

bbl: Boltzmann Bayes Learner for High-Dimensional Inference with Discrete Predictors in R

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Abstract

Non-regression-based inferences, such as discriminant analysis, can account for the effect of predictor distributions that may be significant in big data modeling. We describe **bbl**, an R package for Boltzmann Bayes learning, which enables a comprehensive supervised learning of the association between a large number of categorical predictors and multi-level response variables. Its basic underlying statistical model is a collection of (fully visible) Boltzmann machines inferred for each distinct response level. The algorithm reduces to the naive Bayes learner when interaction is ignored. We illustrate example use cases for various scenarios, ranging from modeling of a relatively small set of factors with heterogeneous levels to those with hundreds or more predictors with uniform levels such as image or genomic data. We show how **bbl** explicitly quantifies the extra power provided by interactions via higher predictive performance of the model. In comparison to deep learning-based methods such as restricted Boltzmann machines, **bbl**-trained models can be interpreted directly via their bias and interaction parameters.

Keywords: Supervised learning, Boltzmann machine, naive Bayes, discriminant analysis, R.

1. Introduction

Many supervised learning tasks involve modeling discrete response variables y using predictors \mathbf{x} that can occupy categorical factor levels (Hastie, Tibshirani, and Friedman 2009). Ideally, it would be best to model the joint distribution $P(\mathbf{x}, y)$ via maximum likelihood,

$$\hat{\Theta} = \arg \max_{\Theta} [\ln P(\mathbf{x}, y | \Theta)], \quad (1)$$

to find parameters Θ . Regression-based methods use $P(\mathbf{x}, y) = P(y | \mathbf{x})P(\mathbf{x}) \simeq P(y | \mathbf{x})$. Their advantages include the wealth of information provided for significance of fit coefficients from rigorous formal results. An alternative is to use $P(\mathbf{x}, y) = P(\mathbf{x} | y)P(y)$ and fit $P(\mathbf{x} | y)$. Since y is low-dimensional, this approach could capture extra information not accessible from regression when there are many covarying predictors. To make predictions for y using $P(\mathbf{x} | y)$, one uses the Bayes' formula. Examples include linear and quadratic discriminant analyses (Hastie *et al.* 2009, pp. 106-119) for continuous \mathbf{x} . For discrete \mathbf{x} , naive Bayes is the simplest approach, where the covariance among \mathbf{x} is ignored via

$$P(\mathbf{x} | y) \simeq \prod_i P(x_i | y) \quad (2)$$

with $\mathbf{x} = (x_1, \dots, x_m)$.

In this paper, we focus on supervised learners taking into account the high-dimensional nature of $P(\mathbf{x}|y)$ beyond the naive Bayes-level description given by Eq. (2). Namely, a suitable parametrization is provided by the Boltzmann machine (Ackley, Hinton, and Sejnowski 1985), which for the simple binary predictor $x_i = 0, 1$,

$$P(\mathbf{x}|y) = \frac{1}{Z_y} \exp \left(\sum_i h_i^{(y)} x_i + \sum_{i < j} J_{ij}^{(y)} x_i x_j \right), \quad (3)$$

where Z_y is the normalization constant, or partition function. Equation (3) is the Gibbs distribution for Ising-type models in statistical mechanics (Chandler 1987). The two sets of parameters $h_i^{(y)}$ and $J_{ij}^{(y)}$ each represent single variable and two-point interaction effects, respectively. When the latter vanishes, the model leads to the naive Bayes classifier. Although exact inference of Eq. (3) from data is in general not possible, recent developments led to many accurate and practically usable approximation schemes (Hyvärinen 2006; Morcos, Pagnani, Lunt, Bertolino, Marks, Sander, Zecchina, Onuchic, Hwa, and Weigt 2011; Nguyen, Zecchina, and Berg 2017; Nguyen and Wood 2016; Nguyen and Wood 2016), making its use in supervised learning a viable alternative to regression methods. Two approximation methods available for use are pseudo-likelihood inference (Besag 1975) and mean field theory (Chandler 1987; Nguyen *et al.* 2017).

A recently described package **BoltzMM** can fit the (‘fully visible’) Boltzmann machine given by Eq. (3) to data using pseudo-likelihood inference (Jones, Nguyen, and Bagnall 2019b; Jones, Bagnall, and Nguyen 2019a). In contrast, classifiers based on this class of models remain largely unexplored. Supervised learners using statistical models of the type (3) usually take the form of the *restricted* Boltzmann machines instead (Hinton 2012), where (visible) predictors are augmented by hidden units and interactions are zero except between visible and hidden units. The main drawback of such layered Boltzmann machine learners, as is common in all deep learning algorithms, is the difficulty in interpreting trained models. In contrast, with the fully visible architecture, $J_{ij}^{(y)}$ in Eq. (3), if inferred with sufficient power while avoiding overfitting, has direct interpretation of interaction between two variables.

We refer to such learning/prediction algorithms using a generalized version of Eq. (3) as Boltzmann Bayes inference. An implementation specific to genomic single-nucleotide polymorphism (SNP) data (two response groups, e.g., case and control, and uniform three-level predictors, i.e., allele counts of $x_i = 0, 1, 2$) has been reported previously (Woo, Yu, Kumar, Gold, and Reifman 2016). However, this C++ software was geared specifically toward genome-wide association studies and is not suitable for use in more general settings. We introduce an R package **bbl** (Boltzmann Bayes Learner), which uses both R and C++ for usability and performance, allowing the user to train and test statistical models in a variety of different usage settings.

2. Model and algorithm

For completeness and for reference to software features described in Section 3, we summarize in this section key relevant formulas (Woo *et al.* 2016) used by **bbl**, generalized such that predictors each can have varying number of factor levels.

2.1. Model description

The discrete response y_k for an instance k takes factor values y among $K \geq 2$ groups; e.g., $y = \text{case}, \text{control}$; $k = 1, \dots, n$ denotes sample (or configuration) index. We also introduce weights w_k , each of which is integral number of times each configuration was observed in data, such that $\sum_k w_k = n_s$ is the total sample size. If the data take the form of one entry per obserbation, $w_k = 1$ and $n = n_s$. The use of frequency w_k can lead to more efficient learning when the number of predictors is relatively small. We use symbol y for a particular factor value and generic response variables interchangeably.

The overall likelihood is

$$L = \sum_k w_k \ln P(\mathbf{x}^k, y_k) = \sum_y \sum_{k \in y} w_k \ln P(\mathbf{x}^k, y) \equiv \sum_y L_y, \quad (4)$$

where the second summation is over all k for which $y_k = y$. The inference is first performed for each group y separately, maximizing L_y given by

$$L_y = \sum_{k \in y} w_k [\ln P(\mathbf{x}^k | y) + \ln P(y)] = \sum_{k \in y} w_k \ln P(\mathbf{x}^k | y) + n_y \ln p_y, \quad (5)$$

where $p_y \equiv P(y)$ is the marginal distribution of y and $n_y = \sum_{k \in y} w_k$ is the size of group y .

In parametrizing the first term in Eq. (5), we assume that predictor variables take discrete factor levels, each with distinct effect on responses, e.g., $x_i = \mathbf{a}, \mathbf{t}, \mathbf{g}, \mathbf{c}$ for DNA sequence data. The group-specific predictor distribution can then be written as

$$P(\mathbf{x} | y) = \frac{1}{Z_y} \exp \left[\sum_i h_i^{(y)}(x_i) + \sum_{i < j} J_{ij}^{(y)}(x_i, x_j) \right]. \quad (6)$$

The number of parameters (d.f.) per group y in $\Theta_y = \{h_i^{(y)}(x), J_{ij}^{(y)}(x, x')\}$ is

$$\text{d.f.} = \sum_i (L_i - 1) + \sum_{i < j} (L_i - 1)(L_j - 1), \quad (7)$$

where L_i is the total number of levels in factor x_i , which contributes one less parameters to d.f. because one of the factors can be taken as reference with the rest measured against it. Internally, **bbi** orders factors, assigns codes $a_i = 0, \dots, L_i - 1$, and set $h_i^{(y)}(a_i) = J_{ij}^{(y)}(a_i, a_j) = 0$ whenever $a_i = 0$ or $a_j = 0$. We refer to $h_i^{(y)}(x)$ and $J_{ij}^{(y)}(x, x')$ as bias and interaction parameters, respectively.

In the special case where predictor levels are binary ($x_i = 0, 1$), one may use the spin variables $s_i = 2x_i - 1 = \pm 1$, as in the package **BoltzMM** (Jones *et al.* 2019a,b). Its distribution (Jones *et al.* 2019a)

$$P(\mathbf{s}) \propto \exp \left(\frac{1}{2} \mathbf{s}^\top \mathbf{M} \mathbf{s} + \mathbf{b}^\top \mathbf{s} \right) \quad (8)$$

is then related to Eq. (3) by

$$b_i = \frac{h_i}{2} + \frac{1}{4} \sum_{j \neq i} J_{ij}, \quad (9a)$$

$$M_{ij} = \frac{1}{4} J_{ij}, \quad (9b)$$

where parameter superscripts were omitted because response group is not present.

