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Topological dynamic Bayesian networks: Application to human face identification across ages

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ABSTRACT

One of the major restrictions of dynamic Bayesian networks (DBNs) is their inability to account for topological features such as shape descriptors, homeomorphy, homotopy, and invariance. The main reason for this shortcoming is explained by the fact that even if dynamic Bayesian networks encode statistical relationships; they are not embedded in a Euclidean space where mathematical structures abound. The goal is to embed DBNs into a Euclidean space such that these topological features can be exploited. This extension of DBNs to topological DBNs (TDBNs) leapfrogs the task of pattern recognition and machine learning by not only classifying objects but revealing how they are related topologically. We have applied the TDBN formalism to facial aging for person identification. Preliminary results reveal that the TDBNs outperform the traditional DBN with an accuracy margin of 8% in average.

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- **Schedule:** Monday, June 14. Half day (Morning)

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- Topological Dynamic Bayesian Networks: Application to
- 0835 Human Face Identification across Ages, Djamel Bouchaffra
- 0855 A Robust Framework for Multiview Age Estimation, Zhen Li, Yun Fu, Thomas S. Huang
- Affect Valence Inference From Facial Action Unit
- 0915 Spectrograms, Daniel McDuff, Rana El Kaliouby, Karim Kassam, Rosalind Picard
- Real Time Head Pose Tracking from Multiple Cameras with a Generic Model, Qin Cai, Aswin

Topological Dynamic Bayesian Networks: Application to Human Face Identification across Ages

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Abstract

One of the major restrictions of dynamic Bayesian networks (DBNs) is their inability to account for topological features such as shape descriptors, homeomorphy, homotopy, and invariance. The main reason for this shortcoming is explained by the fact that even if dynamic Bayesian networks encode statistical relationships; they are not embedded in a Euclidean space where mathematical structures abound. The goal is to embed DBNs into a Euclidean space such that these topological features can be exploited. This extension of DBNs to topological DBNs (TDBNs) leapfrogs the task of pattern recognition and machine learning by not only classifying objects but revealing how they are related topologically. We have applied the TDBN formalism to facial aging for person identification. Preliminary results reveal that the TDBNs outperform the traditional DBN with an accuracy margin of 8% in average.

1. Introduction

One of the most compelling challenges consists of automatically producing models that are capable to, not only predict the category of a single object, but to grasp *topological*¹ relationships between objects as well. Devising machine learning paradigms that compass statistical and topological associations between objects will have a profound impact on the way computers perceive and process objects. Dynamic Bayesian Networks (DBNs) [1,2] that fully explain the traditional hidden Markov models (HMMs) have difficulty modeling continuous structures (surfaces) that are subject to local deformations of their constituents. For example, HMM-based models [3,4,5,6] are not inherently suitable to identify the same human face after it undergoes some slight *continuous* transformations due to aging. Even if this identification task could somehow be performed at a

feature level, it would be more complicated. Therefore, it is necessary to project a DBN in a Euclidean vector space in order to address this issue. One of the ultimate missions of this research is to answer the following questions: *How object A can be deformed in order to obtain object B and conversely?* For example, how can one predict *how facial aging develops?* And *what are the essential facial regions that age faster than others during aging process?* For example, the high school photograph of “John” at the age of fifteen, and his photograph at the age of fifty five should be assigned the same class during a face identification task. Some of the HMM’s extensions such as constrained [7], and situated space [8] represent an attempt to capture structural information by assigning each hidden state a spatial region of a fictitious topology space where a neighborhood between states is defined. However, the objective of these models is not to provide natural Euclidean space embeddings that allow examining topological relationships between objects.

