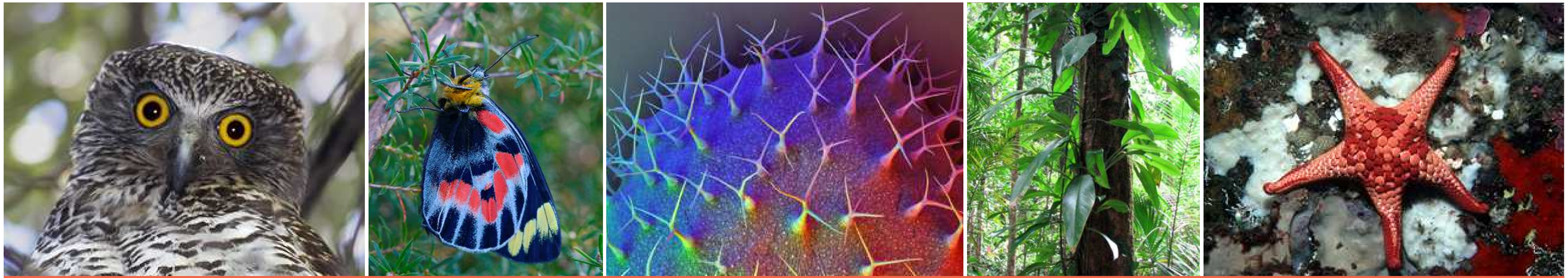


www.ala.org.au

ATLAS OF LIVING AUSTRALIA
sharing biodiversity knowledge

BioloMICS

Presenter: Nathalie van de Wiele

support@ala.org.au

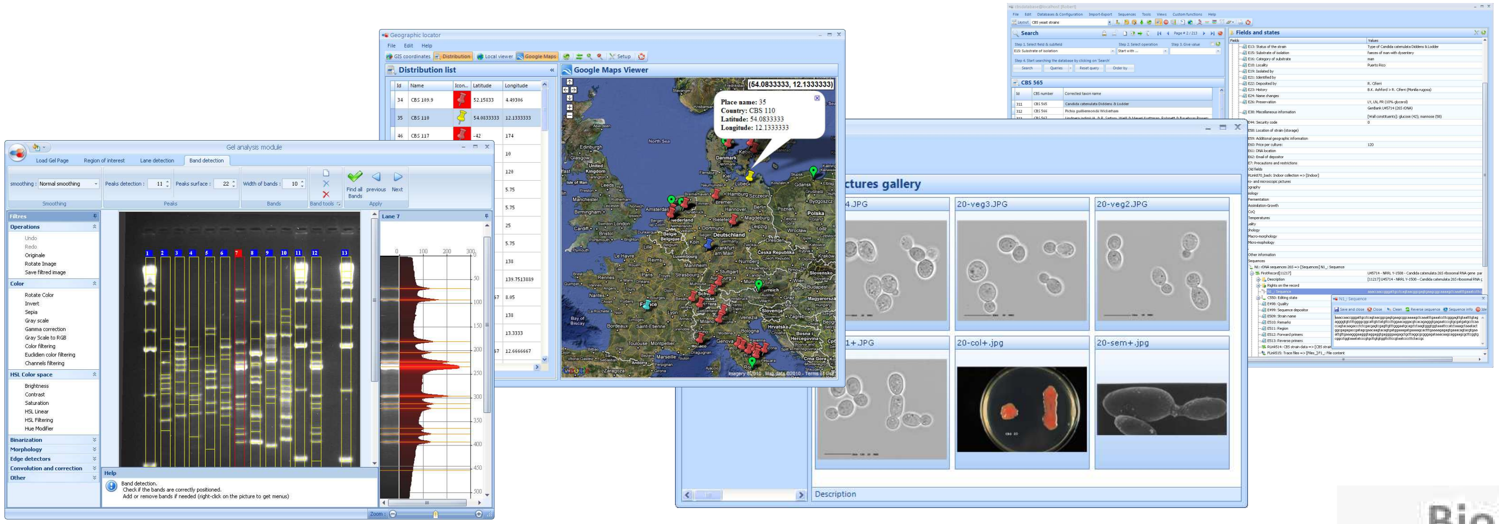
BioloMICS
www.bio-aware.com

The Atlas is funded by the Australian Government under the National Collaborative Research Infrastructure Strategy
and further supported by the Super Science Initiative of the Education Investment Fund

Introduction

Aim of this demonstration:

- Provide an overview of BioloMICS
- Outline the ‘Atlas of Living Australia’ offering for CHACM-member institutions



What is BioloMICS?

- Biological collection management system
- Established in 1999
- Globally used

Health Protection Agency

NCTC
National Collection of Type Cultures
A Health Protection Agency Culture Collection

FIOCRUZ
FUNDAÇÃO OSWALDO CRUZ

ABInBev

Institut Pasteur

CDC

www.cabi.org

CBS

CIDM
centre for infectious diseases & microbiology
Public Health

UNIVERSITÀ DEGLI STUDI DI PERUGIA
FACOLTÀ DI AGRARIA

BOL

The University of Sydney
SIDERE MENS EADEM MUTATO

- Specialised in:
  - Data storage/management
  - Data analysis
  - Publishing of the data

BioloMICS

Why BioloMICS?

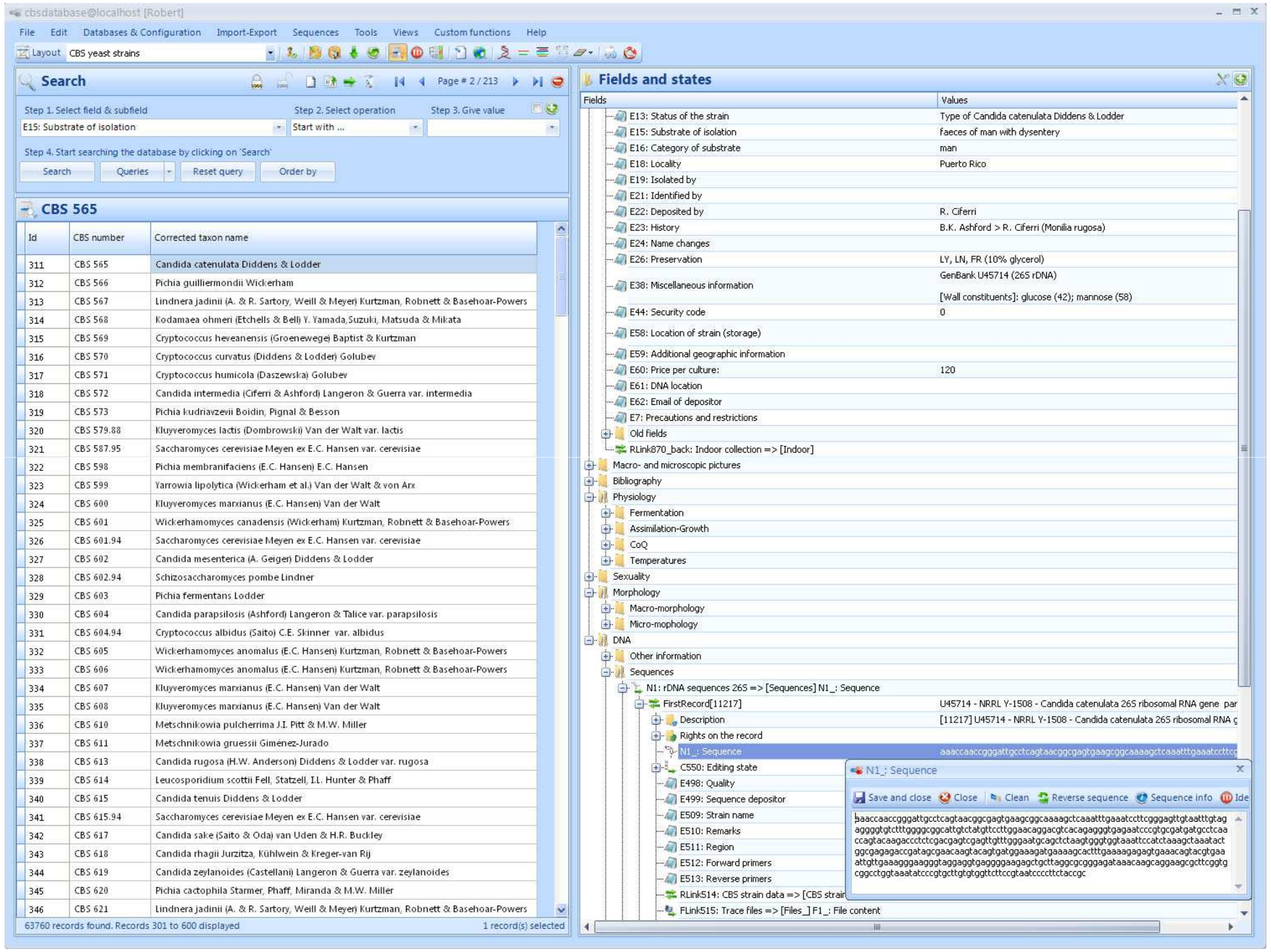
- ✓ High security level
- ✓ Free use and support until at least 2012
- ✓ Multi user access
- ✓ Relational database
- ✓ Virtually any data can be stored *(morphological, administrative, pictures, sequence data, geographical, …)*
- ✓ Option to create/write own scripts
- ✓ Easy import and export of data
- ✓ Many analysis tools available
- ✓ Online instruction movies - *www.bio-aware.com*

What can BioloMICS do?

BioloMICS includes tools to:

- Store and share data
- Customise and secure data
- Search data
- Polyphasic identification and classification
- Gel analysis
- Laboratory Information Management System (LIMS)
- Images analysis
- Geographic manager
- Sequence tools
- Publish (to intranet, ALA and AMRiN)

Main interface



Layout: CBS yeast strains

Step 1. Select field & subfield: E15: Substrate of isolation
Step 2. Select operation: Start with ...
Step 3. Give value:
Step 4. Start searching the database by clicking on 'Search'

CBS 565

Id	CBS number	Corrected taxon name
311	CBS 565	Candida catenulata Diddens & Lodder
312	CBS 566	Pichia guilliermondii Wickerham
313	CBS 567	Lindnera jadinii (A. & R. Sartory, Weill & Meyer) Kurtzman, Robnett & Basehoar-Powers
314	CBS 568	Kodamaea ohmeri (Etchells & Bell) Y. Yamada,Suzuki, Matsuda & Mikata
315	CBS 569	Cryptococcus heveanensis (Groenewege) Baptist & Kurtzman
316	CBS 570	Cryptococcus curvatus (Diddens & Lodder) Golubev
317	CBS 571	Cryptococcus humicola (Daszewska) Golubev
318	CBS 572	Candida intermedia (Ciferri & Ashford) Langeron & Guerra var. intermedia
319	CBS 573	Pichia kudriavzevii Boidin, Pignal & Besson
320	CBS 579.88	Kluyveromyces lactis (Dombrowski) Van der Walt var. lactis
321	CBS 587.95	Saccharomyces cerevisiae Meyen ex E.C. Hansen var. cerevisiae
322	CBS 598	Pichia membranifaciens (E.C. Hansen) E.C. Hansen
323	CBS 599	Yarrowia lipolytica (Wickerham et al.) Van der Walt & von Arx
324	CBS 600	Kluyveromyces marxianus (E.C. Hansen) Van der Walt
325	CBS 601	Wickerhamomyces canadensis (Wickerham) Kurtzman, Robnett & Basehoar-Powers
326	CBS 601.94	Saccharomyces cerevisiae Meyen ex E.C. Hansen var. cerevisiae
327	CBS 602	Candida mesenterica (A. Geiger) Diddens & Lodder
328	CBS 602.94	Schizosaccharomyces pombe Lindner
329	CBS 603	Pichia fermentans Lodder
330	CBS 604	Candida parapsilosis (Ashford) Langeron & Talice var. parapsilosis
331	CBS 604.94	Cryptococcus albidus (Saito) C.E. Skinner var. albidus
332	CBS 605	Wickerhamomyces anomalus (E.C. Hansen) Kurtzman, Robnett & Basehoar-Powers
333	CBS 606	Wickerhamomyces anomalus (E.C. Hansen) Kurtzman, Robnett & Basehoar-Powers
334	CBS 607	Kluyveromyces marxianus (E.C. Hansen) Van der Walt
335	CBS 608	Kluyveromyces marxianus (E.C. Hansen) Van der Walt
336	CBS 610	Metschnikowia pulcherrima J.I. Pitt & M.W. Miller
337	CBS 611	Metschnikowia gruessii Giménez-Jurado
338	CBS 613	Candida rugosa (H.W. Anderson) Diddens & Lodder var. rugosa
339	CBS 614	Leucosporidium scottii Fell, Statzell, I.L. Hunter & Phaff
340	CBS 615	Candida tenuis Diddens & Lodder
341	CBS 615.94	Saccharomyces cerevisiae Meyen ex E.C. Hansen var. cerevisiae
342	CBS 617	Candida sake (Saito & Oda) van Uden & H.R. Buckley
343	CBS 618	Candida rhagii Jurzitza, Kühlwein & Kreger-van Rij
344	CBS 619	Candida zeylanoides (Castellani) Langeron & Guerra var. zeylanoides
345	CBS 620	Pichia cactophila Starmer, Phaff, Miranda & M.W. Miller
346	CBS 621	Lindnera jadinii (A. & R. Sartory, Weill & Meyer) Kurtzman, Robnett & Basehoar-Powers