2.2. Pseudo-likelihood inference

One option for fitting Eq. (6) to data is pseudo-likelihood maximization (Besag 1975):

$$L_y - n_y \ln p_y = \sum_{k \in y} w_k \ln P(\mathbf{x}^k | y) \simeq \sum_{k \in y} w_k \sum_i \ln P_i(x_i^k | y, x_{j \setminus i}^k) \equiv \sum_i L_{iy}, \quad (10)$$

where the effective univariate distribution is conditional to all other predictor values:

$$P_i(x | y, x_{j \setminus i}) = \frac{e^{\bar{h}_i^{(y)}(x | x_{j \setminus i})}}{Z_{iy}(x_{j \setminus i})}, \quad (11)$$

$$Z_{iy}(x_{j \setminus i}) = \sum_x e^{\bar{h}_i^{(y)}(x | x_{j \setminus i})} = 1 + \sum_{a=1}^{L_i-1} e^{\bar{h}_i^{(y)}(a | x_{j \setminus i})}, \quad (12)$$

and

$$\bar{h}_i^{(y)}(x | x_{j \setminus i}) = h_i^{(y)}(x) + \sum_{j \neq i} J_{ij}^{(y)}(x, x_j). \quad (13)$$

Including L_2 penalizers (λ_h, λ) , L_{iy} in Eq. (10) becomes

$$L_{iy} = \sum_{k \in y} w_k \left[\bar{h}_i^{(y)}(x_i^k | x_{j \setminus i}^k) - \ln Z_{iy}(x_{j \setminus i}^k) \right] - \frac{\lambda_h}{2} \sum_x h_i^{(y)}(x)^2 - \frac{\lambda}{2} \sum_{j, x, x'} J_{ij}^{(y)}(x, x')^2 \quad (14)$$

with first derivatives

$$\frac{\partial L_{iy} / n_y}{\partial h_i^{(y)}(x)} = \hat{f}_i^{(y)}(x) - \frac{1}{n_y} \sum_{k \in y} w_k P_i(x | y, x_{j \setminus i}^k) - \lambda_h h_i^{(y)}(x), \quad (15a)$$

$$\frac{\partial L_{iy} / n_y}{\partial J_{ij}^{(y)}(x, x')} = \hat{f}_{ij}^{(y)}(x, x') - \frac{1}{n_y} \sum_{k \in y} w_k \mathbb{1}(x_j^k = x') P_i(x | y, x_{j \setminus i}^k) - \lambda J_{ij}^{(y)}(x, x'), \quad (15b)$$

where

$$\hat{f}_i^{(y)}(x) = \frac{1}{n_y} \sum_{k \in y} w_k \mathbb{1}(x_i^k = x), \quad (16a)$$

$$\hat{f}_{ij}^{(y)}(x, x') = \frac{1}{n_y} \sum_{k \in y} w_k \mathbb{1}(x_i^k = x) \mathbb{1}(x_j^k = x') \quad (16b)$$

are the first and second moments of predictor values and $\mathbb{1}(x)$ is the indicator function. In **bbl**, Eqs. (15) are solved in C++ functions using the quasi-Newton optimization function `gsl_multimin_fdfminimizer_vector_bfgs2` in GNU Scientific Library (<https://www.gnu.org/software/gsl>). By default, $\lambda_h = 0$ and only interaction parameters are penalized. As can be seen from the third equality of Eq. (10), the pseudo-likelihood inference decouples into individual predictors, and the inference for each i in **bbl** is performed sequentially. The resulting interaction parameters, however, do not satisfy the required symmetry,

$$J_{ij}(x, x') = J_{ji}(x', x). \quad (17)$$

After pseudo-likelihood inference, therefore, the interaction parameters are symmetrized as follows:

$$J_{ij}(x, x') \leftarrow \frac{1}{2} [J_{ij}(x, x') + J_{ji}(x', x)]. \quad (18)$$

In **bbl**, the input data are filtered such that predictors with only one factor level (no variation in observed data) are removed. Nevertheless, in cross-validation of the processed data, subdivisions into training and validation sets may lead to instances where factor levels observed for a given predictor within x_i in Eq. (15) are only a subset of those in the whole data. It is thus possible that optimization based on Eqs. (15) is ill-defined when any of the predictors are constant. In such cases, we augment the training data by an extra instance, in which constant predictors take other factor levels.

2.3. Mean field inference

The other option for predictor distribution inference is mean field approximation. In data-driven inference, the interaction parameters are approximated as (Nguyen *et al.* 2017)

$$\hat{J}_{ij}^{(y)}(x, x') = - [\mathbf{C}^{(y)}]_{ij}^{-1}(x, x'), \quad (19)$$

i.e., negative inverse of the covariance matrix,

$$\mathbf{C}_{ij}^{(y)}(x, x') = \hat{f}_{ij}(x, x') - \hat{f}_i(x)\hat{f}_j(x'). \quad (20)$$

Equation (19) can be interpreted as treating discrete \mathbf{x} as if it were multivariate normal: Eq. (6) would then be the counterpart of the multivariate normal p.d.f. with $-J_{ij}^{(y)}(x, x')$ corresponding to the precision matrix. In real data where $n \sim \text{d.f.}$ or less, the matrix inversion is often ill-behaved. It is regularized by interpolation of $\mathbf{C}^{(y)}$ between non-interacting (naive Bayes) ($\epsilon = 0$) and fully interacting limits ($\epsilon = 1$):

$$\mathbf{C}^{(y)} \leftarrow \bar{\mathbf{C}}^{(y)} = (1 - \epsilon) \frac{\text{Tr } \mathbf{C}^{(y)}}{\text{Tr } \mathbf{I}} \mathbf{I} + \epsilon \mathbf{C}^{(y)}, \quad (21)$$

where \mathbf{I} is the identity matrix of the same dimension as $\mathbf{C}^{(y)}$. The parameter ϵ serves as a good handle for probing the relative importance of interaction effects.

The bias parameters are given in mean field by an analog of Eq. (13),

$$\hat{h}_i^{(y)}(x) = \bar{h}_i^{(y)}(x) - \sum_{j \neq i} \sum_{x'} \hat{J}_{ij}^{(y)}(x, x') \hat{f}_j^{(y)}(x'), \quad (22)$$

and

$$\bar{h}_i^{(y)}(x) = \ln \left[\hat{f}_i^{(y)}(x) / \hat{f}_i^{(y)}(0) \right], \quad (23)$$

where $\hat{f}_i^{(y)}(0)$ is the frequency of (reference) factor x_i for which the parameters are zero ($a_i = 0$). Equation (22) relates the effective bias for predictor x_i (the first term on the right) as the sum of univariate bias (left-hand side) and combined mean effects of interactions with other variables (the second term on the right) (Chandler 1987). The effective bias is related to frequency via Eq. (23) because

$$\hat{f}_i^{(y)}(x) = \frac{e^{\bar{h}_i^{(y)}(x)}}{Z_{iy}} = \hat{f}_i^{(y)}(0) e^{\bar{h}_i^{(y)}(x)} \quad (24)$$

where the fact that $\bar{h}_i^{(y)}(0) = 0$ was used in the second equality.

As in pseudo-likelihood maximization, mean field inference also may encounter non-varying predictors during cross-validation. To apply the same inference scheme using Eqs. (20), (22) and (23) to such cases, the single-variable frequency $\hat{f}_i^{(y)}(x)$ and covariance $\hat{f}_{ij}^{(y)}(x, x')$ are computed using data augmented by a prior count of 1 uniformly distributed among all L_i factor levels for each predictor.

2.4. Naive Bayes

When interaction is ignored ($J_{ij}^{(y)} = 0$), the model can be solved analytically. From Eqs. (22) and (23),

$$\hat{h}_i^{(y)}(x) = \ln \left[\hat{f}_i^{(y)}(x) / \hat{f}_i^{(y)}(0) \right] \quad (25)$$

and (Woo *et al.* 2016)

$$L_y - n_y \ln p_y = \sum_{k \in y} w_k \ln P(\mathbf{x}^k | y) = n_y \sum_{i, x} \hat{f}_i^{(y)}(x) \ln \hat{f}_i^{(y)}(x). \quad (26)$$

The likelihood ratio statistic for each predictor, where the null hypothesis is $h_i^{(y)}(x) = h_i(x)$ with $h_i(x)$ the “pooled” inference parameters (same values for all response groups), is then

$$q_i = 2 \sum_y n_y \sum_x \left[\hat{f}_i^{(y)}(x) \ln \hat{f}_i^{(y)}(x) - \hat{f}_i \ln \hat{f}_i(x) \right]. \quad (27)$$

The statistic $q_i \sim \chi^2$ with d.f. = $(K - 1)(L_i - 1)$.

