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Prediction with high dimensional regression via hierarchically structured Gaussian mixtures and latent variables

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Summary. We propose a hierarchical Gaussian locally linear mapping structured mixture model, named HGLLiM, to predict low dimensional responses based on high dimensional covariates when the associations between the responses and the covariates are non-linear. For tractability, HGLLiM adopts inverse regression to handle the high dimension and locally linear mappings to capture potentially non-linear relations. Data with similar associations are grouped together to form a cluster. A mixture is composed of several clusters following a hierarchical structure. This structure enables shared covariance matrices and latent factors across smaller clusters to limit the number of parameters to estimate. Moreover, HGLLiM adopts a robust estimation procedure for model stability. We use three real data sets to demonstrate different features of HGLLiM. With the face data set, HGLLiM shows ability to model non-linear relationships through mixtures. With the orange juice data set, we show that the prediction performance of HGLLiM is robust to the presence of outliers. Moreover, we demonstrate that HGLLiM is capable of handling large-scale complex data by using the data acquired from a magnetic resonance vascular fingerprinting study. These examples illustrate the wide applicability of HGLLiM to handle different aspects of a complex data structure in prediction.

Keywords: Expectation–maximization; High dimension; Magnetic resonance vascular fingerprinting; Mixture of regressions; Robustness

1. Introduction

Building a regression model for prediction is widely used in all disciplines. A large number of applications consist of learning the association between responses and predictors and focusing on predicting responses for the newly observed samples. In this work, we go beyond simple linear models and focus on predicting low dimensional responses by using high dimensional covariates when the associations between responses and covariates are non-linear. Non-linear mappings can be handled through different techniques such as kernel methods (Elisseeff and Weston, 2002; Wu, 2012) or local linearity (De Veaux, 1989; Frühwirth-Schnatter, 2006; Goldfeld and

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Quandt, 1973). In general, the conventional methods adopting local linearity assume assignment independence and are considered as not adequate for regression (Hennig, 2000). Alternatively, one can adopt a mixture modelling strategy and let the membership indicator of a mixture component depend on the values of the covariates. The Gaussian locally linear mapping method called GLLiM (Deleforge *et al.*, 2015) follows this principle.

GLLiM groups data with similar regression associations together. Within the same cluster, the association can be considered as locally linear, which can then be resolved under the classical linear regression setting. Besides adopting the framework of model-based clustering (Banfield and Raftery, 1993; Fraley and Raftery, 2002), GLLiM also takes on a factor-model-based parameterization (Baek *et al.*, 2010; Bouveyron *et al.*, 2007; McLachlan and Peel, 2000; Xie *et al.*, 2010) to accommodate the high dimensional and potentially dependent covariates (see equation (20) in Deleforge *et al.* (2015)). In particular, the high dimensional variables were postulated as a sum of two components: the one that is linearly related to the low dimensional responses, and the other which can be projected onto a factor model and then be presented as augmented latent variables. This data augmentation approach is applicable in many application scenarios, whenever certain variables are only partially observed or corrupted with irrelevant information. The augmentation step, with added latent variables, acts as factor analyser modelling for the noise covariance matrix in the regression model. GLLiM is based on a joint modelling of both the responses and the covariates, observed or latent. This joint modelling framework enables use of an inverse regression strategy to handle high dimensional data.

However, when the covariate dimension is much higher than the response dimension, GLLiM may result in erroneous clusters at the low dimension, leading to potentially inaccurate predictions. Specifically, when the clustering is conducted at a high joint dimension, the distance at low dimension between two members of the same cluster could remain large. As a result, a mixture component might contain several subclusters and/or outliers, violating the Gaussian assumption of the model. This results in a model misspecification effect that can seriously impact prediction performance. We demonstrate this with a numerical example in Section 2. A natural way to lessen this effect is to increase the number of components in the mixture, making each linear mapping even more local. But this practice also increases the number of parameters to be estimated. Estimating parameters in a parsimonious manner is required to avoid overparameterization. In addition, increasing the number of clusters could isolate some data points or lead to singular covariance matrices. Hence, a robust estimation procedure for model stability is also necessary.

In this work, we propose a parsimonious approach combined with a robust estimation procedure which we refer to as HGLLiM for hierarchical Gaussian locally linear mapping to construct a stable model for predicting low dimensional responses. Parsimonious models generally refer to some model instances where the number of parameters is reduced compared with the full parameterization. The goal of parsimonious models is to find a good compromise between model flexibility and parsimony. HGLLiM inherits the advantages from GLLiM on handling high dimensional, non-linear regression with partially latent variables. In terms of the number of parameters, the largest costs usually come from high dimensional covariance matrices. On this front, HGLLiM follows a two-layer hierarchical clustering structure in which we reduce the number of covariance parameters in the model. HGLLiM also includes a pruning algorithm for eliminating outliers as well as determining an appropriate number of clusters. The number of clusters and training outliers determined by HGLLiM can be further used by GLLiM for improving prediction performance.

With the goal of investigating the flexibility in accommodating data structure and the ability to protect from the influences of outliers, we evaluate our method on three data sets with different

characteristics. The face data set contains face images, the associated angles of faces and the source of the light. There is no obvious cluster structure at first glance nor the existence of real outliers. We use this data set to evaluate the ability of HGLLiM in modelling regression through local linear approximations. The orange juice data set contains continuous spectrum predictors and some abnormal observations. Using this data set, we aim to show that HGLLiM is robust and can effectively identify outlying observations. We use these two moderate size data sets to demonstrate how the method works on data with different features and the insensitivity of tuning parameter selection on a wide range of selection domains. Finally, in our last data analysis, we study a problem where researchers are interested in predicting microvascular properties by using so-called magnetic resonance vascular fingerprinting. Hereafter we refer to this data set as the fingerprint data. We use this data set to demonstrate the power of HGLLiM on modelling complex associations over a large number of observations. Results show that HGLLiM can provide comparable prediction performance on one case and much smaller prediction errors on the other, compared with the dictionary matching method in Lemasson *et al.* (2016) with only 25% of the computational time.

This paper is organized as follows. In Section 2 we explain and illustrate the issue that is encountered with unstructured GLLiM in high dimensional settings. In Section 3, we present the structured alternative that we propose. The experiment results on three real data sets are provided in Section 4. Finally, Section 5 concludes with a discussion and potential future directions.

The programs that were used to analyse the data can be obtained from

`https://rss.onlinelibrary.wiley.com/hub/journal/14679876/series-c-datasets`

2. Unstructured Gaussian locally linear mapping

To predict low dimensional data $Y \in \mathbb{R}^L$ by using high dimensional data $X \in \mathbb{R}^D$, $D \gg L$, GLLiM elegantly copes with several challenging issues simultaneously. The high-to-low mapping difficulty is circumvented by inverse regression. And then the desired high-to-low relationship can be easily converted from the low-to-high associations under a proper model construction. Non-linearity is approximated by locally linear associations (chapter 6 of Scott (2015)). The parameter estimation is carried out by an expectation–maximization (EM) algorithm, which nicely incorporates estimation of latent variables.

The original GLLiM groups data into K clusters. For cluster k, the data follow the following distributions:

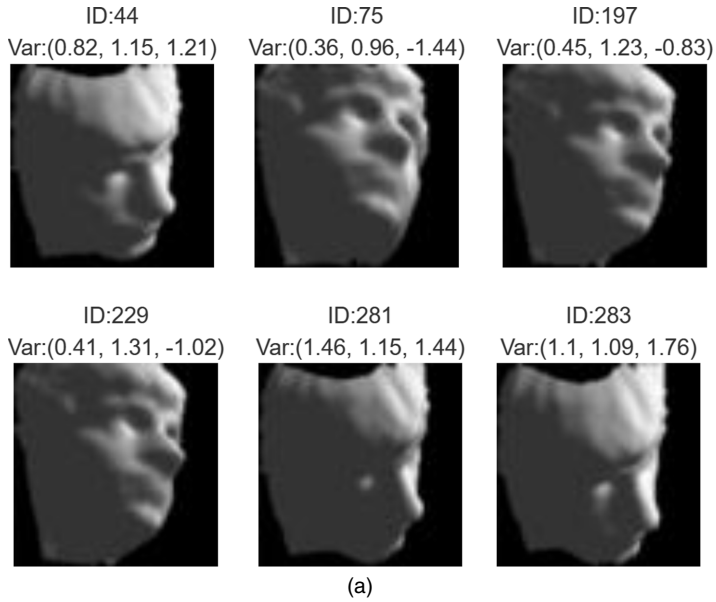
$$p(X = x|Y = y, Z = k; \theta) = \mathcal{N}(x; A_k y + b_k, \Sigma_k). \tag{1}$$

$$p(Y = y|Z = k; \theta) = \mathcal{N}(y; c_k, \Gamma_k), \tag{2}$$

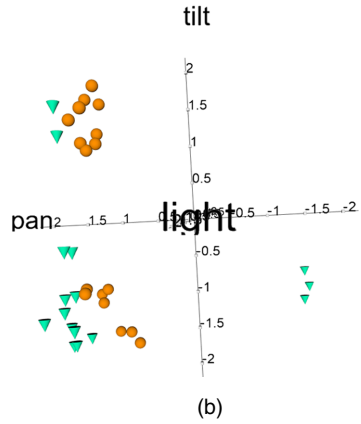
$$p(Z = k; \theta) = \pi_k,$$

where the latent variable Z represents the cluster assignment, and $\theta = \{c_k, \Gamma_k, \pi_k, A_k, b_k, \Sigma_k\}_{k=1}^K$ is a vector denoting the model parameters. For the kth cluster, the centre and the covariance matrix for the mixture at low dimension are c_k and Γ_k. The parameters A_k and b_k are the transformation matrix and intercept, mapping data from low dimension to high dimension with Σ_k capturing the reconstruction errors.