63760 records found. Records 301 to 600 displayed
1 record(s) selected

Fields	Values
E13: Status of the strain	Type of Candida catenulata Diddens & Lodder
E15: Substrate of isolation	faeces of man with dysentery
E16: Category of substrate	man
E18: Locality	Puerto Rico
E19: Isolated by	
E21: Identified by	
E22: Deposited by	R. Ciferri
E23: History	B.K. Ashford > R. Ciferri (Monilia rugosa)
E24: Name changes	
E26: Preservation	LY, LN, FR (10% glycerol)
E38: Miscellaneous information	GenBank U45714 (26S rDNA) [Wall constituents]: glucose (42); mannose (58)
E44: Security code	0
E58: Location of strain (storage)	
E59: Additional geographic information	
E60: Price per culture:	120
E61: DNA location	
E62: Email of depositor	
E7: Precautions and restrictions	
Old fields	
RLink870_back: Indoor collection => [Indoor]	
Macro- and microscopic pictures	
Bibliography	
Physiology	
Fermentation	
Assimilation-Growth	
CoQ	
Temperatures	
Sexuality	
Morphology	
Macro-morphology	
Micro-mophology	
DNA	
Other information	
Sequences	
N1: rDNA sequences 26S => [Sequences] N1_: Sequence	
FirstRecord[11217]	U45714 - NRRL Y-1508 - Candida catenulata 26S ribosomal RNA gene par
Description	[11217] U45714 - NRRL Y-1508 - Candida catenulata 26S ribosomal RNA g
Rights on the record	
N1_: Sequence	aaaccaaccgggattgcctcagtaacggcgagtgaagcggcaaaagctcaaatttgaaatccttcg
C550: Editing state	
E498: Quality	
E499: Sequence depositor	
E509: Strain name	
E510: Remarks	
E511: Region	
E512: Forward primers	
E513: Reverse primers	
RLink514: CBS strain data => [CBS strain	
FLink515: Trace files => [Files_] F1_: File content	

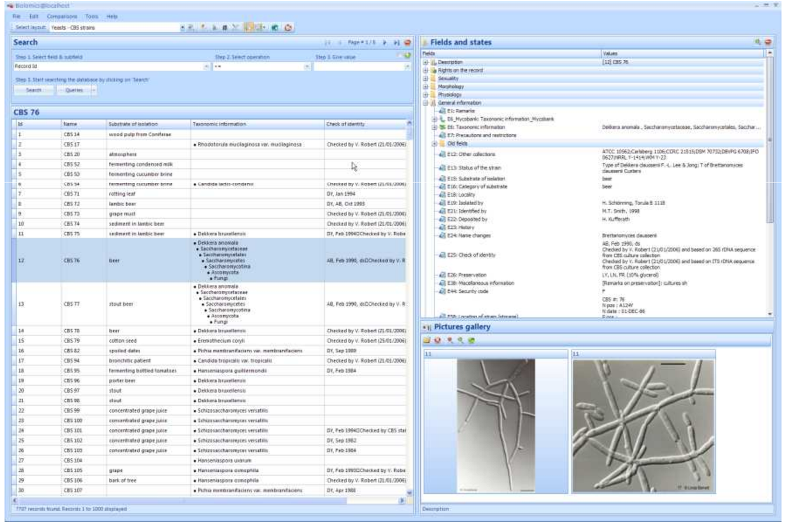
```
aaaccaaccgggattgcctcagtaacggcgagtgaagcggcaaaagctcaaatttgaaatccttcgggagttgtaatttgtag
aggggtgtctttggggcggcattgtctatgttccttggaacaggacgtcacagagggtgagaatcccgtgcgatgatgcctcaa
ccagtacaagaccctctcgacgagtcgagttgtttgggaatgcagctctaagtgggtggtaaattccatctaaagctaaatact
ggcgagagaccgatagcgaacaagtacagtgatggaaagatgaaaagcactttgaaaagagagtgaaacagtacgtgaa
attgttgaaagggaagggtaggaggtgaggggaagagctgcttaggcgcgggagataaacaagcaggaagcgcttcggtg
cggcctggtaaatatcccgtgcttgtgtggttcttccgtaatccccttctaccgc
```

Movie: add new record

BioloMICS

Data sharing

Desktop



Search

Step 1. Select field & subfield: Record Id

Step 2. Select operation: ==

Step 3. Give value

Step 3. Start searching the database by clicking on "Search"

CBS 76

Id	Name	Substrate of isolation	Taxonomic information	Check of identity
1	CBS 14	wood pulp from Coniferae		
2	CBS 17		• Rhodotorula mucilaginosa var. mucilaginosa	Checked by V. Robert (21/01/2006)
3	CBS 20	atmosphere		
4	CBS 52	fermenting condensed milk		
5	CBS 53	fermenting cucumber brine		
6	CBS 54	fermenting cucumber brine	• Candida lactis-condensi	Checked by V. Robert (21/01/2006)
7	CBS 71	rotting leaf		DY, Jan 1994
8	CBS 72	lambic beer		DY, AB, Oct 1993
9	CBS 73	grape must		Checked by V. Robert (21/01/2006)
10	CBS 74	sediment in lambic beer		Checked by V. Robert (21/01/2006)
11	CBS 75	sediment in lambic beer	• Dekkera bruxellensis	DY, Feb 1994Checked by V. Robe
12	CBS 76	beer	• Dekkera anomala • Saccharomycetaceae • Saccharomycetales • Saccharomycetes • Saccharomycotina • Ascomycota • Fungi	AB, Feb 1990, dsChecked by V. R
13	CBS 77	stout beer	• Dekkera anomala • Saccharomycetaceae • Saccharomycetales • Saccharomycetes • Saccharomycotina • Ascomycota • Fungi	AB, Feb 1990, dsChecked by V. R
14	CBS 78	beer	• Dekkera bruxellensis	Checked by V. Robert (21/01/2006)
15	CBS 79	cotton seed	• Eremothecium coryli	Checked by V. Robert (25/01/2006)
16	CBS 82	spoiled dates	• Pichia membranifaciens var. membranifaciens	DY, Sep 1989
17	CBS 94	bronchitic patient	• Candida tropicalis var. tropicalis	Checked by V. Robert (21/01/2006)
18	CBS 95	fermenting bottled tomatoes	• Hanseniaspora guilliermondii	DY, Feb 1984
19	CBS 96	porter beer	• Dekkera bruxellensis	
20	CBS 97	stout	• Dekkera bruxellensis	
21	CBS 98	stout	• Dekkera bruxellensis	
22	CBS 99	concentrated grape juice	• Schizosaccharomyces versatilis	
23	CBS 100	concentrated grape juice	• Schizosaccharomyces versatilis	
24	CBS 101	concentrated grape juice	• Schizosaccharomyces versatilis	DY, Feb 1994Checked by CBS sta
25	CBS 102	concentrated grape juice	• Schizosaccharomyces versatilis	DY, Sep 1982
26	CBS 103	concentrated grape juice	• Schizosaccharomyces versatilis	DY, Feb 1984
27	CBS 104		• Hanseniaspora uvarum	
28	CBS 105	grape	• Hanseniaspora osmophila	DY, Feb 1993Checked by V. Robe
29	CBS 106	bark of tree	• Hanseniaspora osmophila	Checked by V. Robert (21/01/2006)
30	CBS 107		• Pichia membranifaciens var. membranifaciens	DY, Apr 1988

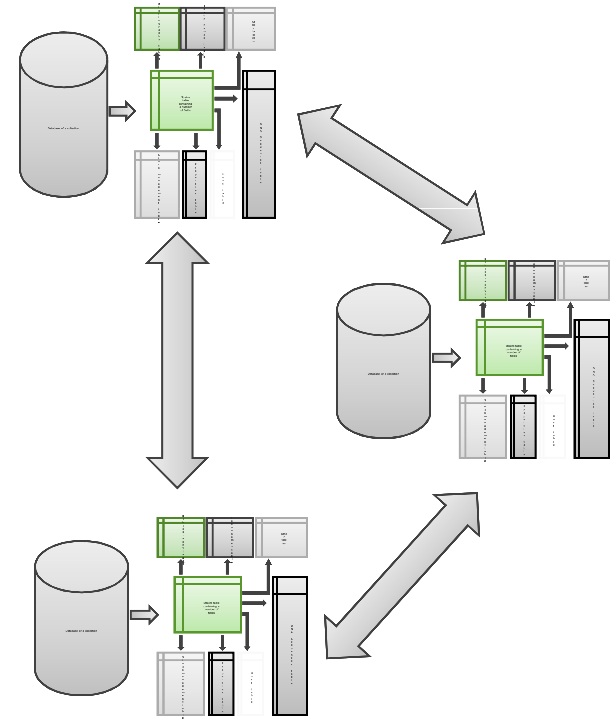
7707 records found. Records 1 to 1000 displayed

Fields and states

Fields	Values
Description	[12] CBS 76
Rights on the record	
Sexuality	
Morphology	
Physiology	
General information	
E1: Remarks	
E6_Mycobank: Taxonomic information_Mycobank	
E6: Taxonomic information	Dekkera anomala , Saccharomycetaceae, Saccharomycetales, Sacchar...
E7: Precautions and restrictions	
Old fields	
E12: Other collections	ATCC 10562;Carlsberg 1106;CCRC 21515;DSM 70732;DBVPG 6708;IFO 0627;NRRL Y-1414;VKM Y-23
E13: Status of the strain	Type of Dekkera claussenii F.-L. Lee & Jong; T of Brettanomyces claussenii Custers
E15: Substrate of isolation	beer
E16: Category of substrate	beer
E18: Locality	
E19: Isolated by	H. Schiönning, Torula B 1118
E21: Identified by	M.T. Smith, 1998
E22: Deposited by	H. Kufferath
E23: History	
E24: Name changes	Brettanomyces claussenii
E25: Check of identity	AB, Feb 1990, ds Checked by V. Robert (21/01/2006) and based on 26S rDNA sequence from CBS culture collection Checked by V. Robert (21/01/2006) and based on ITS rDNA sequence from CBS culture collection
E26: Preservation	LY, LN, FR (10% glycerol)
E38: Miscellaneous information	[Remarks on preservation]: cultures sh
E44: Security code	P
E58: Location of strain (storage)	CBS #: 76 N pos : A124Y N date : 01-DEC-86

Pictures gallery

Connections between (n) collections specific databases

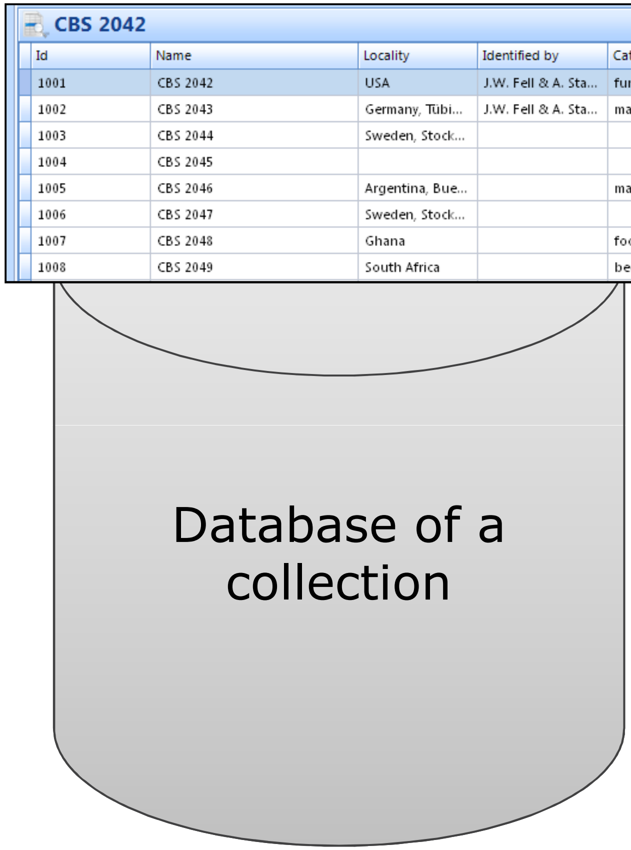


Data storage/management

- Data management
- Analysis Tools
- Publishing Data

- Database
- Tables, Fields, Records
- Layouts
- Security and Rights
- History of Changes
- Search
- Import and Export data
- Programming Manager

