

MNP: R Package for Fitting the Multinomial Probit Model*

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Version 2.6–2

Abstract

MNP is a publicly available R package that fits the Bayesian multinomial probit model via Markov chain Monte Carlo. The multinomial probit model is often used to analyze the discrete choices made by individuals recorded in survey data. Examples where the multinomial probit model may be useful include the analysis of product choice by consumers in market research and the analysis of candidate or party choice by voters in electoral studies. The MNP software can also fit the model with different choice sets for each individual, and complete or partial individual choice orderings of the available alternatives from the choice set. The estimation is based on the efficient marginal data augmentation algorithm that is developed by Imai and van Dyk (2005).

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1 Introduction

This paper illustrates how to use MNP, a publicly available R (R Development Core Team, 2012) package, in order to fit the Bayesian multinomial probit model via Markov chain Monte Carlo. The multinomial probit model is often used to analyze the discrete choices made by individuals recorded in survey data. Examples where the multinomial probit model may be useful include the analysis of product choice by consumers in market research and the analysis of candidate or party choice by voters in electoral studies. The MNP software can also fit the model with different choice sets for each individual, and complete or partial individual choice orderings of the available alternatives from the choice set. We use Markov chain Monte Carlo (MCMC) for estimation and computation. In particular, we use the efficient marginal data augmentation MCMC algorithm that is developed by Imai and van Dyk (2005).

MNP can be installed in the same way as other R packages via the `install.packages("MNP")` command. Appendix A gives instructions for obtaining R and installing MNP on Windows, Mac OS X, and Linux/UNIX platforms. Only three commands are necessary to use the MNP software; `mnpc()` fits the multinomial probit model, `summary()` summarizes the MCMC output, and `predict()` gives posterior prediction based on the fitted model (In addition, `coef()` and `cov.mnp()` allow one to extract the posterior draws of model coefficients and covariance matrix). To run an example script, start R and run the following commands:

```
library(MNP)      # loads the MNP package
example(mnp)      # runs the example script
```

Details of the example script are given in Sections 3 and 4. Three appendices describe installation, the commands, and version history. We begin in Section 2 with a brief description of the multinomial probit model that MNP is designed to fit.

2 The Method

MNP implements the marginal data augmentation algorithms for posterior sampling in the multinomial probit model. The MCMC algorithm we implement here is fully described in Imai and van Dyk (2005); we use Scheme 1 of their Algorithm 1.

2.1 The Multinomial Probit Model

Suppose we have a dataset of size n with $p > 2$ choices and k covariates. Here, choices refer to the number of classes in the multinomial model. The word “choices” is used because the model is often used to describe how individuals choose among a number of alternatives, e.g., how a voter chooses which candidate to vote for among four candidates running for a particular office. We focus on the case when $p > 2$ because when $p = 2$, the model reduces to the standard binomial probit model, which can be fit via the `glm(, family = binomial(probit))` command in R. The multinomial probit model differs from the ordinal probit model in that the former does not assume any inherent ordering on the choices. Thus, although the individuals may have preferences among the available alternatives these ordering are individual specific rather than being characteristics of the alternatives themselves. The ordinal probit model can be fitted via an MCMC algorithm in R by installing a package called MCMCpack (Martin *et al.*, 2009).

Under the multinomial probit model, we assume a multivariate normal distribution on the latent variables, $W_i = (W_{i1}, \dots, W_{i,p-1})$.

$$W_i = X_i\beta + e_i, \quad e_i \sim N(0, \Sigma), \text{ for } i = 1, \dots, n, \quad (1)$$

where X_i is a $(p-1) \times k$ matrix of covariates, β is $k \times 1$ vector of fixed coefficients, e_i is $(p-1) \times 1$ vector of disturbances, and Σ is a $(p-1) \times (p-1)$ positive definite matrix. For the model to be identified, the first diagonal element of Σ is constrained, $\sigma_{11} = 1$. Please note that starting with version 2.6-1, we use the restriction $\text{trace}(\Sigma) = p$ as the default identification strategy following the recommendation of Burgette and Nordheim (2009). This avoids the arbitrariness of fixing one particular diagonal element. The response variable, Y_i , is the index of the choice of individual i among the alternatives in the choice set and is modeled in terms of this latent variable, W_i , via

$$Y_i(W_i) = \begin{cases} 0 & \text{if } \max(W_i) < 0 \\ j & \text{if } \max(W_i) = W_{ij} > 0 \end{cases}, \quad \text{for } i = 1, \dots, n, \text{ and } j = 1, \dots, p-1, \quad (2)$$

where Y_i equal to 0 corresponds to a base category.

The matrix X_i may include both choice-specific and individual-specific variables. A choice-specific variable is a variable that has a value for each of the p choices, and these p values may be different for each individual (e.g., the price of a product in a particular region where an individual lives). Choice-specific variables are recorded relative to the baseline choice and thus there are $p - 1$ recorded values

for each individual. In this way a choice-specific variable is tabulated as a column in X_i . Individual-specific variables, on the other hand, take on a value for each individual, but are constant across the choices, e.g., the age or gender of the individual. These variables are tabulated via their interaction with each of the choice indicator variables. Thus, an individual-specific variable corresponds to $p - 1$ columns of X_i and $p - 1$ components of β .

2.2 The Multinomial Probit Model with Ordered Preferences

In some cases, we observe a complete or partial ordering of p alternatives. For example, we may observe the preferences of each individual among different brands of a product. We denote the outcome variable in such situations by $\mathcal{Y}_i = \{\mathcal{Y}_{i1}, \dots, \mathcal{Y}_{ip}\}$ where $i = 1, \dots, n$ indexes individuals and $j = 1, \dots, p$ represent alternatives. If $\mathcal{Y}_{ij} > \mathcal{Y}_{ij'}$ for some $j \neq j'$, we say j is preferred to j' . If $\mathcal{Y}_{ij} = \mathcal{Y}_{ij'}$ for some $j \neq j'$, we say individual i is indifferent to the choice between alternatives j and j' , but treat the data as if the actual ordering is unknown. In other words, formally we insist on strict inequalities among the preferences, but allow for some inequalities to be unobserved. The preference ordering is assumed to satisfy the usual axioms of preference comparability. Namely, preference is connected: For any j and j' , either $\mathcal{Y}_{ij} \leq \mathcal{Y}_{ij'}$ or $\mathcal{Y}_{ij} \geq \mathcal{Y}_{ij'}$. Preference also must be transitive: for any j, j' , and j'' , $\mathcal{Y}_{ij} \leq \mathcal{Y}_{ij'}$ and $\mathcal{Y}_{ij'} \leq \mathcal{Y}_{ij''}$ imply $\mathcal{Y}_{ij} \leq \mathcal{Y}_{ij''}$. For notational simplicity and without loss of generality, we assume that \mathcal{Y}_{ij} takes an integer value ranging from 0 to $p - 1$. We emphasize that we have not changed the model from Section 2.1. Rather, we simply have more observed data: the index of the choice of the individual i , Y_i , can be computed from \mathcal{Y}_i . Thus, we continue to model the preference ordering, \mathcal{Y}_i , in terms of a latent (multivariate normal) random vector, $W_i = (W_{ij}, \dots, W_{i,p-1})$, via

