

ARB: **a Graphically Oriented Software Package** **Comprising Various Tools for Sequence** **Database Handling and Data Analysis**

**The ARB Project: W. Ludwig, O.Strunk, R.Westram, L. Richter,
H. Meier, A.Buchner, T.Lai, Yadhukumar, G.Jobb, S.Steppi, K. Bader, W. Thomas,
T. Ludwig, W. Förster, H. May, S. Hermann, N. Stuckmann, O. Gross, B. Nonhoff, R. Jost, B.
Reichel, T. Ginhart, A. Vilbig, T. Liss, M. Lenke, A. Bode, K.H. Schleifer**

CANCEL

HELP



ARB - A Software Environment for Sequence Data

ARB is developed at the
Lehrstuhl fuer Mikrobiologie
Technical University of Munich
Germany

<http://www.arb-home.de/>

Authors:

Oliver Strunk, Ralf Westram, Wolfgang Ludwig
Dr. Harald Meier, Gangolf Jobb, Lothar Richter
M. May, S. Hermann, N. Stuckmann, O. Gross
B. Nonhoff, M. Lenke, R. Jost, B. Reichel
W. Foerster, T. Ginhart, A. Vilbig, S. Gerbers

CREATE AND IMPORT

MERGE TWO ARB DATABASES

Existing Files (f) and Direcories (D)

Suffix

```

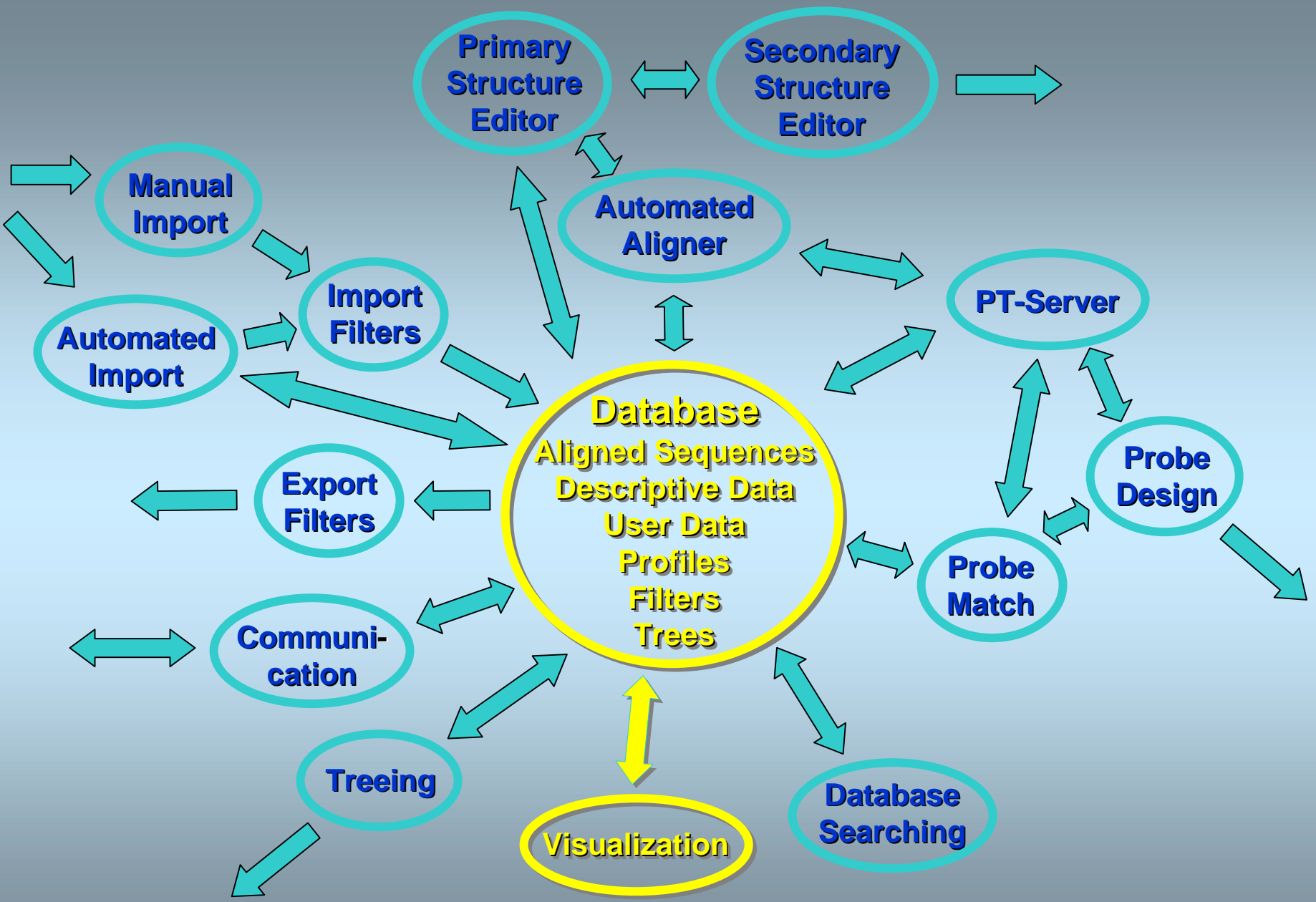
CONTENTS OF '/wl/ludwig/arb/16s'
D ' PARENT DIR      (..)'
D '$ARB_WORKDIR'    (/wl/ludwig)
D '$HOME'           (/wl/ludwig)
D '$PT_SERVER_HOME' (/opt/arb/lib/pts)
D .pics
D 23s
D fields
D march02
D old
D probe
D yassin
f 6feb1702.arb      '106094k Mar 01 18:42 2002'
f 6march0102.arb   '83716k Mar 06 22:39 2002'
f 6pt1350_mrz02.arb '62908k Mar 02 11:27 2002'
f Neu_Aligned_By_Arno.arb '28576k Feb 02 20:05 2002'

```

OPEN SELECTED

DELETE SELECTED

Enable Novice Mode



File Species Sequence SRI Tree Properties Etc

Search1502.arb trees_1490_01mar202 all

SEARCH

Enable edit? Marked?

Close Edit Reload

Enable edit? Marked?

Species Fields

Close Search Help

Enable edit? Marked?

Edit box (select a field and edit in this box)

[EBI] Ophryoglena catenula 185 r-ribosomal (899 genes, complete sequence).

bibliomask

You are editing OpgCaten

Full name [EBI] Ophryoglena catenula

Accession [EBI] J17355 Nucleotides [EBI] 95214538 Medline [EBI] 1745

Bibliography

Author [EBI] Wright A.D., Lynn D.H. [EBI] # Wright A.D., Lynn D.H. # Wright A.-D.G. # Wright A.-D.G.

Title [EBI] Phylogeny of the fish parasite Ichthyophthirius and its relatives Ophryoglena and Tetrahymena (Ciliophora,

Journal [EBI] Mol. Biol. Evol. date 1995 vol 12 pgs 285-290 [EBI] Mol. Biol. Evol. 12(2):285-290(1995).

```

arab
submitted
dbi_check
nuc_dbi_check
nuc_170202
nuc_1746
nuc_170202
nuc_1746
nuc_010302
nuc_1746
nuc_170202
nuc_1746
nuc_170202
nuc_1746
dbi_check_2
dbi_check
db_nuc_n
SGP
DEU
50: [EBI] 185 r-ribosomal SRR
50: [EBI] Submitted (21-MAR-1994) to the EMBL/GenBank/EBI databases. Submitted (10-JUN-1997) to
50: F6602.at_017355.1
50: 1746 017355.1
50: 1746
50: 1746
50: 1746
50: 12search02M
50: [EBI] ARB_4865FEB0
50: [EBI] 1746
50: not in RUP
50: 12search02M up_info
  
```


CLOSE

DATABASE SEARCH

HELP

- ◇ Search species
- ◇ Add species
- ◇ Keep species
- ◇ that match the query
- ◇ that dont match the q.
- ◇ that are marked

QUERY

| | | | | |
|---------------|-----------|---|----------------|---|
| Search fields | aligned | = | Search strings | * |
| and | full_name | = | Glaucomax | |
| and | nuc_term | = | >1600 | |

SEARCH



HITLIST Hits: 3

```

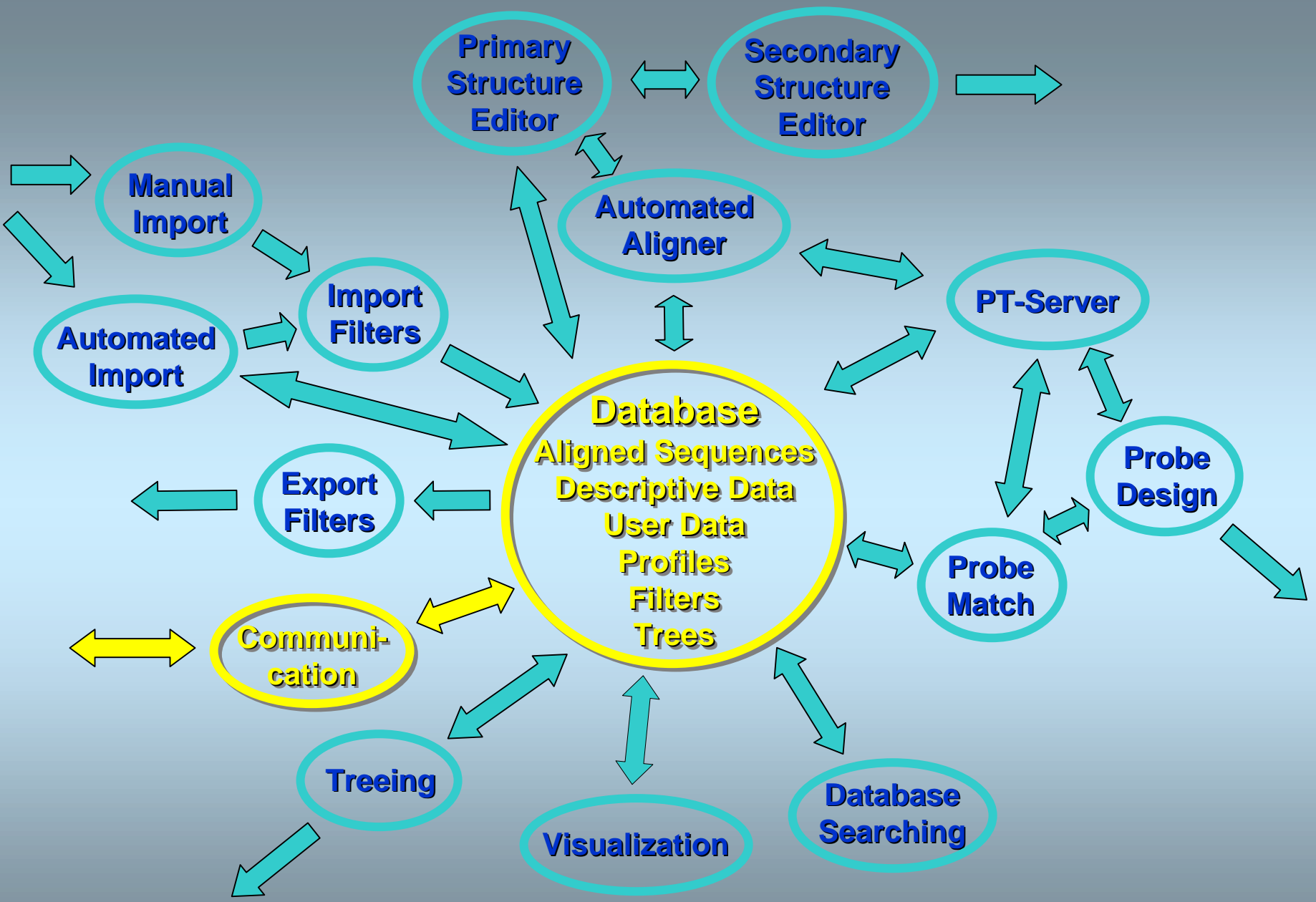
* GucScin3 : 21.ju101UL 21aug01UL 21nov01UL 07c
* GucChatt : 31.ju196UL 11feb01UL 03mar01UL 21.j
* GucChat2 : 31.ju196UL 11feb01UL 03mar01UL 21.j
End of list

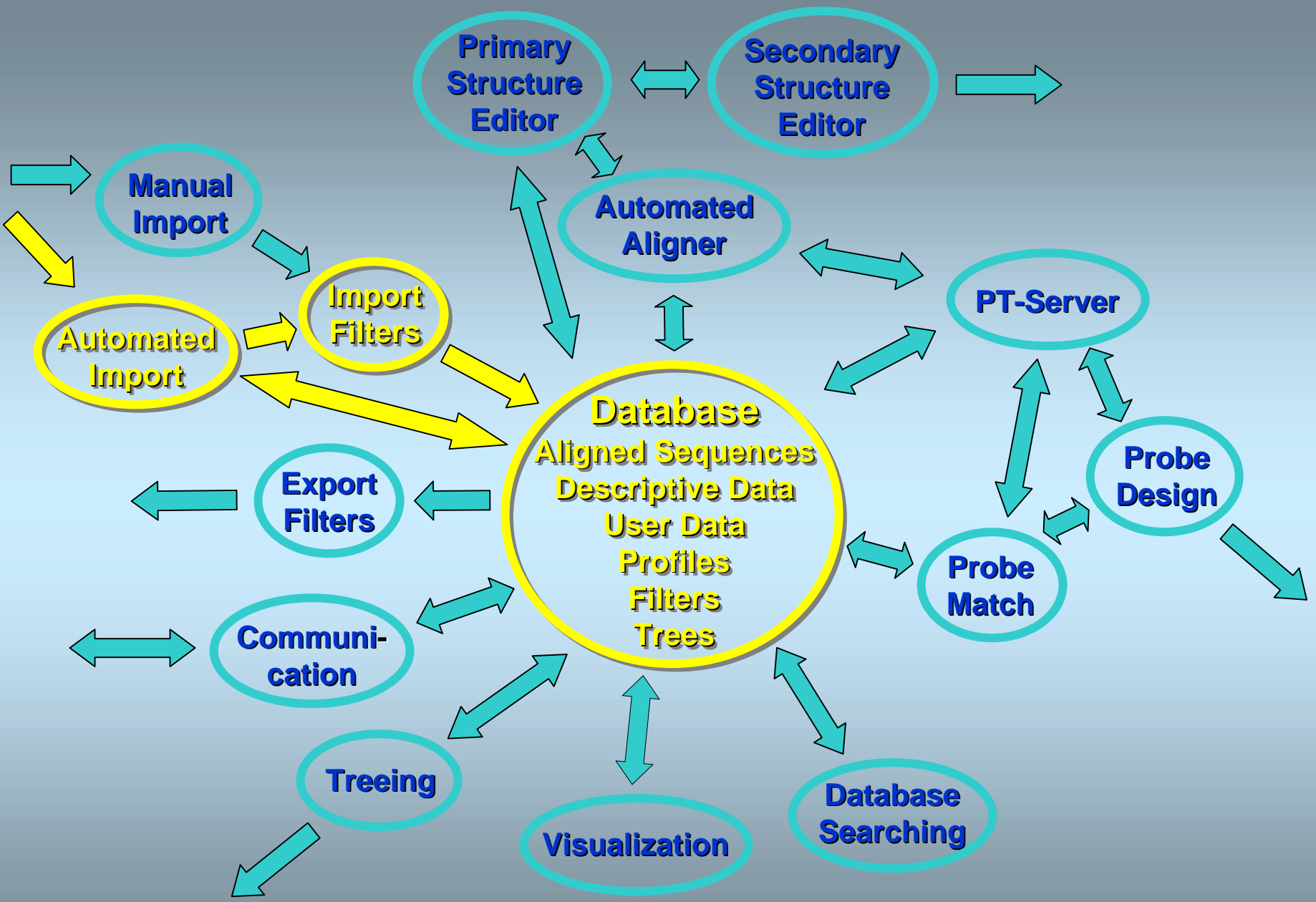
```