The main reason behind the limitation of many traditional machine learning formalisms can be explained as follows: although DBNs encode probabilistic or causal relationships among variables of interest, they are not embedded in a Euclidean space that preserves network connectivity and exhibits topological properties. DBNs need to be *ingrained with a power of merging topological properties (such as homeomorphy, homotopy or invariance) with probabilistic data.*

The branch of topology [9] is fundamental should one needs to understand how objects evolve and whether they are related through some criteria such as “having the same roots (or ancestors)”. Unraveling both statistical and topological information within the standard DBNs represents a major challenge to the pattern recognition community. The inability to capture this vital information has drastically limited the performance of other neighboring areas such as content-based image/video retrieval, signal/image processing and the area of computer vision and robotics in general. Autonomous robots that are capable to relate objects via a fusion of statistics and topology will exhibit a more powerful cognitive skill. There are many other challenges that stem from areas such as: proteomics, and galaxy formation and

¹ From topology: the study of mathematical properties of geometric figures that remain unchanged even when they are distorted, so long as no surfaces are torn, as in the case of a Möbius strip.

evolution that are still to be faced. For example, genes homology which consists of determining sequences, either DNA or protein that shares a common evolutionary origin represents a crucial achievement in genetics and molecular biology. Likewise, the search of protein 3D folds that are similar topologically is vital in the area of proteomics, since structural similarity is correlated with functional similarity. We believe that topology (that grasps structural interconnections) and statistics (that predicts future outcomes based on past experiences) when merged together will play a vital role in the search of solutions.

We introduce a novel formalism whose goal is to embed the vertices of dynamic Bayesian networks into a Euclidean space so that topological features can be incorporated within a single probabilistic framework. The notion of “topological hidden Markov models” (THMMs) which extends the traditional HMM formalism will naturally unfold as a particular DBN’s embedding endowed with topological features.

3. Embedding a Network in a Euclidean Space: Topological Network

The goal is to embed data represented by a network (or a DBN) into a low dimensional Euclidean space. But first, let’s define the context of the word “embedding”:

Definition 1. If $N = (V, E, d)$ where V is a set of vertices, E a set of edges and d a distance measure expressing weights between two vertices, therefore an *embedding* of a network on a Euclidean space Γ (or a surface: compact, connected 2-manifold) is a representation of N on Γ in which vertices of V are mapped to points of Γ and directed edges of E are mapped to simple arcs such that:

- The endpoints of the arc mapped to a directed edge e are the points of Γ associated to the end vertices of e .
- No arcs contain points associated with other vertices.
- Two arcs never cross each other at a point which is interior to either of the arcs.

The purpose of a network embedding is to represent each vertex of the network as a low-dimensional vector that preserves similarities between the vertex pairs. The similarity is measured by a network similarity matrix that expresses certain graphical properties of the data set. Our objective is to: (i) introduce through this embedding, the concept of “topological network” (TN) (or “topological dynamic Bayesian network” (TDBN) if the network is a DBN) and (ii) explore its benefits among practitioners via a selected application.

3.1. Visible Observation Sequence and its Model

We define a visible observation (VO) sequence as a flow of symbols which represents either: (i) temporal data

(times series), generated by some causal process; and (ii) sequential data (such as bio-sequences), where the generating mechanism of this sequence is unknown. Furthermore, it is often the case that the generating mechanism of the symbols forming a VO sequence will be explained by different analytical models (made of the vertices of the entire VO sequence and some latent variables that explain the VO sequence). For example, the same VO sequence $O = o_1, o_2, \dots, o_T$ can be represented by an autoregressive model or a semi-factorial HMM or a semi-HMM with mixtures or simply a standard HMM. These three models depict particular networks. The selection of a suitable “VO sequence model” is executed by the model designer with the help of the expert in the area of application.