2.5. Classification

For prediction, we combine predictor distributions for all response groups via Bayes formula:

$$P(y | \mathbf{x}) = \frac{P(\mathbf{x} | y) p_y}{\sum_{y'} P(\mathbf{x} | y') p_{y'}} = \frac{1}{1 + \sum_{y' \neq y} P(\mathbf{x} | y') p_{y'} / P(\mathbf{x} | y) p_y} = \frac{1}{1 + e^{-F_y(\mathbf{x})}}, \quad (28)$$

where

$$F_y(\mathbf{x}) = \ln \left[\frac{P(\mathbf{x} | y) p_y}{\sum_{y' \neq y} P(\mathbf{x} | y') p_{y'}} \right]. \quad (29)$$

For binary response coded as $y = 0, 1$, Eq. (29) reduces to

$$\begin{aligned} F_1(\mathbf{x}) &= \ln P(\mathbf{x} | y = 1) - \ln P(\mathbf{x} | y = 0) + \ln(p_1/p_0) \\ &= \sum_i \left[h_i^{(1)}(x_i) - h_i^{(0)}(x_i) \right] + \sum_{i < j} \left[J_{ij}^{(1)}(x_i, x_j) - J_{ij}^{(0)}(x_i, x_j) \right] + \ln \frac{Z_0 p_1}{Z_1 p_0}. \end{aligned} \quad (30)$$

Therefore, if $J_{ij}^{(y)}(x, x') = 0$ (naive Bayes), Eq. (28) takes the form of the logistic regression formula. However, the actual naive Bayes parameter values differ from logistic regression fit. No expression for $P(y | \mathbf{x})$ simpler than Eq. (28) exists for data with more than two groups.

In pseudo-likelihood maximization inference, Z_y can be approximated by

$$\ln Z_y = \frac{1}{n_y} \sum_{k \in y} \sum_i \ln \left\{ \sum_x \left[e^{h_i^{(y)}(x) + \sum_{j \neq i} J_{ij}(x, x_j^k)/2} \right] \right\}, \quad (31)$$

or with the same expression without the factor of $1/2$ in the interaction term in the exponent (default). This quantity can be conveniently computed during the optimization process. With the mean field option, the following expression is used:

$$\ln Z_y = -\ln \hat{f}^{(y)}(0) - \frac{1}{2} \sum_{i \neq j} \sum_{x, x'} J_{ij}(x, x') \hat{f}_i(x) \hat{f}_j(x'). \quad (32)$$

For a test data set for which the actual group identity y_k of data instances are known, the prediction score (accuracy) may be defined as

$$s = \frac{1}{n} \sum_k \mathbb{1} [\hat{y}(\mathbf{x}^k) = y_k], \quad (33)$$

where

$$\hat{y}(\mathbf{x}) = \arg \max_y P(y|\mathbf{x}). \quad (34)$$

If response is binary, the score defined by Eq. (33) is sensitive to marginal distributions of the two groups via Eq. (30). The area under curve (AUC) of receiver operating characteristic is a more robust performance measure independent of probability cutoff. In **bb1**, the prediction score given by Eqs. (33) and (34) is used in general with the option to use AUC for binary response using R package **pROC** (Robin, Turck, Hainard, Tiberti, Lisacek, Sanchez, and Müller 2011; Robin, Turck, Hainard, Tiberti, Lisacek, Sanchez, Müller, Siegert, and Doering 2019).

3. Software Usage and Tests

3.1. Logistic regression

To motivate the use of **bb1** and highlight differences, we first consider the use of logistic regression using **glm**. We use the base R data **Titanic** as an example:

```
R> titanic <- as.data.frame(Titanic)
R> titanic
```

	Class	Sex	Age	Survived	Freq
1	1st	Male	Child	No	0
2	2nd	Male	Child	No	0
3	3rd	Male	Child	No	35
4	Crew	Male	Child	No	0
5	1st	Female	Child	No	0
6	2nd	Female	Child	No	0
7	3rd	Female	Child	No	17
8	Crew	Female	Child	No	0
9	1st	Male	Adult	No	118
10	2nd	Male	Adult	No	154
11	3rd	Male	Adult	No	387
12	Crew	Male	Adult	No	670

13	1st Female Adult	No	4
14	2nd Female Adult	No	13
15	3rd Female Adult	No	89
16	Crew Female Adult	No	3
17	1st Male Child	Yes	5
18	2nd Male Child	Yes	11
19	3rd Male Child	Yes	13
20	Crew Male Child	Yes	0
21	1st Female Child	Yes	1
22	2nd Female Child	Yes	13
23	3rd Female Child	Yes	14
24	Crew Female Child	Yes	0
25	1st Male Adult	Yes	57
26	2nd Male Adult	Yes	14
27	3rd Male Adult	Yes	75
28	Crew Male Adult	Yes	192
29	1st Female Adult	Yes	140
30	2nd Female Adult	Yes	80
31	3rd Female Adult	Yes	76
32	Crew Female Adult	Yes	20

```
R> freq <- titanic$Freq
R> titanic <- titanic[, 1:4]
```

Although more detailed versions of the same data set are available [see, e.g., **titanic** (Hendricks 2015) or **stablelearner** (Philipp, Strobl, Zeileis, Rusch, and Hornik 2018b; Philipp, Rusch, Hornik, and Strobl 2018a)], the simpler version above only including factor variables suffices for our purposes because **bbl** requires discrete factors as predictors. Input data can either be of the form above with unique combinations of predictors in each row along with frequency (input to **weights** argument of **glm**) or raw data (one observation per row) we generate using the utility function **freq2raw**:

```
R> library('bbl')
R> titanic_raw <- freq2raw(data = titanic, freq = freq)
R> head(titanic_raw)
```

	Class	Sex	Age	Survived
1	3rd	Male	Child	No
2	3rd	Male	Child	No
3	3rd	Male	Child	No
4	3rd	Male	Child	No
5	3rd	Male	Child	No
6	3rd	Male	Child	No

```
R> summary(titanic_raw)
```

Class	Sex	Age	Survived
1st :325	Male :1731	Child: 109	No :1490


```

2nd :285   Female: 470   Adult:2092   Yes: 711
3rd :706
Crew:885

```

We train a logistic regression model using glm:

```

R> gfit0 <- glm(Survived ~ Class + Sex + Age, family = binomial(),
+   data = titanic, weights=freq)
R> gfit0

```

```

Call:  glm(formula = Survived ~ Class + Sex + Age, family = binomial(),
        data = titanic, weights = freq)

```

Coefficients:

```

(Intercept)      Class2nd      Class3rd      ClassCrew      SexFemale
      0.6853      -1.0181      -1.7778      -0.8577      2.4201
AgeAdult
     -1.0615

```

```

Degrees of Freedom: 23 Total (i.e. Null);  18 Residual

```

```

Null Deviance:      2769

```

```

Residual Deviance: 2210      AIC: 2222

```

```

R> summary(gfit0)

```

Call:

```

glm(formula = Survived ~ Class + Sex + Age, family = binomial(),
    data = titanic, weights = freq)

```

Deviance Residuals:

```

      Min       1Q   Median       3Q      Max
-18.505   -4.247    0.000    4.747   23.915

```

Coefficients:

```

              Estimate Std. Error z value Pr(>|z|)
(Intercept)   0.6853     0.2730   2.510  0.0121 *
Class2nd     -1.0181     0.1960  -5.194 2.05e-07 ***
Class3rd     -1.7778     0.1716 -10.362 < 2e-16 ***
ClassCrew    -0.8577     0.1573  -5.451 5.00e-08 ***
SexFemale     2.4201     0.1404  17.236 < 2e-16 ***
AgeAdult     -1.0615     0.2440  -4.350 1.36e-05 ***
---

```

```

Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

(Dispersion parameter for binomial family taken to be 1)

```

Null deviance: 2769.5  on 23  degrees of freedom

```

Residual deviance: 2210.1 on 18 degrees of freedom
AIC: 2222.1

Number of Fisher Scoring iterations: 5

The fit above included linear terms only. It indicates that survival was strongly associated with class status, sex (female heavily favored), and age. The model below includes all interactions:

```
R> gfit1 <- glm(Survived ~ (Class + Sex + Age)^2, family = binomial(),
+ data = titanic, weights = freq)
R> summary(gfit1)
```

Call:

```
glm(formula = Survived ~ (Class + Sex + Age)^2, family = binomial(),
    data = titanic, weights = freq)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-18.375	-4.565	0.000	3.286	24.014

Coefficients: (1 not defined because of singularities)

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	14.77920	437.96771	0.034	0.97308
Class2nd	0.26021	549.29444	0.000	0.99962
Class3rd	-15.76960	437.96782	-0.036	0.97128
ClassCrew	-0.52215	0.18088	-2.887	0.00389 **
SexFemale	3.59619	0.74781	4.809	1.52e-06 ***
AgeAdult	-15.50683	437.96774	-0.035	0.97176
Class2nd:SexFemale	-0.06801	0.67120	-0.101	0.91929
Class3rd:SexFemale	-2.79995	0.56875	-4.923	8.52e-07 ***
ClassCrew:SexFemale	-1.13608	0.82048	-1.385	0.16616
Class2nd:AgeAdult	-1.93047	549.29453	-0.004	0.99720
Class3rd:AgeAdult	14.85629	437.96787	0.034	0.97294
ClassCrew:AgeAdult	NA	NA	NA	NA
SexFemale:AgeAdult	0.68679	0.52541	1.307	0.19116

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 2769.5 on 23 degrees of freedom
Residual deviance: 2097.5 on 12 degrees of freedom
AIC: 2121.5

Number of Fisher Scoring iterations: 13

The summary of interacting model suggests that class status association arose from the linear effect of being **Crew** and interaction effect of **Female 3rd-class** passengers.