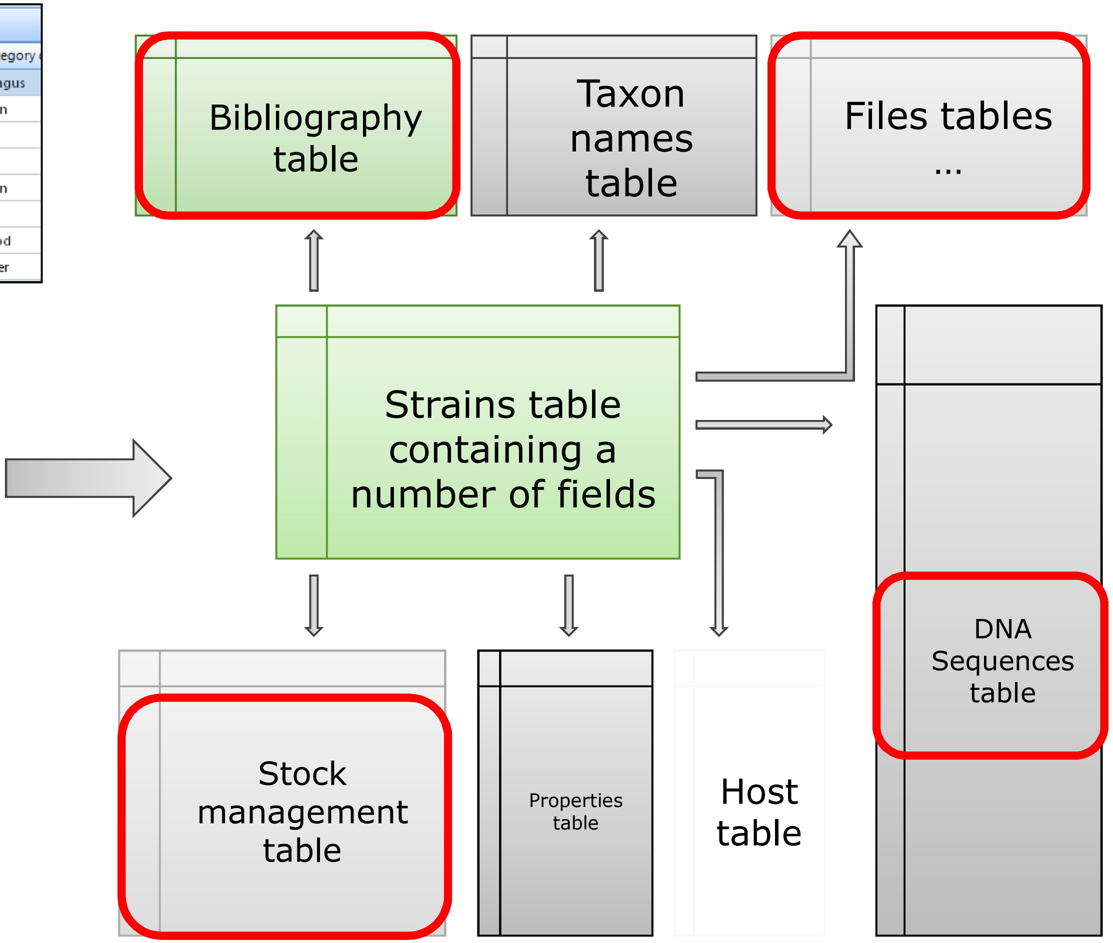
Database



CBS 2042

Id	Name	Locality	Identified by	Category
1001	CBS 2042	USA	J.W. Fell & A. Sta...	fungus
1002	CBS 2043	Germany, Tübi...	J.W. Fell & A. Sta...	man
1003	CBS 2044	Sweden, Stock...		
1004	CBS 2045			
1005	CBS 2046	Argentina, Bue...		man
1006	CBS 2047	Sweden, Stock...		
1007	CBS 2048	Ghana		food
1008	CBS 2049	South Africa		beer

Database of a collection



Bibliography table

Taxon names table

Files tables …

Strains table containing a number of fields

Stock management table

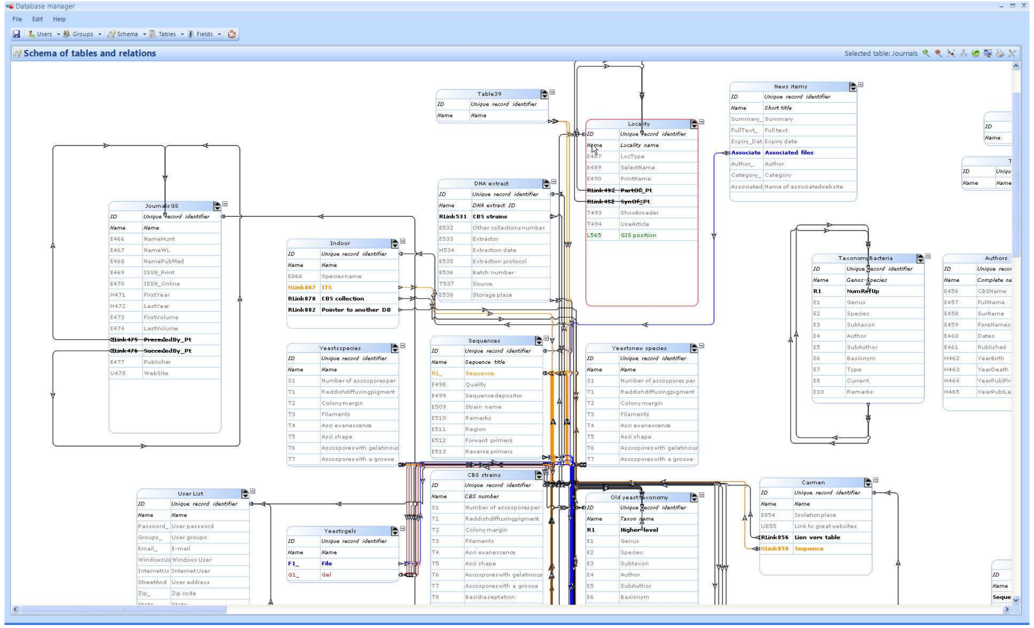
Properties table

Host table

DNA Sequences table

Tables, Fields, Records

- Add, modify and delete:
  - Tables and fields: can only be modified by administrators
  - Records: anyone who has access to the database with writing rights



- 21 field types

Links between tables are visible from the database manager

Layout

- How to display the data
- Not everyone needs to see all tables or fields
  - Various layouts can be created per table
- Layouts can be shared
- When changing a layout the data does not change

Security

- A login and password are required
  - Only registered users can access the system

- Users belong to groups that have specific rights on tables, fields and records

- Only the administrator can add, modify or delete a users profile or a group

- Records can be temporarily protected

Security - Rights

- Rights on tables, fields and records are given to a group of users

- Three levels of access:
  - Read (R), Write (W), Delete (D)

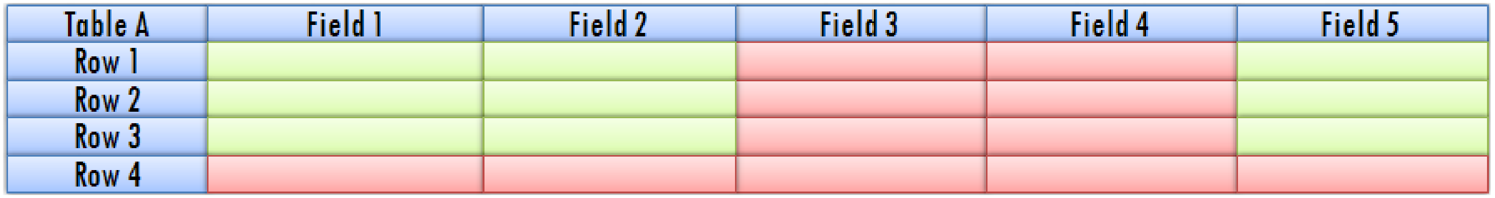
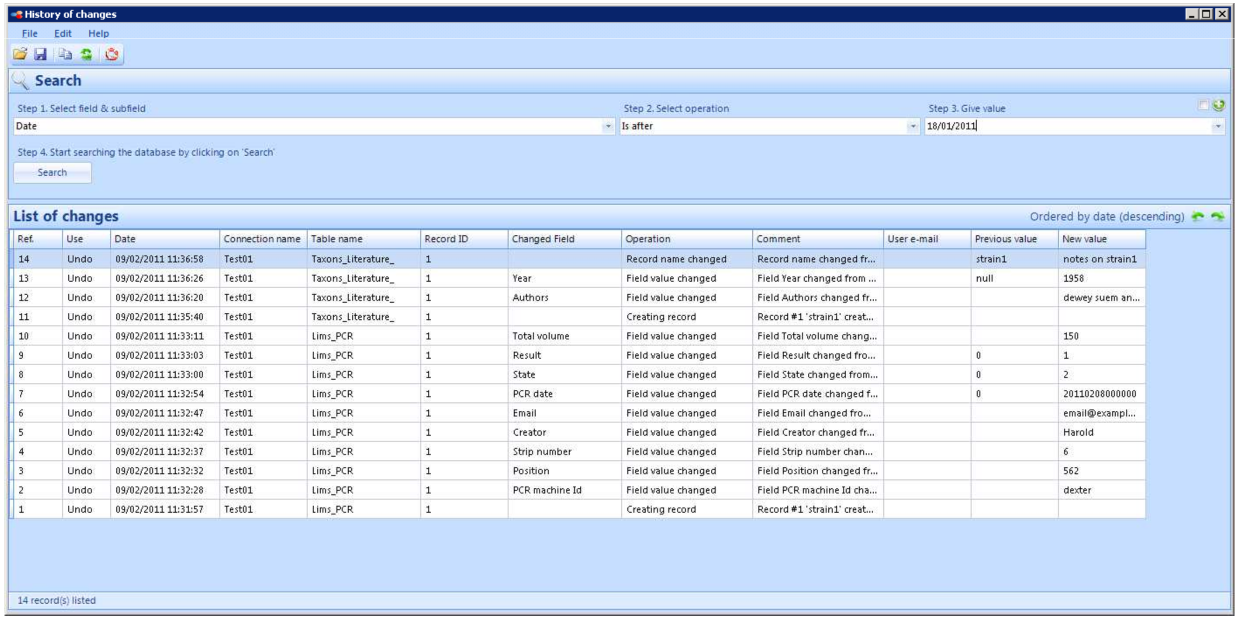


Table A	Field 1	Field 2	Field 3	Field 4	Field 5
Row 1	🟩	🟩	🟥	🟥	🟩
Row 2	🟩	🟩	🟥	🟥	🟩
Row 3	🟩	🟩	🟥	🟥	🟩
Row 4	🟥	🟥	🟥	🟥	🟥

History of changes

- Every modification made to a given database is recorded
- The administrator can search the tracking system and undo or redo a number of actions



Step 1. Select field & subfield: Date

Step 2. Select operation: Is after

Step 3. Give value: 18/01/2011

Step 4. Start searching the database by clicking on 'Search'

List of changes

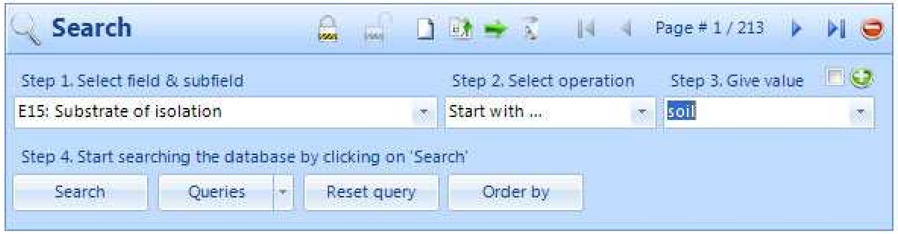
Ordered by date (descending)

Ref.	Use	Date	Connection name	Table name	Record ID	Changed Field	Operation	Comment	User e-mail	Previous value	New value
14	Undo	09/02/2011 11:36:58	Test01	Taxons_Literature_	1		Record name changed	Record name changed fr...		strain1	notes on strain1
13	Undo	09/02/2011 11:36:26	Test01	Taxons_Literature_	1	Year	Field value changed	Field Year changed from ...		null	1958
12	Undo	09/02/2011 11:36:20	Test01	Taxons_Literature_	1	Authors	Field value changed	Field Authors changed fr...			dewey suem an...
11	Undo	09/02/2011 11:35:40	Test01	Taxons_Literature_	1		Creating record	Record #1 'strain1' creat...			
10	Undo	09/02/2011 11:33:11	Test01	Lims_PCR	1	Total volume	Field value changed	Field Total volume chang...			150
9	Undo	09/02/2011 11:33:03	Test01	Lims_PCR	1	Result	Field value changed	Field Result changed fro...		0	1
8	Undo	09/02/2011 11:33:00	Test01	Lims_PCR	1	State	Field value changed	Field State changed from...		0	2
7	Undo	09/02/2011 11:32:54	Test01	Lims_PCR	1	PCR date	Field value changed	Field PCR date changed f...		0	20110208000000
6	Undo	09/02/2011 11:32:47	Test01	Lims_PCR	1	Email	Field value changed	Field Email changed fro...			email@exampl...
5	Undo	09/02/2011 11:32:42	Test01	Lims_PCR	1	Creator	Field value changed	Field Creator changed fr...			Harold
4	Undo	09/02/2011 11:32:37	Test01	Lims_PCR	1	Strip number	Field value changed	Field Strip number chan...			6
3	Undo	09/02/2011 11:32:32	Test01	Lims_PCR	1	Position	Field value changed	Field Position changed fr...			562
2	Undo	09/02/2011 11:32:28	Test01	Lims_PCR	1	PCR machine Id	Field value changed	Field PCR machine Id cha...			dexter
1	Undo	09/02/2011 11:31:57	Test01	Lims_PCR	1		Creating record	Record #1 'strain1' creat...			