- MARK LISTED
UNMARK REST
- UNMARK LISTED
MARK REST
- DELETE LISTED
- WRITE TO FIELDS
OF LISTED

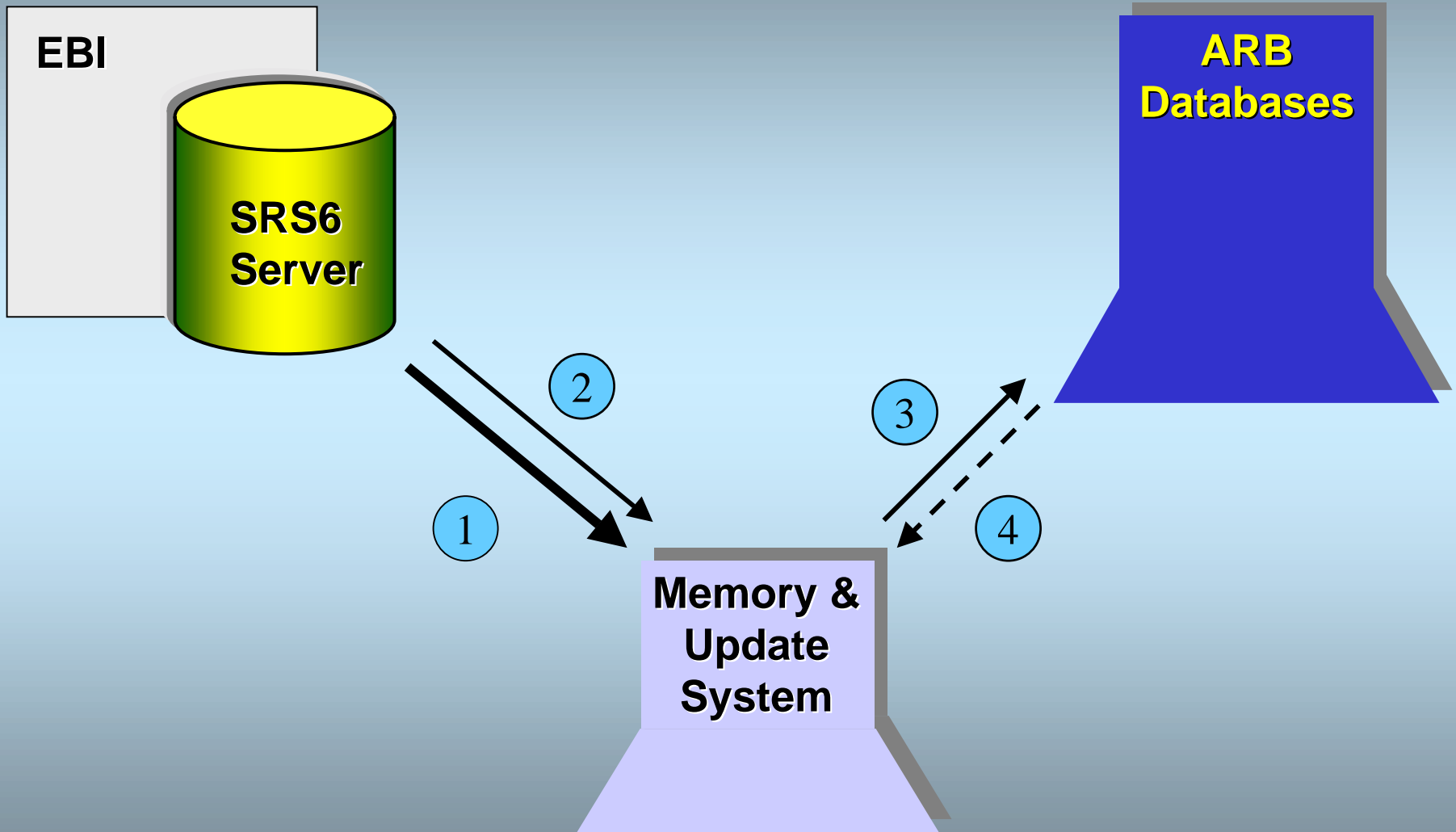
REFRESH

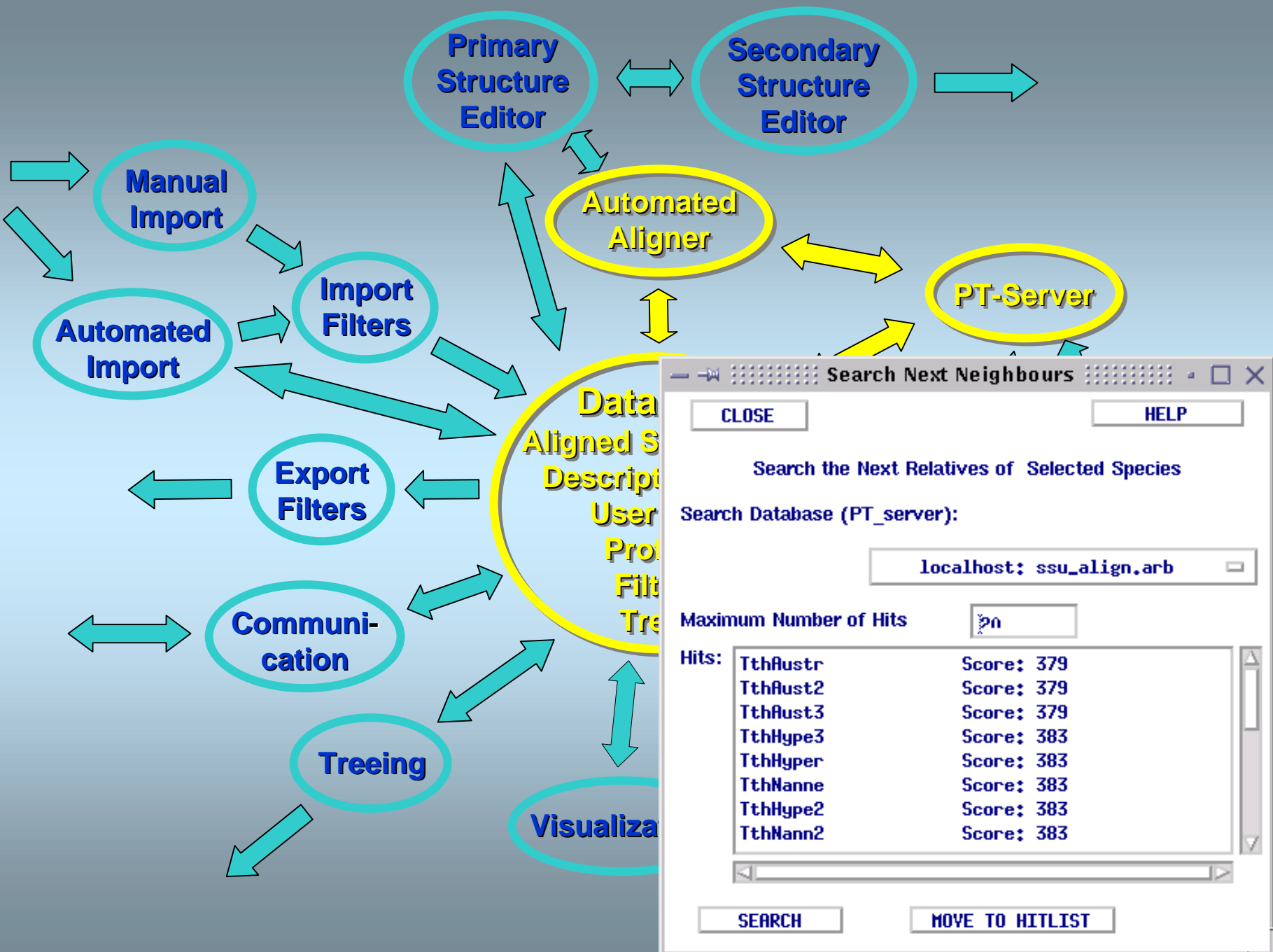
Note: double click item to mark/ unmark

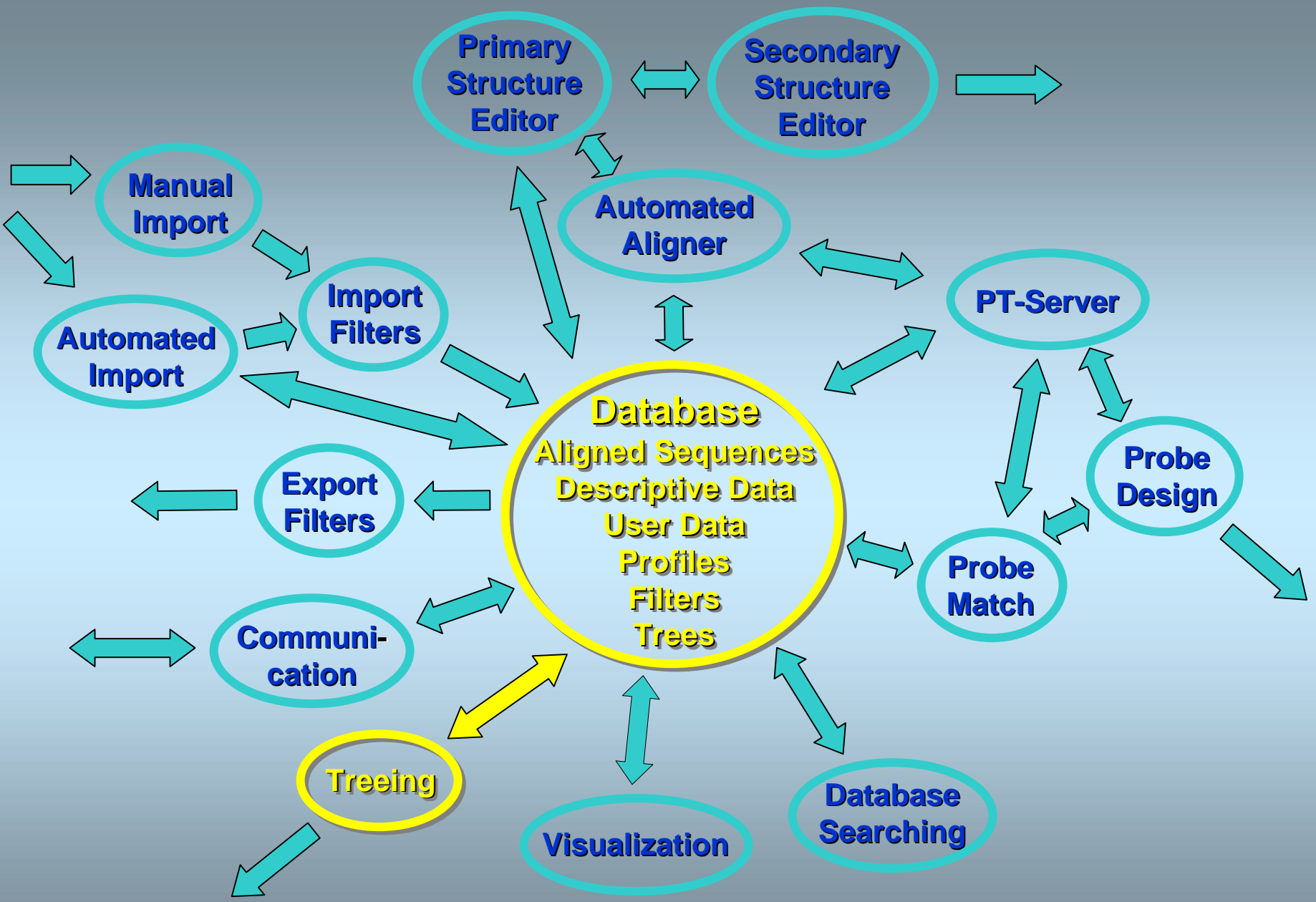




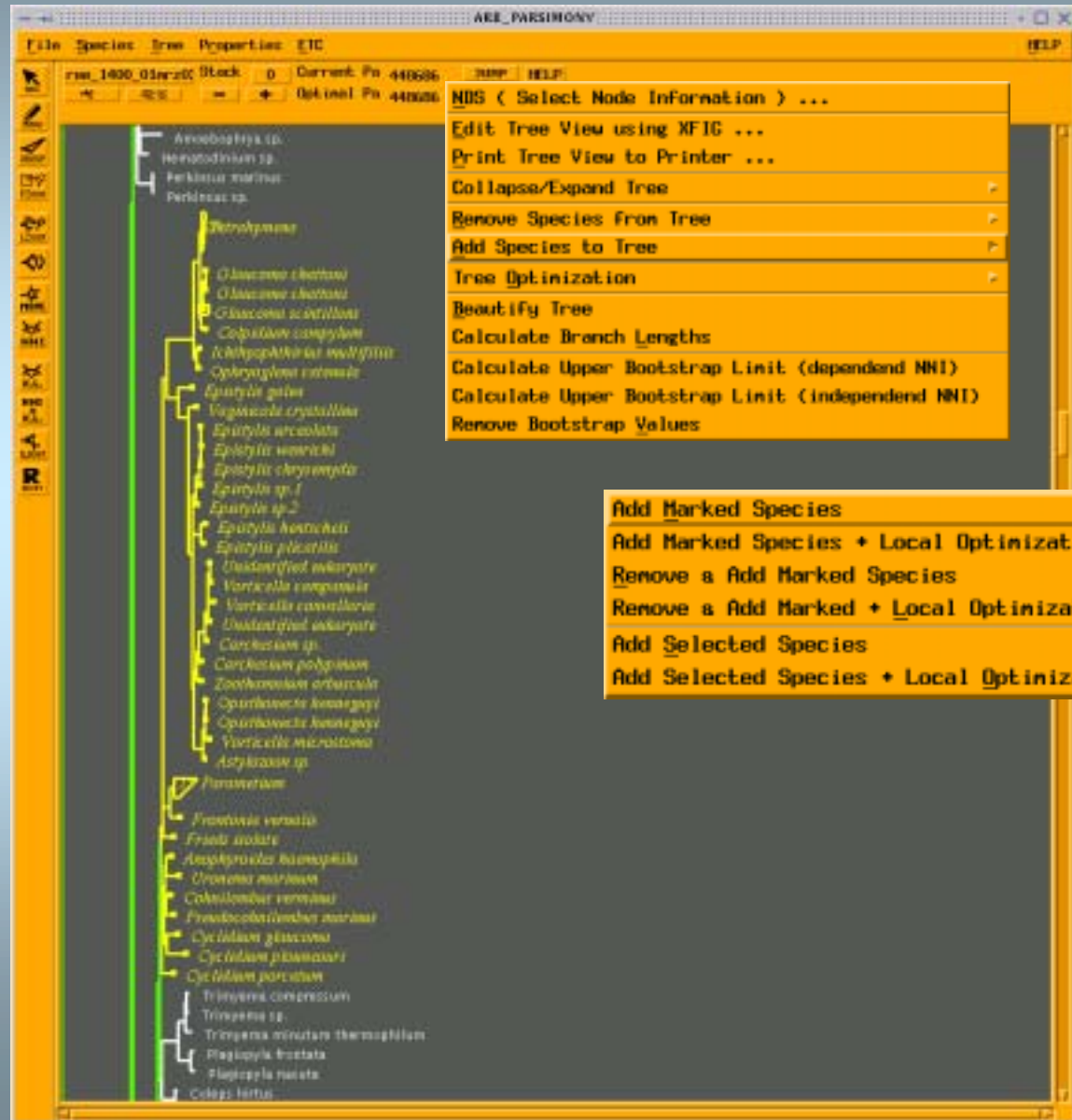
Automation of Data Import



