Point Placement by Phylogenetic Trees and its Application to Visual Analysis of Document Collections

Conference Paper · October 2007

DOI: 10.1109/VAST.2007.4389002 · Source: IEEE Xplore

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University of São Paulo, São Carlos/SP, Brazil
Mathematical and Computer Sciences Institute (ICMC)
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Point Placement by Phylogenetic Trees and its Application to Visual Analysis of Document Collections

Ana M. Cuadros (anamaria@icmc.usp.br)
Fernando V. Paulovich (paulovic@icmc.usp.br)
Rosane Minghim (rminghim@icmc.usp.br)
Guilherme P. Telles (gpt@icmc.usp.br)

Infovis2/MineVis Project: *http://infoserver.lcad.icmc.usp.br/*

Presentation outline

- Problem Statement and motivation
- Multidimensional Projections drawbacks
- Description of the approach
- Results
- Conclusions

Introduction

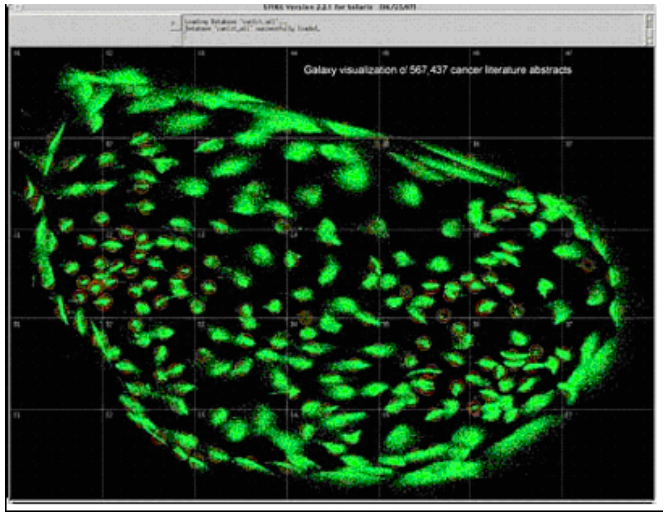
- Problem:
  - Generate a 2D map that reflects relationship among documents
  - Degrees of similarity reflected by proximity in the display
  - Exploratory tasks for document sets based on content
    - Vs. mapping based on metadata

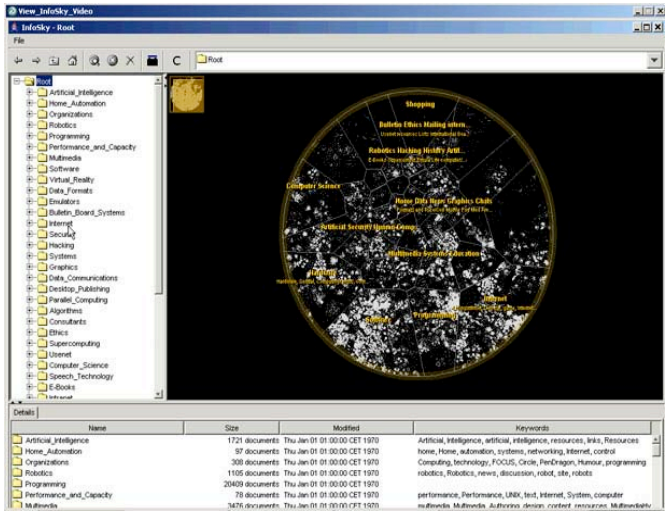
Point placement and multidimensional projections for visualization

- Multidimensional projection technique for data/text analysis:
  - Maps the data into p-dimensional space p={1,2,3}
  - Examples:
    - Principal Component Analysis (PCA) [5]
    - Multidimensional Scaling (MDS) [8]
    - Least-Square Projection (LSP) [11]
  - Projection Explorer (PEx) - http://infoserver.lcad.icmc.usp.br/
- Point Placement Strategies
  - eg. force-directed
- Hybrid Strategies

Maps of documents based on their content

- Ex:
  - IN-SPIRE™ [9]
  - Infosky [1]
- Handle massive amounts of texts and global displays as well as subgroups
- Drawbacks:
  - Documents that should be together get placed in different groups
  - Heterogeneous text sets cause, overlapping regions





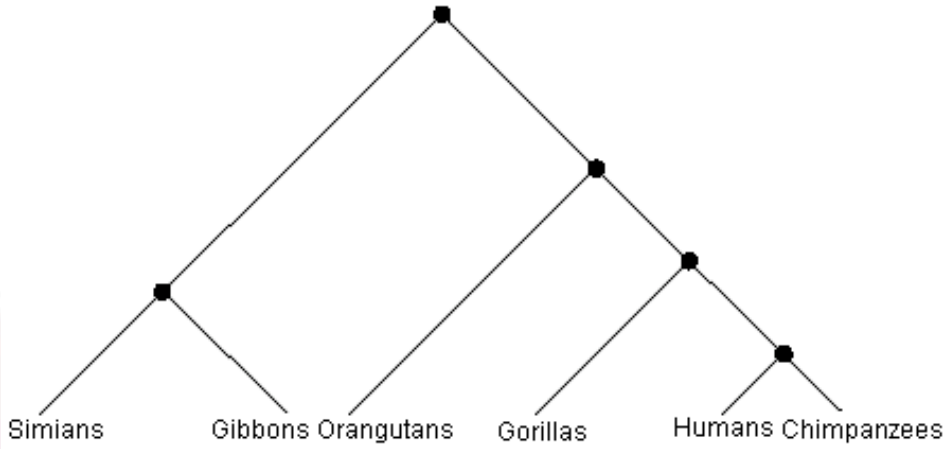
Motivation

- Problem with multidimensional projection techniques
  - Some points are always misplaced
  - Difficulty estimating density of groups
  - Difficulty distinguishing individual points in dense groups

- Alternative:
  - Similarity tree from a distance matrix employing an algorithm for phylogenetic tree reconstruction
    - Reflects the relationships as determined by the similarity measurement

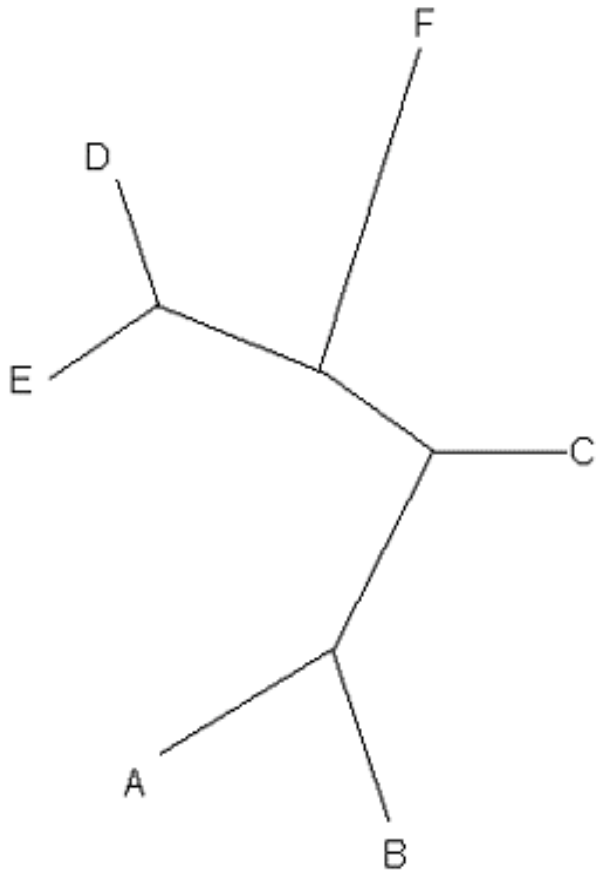
Phylogenetic reconstruction

- Biological problem of building a tree that reflects evolutionary relationship
- Leaves represent species and internal nodes hypothetical ancestors
- Two types of inputs:
  - Character matrix
  - Distance matrix

