τμήμα Ωκεανογραφίας και Θαλάσσιων Βιοεπιστημών

Διδάσκουσα: Μεζίτη Αλεξάνδρα

Εργαστήριο 7: Ανάλυση δεδομένων αλληλούχησης

06/05/2025

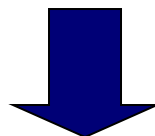
Τι είναι η ευθυγράμμιση αλληλουχιών (sequence alignment);

Προσπάθεια τοποθέτησης των αλληλουχιών ώστε να ευθυγραμμίζονται οι ομόλογες περιοχές των γονιδίων.

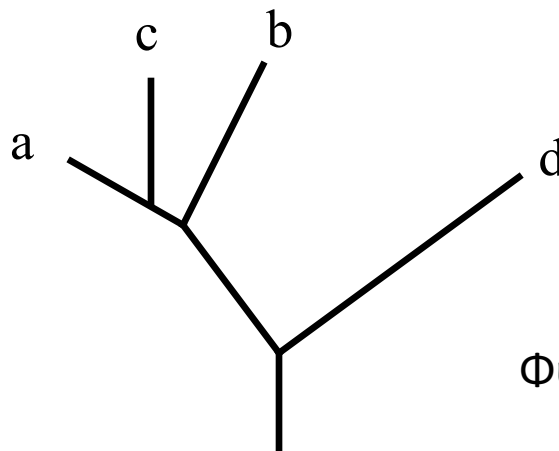
Κατά την ευθυγράμμιση αλληλουχιών από οργανισμούς που έχουν ένα κοινό πρόγονο οι διαφορές μεταφράζονται ως σημειακές μεταλλάξεις και τα κενά ως προσθήκες ή απαλείψεις νουκλεοτιδίων από τη στιγμή που τα δύο είδη απέκλιναν από τον κοινό τους πρόγονο.

Κατασκευή φυλογενετικών δέντρων

είδος a	acgugcucuucaagcuacgugggaacacacugggcgcauuu
είδος b	CC.....
είδος c	C.....
είδος d	AAA.....



Συγκριτική ανάλυση αλληλουχιών



Φυλογενετικό δέντρο

Ευθυγράμμιση ομόλογων νουκλεοτιδίων

The screenshot displays the ARB_EDIT4 software interface, titled "ARB_EDIT4 *1* [ali_16s]". The menu bar includes File, Create, Edit, View, Block, Properties, and HELP. The toolbar contains buttons for QUIT, HELP, Position, E.coli, Base, IUPAC, Helix No., JUMP, GET, Align, Insert, 5'→3', and a search icon. A status bar at the top right indicates "This is ARB Edit4 [Build 03_08_22]".

The main window shows a sequence alignment of 16S rRNA. The top section displays the alignment for "SAI: HELIX_NR" and "SAI: HELIX". Below this, the "SAI: Ecoli (usually)" sequence is shown. The bottom section displays a list of bacterial species with their corresponding sequences aligned in columns. The species listed are:

- Escherichia coli
- Pseudoalteromonas macleodii
- Shewanella benthica
- Roseobacter denitrificans
- Flavobacterium johnsoniae
- Anabaena circinalis
- Rhodococcus rhodnii
- Pirellula sp.
- Mycoplasma bovis
- Aquifex aeolicus

The sequences are aligned in columns, with the first column being the most conserved. The alignment shows that the sequences are highly similar, with many positions having the same nucleotide (A, C, G, U) across all species. The alignment is displayed in a color-coded format, with nucleotides A, C, G, and U represented by different colors (blue, green, red, and yellow respectively). The alignment is also displayed in a table format, with the species names in the first column and the aligned sequences in the subsequent columns.