3.2. Determining the Pivot Vertices of a Network

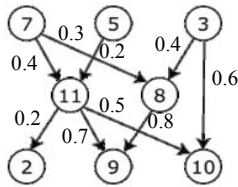
Because a VO sequence model is a network and therefore has a limited mathematical structure, our mission is to build a TN which depicts the set of points created by embedding the vertices of the VO sequence model (network) in an m -dimensional Euclidean space. There exist many algorithms in the literature that perform graph-embedding [10,11]; however, a very few have been dedicated to network embedding. Our approach consists of selecting a set P of m “pivot” vertices ($P = \{v_1, v_2, \dots, v_m\}$) that “best” represent the dimensions (basis) of the Euclidean vector space. The set P is constructed by first conducting a topological sort (TS) on the vertices of the network by edge. The TS procedure orders the vertices such that no incoming edges are first and vertices with only incoming edges are last. Therefore, the set formed by the first vertices produced by TS can be viewed as a generator set of the network. Since we draw an analogy between a generator set and a basis of a vector space, therefore the first vertices produced by TS are considered to be the axis of a Euclidean vector space. We have selected the first m vertices ($m \ll |V|$) produced by TS as forming a basis of a 3-dimensional vector space ($m=3$). The notion of “shortest-distance” (sd) in a general weighted directed acyclic graph (DAG) corresponds to the “longer distance” (ld) in the case where the network is a DBN, since a DBN holds conditional probability values rather than weights. Our approach to network embedding is general but is customized adequately (by transforming sd into ld) when weights between two vertices are conditional probability values. We denote by $d_N(v_i, u)$ the shortest-distance to any vertex u of the network from a source pivot vertex v_i . Each vertex u is mapped to an m -dimensional vector $X_u = [x_1(u), x_2(u), \dots, x_m(u)]^T$, where: $x_i(u) = d_N(v_i, u)$, ($i=1, \dots, m$). It is imperative that this drawing (or embedding) should exhibit the distance preserving embedding property: (i) two vertices u and v that are closely related in the network N ($d_N(v, u) \leq \epsilon$)

should be mapped to two vectors X_u and X_v whose Euclidean distance $d(X_u, X_v)$ is less than $d_N(u, v)$ in Γ . (ii) Conversely, two vertices that are unrelated (or non-adjacent) in the network should be mapped to two vectors that are far apart in Γ . Practically, the dimension of m is reduced to $m=3$ to avoid the curse of dimensionality and to visualize the network layout using Principal Components Analysis (PCA), Nonlinear Components Analysis (NLCA) or Independent Component Analysis (ICA) [12]. The entire embedding process is expressed as:

-
- 1) Conduct a topological sort on the vertices by edge such that vertices with no incoming edges are first and vertices with only incoming edges are last,
 - 2) Select the first m vertices $p_1 \dots p_m$ produced by the topological sort as pivot and set $S = \{p_1, p_2, \dots, p_m\}$
 - 3) **for** each vertex s of S **do** {
 - 4) assign an infinite shortest-distance to every vertex ($sd(v) = \infty$ if $v \neq s$) and a zero shortest-distance to the source s ($sd(s) = 0$)
 - 5) **for** each vertex v in sorted order **do**{
 - 6) **for** each outgoing edge $e(v, u)$ **do**{
 - 7) **if** ($sd(v) + \text{weight}(e) < sd(u)$) **then** {
 $sd(u) = sd(v) + \text{weight}(e);$
 $u = \text{Predecessor}(v);$ }
 - 8) Build the set of points X_u for every vertex u of the network.
-

The set of points X_u formed through this embedding process constitutes the topological network.

Illustration on an arbitrary network N:



By convention: Vertices that are not reachable from any source are assigned a zero shortest-distance from that source.

The topological sorting on the vertices by edge provides: [7, 5, 3, 11, 8, 10, 9, 2]. We then select the first m ($m=3$) vertices of the sorting to be the set of pivot vertices, $S = \{7, 5, 3\}$. Each vertex u of the network is converted to a 3D-point $X_u = [d_N(7, u), d_N(5, u), d_N(3, u)]^T$. This computation provides the 3D-points:

vertex 2: $[0.6, 0.4, 0]^T$; vertex 3: $[0, 0, 0]^T$; vertex 5: $[0, 0, 0]^T$;
vertex 7: $[0, 0, 0]^T$; vertex 8: $[0.3, 0, 0.4]^T$; vertex 9: $[1.1, 0.9, 1.2]^T$;
vertex 10: $[0.9, 0.7, 0.6]^T$; vertex 11: $[0.4, 0.2, 0]^T$.

Figure 1 sketches the points assigned to all vertices in a 3-dimension vector space.

