

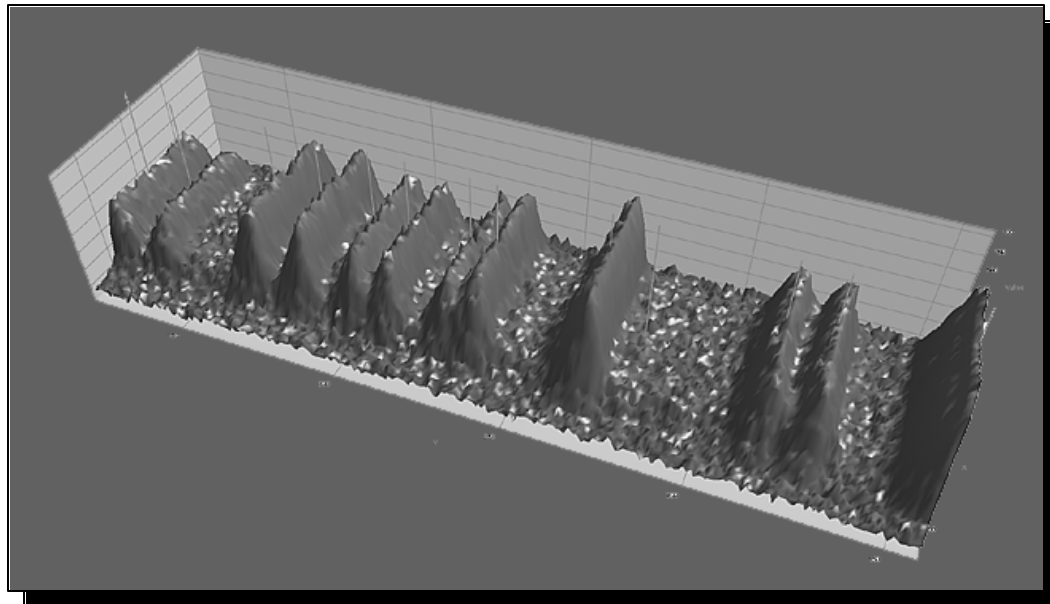
BioNumerics version 3.5

New features

“PulseNet selection”

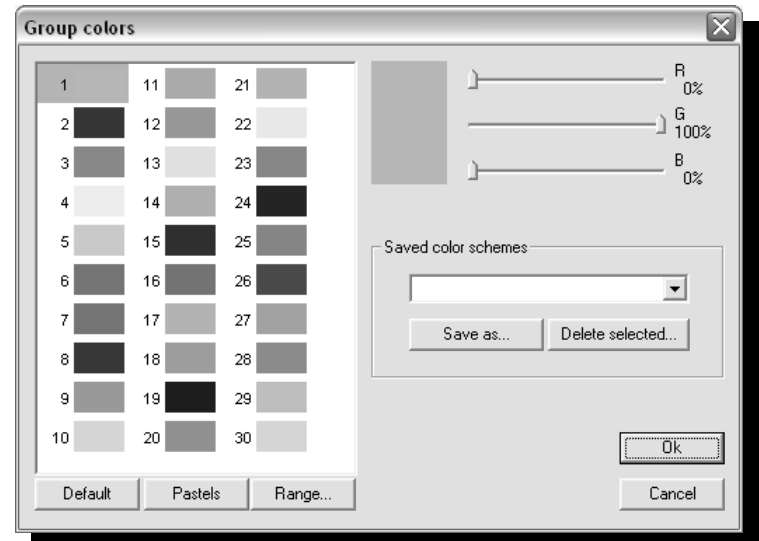
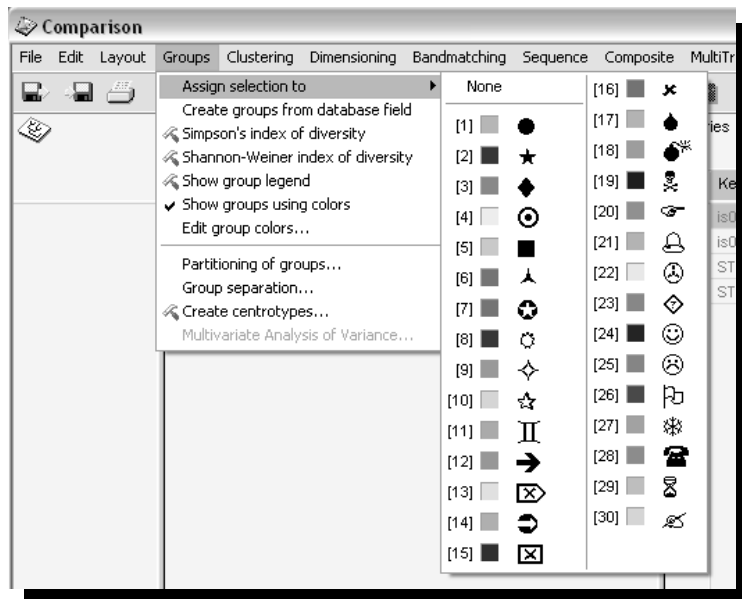
Gel processing