14 record(s) listed

Search

Basic search



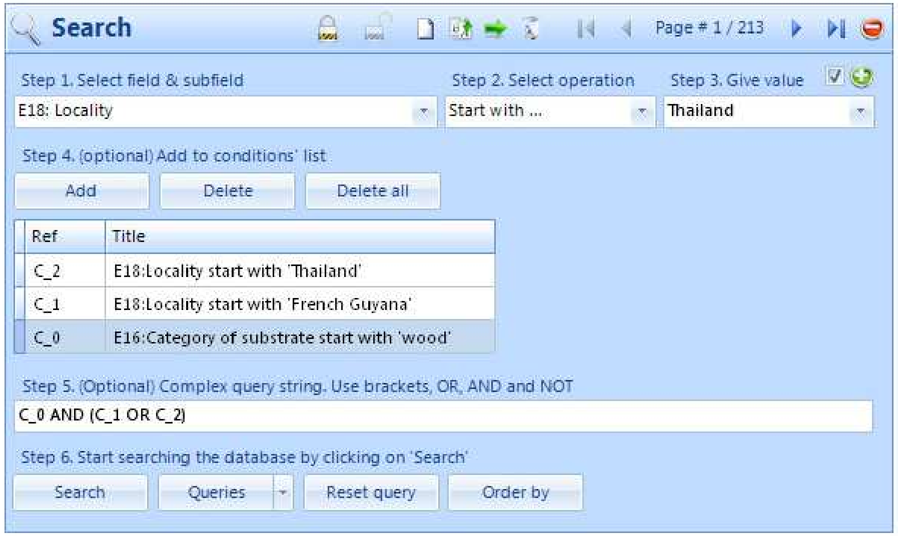
Step 1. Select field & subfield: E15: Substrate of isolation

Step 2. Select operation: Start with ...

Step 3. Give value ☐: soil

Step 4. Start searching the database by clicking on 'Search'

Advanced search



Step 1. Select field & subfield: E18: Locality

Step 2. Select operation: Start with ...

Step 3. Give value ☑: Thailand

Step 4. (optional) Add to conditions' list

Ref	Title
C_2	E18:Locality start with 'Thailand'
C_1	E18:Locality start with 'French Guyana'
C_0	E16:Category of substrate start with 'wood'

Step 5. (Optional) Complex query string. Use brackets, OR, AND and NOT: C_0 AND (C_1 OR C_2)

Step 6. Start searching the database by clicking on 'Search'

Import data

- Everyone with writing rights can enter new data
- Large amounts of data can be imported as tab-delimited (from Excel for example)
- Sequences can be imported in fasta format

  >Species name|collection number| other information…

  ACCTCTTCGATGGCTAGATCGGATCGGATCGATCGATGCT
- Images, text files and PDFs can be attached to records
- Data can be appended, merged or replaced

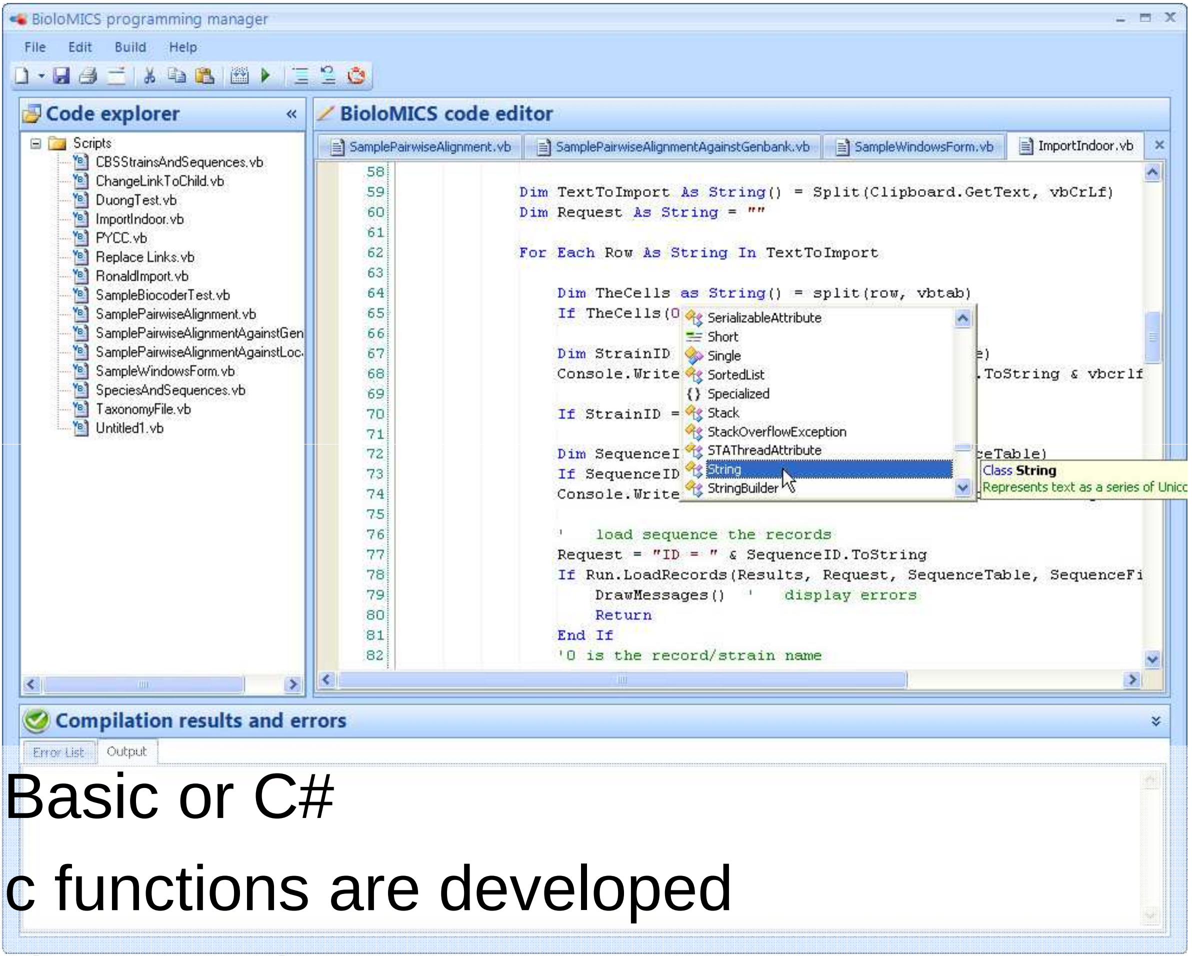
Export data

- All data can be exported using standard formats such as *Tab delimited, text, MS Excel, MS Word, Fasta, etc.*

- Users can define own formats and create reporting templates

- Export to ALA and AMRiN will be part of the standard configuration

Programming manager



```
Dim TextToImport As String() = Split(Clipboard.GetText, vbCrLf)
Dim Request As String = ""

For Each Row As String In TextToImport

    Dim TheCells as String() = split(row, vbtab)
    If TheCells(0

    Dim StrainID                                  e)
    Console.Write                                 .ToString & vbcrlf

    If StrainID =

    Dim SequenceI                                 eTable)
    If SequenceID
    Console.Write

    '   load sequence the records
    Request = "ID = " & SequenceID.ToString
    If Run.LoadRecords(Results, Request, SequenceTable, SequenceFi
        DrawMessages()  '   display errors
        Return
    End If
    '0 is the record/strain name
```

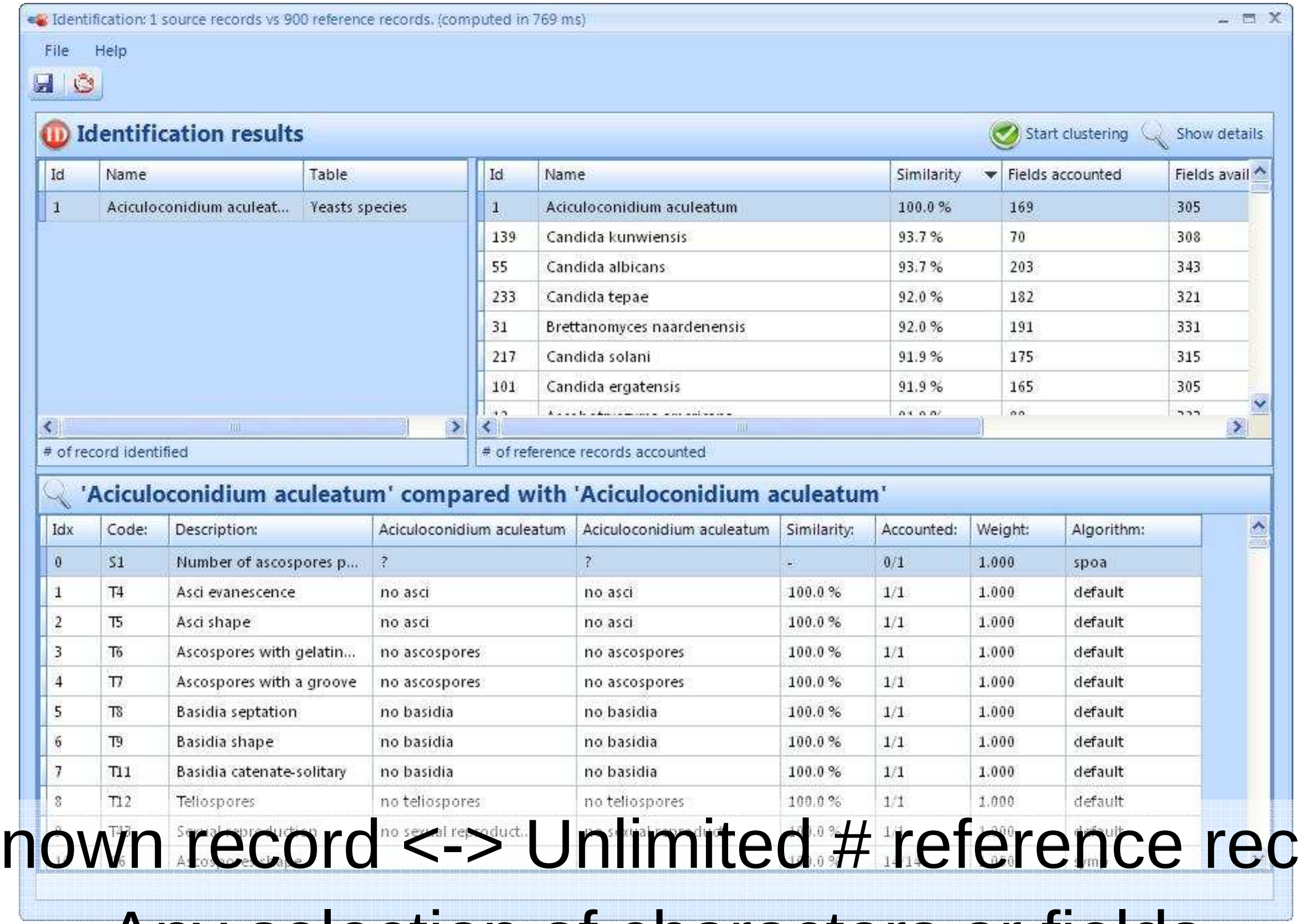
- Visual Basic or C#
- Specific functions are developed
- Add script to main menu

Analysis tools

- Data management
- Analysis Tools
- Publishing Data

- Polyphasic identification
- Polyphasic classification
- Gel analysis
- Laboratory Information Management System (LIMS)
- Images analysis
- Geographic manager
- Sequence tools
  - Pairwise alignment
  - Multiple alignment and trace file edition

Polyphasic identification



Identification: 1 source records vs 900 reference records. (computed in 769 ms)

