

# Nonparametric Bayes Classification via Learning of Affine Subspaces

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based on the paper ***Density Estimation and Classification  
via Bayesian Nonparametric Learning of Affine  
Subspaces*** jointly with David Dunson & Garritt Page, 2012

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- Estimated cell probabilities consistent in weak and strong sense.
- Data applications support the results.

# Affine Subspace Characterization

- Let  $S$  be an affine subspace of  $\mathfrak{R}^m$  of dimension  $k$  ( $k \ll m$ ).
- Let  $\theta \in \mathfrak{R}^m$  be the projection of the origin in  $S$  and  $R \in \mathfrak{R}^{m \times m}$  the projection matrix of the linear subspace parallel to  $S$ .
- Hence  $R = R' = R^2$ ,  $\text{rank}(R) = k$ ,  $R\theta = 0$ .
- Let  $R = UU'$ ,  $U \in V_{k,m} = \{U \in \mathfrak{R}^{m \times k} : U'U = I_k\}$  - the Steifel manifold.
- Any  $x \in S$  can be given isometric coordinates  $\tilde{x} = U'x \in \mathfrak{R}^k$  s.t.  $x = U\tilde{x} + \theta$ .

- For  $x \in \mathfrak{R}^m$ , its projection  $P_S(x) = Rx + \theta$  has coordinates  $U'x \in \mathfrak{R}^k$ .
- The residual  $R_S(x) = x - P_S(x)$  lies in a linear subspace  $S^\perp$  perpendicular to  $S$  with projection matrix  $I - R = VV'$ ,  $V \in V_{m-k,m}$ ,  $V'U = 0$ .
- It has coordinates  $V'(x - \theta)$  in  $\mathfrak{R}^{m-k}$ .

# Joint Density Model

- Let  $X$  denote the predictor in  $\mathfrak{R}^m$  and  $Y$  a categorical response taking values in  $\mathbb{Y} = \{1, \dots, c\}$ .
- Will estimate the conditional class probabilities by modeling the joint of  $(X, Y)$  s.t.  $Y$  depends on  $X$  only through its projection onto  $S$ .
- $(P_S(X), Y)$  has a nonparametric kernel mixture density in  $S \times M_c$  while independently  $R_S(X)$  follows a mean zero parametric model on  $S^\perp$ .

- Say  $(U'X, Y) \sim \int_{\mathfrak{R}^k \times S_c} N_k(x; \mu, \Sigma_1) M_c(y; \nu) P(d\mu d\nu)$  where
- $N_k$  denotes the  $k$ -variate Normal kernel,
- $M_c(y; \nu) = \prod_{l=1}^c \nu_l^{I(y=l)}$  is the multinomial kernel and

$$S_c = \{\nu \in [0, 1]^c : \sum_l \nu_l = 1\}.$$

- Independently  $V'(X - \theta) \sim N_{m-k}(0, \Sigma_2)$ .

- Then  $(X, Y) \sim \int_{\mathbb{R}^k \times \mathcal{S}_c} N_m(x; U\mu + \theta, \Sigma) M_c(y; \nu) P(d\mu d\nu)$   
where
- $\Sigma = U\Sigma_1 U' + V\Sigma_2 V'$ .
- Wlog can take  $\Sigma_1$  and  $\Sigma_2$  to be diagonal.
- For sparsity assume  $\Sigma_2 = \sigma_0^2 I_{m-k}$ , i.e. the  $X$  residuals are homogeneously distributed.
- Let  $\Sigma_1 = \text{diag}(\sigma_1^2, \dots, \sigma_k^2)$ .

- Then  $\Sigma = U(\Sigma_1 - \sigma_0^2 I_k)U' + \sigma_0^2 I_m$  and the model parameters are
- $k, U \in V_{k,m}, \theta \in \mathfrak{R}^m$  satisfying  $U'\theta = 0, \underline{\sigma} = (\sigma_0, \sigma_1, \dots, \sigma_k)$  - a positive vector and  $P$  - a probability on  $\mathfrak{R}^k \times S_c$ .
- For Bayesian n.p. inference set priors on the parameters s.t. the induced prior on the joint density has full support and the posterior estimate is consistent.