- Band search:
 - Possible to keep existing bands
 - Possible to search bands on a single lane or on all lanes
- Show 3D view of gel or lane
- On/Off condition of "Show distortion bars" is saved



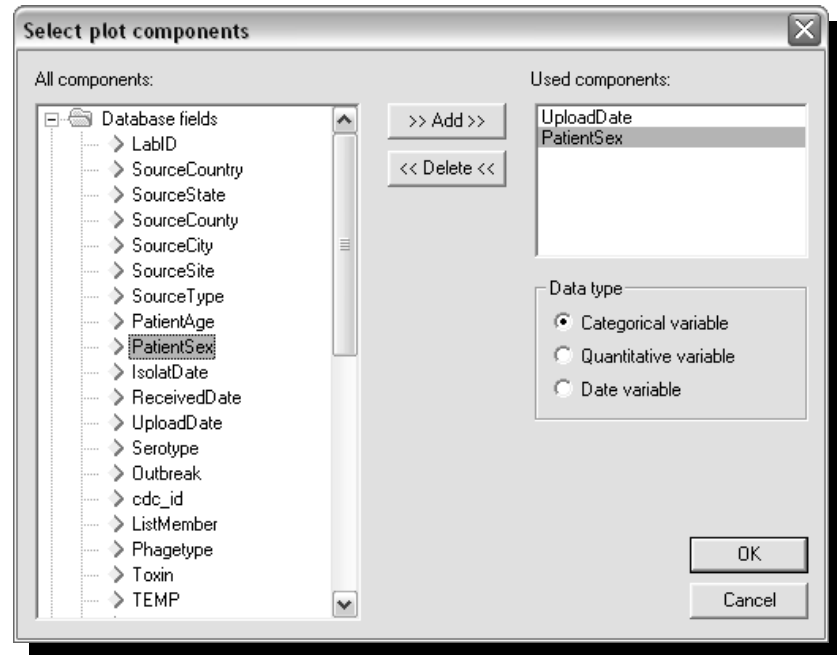
Comparison

- Groups:
 - Up to 30 different group colors are available
 - Possible to modify the group colors



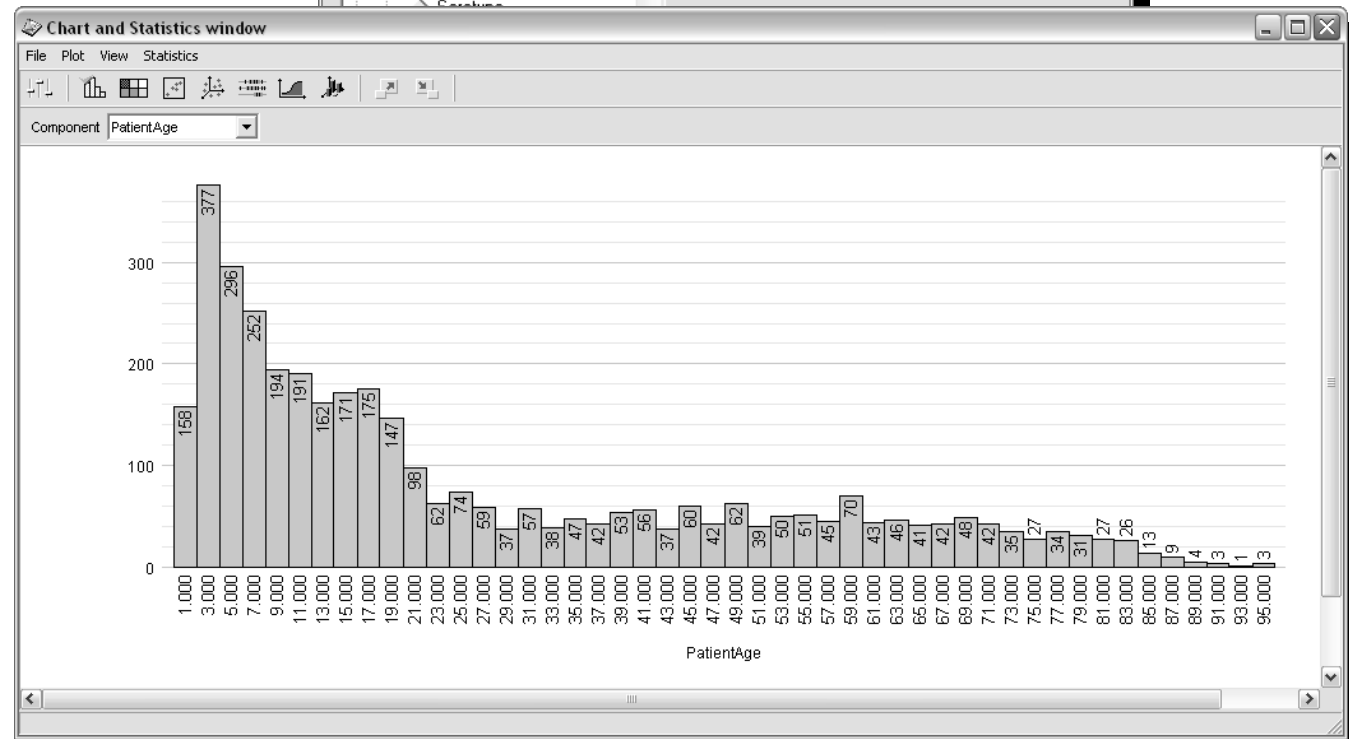
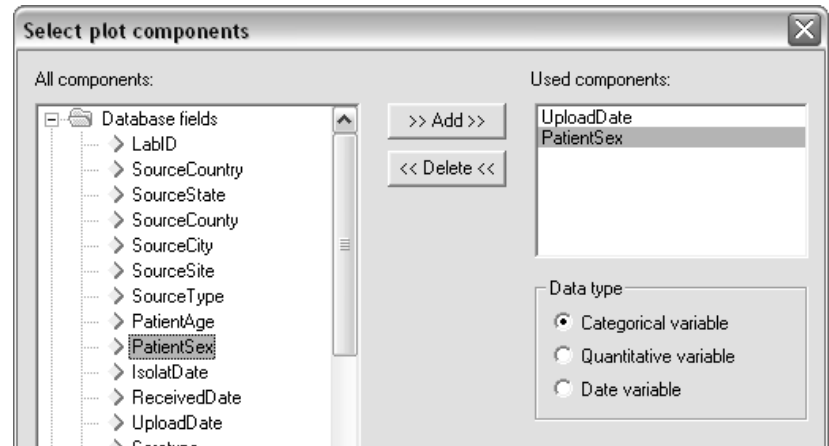
Comparison

