



Molecular Identification Methods and the Importance of Biodiversity Informatics

Pattern Techniques

RFLP

AFLP

ARDRA

RAPD

Protein profiles

Sequence based techniques

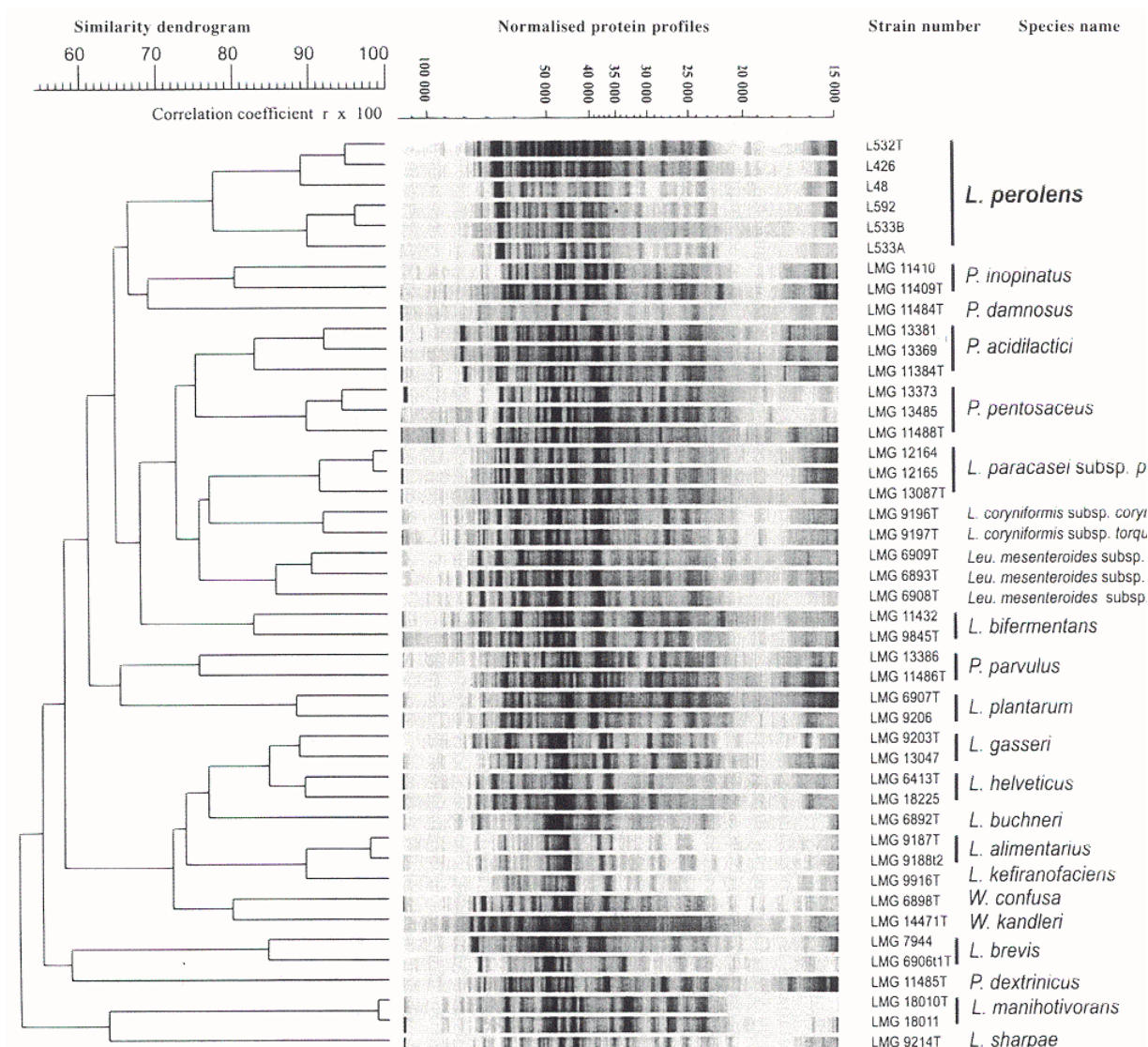
Comparative sequencing

Taxon specific probing
(chips, FISH)

