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Think Globally, Fit Locally: Unsupervised Learning of Nonlinear Manifolds

Lawrence K. Saul lsaul@cis.upenn.edu
Department of Computer and Information Science
University of Pennsylvania
200 South 33rd Street
557 Moore School - GRW
Philadelphia, PA 19104-6389, USA

Sam T. Roweis roweis@cs.toronto.edu
Department of Computer Science
University of Toronto
6 King's College Road
Pratt Building 283
Toronto, Ontario M5S 3G4, CANADA

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Abstract

The problem of dimensionality reduction arises in many fields of information processing, including machine learning, data compression, scientific visualization, pattern recognition, and neural computation. Here we describe locally linear embedding (LLE), an unsupervised learning algorithm that computes low dimensional, neighborhood preserving embeddings of high dimensional data. The data, assumed to lie on a nonlinear manifold, is mapped into a single global coordinate system of lower dimensionality. The mapping is derived from the symmetries of locally linear reconstructions, and the actual computation of the embedding reduces to a sparse eigenvalue problem. Notably, the optimizations in LLE—though capable of generating highly nonlinear embeddings—are simple to implement, and they do not involve local minima. We describe the implementation of the algorithm in detail and discuss several extensions that enhance its performance. The algorithm is applied to manifolds of known structure, as well as real data sets consisting of images of faces, digits, and lips. We provide extensive illustrations of the algorithm's performance.

1. Introduction

Many problems in machine learning begin with the preprocessing of raw multidimensional signals, such as images of faces or spectrograms of speech. The goal of preprocessing is to obtain more useful representations of the information in these signals for subsequent operations such as classification, denoising, interpolation, visualization, or outlier detection. In the absence of prior knowledge, such representations must be learned or discovered automatically. Automatic methods which discover hidden structure from the statistical regularities of large data sets can be studied in the general framework of *unsupervised learning* [Hinton and Sejnowski (1999)].

Two main goals have been proposed for algorithms in unsupervised learning: *density estimation* and *dimensionality reduction*. The goal of density estimation is to learn the parameters of a probabilistic model that can be used to predict or assess the novelty of future observations. The goal of dimensionality reduction is to obtain more compact representations of the original data that capture the information necessary for higher-level decision making. A recent trend in machine learning has been to pursue these goals simultaneously, with probabilistic generative models of raw sensory inputs whose hidden variables represent low dimensional degrees of freedom [Attias (1999), Dayan et al. (1995), Hyvärinen (1998), Roweis (1998), Roweis et al. (2002), Tipping and Bishop (1999)]. However, the goal of dimensionality reduction can also be pursued in a non-probabilistic and non-parametric setting. This is the approach taken here.

Our algorithm addresses a longstanding problem at the intersection of geometry and statistics: to compute a low dimensional embedding of high dimensional data assumed to lie on a nonlinear manifold. Many types of high dimensional data can be characterized in this way—for example, images generated by different views of the same three dimensional object. The use of manifolds to represent continuous percepts is also a recurring theme in computational neuroscience [Seung and Lee (2000)]. The goal of our algorithm is to learn such representations from examples: to discover—in a general setting, without the use of a priori knowledge—the few degrees of freedom that underlie observed modes of continuous variability.

Two canonical forms of dimensionality reduction are the methods of principal component analysis (PCA) [Jolliffe (1986)] and multidimensional scaling (MDS) [Cox and Cox (1994)]. Both PCA and MDS are eigenvector methods designed to model linear variabilities in multidimensional data. In PCA, one computes the linear projections of greatest variance from the top eigenvectors of the data covariance matrix. In MDS, one computes the low dimensional embedding that best preserves pairwise distances between data points. If these distances correspond to Euclidean distances, the results of MDS are equivalent to PCA. Both methods are simple to implement, and their optimizations are well understood and not prone to local minima. These virtues account for the widespread use of PCA and MDS, despite their inherent limitations as linear methods.

Recently, we introduced a more powerful eigenvector method—called locally linear embedding (LLE)—for the problem of *nonlinear dimensionality reduction* [Roweis and Saul (2000)]. This problem is illustrated by the nonlinear manifolds in Fig. 1. In these examples, dimensionality reduction by LLE succeeds in recovering the underlying manifolds, whereas linear embeddings by PCA or MDS map faraway data points to nearby points in the plane, creating distortions in both the local and global geometry. Like PCA and MDS, our algorithm is simple to implement, and its optimizations do not involve local minima. Unlike these methods, however, it is capable of generating highly nonlinear embeddings, and its main step involves a *sparse* eigenvalue problem that scales more naturally to large, high dimensional data sets.

Note that mixture models for local dimensionality reduction [Fukunaga and Olsen (1971), Ghahramani and Hinton (1996), Kambhatla and Leen (1997)], which cluster the data and perform PCA within each cluster, do not address the problem considered here—namely, how to map high dimensional data into a single global coordinate system of lower dimensionality. In particular, while such models can be used to discover and characterize

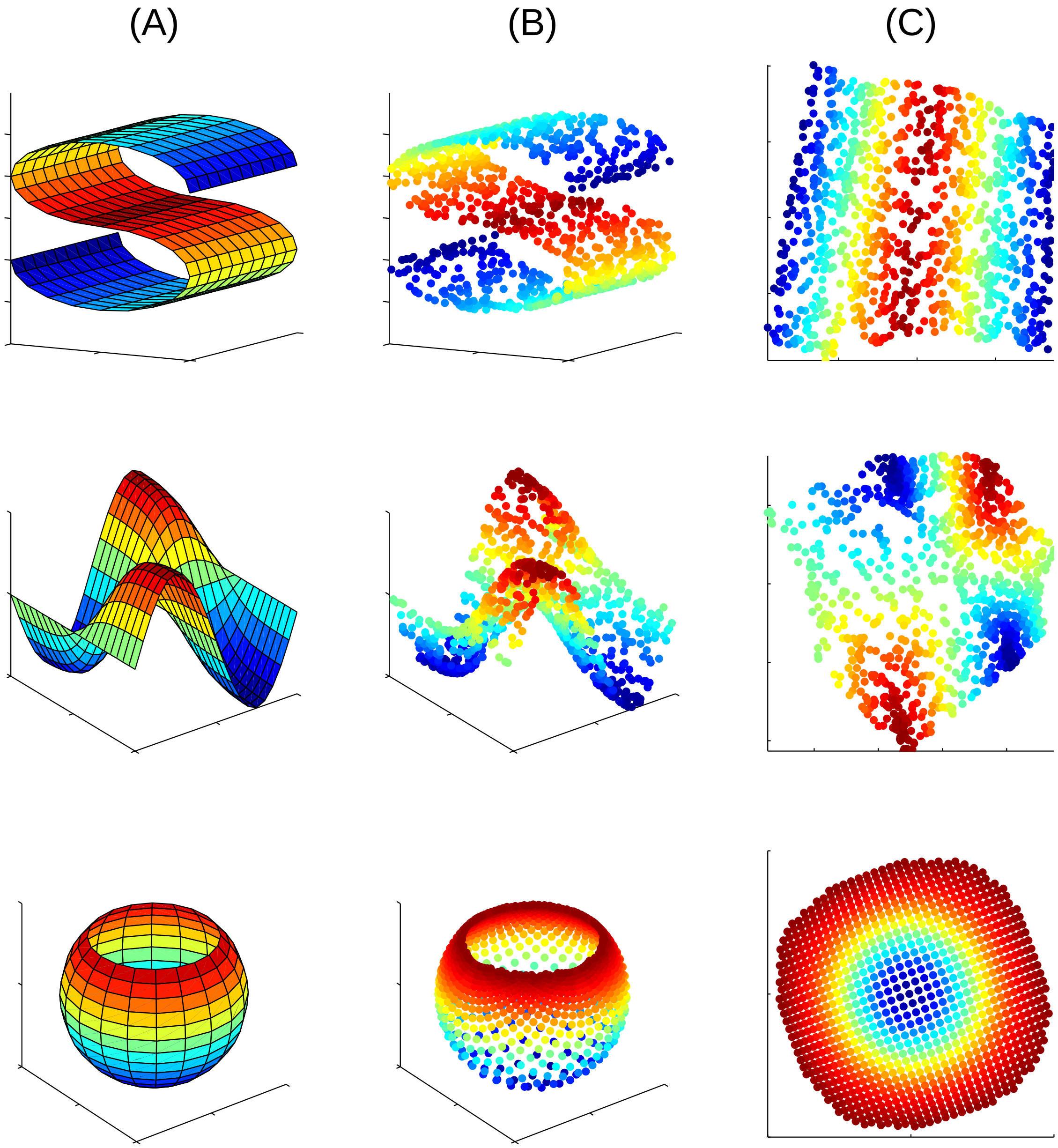

Figure 1: The problem of nonlinear dimensionality reduction, as illustrated for three dimensional data (B) sampled from two dimensional manifolds (A). An unsupervised learning algorithm must discover the global internal coordinates of the manifold without signals that explicitly indicate how the data should be embedded in two dimensions. The color coding in (C) illustrates the neighborhood-preserving mappings as discovered by the LLE algorithm described in this paper.

clusters in high dimensional data, they could not be used to compute the two dimensional embeddings in the rightmost panels of Fig. 1.

In this paper, we review the LLE algorithm and provide significantly more examples and details of its implementation than can be found in earlier work [Roweis and Saul (2000)]. We also discuss a number of extensions that enhance its performance. The organization of this paper is as follows: In section 2, we describe the algorithm in general terms, focusing on its main procedures and geometric intuitions. In section 3, we illustrate the algorithm's performance on several problems of different size and dimensionality. In section 4, we discuss the most efficient ways to implement the algorithm and provide further details on the nearest neighbor search, least squares optimization, and eigenvalue problem. In sections 5 and 6, we describe a number of extensions to LLE, including how to estimate or enforce the dimensionality of discovered manifolds, as well as how to learn both parametric and non-parametric mappings between spaces of different dimensionality. Finally, in section 7, we compare LLE to other eigenvector-based methods for clustering and nonlinear dimensionality reduction [Belkin and Niyogi (2002), Ng et al. (2002), Schölkopf et al. (1998), Shi and Malik (2000), Tenenbaum et al. (2000), Weiss (1999)] and mention several directions for future work.

2. Algorithm

The LLE algorithm, summarized in Fig. 2, is based on simple geometric intuitions. Essentially, the algorithm attempts to compute a low dimensional embedding with the property that *nearby points in the high dimensional space remain nearby and similarly co-located with respect to one another in the low dimensional space.* Put another way, the embedding is optimized to preserve the local configurations of nearest neighbors. As we shall see, under suitable conditions, it is possible to derive such an embedding solely from the geometric properties of nearest neighbors in the high dimensional space. Indeed, the LLE algorithm operates entirely without recourse to measures of distance or relation between faraway data points.

To begin, suppose the data consist of N real-valued vectors $\vec{X}_i$ (or *inputs*), each of dimensionality D, sampled from an underlying manifold. Provided there is sufficient data (such that the manifold is well-sampled), we expect each data point and its neighbors to lie on or close to a locally linear patch of the manifold. More precisely, by "smooth" and "well-sampled" we mean that for data sampled from a d-dimensional manifold, the intrinsic curvature and sampling density are such that each data point has on the order of $2d$ neighbors which define a roughly linear patch on the manifold with respect to some metric in the input space. Under such conditions, we can characterize the local geometry in the neighborhood of each data point by linear coefficients that reconstruct the data point from its neighbors. The LLE algorithm derives its name from the nature of these reconstructions: it is *local*, in the sense that only neighbors contribute to each reconstruction, and *linear*, in the sense that reconstructions are confined to linear subspaces.