• ομόλογες θέσεις στην ίδια κολόνα

Clustal Omega < EMBL-EBI

Clustal Omega < EMBL-EBI

+

←

→

↻

🔍 ebi.ac.uk/jdispatcher/msa/clustalo

☆

🏠

👤 A

Relaunch to update ⋮

Input sequence ⓘ

Sequence Type

☐ Protein ☒ DNA ☐ RNA

Paste your sequence here - or use the example sequence

Choose file

No file chosen

Use the example

Clear sequence

More example inputs

Parameters

OUTPUT FORMAT ⓘ

ClustalW with character counts

▼

More options ▼

Submit

Title

Clustal Omega's job

Submit

Input sequence ⓘ

Sequence Type

☐ Protein ☒ DNA ☐ RNA

Paste your sequence here - or use the example sequence

```
TTACCTACACTTGACATGCAGAGAACTTACTAGAGATAGTTTGGTGCCTTCGGGAAGTCTGACACAGGTGCTGCATGGCT
GTCGTCAGCTCGTGTCGTGAGATGTTGGGTAAAGTCCCGCAACGAGCGCAACCCTTGTCCTTAGTTGCCAGCATTTGGTT
GGGCACTCTAGGAGATGGCCGGTGACAAACCGGAGGAAGGTGGGGACGACGTCAAGTCATCATGGCCCTTACGTGTAG
GGCTACACACGTGCTACAATGGCATTTACAGAGGGAAGCGAGACAGCGATGTGGAGCGGACCCCTTAAAGAATGTCGTA
GTCCGGATTGGAGTCTGCAACTCGACTCCATGAAGTCGGAATCGCTAGTAATCGCAGGTCAGAATACTGCGGTGAATACG
TTCCCGGGCCTTGTACACCGCCCGTCAACCATGGGAGTGGGATGCAAAAGAAGTAGTTAGTTTAACCTTCGGGAGAAC
GATTACCACTTTGTGTT
```

Browse...

No file selected.

Use the example

Clear sequence

More example inputs

Parameters

OUTPUT FORMAT ⓘ

ClustalW



More options ▼

Submit

Title

lab060525

Welcome to the Job Dispatcher website! If you need assistance or have feedback, please [contact](#) us.

Results for Job ID

clustalo-I20250505-115053-0326-23432746-p1m

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Nightingale

COLOR SCHEME

clustal2

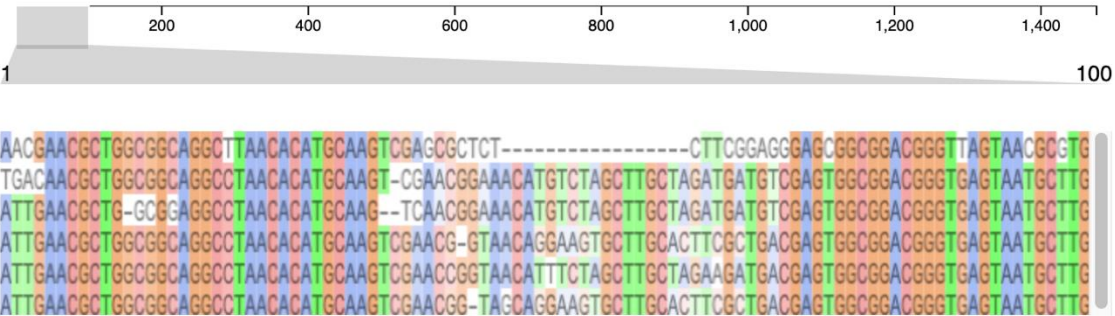
LEGEND

A R N D C Q E G H I L K M F P S T W Y V B X Z

6 sequences



OTU00004
OTU00002
OTU00006
OTU00005
OTU00001
OTU00003



TextEditFileEditFormatViewWindowHelp

Open eClass - Univ. of the AegeanClustal Omega < EMBL-EBI

202202

clustalo

clustalo-I20250505-115053-0326-23432746-p1m.pim

Getting started

clustalo

clustalo-I20250505-115053-0326-23432746-p1m.aln

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clustalo-I20250505-115053-0326-23432746-p1m.tree

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clustalo-I20250505-115053-0326-23432746-p1m.submission

Download

#

#

Percent Identity Matrix - created by Clustal2.1

#

#

1: Otu00004	100.00	74.74	73.15	73.83	75.68	75.09
2: Otu00002	74.74	100.00	93.78	92.21	94.38	93.38
3: Otu00006	73.15	93.78	100.00	91.58	93.39	93.10
4: Otu00005	73.83	92.21	91.58	100.00	95.42	95.41
5: Otu00001	75.68	94.38	93.39	95.42	100.00	95.69
6: Otu00003	75.09	93.38	93.10	95.41	95.69	100.00