3.3. Topological Mapping: Projection onto a Euclidean Space

We focus now on a TDBN which is a particular topological network. The distances between points in the 3D Euclidean space are computed on the basis of: (i) the conditional probability values between pairs of vertices of a DBN; and (ii) the notion of “longest-distance path” from a source vertex to any other vertex of a DBN. Since a TDBN is defined in a discrete set of a Euclidean space, therefore it has is mapped to a continuous set where metrics, homeomorphism, homotopy, as well as invariance properties can be exploited. Once the continuous set assigned to a TDBN is built, our objective is to assign it a set of topological features. This is expressed as follows:

We first map the VO sequence to its model: This mapping is called “VO Sequence Modeling” (**function f**). We then embed (or draw) the VO sequence model in a Euclidean vector space to obtain a TDBN (set of discrete points X): This mapping is called a “VO Sequence Model Embedding” (**function g**). We map the TDBN set to its continuous set: “TDBN Continuous Representation” (**function h**), and finally derive topological features from

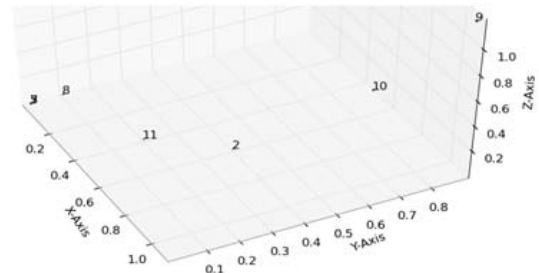


Figure 1. Topological network assigned to the network N: Vertices are embedded in a 3D vector space as points.

the TDBN continuous set: “TDBN Topological Features” (**function i**). Simple DBNs (e.g., HMMs and Kalman filters) are thus ingrained in a Euclidean space where structural information is exhibited.

4. Problems Addressed by Topological Dynamic Bayesian Networks

The problems addressed in the context of a TDBN are:

(i) **Learning a TDBN:** The goal is to learn the positions of the points of the set X (the TDBN) in the Euclidean space. This phase derives directly from the *learning phase of a traditional DBN* [2] but also on the choice of the pivot vertices of the DBN. In other words, the refinement of the DBN structure and the local variable distributions given the data as well as a change of the dimension axes (pivot vertices) of the Euclidean space will decide on the positions of the TDBN points.

(ii) Shape of a TDBN: Since a TDBN X (originated from a DBN) represents a discrete set of points, therefore, the concept of continuity which represents the foundation of topology is difficult to apply. *This is the reason why it is necessary to map a discrete set to a continuous set.* The most natural way to achieve this objective is provided via the notion of “shape”. An efficient means for creating shapes out of point sets is provided by *shape constructors* such as the “ α -shapes” formalism [13]. The α -shape concept represents a formalization of the intuitive notion of “shape” for spatial point set data. *An α -shape is a concrete geometric object that is uniquely defined for a particular set of points.* The parameter α controls the *desired level of details of the shape*. There are several algorithms that construct a family of shapes for a given set of size n in a worst-case time complexity equal to $O(n^2)$ [13]. The “best” alpha-shape assigned to a TDBN is produced only by an optimal DBN given a set of pivot vertices. The α -shapes define a hierarchy of shapes from a set of points (TDBN) that allows features multiscale modeling that are very useful in macromolecule structure exploration as well as in facial aging (identifying changes of human facial compartments: a human face is made of compartments of fat). The α -shapes insert a ball of radius $\sqrt{\alpha}$ around each point and build a simplicial complex that respects the intersections among these balls. The simplicial space formed is defined as the α -shapes. Figure 2 depicts two shapes of the TDBN for different α values. One can notice that more points are connected when $\alpha=2$ compared to when $\alpha=0.5$. *The increase in the connected points is proportional to $(\alpha_2 - \alpha_1)$.*

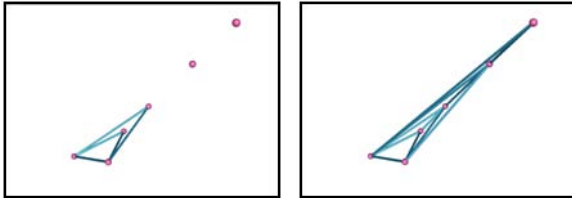


Figure 2. Two α -shapes with $\alpha = 0.5$ and $\alpha = 2$ represent the shape of the TN of the example in section 3.2 at different level of details.