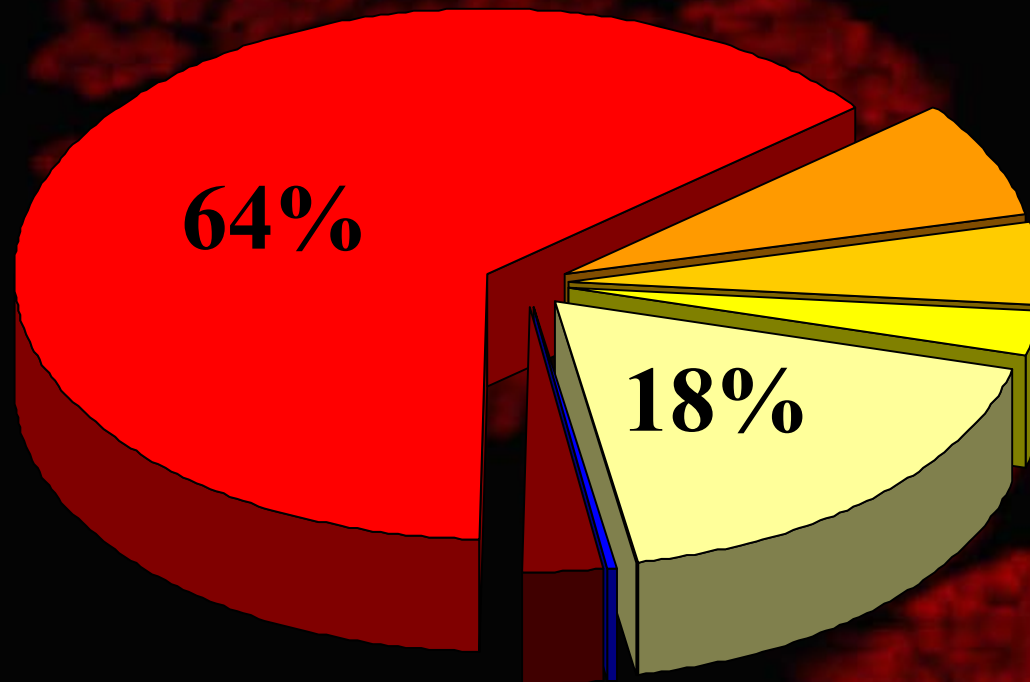
Diagnostic PCR



Molecular Identification Methods



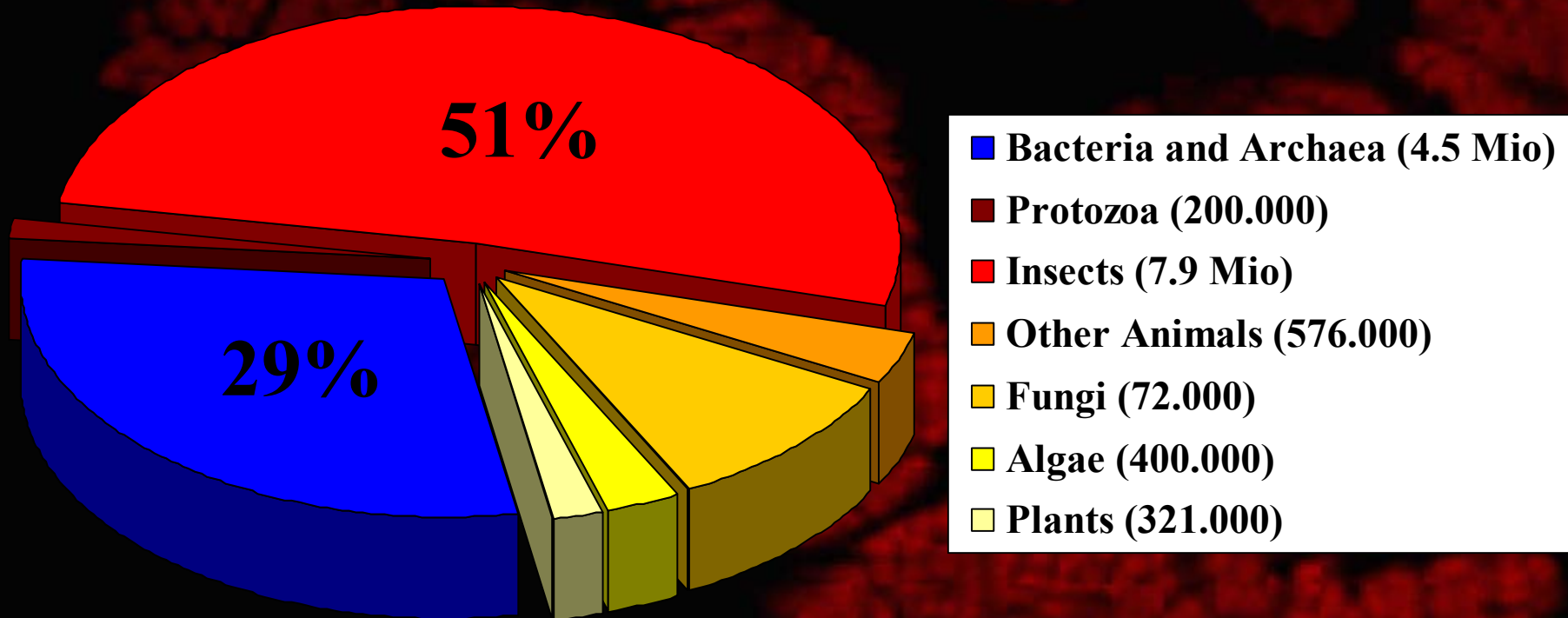
Biodiversity Today



- Bacteria and Archaea (4.500)
- Protozoa (40.000)
- Insects (950.000)
- Other Animals (110.000)
- Fungi (72.000)
- Algae (40.000)
- Plants (270000)