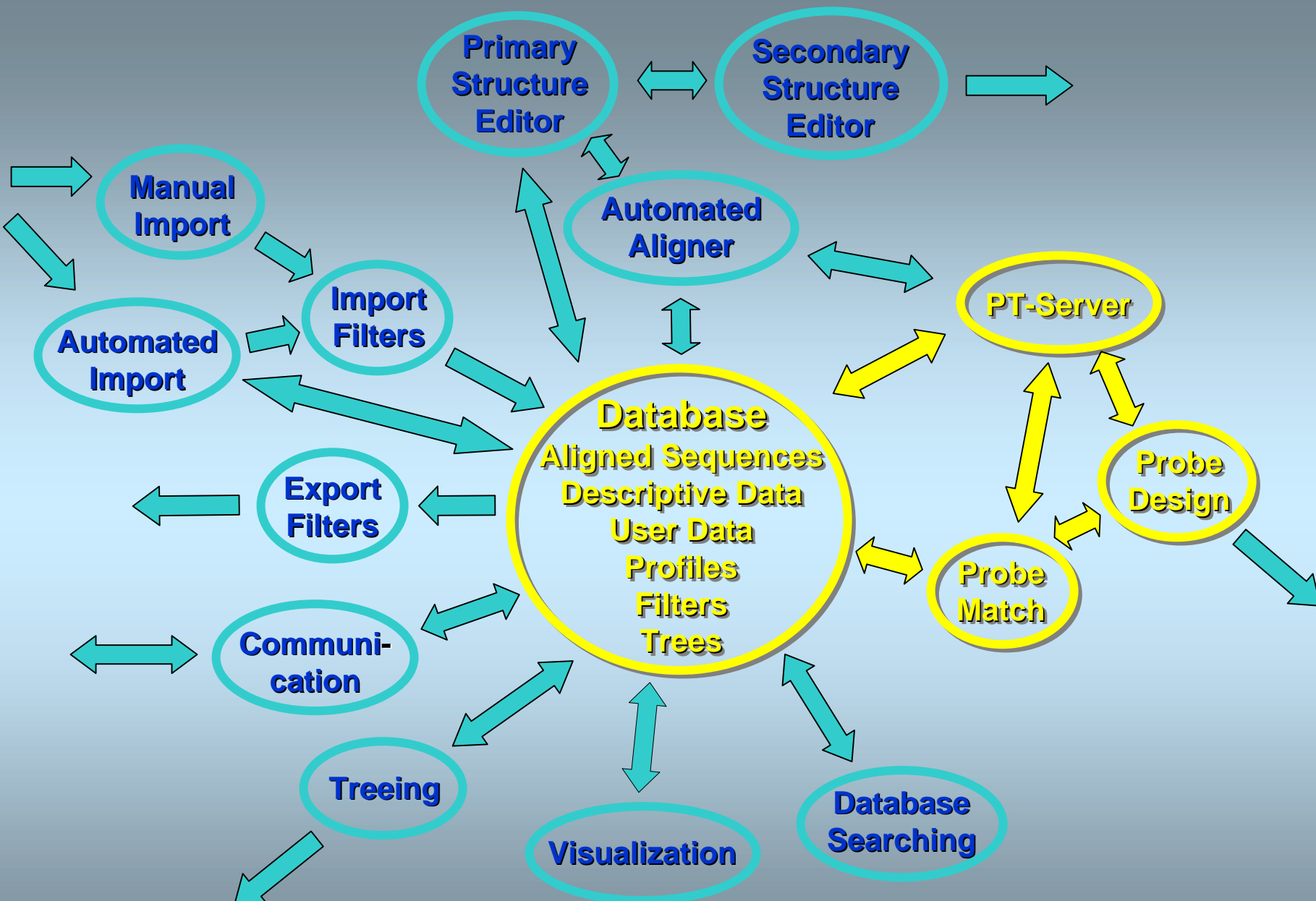


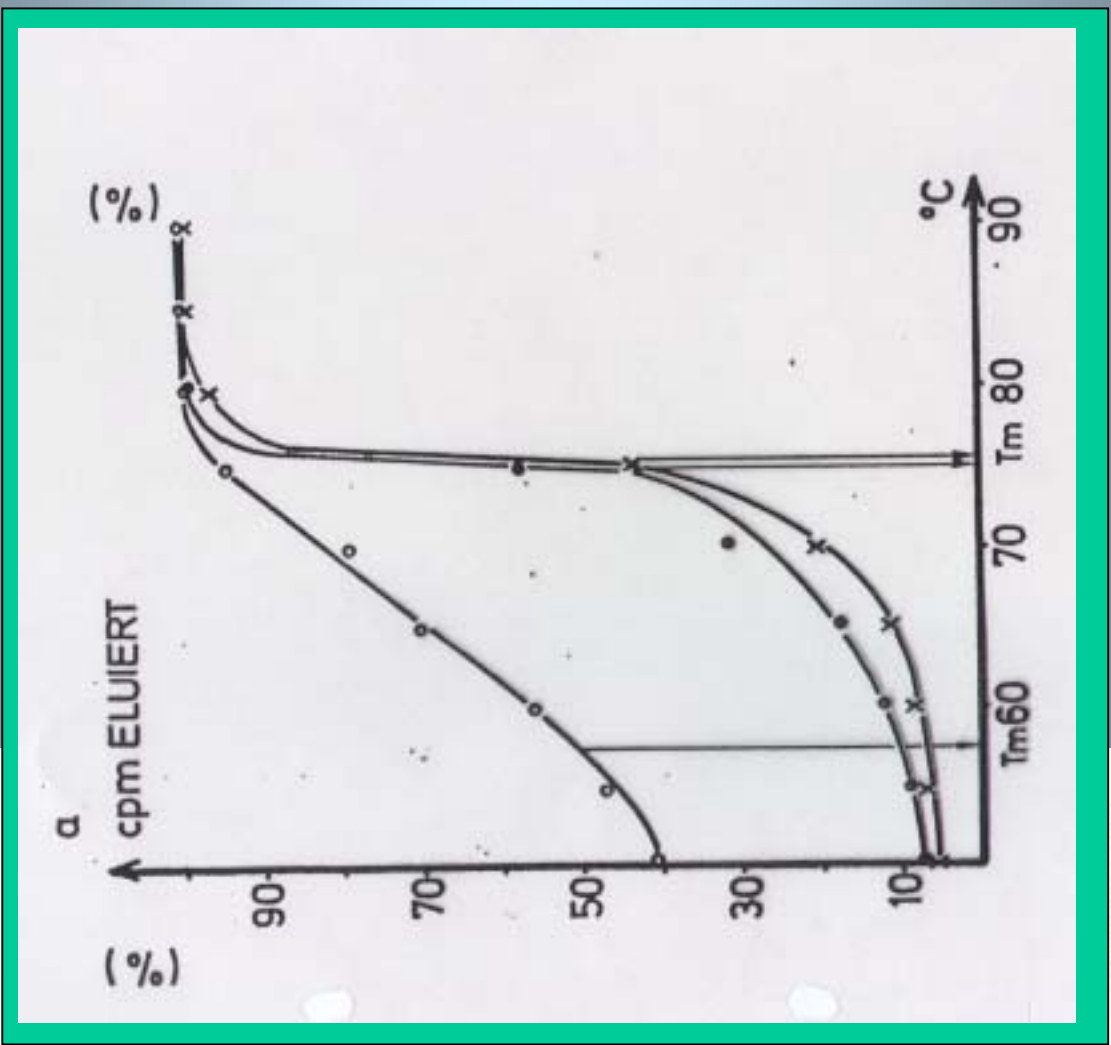
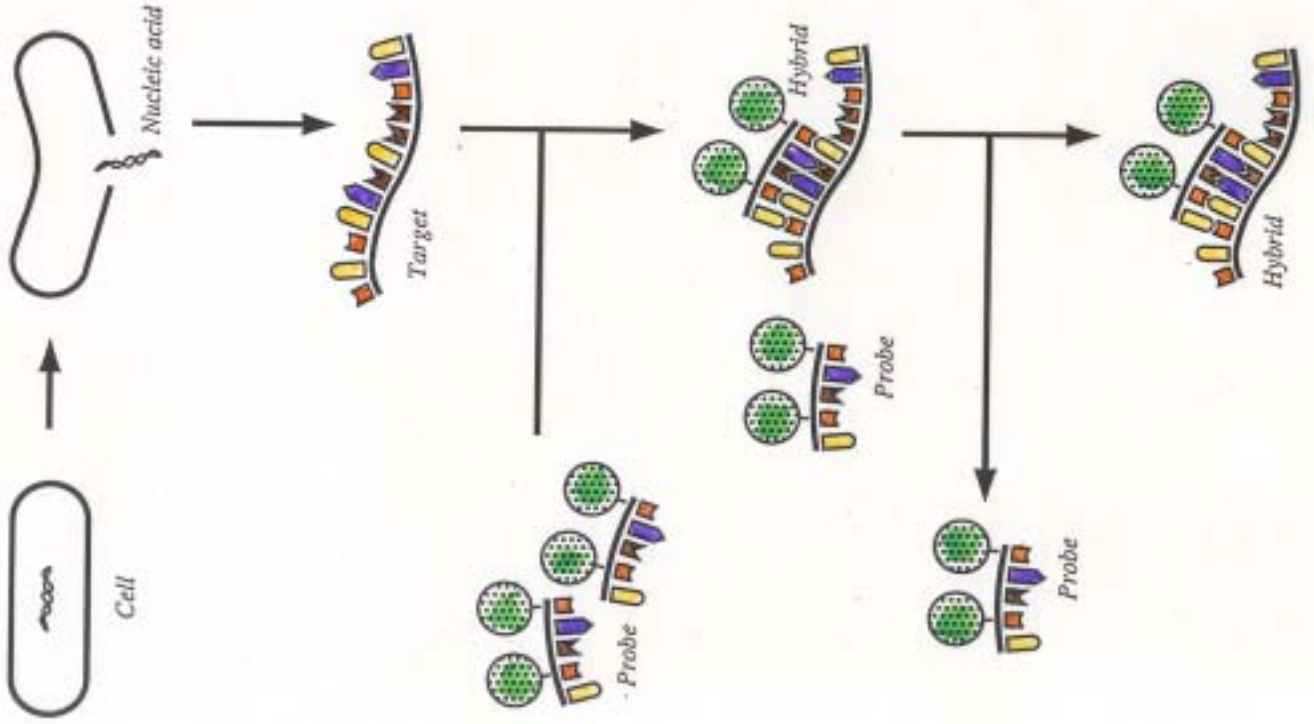


The ARB Parsimony Tool



- Able to handle big trees (e.g. >30.000 16S/18S rRNA sequences)
- Allows optimization of subtrees with different parameters.
- Positioning of sequences possible without changing initial topology.





