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BMT/13/31 Add.
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INTERNATIONAL UNION FOR THE PROTECTION OF NEW VARIETIES OF PLANTS
GENEVA

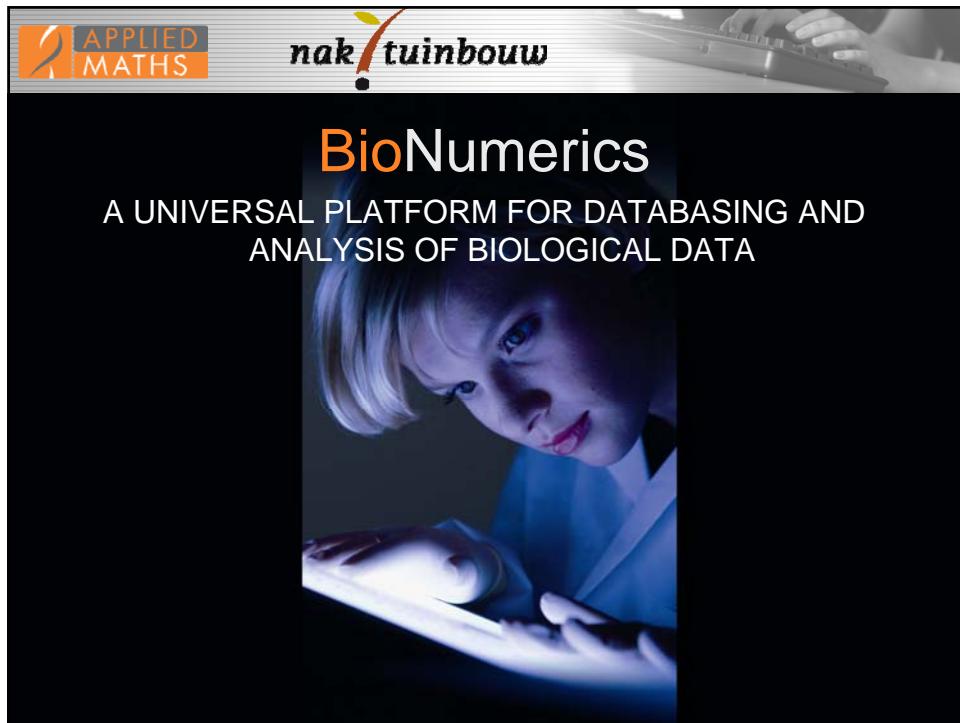
**WORKING GROUP ON BIOCHEMICAL AND MOLECULAR TECHNIQUES,
AND DNA-PROFILING IN PARTICULAR**

**Thirteenth Session
Brasilia, November 22 to 24, 2011**

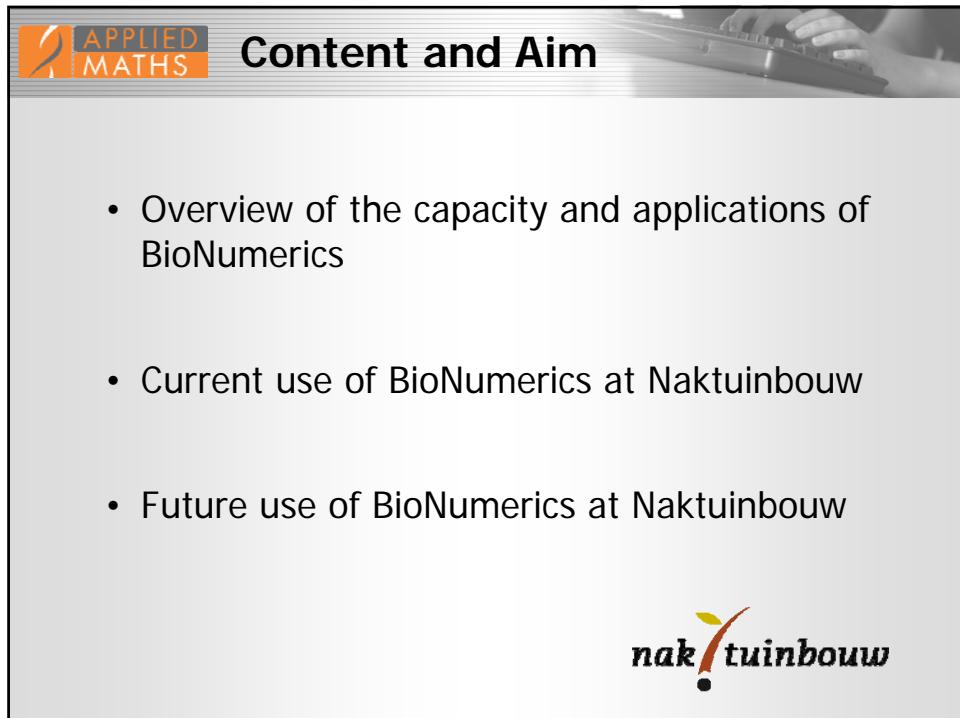
ADDENDUM

**BIONUMERICS: A UNIVERSAL PLATFORM FOR DATABASING AND ANALYSIS
OF BIOLOGICAL DATA**

Document prepared by an expert from the Netherlands



The image shows a screenshot of the BioNumerics software interface. At the top left is the Applied Maths logo. Next to it is the Naktuinbouw logo, which features a stylized orange and yellow 'n' shape followed by the word 'nak tuinbouw'. The main title 'BioNumerics' is displayed in large, bold, orange letters. Below the title, a subtitle reads 'A UNIVERSAL PLATFORM FOR DATABASING AND ANALYSIS OF BIOLOGICAL DATA'. A central image shows a woman in a lab coat looking down at a computer screen displaying a DNA gel electrophoresis pattern.



The image shows a slide titled 'Content and Aim'. The Applied Maths logo is at the top left. The main title 'Content and Aim' is in bold black text. Below the title is a bulleted list:

- Overview of the capacity and applications of BioNumerics
- Current use of BioNumerics at Naktuinbouw
- Future use of BioNumerics at Naktuinbouw

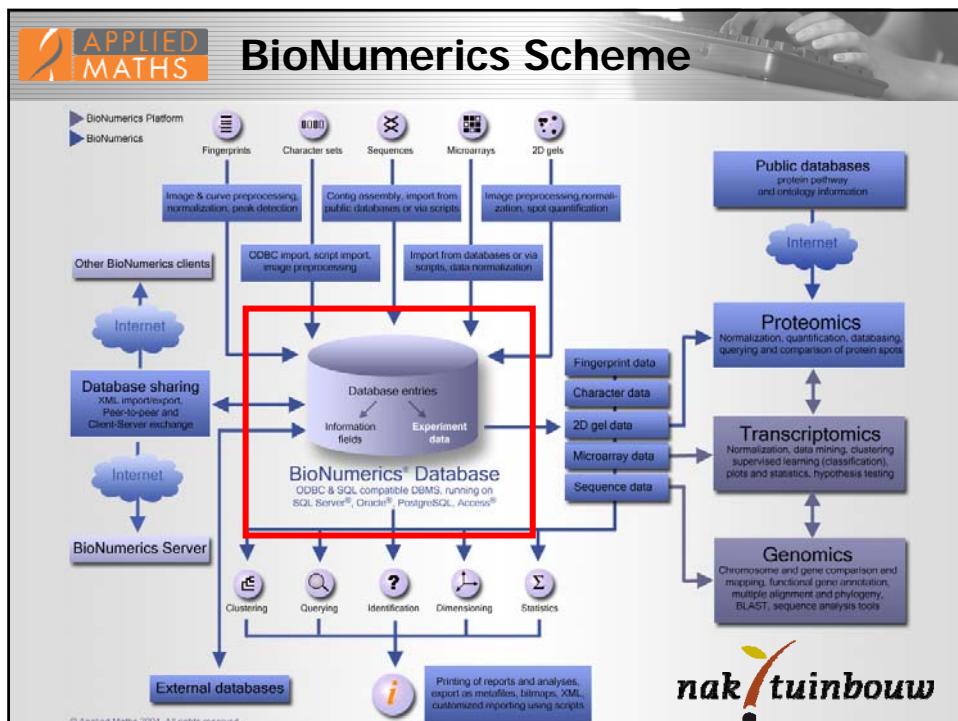
At the bottom right of the slide is the Naktuinbouw logo.