$$\mathcal{Y}_{ij}(W_i) = \#\{W_{ij'} : W_{ij'} < W_{ij}\} \quad \text{for } i = 1, \dots, n, \quad \text{and } j = 1, \dots, p, \quad (3)$$

where $W_{ip} = 0$, the distribution of W_i is specified in equation 1, and $\#\{\dots\}$ indicates the number of elements in a finite set. This model can be fitted via a slightly modified version of the MCMC algorithm in Imai and van Dyk (2005). In particular, we need only modify the way in which W_{ij} is sampled and use a truncation rule based on Equation 3.

2.3 Prior Specification

Our prior distribution for the multinomial probit model is

$$\beta \sim N(0, A^{-1}) \quad \text{and} \quad p(\Sigma) \propto |\Sigma|^{-(\nu+p)/2} [\text{trace}(S\Sigma^{-1})]^{-\nu(p-1)/2}, \quad (4)$$

where A is the prior precision matrix of β , ν is the prior degrees of freedom parameter for Σ , and the $(p-1) \times (p-1)$ positive definite matrix S is the prior scale for Σ ; we assume the first diagonal element of S is one. The prior distribution on Σ is proper if $\nu \geq p-1$, the prior mean of Σ is approximately equal to S if $\nu > p-2$, and the prior variance of Σ increase as ν decreases as long as this variance exists. We also allow for an improper prior on β , which is $p(\beta) \propto 1$ (i.e., $A = 0$).¹

Alternate prior specifications were introduced by McCulloch and Rossi (1994) and McCulloch *et al.* (2000). The relative advantage of the various prior distributions are discussed by McCulloch *et al.* (2000), Nobile (2000), and Imai and van Dyk (2005). We prefer our choice because it allows us to directly specify the prior distribution on the identifiable model parameters, allows us to specify an improper prior distribution on regression coefficient, and results in a Monte Carlo sampler that is relatively quick to converge. An implementation of of the sampler proposed by McCulloch and Rossi (1994) has recently been released in the R package bayesm (Rossi and McCulloch, 2005).

2.4 Prediction under the Multinomial Probit Model

Predictions of individual preferences given particular values of the covariates can be useful in interpreting the fitted model. Consider a value of the $(p-1) \times k$ matrix of covariates, X^* , that may or may not correspond to the values for one of the observed individuals. We are interested in the distribution of the preferences among the alternatives in the choice set given this value of the covariates. Let Y^* be the preferred choice and $\mathcal{Y}^* = (\mathcal{Y}_1^*, \dots, \mathcal{Y}_p^*)$ indicate the ordering of the preferences among the available alternatives. As an example, one might be interested in $\Pr(Y^* = j \mid X^*)$ for some j . By varying X^* , one could explore how preferences are expected to change with covariates. Similarly, one might be interested in how relative preferences such as $\Pr(\mathcal{Y}_j^* > \mathcal{Y}_{j'}^* \mid X^*)$ are expected to change with the covariates.

In the context of a Bayesian analysis, such predictive probabilities are computed via the posterior predictive distribution. This distribution conditions on the observed data, $Y = (Y_1, \dots, Y_n)$ or $\mathcal{Y} = (\mathcal{Y}_1, \dots, \mathcal{Y}_n)$, but averages over the uncertainty in the model parameters. For example,

$$\Pr(Y^* = j \mid X^*, Y) = \int \Pr(Y^* = j \mid X^*, \beta, \Sigma, Y) p(\beta, \Sigma \mid Y) d(\beta, \Sigma). \quad (5)$$

Thus, the posterior predictive distribution accounts for both variability in the response variable given

¹Algorithm 2 of Imai and van Dyk (2005) allows for a non zero prior mean for β . Because the update for Σ in this sampler is not exactly its complete conditional distribution, however, this algorithm may exhibit undesirable convergence properties in some situations.

the model parameters (i.e., the likelihood or sampling distribution) and the uncertainty in the model parameters as quantified in the posterior distribution. Monte Carlo evaluation of the posterior predictive distribution is easy once we obtain a Monte Carlo sample of the model parameters from the posterior distribution: We simply sample according to the likelihood for each Monte Carlo sample from the posterior distribution. This involves sampling the latent variable under the model in (1) and computing the preferred choice using (2) or the ordering of preferences using (3).

3 Example 1: Detergent Brand Choice

In this and the next section, we describe the details of two examples of MNP. In this section we use a market research dataset to illustrate the fitting of the multinomial probit model. In Section 4 we fit the multinomial probit model with ordered preference to a Japanese election dataset. We also describe how to perform convergence diagnostics of the MCMC sampler and analysis of the Monte Carlo output of MNP using an existing R package. Additional examples of MNP can be found in Imai and van Dyk (2005).

3.1 Preliminaries

Our first example analyzes a typical dataset in market research. The dataset contains information about the brand and price of the laundry detergent purchased by 2657 households originally analyzed by Chintagunta and Prasad (1998). The dataset contains the log prices of six detergent brands – Tide, Wisk, EraPlus, Surf, Solo, and All – as well as the brand chosen by each household (Type `help(detergent)` in R for details about the dataset).

We fit the multinomial probit model by using `choice` as the outcome variable and the other six variables as choice-specific covariates. After loading the MNP package, this can be accomplished using the following three commands,

```
data(detergent)
res <- mnp(choice ~ 1, choiceX = list(Surf=SurfPrice, Tide=TidePrice,
                                     Wisk=WiskPrice, EraPlus=EraPlusPrice,
                                     Solo=SoloPrice, All=AllPrice),
          cXnames = c("price"), data = detergent, n.draws = 10000,
          burnin = 2000, thin = 3, verbose = TRUE)
summary(res)
```

The first command loads the example dataset and stores it as the data frame called `detergent`. The second command fits the multinomial probit model. The default base category in this case is `All`.

(The default base category in MNP is the first factor level of the outcome variable, Y .) Each household chooses among the six brands of laundry detergent, i.e., $p = 6$. We specify the choice-specific variables, `choiceX`, using a named list. The elements of the list are the log price of each detergent brand and they are named after the levels of factor variable, `choice`. We also name the coefficient for this set of choice-specific variables by using `cXnames`. The argument `data` allows us to specify the name of the data frame where the data are stored. The model estimates five intercepts and the price coefficient as well as 14 parameters in the covariance matrix, Σ .