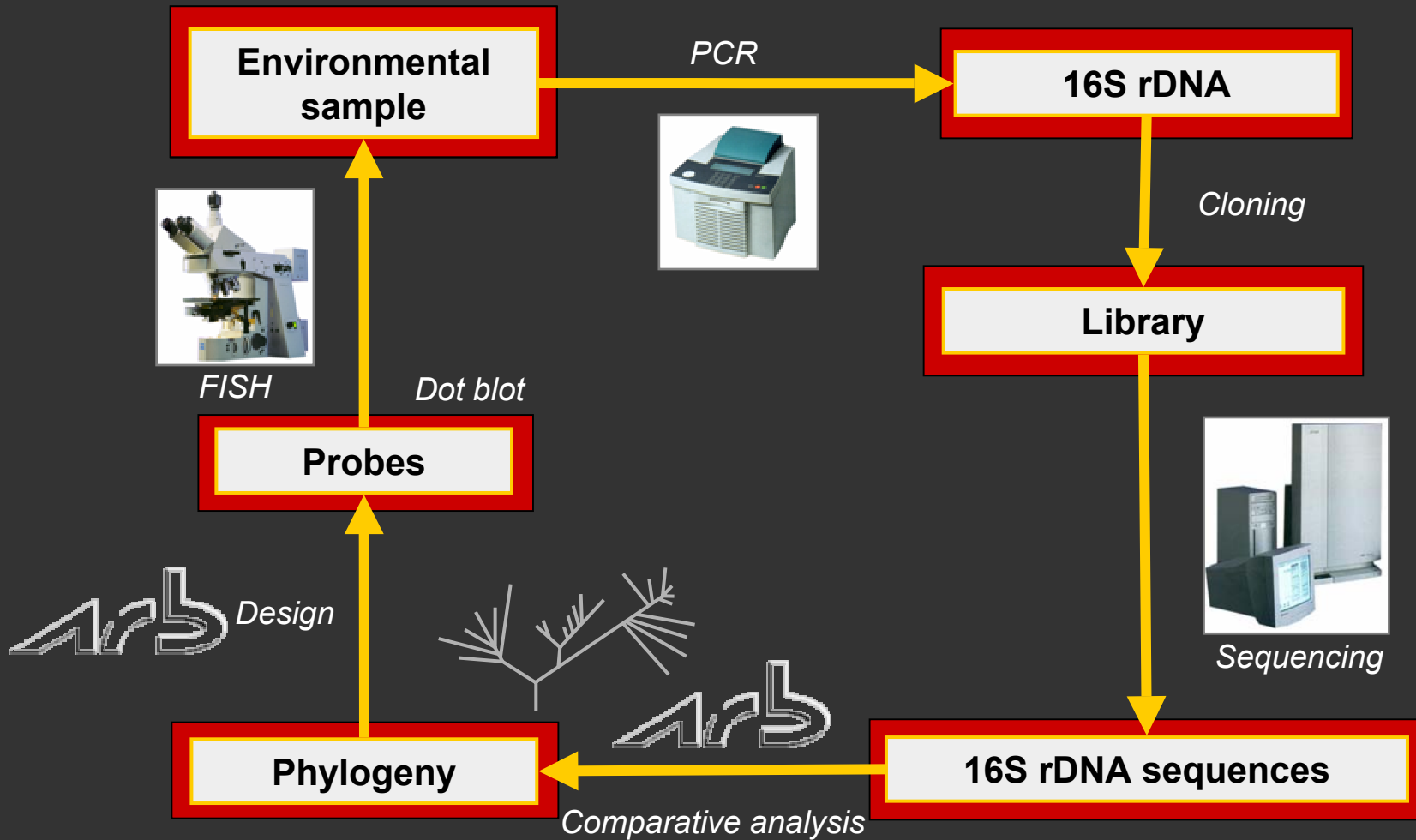
Prokaryotes – The Unseen Majority

(assuming that 0.1% of the prokaryotic species have been isolated)



But every insect contains at least one specific bacterial symbiont

Full-cycle rRNA-approach



20μm

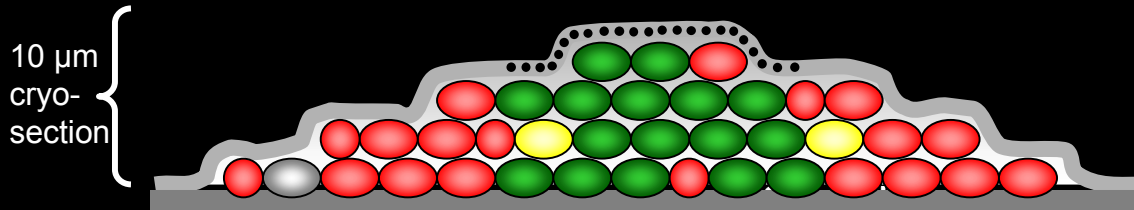
In situ detection of nitrifiers in a biofilm



