A Maximum Likelihood Mixture Approach for Multivariate Hypothesis Testing in case of Incomplete Data

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Abstract: Multivariate hypothesis testing becomes more and more necessary when data is in the process of changing from scalar and univariate format to multivariate format, especially financial and biological data is often constituted of n -dimension vectors. Likelihood ratio test is the best method that applies the test on mean of multivariate sample with known or unknown covariance matrix but it is impossible to use likelihood ratio test in case of incomplete data when the data incompleteness gets popular because of many reasons in reality. Therefore, this research proposes a new approach that gives an ability to apply likelihood ratio test into incomplete data. Instead of replacing missing values in incomplete sample by estimated values, this approach classifies incomplete sample into groups and each group is represented by a potential or partial distribution. All partial distributions are unified into a mixture model which is optimized via expectation maximization (EM) algorithm. Finally, likelihood ratio test is performed on mixture model instead of incomplete sample. This research provides a thorough description of proposed approach and mathematical proof that is necessary to such approach. The comparison of mixture model approach and filling missing values approach is also discussed in this research.

Key words: maximum likelihood, mixture model, multivariate hypothesis testing, incomplete data

1. Likelihood ratio test

Suppose data sample is n -dimension vector space X , which contains m observation vectors $X_1, X_2, \dots, X_m$ where $X_i = \{x_{i1}, x_{i2}, \dots, x_{in}\}$. Note that X_i is identically distributed random variable and it can be called observation, data point, or sample point. We conventionalize that upper-case letter denotes variable and lower-case letter denotes value or instance of variable, for example, x_i is the instance of variable X_i . We test on mean of normal distribution when variance known or unknown, so X_i (s) conforms $N(\mu, \Sigma)$ and the null hypothesis $H_0: \mu = \mu_0$ and H_1 : no constraint on μ . Let $L_0(\mu_0, \Sigma / X)$ and $L_1(\mu, \Sigma / X)$ be the likelihoods for

null hypothesis H_0 and alternative hypothesis H_1 , respectively.

$$\begin{aligned} L_0(\mu_0, \Sigma / X) &= \prod_{i=1}^m P(x_i | \Theta) \\ &= |2\pi\Sigma|^{-n/2} e^{-\frac{1}{2}\sum_{i=1}^m (x_i - \mu_0)^T \Sigma^{-1} (x_i - \mu_0)} \end{aligned}$$

$$\begin{aligned} L_1(\mu, \Sigma / X) &= \prod_{i=1}^m P(x_i | \Theta) \\ &= |2\pi\Sigma|^{-n/2} e^{-\frac{1}{2}\sum_{i=1}^m (x_i - \mu)^T \Sigma^{-1} (x_i - \mu)} \end{aligned}$$

(Where n is the number of dimensions of sample X)
We take the logarithm of likelihood functions so as to convert the repeated multiplication into repeated

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addition, so the log-likelihood function of X is [1, pp. 185-186]:

$$\begin{aligned}
 \text{Log}L_0(\mu_0, \Sigma|X) &= -\frac{n}{2}\log|2\pi\Sigma| \\
 &\quad -\frac{1}{2}\sum_{i=1}^m (x_i - \mu_0)^T \Sigma^{-1} (x_i - \mu_0) \\
 &= -\frac{n}{2}\log|2\pi\Sigma| - \frac{n}{2}\text{tr}(\Sigma^{-1}S) \\
 &\quad -\frac{n}{2}(\bar{x} - \mu_0)^T \Sigma^{-1} (\bar{x} - \mu_0) \\
 \text{Log}L_1(\mu, \Sigma|X) &= -\frac{n}{2}\log|2\pi\Sigma| \\
 &\quad -\frac{1}{2}\sum_{i=1}^m (x_i - \mu)^T \Sigma^{-1} (x_i - \mu) \\
 &= -\frac{n}{2}\log|2\pi\Sigma| - \frac{n}{2}\text{tr}(\Sigma^{-1}S) \\
 &\quad -\frac{n}{2}(\bar{x} - \mu)^T \Sigma^{-1} (\bar{x} - \mu)
 \end{aligned}$$

Where trace operator denoted $\text{tr}(A)$ is the sum of all elements that are on the diagonal of matrix A and $\bar{x} = \frac{1}{m}\sum_{i=1}^m x_i$ is sample mean and S is the sample covariance matrix.