In the simplest formulation of LLE, one identifies K nearest neighbors per data point, as measured by Euclidean distance. (More sophisticated neighborhood criteria are discussed

LLE ALGORITHM

1. **Compute the neighbors of each data point, $\vec{X}_i$.**
2. **Compute the weights W_{ij} that best reconstruct each data point $\vec{X}_i$ from its neighbors, minimizing the cost in eq. (1) by constrained linear fits.**
3. **Compute the vectors $\vec{Y}_i$ best reconstructed by the weights W_{ij}, minimizing the quadratic form in eq. (2) by its bottom nonzero eigenvectors.**

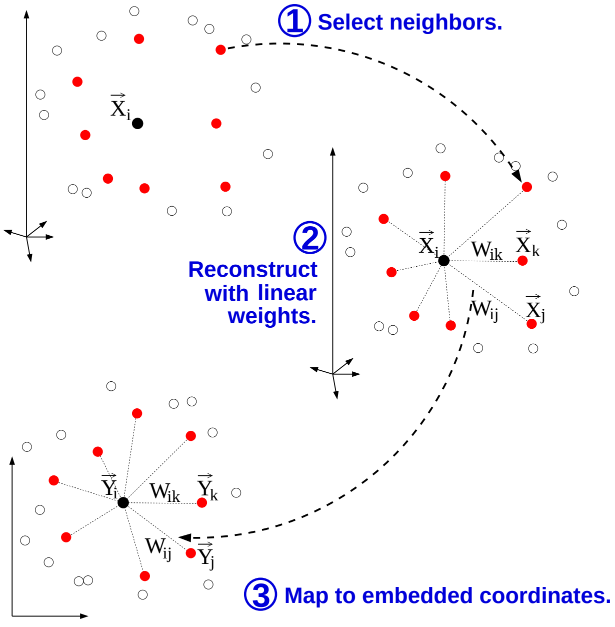

Figure 2: Summary of the LLE algorithm, mapping high dimensional inputs $\vec{X}_i$ to low dimensional outputs $\vec{Y}_i$ via local weights W_{ij}.

in section 4.) Reconstruction errors are then measured by the cost function:

$$\mathcal{E}(W) = \sum_i \left| \vec{X}_i - \sum\nolimits_j W_{ij} \vec{X}_j \right|^2, \tag{1}$$

which adds up the squared distances between all the data points and their reconstructions. The weight W_{ij} summarizes the contribution of the jth data point to the ith reconstruction. To compute the weights, we minimize the cost function in eq. (1) subject to two constraints: a *sparseness* constraint and an *invariance* constraint. The sparseness constraint is that each data point $\vec{X}_i$ is reconstructed only from its neighbors, enforcing $W_{ij} = 0$ if $\vec{X}_j$ does not belong to this set. The invariance constraint is that the rows of the weight matrix sum to one: $\sum_j W_{ij} = 1$. The reason for this latter constraint will become clear shortly. The optimal weights W_{ij} subject to these constraints are found by solving a set of constrained least squares problems, as discussed further in section 4.

Note that the constrained weights that minimize these reconstruction errors obey several important symmetries: for any particular data point, they are invariant to rotations, rescalings, and translations of that data point and its neighbors.[1] The invariance to rotations

[1] Naturally, they are also invariant to global rotations, translations and homogeneous rescalings of all the inputs, but the invariance to local transformations has far more powerful consequences.

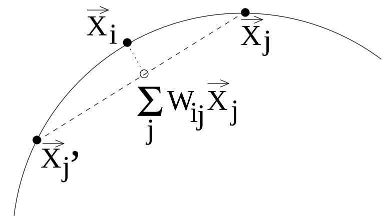

Figure 3: A data point $\vec{X}_i$, its neighbors $\vec{X}_j$, and its locally linear reconstruction $\sum_j W_{ij}\vec{X}_j$.

and rescalings follows immediately from the form of eq. (1); the invariance to translations is enforced by the sum-to-one constraint on the rows of the weight matrix. A consequence of this symmetry is that the reconstruction weights characterize intrinsic geometric properties of each neighborhood, as opposed to properties that depend on a particular frame of reference.

Suppose the data lie on or near a smooth nonlinear manifold of dimensionality $d \ll D$. To a good approximation, then, we imagine that there exists a linear mapping—consisting of a translation, rotation, and rescaling—that maps the high dimensional coordinates of each neighborhood to global internal coordinates on the manifold. By design, the reconstruction weights W_{ij} reflect intrinsic geometric properties of the data that are invariant to exactly such transformations. We therefore expect their characterization of local geometry in the input space to be equally valid for local patches on the manifold. In particular, the same weights W_{ij} that reconstruct the input $\vec{X}_i$ in D dimensions should also reconstruct its embedded manifold coordinates in d dimensions.

(Informally, imagine taking a pair of scissors, cutting out locally linear patches of the underlying manifold, and arranging them in the low dimensional embedding space. If the transplantation of each patch involves no more than a translation, rotation, and rescaling, then the angles between data points on the patch will be preserved. It follows that when the patch arrives at its low dimensional destination, the same weights will provide the optimal reconstruction of each data point from its neighbors.)

LLE constructs a neighborhood preserving mapping based on the above idea. In the third and final step of the algorithm, each high dimensional input $\vec{X}_i$ is mapped to a low dimensional *output* $\vec{Y}_i$ representing global internal coordinates on the manifold. This is done by choosing the d-dimensional coordinates of each output $\vec{Y}_i$ to minimize the embedding cost function:

$$\Phi(Y) = \sum_i \left| \vec{Y}_i - \sum\nolimits_j W_{ij}\vec{Y}_j \right|^2. \tag{2}$$

This cost function—like the previous one—is based on locally linear reconstruction errors, but here we fix the weights W_{ij} while optimizing the outputs $\vec{Y}_i$. Note that the embedding is computed directly from the weight matrix W_{ij}; the original inputs $\vec{X}_i$ are not involved in this step of the algorithm. Thus, the embedding is determined entirely by the geometric information encoded by the weights W_{ij}. Our goal is to find low dimensional outputs $\vec{Y}_i$ that are reconstructed by the same weights W_{ij} as the high dimensional inputs $\vec{X}_i$.

The embedding cost function in eq. (2) defines a quadratic form in the outputs $\vec{Y}_i$. Subject to constraints that make the problem well-posed, the cost function has a unique global minimum. This unique solution for the outputs $\vec{Y}_i$ is the result returned by LLE as the low dimensional embedding of the high dimensional inputs $\vec{X}_i$. The embedding cost function can be minimized by solving a sparse $N \times N$ eigenvalue problem. Details of this eigenvalue problem are discussed in section 4. There, we show that the bottom d non-zero eigenvectors of an easily computed matrix provide an ordered set of embedding coordinates.

Note that while the reconstruction weights for each data point are computed from its local neighborhood—independent of the weights for other data points—the embedding coordinates are computed by an $N \times N$ eigensolver, a global operation that couples all data points (or more precisely, all data points that lie in the same connected component of the graph defined by the neighbors). This is how the algorithm discovers global structure—by integrating information from overlapping local neighborhoods.

Implementation of the algorithm is straightforward. In the simplest formulation of LLE, there exists only one free parameter: the number of neighbors per data point K (or any equivalent neighborhood-determining parameter, such as the radius of a ball to be drawn around each point). Once neighbors are chosen, the optimal weights W_{ij} and outputs $\vec{Y}_i$ are computed by standard methods in linear algebra, as detailed in section 4. The algorithm involves a single pass through the three steps in Fig. 2 and finds global minima of the reconstruction and embedding costs in Eqs. (1) and (2). No learning rates or annealing schedules are required during the optimization and no random initializations or local optima affect the final results.

3. Examples

The embeddings discovered by LLE are easiest to visualize for intrinsically two dimensional manifolds. In Fig. 1, for example, the input to LLE consisted of $N = 1000$ data points sampled off the manifolds shown in panel (A). The resulting embeddings show how the algorithm, using $K = 8$ neighbors per data point, faithfully maps these manifolds to the plane.

The example in the bottom row of Fig. 1 shows that, under the right conditions, LLE can learn the stereographic mapping from the sphere to the plane. For the algorithm to succeed in this case, a neighborhood of the north pole must be excluded, and the data must be sampled uniformly in stereographic coordinates (which corresponds to increasing density as one approaches the north pole). This example suggests that LLE can recover conformal mappings—mappings which locally preserve angles, but not distances. Such a conjecture is also motivated by the invariance of the reconstruction weights in eq. (1) to translations, rotations, *and scalings* of local neighborhoods. Nevertheless, it remains an open problem to prove whether such manifolds can generally be discovered by LLE, and if so, under what sampling conditions.[2]

Fig. 5 shows another intrinsically two dimensional manifold, this one living in a much higher dimensional space. Here, we generated examples—shown in the middle panel of the

[2] Other recent approaches to nonlinear dimensionality reduction [Belkin and Niyogi (2002), de Silva and Tenenbaum (2002)] may also be able to recover conformal mappings under certain assumptions; see section 7.

figure—by translating the image of a single face across a larger background of random noise. The noise was uncorrelated from one example to the next. The only consistent structure in the resulting images thus described a two-dimensional manifold parameterized by the face's center of mass. The input to LLE consisted of $N=961$ grayscale images, with each image containing a 28×20 face superimposed on a 59×51 background of noise. Note that while easy to visualize, the manifold of translated faces is extremely nonlinear in the high dimensional vector space ($D=3009$) of pixel coordinates. The bottom portion of Fig. 5 shows the first two components discovered by LLE, with $K=4$ neighbors per data point. By contrast, the top portion shows the first two components discovered by PCA. It is clear that the manifold structure in this example is much better modeled by LLE. (The minor edge effects are due to selecting a constant number of neighbors per data point. Thus, the neighbors of boundary points lie further away than the neighbors of interior points.)

We also applied LLE to a data set containing many different images of a single person's face. This data set (consisting of frames from a digital movie) contained $N=1965$ grayscale images at 20×28 resolution ($D=560$). Fig. 5 shows the first two components of these images discovered by LLE with $K=12$ nearest neighbors. These components appear correlated with highly nonlinear features of the image, related to pose and expression.

Finally, we applied LLE to images of lips used in the animation of talking heads [Cosatto and Graf (1998)]. This data set contained $N=15960$ color (RGB) images of lips at 144×152 resolution ($D=65664$). Dimensionality reduction of these images is useful for faster and more efficient animation. Fig. 6 shows the first two components of these images discovered by LLE with $K=24$ nearest neighbors. These components appear to capture highly nonlinear degrees of freedom associated with opening the mouth, pursing the lips, and clenching the teeth. Fig. 7 shows how one particular neighborhood of lip images is embedded in this two dimensional space.

Fig. 8 shows the sparsity pattern of a large sub-block of the weight matrix W_{ij} for the data set of lip images. Computing the twenty bottom eigenvectors ($d=20$) for this embedding took about 2.5 hours on a high end workstation, using specialized routines for finding eigenvectors of sparse, symmetric matrices [Fokkema et al. (1998)].

4. Implementation

The algorithm, as described in Fig. 2, consists of three steps: nearest neighbor search (to identify the nonzero weights), constrained least squares fits (to compute the values of the weights), and singular value decomposition (to perform the embedding). We now discuss each of these steps in more detail.