Identification results

Id	Name	Table
1	Aciculoconidium aculeat...	Yeasts species

\# of record identified

Id	Name	Similarity	Fields accounted	Fields avail
1	Aciculoconidium aculeatum	100.0 %	169	305
139	Candida kunwiensis	93.7 %	70	308
55	Candida albicans	93.7 %	203	343
233	Candida tepae	92.0 %	182	321
31	Brettanomyces naardenensis	92.0 %	191	331
217	Candida solani	91.9 %	175	315
101	Candida ergatensis	91.9 %	165	305

\# of reference records accounted

'Aciculoconidium aculeatum' compared with 'Aciculoconidium aculeatum'

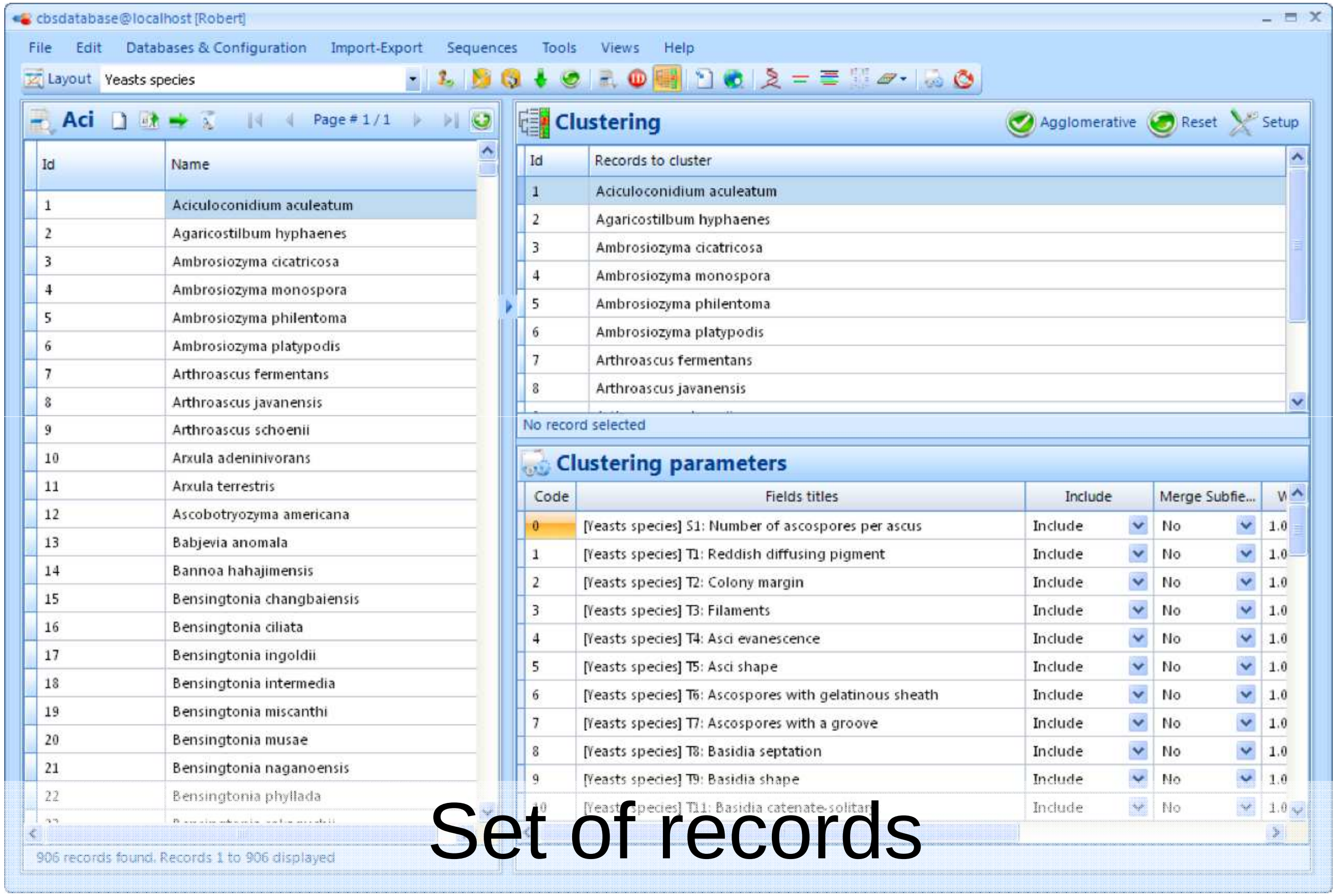
Idx	Code:	Description:	Aciculoconidium aculeatum	Aciculoconidium aculeatum	Similarity:	Accounted:	Weight:	Algorithm:
0	S1	Number of ascospores p...	?	?	-	0/1	1.000	spoa
1	T4	Asci evanescence	no asci	no asci	100.0 %	1/1	1.000	default
2	T5	Asci shape	no asci	no asci	100.0 %	1/1	1.000	default
3	T6	Ascospores with gelatin...	no ascospores	no ascospores	100.0 %	1/1	1.000	default
4	T7	Ascospores with a groove	no ascospores	no ascospores	100.0 %	1/1	1.000	default
5	T8	Basidia septation	no basidia	no basidia	100.0 %	1/1	1.000	default
6	T9	Basidia shape	no basidia	no basidia	100.0 %	1/1	1.000	default
7	T11	Basidia catenate-solitary	no basidia	no basidia	100.0 %	1/1	1.000	default
8	T12	Teliospores	no teliospores	no teliospores	100.0 %	1/1	1.000	default
9	[illegible]	Sexual reproduction	no sexual reproduct...	[illegible]	[illegible]	[illegible]	1.000	default
[illegible]	[illegible]	Ascospore shape	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]

Unknown record <-> Unlimited # reference records

Any selection of characters or fields

BioloMICS

Polyphasic classification



Layout: Yeasts species

Id	Name
1	Aciculoconidium aculeatum
2	Agaricostilbum hyphaenes
3	Ambrosiozyma cicatricosa
4	Ambrosiozyma monospora
5	Ambrosiozyma philentoma
6	Ambrosiozyma platypodis
7	Arthroascus fermentans
8	Arthroascus javanensis
9	Arthroascus schoenii
10	Arxula adeninivorans
11	Arxula terrestris
12	Ascobotryozyma americana
13	Babjevia anomala
14	Bannoa hahajimensis
15	Bensingtonia changbaiensis
16	Bensingtonia ciliata
17	Bensingtonia ingoldii
18	Bensingtonia intermedia
19	Bensingtonia miscanthi
20	Bensingtonia musae
21	Bensingtonia naganoensis
22	Bensingtonia phyllada

906 records found. Records 1 to 906 displayed

Id	Records to cluster
1	Aciculoconidium aculeatum
2	Agaricostilbum hyphaenes
3	Ambrosiozyma cicatricosa
4	Ambrosiozyma monospora
5	Ambrosiozyma philentoma
6	Ambrosiozyma platypodis
7	Arthroascus fermentans
8	Arthroascus javanensis

No record selected

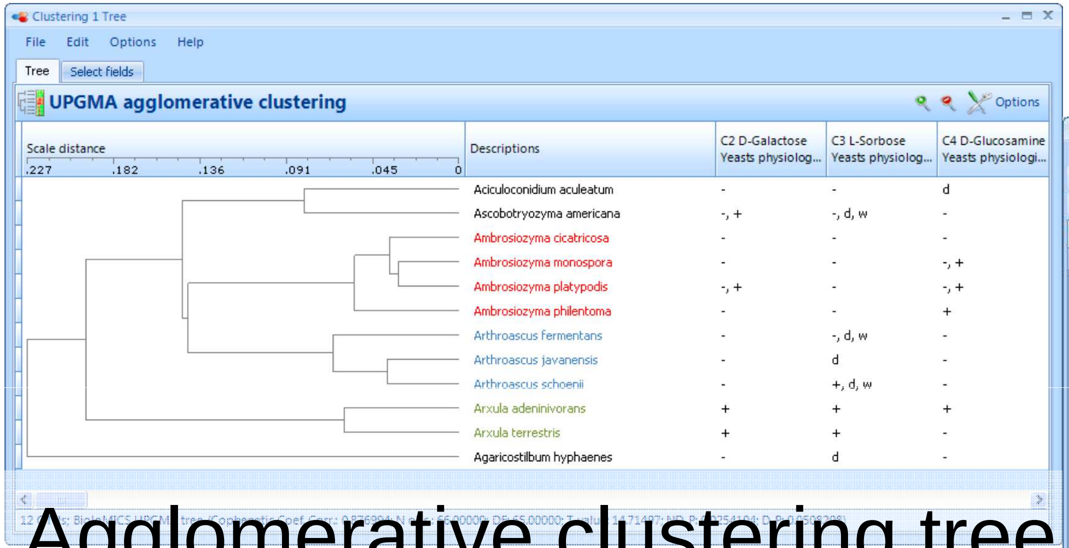
Clustering parameters

Code	Fields titles	Include	Merge Subfie...	W
0	[Yeasts species] S1: Number of ascospores per ascus	Include	No	1.0
1	[Yeasts species] T1: Reddish diffusing pigment	Include	No	1.0
2	[Yeasts species] T2: Colony margin	Include	No	1.0
3	[Yeasts species] T3: Filaments	Include	No	1.0
4	[Yeasts species] T4: Asci evanescence	Include	No	1.0
5	[Yeasts species] T5: Asci shape	Include	No	1.0
6	[Yeasts species] T6: Ascospores with gelatinous sheath	Include	No	1.0
7	[Yeasts species] T7: Ascospores with a groove	Include	No	1.0
8	[Yeasts species] T8: Basidia septation	Include	No	1.0
9	[Yeasts species] T9: Basidia shape	Include	No	1.0
10	[Yeasts species] T11: Basidia catenate-solitar	Include	No	1.0

Set of records

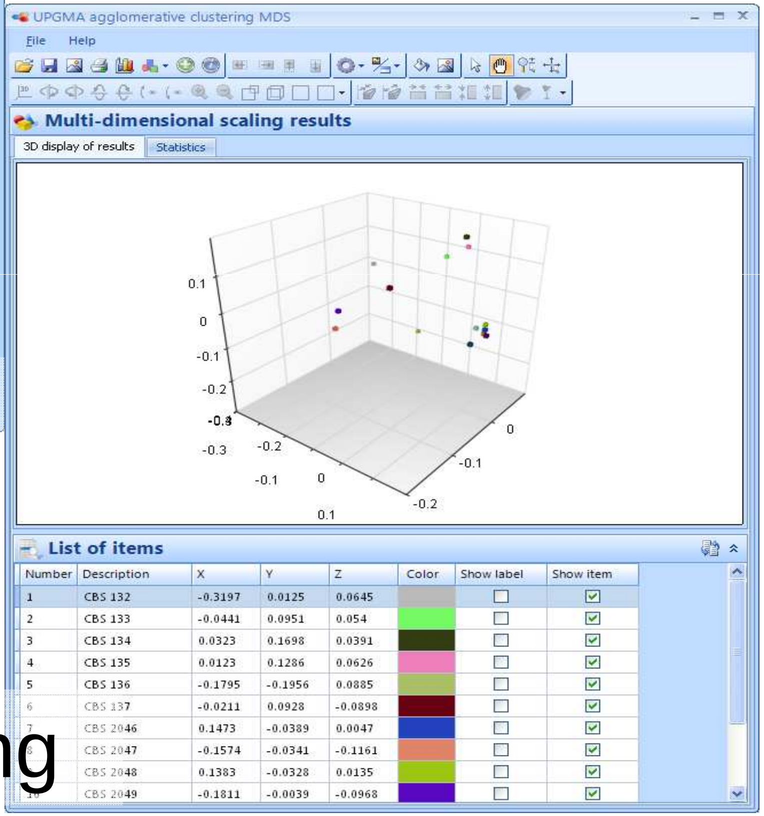
Any selection of characters or fields

Presenting the results



Descriptions	C2 D-Galactose Yeasts physiolog...	C3 L-Sorbose Yeasts physiolog...	C4 D-Glucosamine Yeasts physiologi...
Aciculoconidium aculeatum	-	-	d
Ascobotryozyma americana	-, +	-, d, w	-
Ambrosiozyma cicatricosa	-	-	-
Ambrosiozyma monospora	-	-	-, +
Ambrosiozyma platypodis	-, +	-	-, +
Ambrosiozyma philentoma	-	-	+
Arthroascus fermentans	-	-, d, w	-
Arthroascus javanensis	-	d	-
Arthroascus schoenii	-	+, d, w	-
Arxula adeninivorans	+	+	+
Arxula terrestris	+	+	-
Agaricostilbum hyphaenes	-	d	-

