BRI IZSA&M PROJECT

CENTRI DI REFERENZA NAZIONALI

MicroArray Lab

Collaborating Centre for Veterinary Training, Epidemiology, Food Safety and Animal Welfare

Reference Laboratories Brucellosis, CBPP, Bluetongue

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BRI/IZS&M Microbial Diagnostic Microarray (MDM) database website

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Reference Laboratories
Brucellosis, CBPP, Bluetongue

BRI microarray facility

Italy IZSA&M project (2007):

- Diagnostic microarray for the identification of *Brucella sp.*

Goal; be able to identify other organisms that may cause abortions in animals or that may elicit an immunological response similar to those species.

- Diagnostic microarray for genetic characterisation of rabbits E. coli strains.

Virulence and antimicrobial resistance genes of E. coli.

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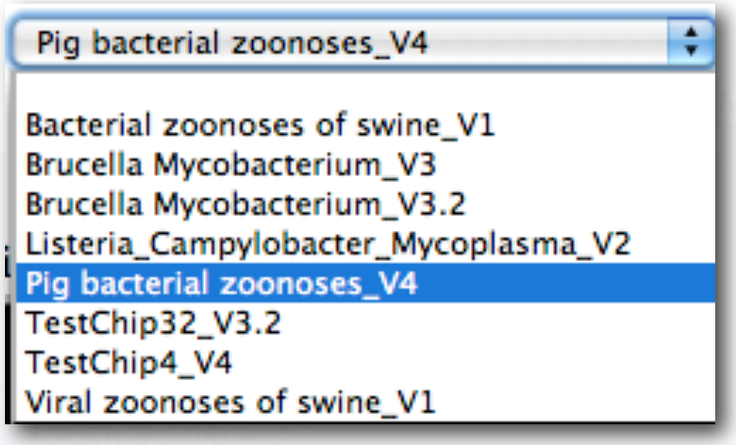
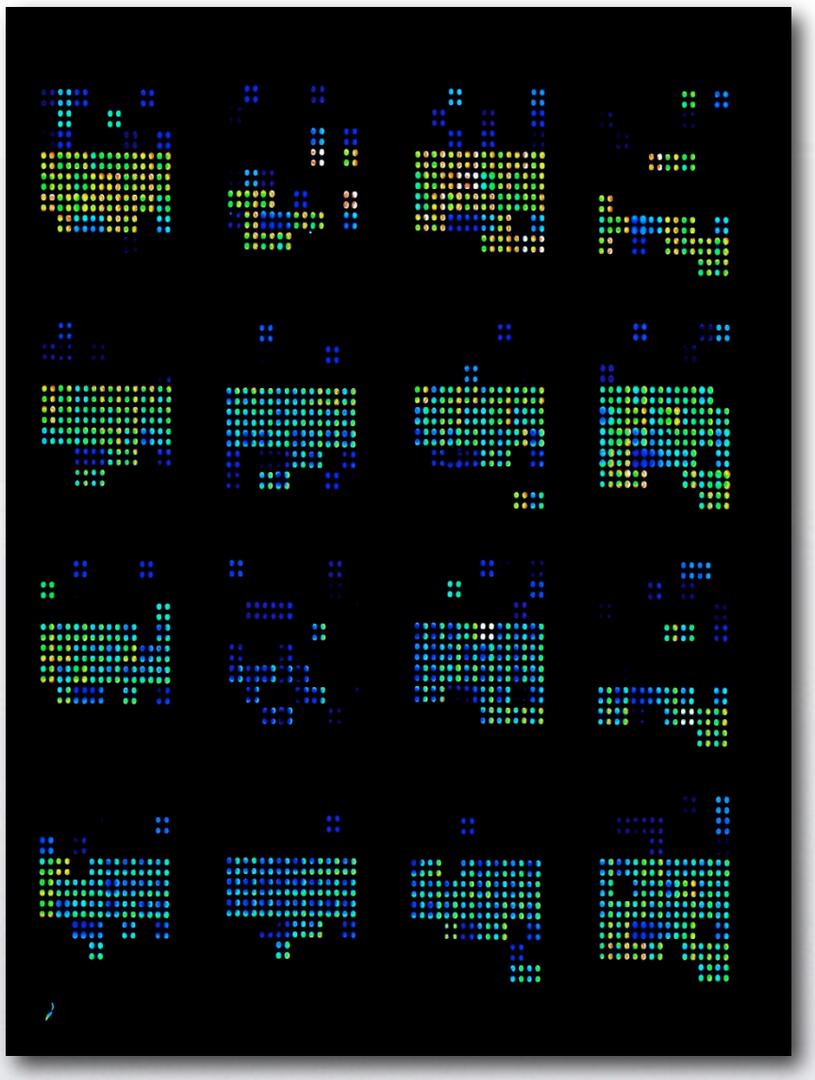
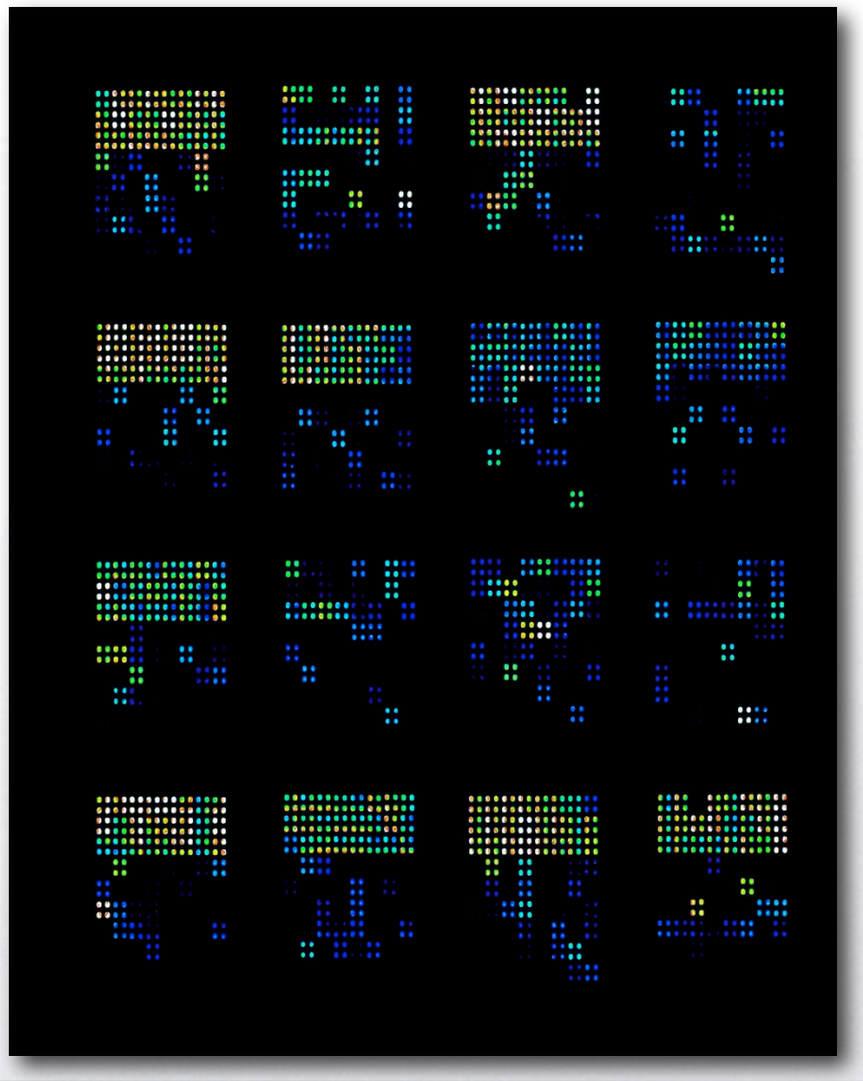
BRI microarray facility