4.1 Neighborhood search

The first step of LLE is to identify the neighborhood of each data point. In the simplest formulation of the algorithm, one identifies a fixed number of nearest neighbors, K, per data point, as measured by Euclidean distance. Other criteria, however, can also be used to choose neighbors. For example, one can identify neighbors by choosing all points within a ball of fixed radius. One can also use locally derived distance metrics (based on a priori knowledge, estimated curvature, pairwise distances, or nonparametric techniques such as box counting) that deviate significantly from a globally Euclidean norm. The number of

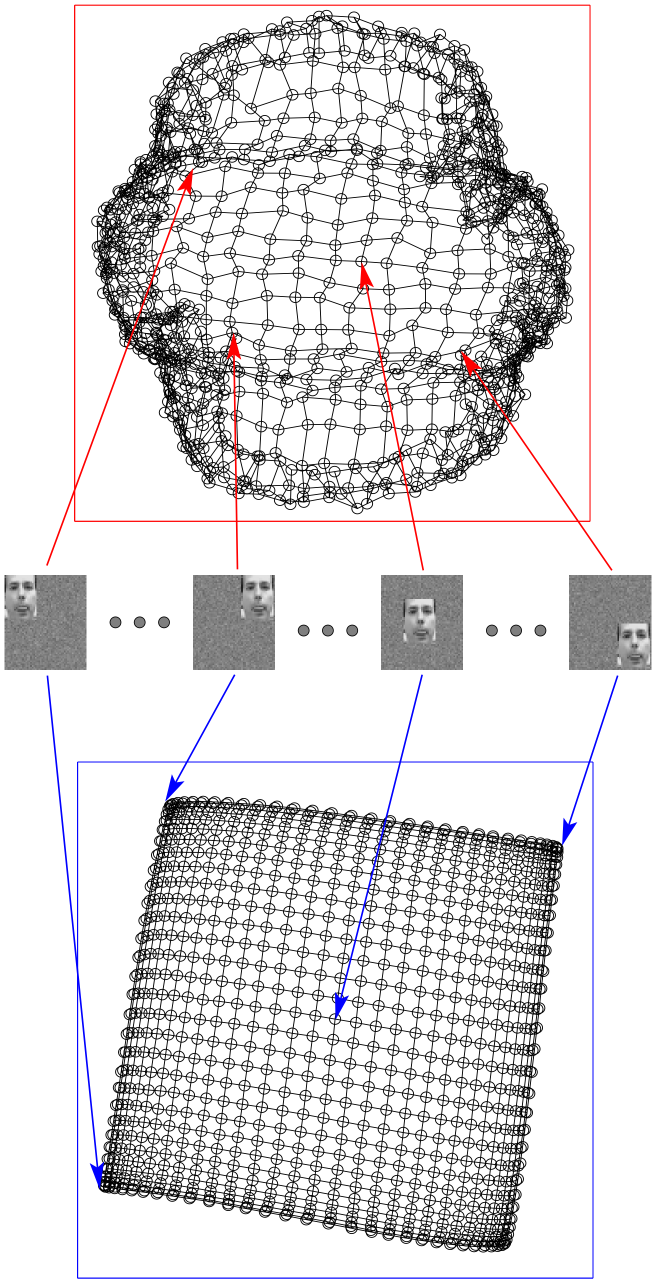

Figure 4: Successful recovery of a manifold of known structure. Shown are the results of PCA (top) and LLE (bottom), applied to $N = 961$ grayscale images of a single face translated across a two-dimensional background of noise. Such images lie on an intrinsically two-dimensional nonlinear manifold, but have an extrinsic dimensionality equal to the number of pixels in each image ($D = 3009$). Note how LLE (using $K = 4$ nearest neighbors) maps the images with corner faces to the corners of its two dimensional embedding ($d = 2$), while PCA fails to preserve the neighborhood structure of nearby images.

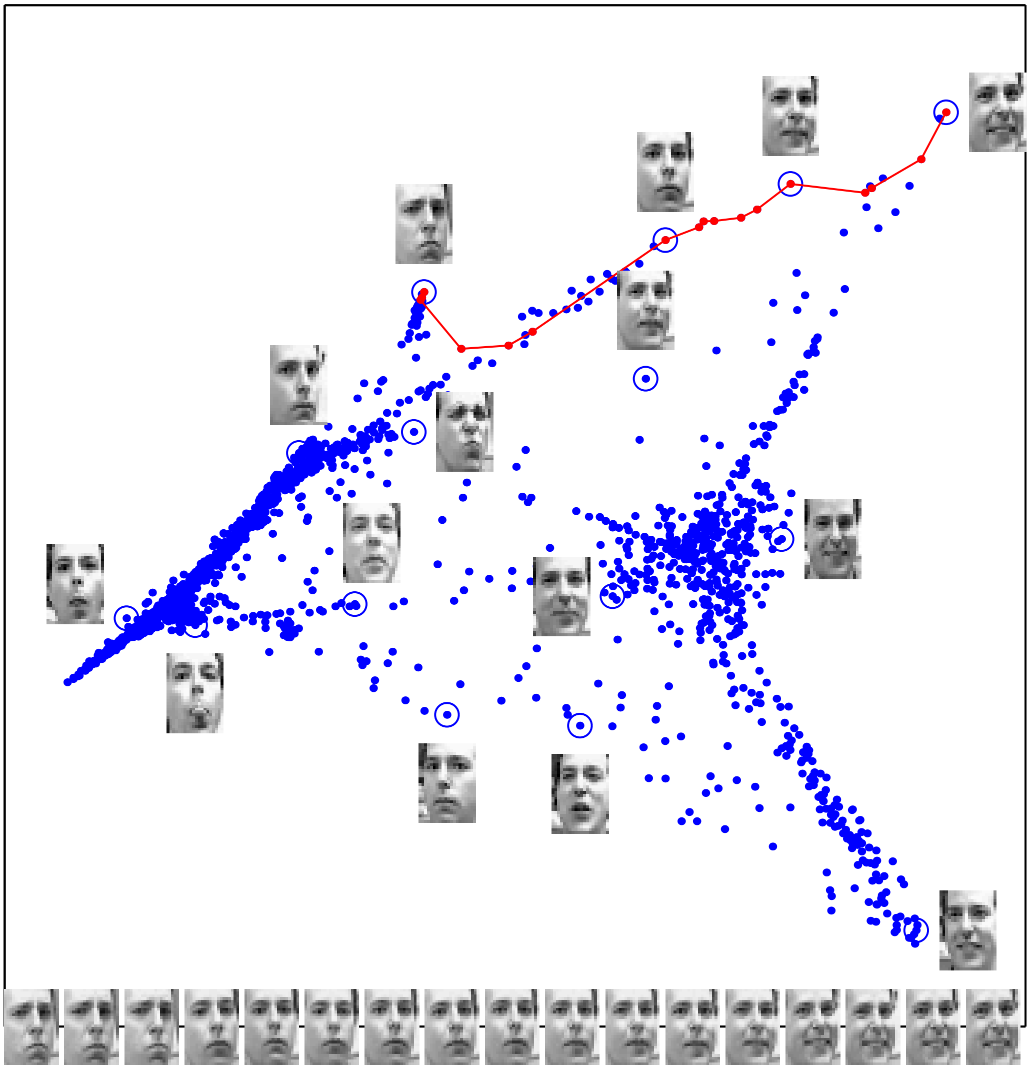

Figure 5: Images of faces mapped into the embedding space described by the first two coordinates of LLE, using $K = 12$ nearest neighbors. Representative faces are shown next to circled points at different points of the space. The bottom images correspond to points along the top-right path, illustrating one particular mode of variability in pose and expression. The data set had a total of $N = 1965$ grayscale images at 20×28 resolution ($D = 560$).

neighbors does not have to be the same for each data point. In fact, neighborhood selection can be quite sophisticated. For example, we can take all points within a certain radius up to some maximum number, or we can take up to a certain number of neighbors but

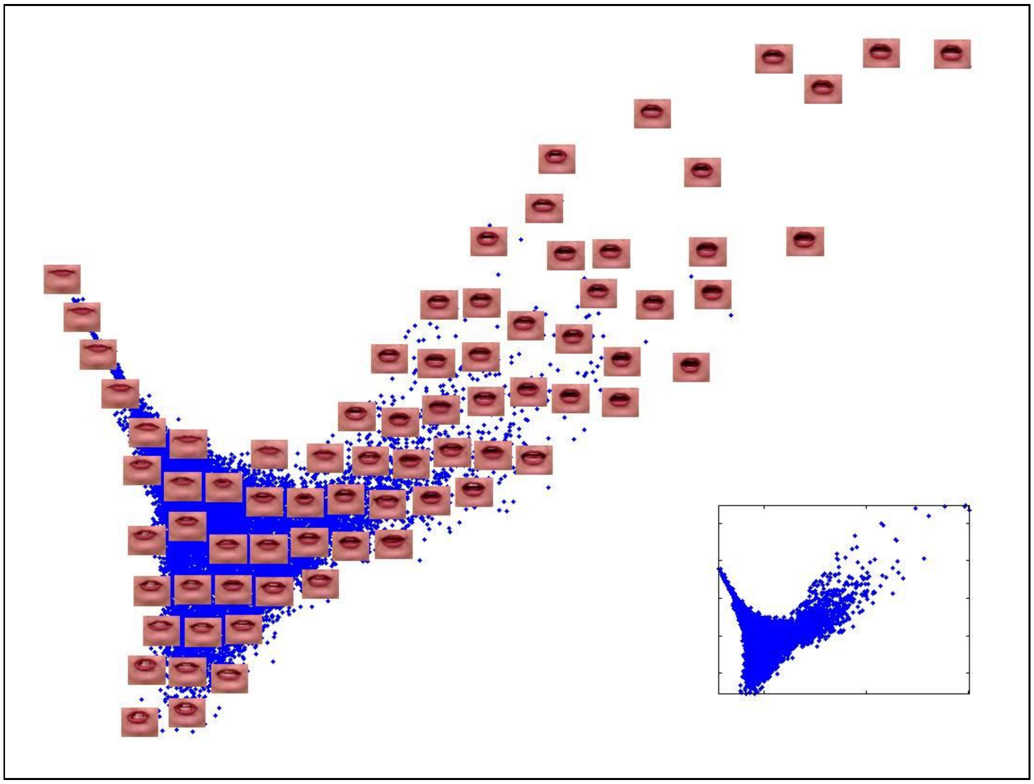

Figure 6: High resolution ($D = 65664$) images of lips, mapped into the embedding space discovered by the first two coordinates of LLE, using $K = 24$ nearest neighbors. Representative lips are shown at different points in the space. The inset shows the first two LLE coordinates for the entire data set ($N = 15960$) without any corresponding images.

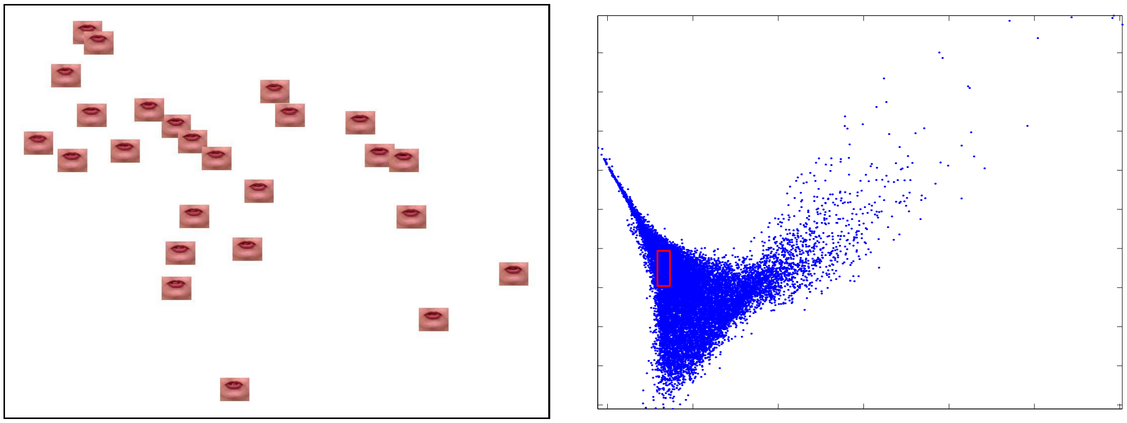

Figure 7: A typical neighborhood of $K = 24$ lip images mapped into the embedding space described by the first two coordinates of LLE. The rectangle in the right plot locates the neighborhood in the overall space of lip images.