To illustrate training and prediction, we divide the sample into train and test sets:

```
R> set.seed(159)
R> nsample <- NROW(titanic_raw)
R> flag <- rep(TRUE, nsample)
R> flag[sample(nsample, nsample/2)] <- FALSE
R> dtrain <- titanic_raw[flag,]
R> dtest <- titanic_raw[!flag,]
```

We train `glm` model with interactions, omitting interaction `Class:Age` because it was rank-deficient, and make prediction on test data:

```
R> gfit2 <- glm(Survived ~ Class * Sex + Sex * Age, family = binomial(),
+   data = dtrain)
R> prl <- predict(gfit2, newdata = dtest)
R> yhat <- ifelse(prl > 0, 'Yes', 'No')
R> mean(yhat == dtest$Survived)
```

```
[1] 0.7718182
```

```
R> gauc <- pROC::roc(response = dtest$Survived, predictor = prl,
+   direction = '<')$auc
R> gauc
```

Area under the curve: 0.7699

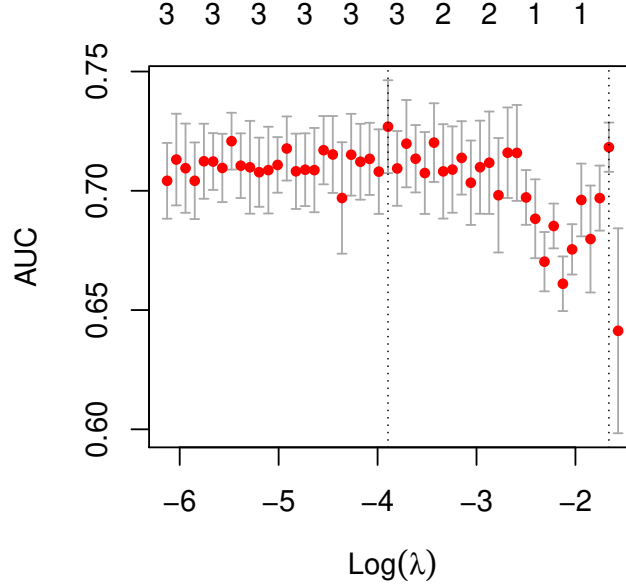
For comparison with **bbl**, which by default includes regularization, we also consider penalized logistic regression fit using **glmnet** (Friedman, Hastie, and Tibshirani 2010; Friedman, Hastie, Tibshirani, Narasimhan, Simon, and Qian 2019)

```
R> if(!require('glmnet'))
+   install.packages('glmnet')
R> library('glmnet')
R> xdat <- data.matrix(dtrain[, 1:3])
R> y <- dtrain[, 4]
R> gnet <- cv.glmnet(x = xdat, y = y, family = 'binomial', alpha = 1,
+   nfolds = 5, type.measure = 'auc')
R> plot(gnet)
```

Note that the above fit used the non-interacting model of three predictors and L_1 penalization ($\alpha = 1$). The input matrix contains integer-coded terms in the linear model (columns):

```
R> head(xdat)
```

```
      Class Sex Age
4         3   1   1
5         3   1   1
```

Figure 1: Cross-validation run of `glmnet` on Titanic data.

7	3	1	1
8	3	1	1
13	3	1	1
14	3	1	1

Figure 1 indicates that the effect of regularization is minimal for this model.

3.2. Boltzmann Bayes learning

The logistic regression shown in Section 3.1 allowed for inference and significance testing of linear and interaction coefficients in association with the response variable. However, the regression fit did not provide any further information regarding the source of association: in the examples in Section 3.1, the survival of Titanic passengers was seen to be associated with being **Female** and not being **Crew** members or **Female 3rd-class** passengers. The corresponding linear regression coefficients, which have the same functional form as in Eq. (30), are measures of the *difference* in enrichment in the two response groups, while the two terms whose difference yielded the coefficient remained unknown. How were the sub-groups distributed among survivor and non-survivor groups? Were there very few **Female 3rd-class** passengers among the survivor group compared to non-survivor, or were they found in both groups but more so among non-survivors?

The **bbl** inference estimates the individual distributions of predictors in response groups separately and subsequently combines them to make predictions. For binary response, this inference provides estimates of the two coefficients whose difference corresponds to the logistic regression outcome. More generally, the availability of the direct estimates of predictor

distributions in each response group given by Eq. (6) facilitates model interpretations in a way not possible for regression-based models, as we show below in this section and Section 3.5.

With this comparison in mind, we use the same Titanic data below to illustrate the Boltzmann Bayes inference. As in **glm**, **bbl** uses formula input to train an S3 object of class **bbl**:

```
R> bfit0 <- bbl(Survived ~ Class + Sex + Age, data = titanic, weights = freq,
+   prior.count = 0)
```

which by default triggers a pair of pseudo-likelihood inferences, solving the maximum pseudo-likelihood equations (15) first under the alternative hypothesis (individual groups have distinct distributions) and then the null hypothesis (all samples have the same distribution). The **print** method on **bbl** shows the structure of model and (subsets) of inferred parameters:

```
R> bfit0
```

Call:

```
bbl(formula = Survived ~ Class + Sex + Age, data = titanic, weights = freq,
    prior.count = 0)
```

3 predictor states:

```
Class = 1st 2nd 3rd Crew
```

```
Sex = Female Male
```

```
Age = Adult Child
```

Responses:

```
Survived = No Yes
```

Coefficients:

```
dh_[Class]^(No):
```

```
      2nd      3rd      Crew
```

```
0.4451514 0.6891838 0.7058579
```

```
dh_[Class]^(Yes):
```

```
      2nd      3rd      Crew
```

```
-0.4112553 -0.9072555 -0.9584859
```

```
dh_[Sex]^(No):
```

```
Male
```

```
1.078173
```

```
dh_[Sex]^(Yes):
```

```
Male
```

```
-1.238999
```

```
dh_[Age]^(No):
```

```
Child
```

```
-0.3651582
```

```
dh_[Age]^(Yes):
```

```

      Child
0.5145496

```

where `dh` represents parameters $\Delta h_i^{(y)} = h_i^{(y)} - h_i$; i.e., individual group parameters offset by the pooled values. Internally, the parameters $h_i^{(y)}$ and $J_{ij}^{(y)}$ are stored as lists with argument order (y, i) and (y, i, j) , respectively. The inner-most elements of the lists are vectors and matrices of dimension $L_i - 1 = c(3, 1, 1)$ and $(L_i - 1, L_j - 1)$, respectively. The `summary` method on `bbl` object prints out parameters and their significance test outcomes under the naive Bayes approximation (no interactions) as a rough overview of model under consideration:

```
R> summary(bfit0)
```

```
Call:
```

```
  bbl(formula = Survived ~ Class + Sex + Age, data = titanic, weights = freq,
      prior.count = 0)
```

```
3 predictor states:
```

```
  Class = 1st 2nd 3rd Crew
```

```
  Sex = Female Male
```

```
  Age = Adult Child
```

```
Responses:
```

```
  Survived = No Yes
```

```
Fit method: mf
```

```
naive Bayes coefficients:
```

```
h_Class:
```

	2nd	3rd	Crew
No	0.3139728	1.4650752	1.7077243
Yes	-0.5425214	-0.1314224	0.0433803
pooled	-0.1313360	0.7757901	1.0017625

chisq = 180.9014, df = 3, Pr(>chisq) = 5.633919e-39

```
h_Sex:
```

	Male
No	2.38189493
Yes	0.06472019
pooled	1.30372186

chisq = 434.4688, df = 1, Pr(>chisq) = 1.730842e-96

```
h_Age:
```

	Child
No	-3.319765
Yes	-2.440056
pooled	-2.954528

chisq = 19.5606, df = 1, Pr(>chisq) = 9.745843e-06

The test results are those from likelihood ratio test applied to the naive Bayes result, Eq. (27), with the null hypothesis $h_i^{(y)}(a) = h_i(a)$. The tables of bias parameters shown above include

those for two survival status groups, which clearly indicate the enrichment of lower **Class** status and **Male** among non-survivors. **Child** are few among both survivors and non-survivors; hence highly negative bias parameters in all groups, although less so in survivor group, as expected. We note that the **summary** method displays naive Bayes results, for which simple analytic expressions for test results are available, even for models containing interactions.

