Unraveling Multi-Dimensional Data using pDView

Luigi Di Caro
Universita' di Torino
Dip. di Informatica
dicaro@di.unito.it

Maria Luisa Sapino
Universita' di Torino
Dip. di Informatica
mlsapino@di.unito.it

K. Selçuk Candan
Arizona State University
Comp. Sci. and Eng
candan@edu.asu

ABSTRACT

We present the *pattern development view (pDView)* system for multidimensional scientific data visualization. The *pDView* system relies on a novel *pattern development tree (pDTree)* structure to unravel patterns in multidimensional data without having to rely on visualizations that require either significant degrees of *projections* that eliminate certain dimensions at the expense of the others or introduce significant visual overhead due to overly-rich multi-dimensional graphic interfaces. Instead, *pDView* maps data along all its *relevant* dimensions onto a *pDTree* structure, capturing and visualizing the underlying fundamental relationships. The user is able to vary contextual parameters to observe the strength and robustness of these relationships under different situations.

Categories and Subject Descriptors

H.2.5 [**Database Management**]: Heterogeneous Databases; H.5.2 [**User Interfaces**]: Graphical user interfaces

General Terms

Algorithms, experimentation

Keywords

Reasoning with scientific data, taxonomy, query language, data visualization

1. MOTIVATION

It is very common in scientific inquiry and other forms of data analysis (such as business intelligence) for the analysts having to look for relationships and patterns across certain data attributes *with respect to* a context defined by other attributes. For example consider an archaeologist making a study on animal bone specimens collected at various sites (possibly for understanding the eating habits of the residents of these sites) using a database `boneCollectionDB(specimen_number, lot_number, species, date)`. For her analysis, this scientist may want to look for the relationships among the species of the animal bones in the context of the places where bones are found.

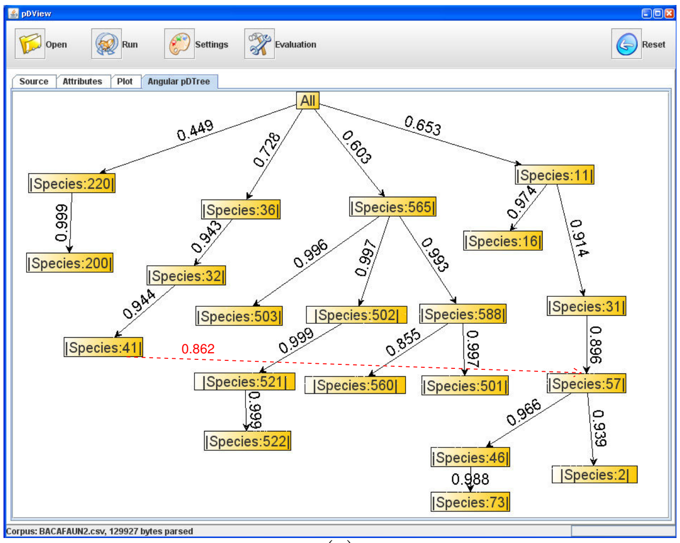
Existing techniques (multi-variate analysis roll-up/drill-down operations in OLAP, multi-dimensional data visualization schemes, such as [11, 6]) for visualizing such multi-dimensional data require either significant degrees of *projections* to cross out (even relevant) dimensions at the expense of the others or introduce significant visual overhead due to overly-rich multi-dimensional graphic interfaces. Research on effective use of 2D spaces for multidimensional data visualization focus on careful selection of the relevant dimensions [10] and organizing data in hierarchical visualization structures along the relevant dimensions and mapping these to 2D spaces [2]. In this demonstration, we present a novel *pattern development view (pDView)* system to visualize multidimensional data without having to rely on high-dimensional visualization mechanisms. We first describe how the underlying *pattern development tree (pDTree)* structures are created and then provide the demonstration scenario for *pDView* (Figure 1).