A distinct feature of GLLiM is that Y need not be a completely observable vector. In fact, it is set to have $Y^{\mathrm{T}} = (T^{\mathrm{T}}, W^{\mathrm{T}})$, where T contains the observable variables, which one intends to predict, and W, being latent, absorbs the remaining dependence and variation in the high dimensional X. The inclusion of W strengthens the chance to reach validity of equation (1).



(a)



(b)

Fig. 1. Clustering results of the face data set obtained from GLLiM: (a) six face images from cluster 7; (b) scatter plot of T for points within clusters 7 (●) and 13 (▼) clustered by GLLiM (the three variables are (Light, Pan, Tilt)

The issue with GLLiM is that the high dimensionality of the data may have an unexpected effect on the posterior probability of the cluster assignment. When the dimensions of X and Y satisfy $D \gg L$, this comes from the following observation: in the expectation step the posterior probabilities r_{nk} (equation (27) in Deleforge *et al.* (2015)) is computed as

$$r_{nk} = p(Z_n = k | x_n, y_n; \theta) = \frac{\pi_k p(x_n, y_n | Z_n = k; \theta)}{\sum_{j=1}^{K} \pi_j p(x_n, y_n | Z_n = j; \theta)} \tag{3}$$

for all n and all k, where $p(x_n, y_n | Z_n = k; \theta)$ can be computed as $p(x_n | y_n, Z_n = k; \theta)\, p(y_n | Z_n = k; \theta)$. The first term is a density with much higher dimension D so its value could dominate the product. In addition, y_n can be decomposed into two parts: the observed variable t_n and the latent variable

Table 1. Comparison of original and post-cluster-division squared error SE†

Image	*GLLiM cluster*	*Original SE*	*Post-division SE*	*Improved ratio (%)*
56	7	0.306	0.043	86.03
223	7	0.016	0.180	−1039.83
293	7	0.060	0.023	61.27
302	7	0.087	0.003	96.99
114	13	0.114	0.118	−2.93
204	13	0.307	0.073	76.19
294	13	3.119	0.120	96.15

†The improved ratio is calculated as the ratio of the difference of SE from pre- to post-cluster division over the original SE. The value is positive if the procedure reduces the SE, and negative otherwise.

w_n. The component w_n reflects the remaining variation in x_n that cannot be explained by x_n's association with t_n. When w_n accounts for explaining most of the variation in x_n, the clustering outcome would highly depend on w_n and weaken the ability of detecting subclusters in T.

Therefore, although GLLiM assumes that within each cluster $p(Y = y|Z = k; \theta)$ is Gaussian and centred on c_k, in practice, the model groups data according to the high dimension term and could fail in imposing the Gaussian shape on the t_ns. In other words, the model rather chooses the clusters to satisfy the assumption in equation (1). And this induces a clustering of the (x_n, y_n)s into groups within which the same affine transformation holds. Thus, a cluster could contain several subclusters and/or outliers since the Gaussian assumption on T, as part of the Y, in equation (2) is sometimes neglected. This may cause a serious effect on the estimation of c_k and Γ_k and consequently on the prediction step.

We illustrate this issue by presenting an example using a face data set (Tenenbaum *et al.*, 2000). This data set contains 698 images (of size 64×64 and being further condensed to 32×32). The pose of each image is defined by three variables in T: *Light*, *Pan* and *Tilt*, as shown in Fig. 1(a). We adopt GLLiM to predict these Ts (low dimensional) by using the image (high dimensional). The superiority of GLLiM in prediction, compared with multiple existing approaches, for this data set was numerically illustrated in Deleforge *et al.* (2015).

Fig. 1(b) shows the scatter plot of T within clusters 7 and 13, grouped by GLLiM. By visual inspection, both clusters seem to consist of two or more subclusters. In GLLiM, samples within the same cluster are assumed to follow Gaussian distributions. This subcluster structure, however, violates the assumption and potentially increases the prediction errors. We demonstrate the difference of prediction performance before and after accounting for the subcluster structure in Table 1. We use prediction squared error for testing data pre- and post-cluster division. We observe that the prediction errors are mostly reduced if we account for the subcluster structure.

Dividing samples at low dimension is an effective and straightforward solution for this issue. However, we could obtain small subclusters after division and then increase the prediction variance. In Table 1, images 114 and 223 were assigned to small and/or tight local clusters and the prediction of T for these two images became worse after cluster division. Conceptually, small clusters could damage the prediction performances for several reasons: the small number of observations in such a cluster leads to estimates with large variation; a small cluster with a small covariance matrix determinant (volume) could lead to instability of the whole likelihood-based

algorithm, and a small or tight cluster could consider a close-by testing sample unfit and force it to be predicted by another less suitable cluster with a larger within-cluster covariance. The last consideration is not relevant to model building but plays an important role in prediction precision.

This observation motivates us to look into enhancing prediction stability by eliminating small clusters and outliers in the training samples. We further explore both issues in Section 4.

3. Hierarchical Gaussian locally linear mapping

In our proposed work, we intend to strike a balance between model flexibility and variation reduction in the estimated predictive model, with the goal of predicting the low dimensional observable variables T, using the high dimensional X. This predictive model need not be the true model but should be effective in prediction. To present the fundamental concepts with clarity, we shall first describe the model structure when $Y = T$, with minimum required notation. The scenario of Y containing W is easily extended in Section 3.2.

3.1. Model description

The joint probability $p(X = x, Y = y; \theta)$ of high dimensional predictor X and low dimensional response Y can be written as

$$\sum_{k=1}^{K} \sum_{l=1}^{M} p(X = x | Y = y, Z = k, U = l; \theta)\, p(Y = y | Z = k, U = l; \theta)\, p(Z = k, U = l; \theta),$$

where θ denotes the vector of parameters; Z and U are respectively latent global and local cluster assignments. The locally linear relationship between X and Y is given by the mixture model

$$X = \sum_{k=1}^{K} \sum_{l=1}^{M} \mathbb{I}(Z = k, U = l)(A_{kl} Y + b_{kl} + E_k),$$

where $\mathbb{I}$ is the indicator function, $A_{kl} \in \mathbb{R}^{D \times L}$ and $b_{kl} \in \mathbb{R}^{D}$ map Y onto X, and $E_k \in \mathbb{R}^{D \times D}$ is the error term that absorbs the remaining uncertainty. Recall that D and L are dimensions of X and Y respectively, and $D \gg L$. Here, we let the local cluster size $M(k) \equiv M$ for notational simplicity only. We assume, within the kth global cluster, that all local clusters share the same error structure which follows a zero-mean Gaussian distribution with covariance matrix Σ_k, i.e. we have

$$p(X = x | Y = y, Z = k, U = l; \theta) = \mathcal{N}(x; A_{kl} y + b_{kl}, \Sigma_k).$$

As in equation (2), the model is completed by assuming that the low dimensional Y, given the clustering assignment indicators $(Z,\ U) = (k,\ l)$, follows a Gaussian distribution with mean c_{kl} and variance Γ_{kl}, and by defining a prior for clustering assignment, $p(Z = k, U = l \mid \theta) = \rho_{kl}$, where $c_{kl} \in \mathbb{R}^{L}$, $\Gamma_{kl} \in \mathbb{R}^{L \times L}$ and $\Sigma_{k=1}^{K} \Sigma_{l=1}^{M} \rho_{kl} = 1$. The vector of parameters in the inverse regression model, θ, is given by

$$\theta = \{c_{kl}, \Gamma_{kl}, \rho_{kl}, A_{kl}, b_{kl}, \Sigma_k\}_{k=1,l=1}^{K,M}. \tag{4}$$

The remaining task is to use the inverse conditional density to construct the exact formulations of the conditional density of Y given X in the forward regression model and the resulting expression of $E[Y|X = x]$. Equivalently to how we define θ in the model of X given Y, we let θ^* denote the parameter vector in the forward regression model of Y given X. We then derive the closed form expression of θ^* as a function of θ, as given in the on-line appendix A. The

prediction of Y given X can then be done by taking the expectation over the forward conditional density, $E[Y|X=x]$, given in equation (12) in appendix A. The use of the closed form expressions that are provided in appendix A makes it computationally efficient in conducting prediction.