We use the default prior distribution; an improper prior distribution for β and a diffuse prior distribution for Σ with $\nu = p = 6$ and $S = I$. We sample 10,000 replications of the parameter from the resulting posterior distribution, saving every fourth sample after discarding the first 2,000 samples as specified by the arguments, `n.draws`, `thin`, and `burnin`. The argument `verbose = TRUE` specifies that a progress report and other useful messages be printed while the MCMC sampler is running. The `summary(res)` command gives a summary of the output including the posterior means and standard deviations of the parameters. The summary is based on the single MCMC chain produced with this call of MNP. Before we can reliably draw conclusions based on these results, we must be sure the chain has converged. Convergence diagnostics are discussed and illustrated in Section 3.2. The result of the call of `summary(res)` are as follows.

Call:

```
mnp(formula = choice ~ 1, data = detergent, choiceX = list(Surf = SurfPrice,
  Tide = TidePrice, Wisk = WiskPrice, EraPlus = EraPlusPrice,
  Solo = SoloPrice, All = AllPrice), cXnames = c("price"),
  n.draws = 10000, burnin = 2000, thin = 3, verbose = TRUE)
```

Coefficients:

	mean	std.dev.	2.5%	97.5%
(Intercept):EraPlus	2.567	0.238	2.123	3.03
(Intercept):Solo	1.722	0.247	1.248	2.25
(Intercept):Surf	1.572	0.163	1.259	1.91
(Intercept):Tide	2.716	0.252	2.269	3.22
(Intercept):Wisk	1.620	0.162	1.328	1.96
price	-82.102	8.952	-99.896	-66.32

Covariances:

	mean	std.dev.	2.5%	97.5%
EraPlus:EraPlus	1.00000	0.00000	1.00000	1.00
EraPlus:Solo	0.82513	0.26942	0.31029	1.36
EraPlus:Surf	0.17021	0.16115	-0.15810	0.48

EraPlus:Tide	0.24872	0.12956	0.00253	0.52
EraPlus:Wisk	0.88170	0.16614	0.54500	1.20
Solo:Solo	2.56481	0.68678	1.53276	4.25
Solo:Surf	0.45246	0.34572	-0.28018	1.13
Solo:Tide	0.50836	0.32706	-0.09069	1.22
Solo:Wisk	1.46997	0.44596	0.65506	2.45
Surf:Surf	1.69005	0.50978	0.92334	2.82
Surf:Tide	0.80762	0.30381	0.34019	1.44
Surf:Wisk	1.01614	0.36503	0.44121	1.85
Tide:Tide	1.32024	0.41669	0.62898	2.25
Tide:Wisk	1.05396	0.30137	0.59323	1.74
Wisk:Wisk	2.58761	0.55076	1.68773	3.82

Base category: All
 Number of alternatives: 6
 Number of observations: 2657
 Number of stored MCMC draws: 2000

We emphasize that these results are preliminary because convergence has not yet been assessed. Thus, we delay interpretation of the fit until Section 3.3, after we discuss convergence diagnostics in Section 3.2. Note that `coef(res)` and `cov.mnp(res)` allow one to extract the posterior draws of model coefficients and covariance matrix if desired. Type `help(mnp)` in R for details.

3.2 Using coda for Convergence Diagnostics and Output Analysis

It is possible to use coda (Plummer, Best, Cowles, and Vines, 2005), to perform various convergence diagnostics, as well as to summarize results. The coda package requires a matrix of posterior draws for relevant parameters to be saved as an `mcmc` object. Here, we illustrate how to use coda to calculate the Gelman-Rubin convergence diagnostic statistic (Gelman and Rubin, 1992). This diagnostic is based on multiple independent Markov chains initiated at over-dispersed starting values. Here, we obtain these chains by independently running the `mnp()` command three times, specifying different starting values for each time. This can be accomplished by typing the following commands at the R prompt,

```
data(detergent)
res1 <- mnp(choice ~ 1, choiceX = list(Surf=SurfPrice, Tide=TidePrice,
                                       Wisk=WiskPrice, EraPlus=EraPlusPrice,
                                       Solo=SoloPrice, All=AllPrice),
           cXnames = c("price"), data = detergent, n.draws = 50000,
           verbose = TRUE)

res2 <- mnp(choice ~ 1, choiceX = list(Surf=SurfPrice, Tide=TidePrice,
                                       Wisk=WiskPrice, EraPlus=EraPlusPrice,
```



```

                                Solo=SoloPrice, All=AllPrice),
coef.start = c(1, -1, 1, -1, 1, -1)*10,
cov.start = matrix(0.5, ncol=5, nrow=5) + diag(0.5, 5),
cXnames = c("price"), data = detergent, n.draws = 50000,
verbose = TRUE)

res3 <- mnp(choice ~ 1, choiceX = list(Surf=SurfPrice, Tide=TidePrice,
                                Wisk=WiskPrice, EraPlus=EraPlusPrice,
                                Solo=SoloPrice, All=AllPrice),
coef.start=c(-1, 1, -1, 1, -1, 1)*10,
cov.start = matrix(0.9, ncol=5, nrow=5) + diag(0.1, 5),
cXnames = c("price"), data = detergent, n.draws = 50000,
verbose = TRUE)

```

where we save the output of each chain separately as **res1**, **res2**, and **res3**. The first chain is initiated at the default starting values for all parameters; i.e., a vector of zeros for β and an identity matrix for Σ . The second chain is run starting from a vector of three 10's and three -10 's for β and a matrix with all diagonal elements equal to 1 and all correlations equal to 0.5 for Σ . Finally, the third chain is run starting from a permutation of the starting value used for β in the second chain, and a matrix with all diagonal elements equal to 1 and all correlations equal to 0.9 for Σ . We again use the default prior specification and obtain 50,000 draws for each chain.

We store the output from each of the three chains as an object of class **mcmc**, and then combine them into a single list using the following commands,

```

library(coda)
res.coda <- mcmc.list(chain1=mcmc(res1$param[,-7]),
                    chain2=mcmc(res2$param[,-7]),
                    chain3=mcmc(res3$param[,-7]))

```

where the first command loads the coda package² and the second command saves the results as an object of class **mcmc.list**, which is called **res.coda**. We exclude the 7th column of each chain, because this column corresponds to the first diagonal element of the covariance matrix which is always equal to 1. The following command computes the Gelman-Rubin statistic from these three chains,

```

gelman.diag(res.coda, transform = TRUE)

```

where **transform = TRUE** applies log or logit transformation as appropriate to improve the normality of each of the marginal distributions. Gelman *et al.* (2004) suggest computing the statistic for each

²If you have not used the coda package before, you must install it. At the R prompt, type `install.packages("coda")`.

scalar estimate of interest, and to continue to run the chains until the statistics are all less than 1.1. Inference is then based on the Monte Carlo sample obtained by combining the second half of each of the chains. The output of the coda command lists the value and a 97.5% upper limit of the Gelman-Rubin statistic for each parameter.