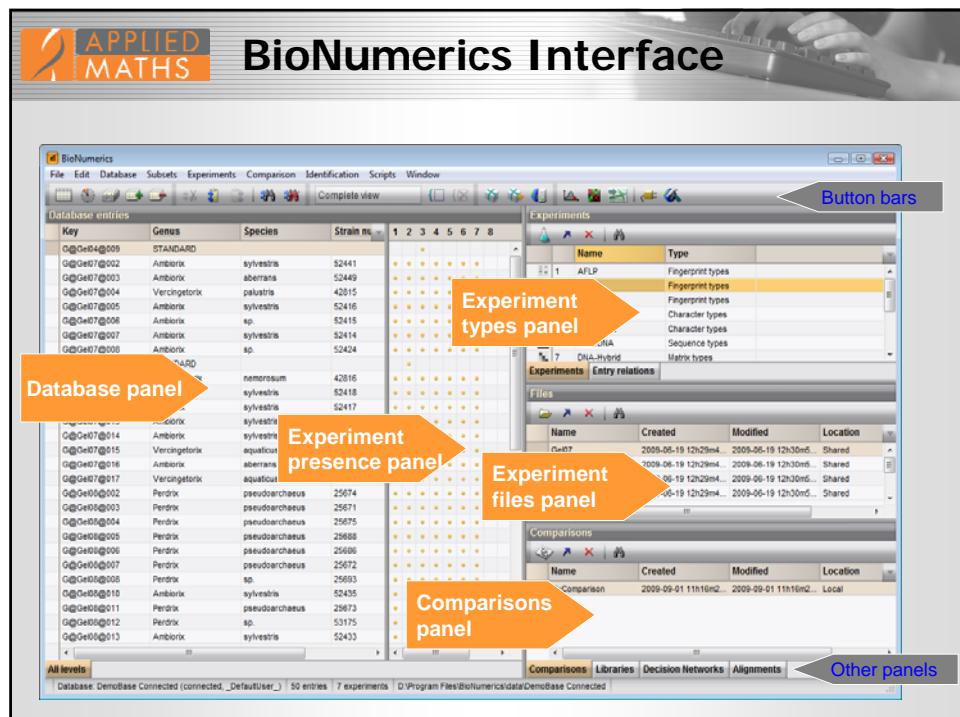
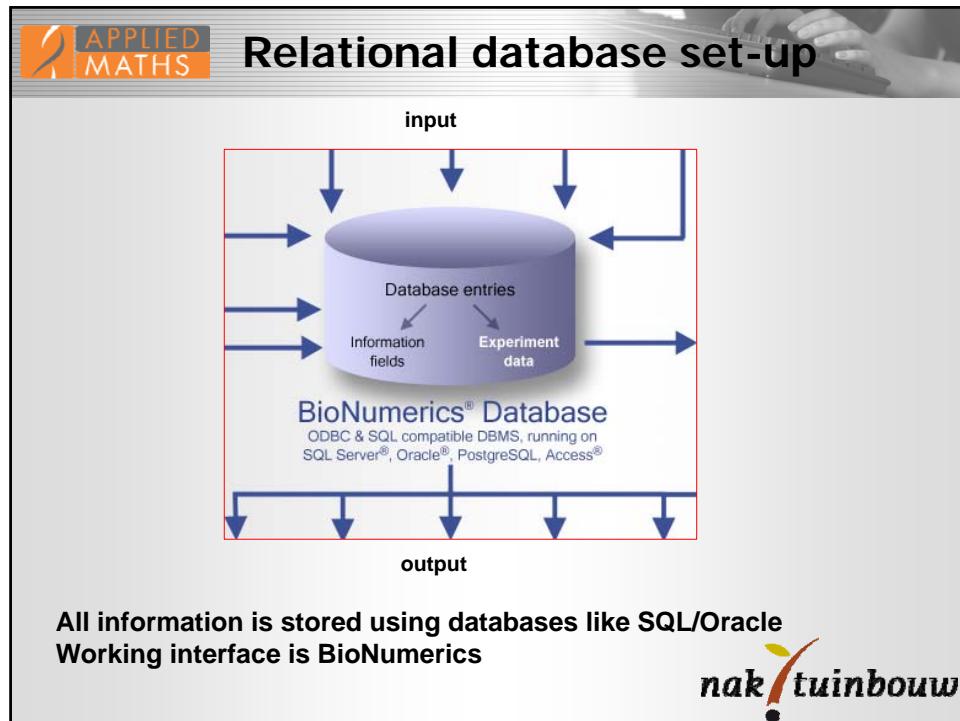
APPLIED MATHS

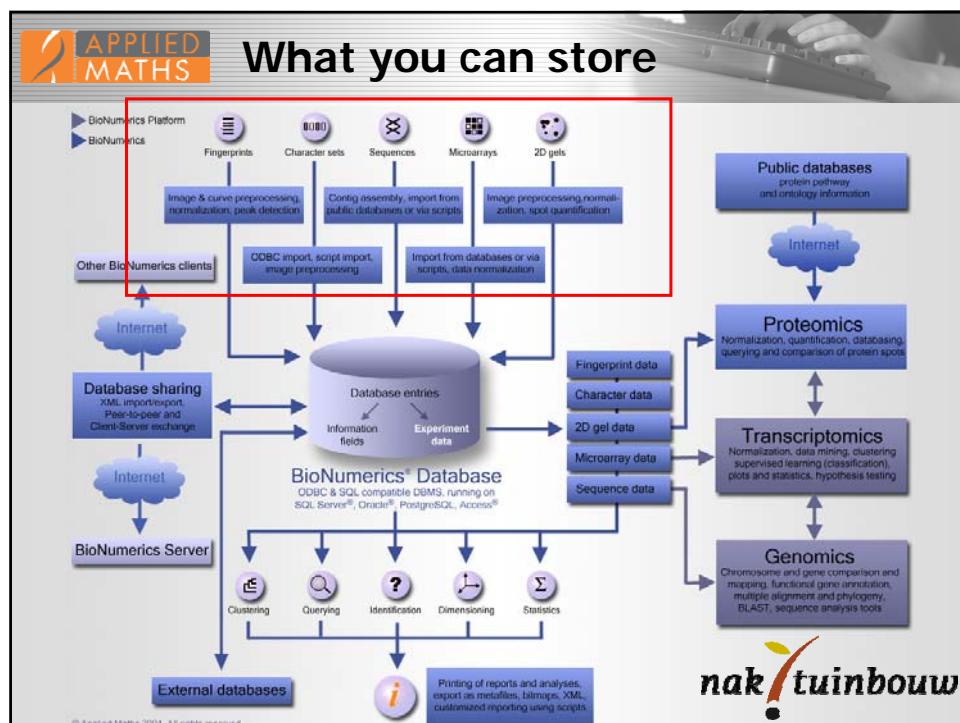
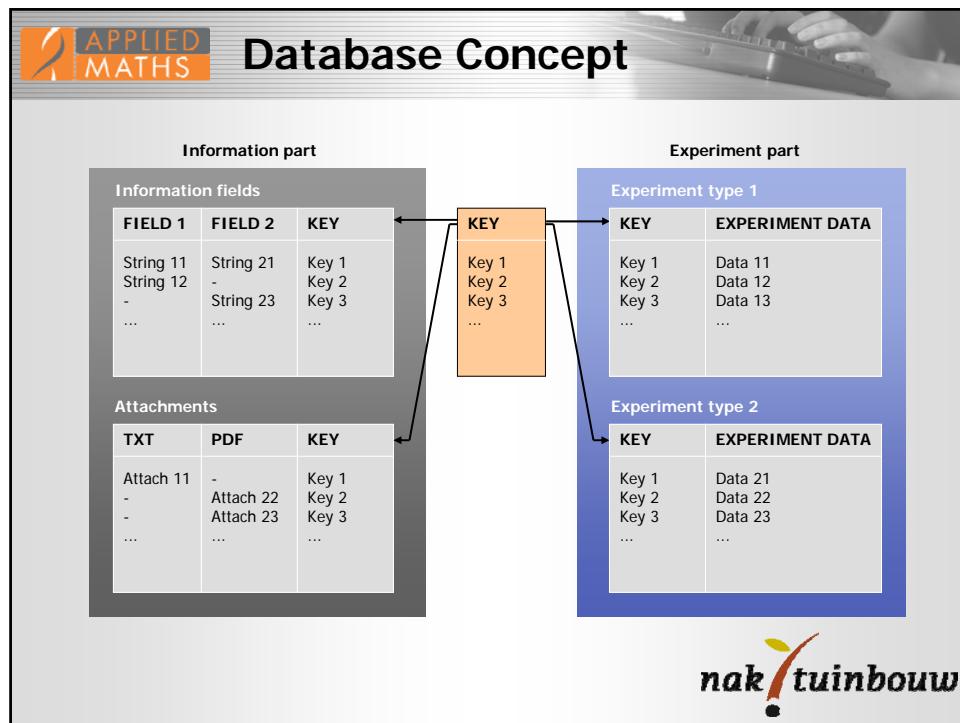
Introduction - Basic features