3.2. Hierarchical Gaussian locally linear mapping model with partially latent responses

Recall that the low dimensional data $Y \in \mathbb{R}^L$ contain a latent component W. Namely, $Y^{\mathrm{T}} = (T^{\mathrm{T}}, W^{\mathrm{T}})$, where $T \in \mathbb{R}^{L_t}$ is observed and $W \in \mathbb{R}^{L_w}$ is latent and thus $L = L_t + L_w$. It is assumed that T and W are independent given Z, and so are W and U. According to the decomposition of Y, the corresponding mean c_{kl}, variance Γ_{kl} and regression parameters A_{kl} of Y, at the local cluster level, are given as

$$\left.\begin{aligned} c_{kl} &= \begin{pmatrix} c_{kl}^t \\ c_k^w, \end{pmatrix}, \\ \Gamma_{kl} &= \begin{pmatrix} \Gamma_{kl}^t & 0 \\ 0 & \Gamma_k^w \end{pmatrix}, \\ A_{kl} &= (A_{kl}^t \; A_k^w). \end{aligned}\right\} \tag{5}$$

That is, when $Z=k$ and $U=l$, at the local cluster level, $T \sim \mathcal{N}(c_{kl}^t, \Gamma_{kl}^t)$; when $Z=k$, at the global cluster level, $W \sim \mathcal{N}(c_k^w, \Gamma_k^w)$. It follows that, locally, the association function between the high dimensional Y and low dimensional X can be written as

$$X = \sum_{k=1}^{K} \mathbb{I}(Z=k) \left\{ \sum_{l=1}^{M} \mathbb{I}(U=l)(A_{kl}^t T + b_{kl}) + A_k^w W + E_k \right\}. \tag{6}$$

Finally, the parameter vector θ in the inverse regression model is rewritten as $\theta = \{\rho_{kl}, c_{kl}^t, \Gamma_{kl}^t, A_{kl}^t, b_{kl}, c_k^w, \Gamma_k^w, A_k^w, \Sigma_k\}_{k=1,l=1}^{K,M}$.

It follows that equation (6) can be rewritten equivalently as

$$X = \sum_{k=1}^{K} \mathbb{I}(Z=k) \left\{ \sum_{l=1}^{M} \mathbb{I}(U=l)(A_{kl}^t T + b_{kl}) + A_k^w c_k^w + E_k' \right\}, \tag{7}$$

where the error vector E_k' is modelled by a zero-centred Gaussian variable with a $D \times D$ covariance matrix given by

$$\Sigma_k' = \Sigma_k + A_k^w \Gamma_k^w A_k^{w\mathrm{T}}. \tag{8}$$

Considering realizations of variables T and X, the addition of the latent W naturally leads to a covariance structure, namely equation (8), where $A_k^w \Gamma_k^w A_k^{w\mathrm{T}}$ is at most of rank L_w. When Σ_k is diagonal, this structure is that of factor analysis with at most L_w factors, and represents a flexible compromise between a full covariance with $O(D^2)$ parameters on one side, and a diagonal covariance with $O(D)$ parameters on the other.

Using the same number of total clusters and considering the fact that Σ_k and A_k^w are estimated only at the global cluster level, we note that the total number of parameters that are needed to model the covariances Σ_k and the latent transformation coefficients A_k^w using HGLLiM is $1/M$ of that required by using GLLiM. In addition, the key emphasis of HGLLiM is to conduct prediction. As shown in equations (5), (7) and (8) at the local *versus* global cluster levels, we now separate the estimation of the mean association functions, which play a key role in prediction, from that of high dimensional covariance matrices, so that the means can be obtained even more locally. Together with the current dependence structures, being stably estimated at the global cluster level by using more data points per cluster, HGLLiM provides a strong prediction tool

built on a structure facilitating sensible approximations to the true underlying distribution of low dimensional T and high dimensional X.

3.3. Robust estimation procedure

HGLLiM contains three sets of latent variables: $Z_{1:N} = \{Z_N\}_{n=1}^N$, $U_{1:N} = \{U_n\}_{n=1}^N$ and $W_{1:N} = \{W_n\}_{n=1}^N$. The first two sets of variables indicate the global and the local cluster assignments and the last is the latent covariates. The model parameters, θ, as defined in equation (4) can be estimated by using the EM algorithm (Dempster *et al.*, 1977). However, even with the inversion step, the prediction procedure still involves a high dimensional predictor and elevated variation in estimated parameters, induced by small clusters or abnormal observations, that could lead to deteriorating prediction quality. The stability can be achieved by constraining the sizes of the clusters (control both covariance volume and prediction variance) and trimming outliers. We design a robust estimation procedure to refine the standard EM algorithm with the purpose of enhancing model stability, which consequently leads to improved prediction performance.

Define the posterior probability of observation n being assigned to cluster (k, l) as

$$r_{nkl} = p(Z_n = k, U_n = l | t_n, x_n; \theta), \tag{9}$$

and let $\Sigma_{n=1}^N r_{nkl}$ represent the cluster size for cluster (k, l). Each data point in a cluster whose cluster size is smaller than a predetermined *minSize* is reassigned to other clusters. The point is kept when the prediction squared error is less than a predetermined *dropThreshold*; otherwise, it would be excluded from the current EM iteration when updating the estimated parameters. With the data points within a cluster playing a dominating role in estimating within-cluster parameters, the cluster size plays the role of the sample size in estimation: when the sample size is too small, the prediction quality deteriorates even if the structure assumed is true. An improved prediction performance might be achieved by assigning such a data point within a small cluster to another cluster that shares similar structures. If no such cluster can be identified, then the data point is excluded from the construction of the prediction model.

An EM algorithm for HGLLiM directly constructed according to models given in Sections 3.1 and 3.2 is described in the on-line appendix A.1. The algorithm iterates between E-steps to update latent W, Z and U and M-steps that update θ. Here, we describe the robust estimation procedure, tailored to ensure stability and outlier trimming. The algorithm is described as follows.

(a) The algorithm is initialized by adopting the parameters θ, mean and covariance, $\tilde{\mu}_{nk}^w$ and $\tilde{S}_k^w$, of latent W of the kth cluster, and cluster assignment r_{nkl} obtained from the EM algorithm that is described in appendix A.1.

(b) The estimating procedure iterates through the following substeps until the algorithm converges.

  (i) Trimming step: to remove outliers, we scan through all local clusters and remove all samples whose in-sample prediction squared errors are greater than a predetermined dropThreshold. The prediction squared error for the nth sample is calculated as

$$E_n^2 = ||t_n^{\text{pred}} - t_n||_2^2, \tag{10}$$

  where t_n is the true value and t_n^{pred} is the prediction from equation (12) in the on-line appendix A. Note that the low dimension data $\{t_n\}_{n=1}^N$ are standardized before training so that each dimension would be equally weighted. The samples with in-sample prediction squared error larger than dropThreshold are considered as outliers and are temporarily removed by assigning r_{n^*kl} to be 0 at that iteration of the M-step, where n^* indicates the training sample whose $E_{n^*}^2 >$ dropThreshold.

(ii) Maximization step with a cluster size constraint: the estimation of θ is the same as the maximization step that is described in the on-line appendix A.1 but with an additional cluster size constraint. Before estimating parameters for each local cluster (k, l), we first check the associated cluster size. If the cluster size is smaller than the given minSize, we force the training data that were originally assigned to this cluster either to be assigned to other clusters during the E-step in updating cluster assignment Z, and U, or, if no appropriate cluster could be found, to be trimmed during the next trimming step.
(iii) Update step for the latent variables: estimation of $\tilde{\mu}_{nk}^{w}$, $\tilde{S}_{k}^{w}$ and r_{nkl} is done by using the E–W and E–Z, U step that is described in appendix A.1.

All outcomes in Section 4 are obtained by using the algorithm that is presented in this section. The procedure to select all tuning parameters, aiming at obtaining better prediction performances, is given in appendix A.2.

4. Numerical investigation

We analyse three data sets and use the outcomes to illustrate the usage of the method proposed. Key features of each data set, and thus the type of data that they represent, are reported in the corresponding subsections. Throughout, we use squared error (equation (10)) to evaluate the prediction performance for each data point. We also calculate the prediction mean-squared error (MSE) among all testing samples with $\text{MSE} = \Sigma_{n=1}^{N_{\text{test}}} E_n^2 / N_{\text{test}}$, where N_{test} is the total number of testing samples.

We calculate and compare the MSE or the quantiles of squared errors over several methods.

(a) HGLLiM is the method proposed. The user-defined parameters K and L_w are set to values by using the method that is described in the on-line appendix A.2. The number of local clusters M is set to 5 to reflect the possible subcluster structure. In each global cluster, the number of local clusters varies and depends on the structure of the data set. Some of the local clusters would be dissolved so the number of local clusters could be less than M. The initial cluster assignment is done by dividing the GLLiM clustering outcomes at the low dimension by using the R package `mclust` (R Core Team, 2018; Scrucca *et al.*, 2017). As stated before, the robust version of the EM algorithm is used throughout the experiments. We set minSize = 5 for all of the analyses and post-analysis checks at the neighbourhood of 5 suggest that this is an appropriate choice. The prediction MSE by using different values of dropThreshold would be calculated and compared.
(b) GLLiM is the original GLLiM algorithm. GLLiM is compared with other methods under the same settings of K and L_w. The initial cluster assignment is done by applying a Gaussian mixture model to a data set that combines the low dimensional T and high dimensional X together.
(c) GLLiM-structure is the method that adopts the number of clusters learned structurally by HGLLiM. In addition, outliers identified by HGLLiM are removed from the training data set. We adopt the same tuning parameters as GLLiM and the initial conditions are obtained from the outcomes of HGLLiM. The key difference between GLLiM-structure and HGLLiM is that GLLiM-structure uses local estimated covariance, which may be more appropriate for a large data set with more local dependence features. Its effectiveness also suggests an additional usage of HGLLiM, in terms of structure learning and identification of outliers.