Detection

Stability of Probe – Target Hybrids

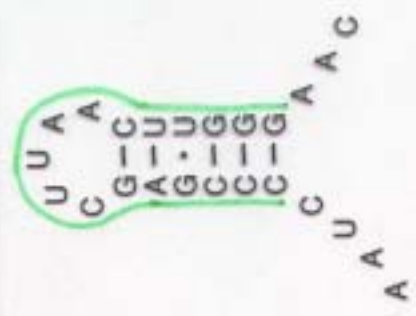
- Size
- G+C Content
- Sequence
- Temperature
- Ionic Strength
- Denaturing Agents
- **Number and Character of Mismatches**

Criteria for *in Silico* Probe Design and Evaluation

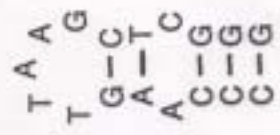
- **Dissociation Temperature**
- **G+C Content**
- **Number of Diagnostic Mismatches**
- **Position of Diagnostic Mismatches**
- **Character of Diagnostic Mismatches**
- **Nearest Neighbors of Diagnostic Mismatches**
- **Intra-probe and –target Base Pairing**
- **Target Position**
- **Hybridization Technique**

3' -GGGCTCGAATTGAACCC-5' 54
Hafnia 5' -AAAUCCCCGAGCUUAACUUGGGAAACA-3'
Yersinia 5' -AAAUCCCCGCGCUUAACGUGGGAAACA-3'
 3' -GGGCGCGAATTGACCC-5' 11

Zielssequenz

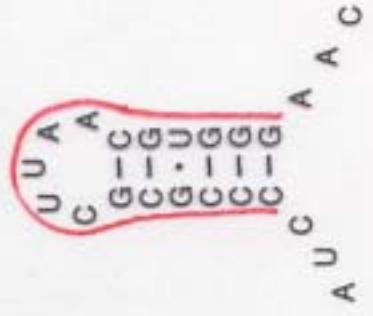


Sonde

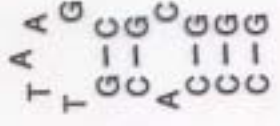


Hafnia alvei

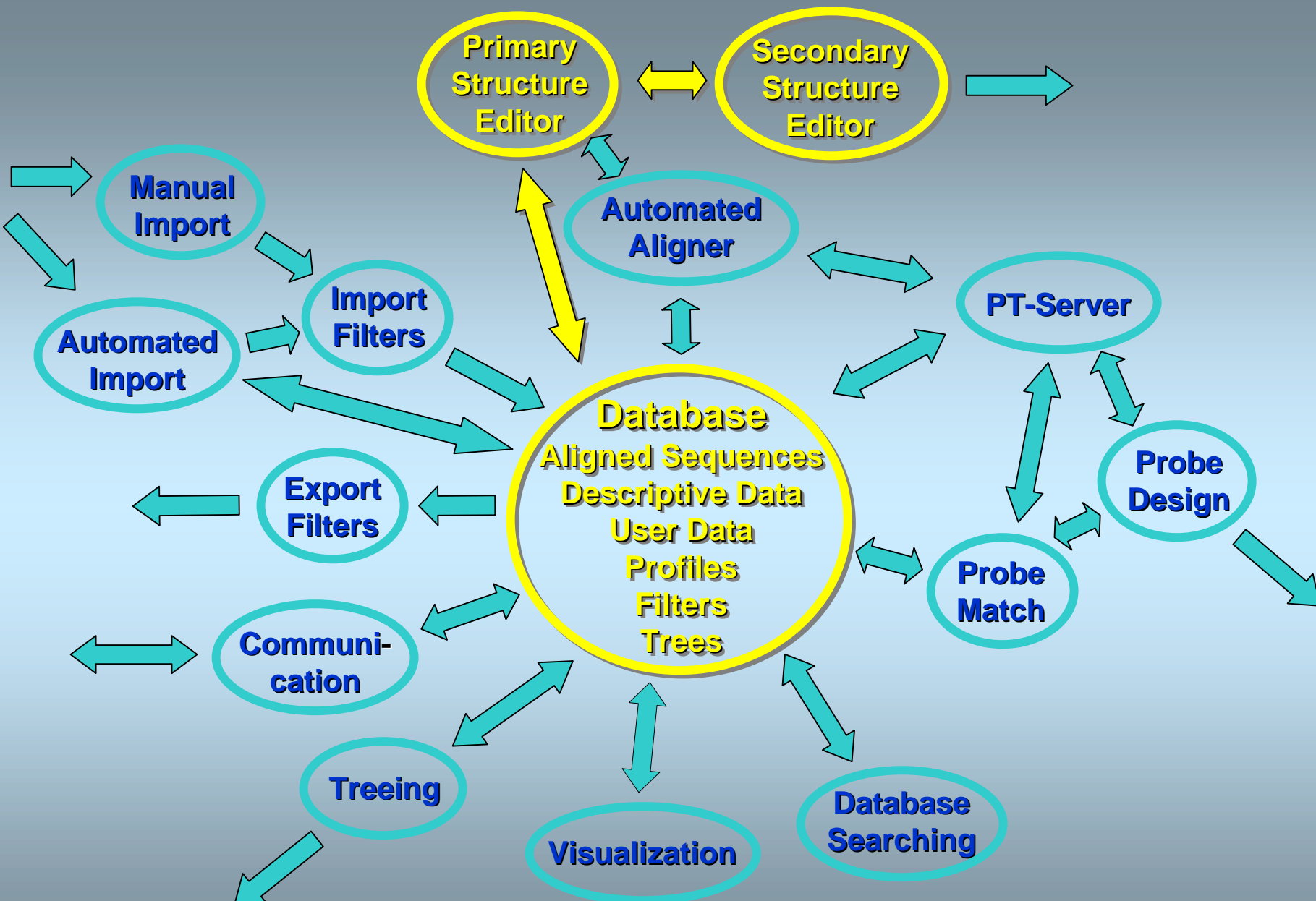
Zielssequenz

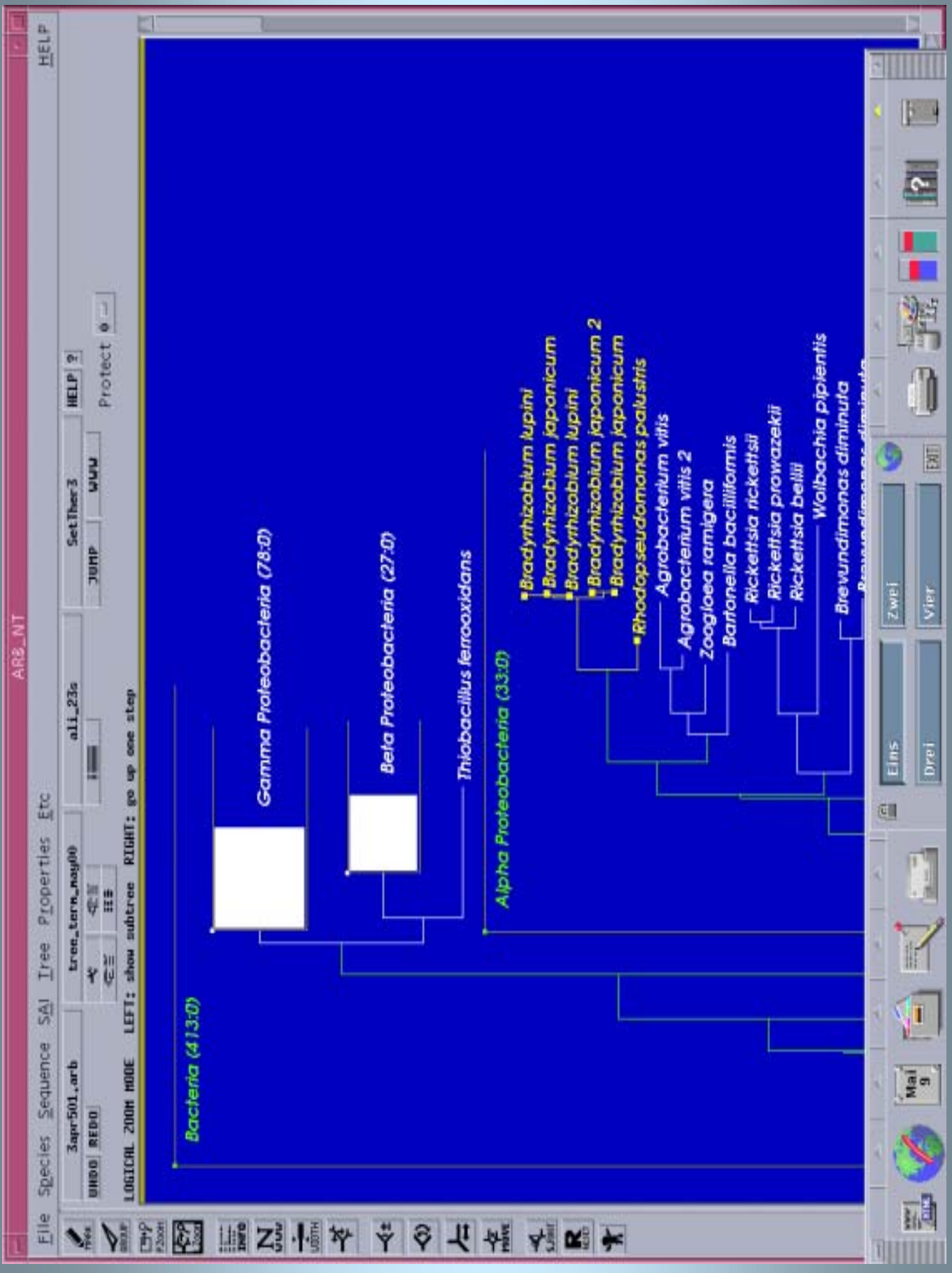


Sonde



Yersinia enterocolytica







UNDO REDO

3apr501.arb

tree_term_wag(0)