Ammonia-oxidizer:
*Nitrosococcus
mobilis*

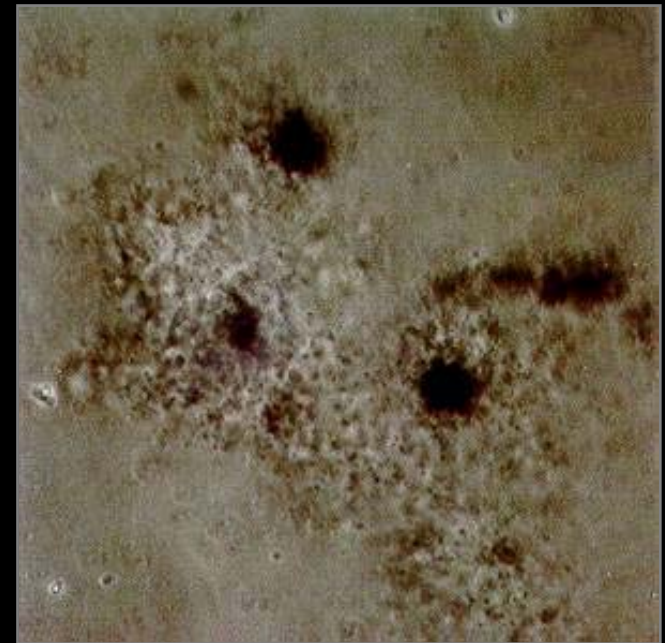
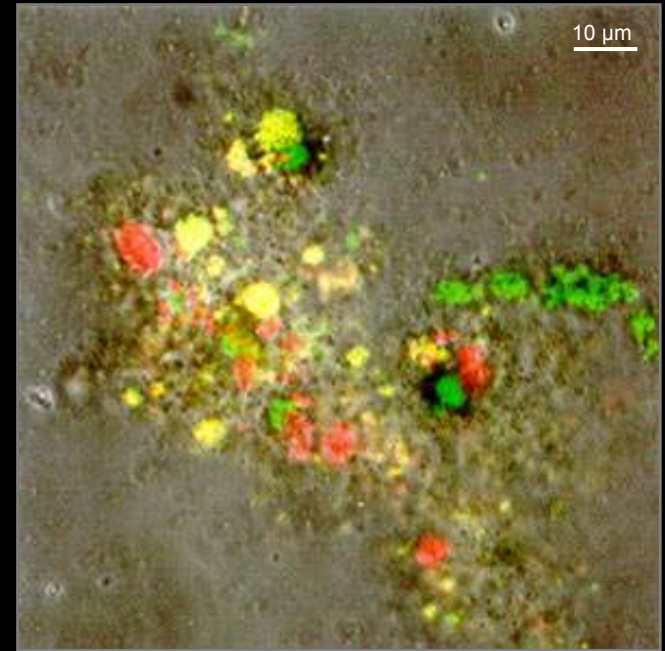
Nitrite-oxidizer:
Novel *Nitrospira*-like
bacteria

FISH - Microautoradiography



Microautoradiography.
Cells which took up
radioactively labeled
substrate induce silver
grain formation.

Fluorescently labeled bacteria

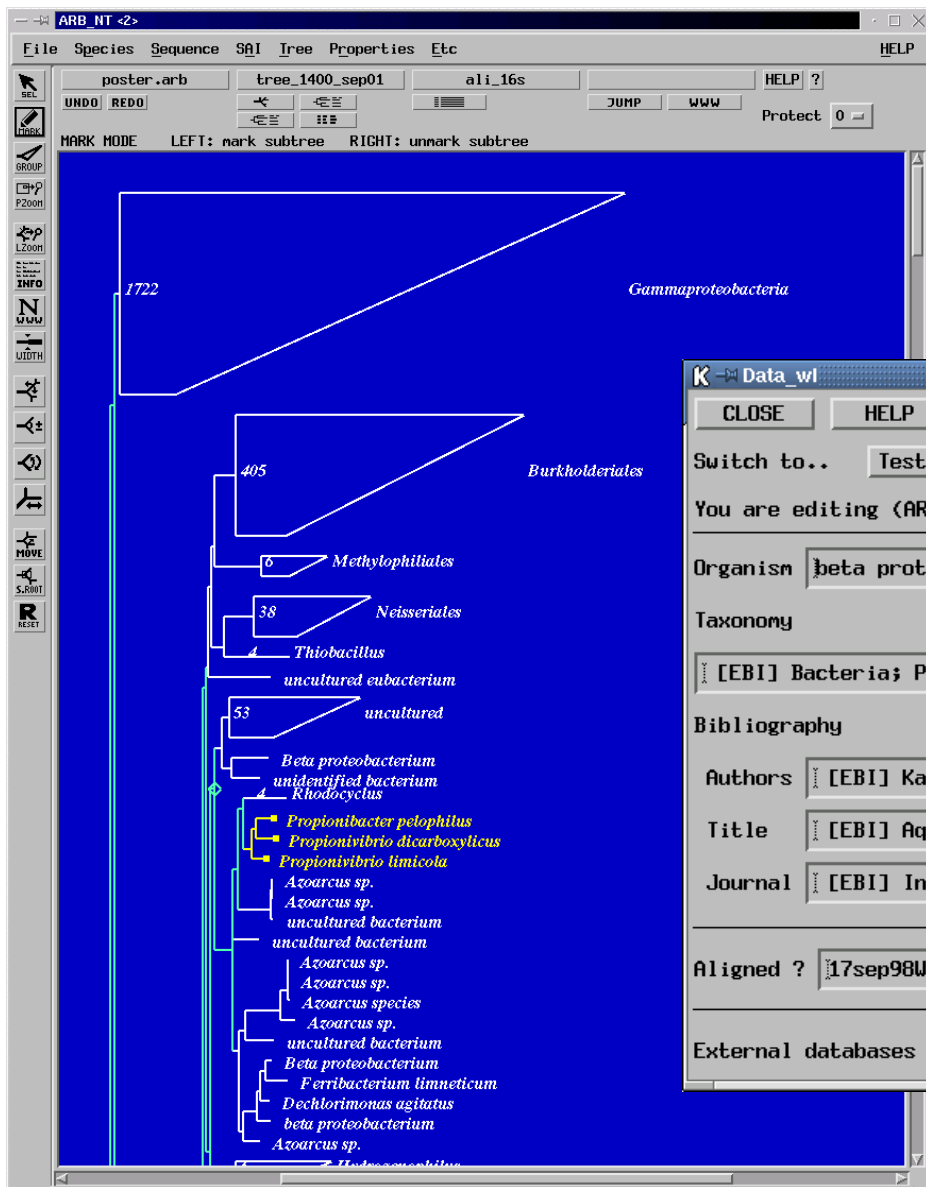




BIOLOG



ARB, a Software Environment for Sequence Data



Data window

CLOSE HELP EDIT RELOAD

Switch to.. Test Basic Expert

You are editing (ARB_ID): Bt0Pro12

Organism: Accnr:

Taxonomy:

Bibliography

Authors:

Title:

Journal:

Aligned ? Sequence: nt Gene: nt

External databases:



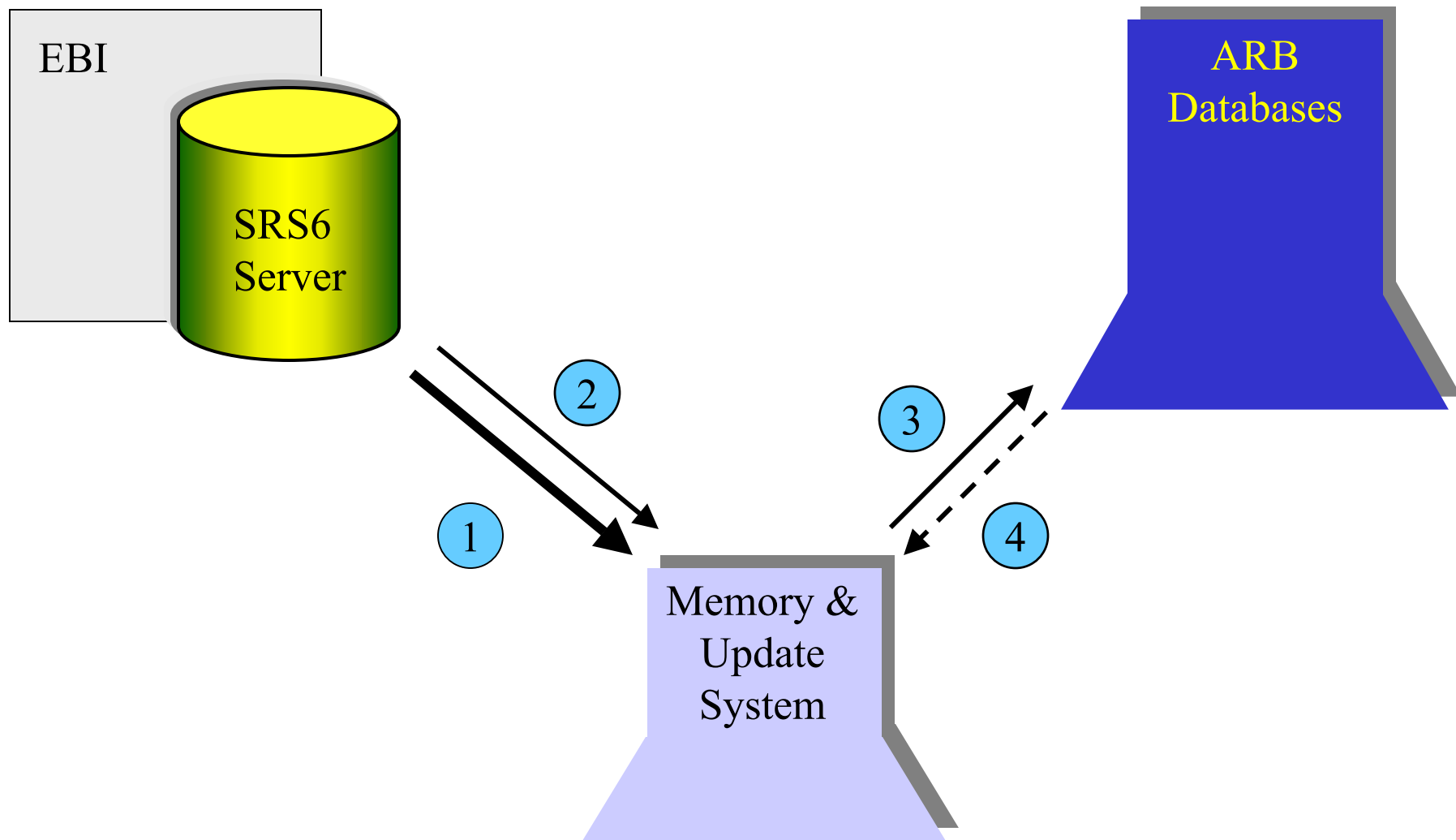
ARB, a Software Environment for Sequence Data

The screenshot shows the ARB_EDIT4 software interface. At the top, there is a menu bar with 'File', 'Create', 'Edit', 'Block', and 'Properties'. Below the menu is a toolbar with various icons for editing and navigation. The main window displays sequence alignment data for three sequences: User1 (aaacucaaa), User2 (ggaacgugcccugaagua), and Probe (RUGGGUAUGGGAAUCUCG). The alignment is shown with positions 0 to 99. Below the alignment, there is a taxonomic tree on the left side, listing various bacterial groups such as Prokaryotes (572), Bacteria (572), Beta-Gammaproteobacteria (572), Betaproteobacteria (562), Burkholderiales (405), Methylophilales (6), Neisseriales (38), Thiobacillus (4), uncultured eubacterium TRA3-20, Rhodocyclales (76), uncultured (53), Beta proteobacterium, unidentified bacterium, Rhodocyclus (4), Propionibacter pelophilus, Propionivibrio dicarboxylicus, Propionivibrio limicola, Azoarcus sp. BS2-3, Azoarcus sp. 6a3, uncultured bacterium SJA-52, uncultured bacterium SJA-109, Azoarcus sp., Azoarcus sp. BS1-14, Azoarcus species, Azoarcus sp. BS20-3, and uncultured bacterium SJA-10.