We now fit an interacting model using **bbl**:

```
R> bfit <- bbl(Survived ~ Class * Sex + Sex * Age, data = titanic,
+   weights = freq)
R> bfit
```

Call:

```
bbl(formula = Survived ~ Class * Sex + Sex * Age, data = titanic,
    weights = freq)
```

3 predictor states:

Class = 1st 2nd 3rd Crew

Sex = Female Male

Age = Adult Child

Responses:

Survived = No Yes

Coefficients:

dh_[Class]^(No):

	2nd	3rd	Crew
	1.486562	2.970599	1.553392

dh_[Class]^(Yes):

	2nd	3rd	Crew
	-0.1036710	-0.7511305	-0.1150225

dh_[Sex]^(No):

	Male
	3.153479

dh_[Sex]^(Yes):

	Male
	-1.07586

dh_[Age]^(No):

	Child
	0.3864377

dh_[Age]^(Yes):

	Child
	-0.177389

```
dJ_[Class,Sex]^(No):
```

```
      Male
2nd  -1.231976
3rd  -2.720271
Crew -1.378106
```

```
dJ_[Class,Sex]^(Yes):
```

```
      Male
2nd  -0.90329177
3rd  -0.01449154
Crew -0.30214334
```

```
dJ_[Sex,Age]^(No):
```

```
      Child
Male -0.493753
```

```
dJ_[Sex,Age]^(Yes):
```

```
      Child
Male  1.167093
```

The parameters printed include those for interactions. The `plot` method shows a barplot of bias parameters and a heatmap of interaction parameters (Fig. 2). Note that **Male** members were predominant (bias parameters; top), while **Male 3rd-class** passengers were under-represented (interactions; bottom left), among non-survivors. In addition, **Male-Child** class had enhanced survival (bottom right).

We now fit the training data and make prediction on test data:

```
R> bfit2 <- bbl(Survived ~ Class * Sex + Sex * Age, data = dtrain)
R> pr <- predict(bfit2, newdata = dtest, type = 'prob')
R> head(pr)
```

	No	Yes	yhat
1	0.8147323	0.1852677	No
2	0.8147323	0.1852677	No
3	0.8147323	0.1852677	No
4	0.8147323	0.1852677	No
5	0.8147323	0.1852677	No
6	0.8147323	0.1852677	No

```
R> auc <- pROC::roc(response = dtest$Survived, predictor = pr[, 2],
+   direction = '<')$auc
R> auc
```

Area under the curve: 0.7707

Here, Eq. (28) was used with **x** from the supplied `newdata`. The `predict` method returns a data frame containing predicted group probabilities and the most likely group for each row.

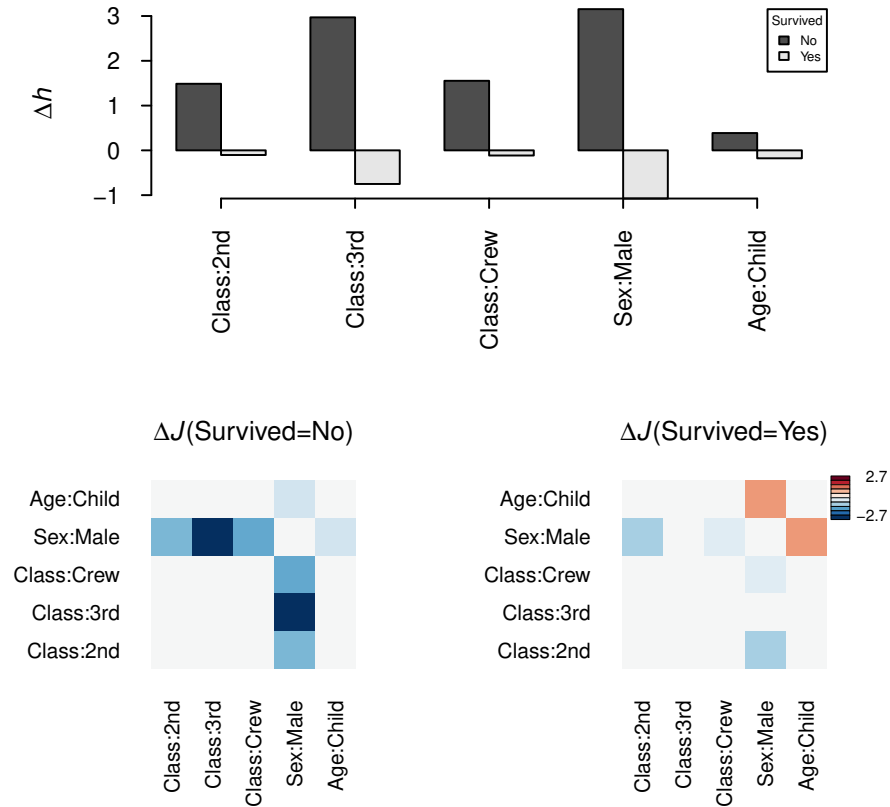


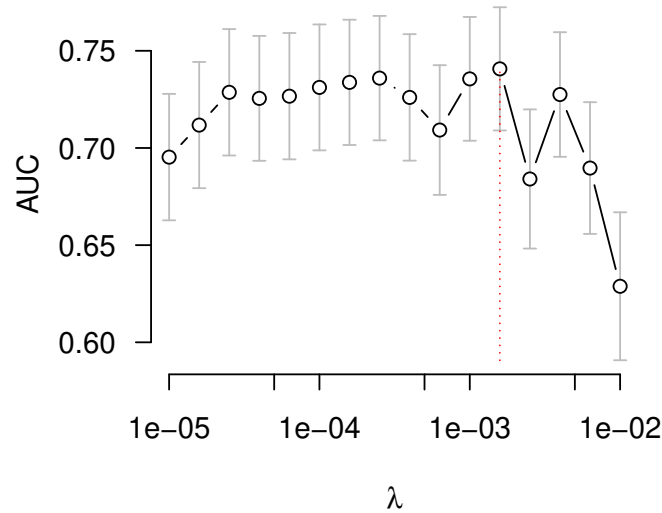
Figure 2: Plot of `bb1` object displays bias (top) and interaction parameters (bottom). All parameters are offset by their pooled (single-group) values.

One can do cross-validation applied to `dtrain` data, dividing it into `nfold = 5` train/validation subsets of 4:1 proportion, and aggregating predictions for validation sets using the trained model:

```
R> cv <- crossVal(Survived ~ .^2, data = dtrain, method = 'pseudo',
+   lambda = 10^seq(-5, -2, 0.2), verbose = 0)
R> cv
```

```
Optimal lambda = 0.001584893
Max. score: 0.7407153
```

	lambda	AUC	ci1	ci2
1	1.000000e-05	0.6952981	0.6627702	0.7278261
2	1.584893e-05	0.7117878	0.6793222	0.7442534
3	2.511886e-05	0.7286483	0.6961300	0.7611665
4	3.981072e-05	0.7255268	0.6933977	0.7576559
5	6.309573e-05	0.7266575	0.6941610	0.7591540

Figure 3: Cross-validation run of *Titanic* data in *bbl*.

```

6  1.000000e-04 0.7311655 0.6987723 0.7635587
7  1.584893e-04 0.7337642 0.7015270 0.7660015
8  2.511886e-04 0.7359441 0.7039356 0.7679526
9  3.981072e-04 0.7260199 0.6934862 0.7585535
10 6.309573e-04 0.7092299 0.6758527 0.7426070
11 1.000000e-03 0.7355622 0.7037121 0.7674124
12 1.584893e-03 0.7407153 0.7090255 0.7724051
13 2.511886e-03 0.6840430 0.6482426 0.7198435
14 3.981072e-03 0.7275102 0.6954548 0.7595655
15 6.309573e-03 0.6896706 0.6557830 0.7235581
16 1.000000e-02 0.6288425 0.5907828 0.6669023

```

```
R> plot(cv, mar=c(4, 4, 3, 3), tck = -0.04, bty = 'n')
```

Here, the model included all interaction terms and returned an object with a `data.frame` of AUCs for multiple `lambda` values as well as 95% confidence intervals and optimal values with maximum AUC. We use this information to make prediction as follows:

```

R> model <- bbl(Survived ~ .^2, data = dtrain, lambda = cv$regstar)
R> pr2 <- predict(model, newdata = dtest)
R> bscore <- mean(dtest$Survived == pr2$yhat)
R> bscore

```

```
[1] 0.7981818
```

```
R> bauc <- pROC::roc(response = dtest$Survived, predictor = pr2[,2],
+   direction = '<')$auc
R> bauc
```

Area under the curve: 0.7709

Alternatively, `predict(cv, ...)` will apply the optimal model within cross-validation to test data. The difference compared to the re-training step above is that the optimal model stored in `cv` was trained on 4/5 of the sample, while `model` above used the whole training set.

A major advantage of the `bb1` fit compared to regression is the availability of predictor distributions in each response group, $P(\mathbf{x}|y)$, given by Eq. (6). In addition to using the model to make predictions of response groups, one can also examine the predictor distributions and identify configurations dominant in each response group. Since the total number of configurations \mathbf{x} grows exponentially with the number of predictors, Markov chain Monte Carlo (MCMC) sampling is necessary for exploration of these distributions except for very low dimensions. The function `mcSample` performs Gibbs sampling of the predictor distributions using `bb1` parameters and outputs the most likely configuration in each response group:

```
R> map <- mcSample(bfit, nstep = 1000, progress.bar = FALSE)
R> map
```

```
$xmax
      No      Yes
Class "3rd"  "1st"
Sex   "Male" "Female"
Age   "Adult" "Adult"
```

```
$emax
      No      Yes
3.380728 0.000000
```

The return value is a list containing the predictor configurations with the highest probability in each response group (columns in `map$xmax` above) and the corresponding “energy” values, which are exponents of Eq. (6).