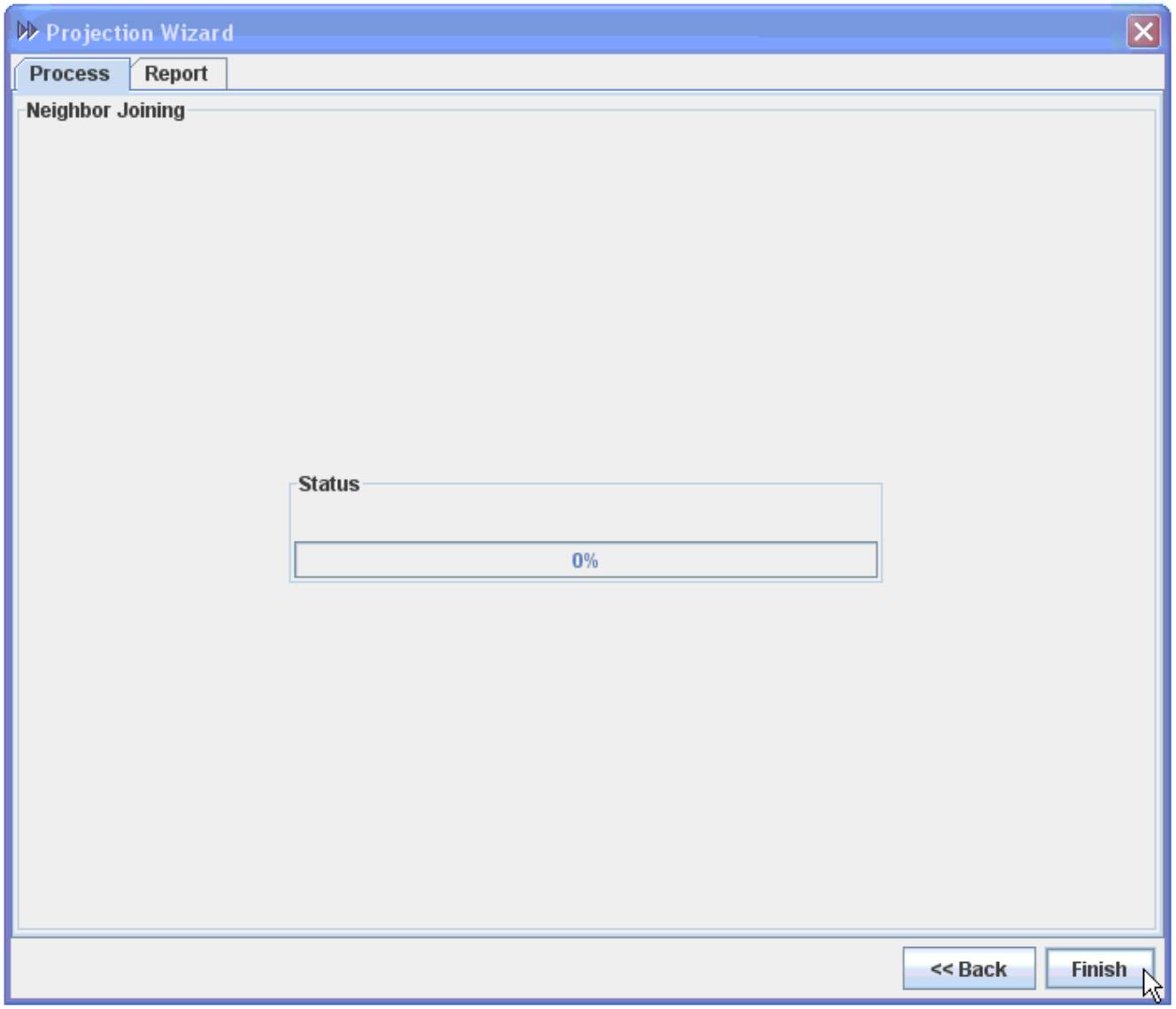


Phylogenetic reconstruction for m-d Vis

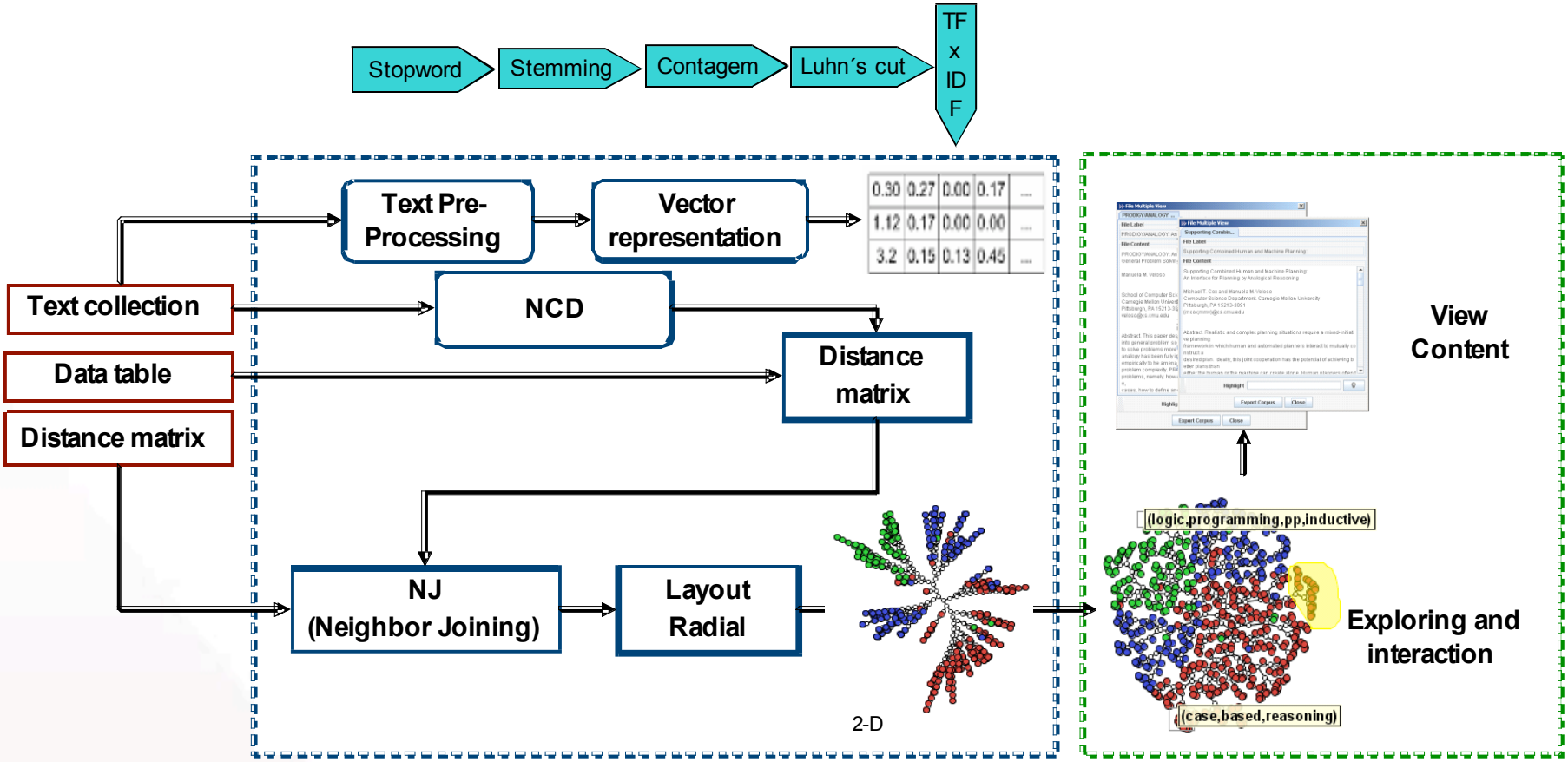
- Generates a distance matrix between all pair of documents
- Builds a similarity tree using a phylogenetic tree reconstruction algorithm (eg. NJ algorithm)
- Employs a lay-out strategy to display the tree
  - Clustered view
- Simplified point placement constrained to branch connections to spread the points around the 2D plane