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Open Source Clustering Software

http://bonsai.ims.u-tokyo.ac.jp/~mdehoon/software/cluster/software.htm

The open source clustering software available here contains clustering routines that can be used to analyze gene expression data. Routines for hierarchical (pairwise simple, complete, average, and centroid linkage) clustering, *k*-means and *k*-medians clustering, and 2D self-organizing maps are included. The routines are available in the form of a C clustering library, an extension module to Python, a module to Perl, as well as an enhanced version of Cluster, which was originally developed by Michael Eisen of Berkeley Lab. The C clustering library and the associated extension module for Python was released under the Python license. The Perl module was released under the Artistic License. Cluster 3.0 is covered by the original Cluster/TreeView license.

Cluster 3.0 for Windows, Mac OS X, Linux, Unix

Pycluster

Algorithm::Cluster for Perl

Reference: M. J. L. de Hoon, S. Imoto, J. Nolan, and S. Miyano: Open Source Clustering Software. *Bioinformatics*, **20** (9): 1453--1454 (2004).

Laboratory of DNA Information Analysis
Human Genome Center
Institute of Medical Science
University of Tokyo

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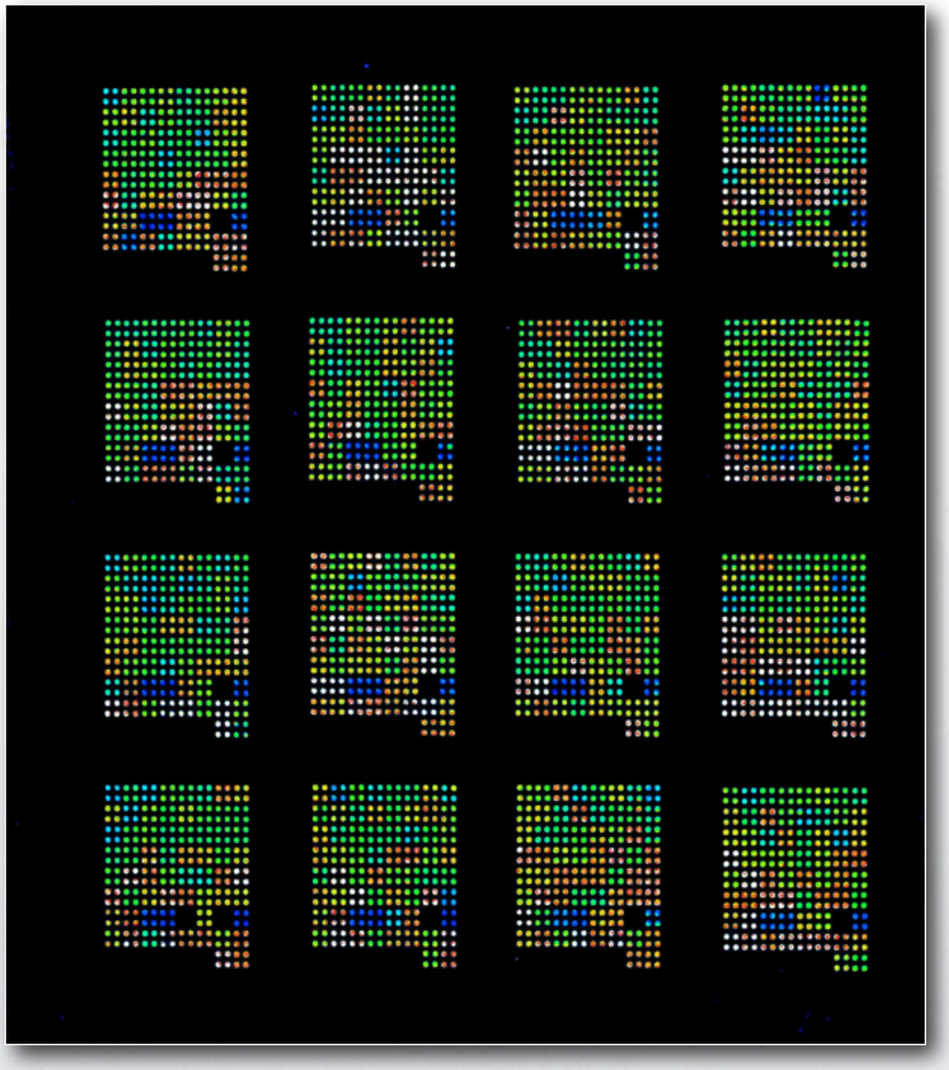
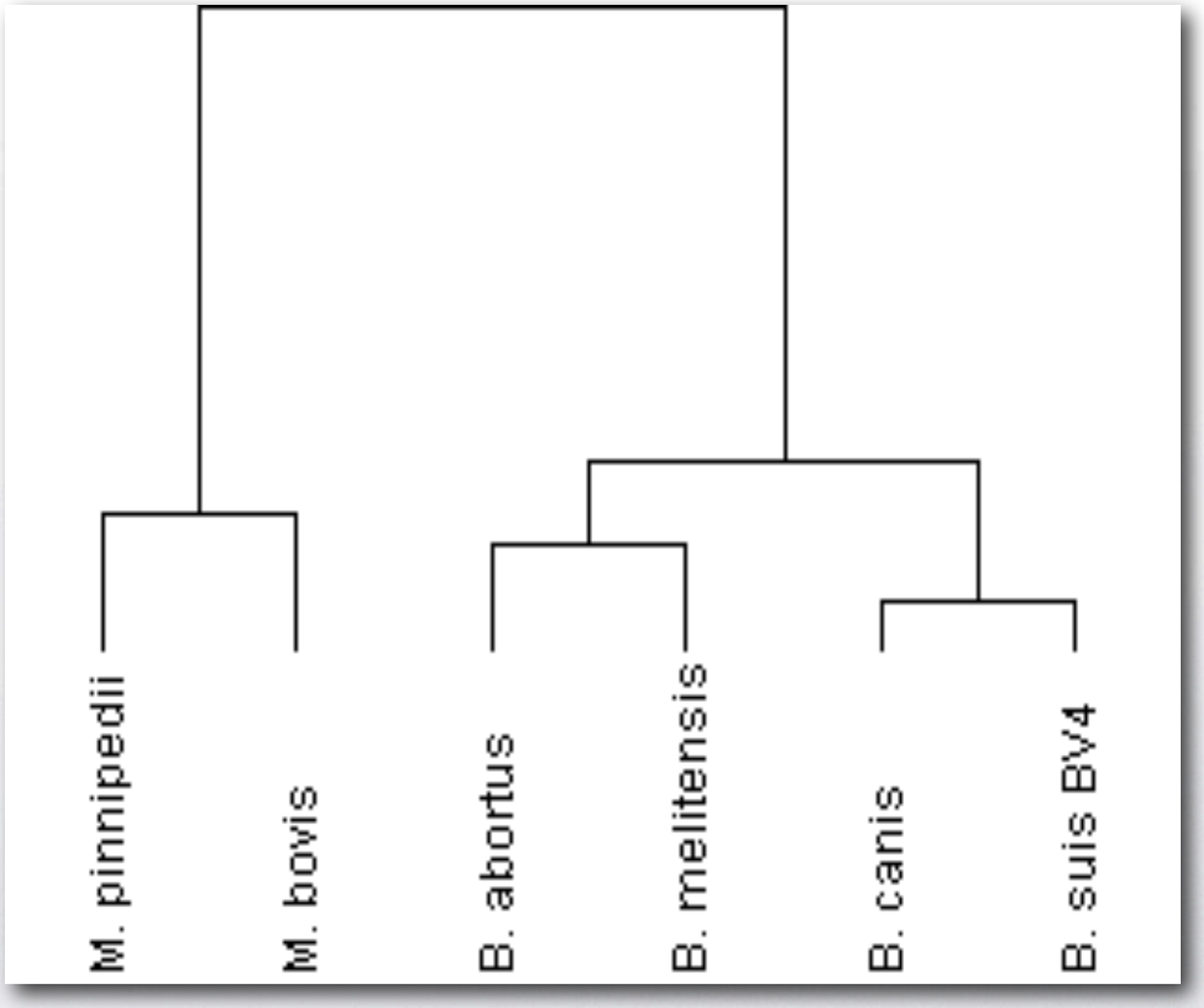
MDM Database