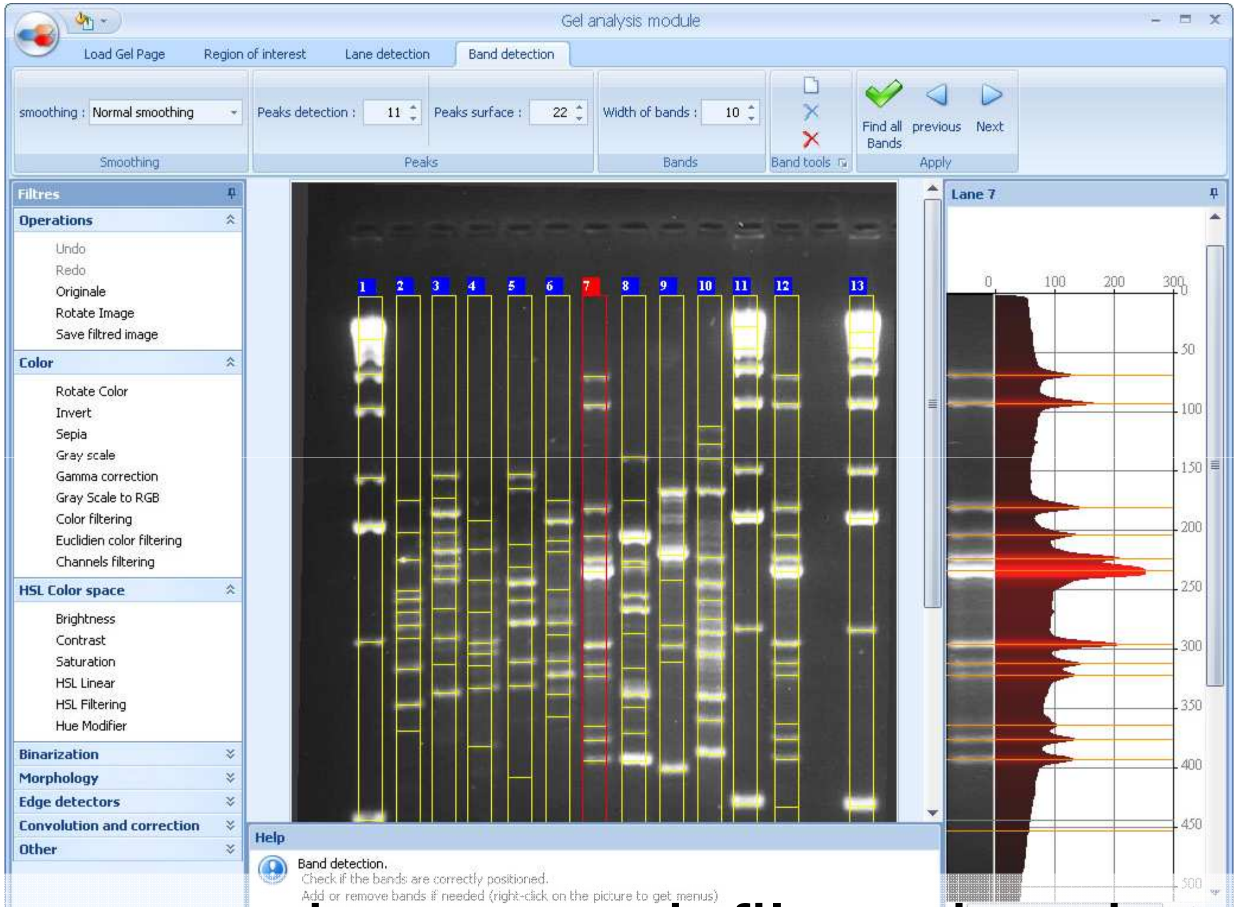
Agglomerative clustering tree



Number	Description	X	Y	Z	Color	Show label	Show item
1	CBS 132	-0.3197	0.0125	0.0645	⬜	☐	☑
2	CBS 133	-0.0441	0.0951	0.054	🟩	☐	☑
3	CBS 134	0.0323	0.1698	0.0391	⬛	☐	☑
4	CBS 135	0.0123	0.1286	0.0626	🟪	☐	☑
5	CBS 136	-0.1795	-0.1956	0.0885	🟩	☐	☑
6	CBS 137	-0.0211	0.0928	-0.0898	🟥	☐	☑
7	CBS 2046	0.1473	-0.0389	0.0047	🟦	☐	☑
8	CBS 2047	-0.1574	-0.0341	-0.1161	🟧	☐	☑
	CBS 2048	0.1383	-0.0328	0.0135	🟩	☐	☑
10	CBS 2049	-0.1811	-0.0039	-0.0968	🟪	☐	☑

Multi-Dimensional Scaling

Gel analysis



smoothing : Normal smoothing

Peaks detection : 11

Peaks surface : 22

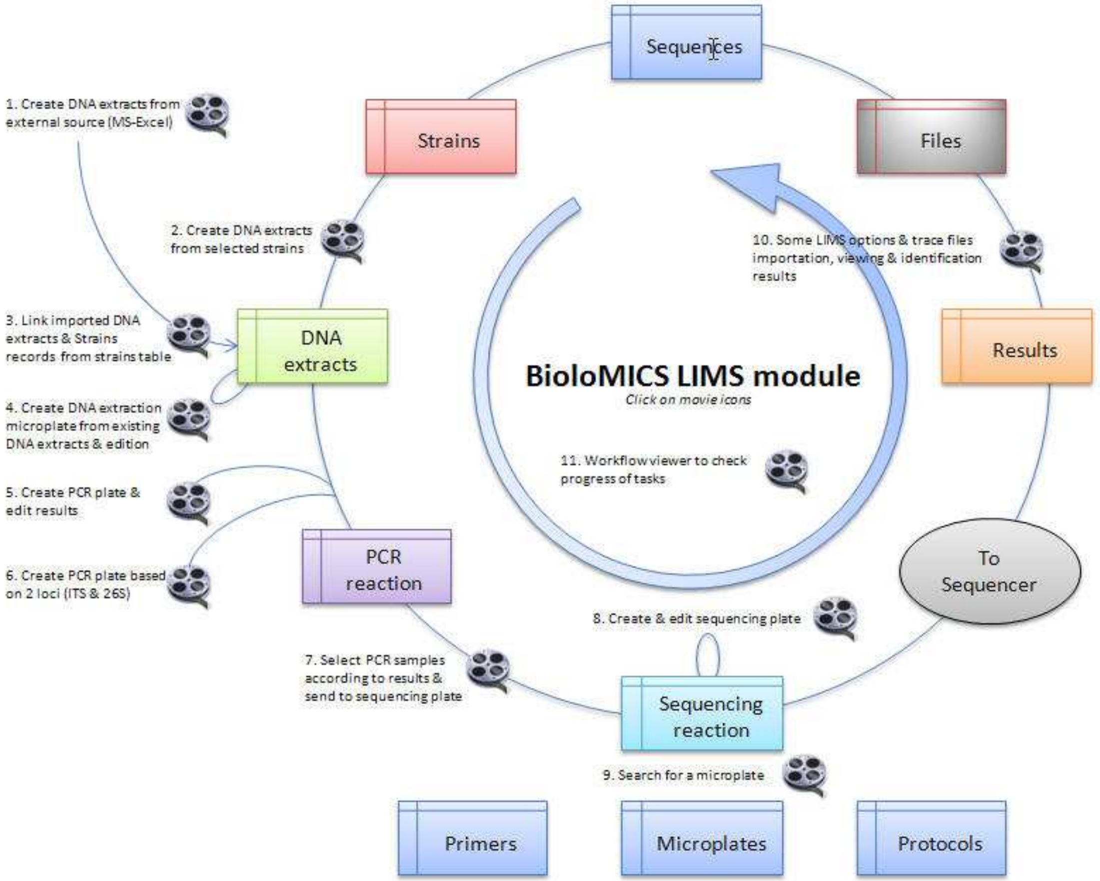
Width of bands : 10

Band detection.
Check if the bands are correctly positioned.
Add or remove bands if needed (right-click on the picture to get menus)

- Any format can be opened, filtered and modified
- Automatic lane and band detection

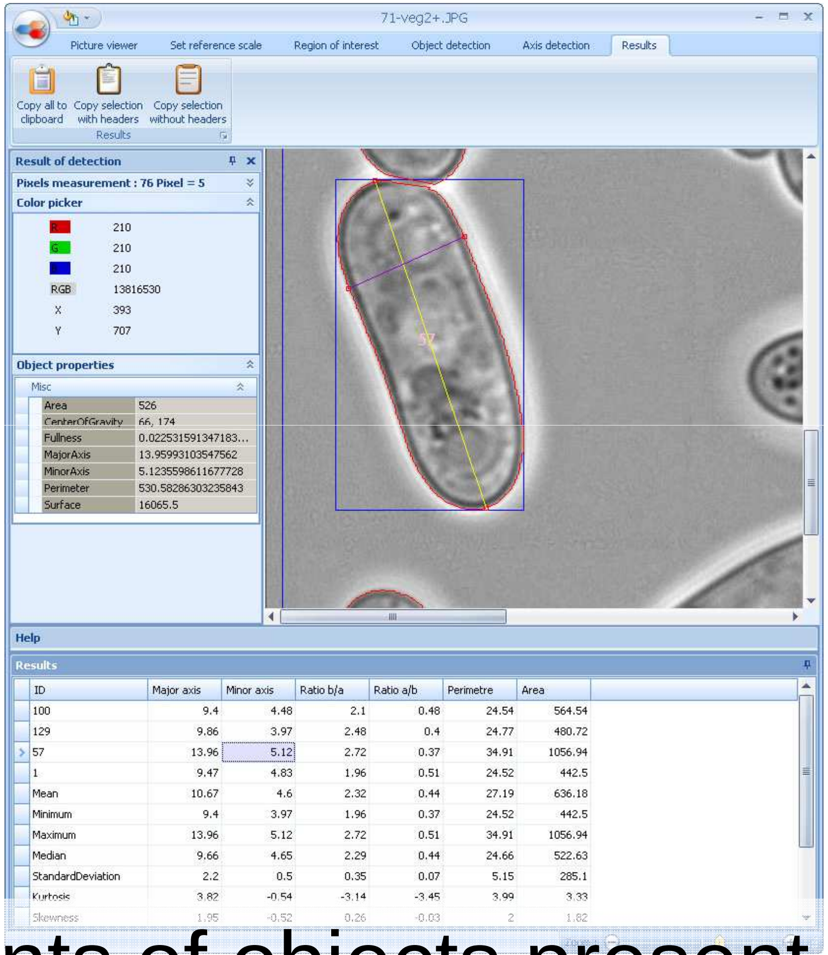
BioloMICS

LIMS



- Laboratory Information Management System
- To manage and track sequencing operations

Image analysis



Result of detection

Pixels measurement : 76 Pixel = 5

Color picker

R	210
G	210
B	210
RGB	13816530
X	393
Y	707

Object properties

Misc

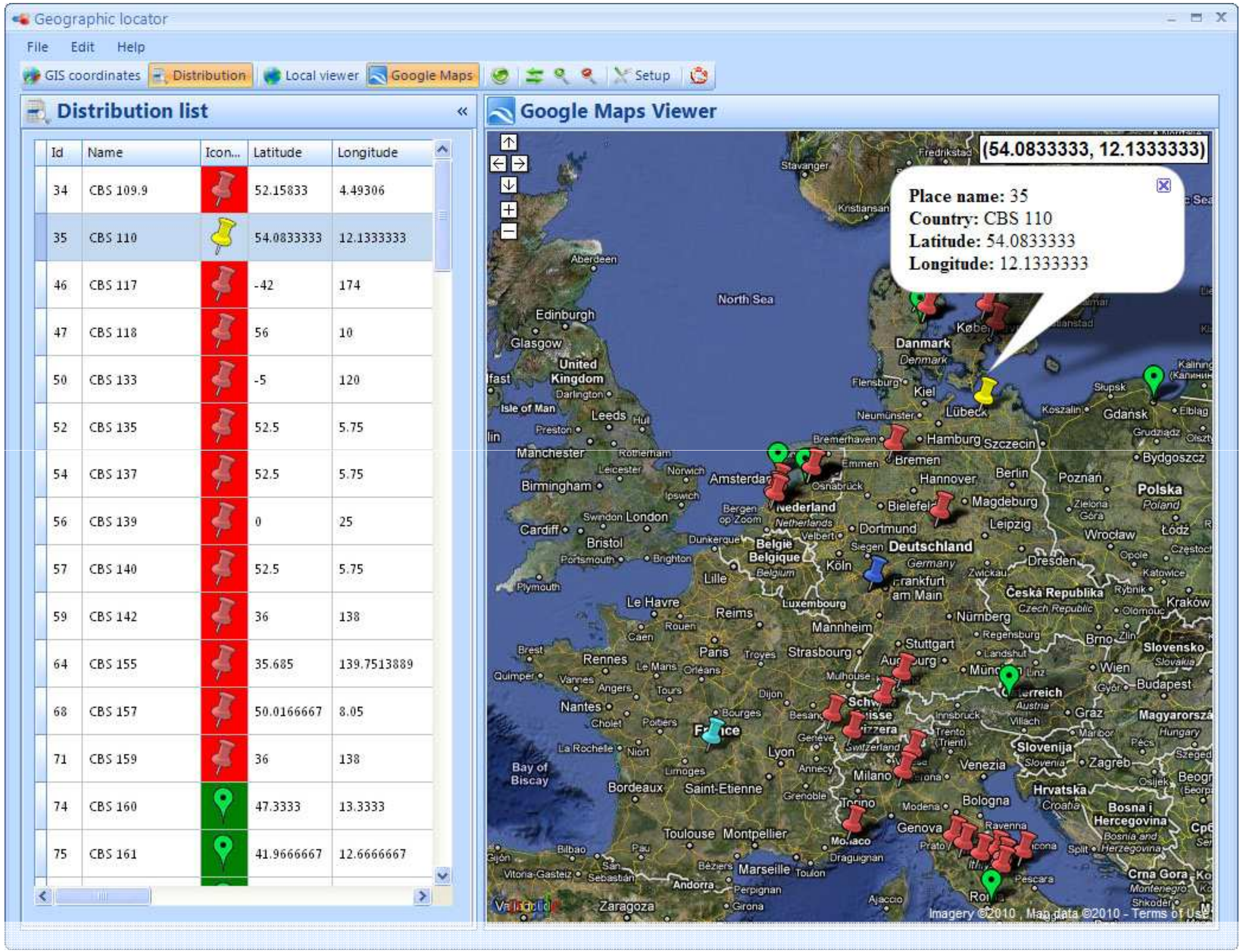
Area	526
CenterOfGravity	66, 174
Fullness	0.022531591347183…
MajorAxis	13.95993103547562
MinorAxis	5.1235598611677728
Perimeter	530.58286303235843
Surface	16065.5