2. PDVIEW AND PDTREE

Let $R(A_1, ...A_n)$ be a table containing the data to be visualized. Without loss of generality, let us take A_1 through A_k as the *context attributes:* they describe the dimensions within which the relationships between the values corresponding to the visualization attributes are to be studied. Let also A_{k+1} through A_m denote the visualization attributes (attributes A_{m+1} through A_n do not have impact on the analysis and visualization). *pDView* queries have the following SQL-like form:

```
CREATE pDVIEW view_name AS
    FREQ $A_{k+1}, \ldots, A_m$
    FROM $R$
    WHERE ...
    INCONTEXT $A_1, \ldots, A_k$
```

Intuitively, as in SQL's `GROUP BY`, the context attributes A_1 through A_k are used for clustering the values corresponding to the visualization attributes, A_{k+1} through A_m. For example given an archaeological database, with the schema `boneCollectionDB(specimen_number, lot_number, species, date)`, having `specimen_number` as the context attribute and `species` as the visualization attribute would mean that the user would like to study the relationships between the *species* of the animals, correspond-



(a)

Coding Sheet

2:	Small Mammal: Rabbit/Rodent-sized
11:	Indeterminate Artiodactyl
16:	Pronghorn
31:	Indeterminate Rabbit
32:	Cottontail
36:	Jackrabbit
41:	Indeterminate Rodents
46:	Pocket Gopher
57:	White-footed Mouse
73:	Prairie Dog
200:	Indeterminate Fishes
220:	Sucker Fish
501:	Indeterminate Small Bird
502:	Indeterminate Medium Bird
503:	Indeterminate Large Bird
521:	Duck
522:	Mallard Duck
560:	Quail
565:	Turkey
588:	StellerŠs Jay

(b)

Figure 1: (a) A sample (angular) *pDTree* created using an archaeological database (Upper Little Colorado prehistory project [1]). The database contains different animal bone specimens collected at an archaeological sites. In this example, the context attribute is the `element_number` (i.e., codes describing types of bones collected at a site; e.g., 43 for "Unidentified skull fragment" and 59 for "Lumbar vertebrae") and the visualization attribute is the `species_number` (i.e., the code for the corresponding species as identified by the archaeologist). Note that, except for a few mis-associations (which secondary linkage analysis -the dashed line- can reveal), the *apDTree* is almost a valid taxonomy of the species

ing to the bones collected within an archaeological study, as a function of their distribution across various specimen collections.

2.1 Data Preparation

Given a *pDView* query, first, the relevant attributes of the data specified in the query are projected, clustered, and the counts for the unique combinations are computed. Let $\alpha_i = \langle a_{1,i}, \ldots, a_{k,i}\rangle$ be an instance of $R[A_1, \ldots, A_k]$. α_i is referred to as a *context-instance*. Let $R_{(\alpha_i)}[A_{k+1}, \ldots, A_m]$ denote the portion of the table R containing the visualization-instances corresponding to the context α_i. Given a visualization-instance $\beta_j = \langle a_{k+1,j}, \ldots, a_{m,j}\rangle$ of the portion $R_{(\alpha_i)}[A_{k+1}, \ldots, A_m]$, the value of $count(i,j)$ is computed as $\mid R_{(\alpha_i)}[A_{k+1} = a_{k+1,j}, \ldots, A_m = a_{m,j}] \mid$. A *visualization-instance frequency* matrix VF, then, reports the frequency (normalized between 0 and 1) of each visualization-instance, $\beta_j = \langle a_{k+1,j}, \ldots, a_{m,j}\rangle$, for each context instance, $\alpha_i = \langle a_{1,i}, \ldots, a_{k,i}\rangle$: $\mathtt{VF}(i,j) = count(i,j)/max_h\{count(h,j)\}$.

The second step in preparing the data for *pDTree* construction involves the identification of a basis consisting of a set of mutually independent unit vectors. This basis defines a space on which the relationships among visualization-instances as well as context-instances can be studied. For this purpose, we use the well known Singular Value Decomposition approach (SVD [3]) on the VF matrix. SVD splits the input matrix into three matrices, $\mathtt{VF} = U\Sigma V^t$, such that U and V are column orthonormal matrices and Σ is a diagonal matrix. The advantage of SVD is that mutually independent columns of U and V can be considered as basis of the space on which visualization- and context-instances can be studied. Also, the weights of the diagonal entries of Σ can be considered as the *significance* of the corresponding columns in U and V.