3.3. Simulated data

We next demonstrate the reliability of `bb1` inference using simulated data.

```
R> predictors <- list()
R> m <- 5
R> L <- 3
R> for(i in 1:m) predictors[[i]] <- seq(0, L-1)
R> par <- randompar(predictors)
R> names(par)
```

```
[1] "h" "j"
```

The utility function `randompar` generates random parameters for predictors. We have set the total number of predictors as $m = 5$, each taking values 0, 1, 2 ($L_i = L = 3$).

```
R> xi <- sample_xi(nsample = 10000, predictors = predictors, h = par$h,
+   J = par$J, code_out = TRUE)
R> head(xi)
```

```
1 0 1 2 2 0
2 0 1 2 0 2
3 0 0 2 1 1
4 1 0 2 1 1
5 1 2 2 2 2
6 1 1 2 0 1
```

The function `sample_xi` will list all possible predictor states and sample configurations based on the distribution (6). The total number of states here is $L^m = 3^5$, which is amenable for exhaustive enumeration. However, this is possible only for small m and L . If either are even moderately larger, `sample_xi` will hang.

Because there is only one response group, we call the main engine `mleestimate` of **bbl** inference directly instead of `bbl`:

```
R> fit <- mleestimate(xi = xi, method = 'pseudo', lambda = 0)
```

```
Predictor 1: 54 iterations, likelihood = 0.902882
Predictor 2: 61 iterations, likelihood = 0.880671
Predictor 3: 45 iterations, likelihood = 0.475724
Predictor 4: 60 iterations, likelihood = 0.860684
Predictor 5: 60 iterations, likelihood = 0.996739
```

In contrast to `bbl` function, which fits a model of multiple response groups and predictors in factors, `mleestimate` is for a single group and requires input matrix `xi` whose elements are integral codes of factors: $a_i = 0, \dots, L_i - 1$. Figure 4 compares the true and inferred parameters. Here, the sample size was large enough that no regularization was necessary.

We next simulate a full binary response data set with four-level predictors:

```
R> nt <- c('a', 'c', 'g', 't')
R> set.seed(135)
R> for(i in 1:m) predictors[[i]] <- nt
R> names(predictors) <- paste0('v', 1:m)
R> par <- list()
R> par[[1]] <- randompar(predictors)
R> par[[2]] <- randompar(predictors, h0 = 0.1, J0 = 0.1)
R> dat <- randomsamp(predictors, response = c('ctrl', 'case'), par = par,
+   nsample = 1000)
```

The function `randomsamp` generates random samples of predictor-response pairs using the supplied `par`. We perform a cross-validation using mean field inference,

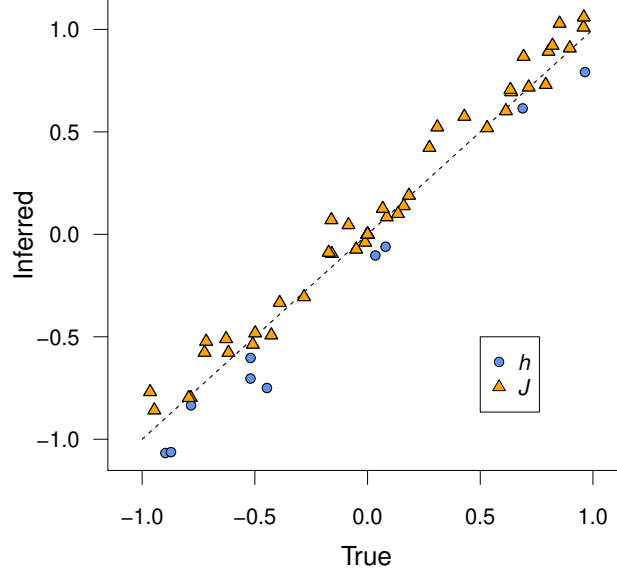


Figure 4: Comparison of true parameters and those inferred from pseudo-likelihood Boltzmann Bayes inference. See the text for conditions.

```
R> cv <- crossVal(y ~ .^2, data = dat, method = 'mf', eps = seq(0, 1, 0.1),
+   verbose=0)
R> cv
```

```
Optimal epsilon = 0.7
Max. score: 0.8845219
```

	epsilon	AUC	ci1	ci2
1	0.0	0.7849546	0.7568076	0.8131017
2	0.1	0.8392593	0.8149947	0.8635240
3	0.2	0.8610941	0.8386831	0.8835051
4	0.3	0.8708767	0.8493991	0.8923543
5	0.4	0.8773411	0.8565066	0.8981756
6	0.5	0.8812357	0.8608067	0.9016647
7	0.6	0.8831850	0.8629906	0.9033795
8	0.7	0.8845219	0.8644845	0.9045594
9	0.8	0.8840456	0.8639740	0.9041172
10	0.9	0.8815880	0.8612527	0.9019232
11	1.0	0.8724978	0.8511909	0.8938047

Here, `bb1` is called inside `crossVal` as before but with `method = 'mf'`, which triggers mean field inference with Eqs. (19) and (22).

As shown in Fig. 5a, prediction AUC is optimized near $\epsilon = 0.7$. The difference between AUC at $\epsilon = 0$ (naive Bayes limit) and the maximum is a measure of the overall effect of interaction. We select three values of ϵ and examine the fit:

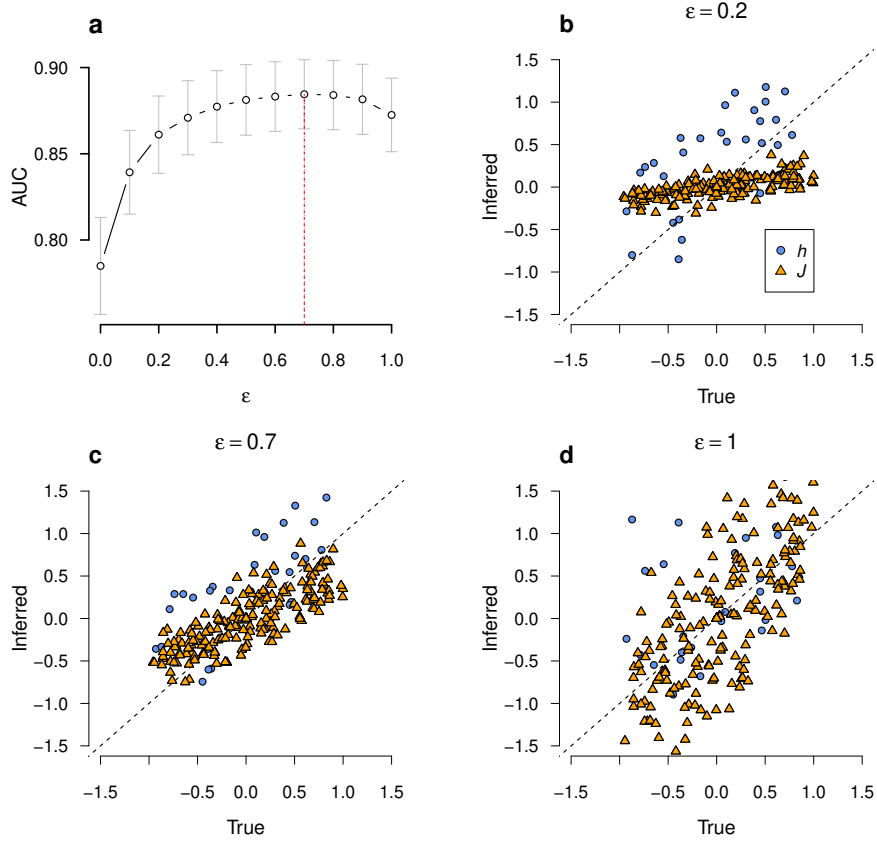


Figure 5: Regularized mean field inference using simulated data. (a) Cross-validation AUC with respect to regularization parameter ϵ . (b-d) Comparison of true and inferred parameters under three ϵ values. Best fit is achieved when AUC is maximum.

```
R> fit <- list()
R> eps <- c(0.2, 0.7, 1.0)
R> for(i in seq_along(eps))
+   fit[[i]] <- bbl(y ~ .^2, data = dat, method = 'mf', eps = eps[i],
+   verbose = 0)
```

Figure 5b-d compares the three inferred parameter sets (`coef(fit[[i]])$h`, `coef(fit[[i]])$J`) with the true values (`par[[iy]]$h`, `par[[iy]]$J`). As ϵ increases from 0 to 1, interaction parameter J grows from zero to large, usually overfit levels. We verify that the bias and variance strike the best balance under $\epsilon = 0.7$ (Fig. 5c), as suggested by cross-validation AUC in Fig. 5a.