- Plot & statistics
 - I. Chose components



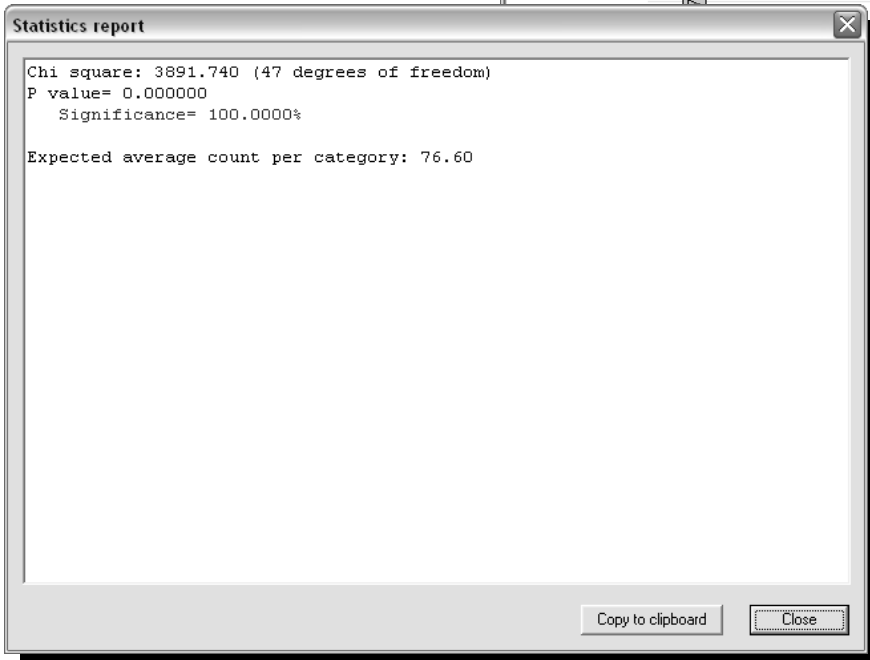
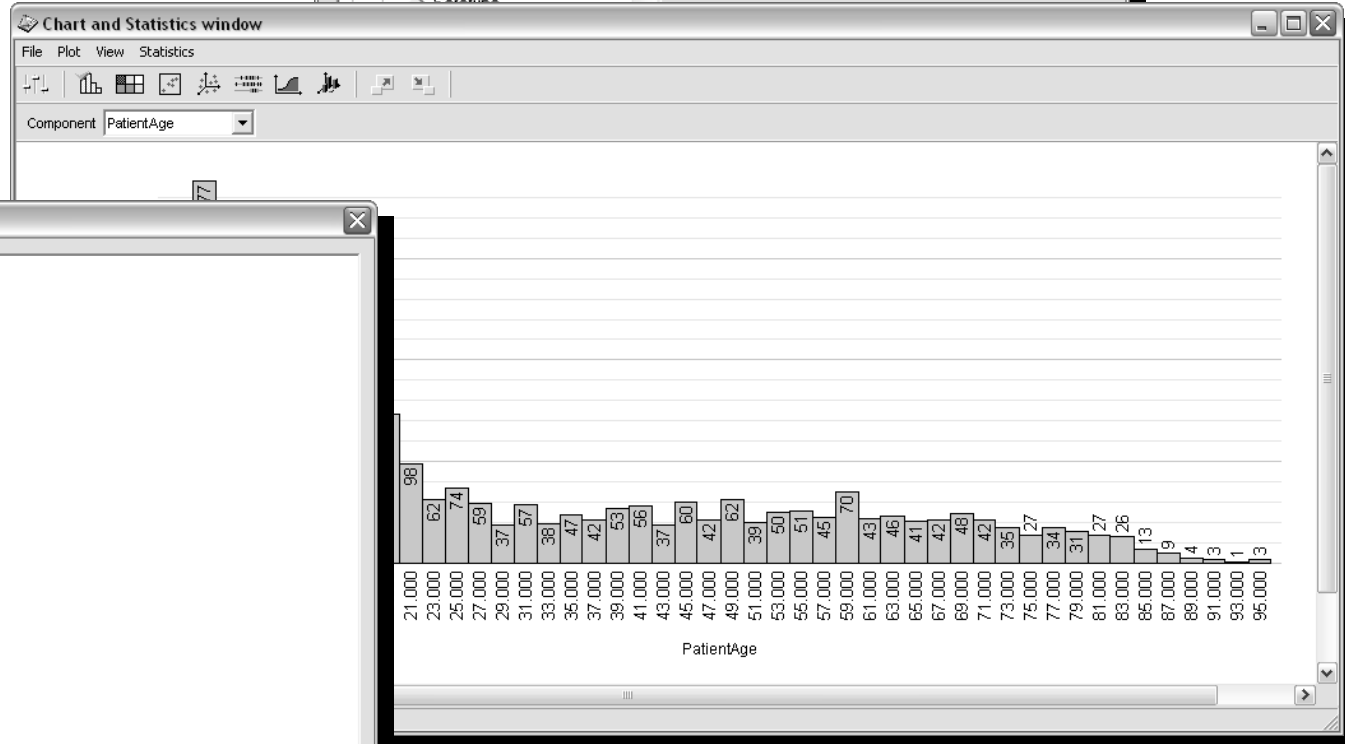
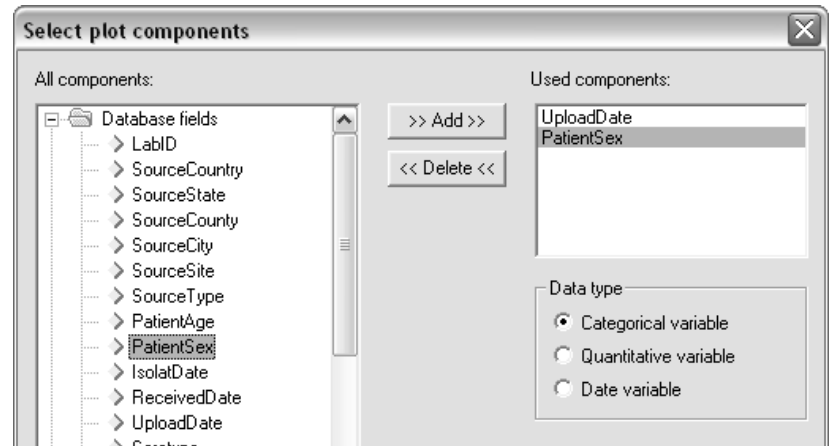
Comparison