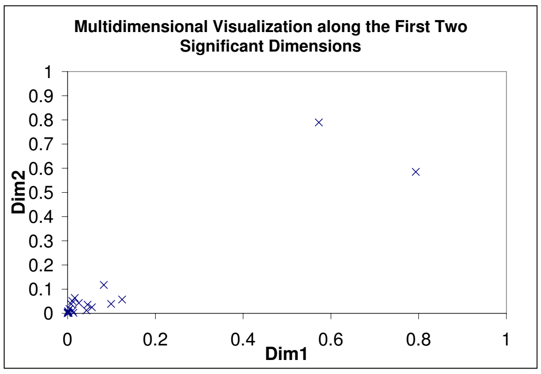
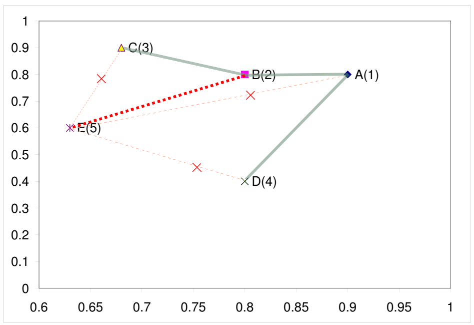


Figure 2: A multidimensional visualization (along the most significant two dimensions) for the data set in Figure 1. Despite major dimensional losses, patterns (easily visible in the *pDTree*) are hard to discern.

2.2 Pattern Development Tree (pDTree)

SVD underlies many data analysis and dimensionality reduction techniques (such as latent semantic analysis [4]). On the other hand, while such principal component based study is highly common we note that it is not sufficient in itself for effective visualization of the data. In particular, the significance values computed by SVD enable reduction in the number of dimensions, but in many cases, the number of relevant dimensions is still beyond what can be visualized effectively. Furthermore, even if the data is compressed to very low-dimensional spaces (2D- or 3D-) to be displayed on screen, simply presenting the data points



	x-std diff.	y-std diff.	ang. diff	avg.
$A \to B$ vs. $A \to B \to E$	0.066	0.115	0.667	**0.283**
$A \to B \to C$ vs.. $A \to B \to C \to E$	0.011	0.068	0.808	0.296
$A \to D$ vs.. $A \to D \to E$	0.066	0.082	0.833	0.327
A vs. $A \to E$	0.191	0.141	0.638	0.323

Figure 3: An example *fpDTree* of line segments: The new visualization instance, E, is connected to the a tree based on its compatibility to the existing branches. Here, E is most compatible with $A \to B$

for scientist's visual interpretation is not effective: in many cases, it is hard for the user to view the data from all relevant points-of-view to identify patterns implying strong relationships among the visualization-instances and/or the context-instances (Figure 2). Therefore, unlike most techniques which effectively amount to dimensionality reduction based on the available significance information, we go further and use the U, V, Σ matrices obtained through SVD to obtain a *pattern development tree (pDTree)*, which does not suffer from the visualization shortcomings of the multi-dimensional spaces. Let us consider the matrix V which maps the visualization-instances onto a multidimensional space defined by the independent basis vectors. Let us call this space, S. For each visualization-instance, $\vec{vi}$, on S, we compute a dominance value ($dom(\vec{vi})$), which describes how dominant the visualization-instance is in space S. We define the $dom(\vec{vi})$ as follows: $dom(\vec{vi}) = |\vec{vi} - \langle 0, 0, \ldots, 0\rangle|$. Intuitively, those visualization-instances that occur frequently (i.e., further away from the null point $\langle 0, 0, \ldots, 0\rangle$) dominate the others. This interpretation is consistent with the observation that the extended boolean model of vector spaces [5] enables one to treat those vectors that are further away from the origin as being also *more general* [7]. This enables us to order the visualization-instances into a tree (where nodes higher up in the hierarchy are more general/dominant) based on their dominance values: the dominant visualization-instances (away from $\langle 0, 0, \ldots, 0\rangle$) are mapped closer to the root.

pDView can use two different strategies to create *pDTrees*: The *free pattern development tree (fpDTree)* strategy relies on the assertion that each branch of the tree represents a set of instances that collectively define a coherent (in terms of overall direction in the space and distribution of instances) pattern in the space. Therefore, new branches are created where instances violate existing patterns. The *angular pattern development tree (apDTree)* strategy, on the other hand, gives more emphasis on the relative value-compositions of

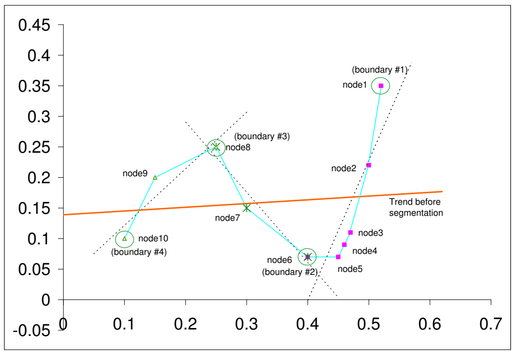


Figure 4: Partitioning of a non-uniform branch (from $node1$ to $node10$) into segments: each partition acts as a coherent pattern in the data and only boundaries are considered for new branches

the instances and only places visualization-instances with similar compositions as part of the same branch.