Results

ID	Major axis	Minor axis	Ratio b/a	Ratio a/b	Perimetre	Area
100	9.4	4.48	2.1	0.48	24.54	564.54
129	9.86	3.97	2.48	0.4	24.77	480.72
57	13.96	5.12	2.72	0.37	34.91	1056.94
1	9.47	4.83	1.96	0.51	24.52	442.5
Mean	10.67	4.6	2.32	0.44	27.19	636.18
Minimum	9.4	3.97	1.96	0.37	24.52	442.5
Maximum	13.96	5.12	2.72	0.51	34.91	1056.94
Median	9.66	4.65	2.29	0.44	24.66	522.63
StandardDeviation	2.2	0.5	0.35	0.07	5.15	285.1
Kurtosis	3.82	-0.54	-3.14	-3.45	3.99	3.33
Skewness	1.95	-0.52	0.26	-0.03	2	1.82

Measurements of objects present on a picture

Geographic manager



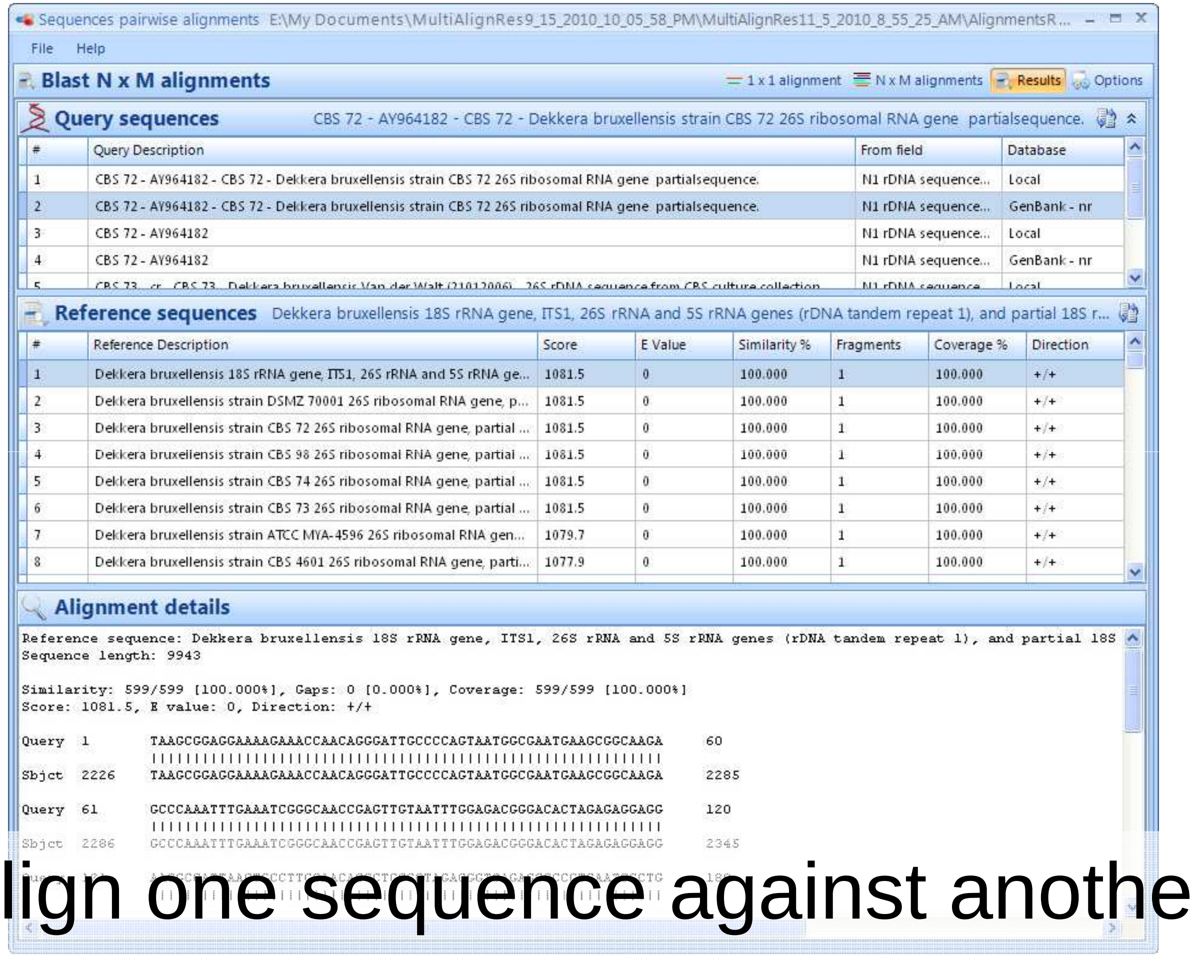
Id	Name	Icon...	Latitude	Longitude
34	CBS 109.9	📌	52.15833	4.49306
35	CBS 110	📌	54.0833333	12.1333333
46	CBS 117	📌	-42	174
47	CBS 118	📌	56	10
50	CBS 133	📌	-5	120
52	CBS 135	📌	52.5	5.75
54	CBS 137	📌	52.5	5.75
56	CBS 139	📌	0	25
57	CBS 140	📌	52.5	5.75
59	CBS 142	📌	36	138
64	CBS 155	📌	35.685	139.7513889
68	CBS 157	📌	50.0166667	8.05
71	CBS 159	📌	36	138
74	CBS 160	📍	47.3333	13.3333
75	CBS 161	📍	41.9666667	12.6666667

(54.0833333, 12.1333333)

Place name: 35
Country: CBS 110
Latitude: 54.0833333
Longitude: 12.1333333

Locate strains on the map by lat/long or text field

Pairwise alignment



Query sequences: CBS 72 - AY964182 - CBS 72 - Dekkera bruxellensis strain CBS 72 26S ribosomal RNA gene partialsequence.

#	Query Description	From field	Database
1	CBS 72 - AY964182 - CBS 72 - Dekkera bruxellensis strain CBS 72 26S ribosomal RNA gene partialsequence.	N1 rDNA sequence...	Local
2	CBS 72 - AY964182 - CBS 72 - Dekkera bruxellensis strain CBS 72 26S ribosomal RNA gene partialsequence.	N1 rDNA sequence...	GenBank - nr
3	CBS 72 - AY964182	N1 rDNA sequence...	Local
4	CBS 72 - AY964182	N1 rDNA sequence...	GenBank - nr
5	CBS 73 - cr - CBS 73 - Dekkera bruxellensis Van der Walt (21012006) - 26S rDNA sequence from CBS culture collection	N1 rDNA sequence...	Local

Reference sequences: Dekkera bruxellensis 18S rRNA gene, ITS1, 26S rRNA and 5S rRNA genes (rDNA tandem repeat 1), and partial 18S r...

#	Reference Description	Score	E Value	Similarity %	Fragments	Coverage %	Direction
1	Dekkera bruxellensis 18S rRNA gene, ITS1, 26S rRNA and 5S rRNA ge...	1081.5	0	100.000	1	100.000	+/+
2	Dekkera bruxellensis strain DSMZ 70001 26S ribosomal RNA gene, p...	1081.5	0	100.000	1	100.000	+/+
3	Dekkera bruxellensis strain CBS 72 26S ribosomal RNA gene, partial ...	1081.5	0	100.000	1	100.000	+/+
4	Dekkera bruxellensis strain CBS 98 26S ribosomal RNA gene, partial ...	1081.5	0	100.000	1	100.000	+/+
5	Dekkera bruxellensis strain CBS 74 26S ribosomal RNA gene, partial ...	1081.5	0	100.000	1	100.000	+/+
6	Dekkera bruxellensis strain CBS 73 26S ribosomal RNA gene, partial ...	1081.5	0	100.000	1	100.000	+/+
7	Dekkera bruxellensis strain ATCC MYA-4596 26S ribosomal RNA gen...	1079.7	0	100.000	1	100.000	+/+
8	Dekkera bruxellensis strain CBS 4601 26S ribosomal RNA gene, parti...	1077.9	0	100.000	1	100.000	+/+

```
Reference sequence: Dekkera bruxellensis 18S rRNA gene, ITS1, 26S rRNA and 5S rRNA genes (rDNA tandem repeat 1), and partial 18S
Sequence length: 9943

Similarity: 599/599 [100.000%], Gaps: 0 [0.000%], Coverage: 599/599 [100.000%]
Score: 1081.5, E value: 0, Direction: +/+

Query  1       TAAGCGGAGGAAAAGAAACCAACAGGGATTGCCCCAGTAATGGCGAATGAAGCGGCAAGA     60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2226    TAAGCGGAGGAAAAGAAACCAACAGGGATTGCCCCAGTAATGGCGAATGAAGCGGCAAGA     2285

Query  61      GCCCAAATTTGAAATCGGGCAACCGAGTTGTAATTTGGAGACGGGACACTAGAGAGGAGG     120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2286    GCCCAAATTTGAAATCGGGCAACCGAGTTGTAATTTGGAGACGGGACACTAGAGAGGAGG     2345
```

Align one sequence against another

Few sequences against Genbank or local database

BioloMICS

Multiple alignment & trace file edition

Consensus:
23 sequences, OptSim=24.5%,
PesSim=0.7%

AY964182 - CBS 72 - Dekkera bruxe...
AY964182
cr - CBS 73 - Dekkera bruxellensis ...
AY969048 - CBS 73 - Dekkera bruxe...
AY969048
d32098 - ifo 1590 - dekkera bruxell...
d32105 - ifo 1590 - dekkera bruxell...
u45738 - nrrl y-12961 - dekkera bru...
af113890 - cbs 74 (type strain) - de...
d32105 - ifo 1590 - dekkera bruxell...
d32105 - ifo 1590 - dekkera bruxell...
cr - CBS 74 - Dekkera bruxellensis ...
EF550257 - NRRL Y-12961 - Dekkera...
AY969049 - CBS 74 - Dekkera bruxe...
D32105 - IFO 1590 - Dekkera bruxe...
D32098 - IFO 1590 - Dekkera bruxe...
U45738 - NRRL Y-12961 - Dekkera b...
AY969049
EF550257
EU011655
cr - CBS 75 - Dekkera bruxellensis ...