- Plot & statistics
 - I. Chose components
 - II. Chose plot type



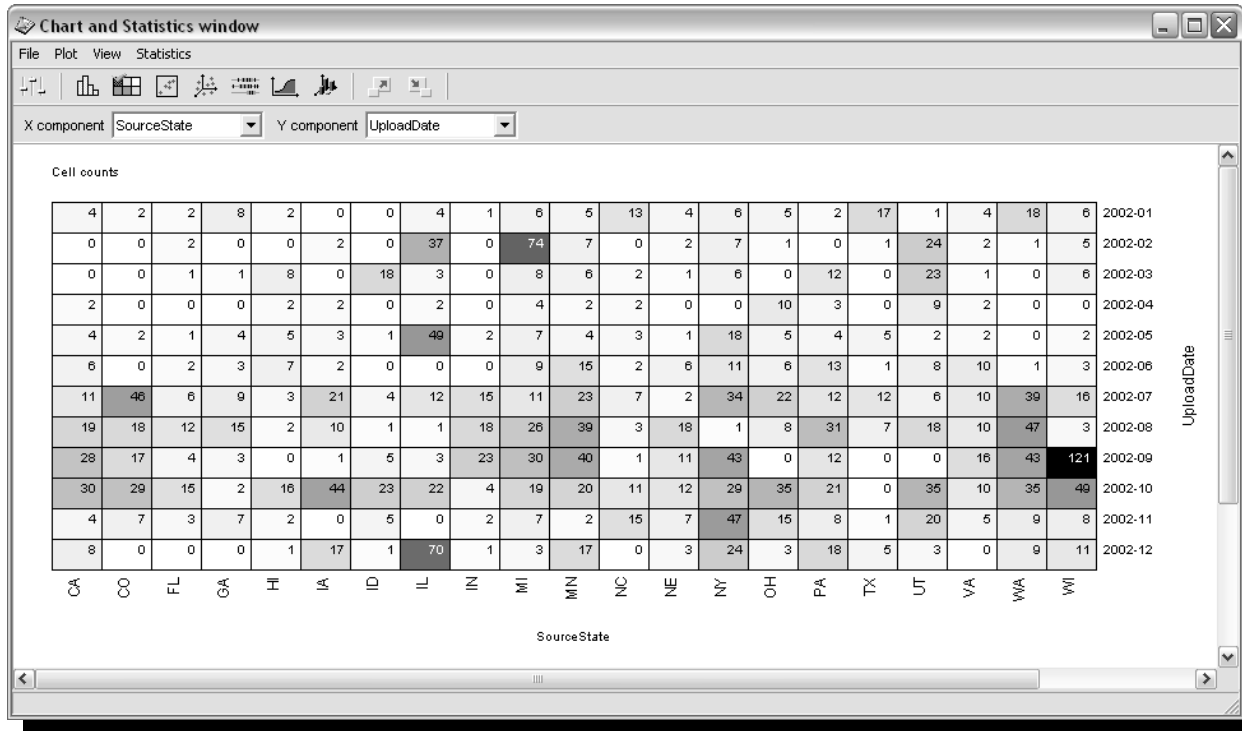
Comparison

- Plot & statistics
 - I. Chose components