Building a Tree from a Set of Documents



Process to create the document map

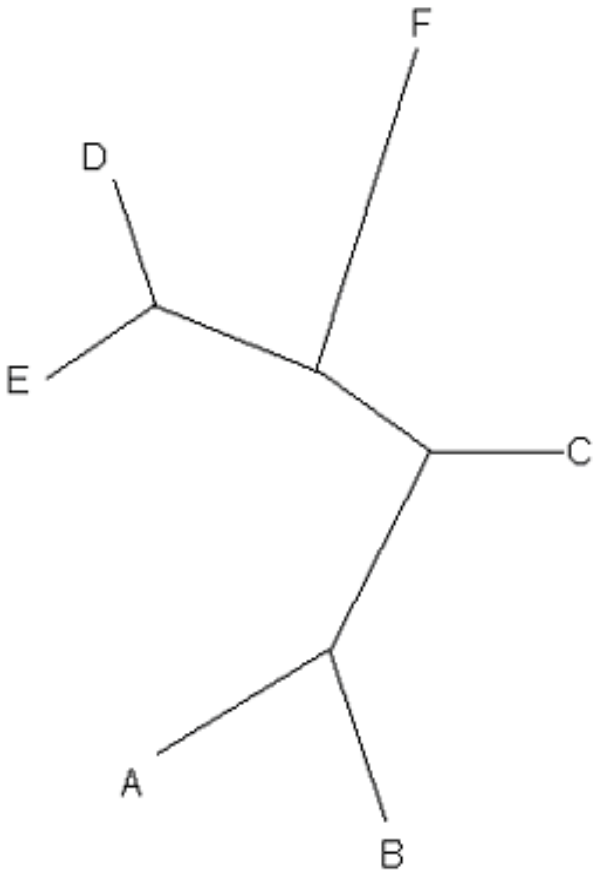


Creating the map NJ

Exploring the map

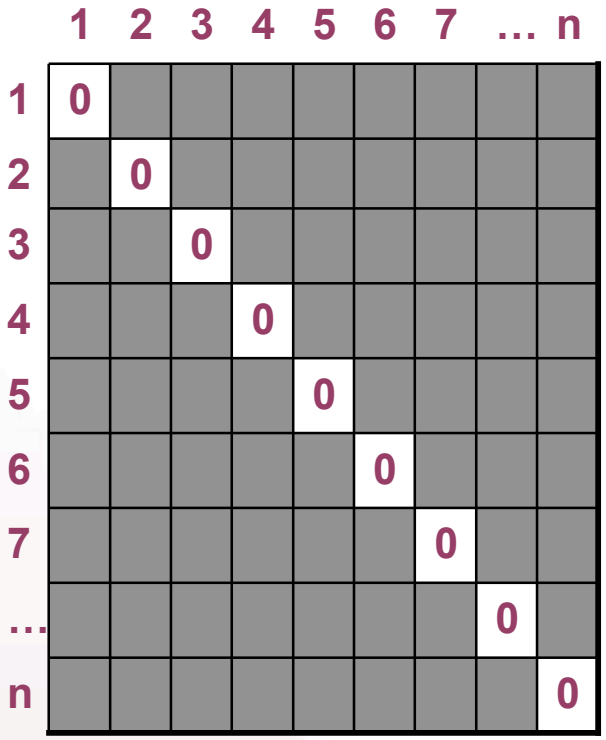
Neighbor-Joining (NJ) [10]

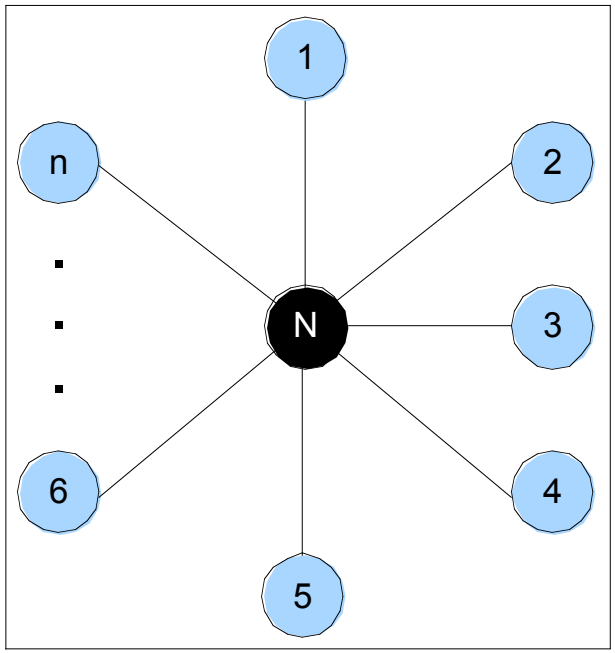
- Neighbor-Joining (NJ) technique [7]:
  - Heuristic algorithm for tree construction
  - Define the tree topology and branches length
  - Builds an unrooted tree
  - Selects the closest pair of documents and joins them into a hypothetical ancestor
  - With text:
    - Leaves: doc.
    - Internal nodes: ancestor hypothetical doc.
    - Edges' lengths: distance between docs.



Neighbor-Joining (NJ) [10]

- Starts with a start-like tree, with n leaves connected to a single internal node



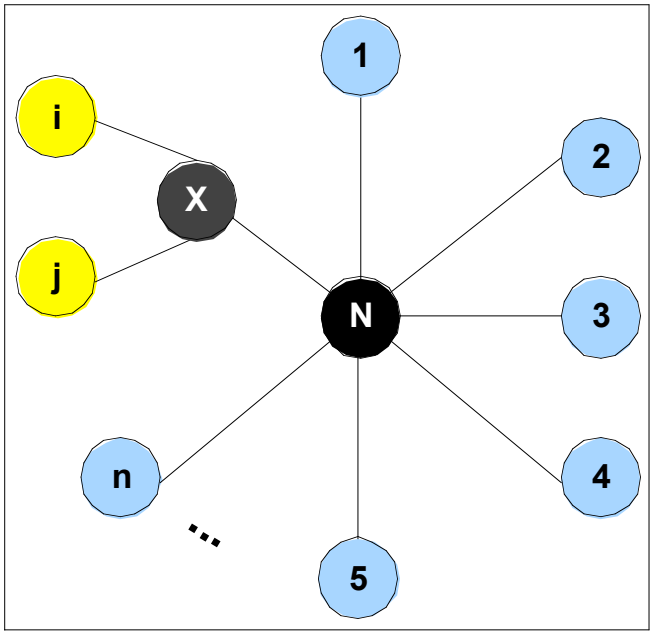


Neighbor-Joining (NJ) [10]

- Selects the smallest sum of branch lengths S_{ij}

$$S_{ij} = \frac{1}{2(n-2)} \sum_{k \neq i,j} (D_{ik} + D_{jk}) + \frac{D_{ij}}{2} + \frac{1}{n-2} \sum_{k,l \neq i,j}^{k<l} D_{kl}$$

- Adds a node x to the tree, with i and j as children and connected to the common ancestor of i and j

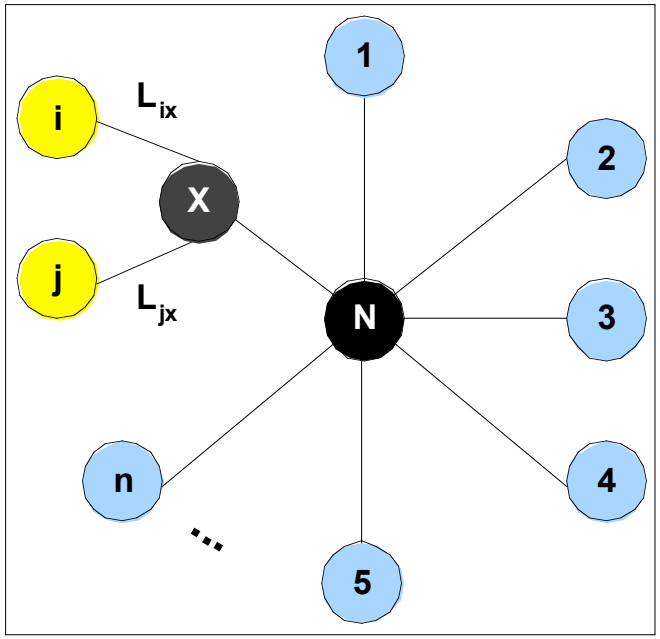


Neighbor-Joining (NJ) [10]