Since the balls around two points in an α -shape have to intersect to express the probabilistic relationship between their corresponding vertices in the DBN therefore, the value of α should obey: $\alpha \geq d_{ij}^2/4$, where d_{ij} is the Euclidean distance between these two points in the TDBN. *It is clear that the α -shapes depend on the positions of the points of X that are driven by the traditional DBN learning phase.* Furthermore, one can extract “signatures” of α -shapes (or any other shape constructor assigned to a TDBN) such as *metric properties*: (volume, area and length), *combinatorial properties*: (number of tetrahedral,

triangles, edges, vertices) and *topological properties*: (number of components, number of independent tunnels, and number of voids). These signatures are put into a *vector form* that characterizes an α -shape (or any other shape constructor).

(iii) Topological Mappings: Because shape constructors (e.g., α -shapes) transform a discrete space (TDBN) into a continuous space, therefore other features such as homeomorphism and homotopy equivalence can also be exploited. If $h(X) = A$ (A is a shape constructor applied to a TDBN = **object of study**) then the pair (A, d) represents a metric space (d is a distance function). A homeomorphism map (bijective, bicontinuous) between two metric spaces (A_1, d_1) and (A_2, d_2) can be built. A_1 and A_2 are two topologically similar objects (or the same object). Similarly, we have the following definition:

Definition 2. Two spaces A_1 and A_2 are homotopy equivalent if there exist continuous maps $f: A_1 \rightarrow A_2$ and $g: A_2 \rightarrow A_1$ such that $g \circ f$ is homotopic to the identity map id_{A_1} and $f \circ g$ is homotopic to id_{A_2} . Intuitively, *two spaces (or objects) A_1 and A_2 are homotopy equivalent if they can be transformed into one another by bending, shrinking and expanding operations.*

(iv) Training: Given a VO sequence as input, the first phase consists of selecting the VO sequence model which is a DBN that explains the VO sequence. The second phase focuses on training the DBN from the data to obtain an optimal DBN. The third phase consists of assigning the optimal DBN to its corresponding embedded DBN to obtain an optimal TDBN. The fourth phase consists of constructing the shapes assigned to the TDBN by applying different geometric constructors (e.g., α -shapes (AS), flow-shapes (FS) and union of balls (UB)) using any state-of-the-art shape constructor algorithm [14]. A set of shapes is formed for different values of α that depend on the TDBN points’ density. Because it has been proven that the α -shapes, the “flow-shapes”, and the “union of balls” constructors are homotopy equivalent [14], therefore they provide “similar” continuous shapes when applied to the same TDBN. Finally, signatures (vectors) of these similar shapes are computed and put together in a cluster to form a *homotopic equivalence class* $[\omega]$. The entire process (from the VO sequence to the homotopic class formation) is undertaken for all VO observation sequences forming the training set. This process is depicted by Figure 3. Two signature vectors of the homotopic equivalence class $[\omega]$ are related since they represent “similar shapes” obtained via the three homotopic constructors (the α -shapes, the “flow-shapes”, and the “union of balls”). This process of assigning homotopic equivalence classes $[\omega_i]$ ($i=1, \dots, c$) is unsupervised and conducted offline during training.