 - II. Chose plot type
 - III. Chose statistic



Comparison

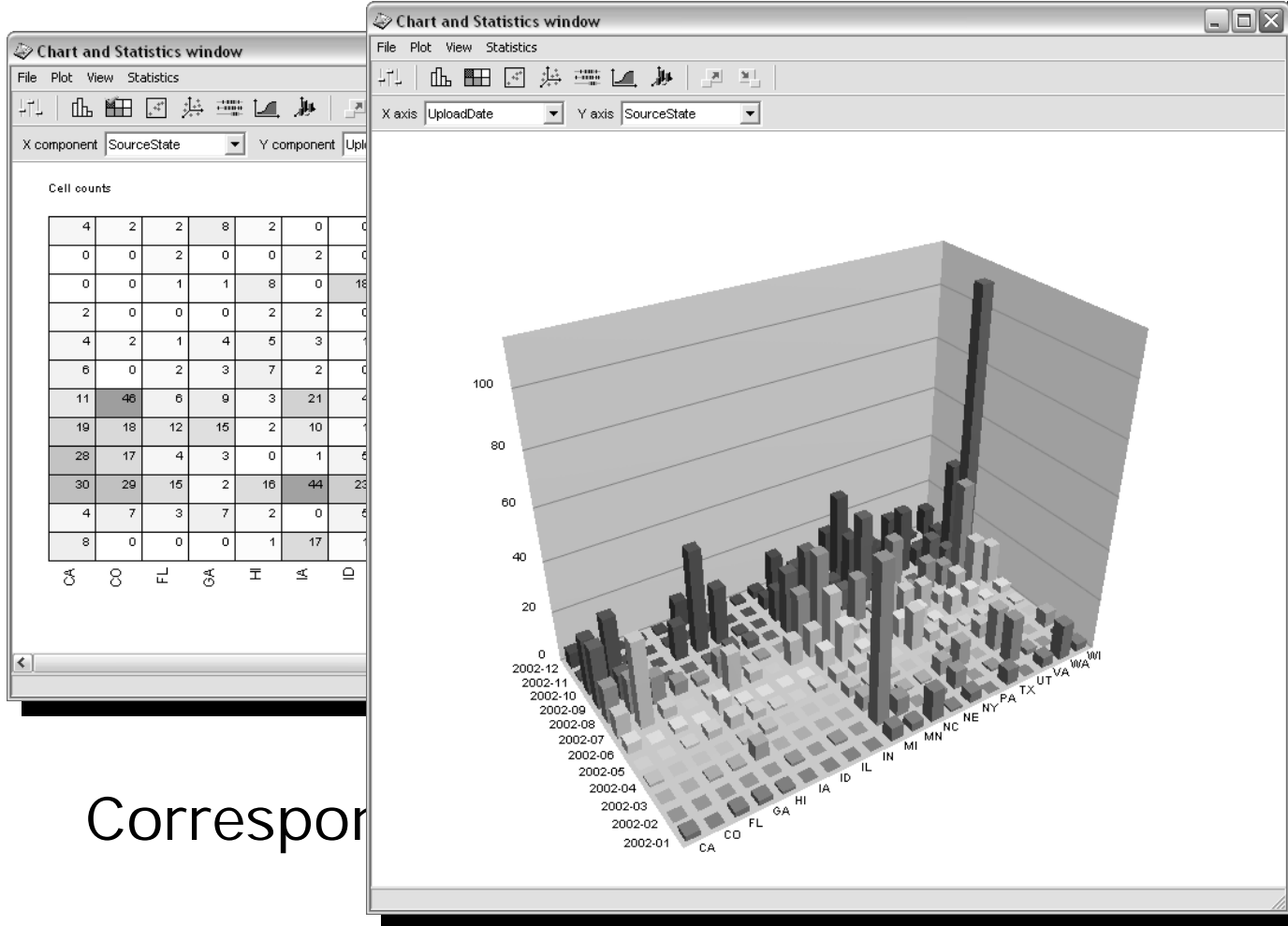
- Contingency tables



Correspondence test (chi-square, Cramer's V)