- Relational database containing taxonomic, typing, and genomic data of biological entities
- Possibility to store many different data sets ("experiments") for each organism or sample studied
- Extensive data import, and export functions
- Advanced statistical analysis, comparison, and identification functions
- Possibility to combine the information from different methods in one single analysis
- Exchange of data over the Internet

nak tuinbouw







 **What you can store**



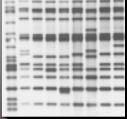
Information fields

- Up to 100 fields (each up to 80 characters)
- Link with external databases



Attachments

- Bitmap images
- HTML and hyperlinks
- Word documents
- Excel spreadsheets
- PDF files
- Text documents



Fingerprints

- 1-D electrophoresis gels scanned as bitmaps (RFLP, PFGE, Ribotyping, RAPD, DGGE & TGGE, etc.)
- Sequencer chromatogram files (AFLP, VNTR, HDA, etc.)
- Spectrophotometric files
- MALDI & SELDI profiles
- All other kinds of densitometric profiles

 **What you can store**



Character data

- Phenotypic test panels (API, Biolog, Vitec, etc.)
- Antibiotic resistance profiles
- Fatty acid and quinolone profiles
- Hybridization blots such as Spoligo typing
- Biochemical & morphological features
- Microarray & Genechip data
- Etc.

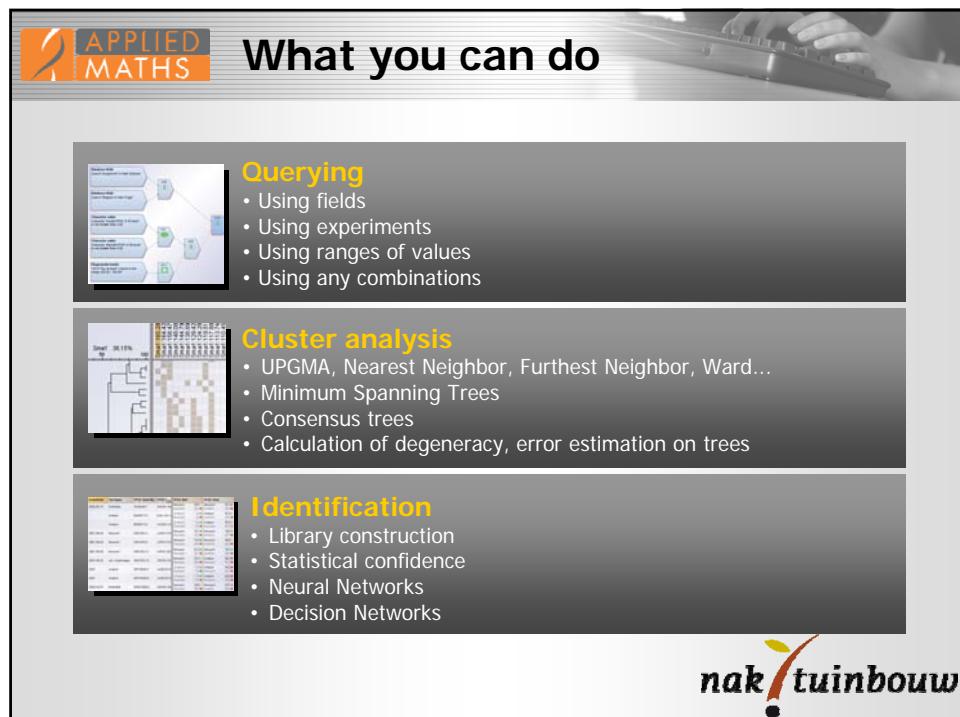
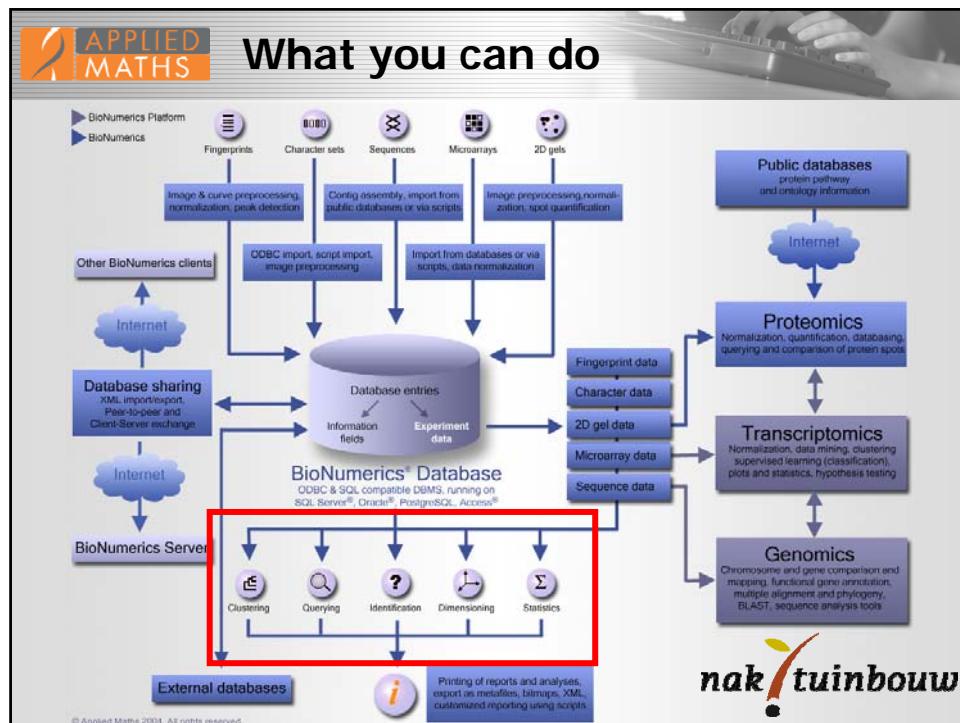


Sequence data

- Sequence trace (chromatogram) files
- Formatted sequences from public databases (EMBL, GenBank)
- Aligned sequences such as from RDP
- Amino acid sequences