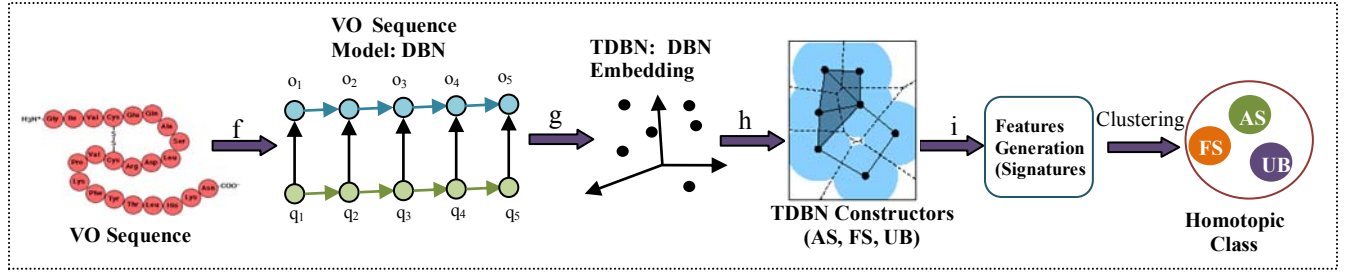


Figure 3. Embedding of a particular DBN (autoregressive HMM) assigned to an amino acid sequence in a Euclidean space. The α -shape (depicted in this figure) is one of the possible constructors that provide a shape to the TDBN from which topological features are generated.

(v) Classification/Testing: Given a VO sequence $O = o_1, o_2, \dots, o_T$, the classification problem is stated as follows: Determine the class ω^* (denoted $[\omega^*]$) among c target classes assigned to this VO sequence such that:

$$\omega^* = \underset{\omega_i}{\operatorname{argmax}} P[\omega_i | o_1, o_2, \dots, o_T], \quad (i = 1, \dots, c).$$

This is equivalent to the determination of the class ω^* such that: $\omega^* = \underset{\omega_i}{\operatorname{argmax}} P[\omega_i | v_1, v_2, \dots, v_n]$, where the sequence (v_1, v_2, \dots, v_n) represents the DBN assigned to the VO sequence (o_1, o_2, \dots, o_T) . However, the idea is to utilize the embedding process g in which $x_i = g(v_i)$; therefore, one can write:

$$P[\omega_i | v_1, v_2, \dots, v_n] \equiv P[\omega_i | (\mathbf{h} \circ \mathbf{g})(v_1, v_2, \dots, v_n)].$$

This latter expression can also be written as: $P[\omega_i | \mathbf{h}(x_1, x_2, \dots, x_n)]$, which consists of evaluating the probability that the shape obtained by applying the geometric constructor h to a TDBN belong to the homotopic class ω . Since, there are three homotopic equivalence constructors with different α values; therefore a set of signature vectors is generated. This set of vectors is represented by its mean vector \bar{S} . In conclusion, the classification problem is expressed as:

$$P[\omega_i | \mathbf{i}(\mathbf{h}(x_1, x_2, \dots, x_n)) = \bar{S}].$$

In other words, for a given TDBN, this classification problem consists of assigning a homotopic equivalence class to an input set of signature vectors characterized by their mean vector. Any continuous deformation of a shape is therefore captured. It is worth to underscore that this investigation goes beyond traditional classification objective since its purpose is not limited only to classifying objects but also to seeking interrelationships between geometric constructors that impact objects. The classification problem is further detailed as:

$$P(\omega_i | \bar{S}) = \frac{P(\bar{S} | \omega_i) \cdot P(\omega_i)}{\sum_{i=1}^{i=c} P(\bar{S} | \omega_i) \cdot P(\omega_i)}.$$

We assume that each class ω_i is made of signature samples (obtained by assigning many different values of α in the

constructors) that come from a known number of 3 mixtures (3 homotopic shapes) whose probability structure is Gaussian.

$$P(\bar{S} | \omega_i) = \sum_{k=1}^{k=3} c_{ik} N(\bar{S}, \mu_{ik}, U_{ik}), \quad 1 \leq i \leq c$$

where c_{ik} is the mixture coefficient for the k -th mixture in class ω_i . Without loss of generality, $N(\bar{S}, \mu_{ik}, U_{ik})$ is assumed to be a Gaussian probability density function with mean vector μ_{ik} and covariance matrix U_{ik} .

Different modules in the TDBN Classifier:

1. Update the DBN parameters through learning via data
2. Map the optimal DBN to its corresponding TDBN
3. Compute α -shapes, “flow-shapes”, and “union of balls”
4. Extract topological feature vectors for training
5. Build homotopic clusters from feature vectors
6. Test incoming patterns for classification.