all_23s

Set Ther-3

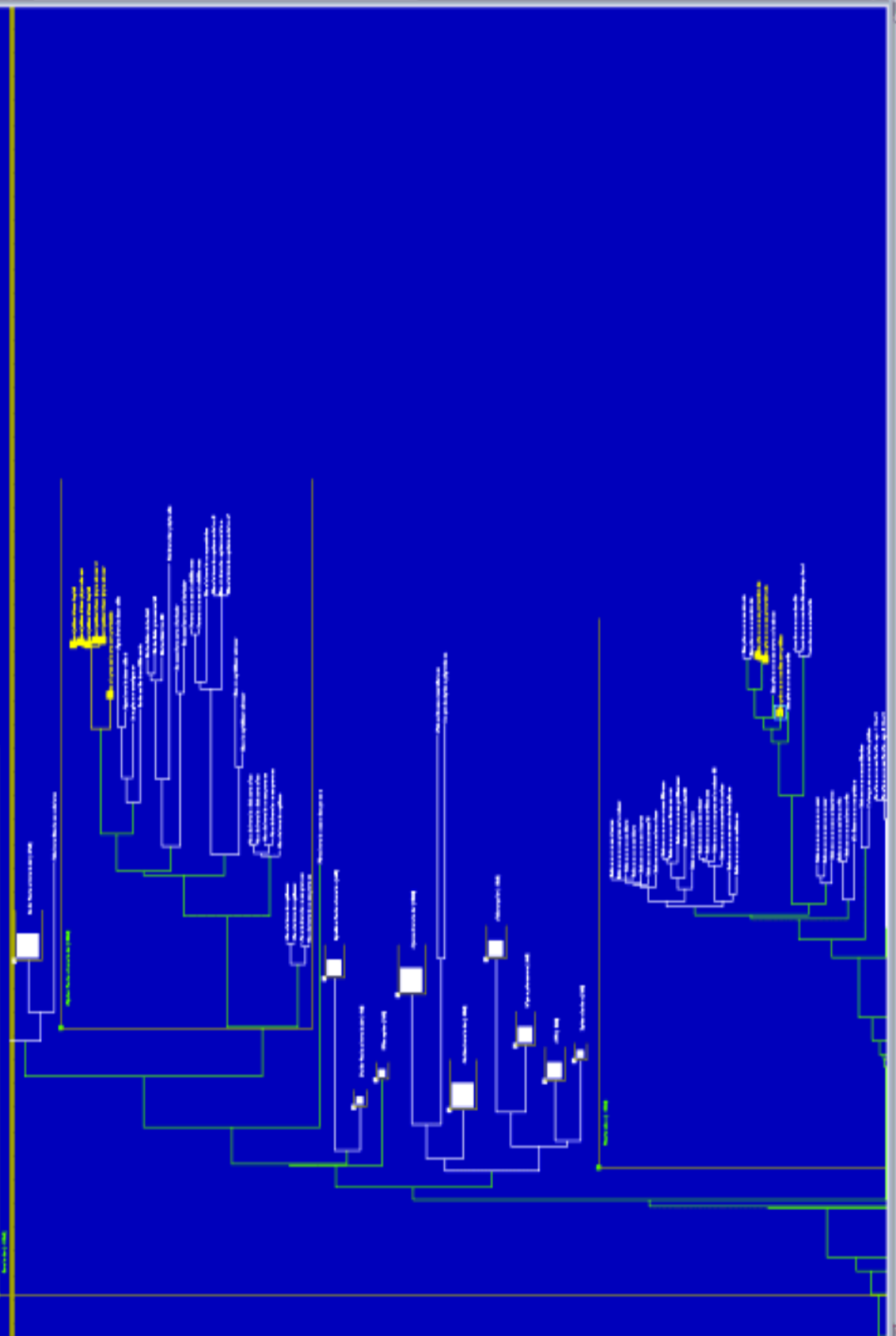
JUMP

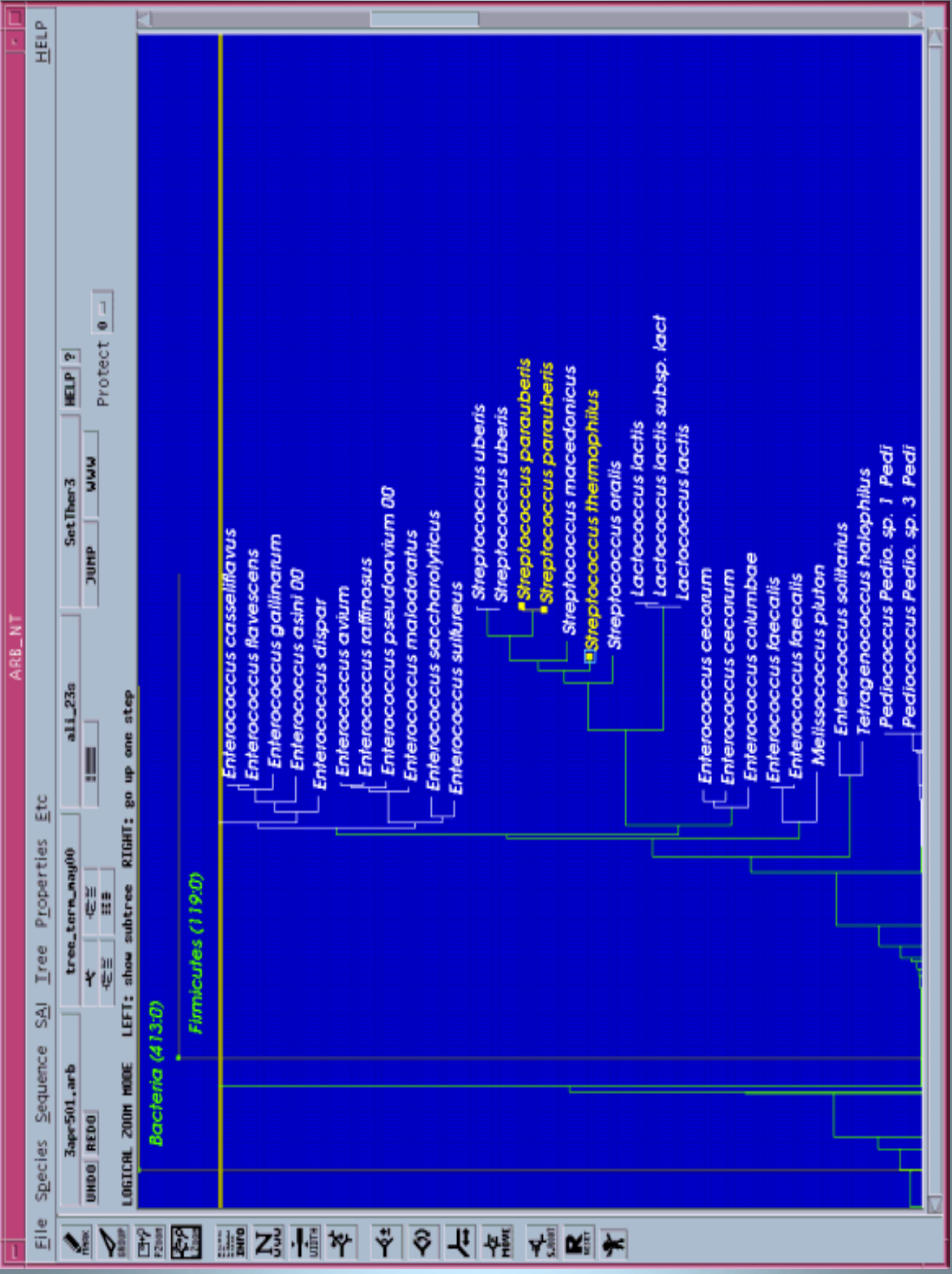
HELP ?



Protect 0

LOGICBL ZOOM MODE LEFT: show subtree RIGHT: go up one step





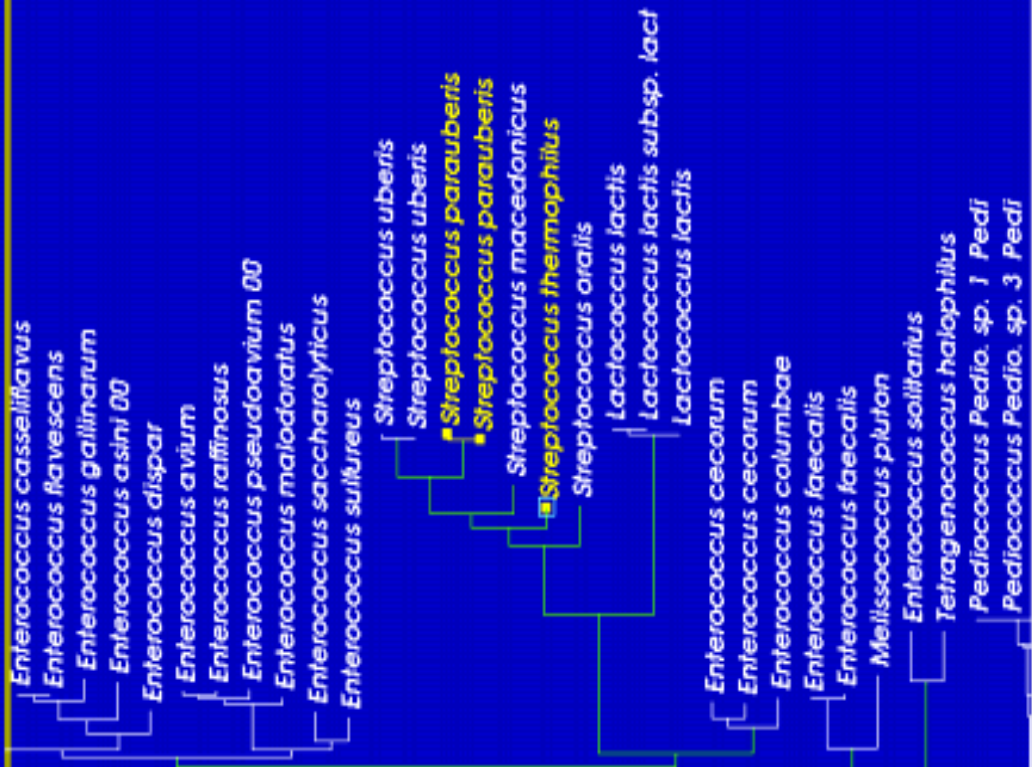
3ape501.arb tree_term_may00 ali_23a Set Ther-3 HELP ?

UNDO REDO tree_term_may00 ali_23a JUMP WWW Protect 0

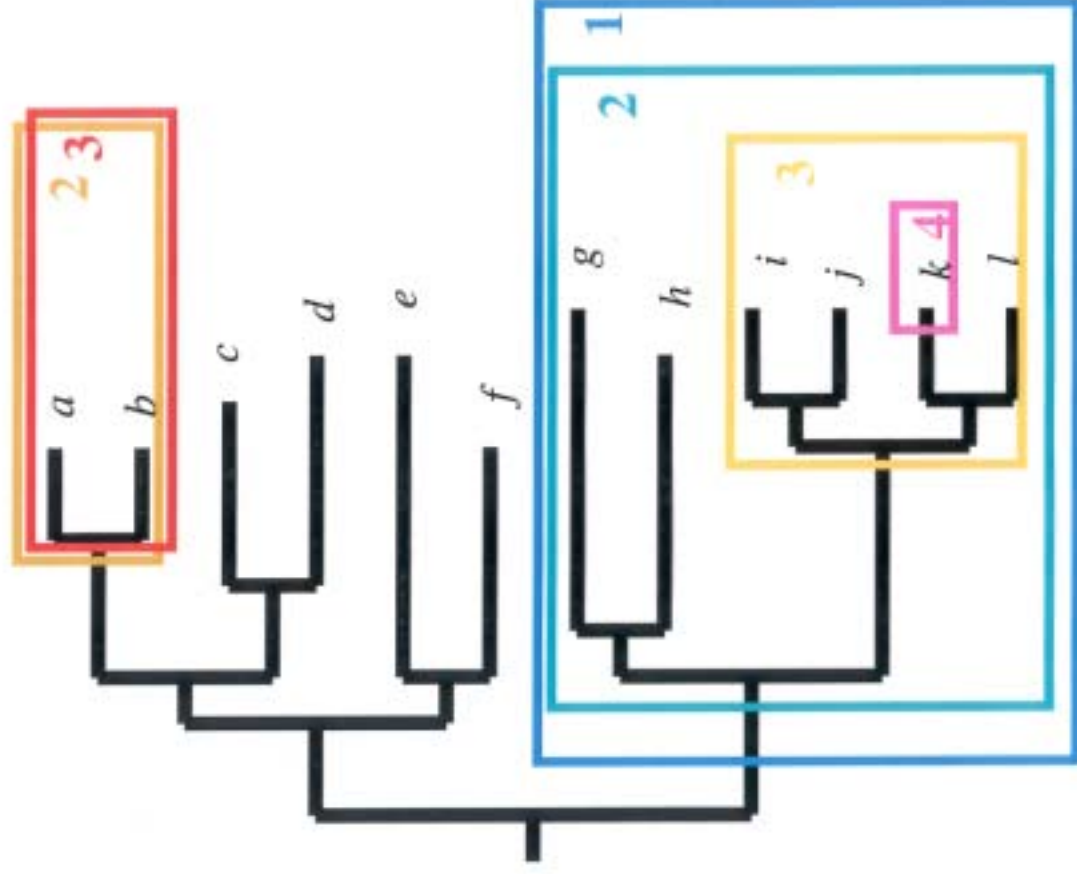
LOGICAL ZOOM MODE LEFT: show subtree RIGHT: go up one step

Bacteria (413:0)

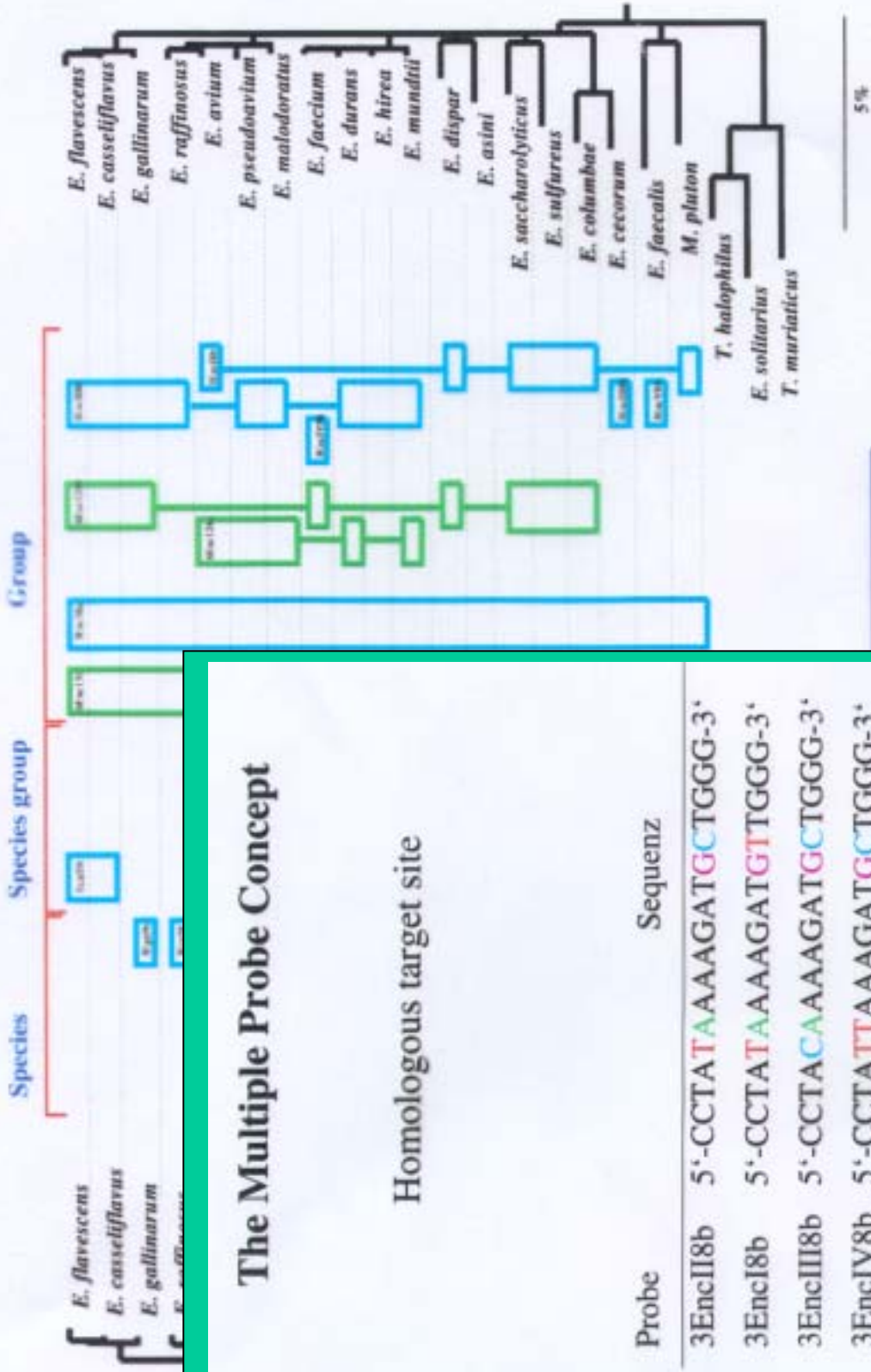
Firmicutes (119:0)