2-D gels
Trendcurve and kinetic reading data



The image shows a screenshot of the Applied Maths software interface. At the top left is the logo 'APPLIED MATHS'. To its right, the text 'What you can do' is displayed in large, bold, black font. In the background, a person's hands are visible on a keyboard. The interface is divided into three main sections, each with an icon and a title:

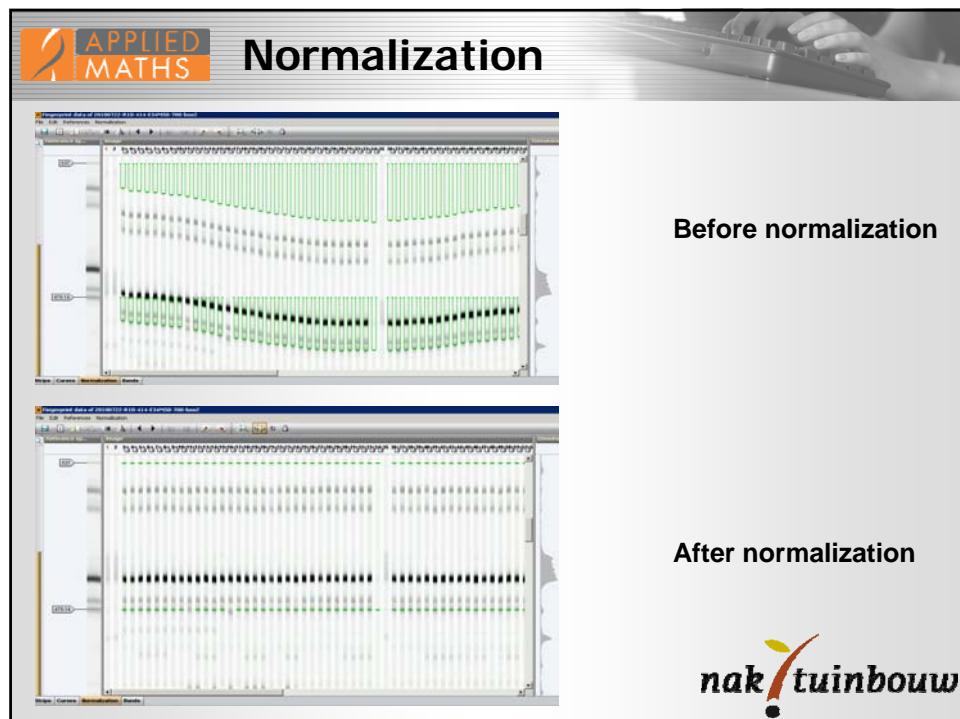
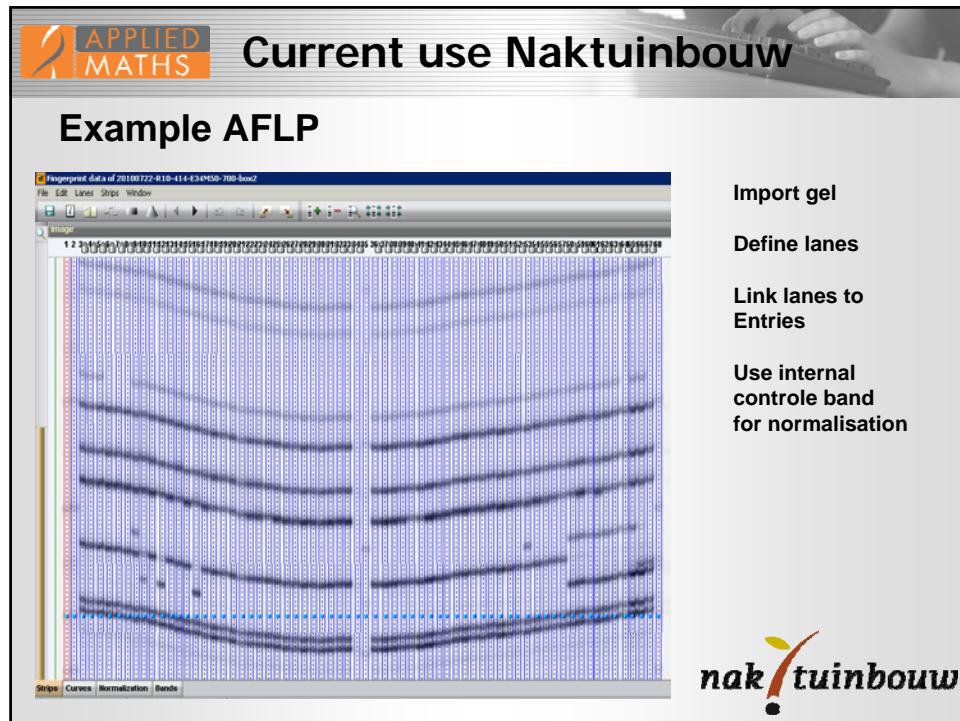
- Dimensioning, ordination**: An icon shows a 3D scatter plot of data points. Below it is a bulleted list:
 - Principal Components
 - Multi-Dimensional Scaling
 - Self-Organizing Maps
- Phylogeny**: An icon shows a phylogenetic tree. Below it is a bulleted list:
 - Pairwise & multiple sequence alignment
 - Neighbor Joining
 - Parsimony
 - Maximum likelihood
- Statistics**: An icon shows a 3D bar chart. Below it is a bulleted list:
 - MANOVA
 - Discriminant analysis
 - K-means partitioning, Jackknife,...
 - Numerous statistical tests and charts

At the bottom right of the interface is the 'nak tuinbouw' logo.

The image shows a screenshot of the Applied Maths software interface. At the top left is the logo 'APPLIED MATHS'. To its right, the text 'Current use Naktuinbouw' is displayed in large, bold, black font. In the background, a person's hands are visible on a keyboard. The interface lists six numbered steps:

1. Storage of sample information and experiment data
2. Query
3. Import of raw fingerprint data into BN
4. Analysis of the DNA fingerprints
5. Clustering/Ordination/ Verification
6. Identification Libraries

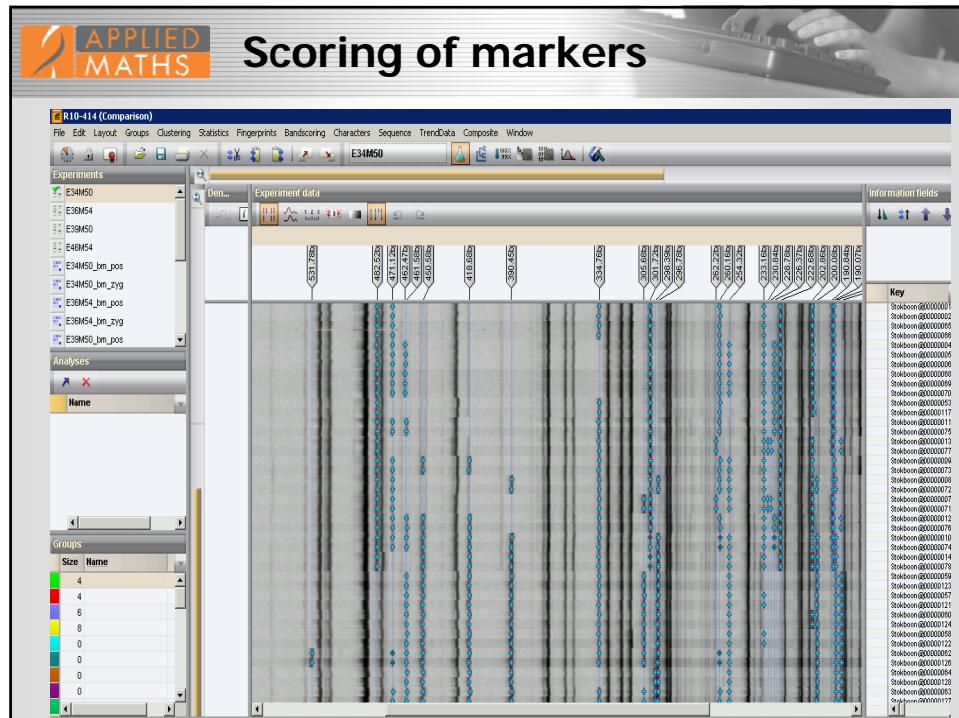
At the bottom right of the interface is the 'nak tuinbouw' logo.