Comparison

- Contingency tables

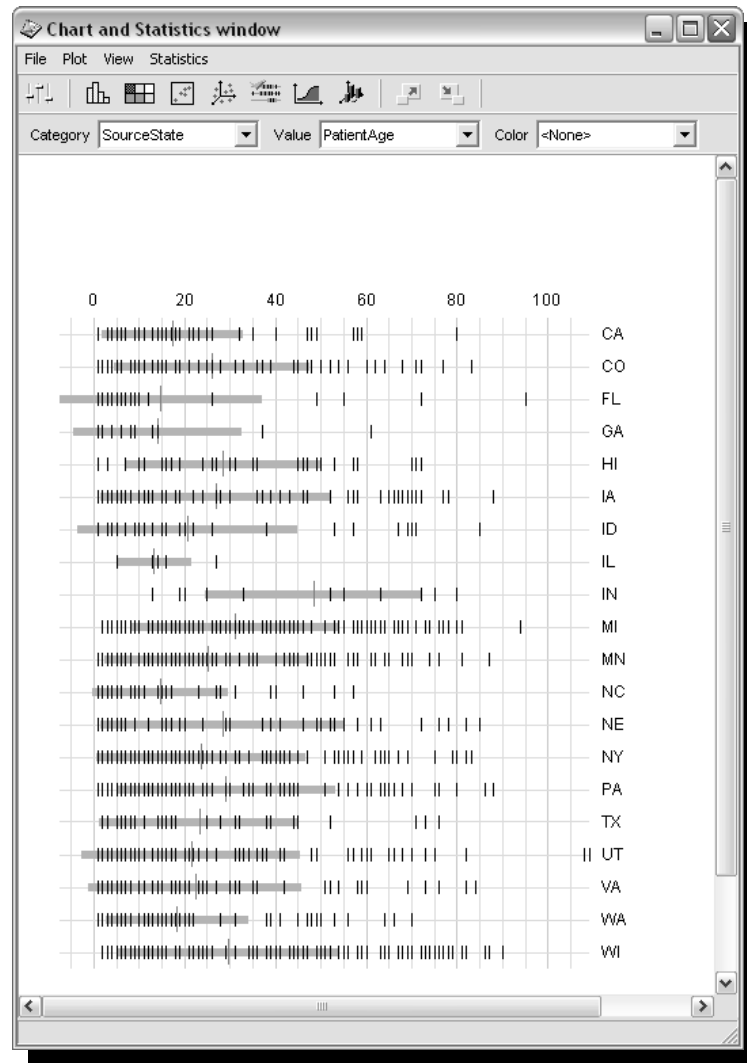


Correspon

s V)