The Multiple Probe Concept



The Multiple Probe Concept



The Multiple Probe Concept

Homologous target site

| Probe | Sequenz |
|-----------|--------------------------|
| 3EncII8b | 5'-CCTA TAAAGATGCTGGG-3' |
| 3EncI8b | 5'-CCTA TAAAGATGTTGGG-3' |
| 3EncIII8b | 5'-CCTA CAAAGATGCTGGG-3' |
| 3EncIV8b | 5'-CCTA TTAAGATGCTGGG-3' |
| 3EncV8b | 5'-CCTA TAAAGATATTGGG-3' |

File Species Sequence 54 Tree Properties ETC

Seq001.arb tree.view.ala ALL.25% HELP 3 Protect 0

00001 01000

VERTICAL ZOOM MODE LEFT: show address RIGHT: go up one step

HELP

get sequence) used as input for multi-probe

0#aggttaagtgaaataaggg
 0#ggtagccagtcacaatttg
 0#tccttagagatgcaagca

LOAD SAVE DELETE Selection: Normal 3 DELETE

of selected sequence to

0 ADD

plement

matches

group hits 5

hits for non group 1.0

hits for group 0.0

File Species Sequence 54 Tree Properties ETC

Seq001.arb tree.view.ala ALL.25% HELP 3 Protect 0

00001 01000

VERTICAL ZOOM MODE LEFT: show address RIGHT: go up one step

HELP

0#aggttaagtgaaataaggg
 0#ggtagccagtcacaatttg
 0#tccttagagatgcaagca

LOAD SAVE DELETE Selection: Normal 3 DELETE

of selected sequence to

0 ADD

plement

matches

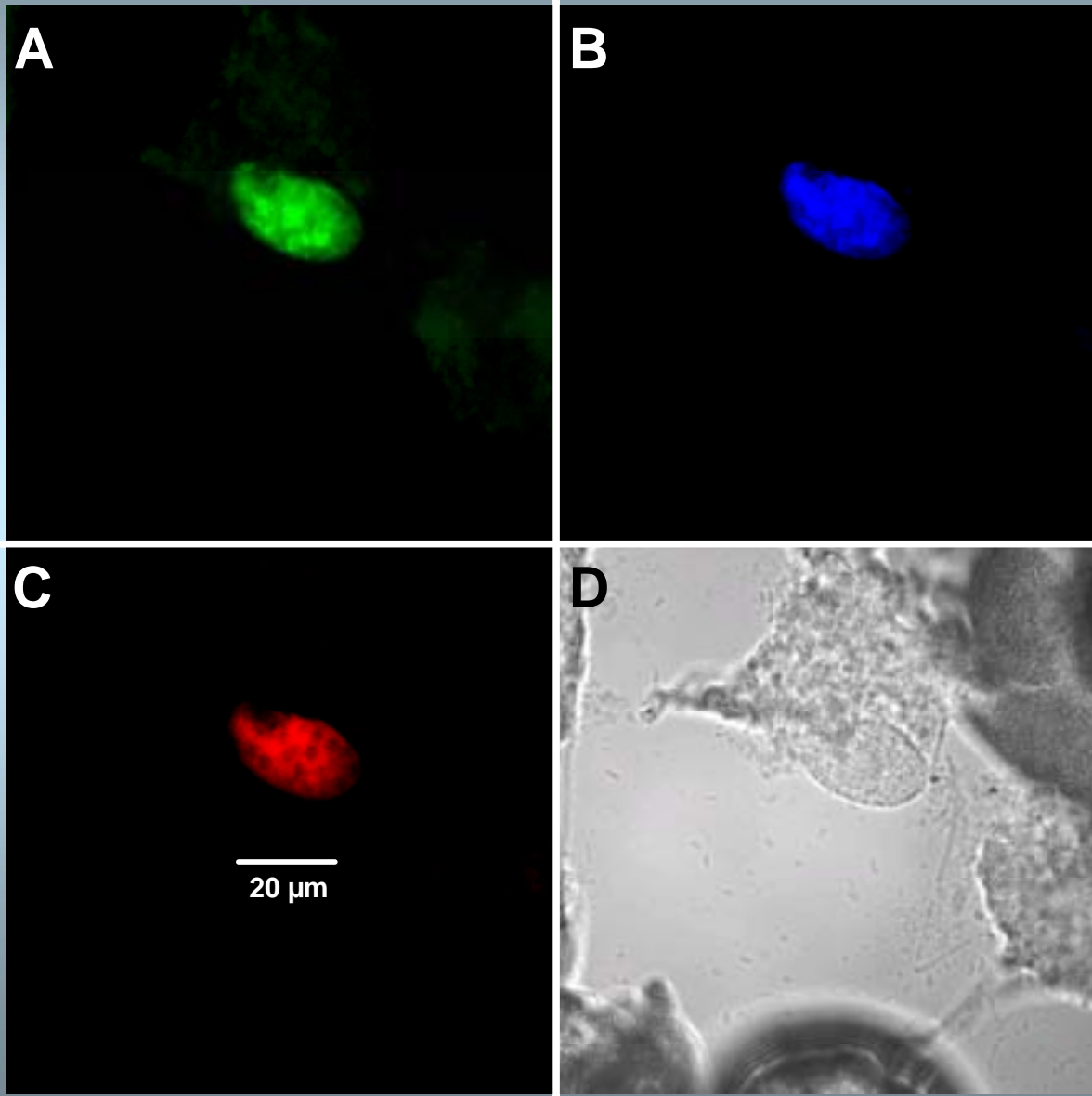
group hits 5

hits for non group 1.0

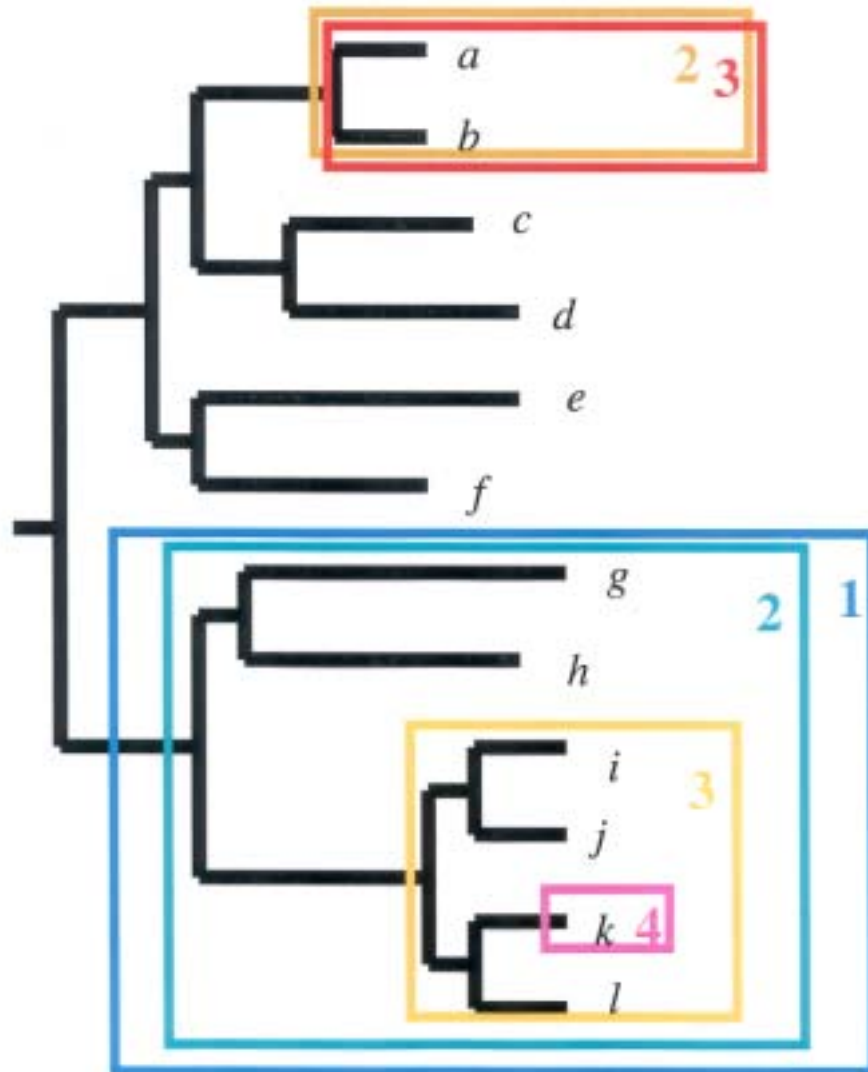
hits for group 0.0

Enterococcus pseudovivum
 Enterococcus hirae
 Enterococcus durans
 Enterococcus mundtii
 Enterococcus faecium
 Enterococcus flavescens
 Enterococcus casseliflavus
 Enterococcus gallinarum
 Enterococcus dispar
 Enterococcus saccharolyticus
 Enterococcus sulfuricus
 Enterococcus avium
 Enterococcus raffinosus
 Enterococcus malodoratus
 Enterococcus cecorum
 Enterococcus columbae
 Enterococcus faecalis
 Melissoecoccus pluton
 Tetragenococcus halophilus
 Enterococcus spilioticus
 Streptococcus parauberis
 Streptococcus uberis
 Streptococcus uberis
 Streptococcus macedonicus
 Streptococcus thermophilus
 Streptococcus oralis
 Lactococcus lactis subsp. lactis
 Lactococcus lactis
 Lactococcus lactis
 Pediococcus Pedio. sp. 1 Pedi
 Pediococcus Pedio. sp. 3 Pedi
 Radiococcus Radio. sp. 1 Rad