4.1. The face data set

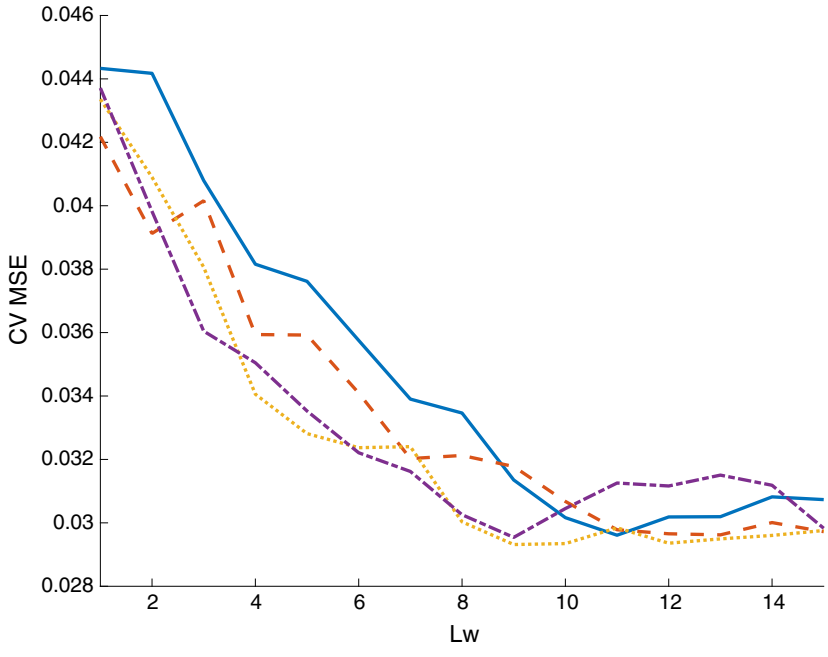
The face data set, consisting of 698 samples, was analysed in the original GLLiM reference (Deleforge *et al.*, 2015). For this data set, we are interested in predicting the pose parameters ($L_t = 3$) by using the image information. The size of each image is condensed to 32×32, and thus $D = 1024$. In addition, T is standardized so that all three dimensions are equally weighted. The histograms of the three T-variables bear no clustering structure. Consequently, the mixture modelling serves the purpose of local linear approximation and the inverse regression is utilized to circumvent the difficulties that are encountered in high dimensional regression.

In each run of cross-validation investigation, we follow the procedure in Deleforge *et al.* (2015) and select 100 testing samples and keep the remaining 598 as training samples. We repeated this procedure 20 times to establish 2000 testing samples. According to the approach that is described in the on-line appendix A.2, we run cross-validation on K from 10 to 25 and L_w from 1 to 15. The cross-validation results in Fig. 2(a) suggest that $K = 20$ and $L_w = 9$. It is noted that the prediction errors decrease with increasing values of L_w. This suggests that the high dimensional X are dependent and that accounting for such dependence via the latent W leads to improvement in prediction. It is also observed that the change of prediction error is relatively small when L_w exceeds a certain value. Therefore, we fix the number of latent factors and compare the prediction performance under $K = 10$, $K = 15$ and $K = 25$.

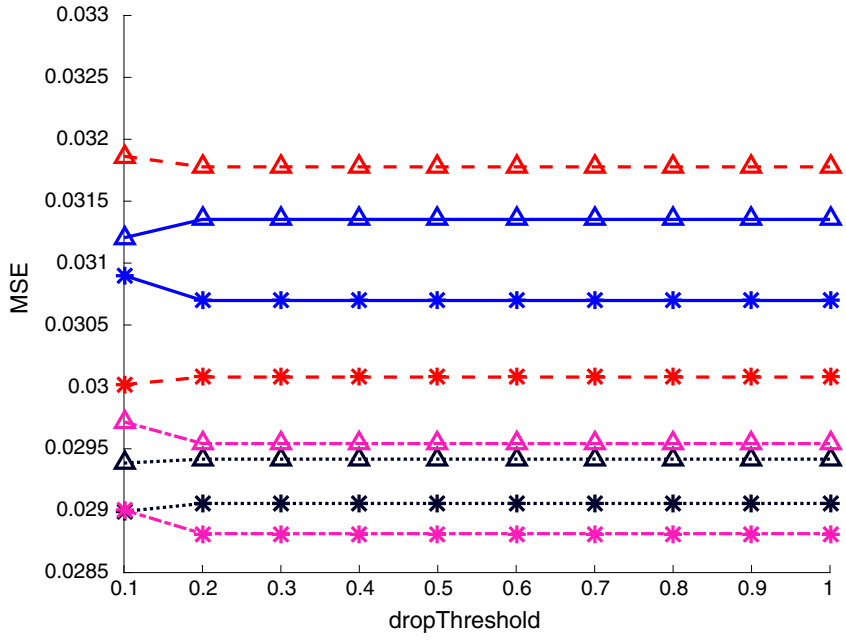
Fig. 2(b) shows prediction outcomes under various values of dropThreshold. We observe that, for different methods and different K, the prediction MSEs are not sensitive to the values of dropThreshold. Thus, we compare the prediction MSE of HGLLiM and GLLiM-structure when dropThreshold $= 0.5$ with GLLiM in Table 2. The prediction MSE for GLLiM decreases as K increases, which indicates that more clusters could be helpful to capture the non-linear relationship between X and T. For HGLLiM, we observe that the prediction MSE is not sensitive to the choice of K. In addition, the numbers of clusters are similar under different choices of K. This indicates that HGLLiM could adjust itself to reach the number of clusters that is suitable to its setting. As for GLLiM-structure, the prediction MSEs are slightly smaller than those of HGLLiM. This is because GLLiM-structure estimates all parameters by using local clusters and local covariances, and the prediction would be less biased when the local structures sufficiently differ. In the face data set, there is no obvious cluster structure and, as a result, clustering serves only the purpose of improving local approximation. Thus, the prediction MSE for GLLiM-structure would be smaller. However, the differences of prediction MSEs between HGLLiM and GLLiM-structure are small, which implies that the settings learned from HGLLiM are appropriate, even though HGLLiM imposes a global cluster structure when there is none. Overall, the prediction performance for HGLLiM is similar when $K = 20$ and $K = 25$. As for GLLiM-structure, the MSE is smaller when $K = 25$ but the difference is negligible.

We further investigate the phenomenon described in Section 2. Specifically, as the dimension of X becomes higher, not only the number of covariance parameters increases, but there is also a higher chance that the clusters that are formed by GLLiM could contain subclusters and/or outliers, which could degrade the prediction quality. We use cluster 7 as our reference to create two clusters. There are two subclusters within cluster 7. We first identify the centre of each subcluster by using the low dimensional T and find 30 nearest samples to each centre. We randomly select 25 data points from each subcluster as the training data and use the rest of the data points as the testing samples. Thus, there will be 50 training samples and 10 testing samples. The procedure is repeated 20 times and the results are aggregated to evaluate the model performance.

To investigate the prediction performance under the different dimensions of X, we resize the face image to $l \times l$ pixels, where we denote l the side length of the image so that the dimension



(a)



(b)

Fig. 2. Results for different user-defined parameters of the face data set: (a) HGLLiM cross-validation results for various K and L_W (——, $K = 10$; – – –, $K = 15$; ·····, $K = 20$; – · – ·, $K = 25$); (b) prediction MSE of various K and different methods against various dropThreshold (△, HGLLiM, $K = 10$; △, HGLLiM, $K = 20$; ✳, GLLiM-structure, $K = 10$; ✳, GLLiM-structure, $K = 20$; △, HGLLiM, $K = 15$; △, HGLLiM, $K = 25$; ✳, GLLiM-structure, $K = 15$; ✳, GLLiM, $K = 25$)

Table 2. Prediction MSE and average cluster number of the face data set when dropThreshold = 0.5

Method	*Results for K = 10*		*Results for K = 15*		*Results for K = 20*		*Results for K = 25*	
	MSE	*Number of clusters*	*MSE*	*Number of clusters*	*MSE*	*Number of clusters*	*MSE*	*Number of clusters*
GLLiM	0.0711	10.00	0.0441	15.00	0.0369	20.00	0.0321	25.00
HGLLiM	0.0314	43.90	0.0318	51.35	0.0294	53.75	0.0295	53.45
GLLiM-structure	0.0307	43.90	0.0301	51.35	0.0291	53.75	0.0288	53.45

of X is $D = l \times l$. For GLLiM, we set the number of clusters, K, to be 2 and the dimension of the latent variables, L_w, to be 9. For HGLLiM, we have one global cluster and two local clusters, i.e. $K = 1$ and $M = 2$. As suggested in Fig. 2(a), we let $L_w = 9$ since this setting results in smaller cross-validation MSE. We disable the robust estimation step, which is equivalent to setting minSize = 0 and dropThreshold = ∞, as described in Section 3.3; also see the on-line appendix A.2. Fig. 3 shows the result of prediction MSE under various dimensions of X. When the dimension of X is low, GLLiM can outperform HGLLiM. However, as the dimension of X increases, we observe that the prediction error of GLLiM increases, suffering from the potentially less suitable cluster assignments. In contrast, HGLLiM maintains appropriate clustering results and thus the prediction performance remains similar for all sizes of image, if not slightly improved with the increasing dimension of X and the enhanced information in the images with higher resolution.