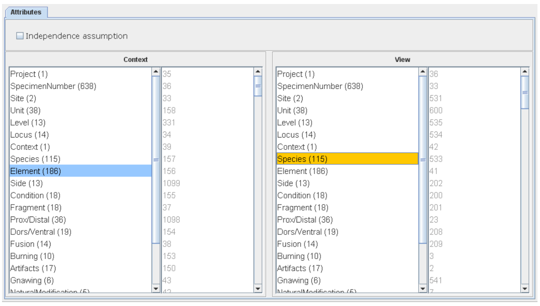
2.2.1 Free Pattern Development Tree (fpDTree)

While dominance helps us order visualization-instances, it does not determine how branching is created in a *pDTree*. Intuitively, if two visualization-instances are related to each other within the current context of analysis, they need to be part of the same branch. In *fpDTrees*, each root-to-instance path is analyzed for pattern developments and shifts (including slope, concentration). For each visualization-instance, considered during the construction of the *fpDTree*, the most compatible branch of the current *fpDTree* is chosen as the connection point. Pattern development analysis underlying the branching decisions involves (a) analysis of the hyper-curves (linear, planar, etc.) defined by branches of the trees, before and after the insertion of the new visualization instance, and (b) checking whether attaching the new visualization instance to that branch will cause a large deviation from the current characteristics of the branch. See Figure 3 for an example *fpDTree* of line segments. Note that, while this figure only illustrates *fpDTree* construction in terms of line segments, *pDView* analyzes planar and hyper-planar pattern developments simultaneously (without requiring exponential growth in analysis time). The user of *pDView*, then can pick the dimensionality of the pattern developments or have *pDView* to scale the number of dimensions needed to create the *fpDTree* as appropriate.

For reducing the computational complexity of branching analysis during *fpDTree* construction as well as to prevent very long branches from causing deformations, *fpDTree* partitions long branches into coherent segments, using multi-dimensional hyper-curvature analysis [9, 8]. It considers only those identified segment boundaries as candidates for branching (Figure 4).

2.2.2 Angular Pattern Development Tree (apDTree)

Unlike the *fpDTree* which analyzes the pattern development along the various branches explicitly using multiple pattern development parameters, *apDTree* treats two visualization-instances to be related only when they have similar compositions with respect to the basis of the underlying multi-dimensional space: *while their dominance in the data set*



Attributes

☐ Independence assumption

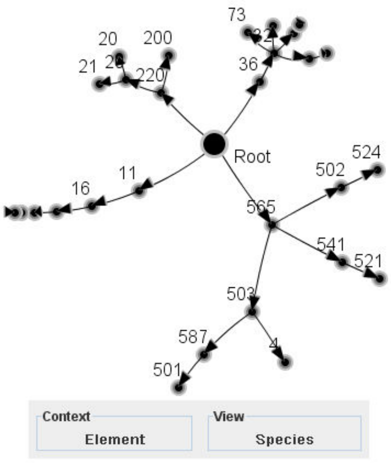
Context

Project (1)	35
SpecimenNumber (638)	36
Site (2)	33
Unit (38)	158
Level (13)	331
Locus (14)	34
Context (1)	39
Species (115)	157
Element (186)	156
Side (13)	1099
Condition (18)	155
Fragment (18)	37
Prox/Distal (36)	1098
Dors/Ventral (19)	154
Fusion (14)	38
Burning (10)	153
Artifacts (17)	150
Gnawing (6)	43
NaturalModification (5)	42

View

Project (1)	36
SpecimenNumber (638)	33
Site (2)	531
Unit (38)	600
Level (13)	535
Locus (14)	534
Context (1)	42
Species (115)	533
Element (186)	41
Side (13)	202
Condition (18)	200
Fragment (18)	201
Prox/Distal (36)	23
Dors/Ventral (19)	208
Fusion (14)	209
Burning (10)	3
Artifacts (17)	2
Gnawing (6)	541
NaturalModification (5)	7

Figure 5: Selection of context- and visualization-attributes.