3.4. Genetic code

We consider a different learning task example with a much larger space of response groups, namely those of amino acids; $K = 21$, which include 20 amino acids plus stop signal ('*'), encoded by DNA sequences ($x_i = \text{a, c, g, t}$). In DNA sequences, three nucleotides combine to encode specific amino acids. We will train a model attempting to discover this genetic code from data.

```
R> set.seed(351)
R> n <- 2000
R> dat <- data.frame(b1 = sample(nt, size = n, replace = TRUE),
+   b2 = sample(nt, size = n, replace = TRUE),
+   b3 = sample(nt, size = n, replace = TRUE))
R> head(dat)
```

```
   b1 b2 b3
1   t  a  g
2   g  t  c
3   t  a  a
4   c  g  g
5   a  a  c
6   c  t  g
```

In the above, we generated random instances of triplet codons for training. We use the package **Biostrings** (Pagès, Aboyoun, Gentleman, and DebRoy 2019) to translate it into amino acids:

```
R> if(!require('Biostrings')){
+   if(!require('BiocManager'))
+     install.packages('BiocManager')
+   BiocManager::install('Biostrings')
+ }
R> aa <- Biostrings::DNAString(paste(t(dat), collapse = ''))
R> aa
```

```
6000-letter "DNAString" instance
seq: TAGGTCTAACGGAACCTGGCGATTATACTTG...AGTAAACTCGACAGTGACCGAAGGTACGGGC
```

```
R> aa <- strsplit(as.character(Biostrings::translate(aa)), split = '')[[1]]
R> xdat <- cbind(data.frame(aa = aa), dat)
R> head(xdat)
```

```
   aa b1 b2 b3
1   *  t  a  g
2   V  g  t  c
3   *  t  a  a
4   R  c  g  g
5   N  a  a  c
6   L  c  t  g
```

We now cross-validate using bbl:

```
R> cv <- crossVal(aa ~ .^2, data = xdat, lambda = 10^seq(-3, 1, 0.5),
+   verbose = 0)
R> cv
```

```
Optimal lambda = 0.3162278
Max. score: 1
```

```
      lambda  score
1 0.001000000 0.9195
2 0.003162278 0.9195
3 0.010000000 0.9875
4 0.031622777 0.9875
5 0.100000000 0.9925
6 0.316227766 1.0000
7 1.000000000 0.9930
8 3.162277660 0.9770
9 10.000000000 0.9770
```

Note that with the multinomial response group, the score used is Eq. (33). The class `cv.bbl` extends `bbl` and stores the model with the optimal λ . In contrast to Section 3.2, we do not refit the model under this λ because the score is maximum. Testing can use all possible codon sequences ($4^3 = 64$ total):

```
R> panel <- expand.grid(b1 = nt, b2 = nt, b3 = nt)
R> head(panel)
```

```
  b1 b2 b3
1  a  a  a
2  c  a  a
3  g  a  a
4  t  a  a
5  a  c  a
6  c  c  a
```

```
R> dim(panel)
```

```
[1] 64  3
```

```
R> p <- predict(cv, panel)
R> ap <- Biostrings::DNASTring(paste(t(panel), collapse = ''))
R> ap <- strsplit(as.character(Biostrings::translate(ap)), split = '')[[1]]
R> score <- mean(ap == p$yhat)
R> score
```

```
[1] 1
```

The trained model has perfect prediction score of 1 and will not make mistakes in any translation of DNA sequences.

3.5. Image data

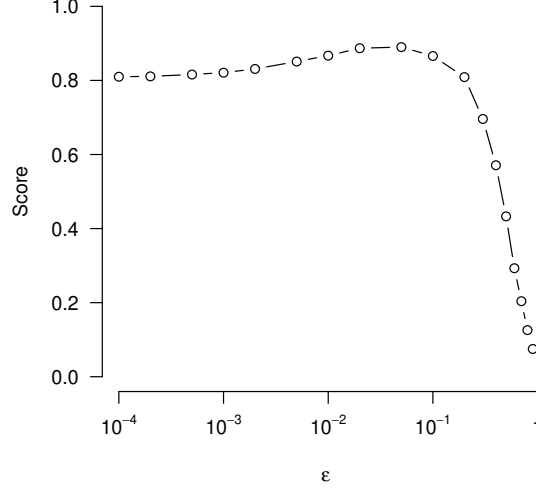


Figure 6: Cross-validation of Boltzmann Bayes inference on MNIST data using mean field option.

We next consider learning examples with data sets containing predictors numbering ~ 100 or more. The MNIST data set (<http://yann.lecun.com/exdb/mnist/>), widely used for benchmarking classification algorithms (Lecun, Bottou, Bengio, and Haffner 1998), contains image data of grayscale levels ($x_i = [0, 255]$) derived from hand-written digits ($y_k = 0, \dots, 9$) for $m = 28 \times 28 = 784$ pixels. We use down-sampled training ($n = 1,000$) and test ($n = 500$) data sets, where grayscale has been transformed into binary predictors ($x_i = 0, 1$):

```
R> dat0 <- read.csv(system.file('extdata/mnist_train.csv', package = 'bbl'))
R> dat <- removeConst(dat0)
R> dat[1:5, 1:10]
```

	y	X40	X41	X45	X46	X47	X64	X65	X66	X67
1	9	0	0	0	0	0	0	0	0	0
2	7	0	0	0	0	0	0	0	0	0
3	1	0	0	0	0	0	0	0	0	0
4	8	0	0	0	0	0	0	0	0	0
5	1	0	0	0	0	0	0	0	0	0

```
R> cv <- crossVal(y ~ .^2, data = dat, method = 'mf', eps = 0.05)
```

Note that before calling `crossVal`, we removed predictors without factor variations (pixels that are always empty) using the utility function `removeConst`. By default, error will occur inside `crossVal` otherwise.

The above run will take a few minutes. By feeding a vector of ϵ values, one can obtain the profile shown in Fig. 6. The jump in performance under $\epsilon^* \sim 0.05$ over $\epsilon \rightarrow 0$ (naive Bayes) limit gives a measure of interaction effects. The relatively small value of ϵ^* at the optimal condition, compared to e.g., Fig. 5a, reflects the sparseness of image data.

We now retrain the model without cross-validation under ϵ^* and classify test set images:

Algorithm	Method	Error rate (%)	Reference/package
Linear classifier	1-layer NN	12.0	Lecun <i>et al.</i> (1998)
K-nearest neighbors	Euclidean (L2)	5.0	Lecun <i>et al.</i> (1998)
2-layer NN	300 hidden units	4.7	Lecun <i>et al.</i> (1998)
RBM	2-layer	0.95	Salakhutdinov and Hinton (2009)
Naive Bayes	Mean field ($\epsilon = 0$)	15.7	bbl
BB	Mean field ($\epsilon = 0.05$)	8.5	bbl

Table 1: Performance comparison of BB inference and other models on MNIST data set. The **bbl** inferences used the full MNIST training and test data sets (see text). BB, Boltzmann Bayes; NN, neural network; RBM, restricted Boltzmann machine.

```
R> mnist <- bbl(y ~ .^2, data = dat, method = 'mf', eps = 0.05)
R> dtest <- read.csv(system.file('extdata/mnist_test.csv', package = 'bbl'))
R> dtest <- dtest[, colnames(dtest) %in% colnames(dat)]
R> pr <- predict(mnist, newdata = dtest[, -1], progress.bar = TRUE)
R> score <- mean(pr$yhat == dtest$y)
R> score
```

Since `mnist` dropped a subset of original predictors, the test data must be filtered accordingly. Note the increase in test score compared to cross-validation score because of the use of full training data.

We performed similar cross-validation and test analyses of the full MNIST data (training $n = 60,000$ and test $n = 10,000$) and obtained the test score of 0.915 (classification error rate 8.5%), which compares favorably with other large-scale neural network algorithms (Table 1).

As with Titanic data, we leverage the unique advantage of `bbl` fit of providing predictor distributions and estimate dominant configurations of each response group (Fig. 7):

```
R> mnist_map <- mcSample(mnist, nstep = 20, progress.bar = TRUE)
R> oldpar <- par(mfrow = c(2, 5), mar = c(1, 1, 1, 1))
R> xvar <- colnames(dat0[, -1])
R> xmap <- apply(mnist_map$xmap, 1:2, as.numeric)
R> xf <- matrix(0, nrow = length(xvar), ncol = 10)
R> rownames(xf) <- xvar
R> for(i in 1:10) xf[rownames(xmap), i] <- xmap[, i]
R> for(i in 1:10){
+   mat <- matrix(t(xf[, i]), nrow = 28, ncol = 28)
+   image(x = 1:28, y = 1:28, z = mat[, 28:1], col = c('white', 'black'),
+         xaxt = 'n', yaxt = 'n', xlab = '', ylab = '')
+ }
R> par(oldpar)
```

It is interesting to note that the model for handwritten digit “1” is a combination of two versions, one slanted forward and the other backward. The images shown in Fig. 7 illustrate examples of model interpretation made possible by the Bayesian formulation used by **bbl**, a significant advantage compared to regression-based methods and other deep learning models whose interpretations are challenging ([Montavon, Samek, and K.-R. Müller 2018](#)).



Figure 7: Maximum probability configurations of digits $(0, \dots, 9)$ estimated from `bbl` fit coefficients using Gibbs sampling.