5. Application and Preliminary Results

(i) Face Identification across Ages:

Problem statement: Given a face sample of an individual at age a_0 ; one determines if this input face is associated with any of a large number of enrolled faces of individuals. However, some face images of the same individual at ages $(a_1 \geq a_0 + 15 \text{ years})$ are *among the enrollees*. In other words, given two faces, can one infer that they represent the same individual at different ages?

A human face is viewed as an ordered visible observation sequence $O = o_1, \dots, o_T$. Each o_i is a vector that captures a facial region such as: “hair”, “forehead”, “eyes”. These vectors are obtained by scanning the image from left to right and top to bottom using a 2D window. Each block image undergoes discrete wavelet transform (DWT) decomposition [15], producing an average image and a sequence of detail images. The sub-image is then decomposed to a certain level and the sub-band energies are selected to form the feature vector o_i . The facial regions (forehead, eyes, mouth, ears, nose) are latent variables (or hidden states) and the o_i are the observables

(feature vectors of sub-band energies); all these variables represent vertices of a dynamic Bayesian network (autoregressive HMM). The weights in this network represent conditional probabilities between a facial region and a feature vector, between two facial regions and two feature vectors. The DBN is embedded in a Euclidean space to form the TDBN subspace of a face. We then apply shape constructors associated to the TDBN to extract the signature vectors of the face. Since we are considering 3 shape constructors (with different α values) that are topologically equivalent, therefore several signature vectors are extracted and gathered to form a homotopic equivalence class ω that represents a face at a particular age (refer to Figure 4).

We have conducted the same task with 3 face images (with different facial expressions) of different ages of the same individual. 2 of these 3 faces are left for training

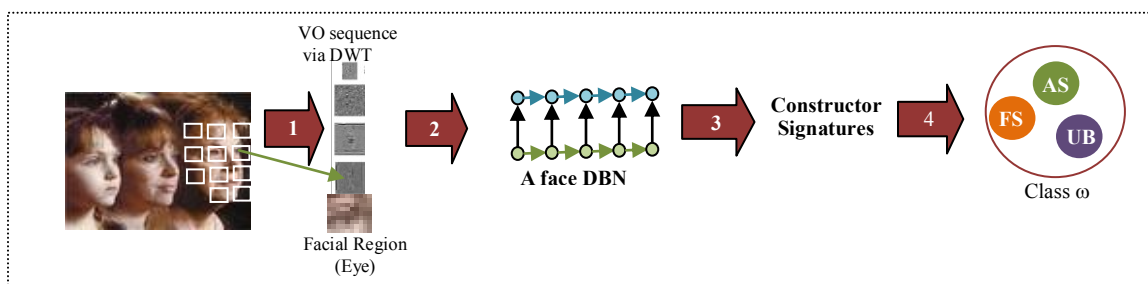


Figure 4. Diagram showing a face as an autoregressive model (DBN) that is embedded in a TDBN whose constructor (AS, FS, UB) signatures are extracted to form the *face homotopic equivalence class*.

whereas 1 face of the same individual is left for testing. The homotopic classes assigned to the 2 training faces of the same individual are merged together to form a “*super homotopic class*”. We have collected $50 \times 3 = 150$ face images *from family members and friends*; but since it is difficult to obtain a large number of faces of same individuals at different ages that would provide a statistical significance, we have used $100 \times 3 = 300$ *simulated faces obtained via dedicated software*. Aging patterns are introduced by changing values of some input parameters. We have therefore built a database of 450 faces in total. In order to measure the power of generalization of the TDBN classifier, we used the m -fold cross-validation estimation technique. We divided the images of the 450 face images into 5 sets ($m=5$), each of which contains 90 face images. We then selected 1 set for testing (validation data) and the other 4 sets (360 face images) for training ensuring that only 1 face of an individual is included in the testing set and the 2 other faces of this individual are part of training. We repeated this procedure 5 times with each time selecting a different set for a validation data. The 5 results from the folds are averaged to produce a single estimation. Finally, testing was undertaken by extracting the mean vector signature

\bar{S} (as described in section 3-v) of the input face and computing the class whose posterior probability $P(\omega_i | \bar{S})$ is maximum. Preliminary results are encouraging; they show that a TDBN outperforms standard DBN using different DWT kernels during a 5-fold cross validation experiment (refer to Table 1).