- Evaluates the branch lengths L_{ix} and L_{jx}

$$L_{ix} = \frac{D_{ij} + \frac{\sum_{k \neq j} D_{ik}}{n-2} - \frac{\sum_{k \neq i} D_{jk}}{n-2}}{2}$$

$$L_{jx} = \frac{D_{ij} + \frac{\sum_{k \neq i} D_{jk}}{n-2} - \frac{\sum_{k \neq j} D_{ik}}{n-2}}{2}$$



Neighbor-Joining (NJ) [10]

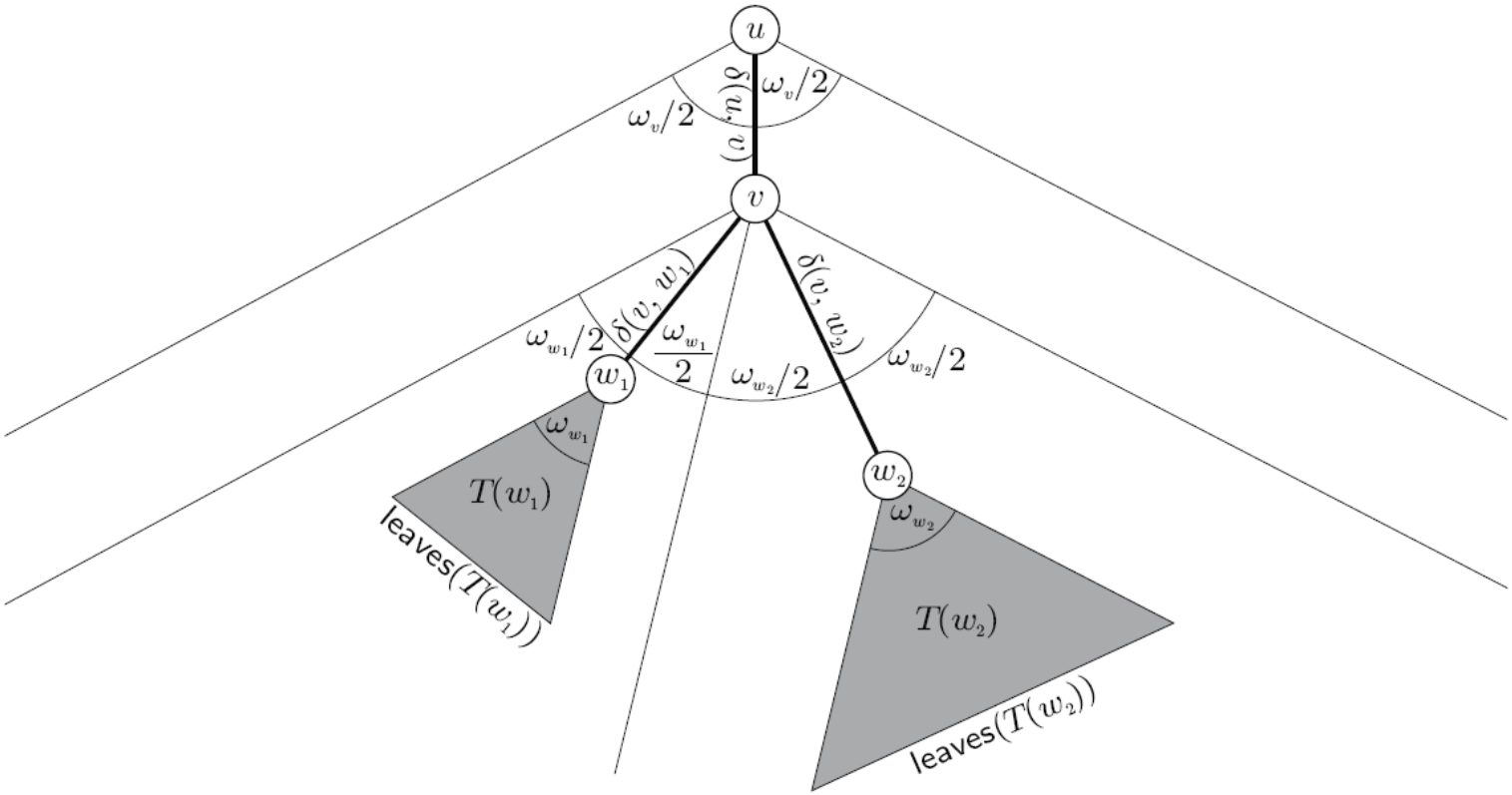
- Replaces i and j by x in the distance matrix evaluating the D_{xy} for every y in the matrix

$$D_{xy} = \frac{D_{iy} + D_{jy}}{2}$$

- Repeats this steps until there is only two nodes remaining in the matrix

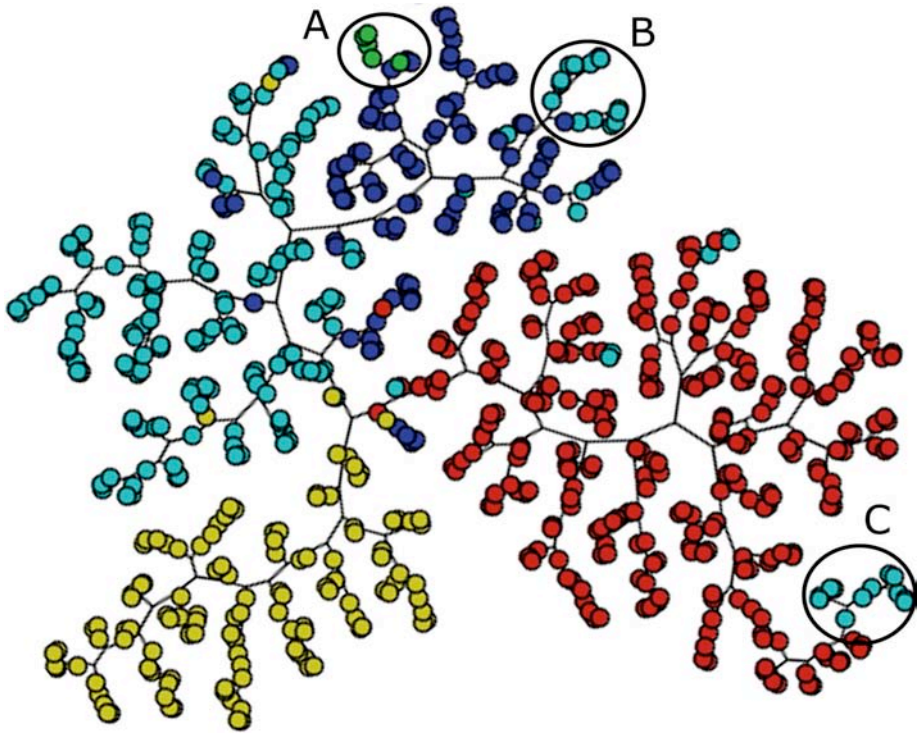
Radial layout [2]

- Preserves edge lengths
- Computed in linear time



Results

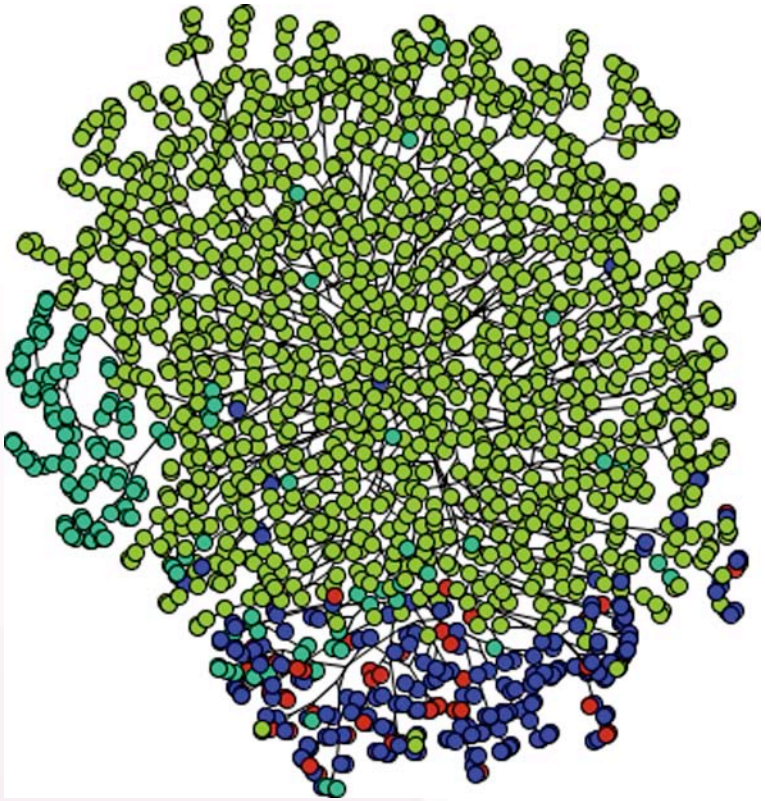
- **Mapping Scientific data sets**
  - CBR+ILP+IR+SON, 680 files, Scientific papers