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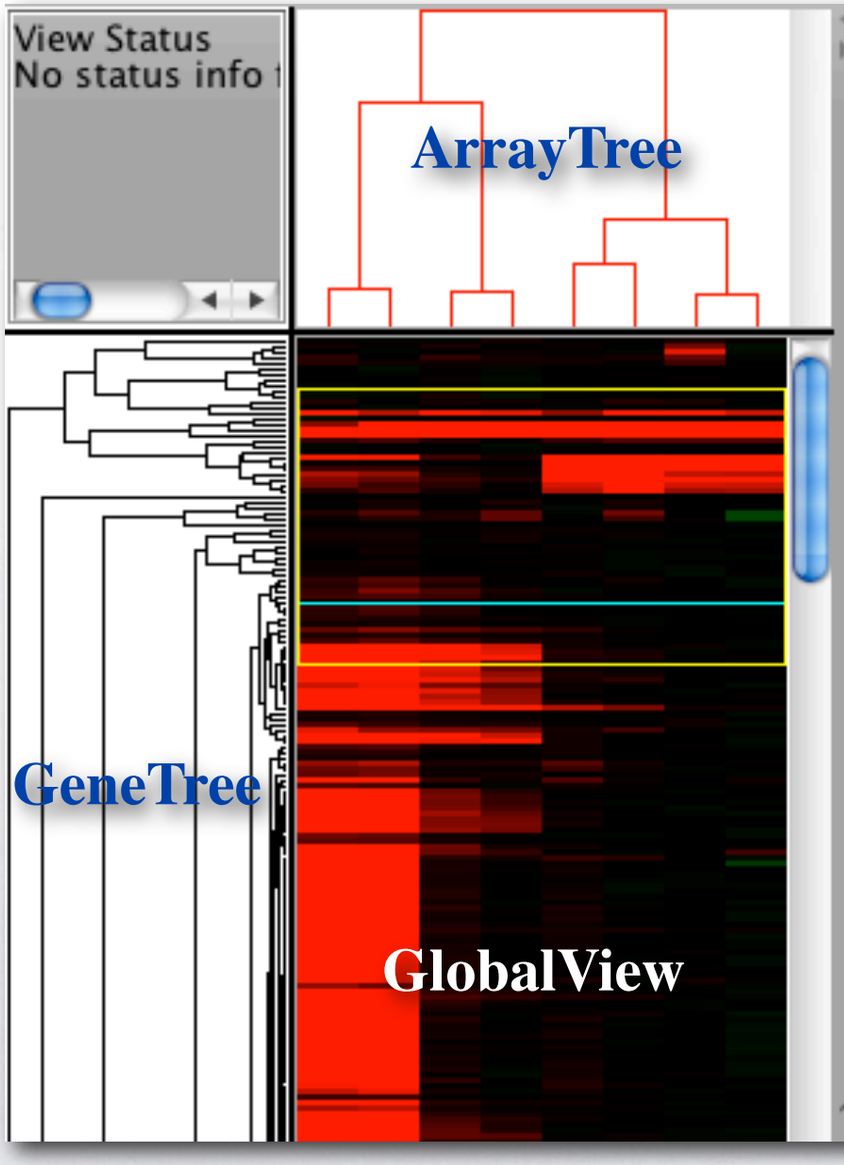