DWT Kernels	Average Precision of DBN	Average Precision of TDBN
Haar	84.2	92.2
Biorth9/7	78.0	89.8
Coiflet(3)	85.6	94.7
Gabor	85.9	91.3

Table 1. Average precisions (%) of TDBNs and DBNs using 5-fold cross validation with different DWT kernels.

The highest precision currently achieved by TDBN is

94.7% via Coiflet. The precision P in each fold is defined by the following ratio:

$$\frac{\# \text{ of face images that were correctly identified}}{\text{Total \# of face images tested}} \times 100\%$$

where the sign “#” means “number”.

(ii) Role of Homotopy Equivalence:

Since the TDBN is determined by a VO sequence and a DBN, therefore what information the α -shapes encapsulate that make it possible for the performance to increase? The answer stems from the idea of extracting several topologically equivalent shapes assigned to the DBN via the TDBN. There is an increase of connected points in the α -shapes faces during a human face aging process as it has been noticed from the example of Figure 2. The generation of many different shapes from the same face DBN allows exploring several deformations of the same human face. All these different shapes are homotopy equivalent. In fact, both α -shapes and flow shapes for example can be applied to generate a hierarchy of shapes from a set of points. This permits multi-scale modeling which appears to be suitable in revealing features at

different length scales such as fat compartments in a human face). This pattern cannot be exploited using the DBN concept alone, since homotopy equivalence is absent in a standard DBN. The different values of α depicts different levels of “aging details” in the α -shape assigned to the face TDBN. In conclusion, it appears that the fusion of statistics (in DBN) and topology (in TDBN) allows deformations of objects to be exhibited and modeled. For example, the changes in facial features (such as appearance of wrinkles, or loss of firmness of the skin, or facial contour deformation) due to aging are captured by some DWT kernels and incorporated in the shape signatures provided by homotopic constructors. Furthermore, signature vectors contain topological invariants that are vital for identifying the same individual at different ages of her life.

(iii) Impact of this Research on Aging:

This investigation allows gaining an insight into one of the most important mysteries related to facial aging. How facial aging is being managed by Mother Nature? It has been conjectured that the face is made up of individual fat compartments that gain and lose fat at different times and different rates as we grow older. Understanding how fat is compartmentalized will allow doctors to be very precise in how facial rejuvenation could be approached. The TDBN approach might help unravel this biological mechanism. The distribution of the components of the signature vectors is the key to providing some clues to this unsolved problem. This distribution helps explaining how these separate compartments change as we age. Our next objective is to analyze the signatures of youthful faces (that exhibit smooth transitions between the fat compartments) with respect to the value assigned to α . The outcomes from this investigation could have tremendous implications in assisting plastic surgeons target facial “deformed” areas and use “injectible fillers” to increase volume to individual regions of the human face. It could also help in designing novel cosmetic and reconstructive surgery techniques. Since aging occurs at a cell level, this research might hold clues to the investigation of other diseases such as diabetes obesity, and cancer.

6. Conclusion

We have introduced an extension of graph embedding to network embedding. Our mission is to focus on dynamic Bayesian networks. The methodology that is proposed allows topological features to be accounted for during a classification task via DBN. This fusion of statistics and topology expressed via the concept of topological dynamic Bayesian network is a preliminary endeavor to connect discrete structures with continuous structures. Experimental results have demonstrated the need for such

formalism that reaches beyond a pure statistical analysis. Many crucial problems such as “find tumors that are similar to a given pattern image-guided radiation therapy”, or “is the morphology of galaxy A related to the morphology of galaxy B?” and others issues in genomics and proteomics will benefit from this fusion. Medical researchers might use a TDBN approach to: (i) repair a damaged brain by transforming it into a healthy one, and (ii) investigate the causes of a brain injury and (iii) identify its location. Similarly, Industry is interested in applications that take into account the elastic nature of objects, such as a piston sliding along a cylinder in response to changes in pressure.

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