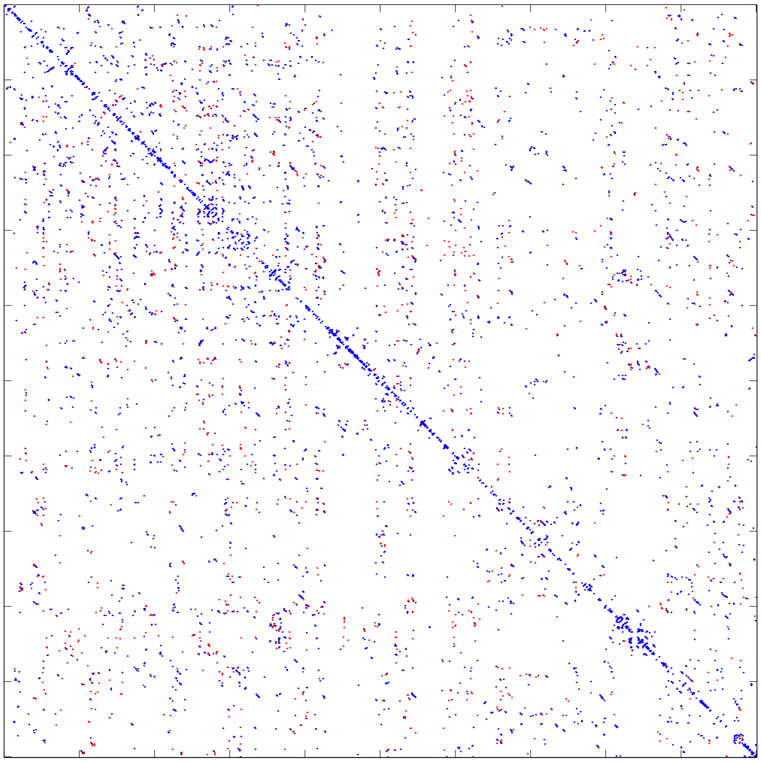

Figure 8: Sparsity pattern of the weight matrix W_{ij} for the data set of lip images. (Only a 1000×1000 sub-block of the matrix is shown to reduce blurring of zero and nonzero elements during printing.) Positive weights are indicated in blue; negative weights, in red. Roughly 99.85% of the elements are zero.

none outside a maximum radius. In general, neighborhood selection in LLE presents an opportunity to incorporate a priori knowledge.

We have not observed the results of LLE to depend sensitively on the choice of the number of nearest neighbors. Several criteria, however, should be kept in mind when choosing this number. First, the algorithm can only be expected to recover embeddings whose dimensionality, d, is strictly less[3] than the number of neighbors, K, and some margin between d and K is desirable to improve the algorithm's robustness. Second, the algorithm is based on the assumption that a data point and its nearest neighbors can be modeled as locally linear; for curved manifolds, choosing K too large will in general violate this assumption. Finally in the unusual case where $K > D$ (indicating that the original data is itself low dimensional), each data point can be reconstructed perfectly from its neighbors, and the local reconstruction weights are no longer uniquely defined. In this case, some further regularization must be added to break the degeneracy.[4] Fig. 9 shows a range of embeddings

[3] The K neighbors span a space of dimensionality at most $K-1$.

[4] A simple regularizer is to penalize the sum of the squares of the weights $\sum_j W_{ij}^2$, which favors weights that are uniformly distributed in magnitude. This is discussed further in section 4.2.

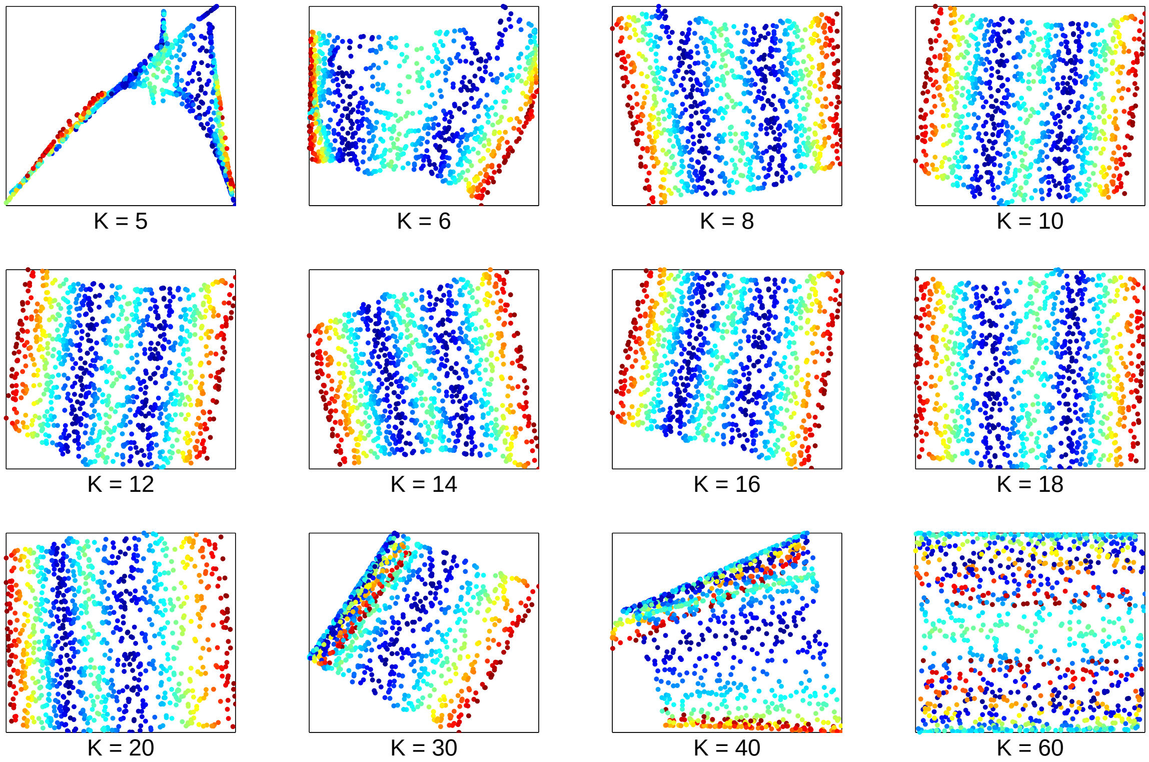

Figure 9: Effect of neighborhood size. Embeddings of the two dimensional S-manifold in the top panels of Fig. 1, computed for different choices of the number of nearest neighbors, K. A reliable embedding from $D=3$ to $d=2$ dimensions is obtained over a wide range of values. If K is too small (top left) or too large (bottom right), however, LLE does not succeed in unraveling the manifold and recovering the two underlying degrees of freedom.

discovered by the algorithm, all on the same data set but using different numbers of nearest neighbors, K. The results are stable over a wide range of values but do break down as K becomes too small or large.

The nearest neighbor step in LLE is simple to implement, though it can be time consuming for large data sets ($N \geq 10^4$) if performed without any optimizations. Computing nearest neighbors scales in the worst case as $O(DN^2)$, or linearly in the input dimensionality, D, and quadratically in the number of data points, N. For many distributions of data, however – and especially for those concentrated on a thin submanifold of the input space – constructions such as K-D trees or ball trees can be used to compute the neighbors in $O(N \log N)$ time [Friedman et al. (1977), Gray and Moore (2001), Moore et al. (2000), Omohundro (1989, 1991)]. More efficient but approximate methods are also possible, some of which come with various guarantees as to their accuracy [Indyk (2000)].

An implementation of LLE also needs to check that the graph formed by linking each data point to its neighbors is connected. Highly efficient algorithms [Tarjan (1972, 1983)] exist for this purpose. If the graph is disconnected (or weakly connected), then LLE should be applied separately to the data in each of the graph's (strongly) connected components. In this case, data from different connected components should be interpreted as lying on distinct manifolds. In theory, such situations could be detected after the fact by zeros in the eigenvalue spectrum [Perona and Polito (2002)] of LLE.[5] In practice, though, it seems much more straightforward to first compute connected components and then apply LLE separately to each component. This not only reduces the computational complexity of the algorithm, but also avoids any possible confounding of results from different components.

4.2 Constrained least squares fits

The second step of LLE is to reconstruct each data point from its nearest neighbors. The optimal reconstruction weights can be computed in closed form. Consider a particular data point $\vec{x}$ with K nearest neighbors $\vec{\eta}_j$ and reconstruction weights w_j that sum to one. We can write the reconstruction error as:

$$\varepsilon \;=\; \left|\vec{x} - \textstyle\sum_j w_j \vec{\eta}_j\right|^2 \;=\; \left|\textstyle\sum_j w_j \left(\vec{x} - \vec{\eta}_j\right)\right|^2 \;=\; \textstyle\sum_{jk} w_j w_k G_{jk}, \tag{3}$$

where in the first identity, we have exploited the fact that the weights sum to one, and in the second identity, we have introduced the "local" Gram matrix,

$$G_{jk} = (\vec{x} - \vec{\eta}_j) \cdot (\vec{x} - \vec{\eta}_k). \tag{4}$$

By construction, this matrix is symmetric and semipositive definite. The reconstruction error can be minimized analytically using a Lagrange multiplier to enforce the constraint that $\sum_j w_j = 1$. In terms of the inverse Gram matrix, the optimal weights are given by:

$$w_j = \frac{\sum_k G^{-1}_{jk}}{\sum_{lm} G^{-1}_{lm}}. \tag{5}$$

The solution, as written in eq. (5), appears to require an explicit inversion of the Gram matrix. In practice, a more efficient and numerically stable way to minimize the error is simply to solve the linear system of equations, $\sum_j G_{jk} w_k = 1$, and then to rescale the weights so that they sum to one (which yields the same result).

In unusual cases, it can arise that the Gram matrix in eq. (4) is singular or nearly singular—for example, for example, when there are more neighbors than input dimensions ($K > D$), or when the data points are not in general position. In this case, the least squares problem for finding the weights does not have a unique solution (see Fig. 10), and the Gram matrix must be conditioned (before solving the linear system) by adding a small multiple of the identity matrix,

$$G_{jk} \leftarrow G_{jk} + \delta_{jk} \left(\frac{\Delta^2}{K}\right) \mathrm{Tr}(G), \tag{6}$$

[5] The corresponding eigenvectors have constant values within each connected component, but different values in different components. This yields a zero embedding cost in eq. (2).