4.2. The orange juice data set

The orange juice data set contains the spectra measured on different kinds of orange juice ($N = 218$). The goal is to use the spectra to predict the level of sucrose ($L_t = 1$). We follow the step that was described in Perthame *et al.* (2018) and decompose the spectra on a spline basis with ($D = 134$) to make $D \approx N$. This data set is known for outliers; the realization of X and T is given in Fig. 4.

We set up the following prediction evaluation procedure. In each run, we randomly select 20 testing samples from the main population (excluding outliers). The remaining 198 samples (including outliers, unless otherwise specified) are used for training. These outliers were identified through leave-one-out cross-validation using GLLiM, with $K = 10$ and $L_w = 2$. Although the set of outliers may differ for different selections of K and L_w, the severe outliers are always selected and they are included here. We identify 11 points, which are the observations with the top 5% of the prediction E^2s (above 4.8) among all data points, as outliers. Removing outliers from testing data prevents the summarized outcomes from being overwhelmed by prediction results of few points, which potentially makes the differences between methods less obvious. All methods were evaluated by using the same settings.

Fig. 5(a) shows the cross-validation results, which suggest the use of $K = 5$ and $L_w = 8$. For comparison, we also provide MSE results for $K = 10$ and $K = 15$. The rest of the setting is the same as the experiment setting that was used for the face data set.

To evaluate the influence of outliers on GLLiM, we conduct an analysis in which we use the same cluster number as in GLLiM-structure but without removing training outliers. This

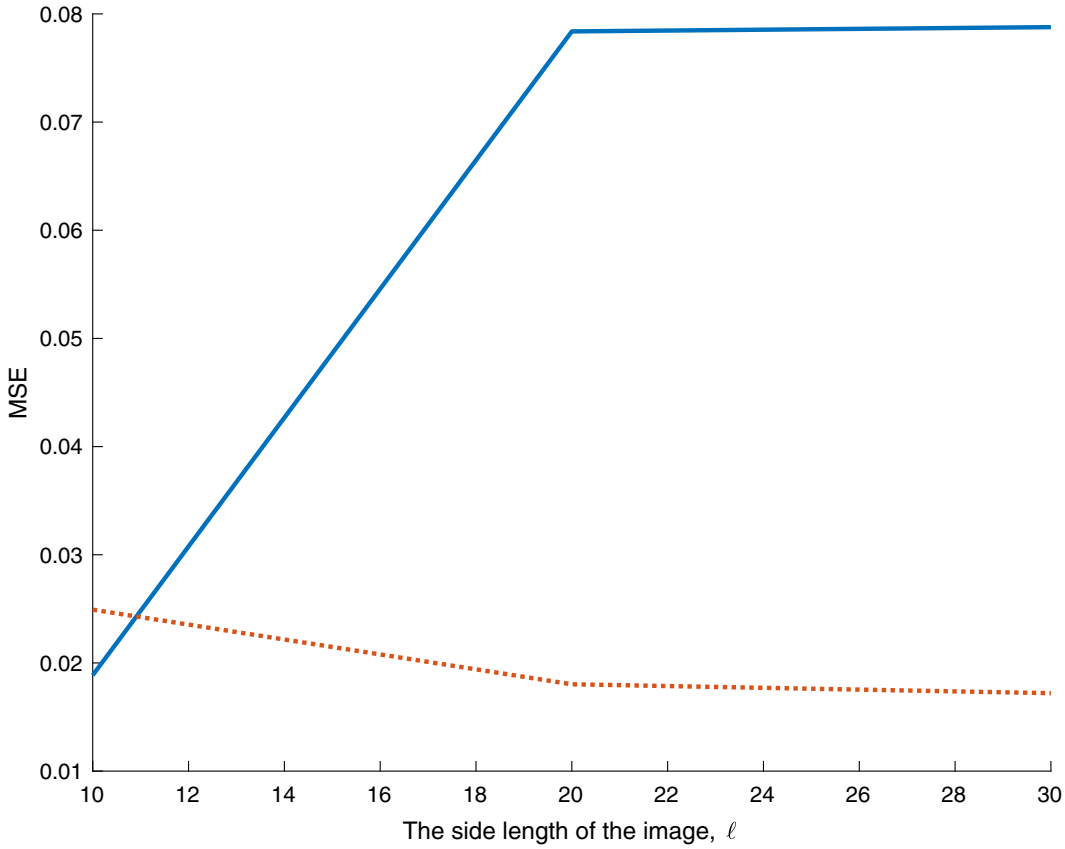


Fig. 3. Prediction MSE of the face data set under different dimensions of X (each image in the face data set consists of $l \times l$ pixels, where l, the side length of the image, is the square root of the dimension of X): ——, GLLiM; – – –, HGLLiM

method is referred to as GLLiM-outlier. In addition, we consider SLLiM in Perthame *et al.* (2018) provided by the R package `xLLiM` (Perthame *et al.*, 2017). SLLiM is a counterpart of GLLiM that accommodates abnormal samples by using Student t-distributions. Precisely, the high dimensional Y is modelled by a mixture of K generalized multivariate Student t-distributions, using the structure that is given in Section 5.5 (page 94) of Kotz and Nadarajah (2004). We also compare SLLiM performances by using the same cluster number learned structurally by HGLLiM. We refer to the resulting procedure as 'SLLiM-structure'. We use the default settings in `xLLiM` for the remaining SLLiM configurations.

Fig. 5(b) shows the prediction MSE for various dropThresholds. The prediction MSEs vary, mainly reflecting the high variation in this data set, partially due to outliers. For a small dropThreshold, the number of training outliers identified is more than expected. This reduces the training data size and makes the prediction unreliable. As dropThreshold reaches a reasonable value, the prediction performance becomes better. However, increasingly more abnormal training samples are included in the training data set as dropThreshold keeps increasing. These outlying data enlarge the model variance and downgrade the prediction performance. Table 3 shows the results for dropThreshold $= 0.5$. We observe that, for $K = 5$, the cluster number is not sufficiently large for GLLiM to capture the non-linear trend in the data, which results in

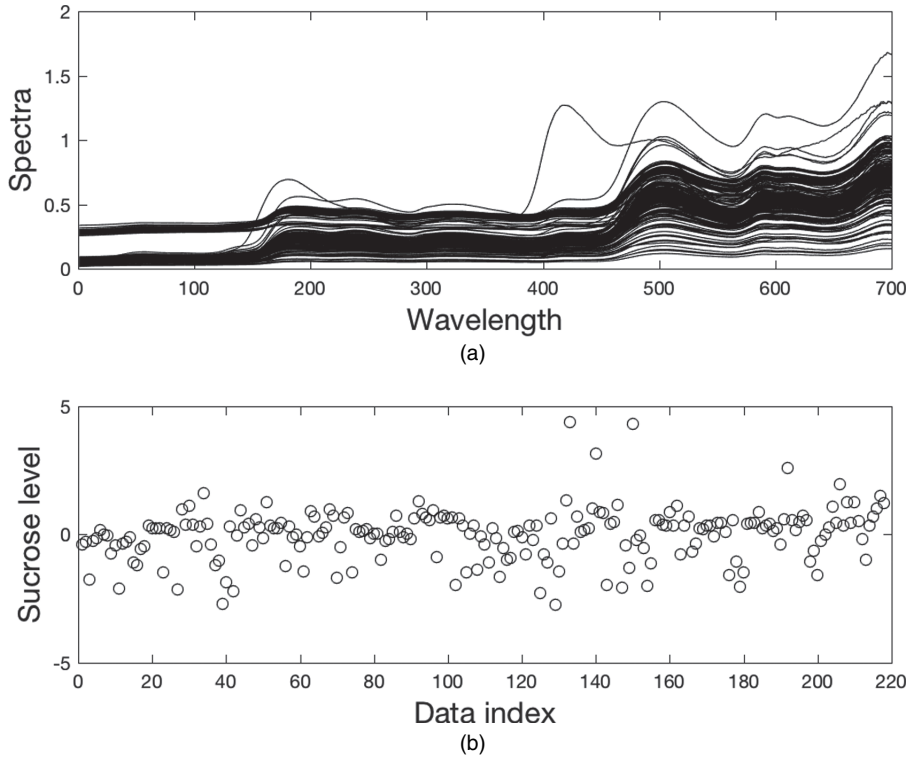


Fig. 4. Orange juice data set: (a) high dimensional data X; (b) low dimensional data T

a relatively large prediction MSE. HGLLiM, in contrast, adjusts the cluster number automatically and the prediction errors are smaller. In addition, HGLLiM removes training outliers that would degrade the model performance. This explains why, even though the cluster number is as large as $K = 15$ (larger than the average size of 12.8 that is used in GLLiM-structure), GLLiM still suffers from large prediction errors. We further observe the benefit of removing outliers by comparing GLLiM-structure and GLLiM-outlier. The prediction errors for GLLiM-structure are smaller than those produced by GLLiM-outlier and the only difference between GLLiM-structure and GLLiM-outlier is whether training outliers, that are identified by HGLLiM, are removed. There are 11 outliers in the training data set. HGLLiM could effectively identify and remove all of them. In addition to these outliers, some potential outlying samples that could result in an unstable model are trimmed as well. Overall, about 6–10% of the training samples would be removed by HGLLiM.