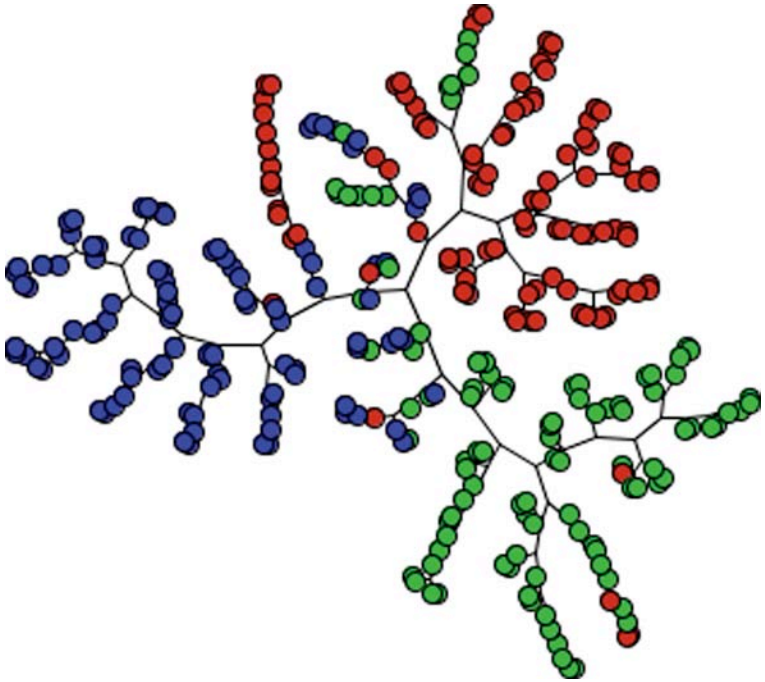


- **Case-based Reasoning**
- **Inductive Logic Programming**
- **Information Retrieval**
- **Sonification**

Results

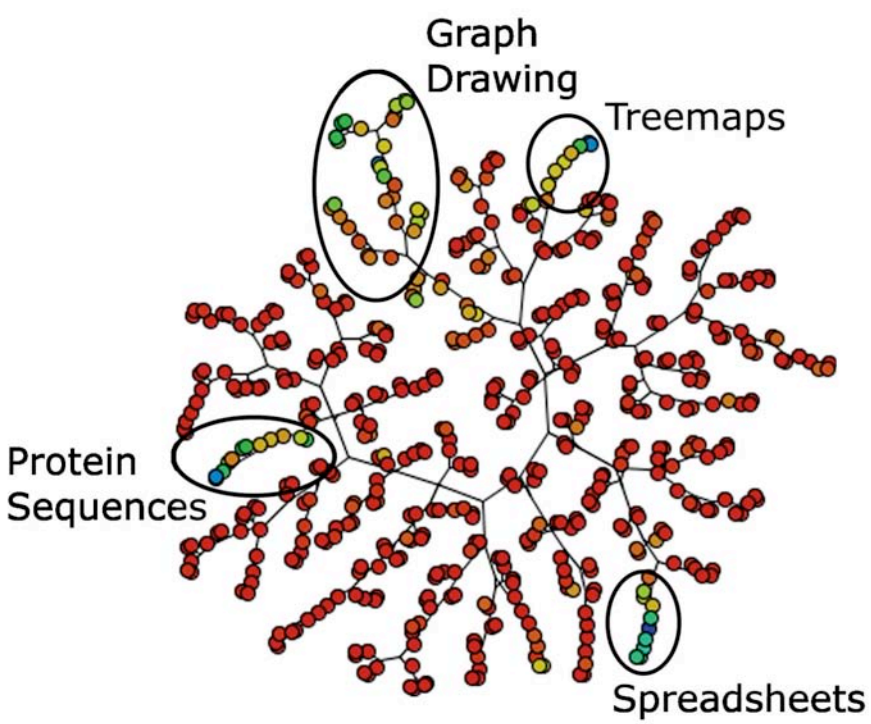
- **Mapping data sets**
  - KDVis, 1,624 files, Scientific papers
  - MESSAGES, 300 files, Discussion groups



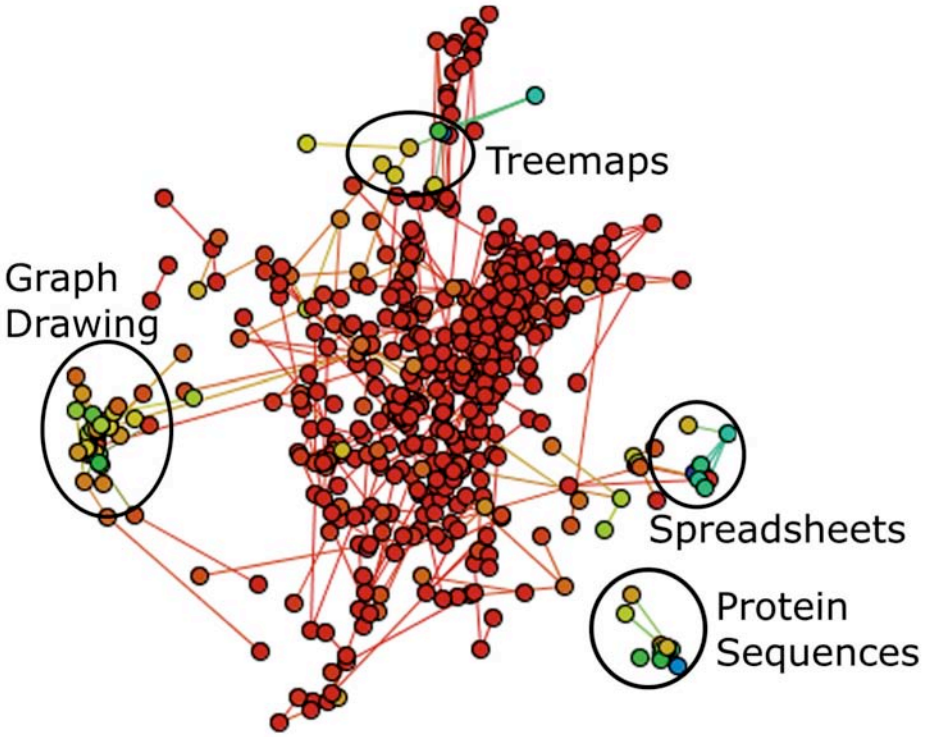


Results

- **Mapping data sets for NJ and projection techniques**
  - 2004 IEEE Infovis Contest, 515 files, Scientific papers