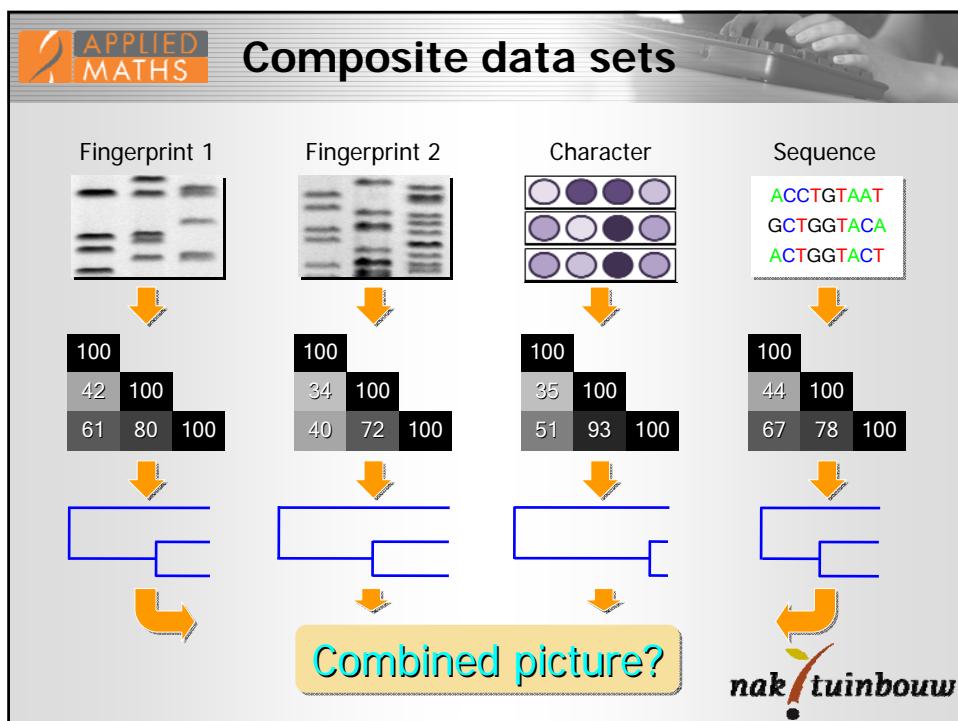
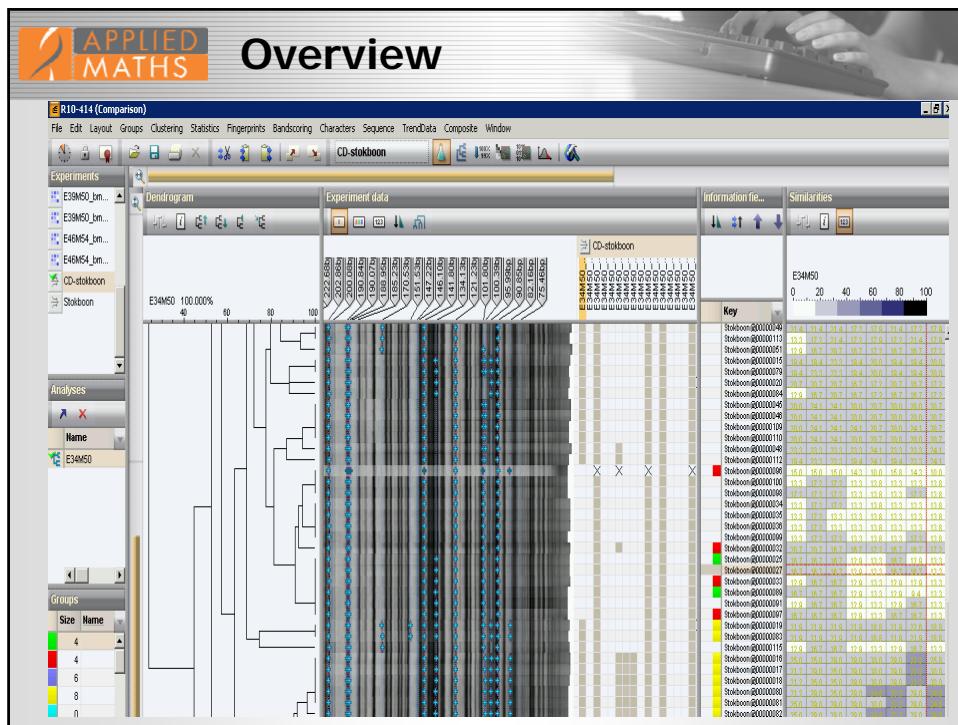


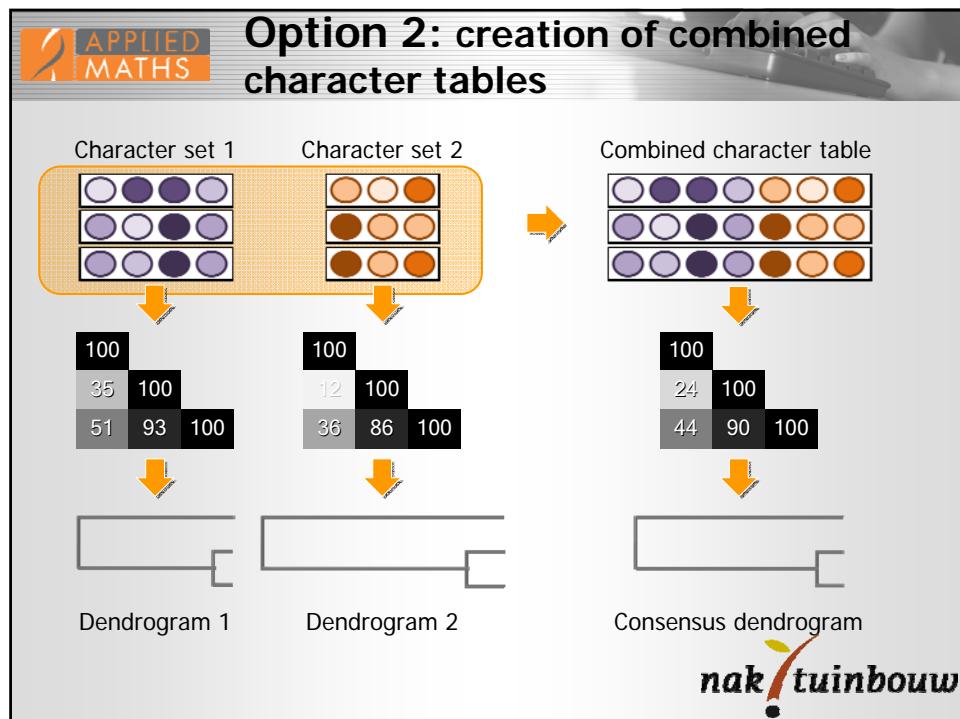
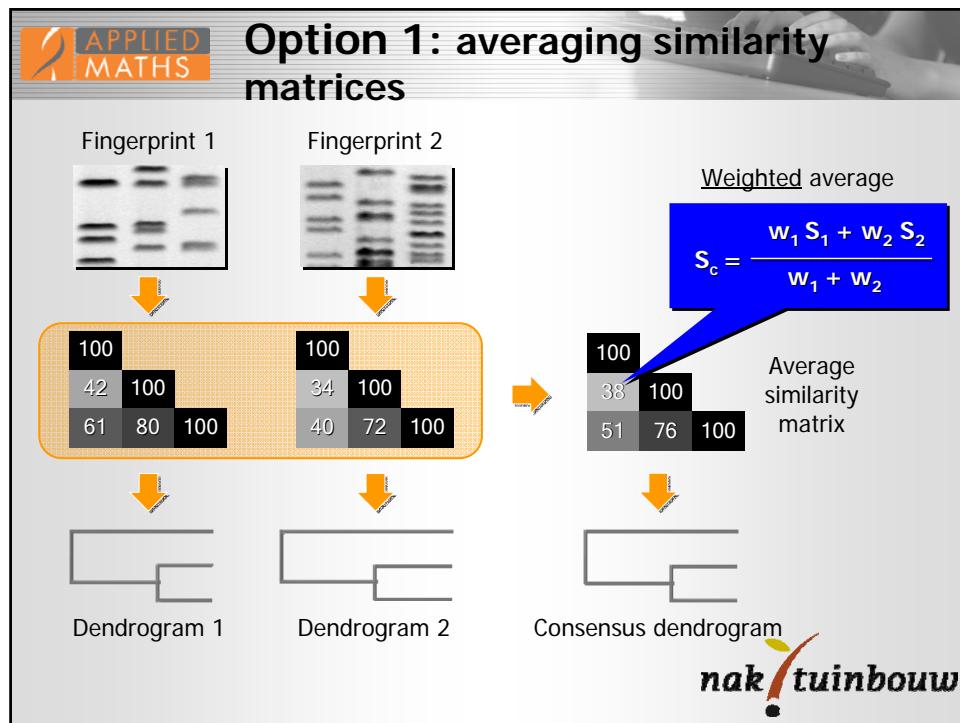
Applied Maths BioNumerics Comparison