Potential scale reduction factors:

	Point est.	97.5% quantile
(Intercept):EraPlus	1.01	1.02
(Intercept):Solo	1.03	1.08
(Intercept):Surf	1.01	1.05
(Intercept):Tide	1.01	1.02
(Intercept):Wisk	1.01	1.04
price	1.01	1.02
EraPlus:Solo	1.02	1.03
EraPlus:Surf	1.02	1.04
EraPlus:Tide	1.03	1.08
EraPlus:Wisk	1.04	1.13
Solo:Solo	1.01	1.04
Solo:Surf	1.01	1.02
Solo:Tide	1.02	1.07
Solo:Wisk	1.00	1.00
Surf:Surf	1.00	1.00
Surf:Tide	1.01	1.04
Surf:Wisk	1.02	1.06
Tide:Tide	1.02	1.06
Tide:Wisk	1.02	1.08
Wisk:Wisk	1.01	1.04

Multivariate psrf

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The Gelman-Rubin statistics are all less than 1.1, suggesting satisfactory convergence has been achieved. (Note that the 97.5conservative user might want to obtain a set of longer Markov chains and recompute the Gelman-Rubin statistics.) It may also be useful to examine the change in the value of the Gelman-Rubin statistic over the iterations. The following commands produce a graphical summary of the progression of the statistics over iterations.

```
gelman.plot(res.coda, transform = TRUE, ylim = c(1,1.2))
```

where `ylim = c(1,1.2)` specifies the range of the vertical axis of the plot. The results appear in Figure 1, as a cumulative evaluation of the Gelman-Rubin statistic over iterations for nine selected

parameters. (Three coefficients appear in the first row; three covariance parameters appear in the second row; and three variance parameters appear in the third row.)

The coda package can also be used to produce univariate time-series plots of the three chains and univariate density estimate of the posterior distribution. The following commands create these graphs for the price coefficient.

```
res.coda <- mcmc.list(chain1=mcmc(res1$param[25001:50000, "price"], start=25001),
                     chain2=mcmc(res2$param[25001:50000, "price"], start=25001),
                     chain3=mcmc(res3$param[25001:50000, "price"], start=25001))
plot(res.coda, ylab = "price coefficient")
```

Figure 2 presents the resulting plots. The left panel overlays the time-series plot for each chain with a different color representing each chain. The right panel shows the kernel-smoothed density estimate of the posterior distribution. One can also apply an array of other functions to `res.coda`. See the coda homepage, <http://www-fis.iarc.fr/coda>, for details.

3.3 Final Analysis and Conclusions

In the final analysis, we combine the second half of each of the three chains. This is accomplished using the following command that saves the last 25,000 draws from each chain as an `mcmc` object and combines the `mcmc` objects into a list,

```
res.coda <- mcmc.list(chain1=mcmc(res1$param[25001:50000,-7], start=25001),
                     chain2=mcmc(res2$param[25001:50000,-7], start=25001),
                     chain3=mcmc(res3$param[25001:50000,-7], start=25001))
summary(res.coda)
```

The second command produces the following summary of the posterior distribution for each parameter based on the combined Monte Carlo sample.

```
Iterations = 25001:50000
Thinning interval = 1
Number of chains = 3
Sample size per chain = 25000
```

1. Empirical mean and standard deviation for each variable,
plus standard error of the mean:

	Mean	SD	Naive SE	Time-series SE
(Intercept):EraPlus	2.5398	0.2300	0.0008400	0.014332
(Intercept):Solo	1.7218	0.2227	0.0008131	0.012972