SLLiM and SLLiM-structure use t-distributions to accommodate the existence of outliers. They are expected to perform better than their Gaussian counterparts (GLLiM and GLLiM-outlier). When K, the cluster number, is small, there would be more samples in each cluster and thus the cluster size, $\Sigma_{n=1}^{N} r_{nkl}$ for cluster (k, l), would be large. In contrast, when K is large, samples would be divided into more clusters, which decreases the cluster size. It is observed that, when K is small, accommodating outliers with t-distributions is not as effective as removing them by comparing SLLiM-structure and GLLiM-structure. When the number of clusters becomes larger, outliers could be assigned to a cluster with less influence on the prediction and thus we can obtain similar prediction performances from SLLiM-structure and GLLiM-structure. However, removing outliers would reduce the cluster size and result in unstable prediction performance. To

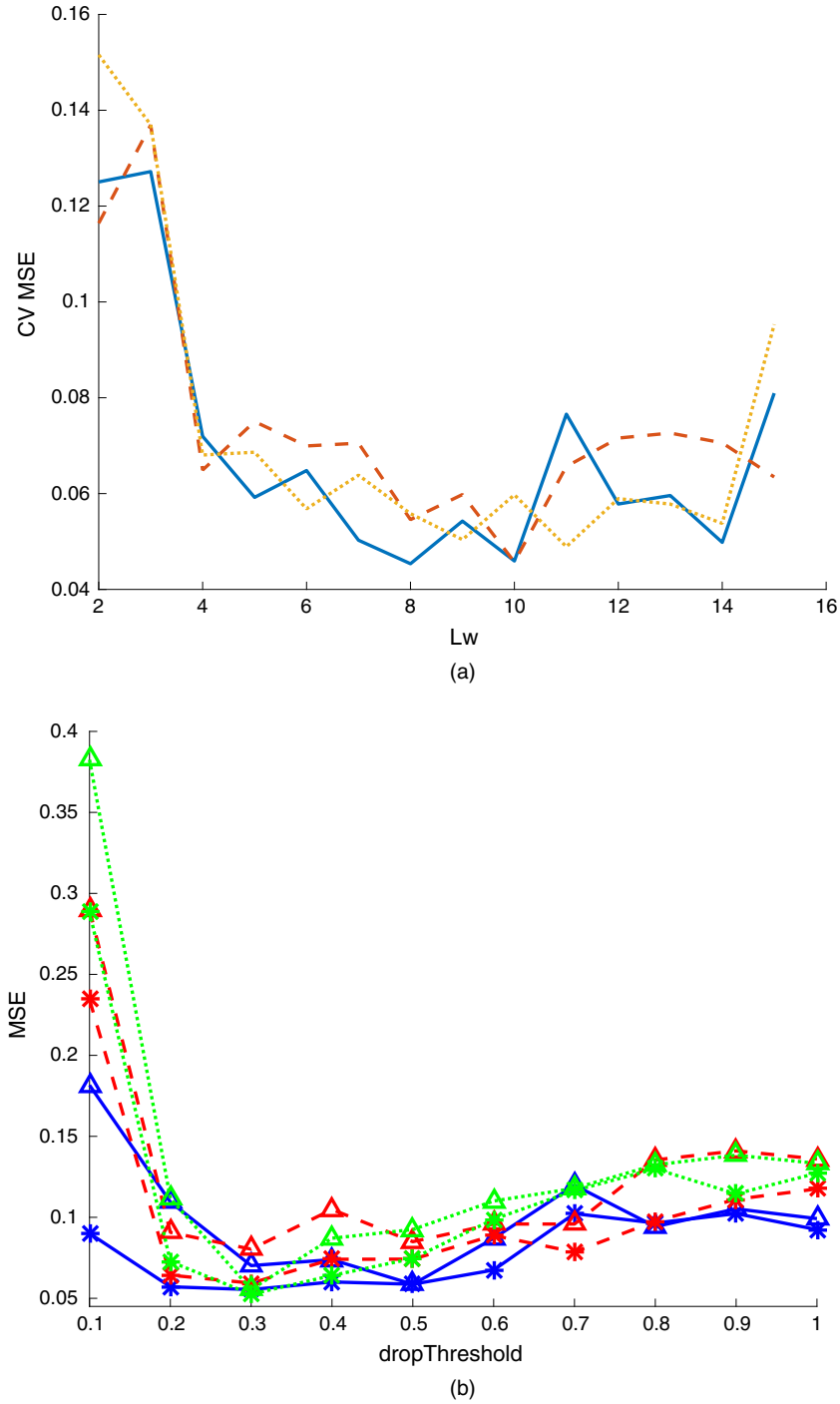


Fig. 5. Results for the user-defined parameters of the orange juice data set: (a) HGLLiM cross-validation results for various K (———, $K = 5$; – – – –, $K = 10$; ·····, $K = 15$) and L_w; (b) prediction MSE of various K and various methods against different dropThreshold (△, HGLLiM, $K = 5$; △, HGLLiM, $K = 10$; △, HGLLiM, $K = 15$; ✱, GLLiM-structure, $K = 5$; ✱, GLLiM, $K = 10$; ✱, GLLiM, $K = 15$)

Table 3. Prediction MSE and average cluster number of the orange juice data set when dropThreshold = 0.5

Method	*Results for* $K = 5$		*Results for* $K = 10$		*Results for* $K = 15$	
	MSE	*Number of clusters*	*MSE*	*Number of clusters*	*MSE*	*Number of clusters*
GLLiM	0.1259	5.00	0.1210	10.00	0.0918	15.00
HGLLiM	0.0587	9.95	0.0681	11.85	0.0692	12.80
GLLiM-structure	0.0621	9.95	0.0742	11.85	0.0746	12.80
GLLiM-outlier	0.0976	9.95	0.1171	11.85	0.1044	12.80
SLLiM	0.1039	5.00	0.0788	10.00	0.0706	15.00
SLLiM-structure	0.0907	9.95	0.0747	11.85	0.0721	12.80

provide reliable model performance, HGLLiM controls the cluster size via the tuning parameter minSize. In addition, HGLLiM estimates the covariance matrices under global cluster level and this estimate is more reliable compared with GLLiM-structure, which estimates covariance matrices locally. SLLiM does not remove any samples and thus the performance would be better than GLLiM-structure when the cluster number K is large. Although removing outliers is more effective, accommodating outliers may still be an alternative to combat outliers when the cluster size is the concern.

4.3. A magnetic resonance vascular fingerprint data set

It is of great interest to the scientific community to be able to assess microvascular properties efficiently, such as blood volume fraction, vessel diameter and blood oxygenation, in the brain so that the ability in diagnosis and management of brain diseases can be improved. Recently, a new approach called magnetic resonance vascular fingerprinting was proposed as an alternative to overcome the limitations of analytical methods in measuring microvascular properties. The approach is built on a system in which the signal that is acquired in each voxel, also called a 'fingerprint', is compared with a dictionary obtained from numerical simulations. Finding the closest match to a fingerprint record in the dictionary allows a direct link between the parameters of the simulations and the microvascular variables (also referred to as parameters in these studies) at the image voxel (Lemasson *et al.*, 2016; Ma *et al.*, 2013).

A synthetic magnetic resonance vascular fingerprint (hereafter referred to as a fingerprint) data set composed of 1383648 observations was created to serve as a 'search–match' library. Each observation in the library consists of a fingerprint measurement and associated parameters: mean vessel radius, Radius, blood volume fraction, BVf, and a measurement of blood oxygenation, DeltaChi. One goal is to predict these parameters ($L_t = 3$) by using the fingerprint measurement ($D = 32$). In addition to these three parameters, other parameters (variables) that have influence over the fingerprint measurements include the apparent diffusion coefficient, ADC, vessel direction, Dir, and vessel geometry, Geo.

In Lemasson *et al.* (2016), numerical performances of a dictionary matching method were presented. For comparison, we implement the dictionary matching method that was adopted in Lemasson *et al.* (2016). The coefficient of determination, r^2, is used to measure the similarity between a testing sample and the training samples (dictionary). The coefficient of determination, r^2, between a testing sample y^{test} and a training sample y^{train} is calculated as

$$r^2 = 1 - \frac{\sum_{d=1}^{D} (y_d^{\text{test}} - y_d^{\text{train}})^2}{\sum_{d=1}^{D} (y_d^{\text{test}} - \bar{y}^{\text{test}})^2}, \tag{11}$$

where $\bar{y}^{\text{test}} = (1/D)\Sigma_{d=1}^{D} y_d^{\text{test}}$. The matched fingerprint is the training fingerprint with the largest r^2 and we predict the parameters of the testing data by using the matched fingerprint.