Consensus:
2 sequences, OptSim=92.8%,
PesSim=60.6%

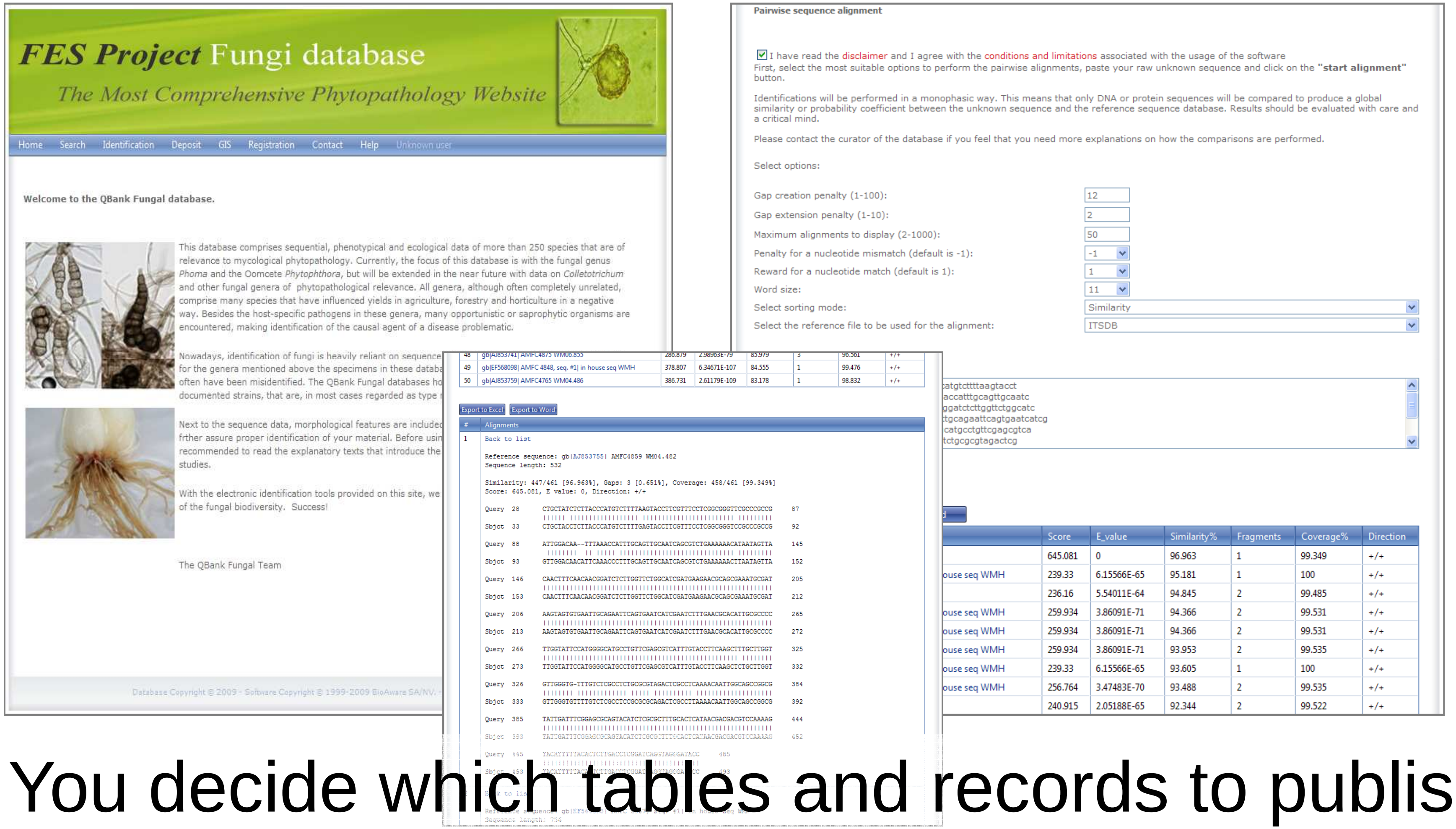
ex 10198_LROR__A07_063.ab1
ex 10198_LR5__A07_063.ab1

Publishing Data

- Data management
- Analysis Tools
- Publishing Data

- To Intranet
- To ALA and AMRiN

Publishing data to intranet



Welcome to the QBank Fungal database.

This database comprises sequential, phenotypical and ecological data of more than 250 species that are of relevance to mycological phytopathology. Currently, the focus of this database is with the fungal genus *Phoma* and the Oomcete *Phytophthora*, but will be extended in the near future with data on *Colletotrichum* and other fungal genera of phytopathological relevance. All genera, although often completely unrelated, comprise many species that have influenced yields in agriculture, forestry and horticulture in a negative way. Besides the host-specific pathogens in these genera, many opportunistic or saprophytic organisms are encountered, making identification of the causal agent of a disease problematic.

Nowadays, identification of fungi is heavily reliant on sequence
for the genera mentioned above the specimens in these databa
often have been misidentified. The QBank Fungal databases ho
documented strains, that are, in most cases regarded as type

Next to the sequence data, morphological features are included
frther assure proper identification of your material. Before usin
recommended to read the explanatory texts that introduce the
studies.

With the electronic identification tools provided on this site, we
of the fungal biodiversity. Success!

The QBank Fungal Team

Database Copyright © 2009 - Software Copyright © 1999-2009 BioAware SA/NV. -

Pairwise sequence alignment

☑ I have read the disclaimer and I agree with the conditions and limitations associated with the usage of the software
First, select the most suitable options to perform the pairwise alignments, paste your raw unknown sequence and click on the **"start alignment"** button.

Identifications will be performed in a monophasic way. This means that only DNA or protein sequences will be compared to produce a global similarity or probability coefficient between the unknown sequence and the reference sequence database. Results should be evaluated with care and a critical mind.

Please contact the curator of the database if you feel that you need more explanations on how the comparisons are performed.

Select options:

Gap creation penalty (1-100): 12
Gap extension penalty (1-10): 2
Maximum alignments to display (2-1000): 50
Penalty for a nucleotide mismatch (default is -1): -1
Reward for a nucleotide match (default is 1): 1
Word size: 11
Select sorting mode: Similarity
Select the reference file to be used for the alignment: ITSDB

```
atgtcttttaagtacct
accatttgcagttgcaatc
ggatctcttggttctggcatc
tgcagaattcagtgaatcatcg
catgcctgttcgagcgtca
tctgcgcgtagactcg
```

	Score	E_value	Similarity%	Fragments	Coverage%	Direction
	645.081	0	96.963	1	99.349	+/+
ouse seq WMH	239.33	6.15566E-65	95.181	1	100	+/+
	236.16	5.54011E-64	94.845	2	99.485	+/+
ouse seq WMH	259.934	3.86091E-71	94.366	2	99.531	+/+
ouse seq WMH	259.934	3.86091E-71	94.366	2	99.531	+/+
ouse seq WMH	259.934	3.86091E-71	93.953	2	99.535	+/+
ouse seq WMH	239.33	6.15566E-65	93.605	1	100	+/+
ouse seq WMH	256.764	3.47483E-70	93.488	2	99.535	+/+
	240.915	2.05188E-65	92.344	2	99.522	+/+

48	gb|AJ853741| AMFC4875 WM06.855	286.879	2.98963E-79	85.979	3	96.561	+/+
49	gb|EF568098| AMFC 4848, seq. #1| in house seq WMH	378.807	6.34671E-107	84.555	1	99.476	+/+
50	gb|AJ853759| AMFC4765 WM04.486	386.731	2.61179E-109	83.178	1	98.832	+/+

1

```
Reference sequence: gb|AJ853755| AMFC4859 WM04.482
Sequence length: 532

Similarity: 447/461 [96.963%], Gaps: 3 [0.651%], Coverage: 458/461 [99.349%]
Score: 645.081, E value: 0, Direction: +/+

Query  28     CTGCTATCTCTTACCCATGTCTTTTAAGTACCTTCGTTTCCTCGGCGGGTTCGCCCGCCG    87
              |||||| |||||||||||||||||| |||||||||||||||||||||||| |||||||||
Sbjct  33     CTGCTACCTCTTACCCATGTCTTTTGAGTACCTTCGTTTCCTCGGCGGGTCCGCCCGCCG    92

Query  88     ATTGGACAA--TTTAAACCATTTGCAGTTGCAATCAGCGTCTGAAAAAACATAATAGTTA    145
               ||||||||  || ||||| ||||||||||||||||||||||||||||| ||||||||||
Sbjct  93     GTTGGACAACATTCAAACCCTTTGCAGTTGCAATCAGCGTCTGAAAAAACTTAATAGTTA    152

Query  146    CAACTTTCAACAACGGATCTCTTGGTTCTGGCATCGATGAAGAACGCAGCGAAATGCGAT    205
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  153    CAACTTTCAACAACGGATCTCTTGGTTCTGGCATCGATGAAGAACGCAGCGAAATGCGAT    212

Query  206    AAGTAGTGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACATTGCGCCCC    265
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  213    AAGTAGTGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACATTGCGCCCC    272

Query  266    TTGGTATTCCATGGGGCATGCCTGTTCGAGCGTCATTTGTACCTTCAAGCTTTGCTTGGT    325
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct  273    TTGGTATTCCATGGGGCATGCCTGTTCGAGCGTCATTTGTACCTTCAAGCTCTGCTTGGT    332

Query  326    GTTGGGTG-TTTGTCTCGCCTCTGCGCGTAGACTCGCCTCAAAACAATTGGCAGCCGGCG    384
              |||||||| ||||||||||||| ||||| |||||||||| ||||||||||||||||||||
Sbjct  333    GTTGGGTGTTTTGTCTCGCCTCCGCGCGCAGACTCGCCTTAAAACAATTGGCAGCCGGCG    392

Query  385    TATTGATTTCGGAGCGCAGTACATCTCGCGCTTTGCACTCATAACGACGACGTCCAAAAG    444
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  393    TATTGATTTCGGAGCGCAGTACATCTCGCGCTTTGCACTCATAACGACGACGTCCAAAAG    452

Query  445    TACATTTTTACACTCTTGACCTCGGATCAGGTAGGGATACC    485

Sequence length: 756
```

You decide which tables and records to publish

BioloMICS

Publishing data to ALA and AMRiN

- Is part of the standard configuration
  - Script available through ‘Programming Manager’
- Two modes:
  - Automatic (scheduled job)
  - Manual (run script to produce file, then upload at http://www.ala.org.au/share/share-data/)

The Atlas is offering to:

- provide BioloMICS licences to organisations that wish to adopt it
- paying licence maintenance fees to at least 2012
- assist with installing and implementing BioloMICS
- assist with migrating existing databases or electronic files to BioloMICS
- provide initial training in BioloMICS
- advise on establishing a web presence for microorganism collections using BioloMICS, if required
- assist to export data from collection databases for sharing through the ALA site and AMRiN.

Summary

- Data is kept safe due to high security rules
- Multiple users can access the data at the same time
- Data can be shared between labs
- There are many Analysis Tools available in the software
- It is available for your use for free.

So, why not take it?

Where to get more information

These slides:
    (ala.org.au)

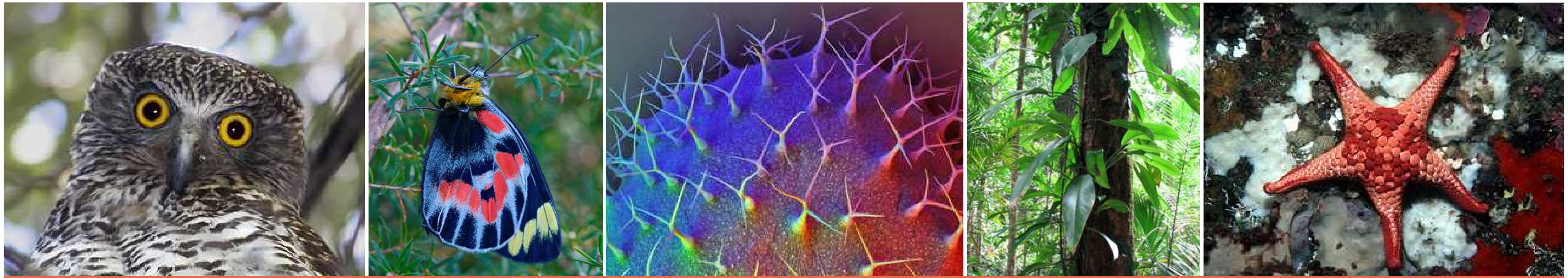
BioloMICS support:
    http://www.bio-aware.com/

Atlas of Living Australia:
    http://www.ala.org.au/support/
    support@ala.org.au

Nathalie van de Wiele:
    nathalie@vdwiele.com

The end

Any questions?



The Atlas of Living Australia Participants

www.ala.org.au

Australian museum
nature culture discover

MUSEUMVICTORIA

Queensland Government

qm
queensland museum
www.qm.qld.gov.au

Tasmanian Museum & Art Gallery

Tasmania
Explore the possibilities

Australian Government
Department of the Environment, Water, Heritage and the Arts

ABRS

CSIRO

Australian Government
Department of Agriculture, Fisheries and Forestry

THE UNIVERSITY OF ADELAIDE
AUSTRALIA

CHAH
Council of Heads of Australasian Herbaria

Southern Cross UNIVERSITY
A new way to think

The Council of Heads of Australian Faunal Collections (CHAFC)

The Council of Heads of Australian Entomological Collections (CHAEC)

Council of Heads of Australian Collections of Microorganisms (CHACM)

The Council of Heads of Australasian Museum Directors (CAMD)

An Australian Government Initiative

National Collaborative Research Infrastructure Strategy

ATLAS OF LIVING AUSTRALIA
sharing biodiversity knowledge

The Atlas is funded by the
Australian Government under the
National Collaborative Research
Infrastructure Strategy
and further supported by the
Super Science Initiative of the
Education Investment Fund