In situ hybridization of *Glaucoma scintillans* with multiple probes



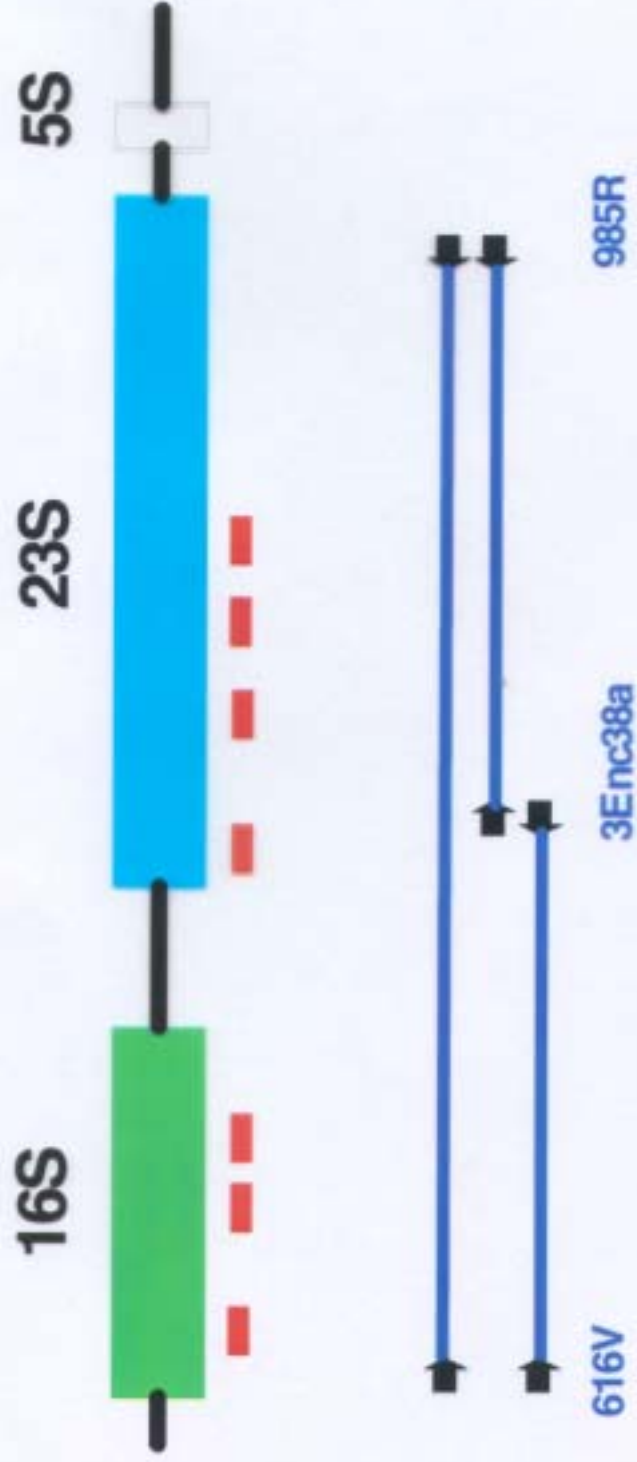
The Multiple Probe Concept



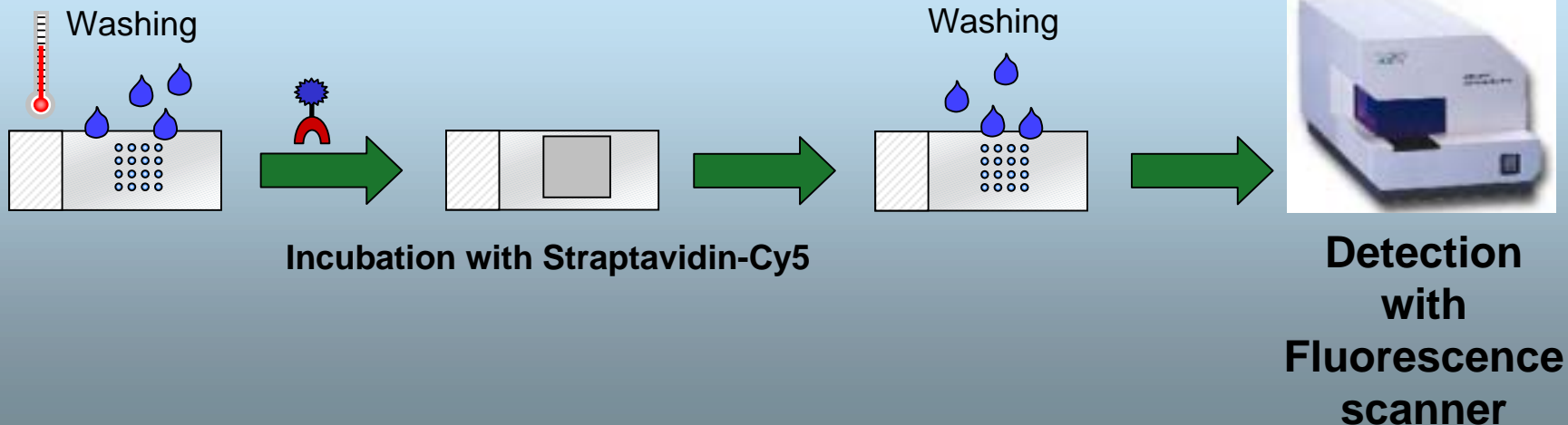
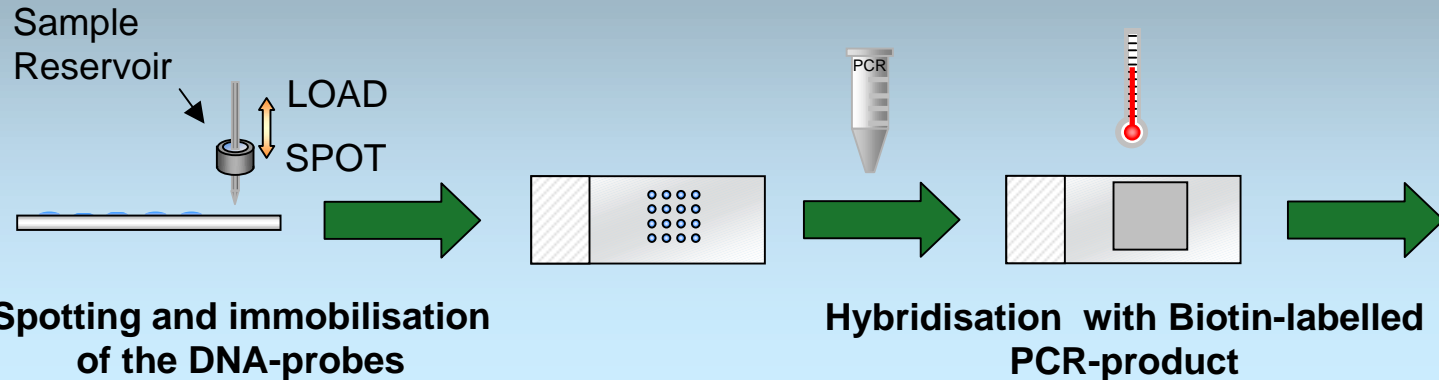
Current Software Development

- All probes on the web
- Multiple probe sets for selected phlogentic groups – chip design
- Chip data analysis and evaluation tool.

Primer - Probe Target Sites



Reverse Hybridisation on DNA Chips



The screenshot shows the ChipAnalyser software interface with several overlapping windows. The main window is titled "ChipAnalyser" and features a menu bar with "File", "View", and "Help". Below the menu bar is a toolbar with icons for file operations (new, open, save, print), a power button, and a search icon. The main area is divided into two tabs: "Chipdata view" and "Threshold view".

The "Chipdata view" tab displays a table of data with the following values:

| |
|-------|
| 18900 |
| 16800 |
| 14700 |
| 12600 |
| 10500 |
| 8400 |
| 6300 |
| 4200 |
| 2100 |

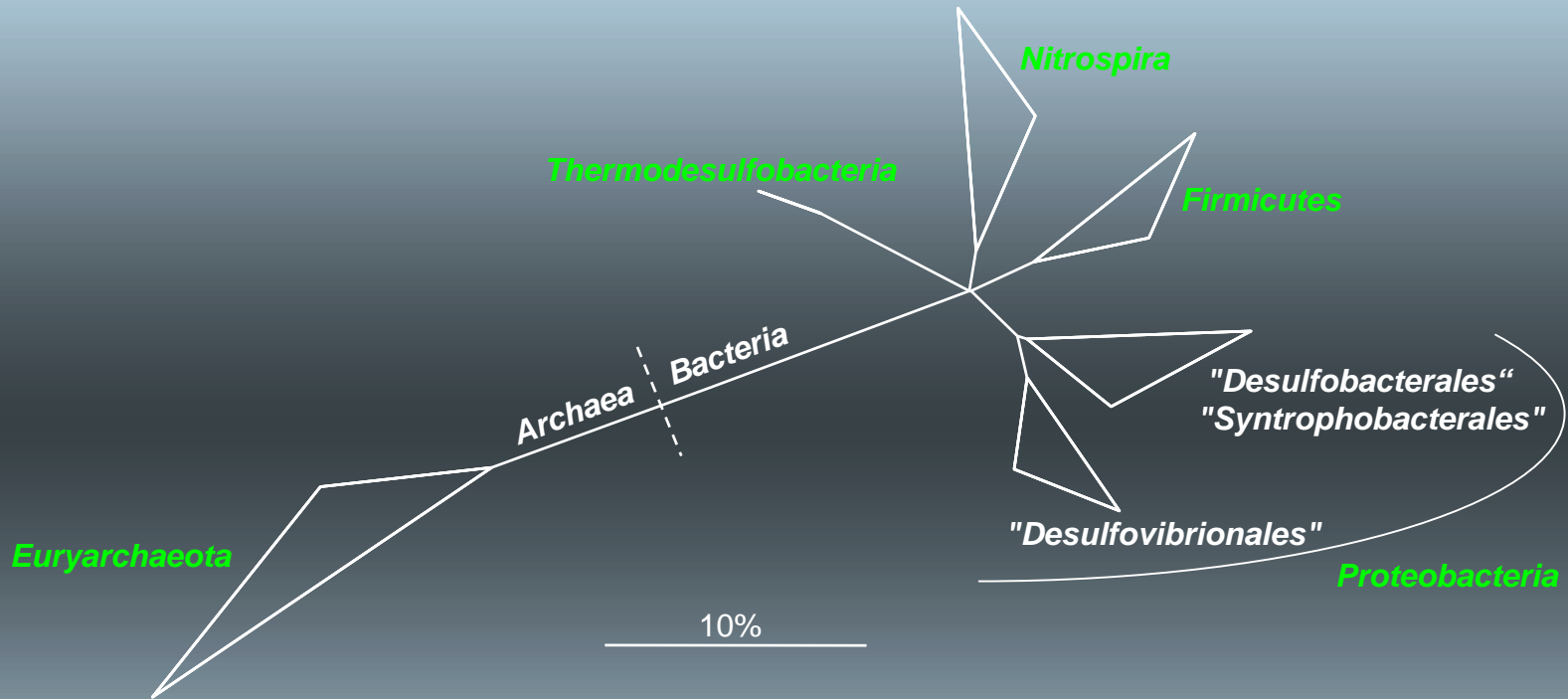
The "Threshold view" tab displays a graph with a red line. The x-axis is labeled with values: 0, 0.2, 0.4, 0.6, 0.81, 1.2, 1.4, 1.6, 1.82, 2.2, 2.4, 2.6, 2.83, 3.2, 3.4, 3.6, 3.84, 4.2, 4.4, 4.64. The y-axis has values: 135.9, 120.8, 105.7, 90.6, 75.5, 60.4, 45.3, 30.2, 15.1. Below the graph, there are two checkboxes: "3 Sigma" and "Delta-background".

Other overlapping windows show the same interface, but with different data points highlighted in green and red in the table.

The SRP PhyloChip - a 16S rRNA gene-based oligonucleotide microarray as biodiversity screening tool for sulfate-reducing prokaryotes in the environment

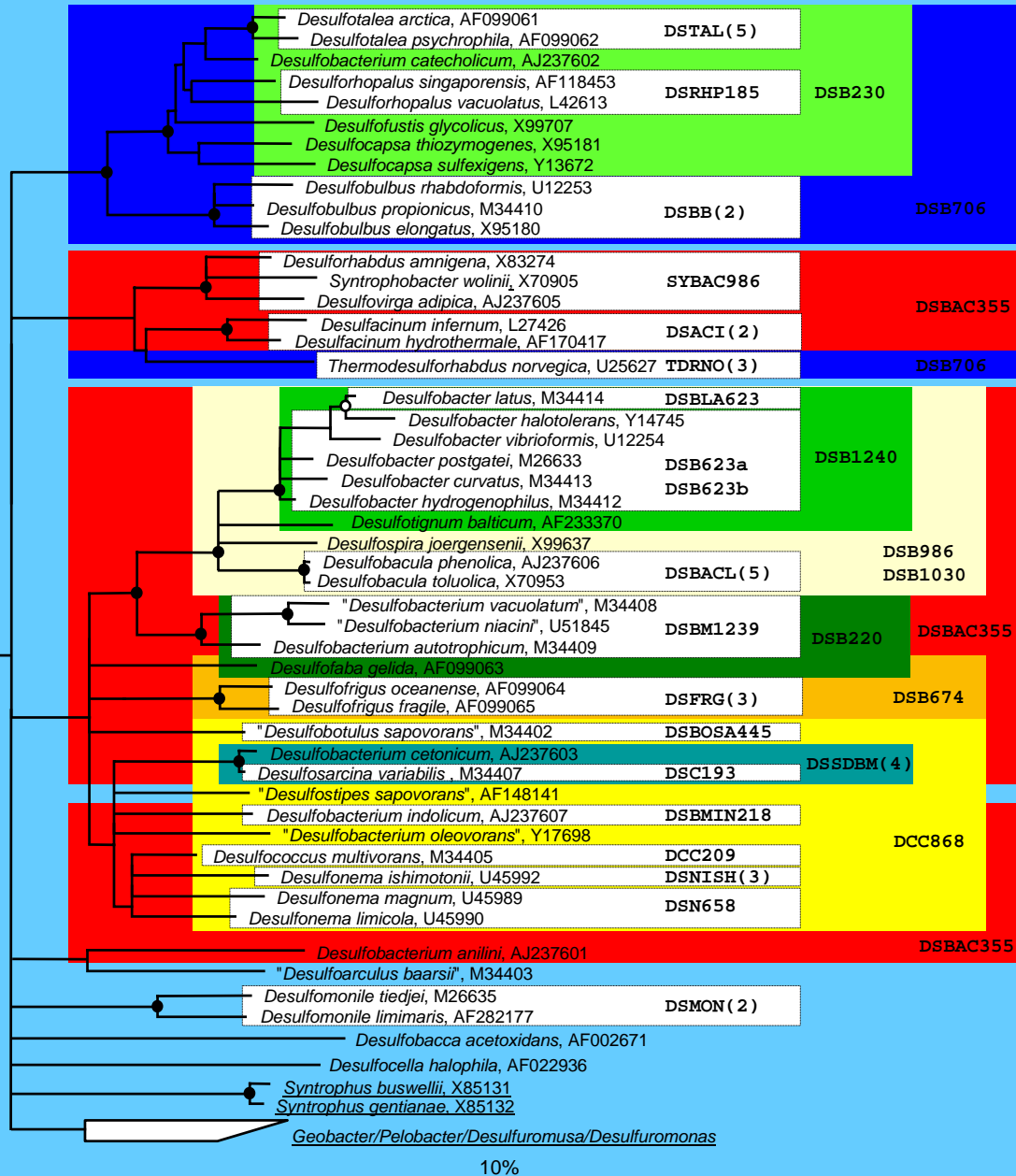
Alexander Loy, Angelika Lehner, Natuschka Lee, Stephan Stubner, Kirsten Küsel, Harold Drake, and Michael Wagner

Limitations of current rRNA-based SRP Diversity Research



DELTA495a
 DELTA495b
 DELTA495c

16S rRNA-based Phylogenetic Tree „Desulfobacterales“, „Syntrophobacterales“ Proteobacteria



Design and Characteristics of SRP-PhyloChip Probes

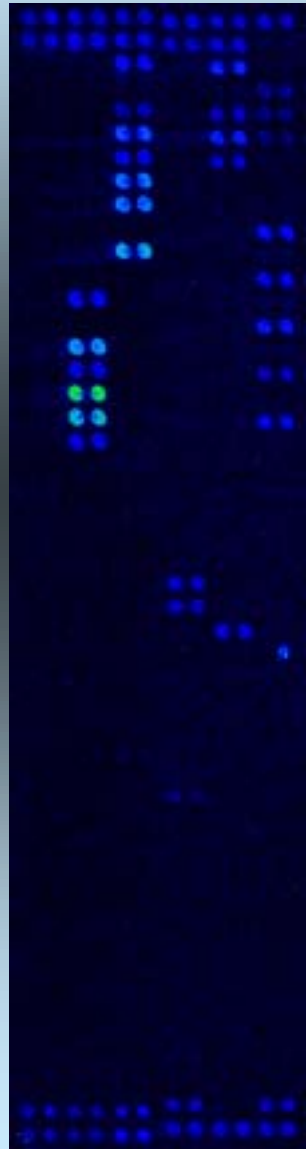
16S rRNA database containing all sequences from recognized SRPs