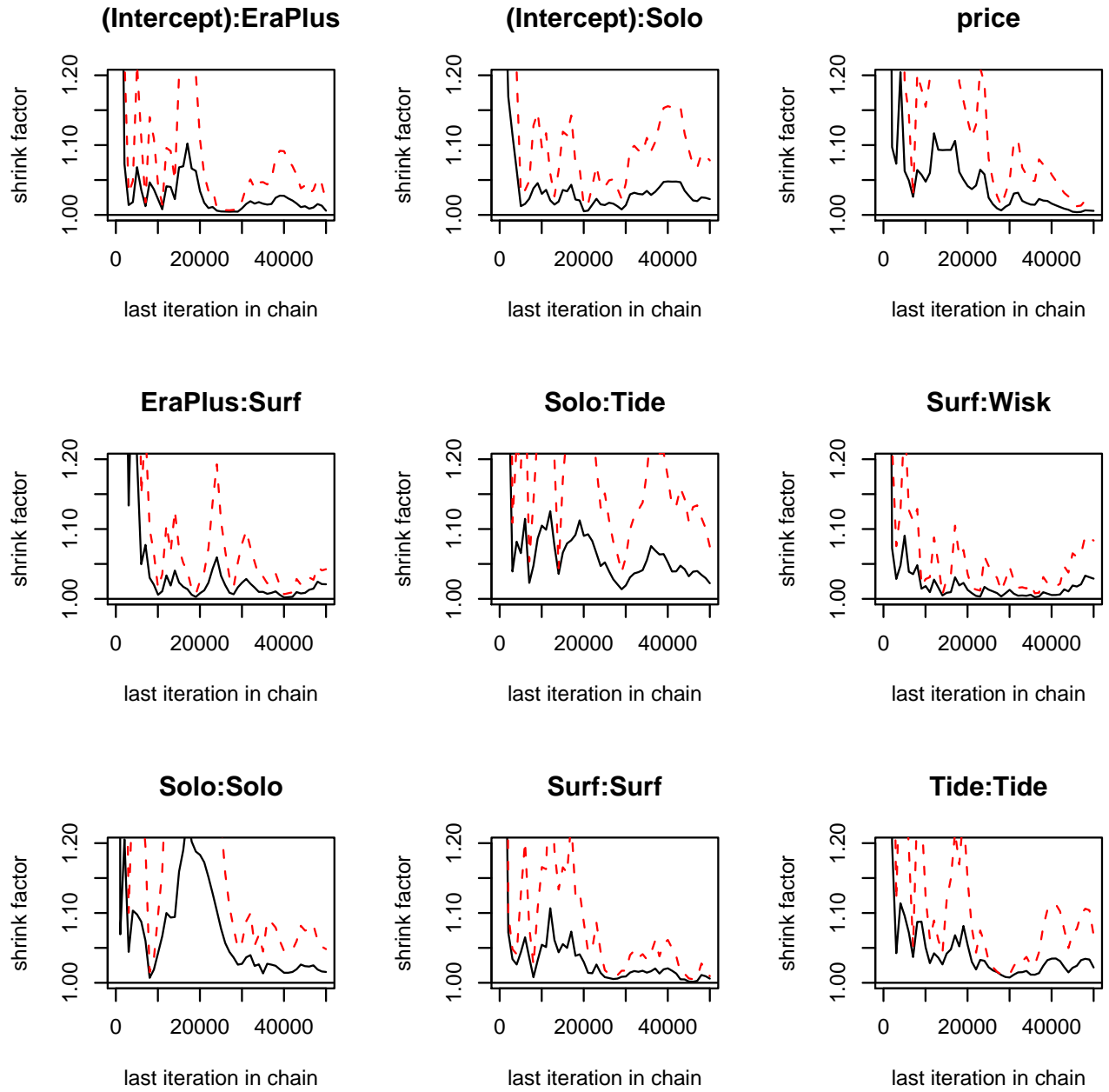


Figure 1: The Gelman-Rubin Statistic Computed with Three Independent Markov Chains for Selected Parameters in the Detergent Example. The first row represents three coefficients, the second row represents three covariances, and the third row represents three variance parameters.

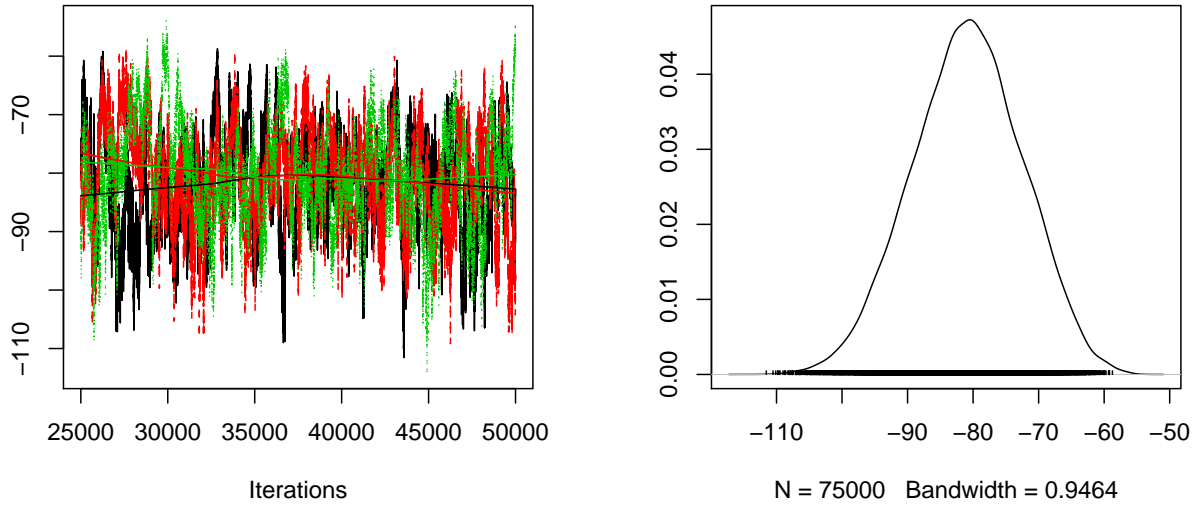


Figure 2: Time-series Plot of Three Independent Markov Chains (Left Panel) and A Density Estimate of the Posterior Distribution of the Price Coefficient (Right Panel). The time-series plot overlays the three chains, each in a different color. A lowess smoothed line is also plotted for each of the three chains. The density estimate is based on all three chains.

(Intercept):Surf	1.5634	0.1663	0.0006072	0.010462
(Intercept):Tide	2.6971	0.2374	0.0008670	0.015153
(Intercept):Wisk	1.6155	0.1594	0.0005822	0.010221
price	-80.9097	8.4292	0.0307791	0.556483
EraPlus:Solo	0.8674	0.2954	0.0010787	0.021698
EraPlus:Surf	0.1226	0.1991	0.0007269	0.014043
EraPlus:Tide	0.2622	0.1525	0.0005568	0.009833
EraPlus:Wisk	0.9062	0.1912	0.0006982	0.012893
Solo:Solo	2.6179	0.7883	0.0028785	0.055837
Solo:Surf	0.5348	0.4307	0.0015728	0.030113
Solo:Tide	0.5570	0.3544	0.0012941	0.024548
Solo:Wisk	1.5442	0.4643	0.0016954	0.031574
Surf:Surf	1.6036	0.4758	0.0017374	0.031269
Surf:Tide	0.7689	0.2992	0.0010926	0.020253
Surf:Wisk	0.9949	0.3548	0.0012955	0.022963
Tide:Tide	1.2841	0.3660	0.0013364	0.024095
Tide:Wisk	1.0658	0.3147	0.0011492	0.020229
Wisk:Wisk	2.5801	0.5523	0.0020167	0.034974

2. Quantiles for each variable:

2.5% 25% 50% 75% 97.5%

(Intercept):EraPlus	2.09105	2.38514	2.5321	2.6926	3.0022
(Intercept):Solo	1.28315	1.57316	1.7219	1.8705	2.1639
(Intercept):Surf	1.24132	1.45272	1.5583	1.6701	1.9023
(Intercept):Tide	2.23562	2.53443	2.6886	2.8544	3.1721
(Intercept):Wisk	1.31120	1.50841	1.6104	1.7191	1.9429
price	-97.62406	-86.61736	-80.7783	-75.1013	-64.9720
EraPlus:Solo	0.32811	0.65755	0.8480	1.0694	1.4666
EraPlus:Surf	-0.24159	-0.01596	0.1131	0.2507	0.5491
EraPlus:Tide	-0.02109	0.16081	0.2571	0.3527	0.5957
EraPlus:Wisk	0.54089	0.77643	0.9035	1.0331	1.2917
Solo:Solo	1.37468	2.02720	2.5225	3.0985	4.4160
Solo:Surf	-0.31143	0.25493	0.5251	0.8180	1.3880
Solo:Tide	-0.05172	0.30518	0.5297	0.7740	1.3106
Solo:Wisk	0.74682	1.21192	1.5131	1.8380	2.5445
Surf:Surf	0.86883	1.25552	1.5377	1.8834	2.6935
Surf:Tide	0.30606	0.55218	0.7285	0.9413	1.4556
Surf:Wisk	0.40231	0.74907	0.9579	1.1957	1.8026
Tide:Tide	0.69841	1.02206	1.2396	1.4999	2.1100
Tide:Wisk	0.51732	0.84824	1.0411	1.2556	1.7579
Wisk:Wisk	1.60662	2.18760	2.5407	2.9238	3.7722

The output shows the mean, standard deviation, and various percentiles of the posterior distributions of the coefficients and the elements of the variance-covariance matrix. The base category is the detergent **All**. Separate intercepts are estimated for each detergent. The price coefficient is negative and highly statistically significant, agreeing with the standard economic expectation that consumers are less likely to buy more expensive goods.