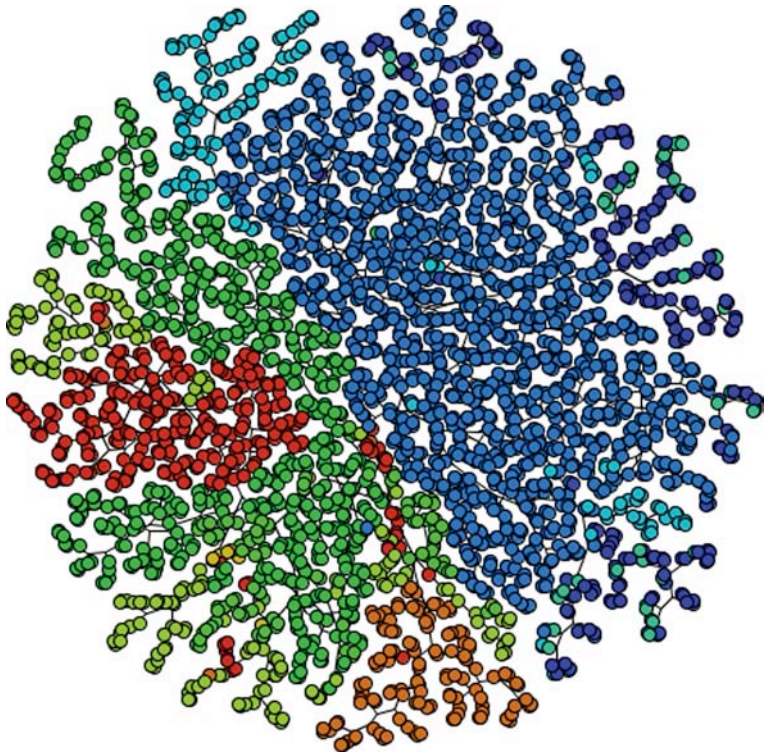
- **NJ**



- **LSP**

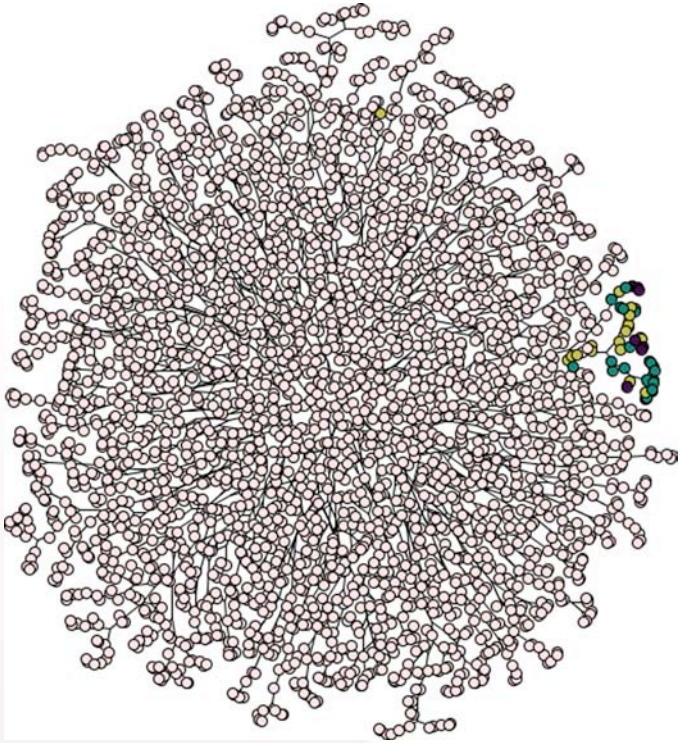
Results

- All scientific data set together using NCD similarity [8]

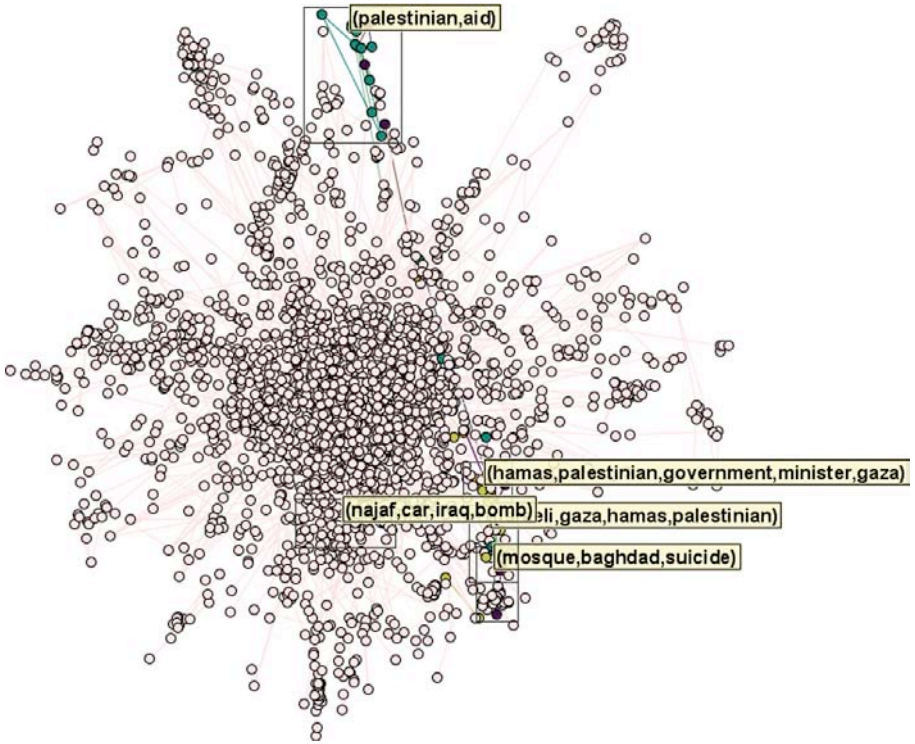


Results

- **Exploring RSS feeds of flash news (Associated Press, BBC, CNN, and Reuters)**
  - NEWS, 2,684 files



- **NJ**



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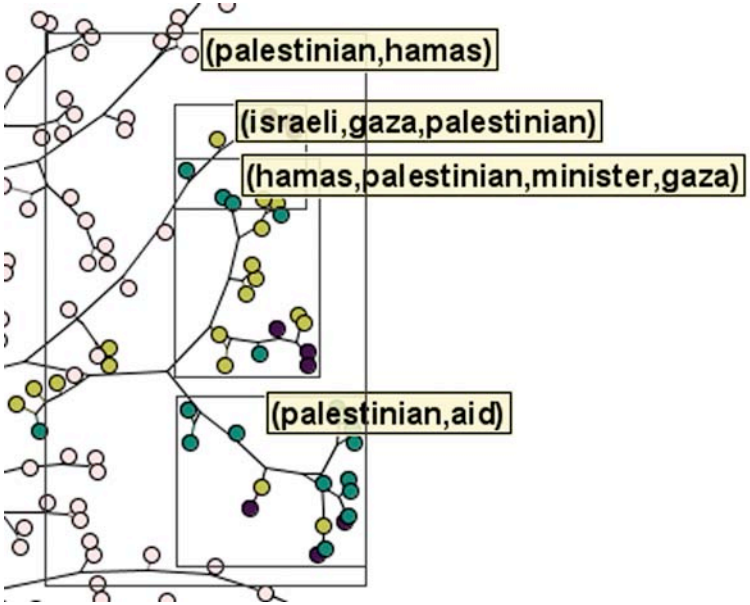