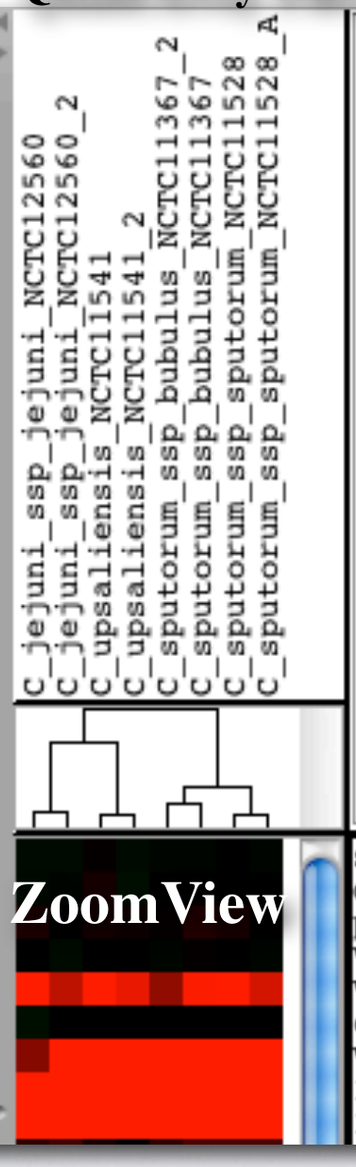
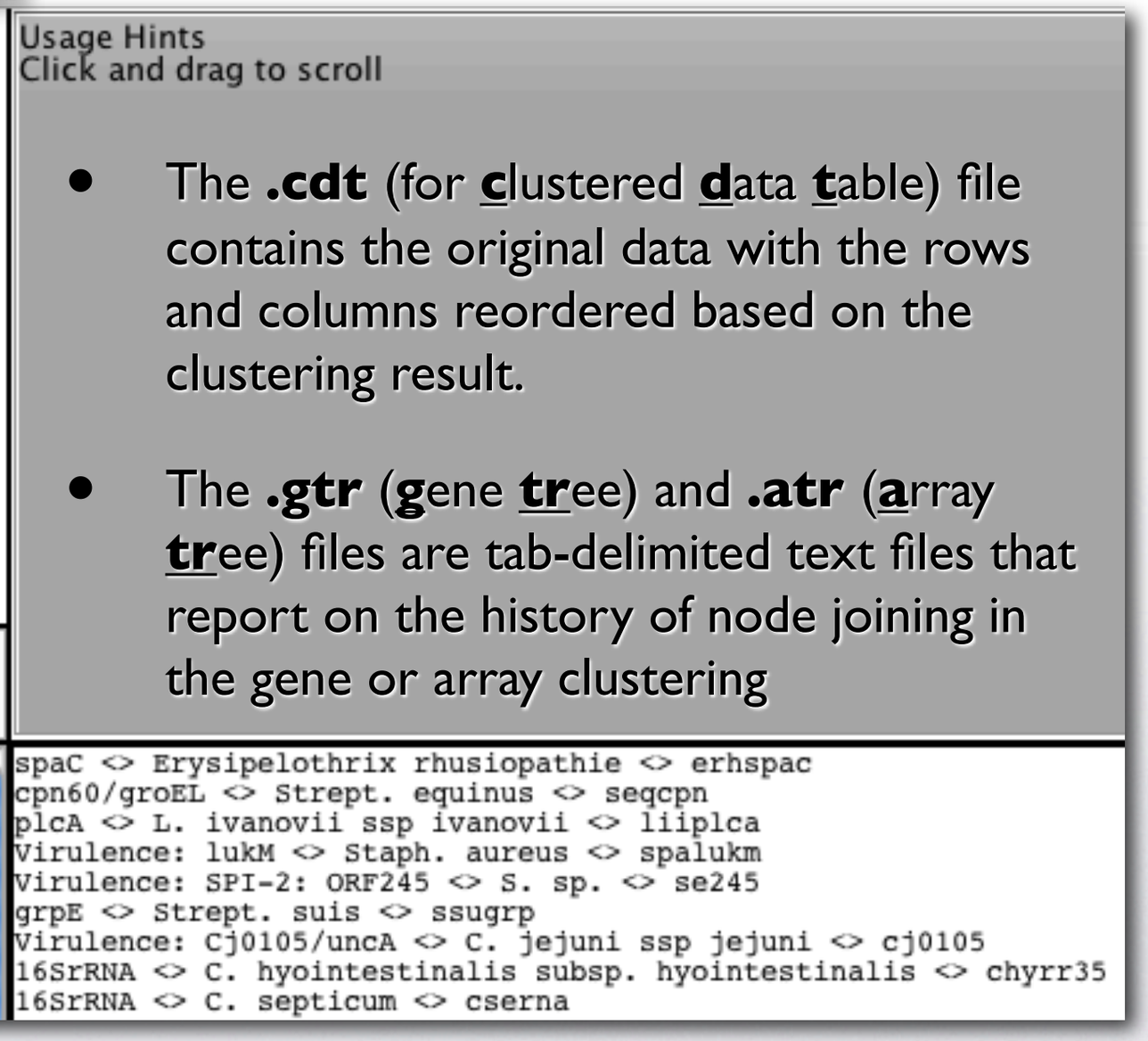
http://jtreeview.sourceforge.net