MNP also allows one to calculate the posterior predictive probabilities of each alternative being most preferred given a particular value of the covariates. For example, one can calculate the posterior predictive probabilities using the covariate values of the first two observations by using the `predict()` command,

```
predict(res1, newdata = detergent[1:2,],
        newdraw = rbind(res1$param[25001:50000,],
                        res2$param[25001:50000,],
                        res3$param[25001:50000,]), type = "prob")
```

where `res1` is the output object from the `mnp()` command, and we set `newdata` to the first two observations of the detergent data set and `newdraw` to the combined draws from the second half of three chains. Setting `type = "prob"` causes the function `predict()` to return the posterior predictive probabilities. Moreover, a new `n.draws` option in `predict()` command allows one to compute the

uncertainty estimates about these predicted probabilities. It is also possible to return a Monte Carlo sample of the the alternative that is most preferred (`type = "choice"`), a Monte Carlo sample of the latent variables (`type = "latent"`), or a Monte Carlo sample of the preference-ordered alternatives (`type = "order"`). (Type `help(predict.mnp)` in R for more details about the `predict()` function in MNP.) The above command yields the following output,

```

           All   EraPlus   Solo      Surf      Tide      Wisk
[1,] 0.01281333 0.1946400 0.12292 0.46208000 0.1401733 0.06737333
[2,] 0.04649333 0.1262133 0.05996 0.03169333 0.3589867 0.37665333

```

The result indicates that the posterior predictive probability of purchasing **Surf** is the largest for households with covariates equal to those in the first household in the data set. Under the model, approximately 46% of such households will purchase **Surf**. On the other hand, **All** is the brand least likely to be purchased by these households. The households with covariates equal to the second household are most likely to buy **Wisk**. Also, they are almost equally likely to purchase **Tide**. (The posterior predictive probabilities of buying **Wisk** and **Tide** are both around 0.35)

4 Example 2: Voters' Preference of Political Parties

Our second example illustrates how to fit the multinomial probit model with ordered preferences (see Section 2.2).

4.1 Preliminaries

We analyze a survey dataset describing the preferences of individual voters in Japan among the political parties. Political scientists may be interested in using the gender, age and education level of voters to predict their party preferences (Type `help(japan)` in R for details about the dataset). The outcome variable is a vector of relative preferences for each of the four parties, i.e., $p = 4$. Each of 418 voters is asked to give a score between 0 and 100 to each party. For example, the first voter in the dataset has the following preferences.

```

LDP NFP SKG JCP
80  75  80   0

```

That is, this voter prefers **LDP** and **SKG** to **NFP** and **JCP**, and between the latter two, she prefers **NFP** to **JCP**. Although **LDP** and **SKG** have the same preference, we do not constrain the estimated preferences to be the same for these two alternatives. Under the Gaussian random utility model, the probability

that the two alternatives having exactly the same preferences is zero. Therefore, inequality constraints are respected, but equality constraints are not.

Furthermore, we only preserve the ranking, not the relative numerical values. Therefore, the following coding of the variables, for our purposes, is equivalent to that given above,

```
LDP NFP SKG JCP
  3   2   3   1
```

Finally, it is possible to have non-response for one of the categories; e.g., no candidate from a particular party may run in a certain district. If $NFP = NA$, we have no information about the relative ranking of NFP.

```
LDP NFP SKG JCP
  3  NA   3   1
```

In this case, there is no constraint when estimating the preference for this alternative; only the inequality constraint, $(LDP, SKG) > JCP$, is imposed.

All three covariates – gender, education, and age of voters – are individual-specific variables rather than choice-specific ones. The model estimates three intercepts and 9 coefficients along with 6 parameters in the covariance matrix. The following commands fit the model,

```
data(japan)
res <- mnp(cbind(LDP, NFP, SKG, JCP) ~ gender + education + age, data = japan,
           n.draws = 10000, verbose = TRUE)
summary(res)
```

The first command loads the dataset, and the second command fits the model. The base category is JCP, which is the last column of the outcome matrix. The default prior distribution is used as in the previous example: an improper prior distribution for β and a diffuse prior distribution for Σ with $\nu = p = 4$ and $S = I$. 10,000 draws are obtained with no burnin or thinning. The final command summarizes the Monte Carlo sample and gives the following output,

```
Call:
mnp(formula = cbind(LDP, NFP, SKG, JCP) ~ gender + education + age,
     data = japan, n.draws = 10000, verbose = TRUE)
```

Coefficients:

```
      mean  std.dev.    2.5% 97.5%
```


(Intercept):LDP	0.615184	0.517157	-0.386151	1.61
(Intercept):NFP	0.689753	0.568109	-0.419521	1.79
(Intercept):SKG	0.133961	0.455960	-0.758883	1.02
gendermale:LDP	0.099748	0.152323	-0.194786	0.40
gendermale:NFP	0.216824	0.166103	-0.102108	0.54
gendermale:SKG	0.132661	0.134605	-0.127145	0.40
education:LDP	-0.107038	0.074792	-0.253483	0.04
education:NFP	-0.107222	0.082324	-0.270127	0.05
education:SKG	-0.003728	0.066429	-0.132496	0.13
age:LDP	0.013518	0.006122	0.001492	0.03
age:NFP	0.006948	0.006783	-0.006572	0.02
age:SKG	0.009653	0.005431	-0.000812	0.02

Covariances:

	mean	std.dev.	2.5%	97.5%
LDP:LDP	1.0000	0.0000	1.0000	1.00
LDP:NFP	1.0502	0.0585	0.9373	1.16
LDP:SKG	0.7070	0.0622	0.5822	0.82
NFP:NFP	1.4068	0.1359	1.1682	1.70
NFP:SKG	0.7452	0.0864	0.5800	0.91
SKG:SKG	0.6913	0.0874	0.5296	0.87

Base category: JCP

Number of alternatives: 4

Number of observations: 418

Number of stored MCMC draws: 10000

4.2 Convergence Diagnostics, Final Analysis, and Conclusions

In order to evaluate convergence of the MCMC sampler, we again obtain three independent Markov chains by running the `mnpc()` command three times with three sets of different starting values. We use starting values that are relatively dispersed given the preliminary analysis of the previous section. Note that when fitting the multinomial probit model with ordered preferences, the algorithm requires the starting values of the latent variable to respect the order constraints of equation (3). Therefore, the starting values of the parameters cannot be too far away from the posterior mode. The following commands fits the model with the default starting value and two sets of overdispersed starting values,

```
res1 <- mnpc(cbind(LDP, NFP, SKG, JCP) ~ gender + education + age, data = japan,
             n.draws = 50000, verbose = TRUE)
```

```
res2 <- mnpc(cbind(LDP, NFP, SKG, JCP) ~ gender + education + age, data = japan,
             coef.start = c(1, -1, 1, -1, 1, -1, 1, -1, 1, -1, -1),
```

```

cov.start = matrix(0.5, ncol=3, nrow=3) + diag(0.5, 3),
n.draws = 50000, verbose = TRUE)

res3 <- mnp(cbind(LDP, NFP, SKG, JCP) ~ gender + education + age, data = japan,
  coef.start = c(-1, 1, -1, 1, -1, 1, -1, 1, -1, 1, -1, 1),
  cov.start = matrix(0.9, ncol=3, nrow=3) + diag(0.1, 3),
  n.draws = 50000, verbose = TRUE)