3.6. Transcription factor binding site data

One of machine learning tasks of considerable interest in biomedical applications is the detection of transcription factor binding sites within genomic sequences (Wasserman and Sandelin 2004). Transcription factors are proteins that bind to specific DNA sequence segments and regulate gene expression programs. Public databases, such as JASPAR (Khan, Fornes, Stigliani, Gheorghe, Castro-Mondragon, van der Lee, Bessy, Chéneby, Kulkarni, Tan, Baranasic, Arenillas, Sandelin, Vandepoele, Lenhard, Ballester, Wasserman, Parcy, and Mathelier 2018), host known transcription factors and their binding sequence motifs. Supervised learners allow users to leverage these data sets and search for binding motifs among candidate sequences.

Here, we illustrate such an inference using an example set (MA0014.3) of binding motif sequences from JASPAR (<http://jaspar.genereg.net>):

```
R> seq <- readFasta(system.file('extdata/MA0014.3.fasta', package = 'bbl'))
R> head(seq)
```

```
  1 2 3 4 5 6 7 8 9 10 11 12
1 G G G C G T G A C T T C
2 C A G C G T G A C G C G
3 G C G C G T C A C G C T
4 C A G C T T G A C C A G
5 G A C C G T G A C C A C
6 A G G C G C G A C G C C
```

```
R> dim(seq)
```

```
[1] 948 12
```

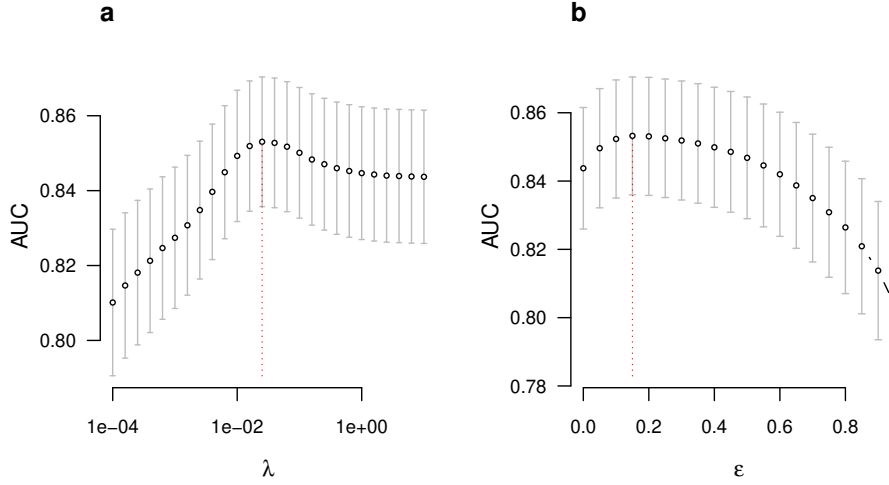


Figure 8: Cross-validation of transcription factor binding motif model using **bbl** with control sequences generated by 3 nucleotide mutations. Data set is from [Khan *et al.* \(2018\)](#) (sample ID MA0014.3; see text). (a) Pseudo-likelihood and (b) mean field inferences.

The data set consists of common nucleotide segments from $n = 948$ raw sequences used for motif discovery. We simulate a training set by generating non-binding sequences with random mutation of 3 nucleotides:

```
R> set.seed(561)
R> nsample <- NROW(seq)
R> m <- NCOL(seq)
R> nt <- c('A', 'C', 'G', 'T')
R> ctrl <- as.matrix(seq)
R> for(k in seq_len(nsample))
+   ctrl[k, sample(m, 3)] <- sample(nt, 3, replace = TRUE)
R> colnames(ctrl) <- 1:m
R> data <- rbind(data.frame(y = rep('Binding', nsample), seq),
+   data.frame(y = rep('Non-binding', nsample), ctrl))
R> data <- data[sample(NROW(data)), ]
```

We assess the performance of pseudo-likelihood and mean field inferences below using cross-validation:

```
R> ps <- crossVal(y ~ .^2, data = data, method = 'pseudo',
+   lambda = 10^seq(-2, -1, 0.2), verbose = 0)
R> ps
```

```
Optimal lambda = 0.02511886
Max. score: 0.8530506
```

lambda	AUC	ci1	ci2
--------	-----	-----	-----

```

1 0.01000000 0.8492785 0.8317472 0.8668099
2 0.01584893 0.8519168 0.8345200 0.8693135
3 0.02511886 0.8530506 0.8357371 0.8703641
4 0.03981072 0.8527546 0.8354393 0.8700699
5 0.06309573 0.8517454 0.8343829 0.8691079
6 0.10000000 0.8501086 0.8326675 0.8675497

```

```

R> mf <- crossVal(y ~ .^2, data = data, method = 'mf',
+   eps = seq(0.1, 0.4, 0.1), verbose = 0)
R> mf

```

```

Optimal epsilon = 0.2
Max. score: 0.8530829

```

	epsilon	AUC	ci1	ci2
1	0.1	0.8523296	0.8350451	0.8696140
2	0.2	0.8530829	0.8357946	0.8703712
3	0.3	0.8518778	0.8344548	0.8693008
4	0.4	0.8498872	0.8322967	0.8674777

In both cases, there is an optimal, intermediate range of regularization with maximum AUC (Fig. 8). The level of performance attainable with non-interacting models, such as position frequency matrix (Wasserman and Sandelin 2004), corresponds to the $\epsilon = 0$ limit in Fig. 8b. The AUC range obtained above is representative of the sensitivity and specificity levels one would get when scanning a genomic segment using a trained model for detection of a binding site to within resolution of ~ 3 base pairs.

We analyzed 684 data sets with at least 30 sequences from JASPAR database of varying sample sizes and segment lengths with the same protocol. Differences between fully optimized AUC scores and those from non-interacting models (naive Bayes) were most pronounced above the intermediate range of AUC (Fig. 9).

4. Summary

We introduced a user-friendly R package **bbl**, implementing general Boltzmann Bayes classifiers applicable to heterogeneous, multifactorial predictor data associated with a discrete multi-class response variable. The currently available R package **BoltzMM** is limited to fitting data into a single fully visible Boltzmann distribution without reference to response variables, and assumes binary predictors. The package **bbl** employs a more general statistical distribution accommodating heterogeneous, factor-valued predictors via Eq. (6), embedding it in a Bayesian classifier to build supervised learning and prediction models. The basic implementation architecture of **bbl** follows those of standard base R packages such as **glm**.

Compared to more widely applied restricted Boltzmann machine algorithms (Hinton 2012), the Boltzmann Bayes model explicitly infers interaction parameters for all pairs of predictors, making it possible to interpret trained models directly, as illustrated in Figs. 2 and 7, the latter using MCMC sampling of predictor distributions. The **bbl** inference is especially suited to data types where a moderate number of unordered features (such as nucleotide sequences)

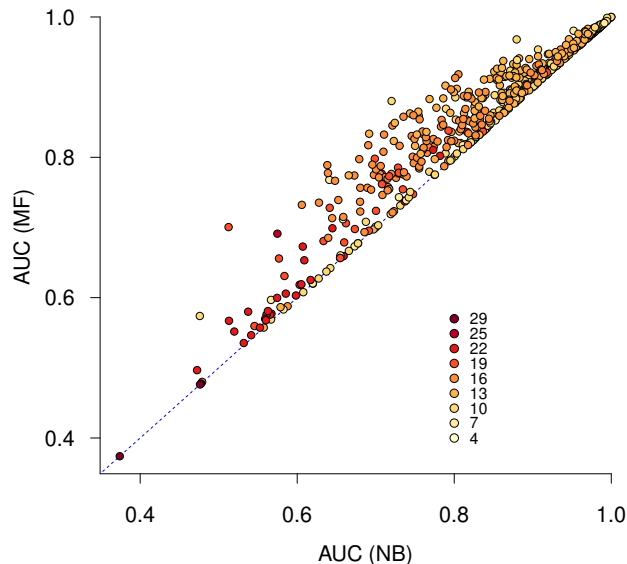


Figure 9: AUC scores of **bbl** model trained on 684 transcription factor binding site sequence data sets from JASPAR (Khan *et al.* 2018) under the same protocol as in Fig. 8. Naive Bayes (NB; mean field with $\epsilon = 0$) and full mean field (MF) results are compared. The symbol colors show the segment length of each binding site data (color-map in legend).

combine to determine class identity, as in transcription factor binding motifs (Section 3.6). Among the two options for inference methods, mean field (`method = 'mf'`) is faster but can become memory intensive for models with a large number of predictors. Pseudo-likelihood maximization (`method = 'pseudo'`) is slower but usually provides better performance.

Computational details

The current version of **bbl** is available at the Comprehensive R Archive Network (CRAN) at <https://CRAN.R-project.org/package=bbl>. Installation of **bbl** requires the GNU Scientific library <https://www.gnu.org/software/gsl> installed. The results in this paper were obtained using R 3.6.2. R itself and all packages used are available from the CRAN at <https://CRAN.R-project.org> and Bioconductor at <https://bioconductor.org>.

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