QuantArray Files







- The **.cdt** (for **c**lustered **d**ata **t**able) file contains the original data with the rows and columns reordered based on the clustering result.
- The **.gtr** (**g**ene **tr**ee) and **.atr** (**a**rray **tr**ee) files are tab-delimited text files that report on the history of node joining in the gene or array clustering

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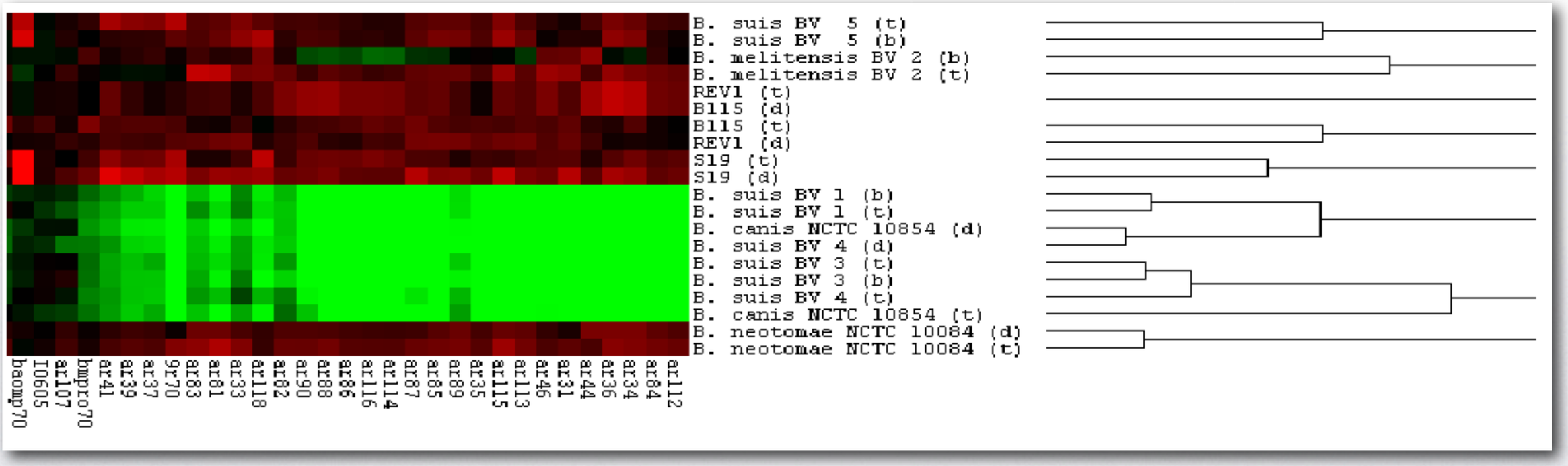
Java TreeView

http://jtreeview.sourceforge.net



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Listeria_Campylobacter_Mycoplasma V2

Please, make sure you use the correct microarray!

Add NEW Quantarray raw-data files ...

- Species
- **... OR ...** *New Species*
- **Strain names/descriptions** are defined by the QA file name.
- **Single** QA File — Browse...
- **... OR ...** **Zipped** directory — Browse...
- Make this file (these files) **PUBLIC** to all users ☐ Yes.
- **... OR ...** Give file-access to group only.

*Note: *** Only Tab delimited Text files (zipped) should be upload ****
Note: Uploading and parsing QA zip files can take a minute or two.

Upload

Add NEW Clusters ...

ClusterName

Method: A: Pairwise average-linkage clustering

Distance: C: correlation

Filter ☐ Clustering using the Log2 signal (no division by empty spot signal).

- Make this cluster **PUBLIC** to all users ☐ Yes.
- **... OR ...** Give access to group only.

Start Clustering

Quantarray raw data files:

- Campylobacter ...
- Campylobacter_Field_Strains ...
- E.coli ...
- Listeria ...
- Listeria_Field_Strain ...
- Mycoplasma ...
- Mycoplasma_Field_Strains ...
- Mycoplasma_mycoides ...
- Namibia_Strains ...
- Other ...

Clusters:

- http://candida2.bri.nrc.ca/IZSAM/

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Reference Laboratories Brucellosis, CBPP, Bluetongue

Select Microarray | Pig bacterial zoonoses_V4 | logout marcovth | Forum | Download Key File

Pig bacterial zoonoses_V4
- Bacterial zoonoses of swine_V1
- Brucella Mycobacterium_V3
- Brucella Mycobacterium_V3.2
- Listeria_Campylobacter_Mycoplasma_V2
- Pig bacterial zoonoses_V4
- TestChip32_V3.2
- TestChip4_V4
- Viral zoonoses of swine_V1

Pig bacterial zoonoses V4

Please, make sure you use the correct microarray!

Add NEW Quantarray raw-data files ...

- Species
- ... OR ... *New Species*

Quality Control Species
- E. coli
- Campylobacter
- Listeria
- Yersinia
- Vibrio cholerae
- Staphylococcus
- Salmonella
- Enterococcus
- Listeria Cheese Project

- **Strain names/descriptions** are defined by the QA file name.
- **Single** QA File — Browse...
- ... OR ... **Zipped** directory — Browse...
- Make this file (these files) **PUBLIC** to all users — Yes.
- ... OR ... Give file-access to group — only.

*Note: *** Only Tab delimited Text files (zipped) should be upload ****
Note: Uploading and parsing QA zip files can take a minute or two.

Upload

Add NEW Clusters ...

ClusterName

Method: A: Pairwise average-linkage clustering

Distance: C: correlation

Filter: Clustering using the Log2 signal (no division by empty spot signal).

- Make this cluster **PUBLIC** to all users — Yes.
- ... OR ... Give access to group — only.

Start Clustering

Do you want to share your files/clusters with other users ?

- Each Microarray has a key file. There may be different versions (e.g 1.0 and 1.1) when more samples are added to the chips.

- Each coordinate in a QA-file is checked against the same coordinate in the key file.

- If the coordinate description of the key file doesn't match the description in the QA-file, we will check if it's a small error. The website will correct small errors in the QA-file, if possible.