Validation of SRP phylogeny (cultured bacteria and available clone sequences)

14 universal, bacterial, and group-specific probes

26 published oligonucleotide probes specific for different SRPs

**102 newly designed probes of identical or hierarchical specificity
monophyletic groups of SRPs**



Application of the SRP-PhyloChip in Clinical and Environmental Samples

Tooth pocket material from patients
with periodontitis



Chemocline of a cyanobacterial hypersaline mat
(Solar Lake, Sinai)

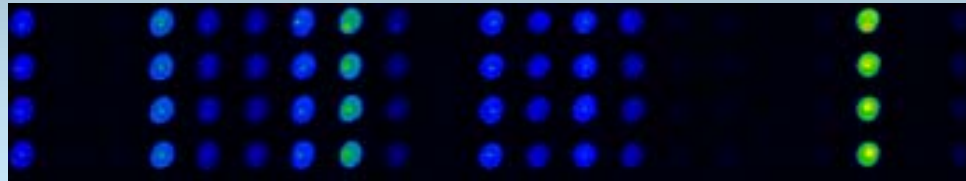
Sphagnum moss- and *Molinia* grass-covered
moor soils (Fichtelgebirge, Germany)



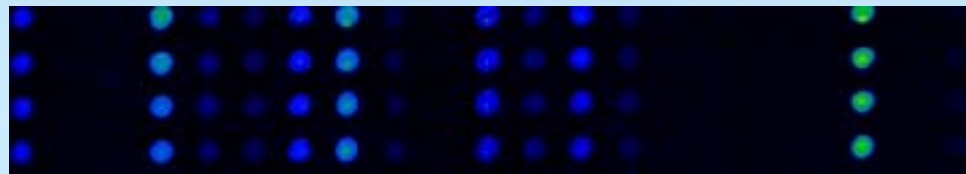
Hybridization with Cy5 labelled PCR product to Dsvha -test Chip

target: Dsv.ha.16s
PCR product

EUB338I
EUB338II
EUB338III
Srb385a
Dsv68
Dsv698
Dsv1292
Dsvha831
Dsvha130
Dsvha588
Dsvha733
Dsvha1424
Srb385b
Dsv820
Dsv7849
Dsv11350
Dsv887
Dsv9199
Dsv1019
4

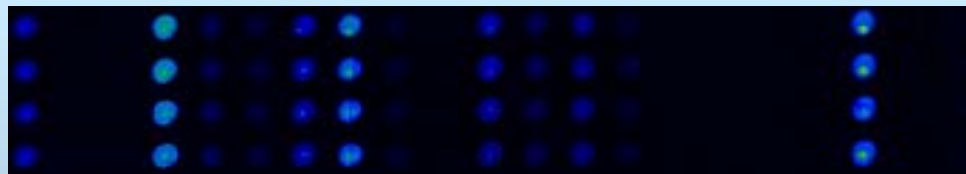


10% FA



15% FA

perfect match
one mismatch
two or more
mismatches



20% FA

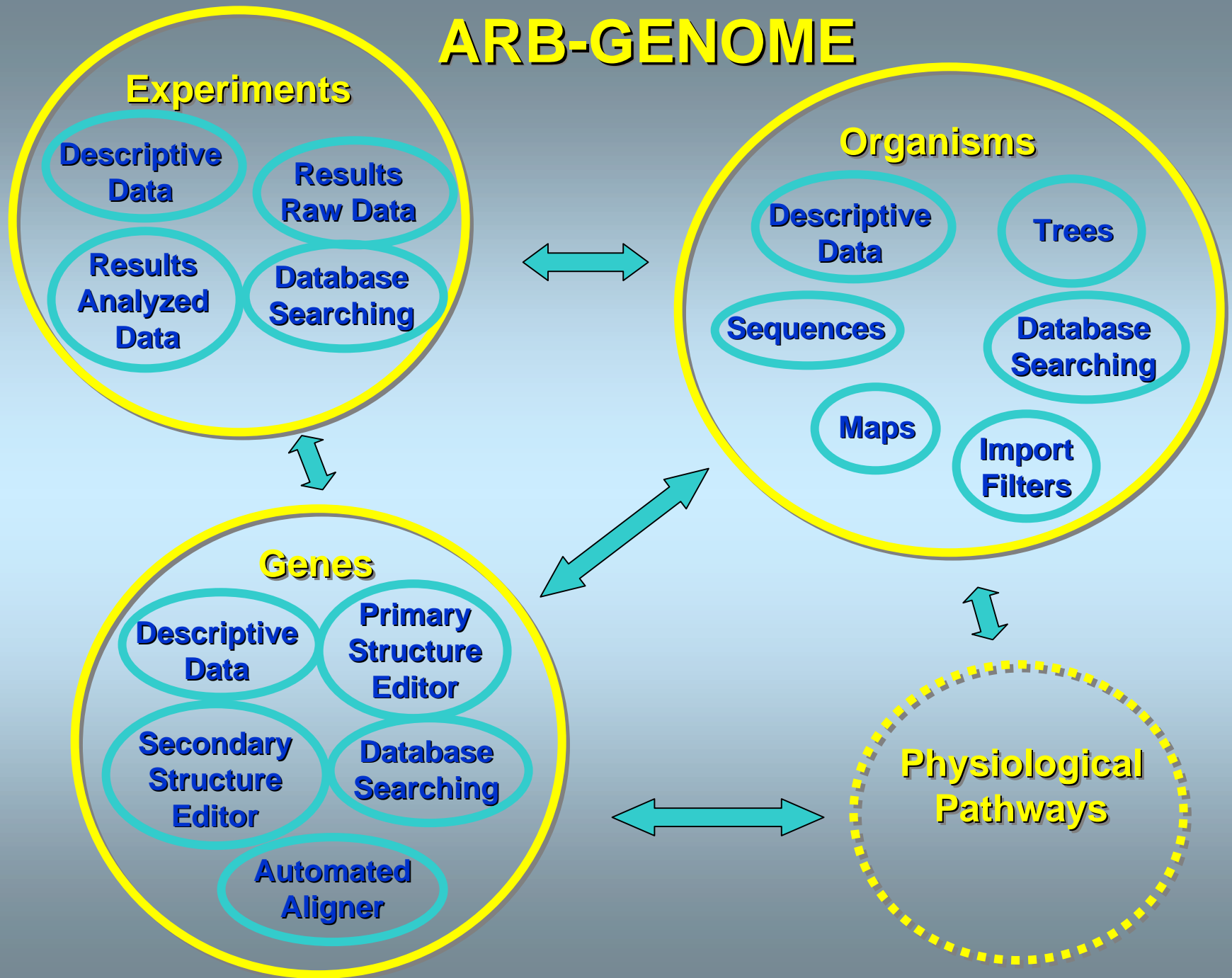


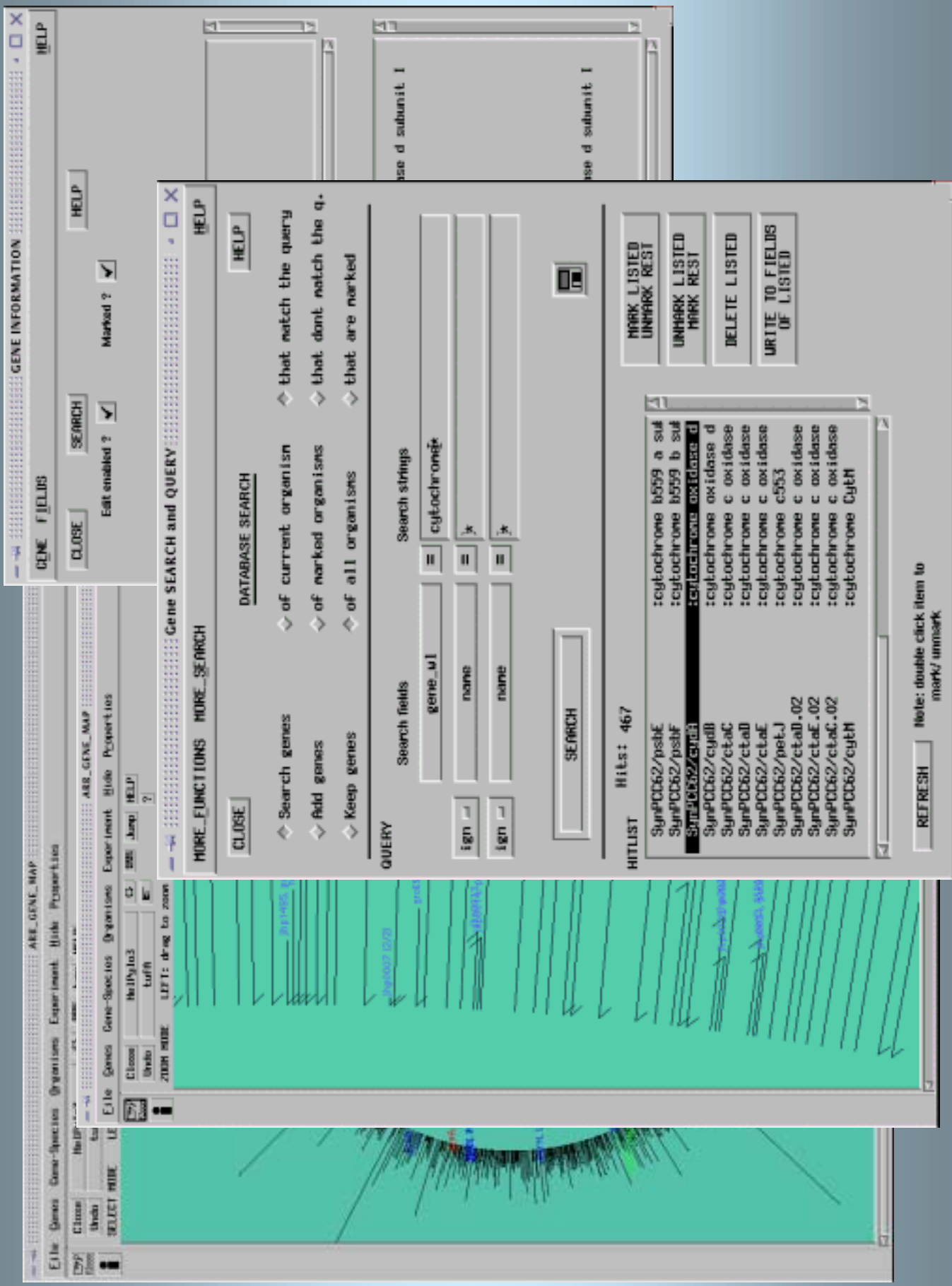
25% FA



30% FA

ARB-GENOME





GENE INFORMATION

HELP

SEARCH

Close

Marked ?

Gene SEARCH and QUERY

HELP

SEARCH

Close

Marked ?

More Functions MORE SEARCH

Database Search

Search genes of current organism that match the query

Add genes of marked organisms that dont match the q.

Keep genes of all organisms that are marked

QUERY

Search fields

gene_ul = cytochrome*

name = *

name = *

SEARCH

HITLIST Hits: 467

SynPCC62/psfE

SynPCC62/psfF

SynPCC62/cytlb

SynPCC62/cytlc

SynPCC62/ctaC

SynPCC62/ctaD

SynPCC62/ctaE

SynPCC62/petJ

SynPCC62/ctaB.02

SynPCC62/ctaE.02

SynPCC62/ctaC.02

SynPCC62/cytlH

MARK LISTED UNMARK REST

UNMARK LISTED MARK REST

DELETE LISTED

WRITE TO FIELDS OF LISTED

REFRESH

Note: double click item to mark/ unmark

GENE MAP

Close

Search

Marked ?

More Functions MORE SEARCH

Database Search

Search genes of current organism that match the query

Add genes of marked organisms that dont match the q.

Keep genes of all organisms that are marked

QUERY

Search fields

gene_ul = cytochrome*

name = *

name = *

SEARCH

HITLIST Hits: 467

SynPCC62/psfE

SynPCC62/psfF

SynPCC62/cytlb

SynPCC62/cytlc

SynPCC62/ctaC

SynPCC62/ctaD

SynPCC62/ctaE

SynPCC62/petJ

SynPCC62/ctaB.02

SynPCC62/ctaE.02

SynPCC62/ctaC.02

SynPCC62/cytlH

MARK LISTED UNMARK REST

UNMARK LISTED MARK REST

DELETE LISTED

WRITE TO FIELDS OF LISTED

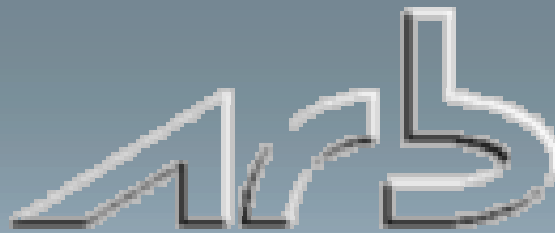
REFRESH

Note: double click item to mark/ unmark

Currently Maintained ARB Databases

(Eucarya, Archaea, Bacteria)

- Small subunit rRNA
- Large subunit rRNA
- Ribosomal Proteins
- Elongation – initiation factors
- Proton translocating ATPase subunits
- Heat shock proteins
- recA
- RNA polymerases
- DNA gyrases
- Aminoacyl tRNA synthetases
- Cytochrome oxidase



The ARB Project: Integrated Gene and Genome Databases, Tools for Phylogeny, Taxonomy and Identification

W. Ludwig, O.Strunk, R.Westram,

**L. Richter, H. Meier, A.Buchner, T.Lai, Yadhukumar, G.Jobb, S.Steppi, K. Bader, W.
Thomas, T. Ludwig**

**W. Förster, H. May, S. Hermann, N. Stuckmann, O. Gross, B. Nonhoff, R. Jost, B. Reichel, T. Ginhart,
A. Vilbig, T. Liss,
M. Lenke, A. Bode, K.H. Schleifer**