The screenshot shows the ARB_SECEDIT software interface. The main window displays a 3D RNA secondary structure model of an RNA sequence. The structure is shown as a complex, folded chain of nucleotides, with various loops and stems. The sequence is color-coded by base pair: A (green), U (yellow), G (red), and C (blue). The structure is labeled with positions 700, 1000, 1050, 1100, 1150, 1200, and 1250. The interface includes a menu bar with 'File', 'Properties', 'Close', 'HELP', '?', 'Undo', 'Redo', and 'Center'. Below the menu is a toolbar with icons for zooming and rotating the structure. The main window is titled 'ROTATE MODE' and has instructions: 'LEFT: Rotate SUBhelix RIGHT: rotate strand'.



Automation of Data Import



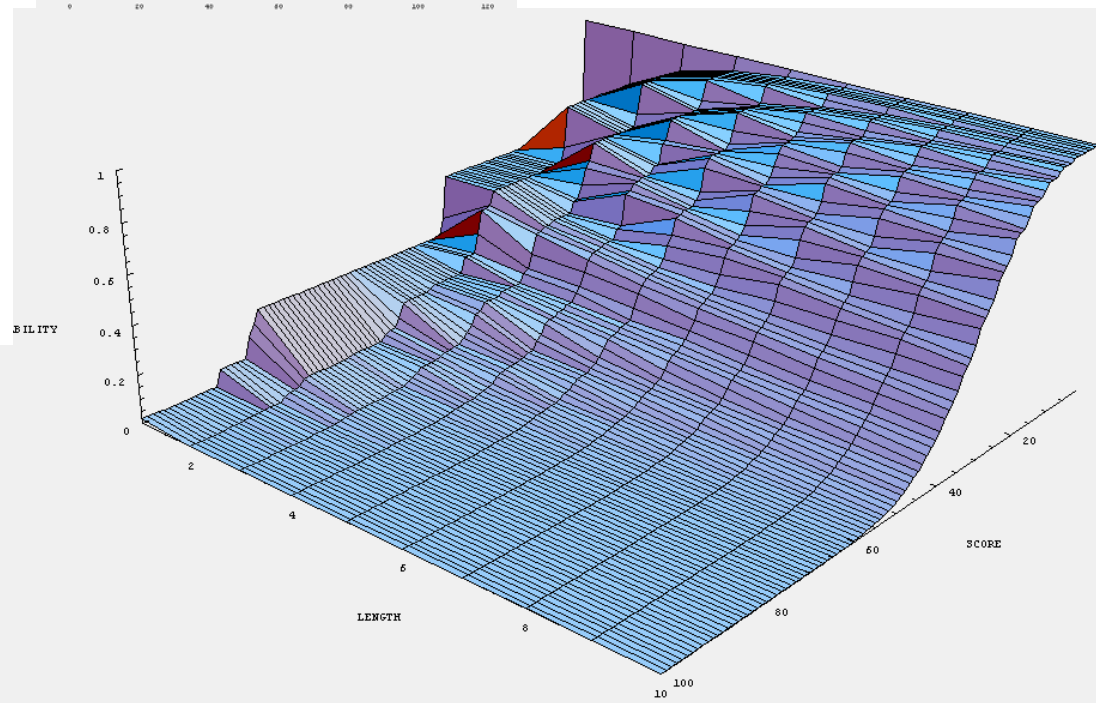
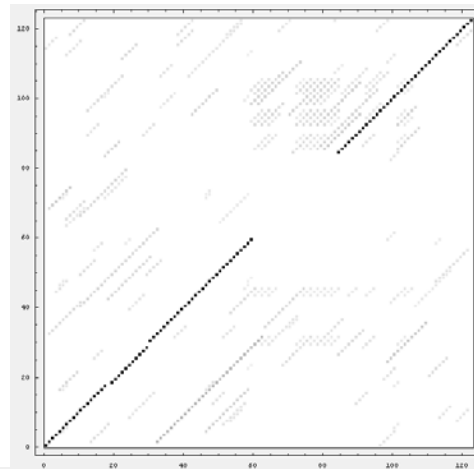
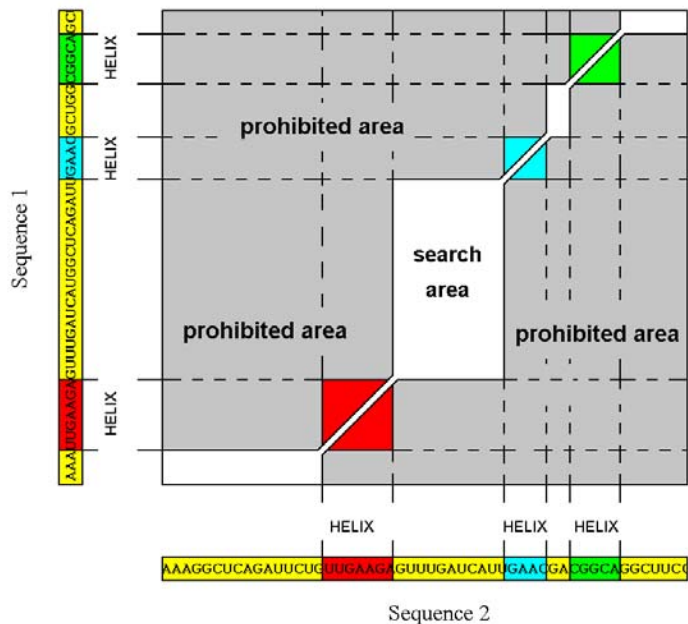