- If more than 5 descriptions don't match (or can not be corrected), you are likely uploading a QA-file for the wrong Microarray, and the QA-file will be refused. ***The best solution will be to download the latest key file, and re-analyse your chips with QuantArray.***

- If your QA-file contains more coordinates (data lines) than the key file, we will also refuse the file.
This simply means that a new version of the key was not uploaded to the website yet. **(Please contact Admin!)**

```
1       1       1       1       yf5 [seq-yf-5 <> Y. frederiksenii <> Yersinia]
1       1       1       2       yf5 [seq-yf-5 <> Y. frederiksenii <> Yersinia]
1       1       1       3       yf5 [seq-yf-5 <> Y. frederiksenii <> Yersinia]
1       1       1       4       yeypla [yplA <> Y. enterocolitica (type 0:8) <> Yersinia]
```

Key File

QA-file

Number	Array Row	Array Column	Row	Column	Name	X Location	Y Location	ch1 Intensity	ch1 Background
1	1	1	1	1	yf5 [seq-yf-5 <> Y. frederiksenii <> Yersinia]	740	1210	1861.9104	48.268
2	1	1	1	2	yf5 [seq-yf-5 <> Y. frederiksenii <> Yersinia]	960	1250	1720.80603	36.268
3	1	1	1	3	yf5 [seq-yf-5 <> Y. frederiksenii <> Yersinia]	1140	1230	1808.223877	44.910
4	1	1	1	4	yeypla [yplA <> Y. enterocolitica (type 0:8) <> Yersinia]		1340	1230	959.05

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Add NEW Clusters ...

ClusterName: ClusterCampy

Method: A: Pairwise average-linkage clustering

Distance: C: correlation

Filter: ☐ Clustering using the Log2 signal (no division by empty spot signal).

- Make this cluster **PUBLIC** to all users ☑ Yes.
- **... OR ...** Give access to group ____ only.

Start Clustering

Quantarray raw data files:

» ☑ **Campylobacter ...**				
☑	C_jejuni_ssp_jejuni_NCTC12560	QAfile	Norm.	Public
☑	C_jejuni_ssp_jejuni_NCTC12560_2	QAfile	Norm.	Public
☑	C_sputorum_ssp_bubulus_NCTC11367	QAfile	Norm.	Public
☑	C_sputorum_ssp_bubulus_NCTC11367_2	QAfile	Norm.	Public
☑	C_sputorum_ssp_sputorum_NCTC11528	QAfile	Norm.	Public
☑	C_sputorum_ssp_sputorum_NCTC11528_A	QAfile	Norm.	Public
☑	C_upsaliensis_NCTC11541	QAfile	Norm.	Public
☑	C_upsaliensis_NCTC11541_2	QAfile	Norm.	Public
» ☐ **E. coli ...**				
» ☐ **Enterococcus ...**				
» ☐ **Listeria ...**				
» ☐ **Listeria Cheese Project ...**				
» ☐ **Quality Control Species ...**				
» ☐ **Salmonella ...**				
» ☐ **Staphylococcus ...**				
» ☐ **Vibrio cholerae ...**				
» ☐ **Yersinia ...**				

Select species files

A: Pairwise average-linkage clustering
- A: Pairwise average-linkage clustering
- M: Pairwise maximum-linkage clustering
- S: Pairwise single-linkage clustering
- C: Pairwise centroid-linkage clustering

C: correlation
- C: correlation
- A: absolute value of the correlation
- U: uncentered correlation
- X: absolute uncentered correlation
- S: Spearman's rank correlation
- K: Kendall's
- E: Euclidean distance
- B: City-block distance

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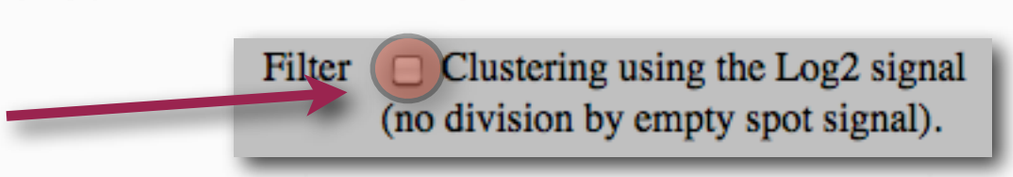
- Normalization.

  - Log2((Signal-Bkg)/Empty) *Selected by default*

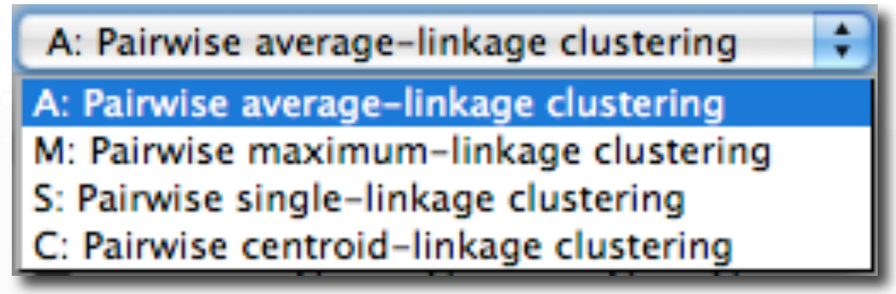
  - Log2(Signal-Bkg)