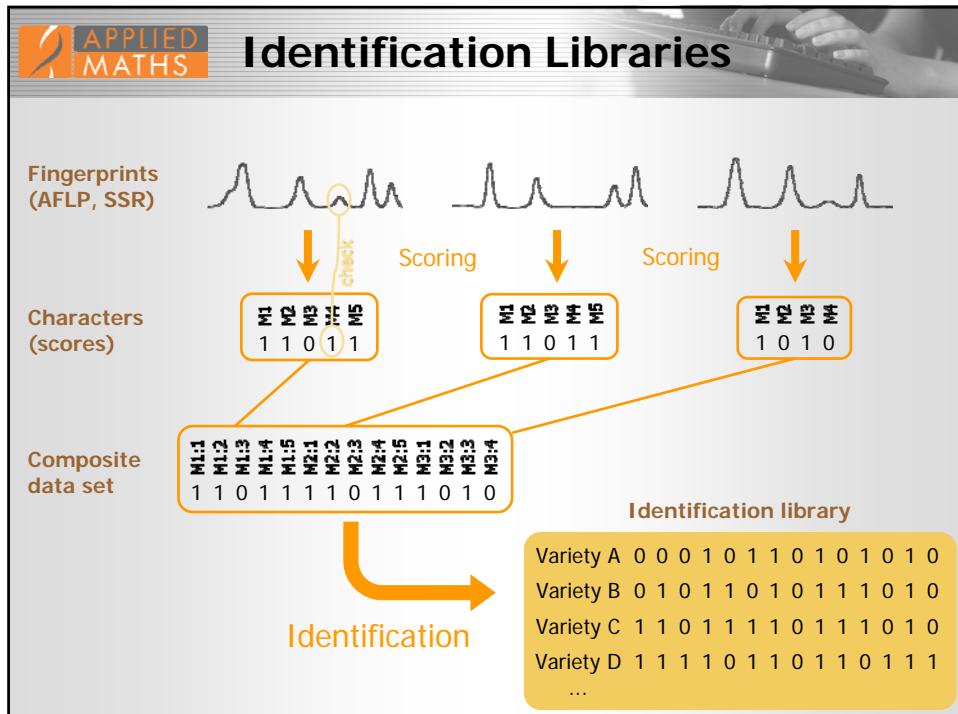
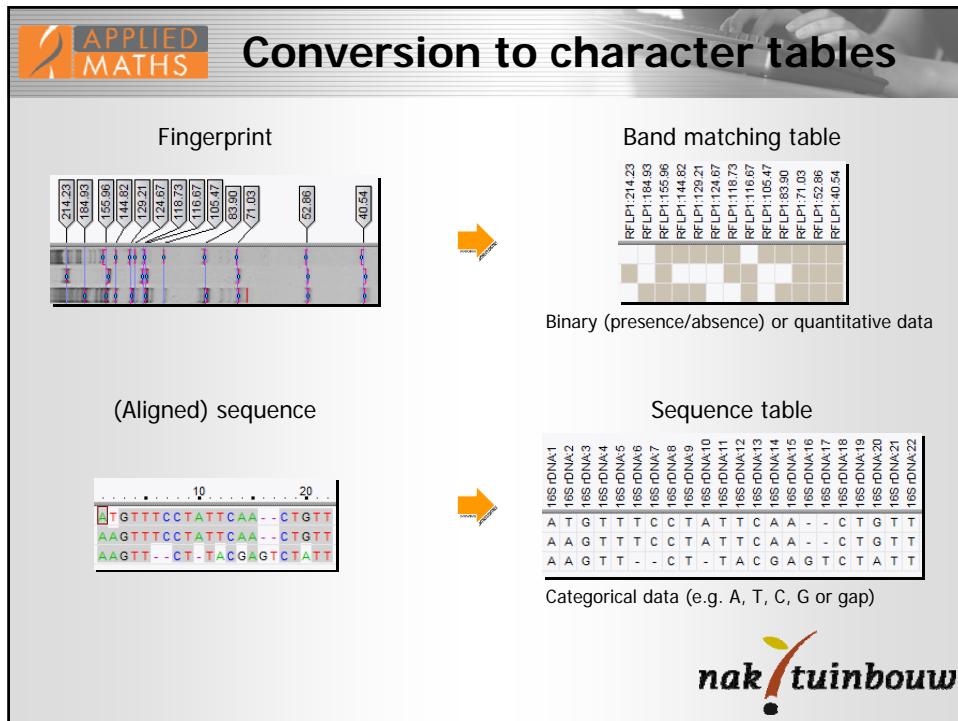
The screenshot shows the BioNumerics software interface for comparison analysis. The main window displays a database of samples (Stabion@...) with columns for Key, Pijnadresnr, Aficode, Vastgestelde naam, Voorklopte aand..., and Aanvraagnr. The experiments section shows a grid of samples (1-10) across lanes (1-11). The right side of the interface includes tabs for Experiments, Comparisons, Alignments, and Annotations.