Context: Element

View: Species

Figure 6: Dynamic fish-eye view of the angular Pattern Development Tree created with the settings shown in Figure 5.

may differ significantly, such a pair of entries are related to the underlying context-instances in a similar manner. Thus, in *apDTree*s, for branch differentiation, we rely on the angular differences (i.e. difference in *compositions*) of the visualization-instances. Visualization-instances with similar compositions are part of the same branch of the *apDTree*, while visualization-instances with different compositions should be mapped onto different branches. To achieve this, we incrementally construct the *apDTree* by considering the visualization-instances in the decreasing order of their dominance values (as in *fpDTree*s) and by connecting each visualization-instance, $\vec{vi}_i$, to the one, $\vec{vi}_j$, most similar (in terms of their compositions; i.e., $cosine(\vec{vi}_i, \vec{vi}_j)$) already included in the *apDTree*. See Figure 1(a) for a sample angular *pDTree* created using a database containing different animal bone specimens collected at an archaeological site. Note that, except for a few mis-associations (which secondary linkage analysis -the dashed line- provided by *pDView* can reveal), the *apDTree* is almost a valid taxonomy of the species.

3. DEMO SCENARIO

We demonstrate the pattern development view system for visualization of multidimensional data through its use in an archaeological domain. Specifically, we will use the Upper Little Colorado prehistory project data set [1], consisting of a relation with ~30,000 tuples on 20 attributes, and show how (a) the context of interest and the visualization attributes are interactively selected, as shown in Figure 5, (b) how the patterns on the visualization attributes are visualized in *fPDTree*s and *aPDTree*s as a function of the context (Figure 6 shows a fish-eye exploration view), and (c) how the user can focus on a node of the *pDTree* for further exploration tasks like manual or automatic selections of dimensions relevant to the pattern selected and visualized, or ranking of context-instances based on cosine similarity (Figure 7).

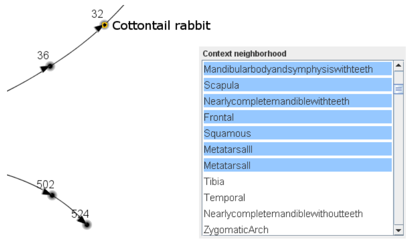


Figure 7: The selection of a visualization-instance (Cottontail rabbit) triggers the ranking of the context-instances based on cosine similarity.

4. ACKNOWLEDGMENTS

We thank Prof. Keith Kintigh for the data set and his help with the interpretations of the results.

5. REFERENCES

[1] T.C.Clark. Assessing Room Function Using Unmodified Faunal Bone: A Case Study from East-central Arizona. Kiva64(1): 1998.

[2] G.Chintalapani, C. Plaisant, B.Shneiderman: Extending the Utility of Treemaps with Flexible Hierarchy. IV, 2004.

[3] C. Eckart, G. Y. The Approximation of One Matrix by Another of Lower Rank. Psychometrika, 1936.

[4] S. Deerwester, S. Dumais, G.Furnas, R. Harshman, T. Landauer, K. Lochbaum and L. Streeter. Computer Information Retrieval using latent semantic Structure, US Patent, 1989.

[5] G. Salton, E.A. Fox, and H. Wu. Extended Boolean Information Retrieval. CACM, 26(11). 1983.

[6] T. Jirka. Multidimensional Data Visualization, Technical Report (DCSE/TR-2003-03), 2003.

[7] J.W. Kim and K.S. Candan. CP/CV: Concept Similarity Mining without Frequency Information from Domain Describing Taxonomies. CIKM, 2006.

[8] David G. Lowe. Three-dimensional object recognition from single two-dimensional images. AI, 1987.

[9] Y. Qi, K. S. Candan: CUTS: CUrvature-based Development Pattern Analysis and Segmentation for Blogs and other Text Streams. Hypertext, 2006.

[10] J.Seo and B.Shn. A Rank-by-Feature Framework for Unsupervised Multidimensional Data Exploration Using Low Dimensional Projections. IV 2004..

[11] K. Techapichetvanich, A. Datta, Interactive Visualization for OLAP, LNCS, Vol. 3482, 2005.