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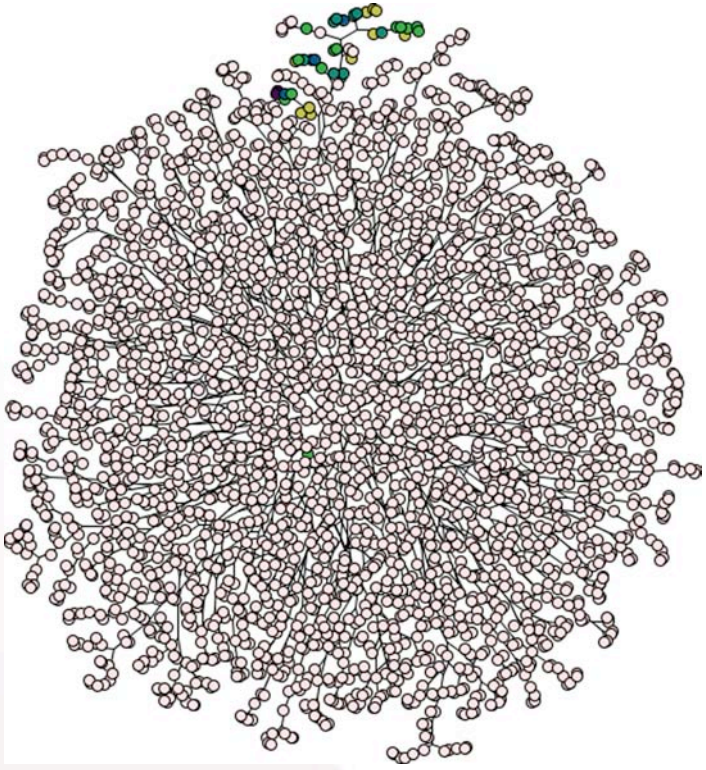
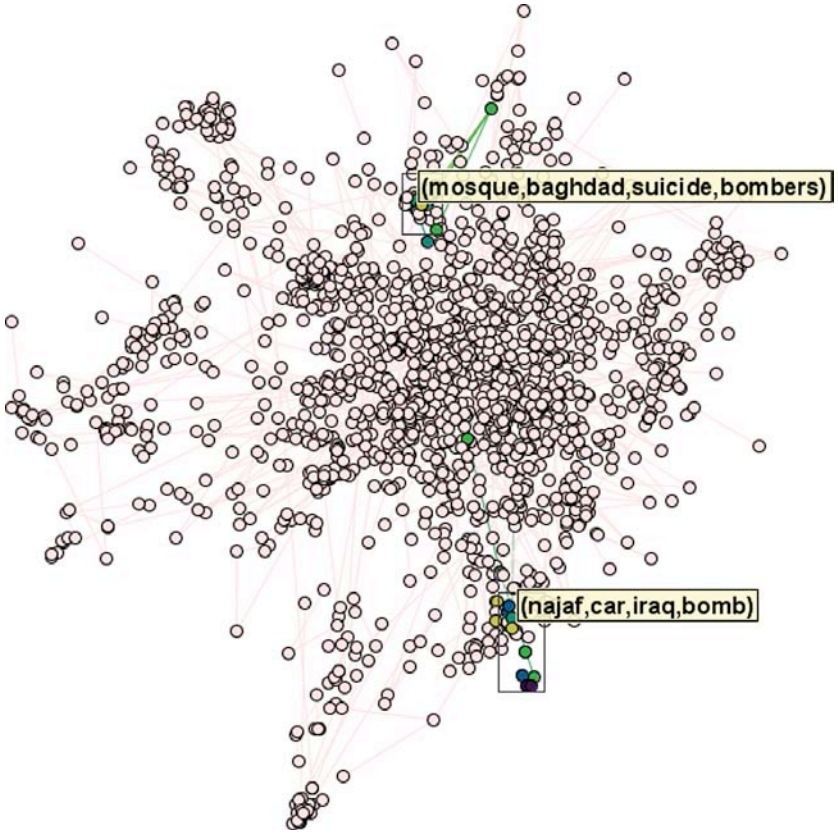


- **NJ**



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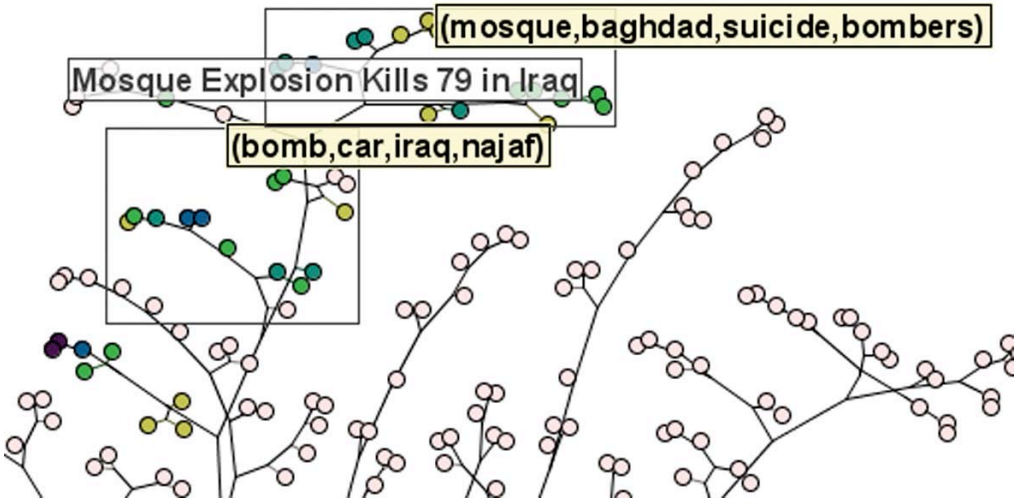
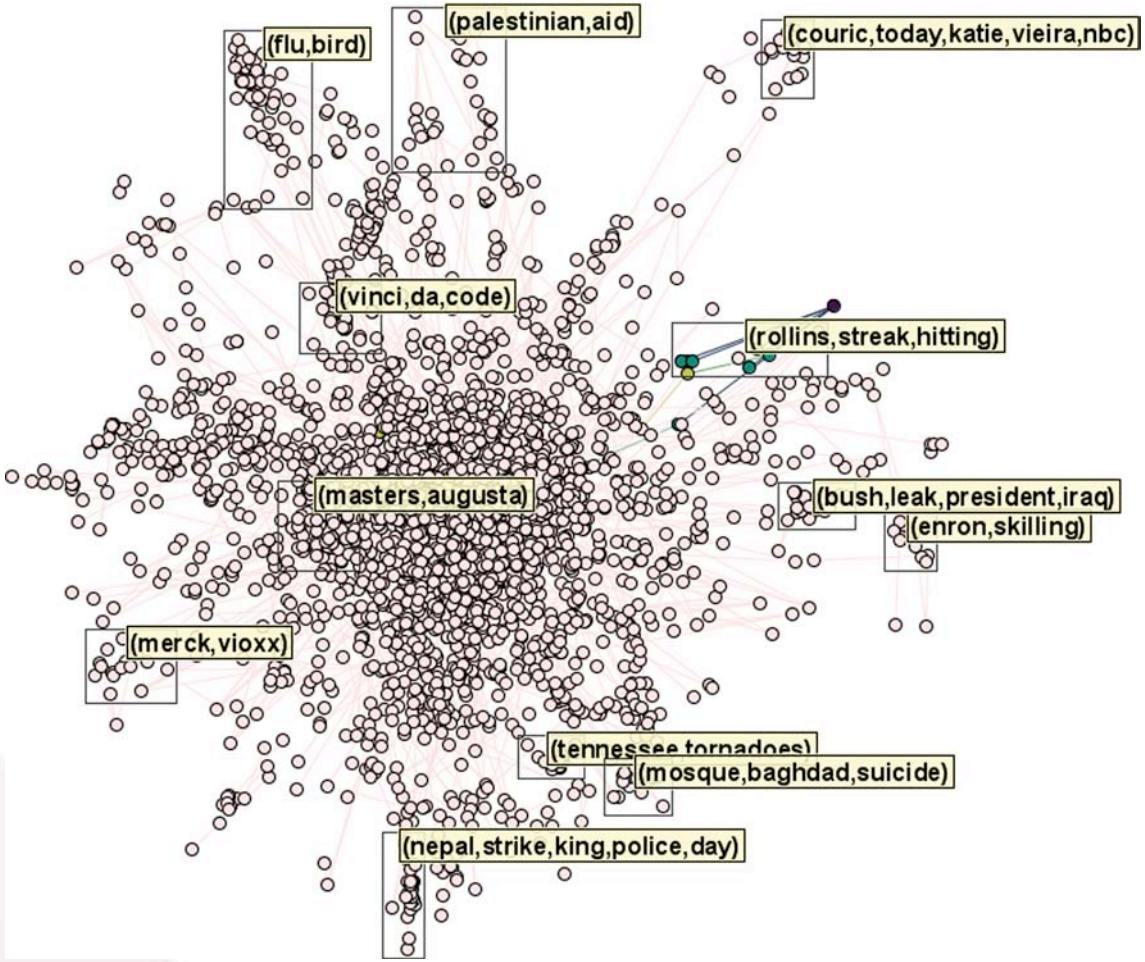