## Prior Choice on $\Theta$

- Common prior choice on  $\Theta = (k, U, \theta, \underline{\sigma}, P)$  that preserves conjugacy can be
  - a discrete prior on  $k$  and given  $k$ ,
  - a matrix Bingham-von Mises-Fisher density on  $U$  which has the form proportional to  $\exp \text{Tr}(UA + UBU'C)$ ,
  - a  $m$ -variate Normal on  $\theta$  restricted to the space of vectors orthogonal to  $U$ ,
  - inverse-Gamma priors on the elements of  $\underline{\sigma}$ , and,

- a Dirichlet process (DP) prior on  $P$ :  $P \sim \text{DP}(w_0(P_0 \otimes Q_0))$ , where  $P_0$  is a  $k$ -variate Normal and  $Q_0$  a Dirichlet distribution on  $S_c$ .
- When  $P$  is discrete, say,  $P = \sum_{j=1}^{\infty} w_j \delta_{(\mu_j, \nu_j)}$ , then

$$P(Y = y | X = x; \Theta) = \sum_{j=1}^{\infty} \tilde{w}_j(U'x) M_c(y; \nu_j)$$

where  $\tilde{w}_j(x) = \frac{w_j N_k(x; \mu_j, \Sigma_1)}{\sum_{i=1}^{\infty} w_i N_k(x; \mu_i, \Sigma_1)}$ ,  $x \in \mathfrak{R}^k$ .

- Markov chain Monte Carlo (MCMC) methods can be employed to draw from the posterior.
- Choice of o.n. basis leads to rapid convergence and avoids large dimensional matrix inversion.

# Consistency of the Conditional Class Probabilities

To show that the conditional density of  $Y$  given  $X$  under the posterior is consistent.

Assume the following on  $f_t$  - the true joint density of  $(X, Y)$ .

- 1  $0 < f_t(x, y) < A$  for some constant  $A$  for all  $(x, y) \in \mathbb{R}^m \times \mathbb{Y}$ .
- 2  $E_t |\log \{f_t(X, Y)\}| < \infty$ .
- 3 For some  $\delta > 0$ ,  $E_t \log \frac{f_t(X, Y)}{f_\delta(X, Y)} < \infty$ , where  
 $f_\delta(x, y) = \inf_{\tilde{x}: \|\tilde{x} - x\| < \delta} f_t(\tilde{x}, y)$ .
- 4 For some  $\alpha > 0$ ,  $E_t \|X\|^{2(1+\alpha)m} < \infty$ .

Here  $E_t$  denotes expectation under  $f_t$ .

- Define probability  $\tilde{P}_t$  on  $\mathfrak{R}^m \times \mathcal{S}_c$  as

$$\tilde{P}_t(d\mu d\nu) = \sum_{j=1}^c f_t(\mu, j) d(\mu) \delta_{e_j}(d\nu)$$

where  $e_j$  is the vector with 1 as  $j$ th coordinate and zeros elsewhere.

- Set priors on the parameters such that given  $k$ ;  $(U, \theta)$ ,  $\underline{\sigma}$  and  $P$  are conditionally independent.
- Let  $(\mathbb{X}_n, \mathbb{Y}_n) = (X_1, Y_1), \dots, (X_n, Y_n)$  iid  $f_t$ .

# Weak Posterior Consistency (WPC)

## Theorem (Weak Posterior Consistency (WPC))

*Let  $Pr(k = m) > 0$  and the conditional priors on  $\underline{\sigma}$  and  $P$  given  $k = m$  contain  $\underline{0}$  and  $\tilde{P}_t$  in their weak supports respectively. Then under assumptions **1-4** on  $f_t$ , the Kullback-Leibler (KL) condition is satisfied by the induced prior on  $f$  at  $f_t$ .*

The proof runs on the same lines of the proof of Theorem 3.1.  
*Bhattacharya, Page & Dunson 2012.*

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This in turn implies a.s. WPC which implies  $\forall \epsilon > 0$ ,

$$\Pi_n \{ |P(Y = y|X \in U; \Theta) - P_t(Y = y|X \in U)| > \epsilon \} \rightarrow 0 \text{ a.s. } P_t$$

where  $\Pi_n$  denotes the posterior of  $\Theta$  given  $(\mathbb{X}_n, \mathbb{Y}_n)$ .