Computation time is a critical issue when analysing large data sets. To speed up the computation, we could take advantage of the hierarchical structure of HGLLiM by subsetting the data set into smaller groups and applying HGLLiM on the resulting groups in parallel. Our current study consists of two components. Through cross-validation, we first evaluate the feasibility and effectiveness of the parallel computation algorithms and utilize it to compare the performance of different methods on the synthetic data set. We then apply these methods to a fingerprint data set that was collected in an animal study, in which, besides predicting the variable BVf (a main goal of Lemasson *et al.* (2016)), we focus on predicting another variable, ADC, a more challenging scenario which has not been reported before.

We divide the synthetic library into 20 groups and apply the parallelization techniques to accelerate the model building process (see the on-line appendix B and appendix C for more details). When conducting the analysis in the animal study, we add a small amount of the *in vivo* data in the training data set. We noted that fingerprint samples from the real world are noisier than their synthetic counterparts and thus this practice, as a calibration step, enables the training model to accommodate readily the real fingerprint samples in prediction. The ratio of the synthetic samples to the real image samples is 4 to 1. The cluster number and latent factor number are selected by using the method that is described in appendix A.2 and are set to $K = 1240$ and $L_w = 9$ respectively. We evaluate and compare the performance of various methods on the synthetic data set through cross-validation. The cross-validation results in predicting Radius, BVf and DeltaChi demonstrate that the model-based methods (GLLiM, HGLLiM and GLLiM-structure) can achieve comparative prediction performance (appendix D). Next, we apply these methods to a fingerprint data set collected in an animal study.

This animal study data set contains samples from 115 rats categorized into five groups: healthy, three kinds of tumours (9L, C6 and F98) and stroke. For each rat, there are five brain slices of 128×128 voxels and each voxel contains 32-dimension fingerprint information. For each slice, the lesion (unhealthy) and the striatum (healthy) areas are labelled and they form the region of interest (ROI). Fig. 6 shows the predicted BVf-image by using various methods. As indicated in Lemasson *et al.* (2016), the value of the true BVf is not available at the voxel level and, instead, they are measured over the whole ROIs. Nevertheless, the comparison between the true values and those obtained by the dictionary matching method, at the ROI level, indicates that the method has successfully provided a close-to-truth match; see Lemasson *et al.* (2016). Table 4 shows the mean prediction results within the ROIs obtained by the methods. The three additional methods that are considered here, besides the dictionary matching method that was used in Lemasson *et al.* (2016), are GLLiM, HGLLiM and GLLiM-structure. All four methods provide similar results in predicting BVf.

There are 1385509 samples in the real image data set. For the dictionary matching method, using a parallel for-loop (*parfor*) and a preprocessing technique (Lemasson *et al.*, 2016) it took about 2.4 h (precisely 8639.53 s) to match the whole animal image samples to the training data set ($N^{\text{train}} = 1383648$). A direct computation without parfor and preprocessing took 429507.79 s and reached the same outcomes. For the model-based method, utilizing the grouped structure and the parallel computing technique, it takes 1058.32, 2133.51 and 1922.37 s for GLLiM,

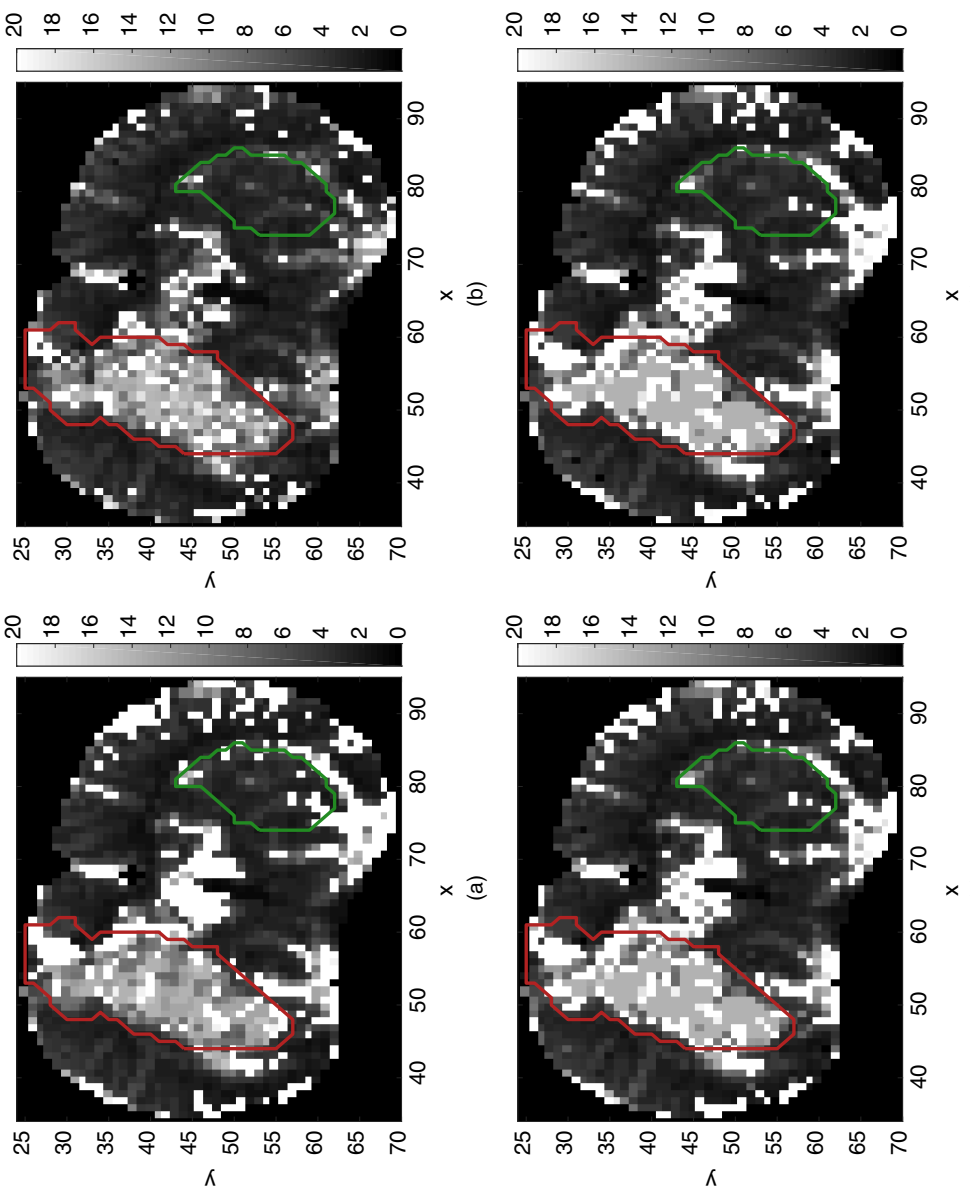


Fig. 6. Predicted BVf-images of one animal from the 9L group by using either (a) dictionary matching, (b) GLLiM, (c) HGLLiM or (d) GLLiM-structure: in each plot, the ROI on the left marks the lesion region and the ROI on the right is from the healthy striatum

Table 4. Mean predicted values within ROIs of various vascular parameters from different categories

Category	*Parameter*	*Results for the following methods:*			
		Dictionary matching	*GLLiM*	*HGLLiM*	*GLLiM-structure*
9L	Radius	21.85	20.14	22.12	21.52
	BVf	14.49	14.33	14.71	14.25
	DeltaChi	0.98	0.93	1.03	0.94
C6	Radius	13.59	16.01	13.67	13.81
	BVf	4.17	4.01	4.25	4.52
	DeltaChi	0.77	0.76	0.79	0.74
F98	Radius	11.56	13.14	11.13	11.23
	BVf	3.86	3.96	4.01	3.97
	DeltaChi	0.65	0.66	0.62	0.61
Stroke	Radius	14.69	13.51	14.31	14.41
	BVf	4.22	4.49	4.13	4.25
	DeltaChi	0.60	0.63	0.62	0.63
Healthy	Radius	8.16	7.96	8.54	8.34
	BVf	3.58	3.51	3.63	3.56
	DeltaChi	0.76	0.72	0.74	0.80

HGLLiM and GLLiM-structure respectively to process the animal image data set. Thus, the prediction procedure of GLLiM, HGLLiM and GLLiM-structure is much more efficient than the dictionary matching method.

The parameter ADC was not thoroughly investigated in Lemasson *et al.* (2016). The main reason is that the predicted ADC-values, obtained by using the dictionary matching approach, were not comparable with those measured *in vivo* by magnetic resonance imaging. With the *in vivo* ADC-values that are available at the voxel level, being able to understand how the synthetic and real measurements differ for a given parameter is scientifically important to developing new instruments and to future knowledge advancements. Here, we study ADC and use it to evaluate the prediction performances of various methods. Fig. 7 shows the true ADC-image and the images of the differences between the true and predicted ADC-values. The differences are shown in the ratio against the signal levels for each ROI. Most of the predictions that were made by dictionary matching deviated from the true values. In contrast, HGLLiM and GLLiM-structure provide better ADC-images. There are some voxels with extreme differences that none of the methods can predict well. When no suitable training information could be provided by the synthetic fingerprint data, the prediction quality on these voxels tends to be dreadful regardless of which method is used.