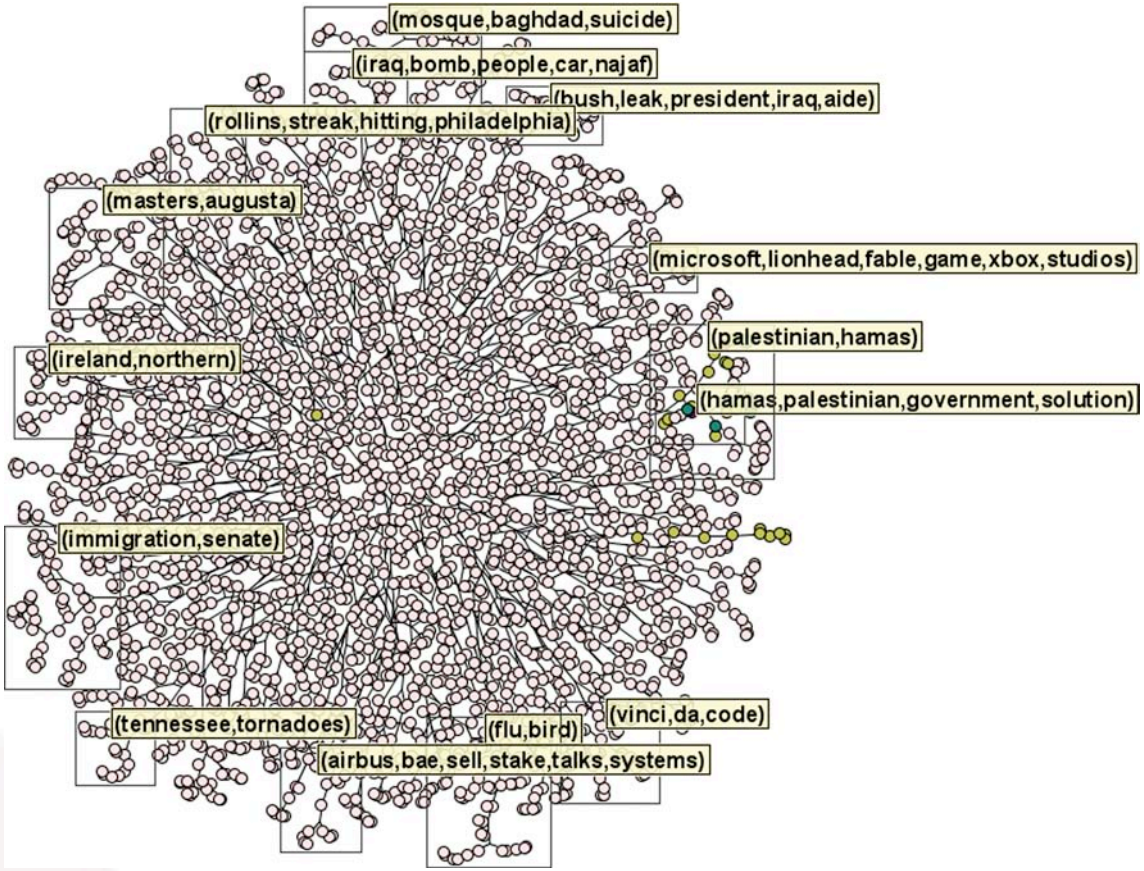
Results

- Grouping by topic (LSP)



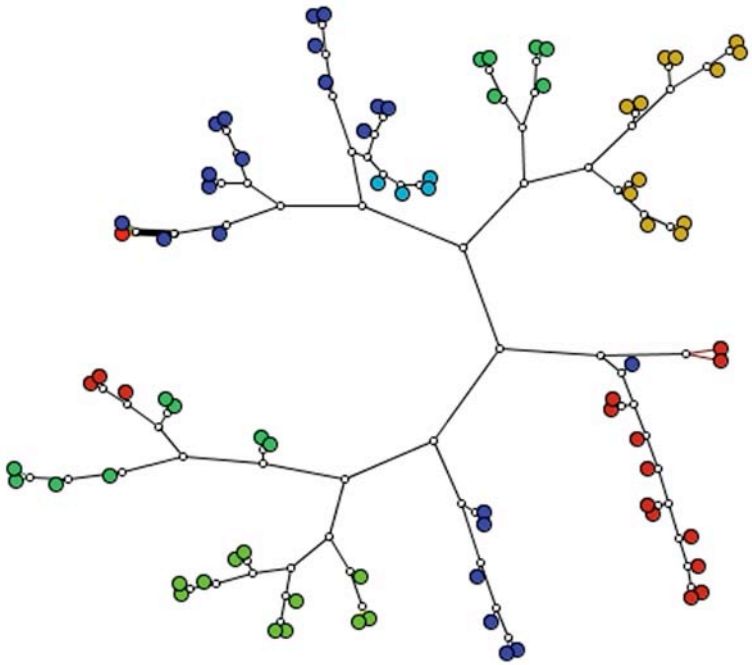
Results

- Grouping by topic (NJ)



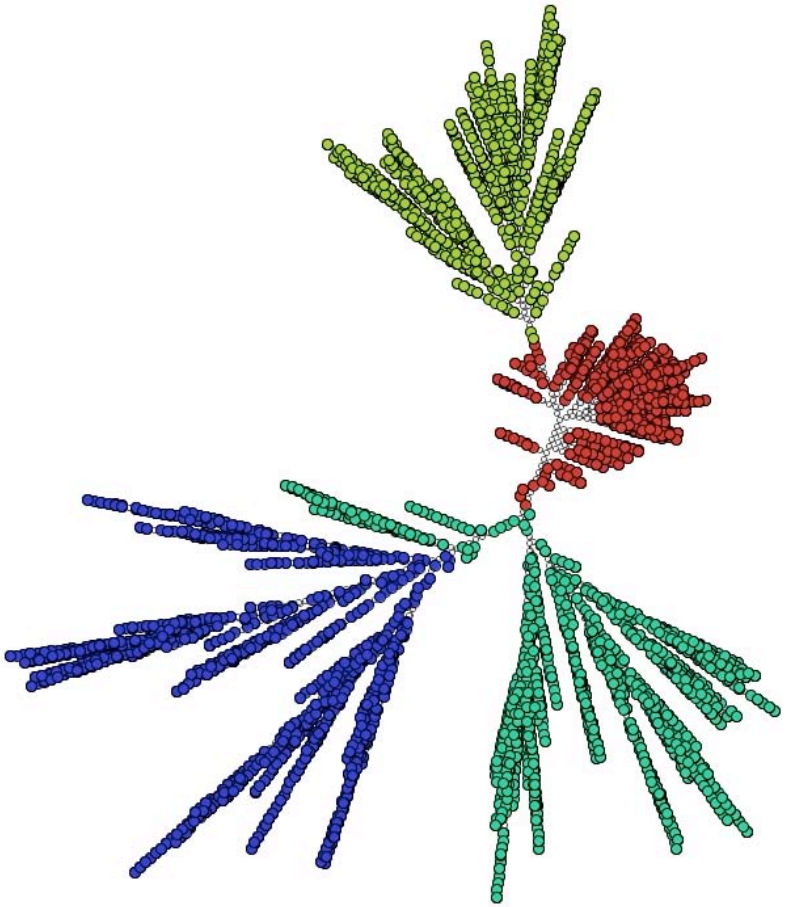
Results

- **Stream-flow in hydroelectric plants of Paraná River (Brazil)**
  - Color is sub-basin of the river



Results

- **Quadrupeds mammals data set**
  - 10,000 data instances



Results

- Time in seconds to create maps in a 3.2 GHz Pentium 4

Data Set	NJ	Layout	Total
CBR+ILP+IR+SON	4,55	0,52	5,17
KDVis	66,20	1,26	67,46
INFOVIS04	1,83	0,45	2,28
ALL	454,66	2,17	456,83
MESSAGES	0,35	0,31	0,66
NEWS	359,63	1,70	361,33

Concluding remarks

- NJ
  - Reflects content relationship visually
  - Constructs a hierarchy
- Interpretation of display
  - Makes good use of the visual space
  - Complementary of the projections
- Same distance matrix always generates the same tree
  - Helps evaluating the similarity measurement

Concluding Remarks

- Further work
  - Construct a set of tools for proper exploration of phylogenetic trees
  - Reduce processing time
  - Hybrid and hierarchical approaches
  - Test with other phylogenetic reconstruction methods

- Brazilian financial agencies
  - FAPESP
  - CNPq

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