# Strong Posterior Consistency (SPC)

## Theorem (Strong Posterior Consistency (SPC))

*Assume the conditions for WPC hold. Pick positive constants  $a, b, \{\tau_k\}_{k=1}^m$  and  $A$  and set the prior s.t. for  $k \leq m - 1$ ,  $\|\theta\|^a$  follows a Gamma density,  $\max(\underline{\sigma}) \leq A^{1/b}$ , and  $\Pr(\min(\underline{\sigma}) < n^{-1/b} | k)$  decays exponentially with  $n$ . This holds for e.g. with  $\sigma_j$ s all equal and  $\sigma_j^{-b}$  following a Gamma density truncated to  $[A^{-1}, \infty)$ . For the DP ( $w_k(P_k \otimes Q_0)$ ) prior on  $P$ ,  $k \geq 1$ , choose  $P_k$  to be a Normal density on  $\mathbb{R}^k$  with variance  $\tau_k^2 I_k$ . Then a.s. SPC results if the constants satisfy  $\tau_k^2 > 4A^2$ ,  $a < 2(1 + \alpha)m$  and  $1/a + 1/b < 1/m$ .*

Proof follows from the proof of Theorem 3.5. *Bhattacharya, Page & Dunson 2012.*

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SPC implies

$$\Pi_n \left\{ \int_{\mathfrak{R}^m} |P(Y = y|X = x; \Theta) - P_t(Y = y|X = x)| g_t(x) dx > \epsilon \right\} \\ \rightarrow 0 \text{ a.s. } P_t \forall y$$

with  $g_t$  the density of  $X$  under  $P_t$ .

- A Inverse Gamma prior on  $\underline{\sigma}$  satisfies the requirements for weak but not strong posterior consistency.

- A Inverse Gamma prior on  $\underline{\sigma}$  satisfies the requirements for weak but not strong posterior consistency.
- In *Bhattacharya & Dunson 2011*, a gamma prior is proved eligible when  $k = m$  as long as the hyperparameters are allowed to depend on sample size  $n$  in a suitable way.
- However there it is assumed that  $f_t$  has a compact support.
- The result is expected to hold true in this context too.

# Principal Subspace Classifier (PSC)

- The marginal density of  $X$  is

$$X \sim g(x; \Theta) = \int_{\mathbb{R}^k} N_m(x; \phi(\mu), \Sigma) P_1(d\mu),$$
$$\phi(\mu) = U\mu + \theta, \quad \Sigma = U\Sigma_1 U' + V\Sigma_2 V',$$

$P_1$  is the  $\mu$  marginal of  $P$ .

- The  $X$  component on which  $Y$  depends is the  $k$ -principal component of  $X$  if the eigenvalues of  $\Sigma_1$  are greater than or equal to those of  $\Sigma_2$  (and  $P$  is non-degenerate).
- This holds if  $\Sigma = \sigma_0^2 I$ .

- In some sense the model can be considered a Bayesian nonparametric extension of the probabilistic PCA of *Tipping & Bishop 1999* and *Nyamundanda et. al. 2010*.
- The model could also be thought of as a nonparametric extension of the Bayesian Gaussian process latent variable models of *Titsias & Lawrence 2010* and SVD models of *Hoff 2007*.

# Estimating $S$

- To obtain a Bayes estimate for the subspace  $S$ , choose an appropriate loss function and minimize the Bayes risk w.r.t. the posterior distribution.
- $S$  is characterized by its projection matrix  $R$  and origin  $\theta$ , i.e. the pair  $(R, \theta)$ .
- $R \in \mathfrak{R}^{m \times m}$ ,  $\theta \in \mathfrak{R}^m$  satisfy  $R = R' = R^2$  and  $R\theta = 0$ . We use  $\mathcal{S}_m$  to denote the space of all such pairs.

- One particular loss function on  $\mathcal{S}_m$  is

$$L((R_1, \theta_1), (R_2, \theta_2)) = \|R_1 - R_2\|^2 + \|\theta_1 - \theta_2\|^2, \quad (R_i, \theta_i) \in \mathcal{S}_m,$$

where  $\|A\|^2 = \sum_{ij} a_{ij}^2 = \text{Tr}(AA')$ .

- Then a point estimate for  $(R, \theta)$  is the  $(R_1, \theta_1)$  minimizing the posterior expectation of loss  $L$  over  $(R_2, \theta_2)$ , provided there is a unique minimizer.