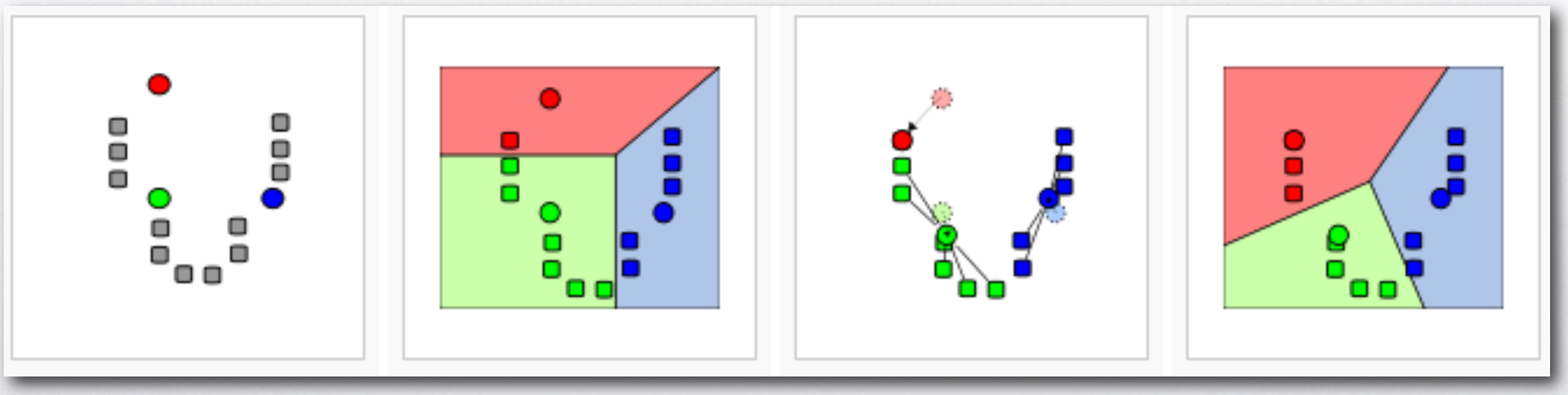


MDM Database

- **Option of 4 different clustering algorithms.**

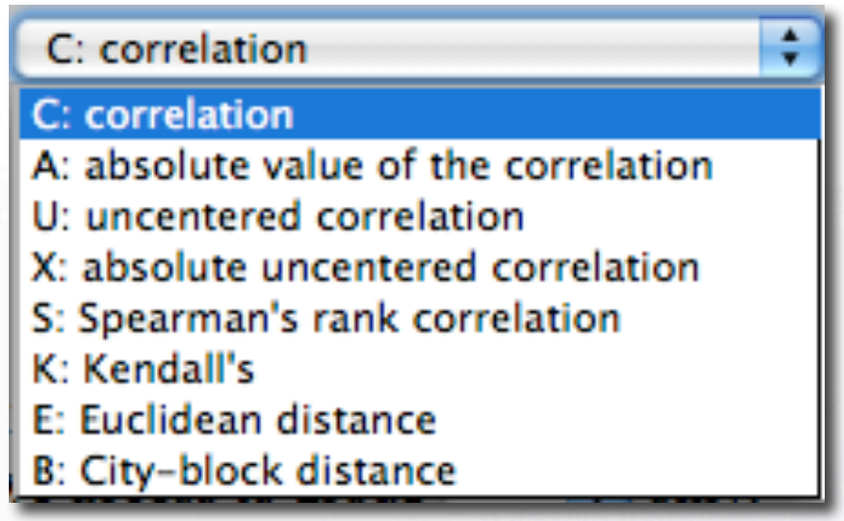
  Specifies how the distance between clusters is defined (clustering algorithm):



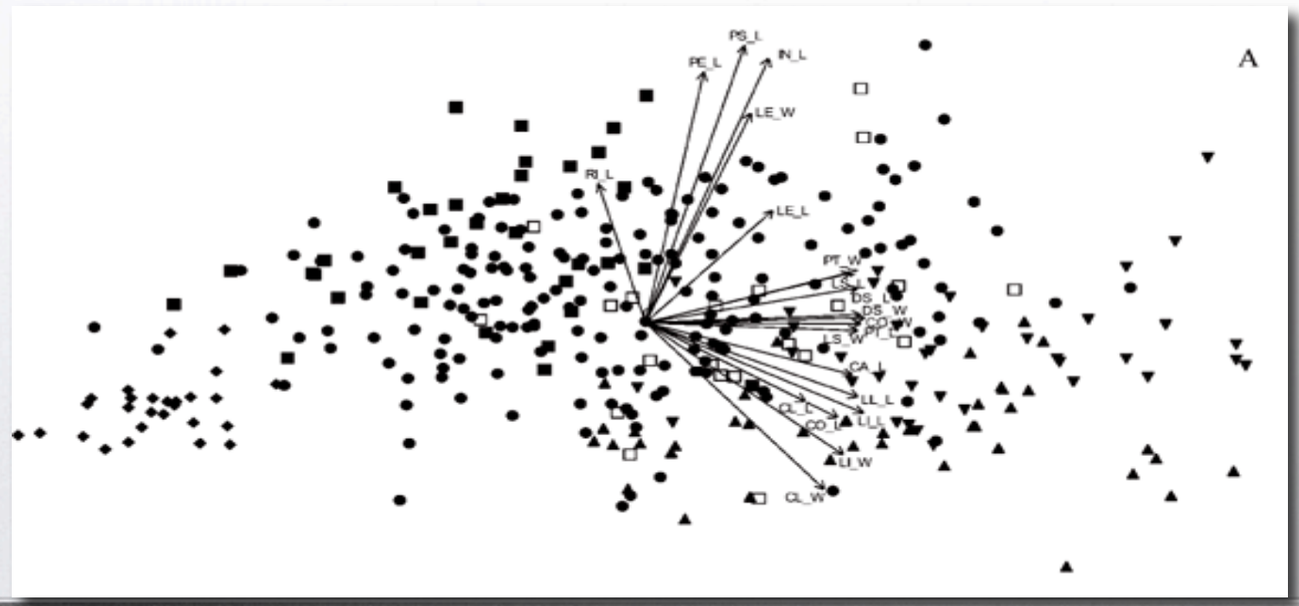


MDM Database

- **Option of 8 different options of distance calculation.**



How the similarity/distance of two elements is calculated



- Parsing normalized files: * * * * * * * *
- Generating Matrix file: * * * * * * *

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IZSAM FORUM

Conference: IZSAM Website		
Forum	**Messages**	**Last Post**
General discussions *General discussions*	4	Microarrays 3/3/10 at 2:50 PM by alfredaADM
Conference: Microarrays		
Forum	**Messages**	**Last Post**
Bacterial zoonoses of swine	0	*None*
Pig bacterial zoonoses • *Listeria* • *Salmonella* • *E. coli* • *Vibrio cholerae* • *Yersinia* • *Staphylococcus* • *Campylobacter* • *Enterococcus* • *Quality Control Species* • *Listeria Cheese Project*	0	*None*
Brucella Mycobacterium • *Brucella* • *Campylobacter* • *E.coli* • *Listeria* • *Mycobacterium* • *Others* • *Mycobacterium_Field* • *Mycobacterium_tuberculosis_complex* • *Mycobacterium_bovine_strains*	0	*None*