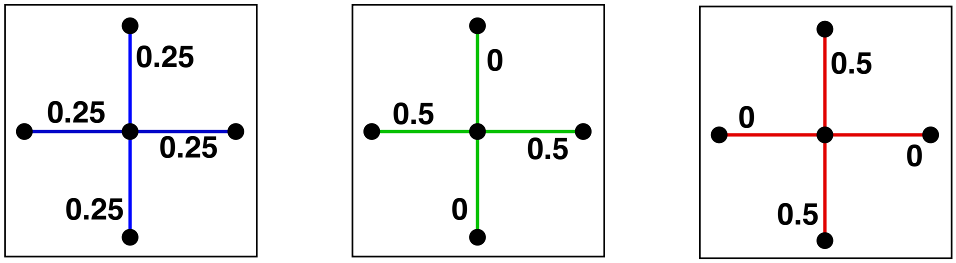

Figure 10: Degeneracy of reconstruction weights. If there are more neighbors (K) than input dimensions (D), then the weights which minimize the reconstruction error in eq. (1) do not have a unique solution. Consider, for example, a two dimensional data point whose four neighbors lie at the corners of a diamond. In this case, many different settings of the weights lead to zero reconstruction error. Three possible settings are shown above. Adding a regularizer that penalizes the squared magnitude of the weights favors the left solution over all others. Note that while this example has particular symmetries (chosen for ease of visualization), the degeneracy arises whenever $K > D$, even for points in general position.

where $\mathrm{Tr}(G)$ denotes the trace of G, and $\Delta^2 \ll 1$. This amounts to adding a regularization term to the reconstruction cost that measures the summed squared magnitude of the weights.

The regularization term acts to penalize large weights that exploit correlations beyond some level of precision in the data sampling process. It may also introduce some robustness to noise and outliers. This form of regularization (with $\Delta = 0.1$) was used, for example, to compute all the embeddings in Fig. 1. For these synthetic manifolds, the regularization is essential because there are more neighbors ($K = 8$) than input dimensions ($D = 3$). (For most data sets requiring dimensionality reduction, however, D is much larger than K.)

Computing the reconstruction weights W_{ij} is typically the least expensive step of the LLE algorithm. The computation scales as $O(DNK^3)$; this is the number of operations required to solve a $K \times K$ set of linear equations for each data point. It is linear in both the number of data points and the number of input dimensions. The weight matrix can be stored as a sparse matrix with NK nonzero elements. The inputs $\vec{X}_i$ do not all need to be in memory at once for this step because the algorithm fills in the weights based on a purely local computation.

4.3 Eigenvalue problem

The final step of LLE is to compute a low dimensional embedding based on the reconstruction weights W_{ij} of the high dimensional inputs $\vec{X}_i$. Note that only information captured by the weights W_{ij} is used to construct an embedding; the actual inputs $\vec{X}_i$ do not appear anywhere in the final step of the algorithm (and hence do not need to remain in memory once the weights are computed). The low dimensional outputs $\vec{Y}_i$ are found by minimizing the cost function, eq. (2), for fixed weights W_{ij}. This cost function is minimized when the outputs $\vec{Y}_i$ are reconstructed (or nearly reconstructed) by the *same* weighted linear combinations of neighbors as computed for the inputs. Note that the assignment of neighbors is always based on the locations of the inputs $\vec{X}_i$; the algorithm does not dynamically recompute neighbors based on the locations of the outputs $\vec{Y}_i$.

To optimize the embedding cost function in eq. (2), we rewrite it as the quadratic form:

$$\Phi(Y) = \sum_{ij} M_{ij} (\vec{Y}_i \cdot \vec{Y}_j), \tag{7}$$

involving inner products of the outputs $\vec{Y}_i$. The square $N \times N$ matrix M that appears in eq. (7) is given by:

$$M_{ij} = \delta_{ij} - W_{ij} - W_{ji} + \sum_k W_{ki} W_{kj}, \tag{8}$$

where δ_{ij} is 1 if $i = j$ and 0 otherwise. The matrix M is sparse, symmetric, and semipositive definite.

The optimization of eq. (7) is performed subject to constraints that make the problem well posed. Note that we can translate the outputs $\vec{Y}_i$ by a constant displacement without affecting the cost, $\Phi(Y)$, in eq. (2). We remove this translational degree of freedom by requiring the outputs to be centered on the origin:

$$\sum_i \vec{Y}_i = \vec{0}. \tag{9}$$

We can also rotate the outputs $\vec{Y}_i$ without affecting the cost, $\Phi(Y)$, in eq. (2). To remove this rotational degree of freedom (as well as to fix the scale of the outputs), we constrain the outputs to have unit covariance, with outer products that satisfy

$$\frac{1}{N} \sum_i \vec{Y}_i \vec{Y}_i^\top = I, \tag{10}$$

where I is the $d{\times}d$ identity matrix. The constraint that the covariance is equal to the identity matrix embodies three assumptions: first, that the different coordinates in the embedding space should be uncorrelated to second-order; second, that reconstruction errors for these coordinates should be measured on the same scale; and third, that this scale should be of order unity. (Note that these assumptions are rather mild. Since we are free to rotate and homogeneously rescale the outputs, we can always make the covariance of $\vec{Y}$ to be diagonal and of order unity. Further restricting the covariance to be the identity matrix only introduces the additional assumption that all the embedding coordinates should be of the same scale.)

Under these restrictions, the optimal embedding—up to a trivial global rotation of the embedding space—is found by minimizing eq. (2) subject to the constraints in eqs. (9–10). This can be done in many ways, but the most straightforward is to find the bottom $d+1$ eigenvectors of the matrix, M. (This equivalence between extremization of a normalized quadratic form and the computation of largest or smallest eigenvectors is a version of the Rayleitz-Ritz theorem [Horn and Johnson (1990)].) The bottom eigenvector of this matrix, which we discard, is the unit vector with all equal components; it represents the free translation mode of eigenvalue zero. Discarding this eigenvector enforces the constraint in eq. (9) that the outputs have zero mean, since the components of other eigenvectors must sum to zero, by virtue of orthogonality with the bottom one. The remaining d eigenvectors constitute the d embedding coordinates found by LLE.

Note that the bottom $d+1$ eigenvectors of the sparse, symmetric matrix M (that is, those corresponding to its smallest $d+1$ eigenvalues) can be found without performing a full matrix diagonalization [(Bai et al., 2000)]. Moreover, the matrix M can be efficiently stored and manipulated in a way that exploits its sparseness,

$$M = (I - W)^{\top}(I - W), \tag{11}$$

giving substantial computational savings for large values of N. In particular, left multiplication by M (the subroutine required by most sparse eigensolvers) can be performed as:

$$M\vec{v} = (\vec{v} - W\vec{v}) - W^{\top}(\vec{v} - W\vec{v}), \tag{12}$$

requiring just one multiplication by W and one multiplication by $W^{\top}$, both of which are extremely sparse. Thus, the matrix M never needs to be explicitly created or stored; it is sufficient just to store and multiply the (even sparser) matrix W. An efficient implementation of the multiplication $\vec{v} \leftarrow M\vec{v}$ can be achieved using the update $\vec{v} \leftarrow \vec{v} - W\vec{v}$ followed by the update $\vec{v} \leftarrow \vec{v} - W^{\top}\vec{v}$.

The final step of LLE is typically the most computationally expensive. Without special optimizations, computing the bottom eigenvectors scales as $O(dN^2)$, linearly in the number of embedding dimensions, d, and quadratically in the number of data points, N. Specialized methods for sparse, symmetric eigenproblems [Bai et al. (2000), Fokkema et al. (1998)], however, can be used to reduce the complexity to subquadratic in N. Note that as more dimensions are added to the embedding space, the existing ones do not change. Thus, for efficiency or convenience, we can compute the bottom eigenvectors of eq. (8) one at a time, yielding a "nested" set of embeddings in successively higher dimensions. For very large problems, one can consider alternative methods for optimizing the embedding cost function, such as direct descent by conjugate gradient methods [Press et al. (1993)], iterative partial minimizations, or stochastic gradient descent [LeCun et al. (1998)].

5. Extensions

In this section, we describe several useful extensions to the basic LLE algorithm, including the handling of input in the form of pairwise distances, the use of nonnegative reconstruction weights, and the estimation of a manifold's intrinsic dimensionality.

5.1 LLE from pairwise distances

The LLE algorithm, as described in Fig. 2, takes as input the N high dimensional vectors, $\vec{X}_i$. In many settings, however, the user may not have access to data of this form, but only to measurements of dissimilarity or distance between data points. A simple variation of LLE can be applied to input of this form. In this way, matrices of pairwise distances can be analyzed by LLE just as easily as by MDS [Cox and Cox (1994)] or other distance-based approaches to dimensionality reduction [Tenenbaum et al. (2000)].

The first step of the algorithm remains to identify nearest neighbors. These can be identified by the smallest non-zero elements of each row in the distance matrix. To derive the reconstruction weights for each data point, we need to compute the Gram matrix G_{jk} between its nearest neighbors, as defined by eq. (4). This matrix can be found by inferring dot products from pairwise distances in exactly the same manner as MDS. In particular, consider a point $\vec{x}$ and its K neighbors η_i, and let S_{ij} denote the symmetric square matrix, of size $(K+1)\times(K+1)$, that records pairwise *squared* distances between these points. (In a slight abuse of notation, here we will allow the indices to range from $i, j = 0, 1, \ldots, K$, where positive values refer to the K neighbors of $\vec{x}$ and the zero index refers to the point $\vec{x}$ itself.) For the purpose of computing the Gram matrix G in eq. (4), we can assume without loss of generality that these $K+1$ points are centered on the origin. In this case, their dot products are given exactly in terms of their pairwise distances by:

$$\rho_{ij} = \frac{1}{2}\left[\left(\frac{1}{K+1}\right)\sum_{k=0}^{K}(S_{ik}+S_{kj}) - \left(\frac{1}{K+1}\right)^2 \sum_{k,\ell=0}^{K} S_{k\ell} - S_{ij}\right]. \qquad (13)$$

Consistent with our earlier notation, the elements in this matrix also record the dot products $\rho_{00} = |\vec{x}|^2$, $\rho_{0j} = \vec{x}\cdot\vec{\eta}_j$ (for $j>0$), and $\rho_{ij} = \vec{\eta}_i\cdot\vec{\eta}_j$ (for $i, j>0$). The "local" Gram matrix G_{ij} is given in terms of the matrix of dot products ρ_{ij} by:

$$G_{ij} \;=\; (\vec{x}-\vec{\eta}_i)\cdot(\vec{x}-\vec{\eta}_j) \;=\; \rho_{00} - \rho_{i0} - \rho_{0j} + \rho_{ij}. \qquad (14)$$

Note that G_{ij} is a $K\times K$ square matrix, whereas ρ_{ij} is one dimension larger. In terms of the Gram matrix G_{ij}, the reconstruction weights for each data point are given by eq. (5). The rest of the algorithm proceeds as usual.

Note that this variant of LLE does not in fact require the complete $N\times N$ matrix of pairwise distances. Instead, for each data point, the user needs only to specify its nearest neighbors, the pairwise distances between the data point and its neighbors, and the pairwise distances between the neighbors themselves.

Is it possible to recover manifold structure from even less user input—say, just the pairwise distances between each data point and its nearest neighbors? A simple counterexample in Fig. 11 shows that this is not in general possible. Consider the three dimensional data set whose points have integer coordinates satisfying $x+y+z=0$; that is, they lie at the sites of a planar square lattice. Suppose that points with even x-coordinates are colored black and those with odd x-coordinates are colored white. The degenerate "two point" embedding that maps all black points to the origin and all white points one unit away *exactly* preserves the distance between each point and its four nearest neighbors. Nevertheless, this embedding completely fails to preserve the structure of the underlying manifold.