## Theorem (Subspace Estimator)

Let  $f(R, \theta) = \int_{(R_2, \theta_2)} L((R, \theta), (R_2, \theta_2)) dP_n(R_2, \theta_2)$ ,  $(R, \theta) \in \mathcal{S}_m$ .

This function is minimized by  $R = \sum_{j=1}^k U_j U_j'$  and  $\theta = (I - R)\bar{\theta}$  where  $\bar{R}$  and  $\bar{\theta}$  are the posterior means of  $R_2$  and  $\theta_2$  respectively,

$$2\bar{R} - \bar{\theta}\bar{\theta}' = \sum_{j=1}^m \lambda_j U_j U_j', \quad \lambda_1 \geq \dots \geq \lambda_m$$

is a s.v.d. of  $2\bar{R} - \bar{\theta}\bar{\theta}'$ , and  $k$  minimizes  $k - \sum_{j=1}^k \lambda_j$ . The minimizer is unique iff there is a unique minimizer  $k$  and  $\lambda_k > \lambda_{k+1}$  for that  $k$ .

- Proof follows from *Bhattacharya et. al. 2012* and *Bhattacharya, A. & Bhattacharya, R. 2012*.

- Proof follows from *Bhattacharya et. al. 2012* and *Bhattacharya, A. & Bhattacharya, R. 2012*.
- The relative importance of different features  $\{X_1, \dots, X_m\}$  in explaining  $Y$  can then be judged by the magnitude of the corresponding diagonal entry of  $R$ .
- The magnitudes can also be used to group the features according to their relative importance.

# Identifiability of $S$

- $X \sim N_m(0, \Sigma) * (P_1 \circ \phi^{-1})$ , with “ $*$ ” denoting convolution.
- The characteristic function of  $X$  is

$$\Phi_X(t) = \exp(-1/2t'\Sigma t)\Phi_{P_1 \circ \phi^{-1}}(t), \quad t \in \mathfrak{R}^m.$$

- If a discrete  $P$  is employed, then  $\Sigma$  and  $P_1 \circ \phi^{-1}$  can be uniquely determined from the marginal of  $X$ .
- $P_1 \circ \phi^{-1}$  is a distribution on  $\mathfrak{R}^m$  supported on  $S = \phi(\mathfrak{R}^k)$ .

- Define the *affine support* of a probability  $Q$ ,  $\text{asupp}(Q)$  as the intersection of all affine subspaces having prob. 1. It contains the support  $\text{supp}(Q)$  (but may be larger).
- To identify  $S$  and  $k$  we assume that  $\text{asupp}(P_1)$  is  $\mathbb{R}^k$ .
- Then  $\text{asupp}(P_1 \circ \phi^{-1})$  is an affine subspace of  $\mathbb{R}^m$  of dimension equal to that of  $\text{asupp}(P_1) = k$ .

- Since  $\text{asupp}(P_1 \circ \phi^{-1})$  is identifiable, this implies that  $k$  is also identifiable as its dimension.
- Since  $S$  contains  $\text{asupp}(P \circ \phi^{-1})$  and has dimension equal to that of  $\text{asupp}(P \circ \phi^{-1})$ ,  $S = \text{asupp}(P \circ \phi^{-1})$ .
- Then  $R = UU'$  and  $\theta$  are identifiable as the projection matrix and origin of  $S$ .

# Real Data Examples

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- The classifier built (PSC) is used in real data examples and its performance compared with other well known classification methods.
- Three such competitors considered are  $k$  nearest neighbor (KNN), mixture discriminant analysis (MDA), and support vector machine (SVM).

- KNN is algorithmic based and classifies well in a variety of settings. A range of neighborhood sizes are considered with the one producing the best out of sample prediction ultimately used.

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- MDA is a flexible model based Gaussian mixture classifier (see *Hastie & Tibshirani 1996*). The number of components in the Gaussian mixture chosen to produce the best out of sample prediction.
- SVM is a very accurate classifier and is therefore included.
- Out of sample prediction error rates used to compare PSC to the 3 competitors.

# Brain Computer Interface (BCI) Data

- The BCI dataset consists of a single person performing 400 trials in each of which he imagined movements with either the left hand or the right hand.
- For each trial, EEG recorded from 39 electrodes.
- An autoregressive model of order 3 was fit to each of the resulting 39 time series.