**Open comparison window
To compare several different experiments from different samples**









Identification Libraries

Unknowns	sample number	sample number given by supplier	variety name from analysis	Matches
981	onbekend	Nicola		CPVO
984	10.203	Bellini		Nicola 100
1752		Désirée		Bellini 100
1753		Désirée		Désirée 100
1754	labor 71039	Rode Pipo		Désirée 100
				Rode Pipo 98.2

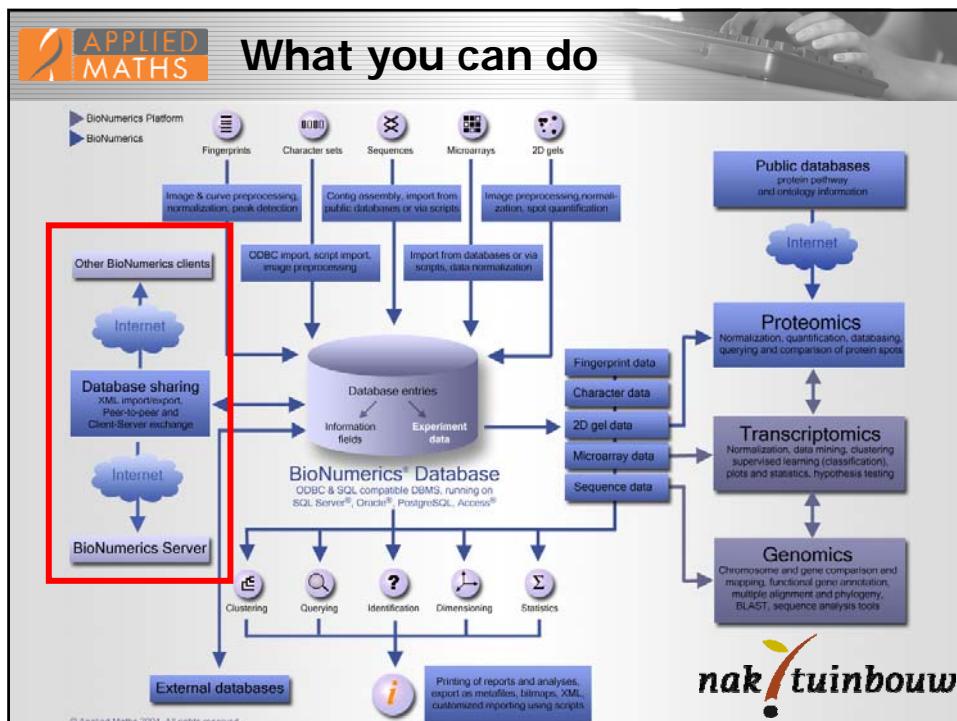
Best hit for unknown Sample with samples in library

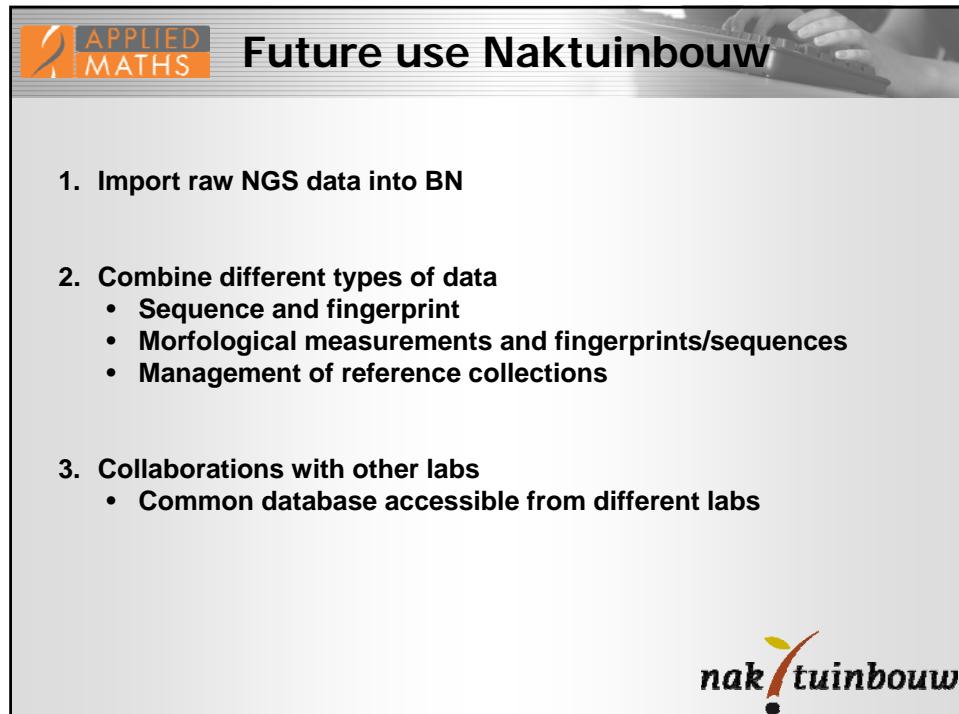
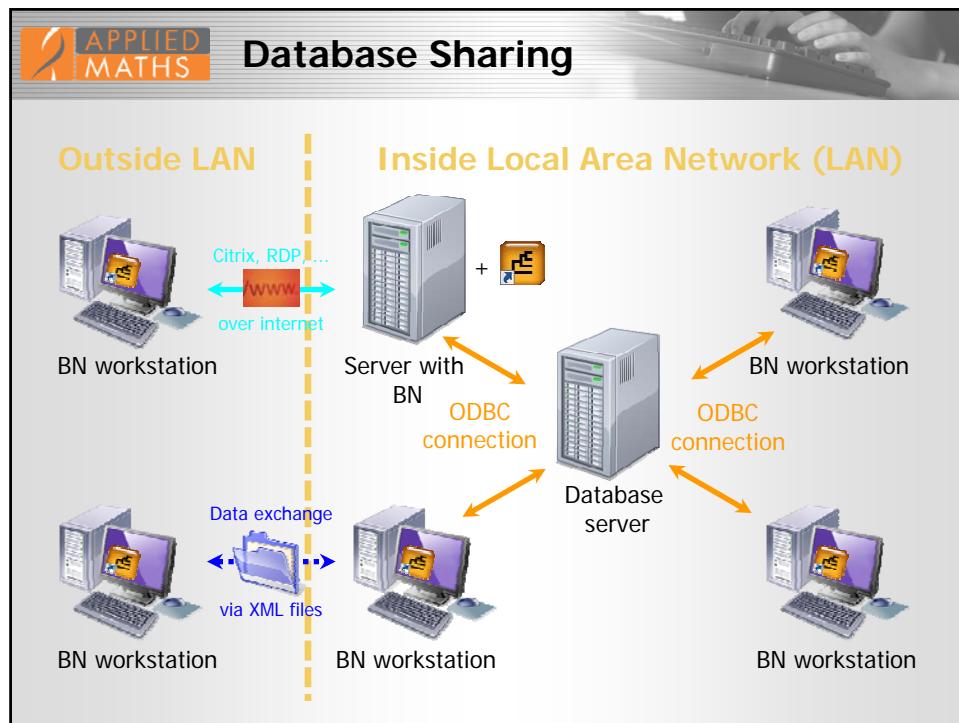
Comparison settings