5.2 Convex reconstructions

The rows of the weight matrix W_{ij} computed by the second step of LLE are constrained to sum to one. One can additionally constrain these weights to be non-negative, thus requiring the reconstruction of each data point to lie within the convex hull of its neighbors. It is more expensive to compute the least squares solution with non-negativity constraints, but the

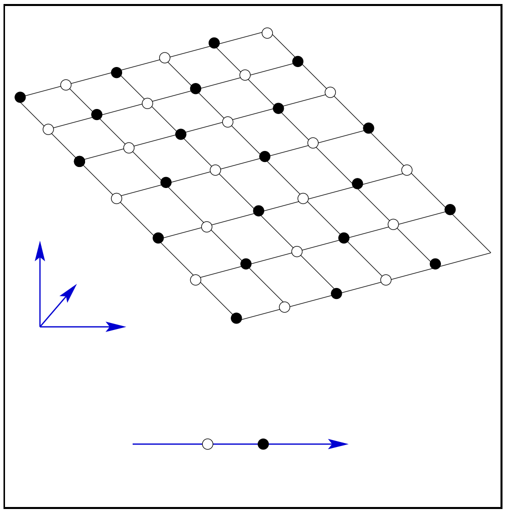

Figure 11: Distances to neighbors are not sufficient to infer the structure of a manifold. Shown above is a trivial "two-point" embedding that exactly preserves the distances between each point and its four nearest neighbors, but does not preserve the underlying structure of the manifold.

additional cost is usually negligible compared to the other two steps of LLE.[6] In conjunction with the sum-to-one constraint, the constraint of nonnegativity limits the weights strictly to the range [0,1]. Such a constraint has both advantages and disadvantages. On one hand, it tends to increase the robustness of the linear fits to outliers. On the other hand, it can degrade the reconstruction of data points that lie on the boundary of a manifold and outside the convex hull of their neighbors.

A general prescription for using convex versus linear reconstructions does not exist to cover all applications of LLE. In certain applications, it may be straightforward to identify neighborhoods that are not plagued by outliers; in others, it may be simpler to choose K nearest neighbors everywhere and use only nonnegative weights. A useful heuristic is to inspect a histogram of the reconstruction weights obtained without non-negativity constraints. If certain data points have very large (positive or negative) reconstruction weights, it may be wise to re-assign their neighbors or to constrain their linear reconstructions to be convex.

5.3 Estimating the intrinsic dimensionality, d

Given data sampled from a nonlinear manifold, it is naturally of interest to estimate the manifold's intrinsic dimensionality, d. Recall how PCA solves this problem for linear manifolds: the dimensionality is estimated by the number of eigenvalues of the sample covariance

[6] In particular, one must solve a problem in quadratic progamming: minimize $\sum_{jk} w_j w_k G_{jk}$ from eq. (3) subject to $\sum_j w_j = 1$ and $w_j \geq 0$. The required optimization is convex, with solutions that often lie on the edge of the constraint region [Judge and Takayama (1966)].

matrix that are comparable in magnitude to the largest eigenvalue. An analogous strategy for nonlinear manifolds and LLE [Perona and Polito (2002)] immediately suggests itself—that is, to estimate d by the number of eigenvalues that are appreciable in magnitude to the smallest nonzero eigenvalue of the cost matrix, M, from eq. (8). In practice, we have found this procedure to work only for highly contrived examples, such as data that lies on an essentially linear manifold, or data that has been sampled in an especially uniform way (so that the lowest nonzero eigenvalues are equal or nearly equal due to symmetry). More generally, though, we have not found it to be reliable. Fig. 12 plots the eigenvalue spectrum of the cost matrix in eq. (8) for several data sets of intrinsic dimensionality $d=2$. The eigenvalues reveal a distinguishing signature at $d=2$ in some of these plots, but not in others.

In our work, we have relied on various classical methods to estimate the intrinsic dimensionality d of the data set. One way to estimate this dimensionality is to examine the eigenvalue spectra of local covariance matrices. Performing in essence a local PCA in the neighborhood of each data point, we can then ask whether these analyses yield a consistent estimate of the intrinsic dimensionality. Yet another estimate can be obtained by box-counting. Suppose we consider two points to be neighbors if they lie within a distance, ϵ. If the data are uniformly sampled over the manifold, then the number of neighbors should scale for small ϵ as $K_\epsilon \propto \epsilon^d$, where d is the intrinsic dimensionality. Both these methods can be used prior to the final step of LLE to fix the number of embedding coordinates computed by the algorithm.

5.4 Enforcing the intrinsic dimensionality, d

LLE normally computes an ordered set of embedding coordinates without assuming the particular number that will be used. In some applications, however, a manifold's intrinsic dimensionality may be known a priori, or the user may wish to bias the results of LLE toward an embedding of a particular dimensionality (such as $d=2$, which is easily visualized). In these circumstances, the second step of LLE can be modified in a simple way[7] to suppress spurious or noisy degrees of freedom and force a desired intrinsic dimensionality, d. For each data point, the idea is to project its neighbors into their d-dimensional subspace of maximal variance before performing the least squares reconstruction. The subspace is computed from the d dominant eigenvectors of the Gram matrix G in eq. (4). The effect of this projection is to limit the rank of G before solving for the reconstruction weights. The reconstruction weights are then computed as before, but from the rank-limited Gram matrix (and using the minimum norm solution to the least squares problem).

As an example of this technique, Fig. 13 shows the results of LLE on a data set of handwritten digits [Hull (1994)]. For this run of LLE, neighbors were projected into an eight dimensional subspace ($d = 8$) before performing the least squares reconstructions and computing the weights W_{ij}. Interestingly, the resulting embedding provides a low dimensional clustering of the handwritten digits based on their labels (ZERO to NINE).

[7] Another possible strategy, although a bad one, is to reduce the number of neighbors of each data point, thus automatically limiting the dimensionality of the subspace spanned by the neighborhood.

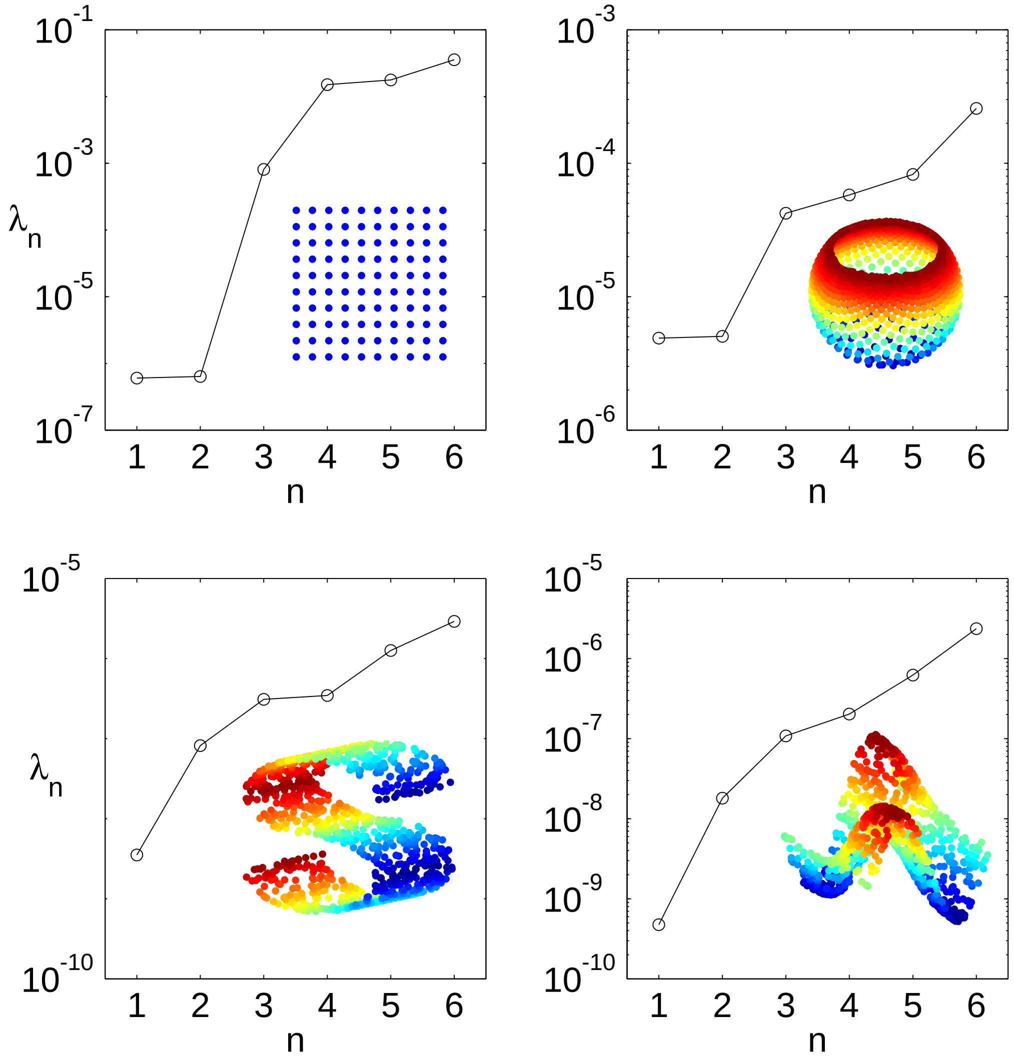

Figure 12: Eigenvalues from the third step of LLE are not reliable indicators of intrinsic dimensionality. Plots show the smallest nonzero eigenvalues λ_n of the embedding cost matrices for several data sets. The gap between the $n = 2$ and $n = 3$ eigenvalues reveals the true dimensionality $(d = 2)$ of regularly sampled data in the plane and on the sphere. There is no similar signature, however, for the randomly sampled data on the two bottom manifolds.

6. Generalization

LLE provides an embedding for the fixed set of training data to which the algorithm is applied. Suppose, however, that we are asked to compute the output $\vec{y}$ for a new input $\vec{x}$, or vice versa. In this case, we need to *generalize* the results of LLE to new locations on the manifold. For the purpose of generalization, it is useful to derive an explicit mapping

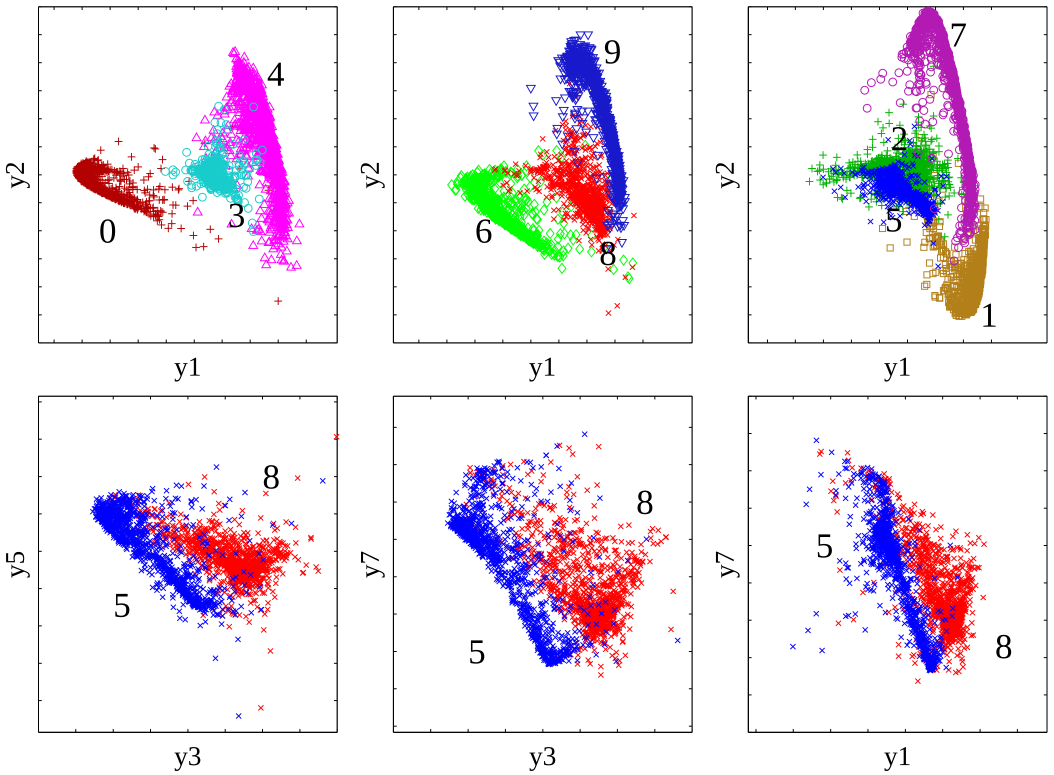

Figure 13: Embeddings of $N = 11000$ handwritten digits. The inputs $\vec{X}_i$ were grayscale images of handwritten numerals (zero through nine) taken from the USPS data set [Hull (1994)] at 16×16 resolution ($D = 256$) A maximum manifold dimensionality of $d=8$ was enforced by singular value decomposition of the local Gram matrices, as described in section 5.4. The top panels show the first two coordinates discovered by LLE. Many digit classes (labelled) are well clustered in just these two dimensions. Classes that overlap in the first two dimenions are typically separated in others, as the bottom panels show for fives versus eights in the third, fifth and seventh LLE coordinates.