```

We follow the commands used in Section 3.2 and compute the Gelman-Rubin statistic for each parameter. Upon examination of the resulting statistics, we determined that satisfactory convergence has been achieved. For example, the value of the Gelman-Rubin statistic is less than 1.01 for all the parameters. Hence, we base our final analysis on the combined draws from the second half of the three chains (i.e., a total of 75,000 draws using 25,000 draws from each chain). Posterior summaries can be obtained using the coda package as before,

```

Iterations = 25001:50000
Thinning interval = 1
Number of chains = 3
Sample size per chain = 25000

```

1. Empirical mean and standard deviation for each variable,
plus standard error of the mean:

	Mean	SD	Naive SE	Time-series SE
(Intercept):LDP	0.60167	0.51421	1.88e-03	8.05e-03
(Intercept):NFP	0.68294	0.56867	2.08e-03	7.95e-03
(Intercept):SKG	0.12480	0.45680	1.67e-03	7.25e-03
gendermale:LDP	0.10668	0.15448	5.64e-04	2.95e-03
gendermale:NFP	0.22240	0.16983	6.20e-04	2.91e-03
gendermale:SKG	0.13897	0.13753	5.02e-04	2.70e-03
education:LDP	-0.10517	0.07643	2.79e-04	1.35e-03
education:NFP	-0.10634	0.08448	3.08e-04	1.28e-03
education:SKG	-0.00258	0.06766	2.47e-04	1.18e-03
age:LDP	0.01361	0.00617	2.25e-05	9.90e-05
age:NFP	0.00698	0.00680	2.48e-05	1.01e-04
age:SKG	0.00972	0.00547	2.00e-05	9.13e-05
LDP:NFP	1.05535	0.05508	2.01e-04	1.15e-03
LDP:SKG	0.71199	0.06125	2.24e-04	1.59e-03
NFP:NFP	1.41860	0.13540	4.94e-04	2.45e-03
NFP:SKG	0.75391	0.08262	3.02e-04	2.12e-03
SKG:SKG	0.70007	0.08488	3.10e-04	2.16e-03

2. Quantiles for each variable:

	2.5%	25%	50%	75%	97.5%
(Intercept):LDP	-0.405757	0.25198	0.60033	0.9476	1.6172
(Intercept):NFP	-0.428421	0.30016	0.68058	1.0657	1.7981
(Intercept):SKG	-0.769018	-0.18476	0.12335	0.4303	1.0258
gendermale:LDP	-0.197199	0.00328	0.10643	0.2105	0.4096
gendermale:NFP	-0.110730	0.10856	0.22135	0.3361	0.5566
gendermale:SKG	-0.131661	0.04702	0.13905	0.2307	0.4096
education:LDP	-0.254631	-0.15718	-0.10519	-0.0533	0.0447
education:NFP	-0.271657	-0.16329	-0.10654	-0.0496	0.0595
education:SKG	-0.135829	-0.04833	-0.00248	0.0429	0.1306
age:LDP	0.001591	0.00941	0.01361	0.0177	0.0257
age:NFP	-0.006336	0.00240	0.00697	0.0115	0.0203
age:SKG	-0.000947	0.00603	0.00967	0.0134	0.0206
LDP:NFP	0.944577	1.01919	1.05564	1.0924	1.1623
LDP:SKG	0.587135	0.67120	0.71364	0.7544	0.8266
NFP:NFP	1.181667	1.32454	1.40803	1.5028	1.7125
NFP:SKG	0.590798	0.69778	0.75463	0.8104	0.9125
SKG:SKG	0.538858	0.64219	0.69806	0.7564	0.8711

Here, one of the findings is that older voters tend to prefer LDP as indicated by the statistically significant positive age coefficient for LDP. This is consistent with the conventional wisdom of Japanese politics that the stronghold of LDP is elderly voters.

To further investigate the marginal effect of age, we calculate the posterior predictive probabilities of party preference under two scenarios. First, we choose the 10th individual in the survey data and compute the predictive probability that a voter with this set of covariates prefers each of the parties. This can be accomplished by the following commands,

```
japan10a <- japan[10,]
predict(res1, newdata = japan10a,
        newdraw = rbind(res1$param[25001:50000,],
                        res2$param[25001:50000,],
                        res3$param[25001:50000,]), type = "prob")
```

where the first command extracts the 10th observation from the Japan data, and the second command computes the predictive probabilities. Note that this individual has the following attributes,

```
gender education age
male          4   50
```

The resulting posterior predictive probabilities of being the most preferred party are,

```
      JCP      LDP      NFP      SKG
[1,] 0.107707 0.359267 0.324613 0.208413
```

The result indicates that under the model, we should expect 36% of voters with these covariates to prefer LDP, 32% to prefer NFP, 21% to prefer SKG, and 11% to prefer JCP. Next, we change the value of the age variable of this voter from 50 to 75, while holding the other variables constant. We then recompute the posterior predictive probabilities and examine how they change. This can be accomplished using the following commands,

```
japan10b <- japan10a
japan10b[,"age"] <- 75
predict(res1, newdata = japan10b,
        newdraw = rbind(res1$param[25001:50000,],
                        res2$param[25001:50000,],
                        res3$param[25001:50000,]), type = "prob")
```

where the first two commands recode the age variable for the voter and the second command makes the prediction. We obtain the following results,

	JCP	LDP	NFP	SKG
[1,]	0.06548	0.485467	0.249667	0.199387

The comparison of the two results shows that changing the value of the age variable from 50 to 75 increases the estimated posterior predictive probability of preferring LDP most and by more than 10 percentage points. Interestingly, the predictive probability for SKG changes very little, while that of NFP decreases significantly. This suggests that older voters tend to prefer LDP over NFP.

Appendices

A Installation

To use MNP, you must install the statistical software R (if it is not already installed) as well as the MNP package.