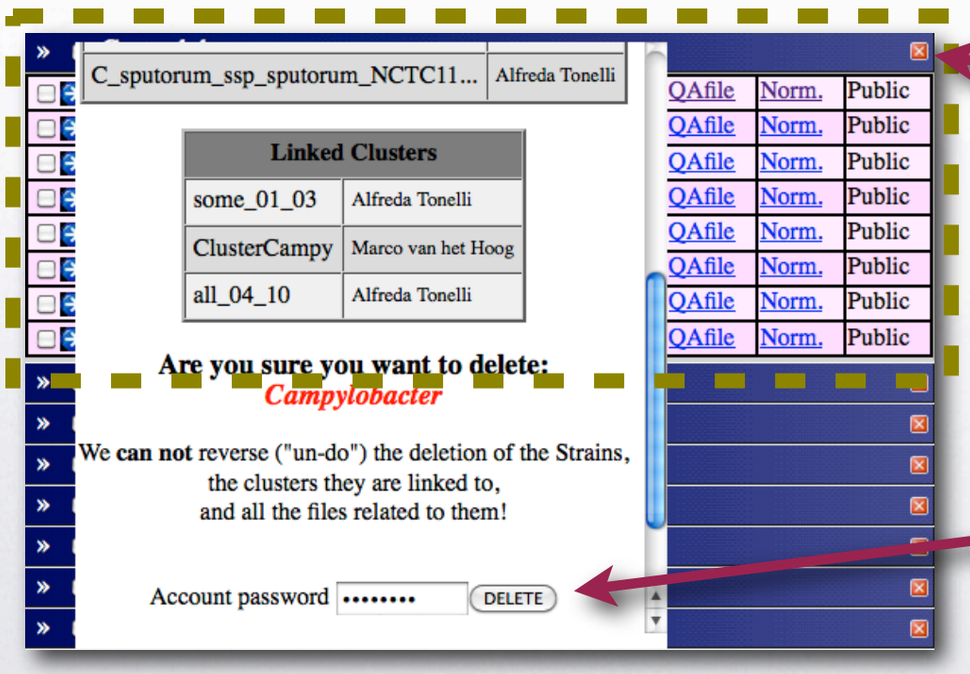
- ***Administration*** features.

Add new Microarrays ...

ADMIN: Add a new Microarray: Name | Version *(V.)* | KeyFile | Browse... | Add

Change the key of a Microarray to a new version ...

Pig bacterial zoonoses ***V4*** **ADMIN:** KeyVersion *(V.)* | KeyFile | Browse... | Add/Update



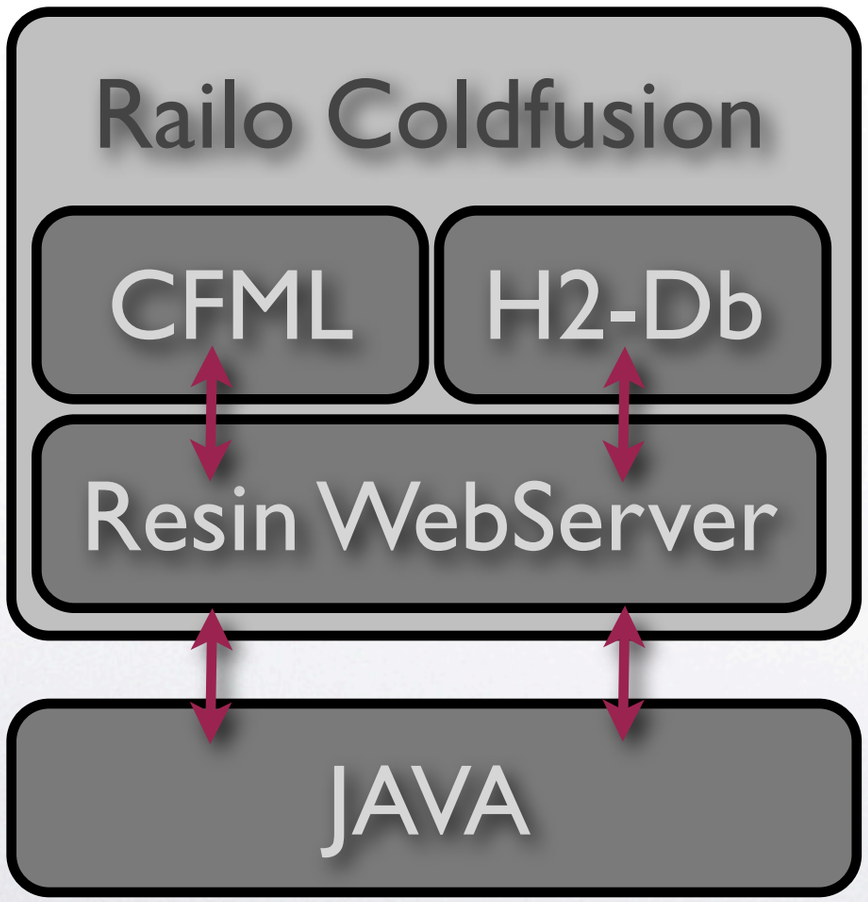
Delete a specie and all the files linked to it.

- QuantArray + Normalized files.

- All the clusters (files) linked to it.

Requires administration password !

• ***Web-server*** platform



- Railo open-source Coldfusion server.
- "H2" (Java) database *(similar to MySQL)*.
- CFML-engine + H2-Db are integrated in one server.
- CFML language is an extension of HTML language.

```
<cfquery name="ClusterStrains" dbtype="query">
    SELECT strainID, specieID AS sID, strainname, speciename, qafile, publicfile, reference, sessionid
    FROM ClusterStrains
</cfquery>
<dt id="#clusterID#Header" name="#clusterID#Header">
    <table width="100%"><td><font size="4" color="WHITE"> &raquo;  #clusterName# ... </font></td>
        <td></td>
    <td align="right"><font color="WHITE">#DateFormat(clusterDate,"YYYY-mmm-dd")#</font>
        <cfif access IS 3 OR ownerID IS memberID><a href="#homepage#?chipID=#chipID#&delClID=#clusterID#"><img
            height="12" src="./gifs/close.jpg" border="0"></a></cfif>
    </td></table>
</dt>
```

http://www.getrailo.org

http://www.h2database.com