BIOLOG

Development of an Improved Sequence Aligner



Smith-Waterman-Matrix with Constraints imposed by Secondary Structure



“Island Hopping”



Database Access

http://www.arb-home.de

Netscape: The ARB project

File Edit View Go Communicator Help

Back Forward Reload Home Search Netscape Print Security Shop Stop

Bookmarks Location: http://www.arb-home.de/

Linux WebMail Calendar Radio People Yellow Pages Download

Development of a phylogenetic environment

ARB The ARB Project

Introduction

The rapidly increasing number of available rRNA sequence data, the growing missing of an integrated package of cooperating software tools for data handling and analysis led to the formation of the [bioinformatics group](#) some years ago.

The ARB project (latin, "arbor"=tree) is a joint initiative of the [Lehrstuhl für Rechnerorganisation](#) of the Technical University of Munich.

What is ARB?

The ARB software is a graphically oriented package comprising various tool database of processed (aligned) sequences and any type of additional data phylogeny or other user defined criteria. [Take a look at some features](#)

Currently [research projects](#) for software development and database maintenance foundation.

Last updated on 21 Oct 2004
by [Eduard Richter](#) and [Ralf Westram](#)

[About ARB](#)
[News](#)
[Documentation](#)
[Downloads](#)
[Projects](#)
[People](#)
[Jobs](#)
[Links](#)

Netscape: The home of ARB: Downloads

File Edit View Go Communicator Help

Back Forward Reload Home Search Netscape Print Security Shop Stop

Bookmarks Location: http://www2.mikro.biologie.tu-muenchen.de/arb/downloads.html

Linux WebMail Calendar Radio People Yellow Pages Download Customize...

Development of a phylogenetic environment

ARB Downloads

ARB databases:

- [databases](#) Last update: 2001-May-10

Important: If you download databases using windows, only download the .gz files! Otherwise the file will be corrupted.

Files needed to install arb:

- [arb_install.sh](#) installation script
- [arb.tgz](#) ARB program
- [zcat](#) decompress programm (gzip)

Important: Do not uncompress and untar arb.tgz directly, use the install script!

Installation instructions:

- [arb_README.txt](#) Last update: 1998-Oct-22

Beta-Versions:

Warning: This are medium stable versions. Please do not delete your old ARB-installation and install into a different directory.

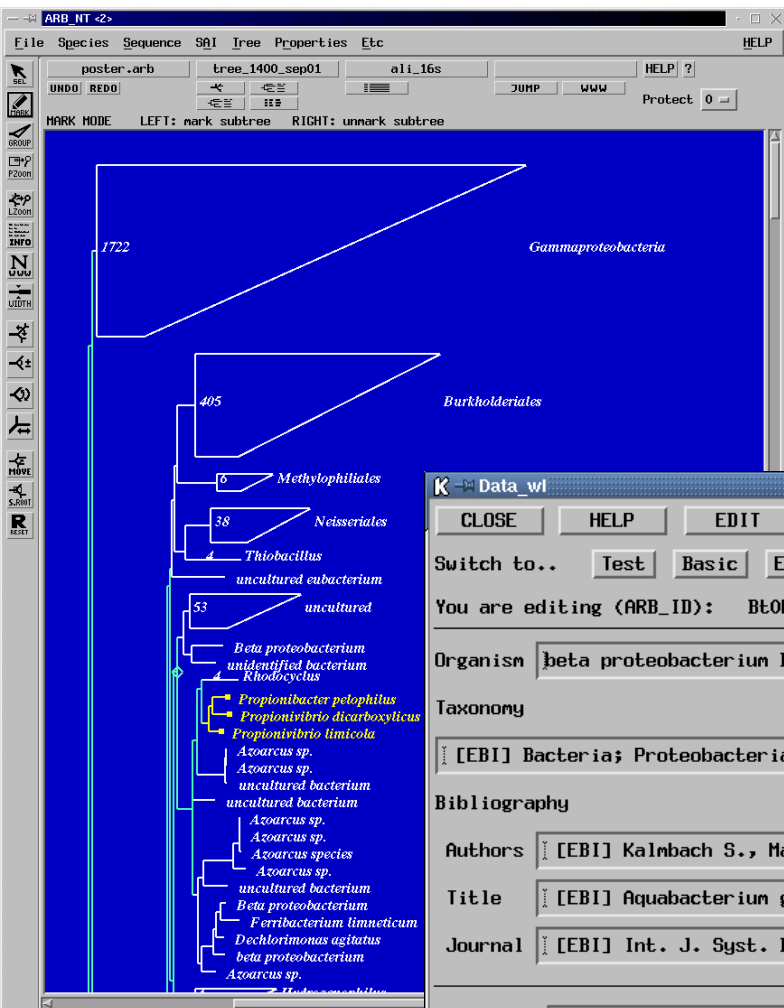
- [Linux Beta 011107](#) Last update: 2001-Nov-07
- [Solaris Beta 011107](#) Last update: 2001-Nov-07
- [Recent changes](#)

Linux-Requirements: A recent version of Linux (based on libc 6)
To detect which version you have type 'ldd /bin/su'. If libc.so.6 shows up you have a version based on libc 6.