A.1 Windows systems

1. **Installing the latest version of R.** You may skip this step if the latest version of R is already installed on your system. If R is not installed on your system, go to the Comprehensive R Archive Network (CRAN) website (<http://cran.r-project.org>) and download the latest R installer for Windows. Double-click on the `.exe` file to launch the installer. We recommend that you accept the default installation options.
2. **Installing MNP.** Start R and type at the prompt:

```
install.packages("MNP")
```

A.2 Unix/Linux systems

1. **Installing the latest version of R.** You may skip this step if the latest version of R is already installed on your system. If R is not installed on your system, it may either be installed locally (e.g., in an individual user's `bin` directory) or globally (e.g., in the `/bin` directory). The latter requires administrative privileges. In either case, the latest release of R may be downloaded from the CRAN website (<http://cran.r-project.org>).
2. **Installing MNP.**

- (a) Create a local library directory if it does not exist already. Here, we use `~/Rlib/library` but you can specify a different directory. This directory can be created by typing the following command at the command prompt,

```
mkdir ~/Rlib ~/Rlib/library
```

- (b) Open the `~/.Renviron` file in your home directory (or create it if it does not exist) and add the following line,

```
R_LIBS="~/Rlib/library"
```

Alternatively, one can define the environmental variable. For example, add the following line to your Bourne shell startup file (e.g., `.bashrc` file if you are using a bash shell),

```
export R_LIBS="$HOME/Rlib/library"
```

(c) Start R and type at the prompt:

```
install.packages("MNP", lib=~ /Rlib/library/)
```

A.3 MacOS X systems

1. **Installing the latest version of R.** You may skip this step if the latest version of R is already installed on your system. If R is not installed on your system, you may download it from the CRAN website (<http://cran.r-project.org>).
2. **Installing MNP.** If you are using RAqua, typing the following command at the prompt,

```
install.packages("MNP")
```

will install MNP into the default local library directory, `~/Library/R/library`.

If you are using the command line R, then the installation of the MNP package can be done exactly in the same way as in Unix/Linux systems. You might want to set `R_LIBS` to `~/Library/R/library` so that the command line R and RAqua can share the same local library directory.

B What's New?

version	date	changes
2.6 – 4	6.09.13	a label error for latent variables (thanks to Sky Xue).
2.6 – 3	12.06.11	a minor change to eliminate warnings for R2.14-0.
2.6 – 2	10.27.10	a bug fixed in <code>predict()</code> (thanks to Lane Burgette).
2.6 – 1	09.23.09	trace restriction used as the default (thanks to Lane Burgette).
2.5 – 6	03.24.08	an important bug fix for the treatment of base categories (thanks to Ryan Black and Taeyoung Park)
2.5 – 5	08.01.07	returning X matrix from <code>predict()</code>
2.5 – 4	05.24.07	another bug fix in <code>predict()</code> (thanks to Andrew Owen).
2.5 – 3	12.04.06	a minor change.
2.5 – 2	11.30.06	a bug fix in <code>predict()</code>
2.5 – 1	11.21.06	rewrite <code>predict()</code> in C for speedup. Changed <code>moredraw</code> to <code>n.draws</code> .
2.4 – 2	10.17.06	bug fix in <code>moredraw</code> option (thanks to Ken Benoit).
2.4 – 1	10.05.06	added an option, <code>moredraw</code> , to <code>predict.mnp()</code> (thanks to Ken Benoit).
2.3 – 9	09.21.06	minor changes to be consistent with R version 2.4-0.
2.3 – 8	04.26.06	removing C warnings for Windows platform.
2.3 – 7	04.24.06	some very minor fixes to the C code.
2.3 – 6	01.11.06	print the number of estimated parameters in <code>summary()</code> (thanks to S.C. Wang)
2.3 – 5	12.27.05	-1 is allowed in <code>formula</code> (thanks to Daeyoung Koh)
2.3 – 4	09.06.05	added inverse CDF method option for truncated normal sampling
2.3 – 3	06.23.05	made Gibbs sampler slightly more efficient
2.3 – 2	06.02.05	minor changes to NAMESPACE and DESCRIPTOIN files
2.3 – 1	05.27.05	added <code>coef.mnp()</code> and <code>cov.mnp()</code> (thanks to Natasha Zharinova).
2.2 – 3	05.12.05	minor changes to the documentation; version published in <i>Journal of Statistical Software</i>
2.2 – 2	05.09.05	minor changes to the documentation
2.2 – 1	05.01.05	stable release for R 2.1.0; The observations with missing values in X will be deleted in <code>mnp()</code> and <code>predict()</code> (thanks to Natasha Zharinova).
2.1 – 2	03.22.05	added an option, <code>newdraw</code> , for <code>predict()</code> method
2.1 – 1	02.25.05	improved <code>predict()</code> method; documentation enhanced and edited
2.0 – 1	02.12.05	added <code>predict()</code> method (thanks to Xavier Gerard and Saleem Shaik)
1.4 – 1	12.16.04	improved error handling (thanks to Kjetil Halvorsen)
1.3 – 2	11.17.04	stable release for R 2.0.1; minor updates of the documentation
1.3 – 1	10.09.04	stable release for R 2.0.0; updating vector.c
1.2 – 1	09.26.04	optionally stores the latent variable (thanks to Colin McCulloch)
1.1 – 2	09.14.04	minor fix in <code>mnp()</code> (thanks to Ken Shultz)
1.1 – 1	08.28.04	major and minor changes: namespace implemented
1.0 – 4	07.14.04	users can interrupt the C process within R (thanks to Kevin Quinn)
1.0 – 3	06.30.04	bug fix in <code>xmatrix.mnp()</code> (thanks to Andrew Martin)
1.0 – 2	06.29.04	removed <code>p.alpha0</code> parameter
1.0 – 1	06.23.04	official release

version	date	changes
0.9 – 13	05.28.04	bug fix in <code>ymatrix.mnp()</code>
0.9 – 12	05.23.04	updating the documentation and help files
0.9 – 11	05.08.04	bug fix in <code>cXnames()</code> (thanks to Liming Wang)
0.9 – 10	05.03.04	first stable version; bug fix in labeling
0.9 – 9	05.02.04	bug fix in sampling of W ; added <code>summary.mnp()</code> and <code>print.summary.mnp()</code>
0.9 – 8	04.29.04	improving sampling of W , replace <code>printf()</code> with <code>Rprintf()</code>
0.9 – 7	04.27.04	missing data allowed for all models, varying choice sets allowed.
0.9 – 6	04.26.04	missing data allowed in the response variable for standard MNP; a major bug fixed for MoP (thanks to Shigeo Hirano)
0.9 – 5	04.25.04	improper prior handled by algorithm 1
0.9 – 4	04.21.04	bug fix in MoP, R 1.9.0 compatible, changes in <code>mprobit.R</code>
0.9 – 3	04.10.04	<code>rWish()</code> modified with an improved algorithm
0.9 – 2	03.22.04	first public beta version
0.9 – 1	03.20.04	first beta version

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