Comparison

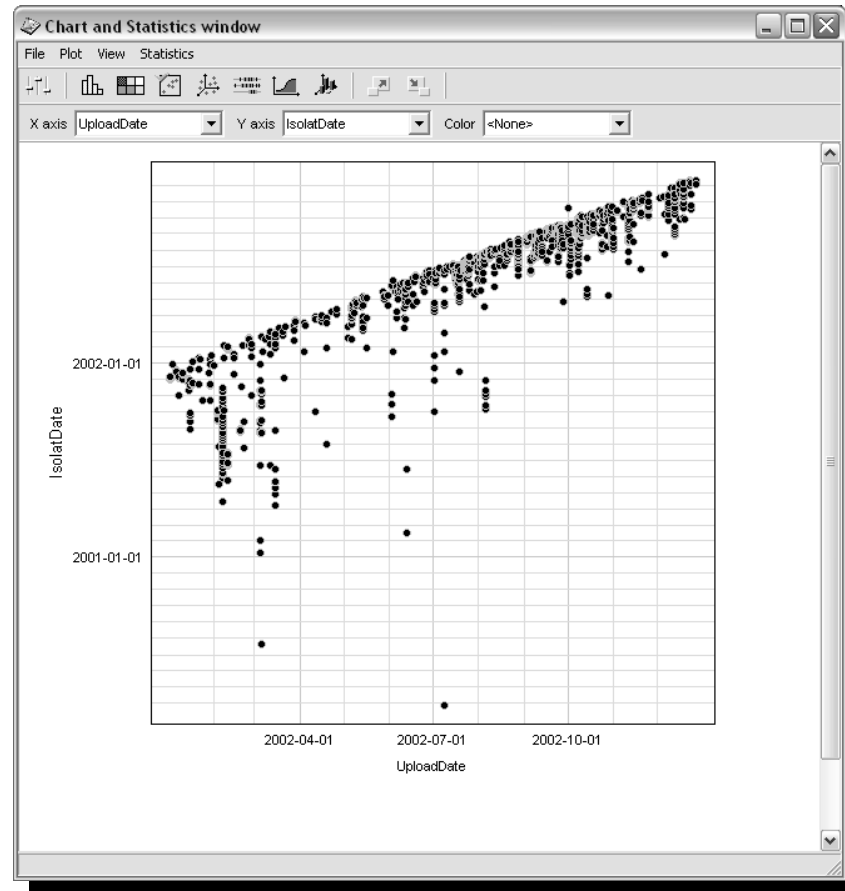
- ANOVA plots



T-test, Mann-Witney, ANOVA, Kruskal-Wallis

Comparison

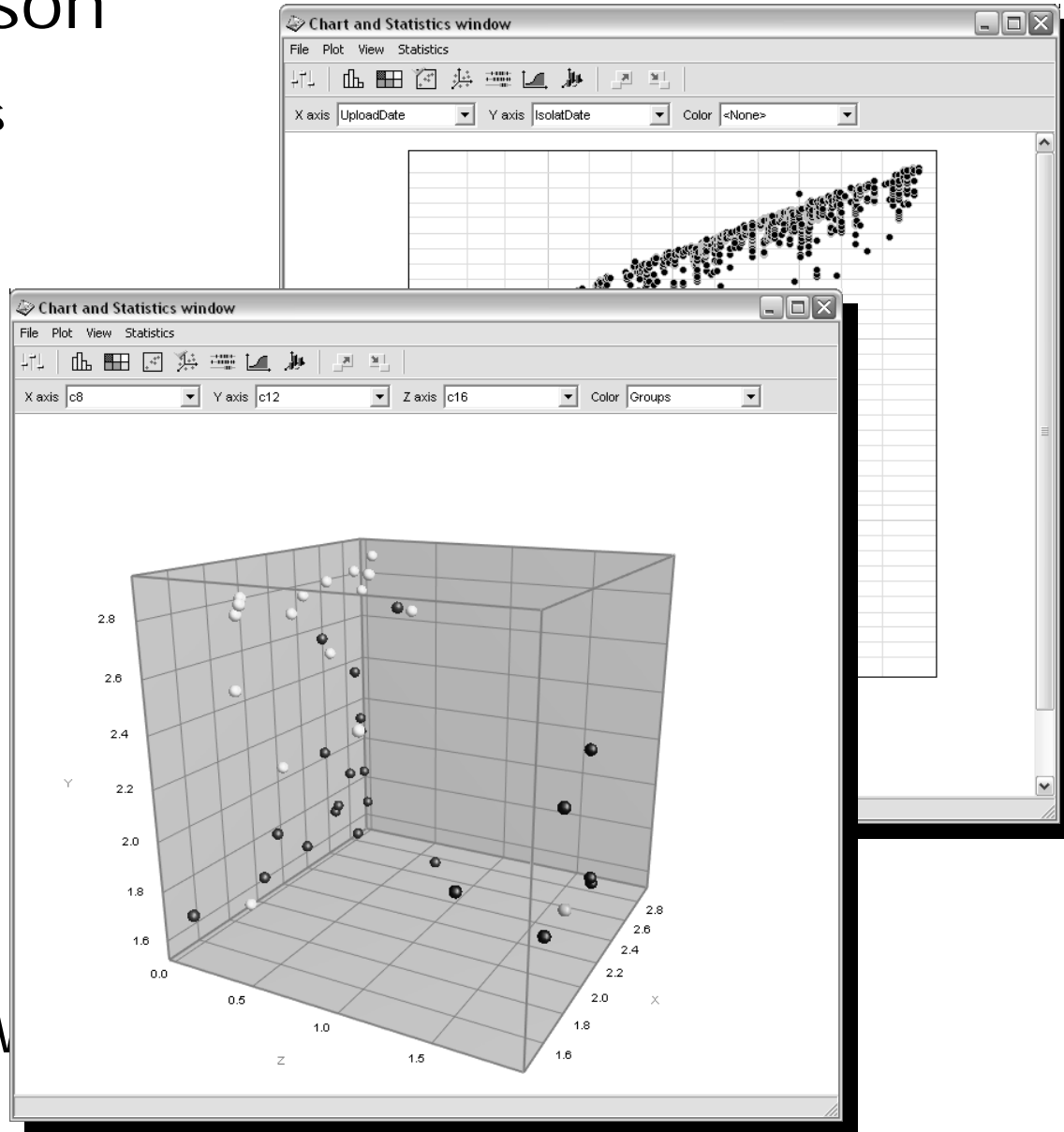
- Scatter plots



T-test, Wilcoxon, Pearson, Spearman

Comparison

- Scatter plots



T-test, V

Minimum Spanning Trees

What is it?