between the high and low dimensional spaces of LLE that does not require an expensive eigenvector calculation for each new query. A natural question is how to construct such a mapping given the results of LLE from a previous run of the algorithm. In this section, we describe two possible solutions—one non-parametric, one parametric—to this problem.

6.1 Non-parametric model

The non-parametric model relies on a natural mapping between the low and high dimensional spaces of LLE. In particular, to compute the output $\vec{y}$ for a new input $\vec{x}$, we can do the following: (i) identify the K nearest neighbors of $\vec{x}$ among the training inputs; (ii) compute the linear weights w_j that best reconstruct $\vec{x}$ from its neighbors, subject to the sum-to-one constraint, $\sum_j w_j = 1$; (iii) output $\vec{y} = \sum_j w_j \vec{Y}_j$, where the sum is over the outputs corresponding to the neighbors of $\vec{x}$. A non-parametric mapping from the embedding space to the input space can be derived in the same manner. (Note that in this direction, moreover, there does not exist the option of rerunning LLE on an augmented data set.)

The non-parametric mappings derived in this way are based on the same underlying intuitions as LLE. They provide a simple and effective way to generalize to new data when the assumptions of local linearity are met. Though straightforward to implement, this approach to generalization has the disadvantage that it requires access to the entire set of previously analyzed inputs and outputs — potentially a large demand in storage. An open problem is to establish the asymptotic conditions under which these mappings yield the same (or nearly the same) result as rerunning LLE on the augmented data set of original plus new inputs.

6.2 Parametric model

Methods in supervised learning can be used to derive more compact mappings that generalize over large portions of the input and embedding space. In particular, one can take the input-output pairs of LLE as training data for an invertible function approximator and learn a parametric mapping between the two spaces. Here, we discuss one such approach that is based on similar intuitions as its non-parametric counterpart.

Given the results of LLE, we consider how to learn a probabilistic model of the joint distribution, $P(\vec{x}, \vec{y})$, over the input and embedding spaces. The joint distribution can be used to map inputs to outputs and vice versa by computing the expected values $\mathrm{E}[\vec{y}|\vec{x}]$ and $\mathrm{E}[\vec{y}|\vec{x}]$. To represent the joint distribution, we propose a mixture model [McLachlan and Basford (1988)] that is specifically tailored to data that lies on a low dimensional nonlinear manifold. The individual components of this mixture model are used to represent the densities of locally linear neighborhoods on the manifold. Mixture models have been widely used for this purpose [Beymer and Poggio (1996), Bregler and Omohundro (1995), Hinton et al. (1997), Kambhatla and Leen (1997), Roweis et al. (2002), Saul and Rahim (1999), Vlassis et al. (2002)], so their treatment here is necessarily brief.

The model that we consider is a mixture of linear models with Gaussian distributions. It describes a three-step generative process for high and low dimensional vectors $\vec{x} \in \mathcal{R}^D$ and $\vec{y} \in \mathcal{R}^d$. First, a discrete hidden variable z is sampled from its prior distribution, $P(z)$, to select a particular neighborhood on the manifold. Next, a d-dimensional vector $\vec{y}$ is sampled from a conditional Gaussian distribution, $P(\vec{y}|z)$, with mean vector $\vec{\nu}_z$ and (full) covariance matrix Σ_z. Finally, a D-dimensional vector $\vec{x}$ is sampled from a conditional Gaussian distribution, $P(\vec{x}|\vec{y}, z)$ with mean vector $\Lambda_z \vec{y} + \vec{\mu}_z$ and diagonal covariance matrix Ψ_z. Here, Λ_z is a $D \times d$ loading matrix that describes the locally linear mapping from low to high dimensional observations. The model is similar to a mixture of factor analyzers [Rubin and Thayer (1982), Ghahramani and Hinton (1996)], except that the low dimensional variable $\vec{y}$ is observed, not hidden, and the Gaussian distributions $P(\vec{y}|z)$ have nonzero mean vectors and full covariance matrices. The overall distribution is given by:

$$
\begin{aligned}
P(\vec{x}, \vec{y}, z) &= P(\vec{x}|\vec{y}, z) P(\vec{y}|z) P(z) && (15) \\
P(\vec{x}|\vec{y}, z) &= \frac{|\Psi_z|^{-1/2}}{(2\pi)^{D/2}} \exp\left\{ -\frac{1}{2} \left[\vec{x} - \Lambda_z \vec{y} - \vec{\mu}_z\right]^T \Psi_z^{-1} \left[\vec{x} - \Lambda_z \vec{y} - \vec{\mu}_z\right] \right\} && (16)
\end{aligned}
$$

$$P(\vec{y}|z) \quad = \quad \frac{|\Sigma_z|^{-1/2}}{(2\pi)^{d/2}} \exp\left\{-\frac{1}{2}\left[\vec{y}-\vec{\nu}_z\right]^T \Sigma_z^{-1}\left[\vec{y}-\vec{\nu}_z\right]\right\}. \tag{17}$$

The parameters in this model which need to be estimated from data are the prior probabilities $P(z)$, the mean vectors $\vec{\nu}_z$ and $\vec{\mu}_z$, the full covariance matrices Σ_z and the diagonal covariance matrices Ψ_z, and the loading matrices Λ_z. The training examples for the model consist of the input-output pairs from a D-dimensional data set and its d-dimensional locally linear embedding.

The parameters in this model can be learned by an Expectation-Maximization (EM) algorithm for maximum likelihood estimation [Dempster et al. (1977)]. The EM algorithm is an iterative procedure that attempts to maximize the total log-likelihood of observed input-output pairs in the training set. The re-estimation formulae for this model are given in Appendix A.

Fig. 14 shows a model with 32 mixture components learned from the results of LLE on the S-shaped manifold in Fig. 1. The Gaussian distributions $P(\vec{x}|\vec{y}, z)$ are depicted by planes centered on the points $\Lambda_z\vec{\nu}_z + \vec{\mu}_z$, whose normal vectors are perpendicular to the subspaces spanned by the rows of Λ_z. These subspaces very accurately model the locally linear neighborhoods on the manifold ($d = 2$) from which the data was generated. Note that mixture models in high dimensional spaces (even $D=3$) are typically plagued by very poor local minima, and that an unsupervised mixture of factor analyzers—treating $\vec{y}$ as a hidden variable—would be unlikely to discover a solution of this quality. Clamping these latent variables to the outputs of LLE makes learning much easier.

7. Discussion

We conclude by tracing the origins of this work, comparing LLE to other well known algorithms for nonlinear dimensionality reduction, and mentioning some open problems for future research.

The motivation for LLE arose from an extended line on work on mixture models. A number of researchers had shown that nonlinear manifolds could be learned from examples and parameterized by mixtures of locally linear models [Bregler and Omohundro (1995), Kambhatla and Leen (1997), Ghahramani and Hinton (1996), Hinton et al. (1997), Saul and Rahim (1999)]. These models, however, exhibited a peculiar degeneracy: their objective functions (measuring either least squares reconstruction error or log likelihood) were invariant to arbitrary rotations and reflections of the local coordinate systems in each linear model. In other words, their learning algorithms did not favor a consistent alignment of the local linear models, but instead yielded internal representations that changed unpredictably as one traversed connected paths on the manifold.

LLE was designed to overcome this shortcoming—to discover a single global coordinate system of lower dimensionality. Initially, we imagined that such a coordinate system could be obtained by patching together the local coordinate systems of individual components in a mixture model [Hinton and Revow (1998)]. Difficulties with this approach led us to consider a non-parametric setting in which the local coordinate systems were defined by each data point and its nearest neighbors. The main novelty of LLE lies, we believe, in its appeal to particular symmetries. The reconstruction weights in LLE capture the intrinsic geometric properties of local neighborhoods—namely, those properties invariant to

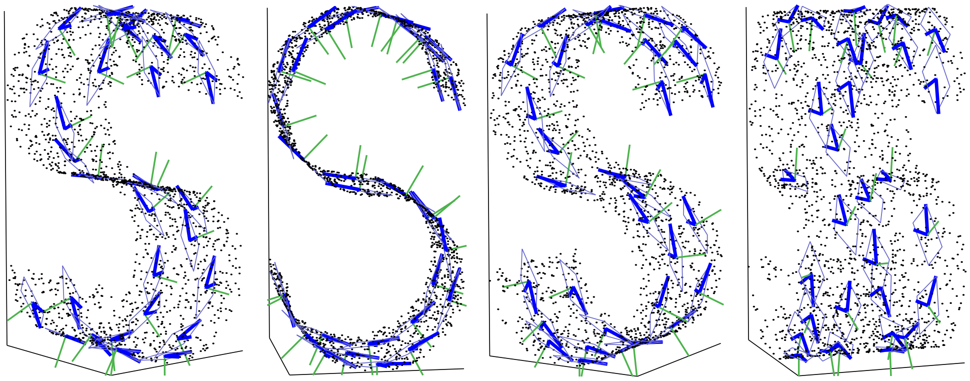

Figure 14: Mixture of linear models learned from data sampled from the surface of a two dimensional manifold. Each mixture component parameterizes the density over a locally linear neighborhood on the manifold. The mixture model with 32 components was trained on the input-output pairs of LLE shown in the top row of Fig. 1. Thick lines indicate increasing coordinates on the manifold, while light squares (and their normals) indicate the neighborhoods modeled by individual mixture components. Parameters of the mixture model were estimated by the EM algorithm described in section 6.2 and appendix A. A three-dimensional animation of these results can be viewed at `http://www.cs.toronto.edu/∼roweis/lle/images/mfaspin.gif`.

translation, rotation, and scaling. The appeal to these symmetries was directly motivated by the degeneracy observed in earlier work on mixture models.

While LLE is a non-parametric method, recent studies [Roweis et al. (2002), Verbeek et al. (2002a)] have, in fact, shown how to learn a probabilistic mixture model whose individual coordinate systems are aligned in a consistent way. These approaches rely on LLE to initialize certain parameter estimates and overcome the otherwise difficult problem of local maxima.