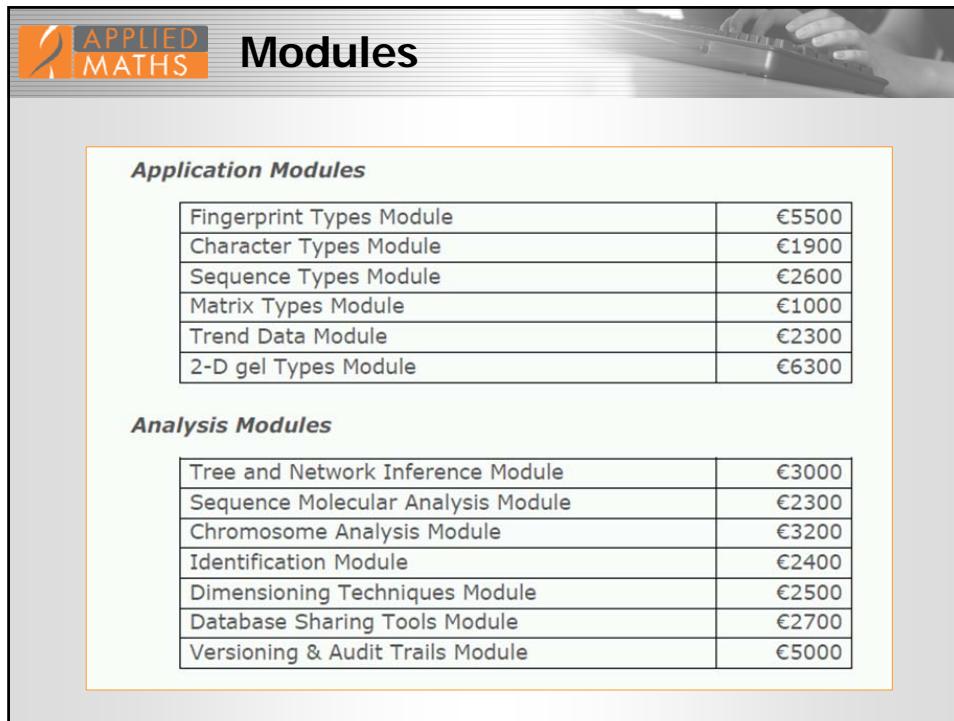
CPVO settings

- Comparison
 - Similarity coefficient
 - Average from experiments
SSR1_bm_zyg + STM0019_bm_zyg + STM2005_bm_zyg + STM2028_bm_zyg + t
 - SSR1_bm_zyg settings
SSR1_bm_zyg numerical values, closed data set (14 characters)
 - Comparison
 - Similarity coefficient
 - Pearson correlation
Use square root conversion: No
Negative similarities: Clip to zero
 - STM0019_bm_zyg settings
STM0019_bm_zyg numerical values, closed data set (10 characters)
 - Comparison
 - Similarity coefficient
 - Pearson correlation
Use square root conversion: No

nak tuinbouw







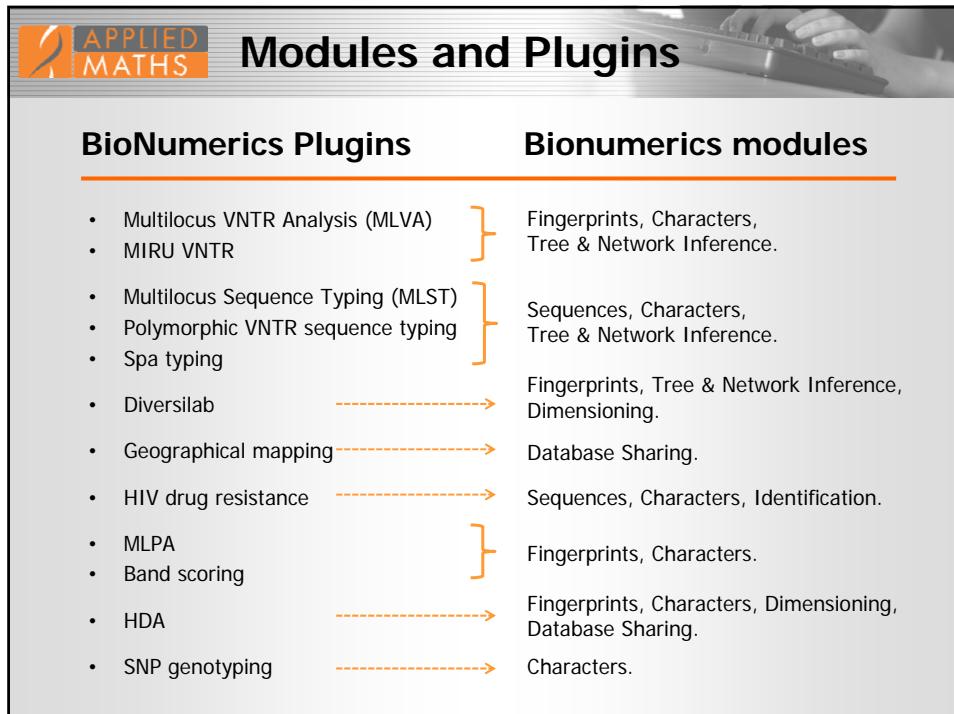
APPLIED MATHS Modules

Application Modules

Fingerprint Types Module	€5500
Character Types Module	€1900
Sequence Types Module	€2600
Matrix Types Module	€1000
Trend Data Module	€2300
2-D gel Types Module	€6300

Analysis Modules

Tree and Network Inference Module	€3000
Sequence Molecular Analysis Module	€2300
Chromosome Analysis Module	€3200
Identification Module	€2400
Dimensioning Techniques Module	€2500
Database Sharing Tools Module	€2700
Versioning & Audit Trails Module	€5000



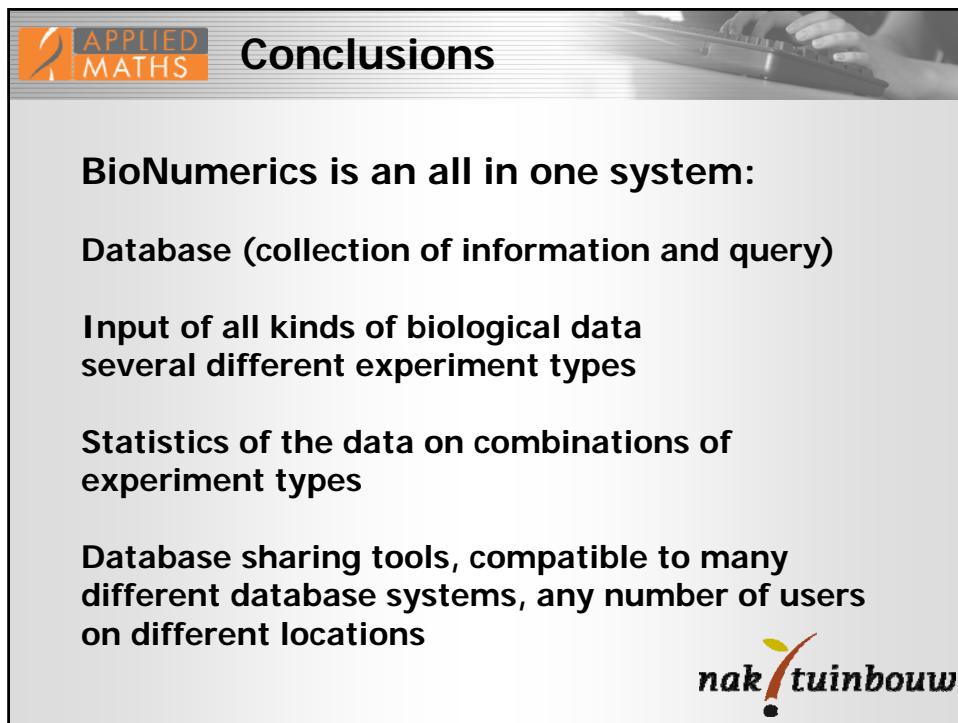
APPLIED MATHS Modules and Plugins

BioNumerics Plugins

- Multilocus VNTR Analysis (MLVA)
- MIRU VNTR
- Multilocus Sequence Typing (MLST)
- Polymorphic VNTR sequence typing
- Spa typing
- Diversilab
- Geographical mapping
- HIV drug resistance
- MLPA
- Band scoring
- HDA
- SNP genotyping

Bionumerics modules

- Fingerprints, Characters, Tree & Network Inference.
- Sequences, Characters, Tree & Network Inference.
- Fingerprints, Tree & Network Inference, Dimensioning.
- Database Sharing.
- Sequences, Characters, Identification.
- Fingerprints, Characters.
- Fingerprints, Characters, Dimensioning, Database Sharing.
- Characters.



The slide has a header section with the Applied Maths logo and the word "Conclusions". Below this, the text "BioNumerics is an all in one system:" is followed by four bullet points describing the software's features: "Database (collection of information and query)", "Input of all kinds of biological data several different experiment types", "Statistics of the data on combinations of experiment types", and "Database sharing tools, compatible to many different database systems, any number of users on different locations". At the bottom right is the logo for "nak tuinbouw".

Conclusions

BioNumerics is an all in one system:

- Database (collection of information and query)**
- Input of all kinds of biological data
several different experiment types**
- Statistics of the data on combinations of
experiment types**
- Database sharing tools, compatible to many
different database systems, any number of users
on different locations**

nak tuinbouw

[End of document]