- The trial is then represented by the total of  $117 = 39 \times 3$  dimensional feature space.
- Goal is to classify each trial as left or right hand movements using the 117 features.
- 200 observations randomly selected to serve as testing data.
- Posterior combinations done with dimension  $k$  fixed.

- To select a  $k$  the out of sample prediction error rates and area under the receiver operating characteristic (ROC) curve are employed.
- Since low out of sample prediction error rates and large areas under the curve are desirable, a  $k$ -value at-most 25 that maximized the difference between them is selected.
- Following this criteria,  $k = 3$  chosen.
- PSC produces an out of sample prediction error rate of 0.205 compared to 0.51 for KNN, 0.25 for MDA and 0.23 for SVM.

## Wisconsin Breast Cancer (WBC) data set

- In this data set the response is breast cancer diagnosis while the covariates consists of 9 nominal variables describing some type of breast tissue cell characteristic.
- Although this data set is not high dimensional, it provides a nice illustration of the type of information the PSC can provide regarding associations between covariates and response.
- Similar to what was done with the BCI data set  $k = 3$  is selected.
- This results in an out of sample prediction error rate of 0.017 which is smaller than the error rate for KNN (0.035), MDA (0.028) and SVM (0.028).

- Even though the PSC classifies more accurately than the other methods, what is of particular interest is how each of the 9 tumor attributes influence classification.
- The 9 attributes (clump thickness, uniformity of cell size, uniformity of cell shape, marginal adhesion, single epithelial cell size, bare nuclei, bland chromatin, normal nucleoli, and mitosis) are all related to a lump being benign or not.
- From the theorem on subspace estimation the estimated principal directions are found in the Table below.

## Theorem (Subspace Estimator)

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This function is minimized by  $R = \sum_{j=1}^k U_j U_j'$  and  $\theta = (I - R)\bar{\theta}$  where  $\bar{R}$  and  $\bar{\theta}$  are the posterior means of  $R_2$  and  $\theta_2$  respectively,

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is a s.v.d. of  $2\bar{R} - \bar{\theta}\bar{\theta}'$ , and  $k$  minimizes  $k - \sum_{j=1}^k \lambda_j$ . The minimizer is unique iff there is a unique minimizer  $k$  and  $\lambda_k > \lambda_{k+1}$  for that  $k$ .

**Table :** The  $k = 3$  principal directions of the Breast Cancer data set along with the row norms

Variable	$U_{[,1]}$	$U_{[,2]}$	$U_{[,3]}$	norm
clump thickness	-0.294	0.233	0.453	0.588
uniformity of cell size	-0.399	-0.132	-0.189	0.460
uniformity of cell shape	-0.395	-0.102	0.0172	0.408
marginal adhesion	-0.314	-0.007	-0.477	0.571
single epithelial cell size	-0.231	-0.181	-0.307	0.424
bare nuclei	-0.450	0.713	0.101	0.849
bland chromatin	-0.295	-0.032	-0.194	0.354
normal nucleoli	-0.376	-0.587	0.543	0.883
mitosis	-0.121	-0.173	-0.305	0.371

- A way to assess the relative importance of each variable and also provide a means of grouping the variables is to calculate the norm associated with each row of  $U$  (i.e. the norm of the corresponding diagonal entry of  $R = UU'$ ).
- These values can be found under the header “norm” in the Table.
- It appears that a bare nuclei and normal nucleoli form a group.
- Another is formed by clump thickness and marginal adhesion.
- Finally it appears that uniformity of cell size, uniformity of cell shape and single epithelial cell size form a group.

# Summary

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- A flexible nonparametric model proposed for classification via feature space dimension reduction.
- The model satisfies large support & consistency conditions.
- A simple Gibbs sampler can be implemented with conjugate sampling steps for posterior sampling.
- Better performance than commonly used machine learning, computer science and parametric statistical methods.

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- In addition to building efficient classifiers, the proposed methodology provides insight regarding predictors that are influential in explaining the response - an information applied scientists often highly value.
- Can easily be extended to other regression setup.

## Further Work possible

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- Change the notion of inner product to use non linear predictor transformations to explain the response.
- A nonparametric model may be fit on the non-signal predictors as well.
- Use other priors besides Dirichlet Process.
- Extend to nonparametric hypothesis testing on the lines of *Bhattacharya & Dunson 2012*.

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