At its core, LLE uses linear methods—least squares optimization and matrix diagonalization—to obtain highly nonlinear embeddings. The only element of nonlinearity is introduced by the first step of the algorithm—a nearest neighbor search—which can be viewed as a highly nonlinear thresholding procedure. Because its optimizations are straightforward to implement and do not involve local minima, LLE compares favorably to purely linear methods, such as PCA and classical MDS. Unlike these methods, however, LLE can be used to address problems in nonlinear dimensionality reduction. LLE also generates a sparse eigenvalue problem, as opposed to the dense eigenvalue problems in PCA and MDS. This has many computational advantages for scaling its performance up to large data sets.

LLE illustrates a general principle, elucidated by earlier studies [Martinetz and Schulten (1994), Tenenbaum (1998)], that overlapping local neighborhoods—collectively analyzed—can provide information about global geometry. The formulation of LLE in terms of reconstruction weights and eigenvectors arose, somewhat serendipitously, from a completely unrelated line of work in signal processing [Saul and Allen (2001)]. LLE is more properly viewed, however, as belonging to a family of recently proposed algorithms that use eigenvector methods to solve highly nonlinear problems in dimensionality reduction, clustering, and image segmentation [Belkin and Niyogi (2002), Ng et al. (2002), Shi and Malik (2000), Tenenbaum et al. (2000), Weiss (1999)]. These algorithms—discussed in more detail below—avoid many of the pitfalls that plague other nonlinear approaches, such as autoencoder neural networks [DeMers and Cottrell (1993), Kramer (1991)], self-organizing maps [Durbin and Wilshaw (1987), Kohonen (1988)], latent variable models [Bishop et al. (1998)], principal curves and surfaces [Hastie and Stuetzle (1989), Verbeek et al. (2002b)], and many variants on multidimensional scaling [Cox and Cox (1994), Klock and Buhmann (1999), Littman et al. (1992), Takane and Young (1977)]. These latter approaches, especially those based on hill-climbing methods, do not have the same guarantees of global optimality or convergence as eigenvector methods; they also tend to involve many free parameters, such as learning rates, initial conditions, convergence criteria, and architectural specifications—all of which must be tuned by the user or set by tedious cross validation.

The first and third steps of LLE are similar to those of the normalized cut algorithm for image segmentation [Shi and Malik (2000)] and related Laplacian-based methods for clustering [Ng et al. (2002)] and dimensionality reduction [Belkin and Niyogi (2002)]. At the heart of all these algorithms is a sparse eigenvalue problem derived from a weighted graph representing neighborhood relations. Recent work [Belkin and Niyogi (2002)] has related LLE to the Laplacian-based methods and argued that all these approaches can be understood in terms of a unified framework for clustering and dimensionality reduction. There have been several extensions of the normalized cut algorithm for clustering and image segmentation—to directed graphs [Yu and Shi (2001)] and to probabilistic settings [Meila and Shi (2000)]–that would be interesting to explore for problems in manifold learning. Likewise, Fig. 13 gives an indication that LLE might be useful for certain types of clustering: the algorithm's unsupervised dimensionality reduction of $N = 11000$ handwritten digits (from $D = 256$ to $d = 8$) largely preserves the separation between different classes.

A different but equally successful approach to nonlinear dimensionality reduction is the Isomap algorithm [Tenenbaum (1998), Tenenbaum et al. (2000)]. Isomap is a nonlinear generalization of MDS in which embeddings are optimized to preserve "geodesic" distances between pairs of data points—that is to say, distances along the manifold from which the data is sampled. These distances are estimated by computing shortest paths through large sublattices of data. Like LLE, the Isomap algorithm has three steps: (i) construct a graph in which each data point is connected to its nearest neighbors; (ii) compute the shortest distance between all pairs of data points among only those paths that connect nearest neighbors; (iii) embed the data via MDS so as to preserve these distances. Though similiar in its aims, Isomap is based on a radically different philosophy than LLE (as well as the other Laplacian-based spectral methods discussed above). In particular, Isomap attempts to preserve the global geometric properties of the manifold, as characterized by the geodisic distances between faraway points, while LLE attempts to preserve the local geometric properties of the manifold, as characterized by the linear coefficients of local reconstructions.

As LLE and Isomap are based on somewhat different intuitions, when they break down, they tend to make different errors. The embeddings of LLE are optimized to preserve the geometry of nearby inputs; though the collective neighborhoods of these inputs are overlapping, the coupling between faraway inputs can be severely attenuated if the data is noisy, sparse, or weakly connected. Thus, the most common failure mode of LLE is to map faraway inputs to nearby outputs[8] in the embedding space. By contrast, the embedding cost for Isomap is dominated by the (geodesic) distances between faraway inputs. Thus, its embeddings are biased to preserve the separation of faraway inputs at the expense of distortions in the local geometry. Depending on the application, one algorithm or the other may be most appropriate.

Other important differences between LLE and Isomap are worth mentioning. In section 3, we conjectured that under appropriate conditions, LLE can recover conformal mappings—mappings which locally preserve angles, but not necessarily distances. Such mappings cannot generally be recovered by Isomap, whose embeddings explicitly aim to preserve the distances between inputs.[9] In terms of computational requirements, LLE does not involve the need to solve large dynamic programming problems, such as computing the geodesic distances between data points. It also creates only very sparse matrices, whose structure can be exploited for savings in time and space. This efficiency gain is especially important when attempting to diagonalize large matrices. By subsampling the data to use only certain "landmark" points, Isomap's optimization can also be made relatively sparse, although at the expense of approximating its original objective function.

Yet another eigenvector-based algorithm for nonlinear dimensionality reduction is kernel PCA [Schölkopf et al. (1998)]. This approach builds on the observation that PCA can be formulated entirely in terms of dot products between data points. In kernel PCA, one substitutes the inner product of a Hilbert space for the normally Euclidean dot products of PCA. This amounts to performing PCA on a nonlinear mapping of the original inputs into a different (possibly infinite dimensional) space where their intrinsically low dimensional structure is easier to discover. Williams (2001) has pointed out a connection between kernel PCA and metric MDS. Unlike LLE, kernel PCA does not appeal explicitly to the notion that the data lies on a manifold. However, LLE can be cast as particular form of kernel PCA [(Schölkopf and Smöla, 2002, see p. 455)], and a "kernalized" version of LLE has been proposed [DeCoste (2001)] to visualize the effects of different kernels.

This paper has focused on the application of LLE to high dimensional data sampled (or believed to be sampled) from a low dimensional manifold. LLE can also be applied to data for which the existence of an underlying manifold is not obvious. In particular, while we have focused on real valued signals such as images, relationships between categorial or discrete valued quantities can also be analyzed with LLE. In previous work [Roweis and Saul (2000)], for example, we applied LLE to documents of text, where it can be viewed

[8] Such failures can be detected by computing pairwise distances between *outputs* and testing that nearby outputs correspond to nearby inputs. Note that one could modify the embedding cost function in eq. (2) to include repulsive as well as attractive terms—in other words, to push non-neighbors apart as well as to keep neighbors close. This, however, creates a less sparse eigenvalue problem.

[9] Noting this, de Silva and Tenenbaum (2002) recently proposed an extension to Isomap that does not strictly attempt to preserve distances between inputs. It is able to recover conformal mappings by relaxing certain distance constraints imposed by the original algorithm.

as a nonlinear alternative to the traditional method of latent semantic analysis [Deerwester et al. (1990)].

Whatever the application, though, certain limitations of the algorithm should be kept in mind. Not all manifolds can be recovered by LLE, even in the asymptotic limit of infinite data. How should we handle manifolds, such as the sphere and the torus, that do not admit a uniformly continuous mapping to the plane [Pless and Simon (2001)]? Likewise, how should we embed data sets whose intrinsic dimensionality is not the same in all parts of space, or whose structure is better described as fractal? Further work is needed in these settings. A closely related issue—how to cope with poorly or nonuniformly sampled data—should also be investigated.

In this paper, we have provided a thorough survey of the LLE algorithm—the details of its implementation, an assortment of possible uses and extensions, and its relation to other eigenvector methods for clustering and nonlinear dimensionality reduction. LLE is, of course, an unsupervised learning algorithm, one that does not require labeled inputs or other types of feedback from the learning environment. An oft-made criticism of such algorithms is that they attempt to solve a harder problem than is necessary for any particular task (or in some cases, even the wrong problem altogether). In our view, LLE belongs to a new class of unsupervised learning algorithms that removes much of the force behind this argument. These algorithms do not make strong parametric assumptions, and they are distinguished by simple cost functions, global optimizations, and the potential to exhibit highly nonlinear behavior. We expect these algorithms to be broadly useful in many areas of information processing, and particularly as a tool to simplify, accelerate, and revive other forms of machine learning in high dimensional spaces.

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Appendix A. EM Algorithm for Mixture of Linear Models

In this section, we present the update rules for the EM algorithm in section 6.2. The algorithm is used to estimate the parameters of that section's generative model for input-output pairs of LLE, here denoted by $\{\vec{x}_n, \vec{y}_n\}_{n=1}^{N}$. The derivation is a special case of the full derivation of the EM algorithm for mixtures of factor analyzers [Ghahramani and Hinton (1996)] and is not repeated here. The E-step of the EM algorithm uses Bayes' rule to compute the posterior probabilities:

$$P(z|\vec{y}_n, \vec{x}_n) = \frac{P(\vec{x}_n|\vec{y}_n, z)P(\vec{y}_n|z)P(z)}{\sum_{z'} P(\vec{x}_n|\vec{y}_n, z')P(\vec{y}_n|z')P(z')}. \tag{18}$$

The M-step uses these posterior probabilities to re-estimate the parameters of the model. To simplify the updates in the M-step, we introduce the following notation:

$$\begin{aligned} \gamma_{zn} &= P(z|\vec{x}_n, \vec{y}_n), & (19)\\ \omega_{zn} &= \frac{\gamma_{zn}}{\sum_{n'} \gamma_{zn'}}. & (20) \end{aligned}$$

Here, γ_{zn} and ω_{zn} are the elements of $M \times N$ matrices, where M is the number of mixture components and N is the number of examples. In terms of this notation, the M-step consists of the following updates, to be performed in the order shown:

$$
\begin{aligned}
\vec{\nu}_z &\leftarrow \sum_n \omega_{zn} \vec{y}_n, &(21)\\
\vec{\Sigma}_z &\leftarrow \sum_n \omega_{zn} \left[\vec{y}_n - \vec{\nu}_z\right] \left[\vec{y}_n - \vec{\nu}_z\right]^T, &(22)\\
\Lambda_z &\leftarrow \sum_n \omega_{zn} \vec{x}_n (\vec{y}_n - \vec{\nu}_z)^T \Sigma_z^{-1}, &(23)\\
\vec{\mu}_z &\leftarrow \sum_n \omega_{zn} \left[\vec{x}_n - \Lambda_z \vec{y}_n\right], &(24)\\
\left[\vec{\Psi}_z\right]_{ii} &\leftarrow \sum_n \omega_{zn} \left[\vec{x}_n - \Lambda_z \vec{y}_n - \vec{\mu}_z\right]_i^2, &(25)\\
P(z) &\leftarrow \frac{\sum_n \gamma_{zn}}{\sum_{z'n'} \gamma_{z'n'}}. &(26)
\end{aligned}
$$

The total log-likelihood, $\mathcal{L} = \sum_n \log P(\vec{x}_n, \vec{y}_n)$, can also be computed at each iteration. The updates in eqs. (21–26) are derived in a standard way from the auxiliary function for EM algorithms [Dempster et al. (1977)]. Thus, they lead to monotonic improvement in the total log-likelihood and converge to a stationary point in the model's parameter space.