Table 5 shows the 50%, 90% and 99% quantiles of the ADC squared errors. The outcomes that are reported under the 50th and 90th percentiles give the indication of 'average' and 'almost-all' prediction performances for each method. The 99th-percentile values enable comparisons of worse-case scenarios. We still obtain some predictions with large errors by using GLLiM, HGLLiM and GLLiM-structure. However, for the majority of the data, the squared errors are smaller than those obtained by the dictionary matching method. We conclude that here there is no suitable cluster to conduct prediction for these data. For GLLiM, HGLLiM and GLLiM-structure, if a suitable cluster for conducting prediction does not exist, the cluster with the closest Mahalanobis distance is applied for prediction. However, the largest membership

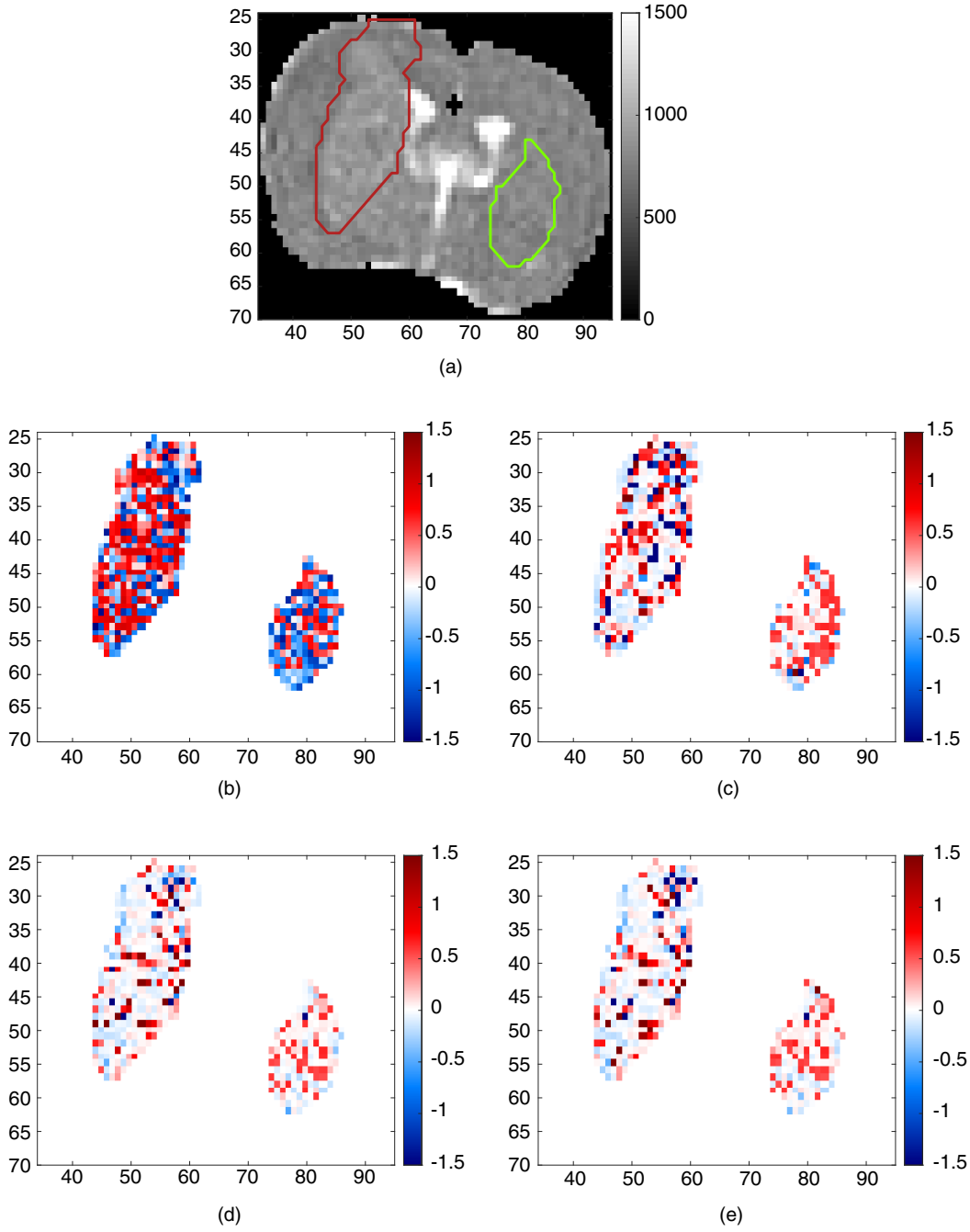


Fig. 7. True ADC-image and the differences between the true values and the predicted values against the signal levels of one animal from the 9L group (differences are normalized by the average true ADC-values in each ROI): (a) true ADC-image; difference maps between true values and predicted values against the signal levels by using either (b) the dictionary matching method, (c) GLLiM, (d) HGLLiM or (e) GLLiM-structure

Table 5. 50%, 90% and 99% quantiles of squared errors of predicting ADC for various methods under various image categories

Category	*Results for dictionary matching*			*Results for GLLiM*			*Results for HGLLiM*			*Results for GLLiM-structure*		
	50%	*90%*	*99%*	*50%*	*90%*	*99%*	*50%*	*90%*	*99%*	*50%*	*90%*	*99%*
9L	1.1180	3.9803	10.6829	0.2392	0.5684	14.5668	0.1132	0.7613	11.8721	0.1018	0.7154	10.9574
C6	1.1208	4.4719	14.4888	0.3043	2.6091	26.7575	0.3252	1.9840	22.5427	0.3138	1.7764	20.0213
F98	1.0994	4.2373	14.4888	0.3802	3.4129	55.4479	0.2951	2.3672	35.3199	0.2801	2.4129	50.8133
Stroke	1.1663	5.8045	14.8888	0.4779	4.5668	66.1164	0.3218	3.0975	55.7821	0.3192	3.1424	53.9315
Healthy	1.0931	3.8086	7.7912	0.2131	1.2510	14.5668	0.1527	1.1087	11.9597	0.1054	1.1145	13.2165

posterior probability r_{nkl} among all k and l in equation (9) would be smaller than the majority of the data. This information could be utilized to identify unreliable prediction results. The worst case of dictionary matching seems to produce smaller prediction error when being compared with other methods. Nevertheless, this is due to the nature of the difference between approaches. The dictionary matching method always predicts using values obtained from a member in the dictionary, so its prediction error cannot go beyond what would be provided by the possible values in the dictionary. This phenomenon does not apply to model-based methods. When prediction is conducted on the data outside the range of the training data set, the prediction error could become considerably large, as shown by the outcome of 99th percentiles of prediction squared errors. As a result, even though dictionary matching seems to outperform other model-based methods at these extreme cases, it does not necessarily indicate that the dictionary method is practically useful for these cases, with the outcomes being so much worse than predicting the rest of the data set. Our model-based approaches, in contrast, do have the advantage of identifying these troublesome cases for further consideration.

5. Discussion and conclusion

We propose HGLLiM as a parsimonious and structured version of GLLiM. HGLLiM adopts a two-level hierarchical structure of clusters. The structure assumed enables us to assess the parameters in the mean association functions more locally without suffering from the clustering outcomes being dominated by the dependence structures in the high dimensional predictors. Under the same construction, we also estimate the reduced number of covariance parameters with more data points. In addition, we implement a robust version of HGLLiM to enhance model stability and to reduce prediction variation. HGLLiM further leads to a post-learning version of GLLiM, called GLLiM-structure. By using local means and local variances, although with unfitted points removed, GLLiM-structure tends to attain improved empirical performances.

The motivation behind HGLLiM and GLLiM-structure is to obtain precise predictions by constructing stable training models. Eliminating the existence of small clusters and removing outliers assist in achieving this goal. The fact that HGLLiM focuses only on preserving primary structures learned from the training data set may reduce the quality of its predictions of rare data points, which are insufficiently presented therein. Nevertheless, by utilizing the largest membership posterior probability r_{nkl} among all clusters (k, l) and by recognizing when this maximum will be much smaller than those obtained from the majority of the data, we can identify such testing samples with unreliable prediction results.

In the analysis of the fingerprint data set, we experimented with predicting these testing samples by using the average predicted values based on nearest neighbour matching (the results are not shown). At the cost of slightly elevated computation time, such replacement does have the predicted values within the range of training measurements. The prediction quality for these difficult-to-predict cases is similar to that of the dictionary matching method. However, it is important to note that such quality, as for the dictionary matching method, remains unsatisfactory. This outcome is not a surprise because these data points are either not present or poorly represented in the training samples.

Notwithstanding this drawback that the resulting training model that is obtained by HGLLiM may or may not reflect the exact true model that generates all the data, it nevertheless captures the critical structure and establishes a model that can be stably estimated by using the available data. The size and complexity of this model would be determined by the data. Finally, the learning procedure could be accelerated by dividing data into groups and adopting parallelization

computation techniques. We illustrate that this practice is readily accommodated by HGLLiM's hierarchical model structure.

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Supporting information

Additional 'supporting information' may be found in the on-line version of this article:

'Prediction with high-dimensional regression via hierarchically structured Gaussian mixtures and latent variables'.