Percent Identity Matrix

clustalo-I20250505-115053-0326-23432746-p1m.pim

Download

Submission Details

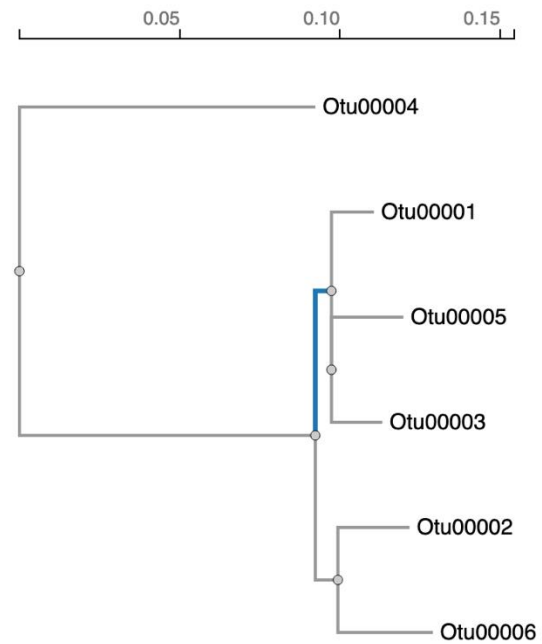
clustalo-I20250505-115053-0326-23432746-p1m.submission

Download

Phylogram



Selected 3 branches with current label



Meziti et al. 2010

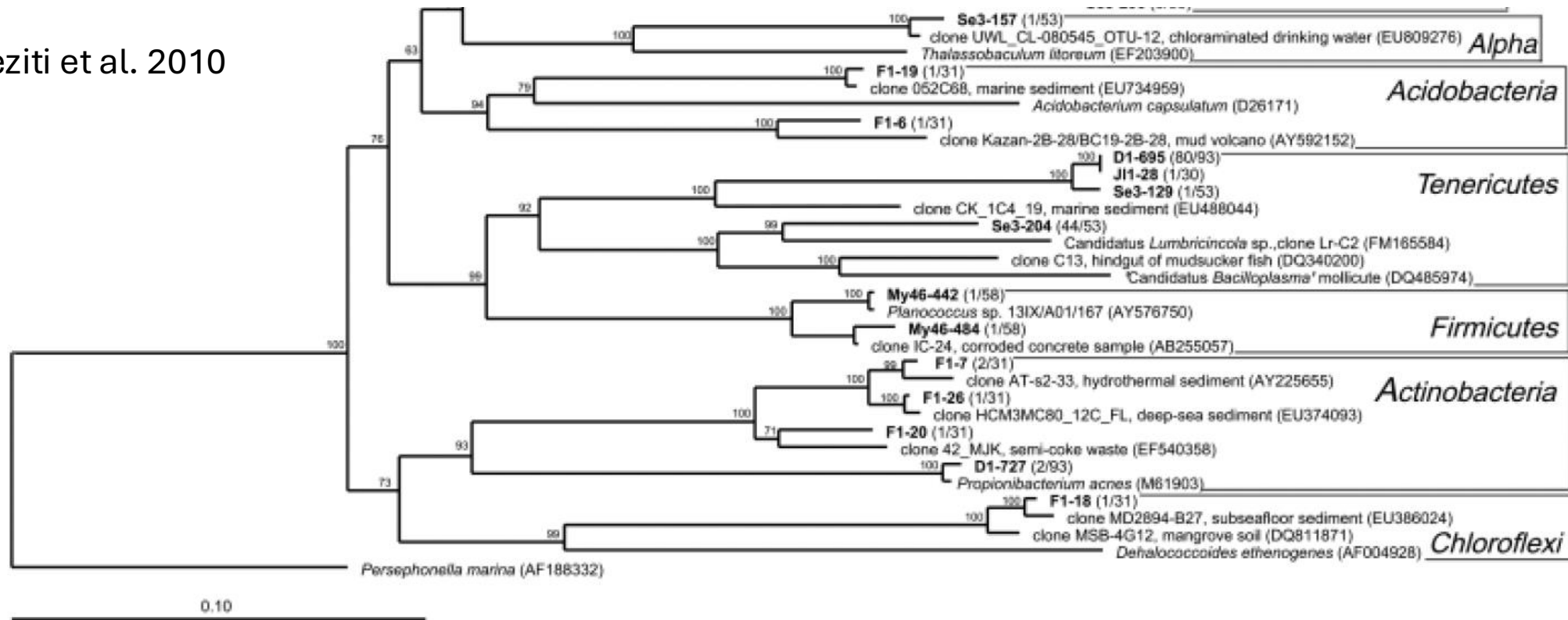


Fig. 2. Neighbor-joining tree based on 16S rRNA gene sequences from the midgut of *Nephrops norvegicus*. *Persephonella marina* (*Aquificae*) was used as an outgroup. The bar corresponds to 10% nucleotide difference and bootstrap values were calculated from 1000 replicate trees. Relative abundances of retrieved phylotypes in each clone library are shown in parentheses. Only bootstrap values over 50% are shown in the tree.

Που ανήκει ταξινομικά το OTU Se3-204?
Ποιος είναι ο κοντινότερος συγγενής του;