BIOLOG

The Integrated Database



Data window

Switch to.. **Test** Basic Expert

You are editing (ARB_ID): BtOPro12

Organism: beta proteobacterium B2

Taxonomy: [EBI] Bacteria; Proteobacteria; beta subdivision.

Bibliography:

Authors: [EBI] Kalmbach S., Manz U., Wecke J., Szezyk U. Kalmbach

Title: [EBI] Aquabacterium gen. nov., with description of Aquabacterium

Journal: [EBI] Int. J. Syst. Bacteriol. 49:769-777(1999). Submitted

Aligned ? 17sep98WL 12Feb00WL 10dec00WL Sequence: 1417 nt

External databases: **EBI** GENBANK PUBMED **SYNTAX**

Netscape: Frameset 21

File Edit View Go Communicator

Back Forward Reload Home Search Netscape Print Security Shop

Bookmarks Location: http://www.biologie.uni-ulm.de/systax/daten/index.html

Linux WebMail Calendar Radio People Yellow Pages Download Custom

Suche nach Taxa Hilfe

1- Suchmuster: I

2- Datenbank: SysTax

3- Start: Zurücksetzen Suchen

4- Suchergebnis:

Das Suchergebnis wird hier angezeigt.

- Klicken Sie auf den Namen zum "Navigieren" im System
- Markieren Sie ein Taxon und lassen Sie sich die unter (5) ausgewählten Informationen anzeigen.

5- Optionen:

Taxonomie: Synonyme nein ja
Literatur nein ja
alternative Taxonomie nein ja

Einheimische Namen

Sammlungsdaten: alle Sammlungen

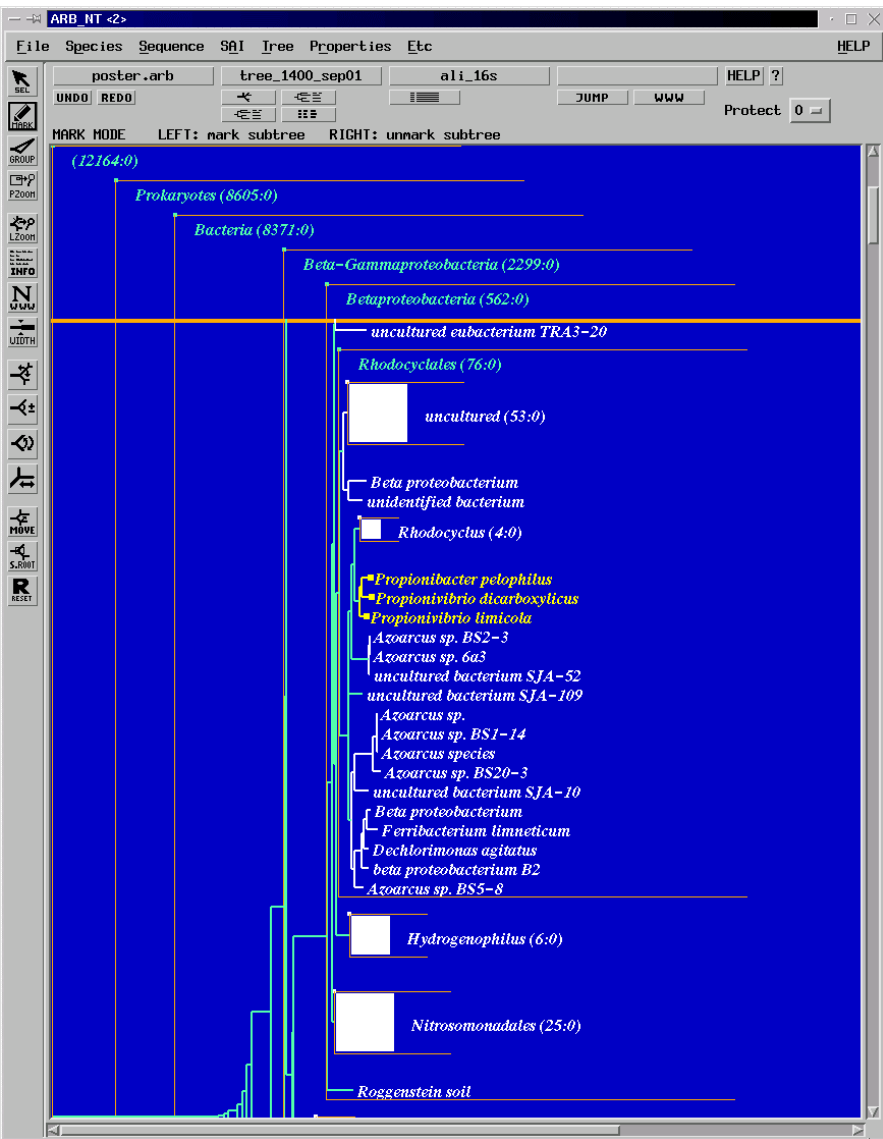
Merkmale: alle Merkmale

Literatur Rote Listen

Verbreitung Abbildungen

Experten Bemerkungen

Adressen
Stichworte
Taxon
Volksnamen
Literatur
Abbildungen
Informationssystem
Botanischer Gärten
Projekte
Technisches
Handbuch
Adressen
download
upload



BIOTA:

Integrated database of rRNA sequences and physiological, morphological and other characteristics

DNATAX & MOLART:

Databases of rRNA, elongation factors, cytochrome sequences for Identification

SYSTAX:

Integrated database of rRNA sequences and morphological, physiological, geographical, and other data



BIOLOG

BIOTA S04