Data set: a number of organisms with a set of categorical variables

- MLST
- MLVA (VNTR's)
- PFGE data after band matching

A 1 5 6 4
B 1 6 6 4
C 2 5 6 4
D 1 8 2 1



Between any pair of organisms:
Distance = number of different
characters

$$d(\mathbf{A}, \mathbf{B}) = 1$$

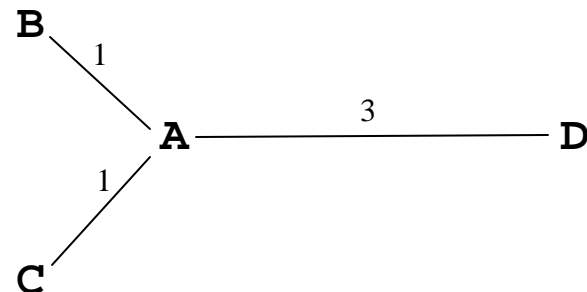
$$d(\mathbf{A}, \mathbf{C}) = 1$$

$$d(\mathbf{B}, \mathbf{C}) = 2$$

...



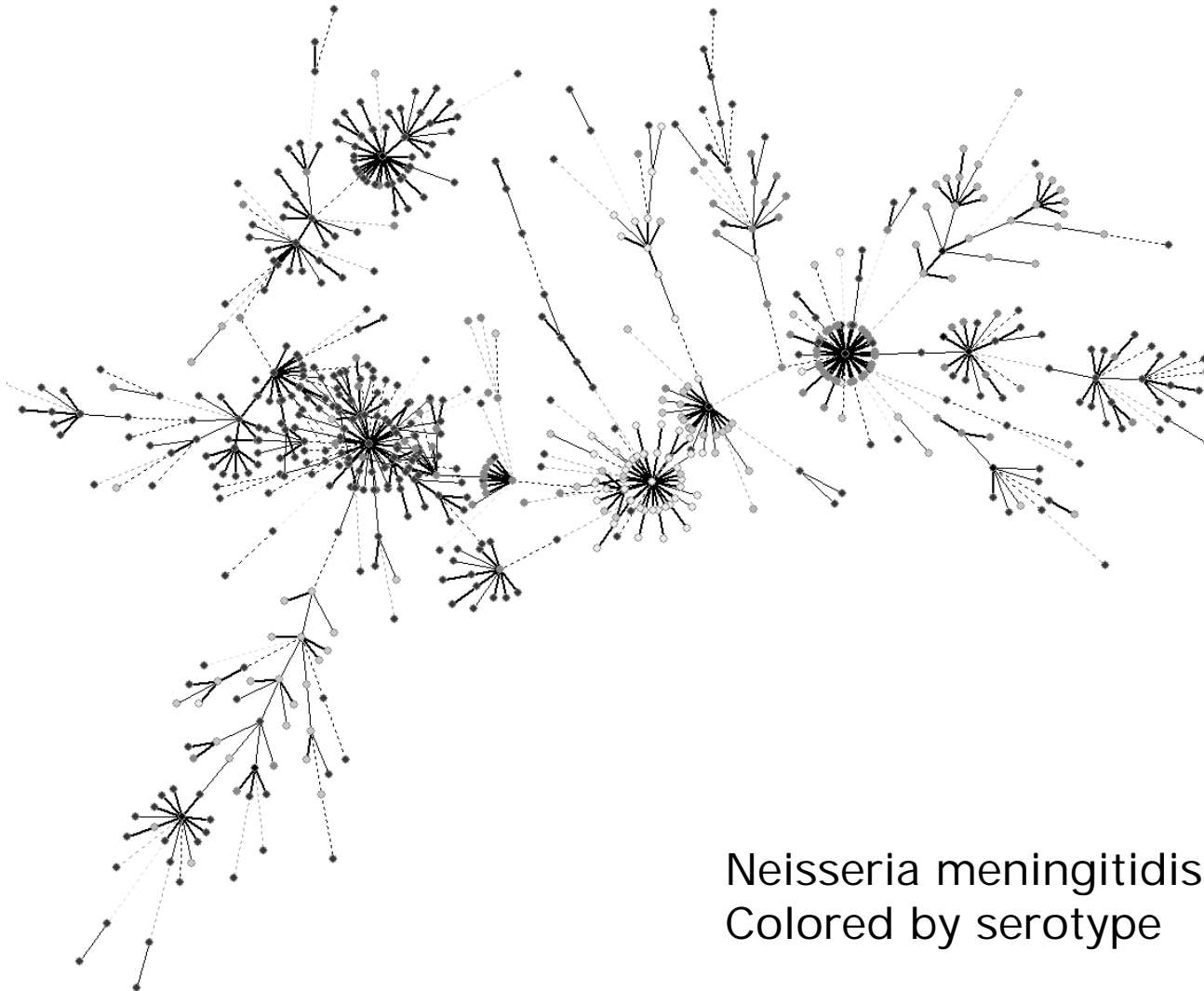
A tree is constructed so
that the total summed
distance along the
branches is minimal



Minimum Spanning Trees

Why?

A very powerful way of summarizing up the relations between a large set of organisms in a single image



Neisseria meningitidis
Colored by serotype