$L_0(\mu_0, \Sigma | X)$ and $L_1(\mu, \Sigma | X)$ get maximal if and only if $\text{Log}L_0(\Theta | X)$ and $\text{Log}L_1(\Theta | X)$ get maximal. It is proved that $\text{Log}L_0(\mu_0, \Sigma | X)$ and $\text{Log}L_1(\mu, \Sigma | X)$ get maximal if and only if $\mu = \bar{x}$ and $\Sigma = S$ when $\mu = \bar{x}$ and $\Sigma = S$ are solutions of equation formed by setting first-order derivative with regard to μ and Σ to be zero.

$$\begin{aligned}
 &\left\{ \frac{\partial \left(-\frac{n}{2}\log|2\pi\Sigma| - \frac{n}{2}\text{tr}(\Sigma^{-1}S) - \frac{n}{2}(\bar{x} - \mu)^T \Sigma^{-1} (\bar{x} - \mu) \right)}{\partial \mu} = 0 \right. \\
 &\left. \frac{\partial \left(-\frac{n}{2}\log|2\pi\Sigma| - \frac{n}{2}\text{tr}(\Sigma^{-1}S) - \frac{n}{2}(\bar{x} - \mu)^T \Sigma^{-1} (\bar{x} - \mu) \right)}{\partial \Sigma} = [0] \right\} \\
 &\Leftrightarrow \begin{cases} \mu = \bar{x} \\ \Sigma = S \end{cases}
 \end{aligned}$$

Let L_0^* and L_1^* be the maximal likelihoods for null hypothesis H_0 and alternative hypothesis H_1 . If we substitute $\mu = \bar{x}$ and $\Sigma = S$ to $L_0(\mu_0, \Sigma | X)$ and $L_1(\mu, \Sigma$

$| X)$, then $L_0(\mu_0, \Sigma | X)$ and $L_1(\mu, \Sigma | X)$ is totally determined.

$$\begin{aligned}
 L_0^* &= L_0(\mu_0, S | X) \\
 &= |2\pi S|^{-n/2} e^{-\frac{1}{2}\sum_{i=1}^m (x_i - \mu_0)^T S^{-1} (x_i - \mu_0)} \\
 L_1^* &= L_1(\bar{x}, S | X) \\
 &= |2\pi S|^{-n/2} e^{-\frac{1}{2}\sum_{i=1}^m (x_i - \bar{x})^T S^{-1} (x_i - \bar{x})}
 \end{aligned}$$

The likelihood ratio R [1, pp. 184-192] is defined as the ratio of the maximum likelihood of null hypothesis to the maximum likelihood of alternative hypothesis.

$$R = \frac{L_0^*(X)}{L_1^*(X)}$$

It is proved that $-2\log(R)$ is approximate to chi-square distribution χ^2 with n degrees of freedom when Σ is known; so H_0 is rejected in favor of H_1 if $-2\log(R) > \chi_{\alpha, n}^2$ with significant level α . This introduction is a brief principle of likelihood ration test. In general, likelihood ration test is a very effective testing method because it simplifies the complexity of n -dimension data by transforming multivariate testing criterion into univariate testing criterion based on scalar likelihood ratio.

2. Mixture model test on incomplete data

Suppose data sample is n -dimension vector space, which contains m observation vectors $X_1, X_2, \dots, X_m$ where $X_i = \{x_{i1}, x_{i2}, \dots, x_{in}\}$. Thus, $X = \{X_1, X_2, \dots, X_m\}$ compose a matrix whose each row is observation X_i . In case of incomplete data, X is sparse matrix and observation X_i is not always complete vector when it can lack some components x_{ij} (s). Likelihood ration test cannot apply into incomplete sample as X because it is impossible to calculate statistics such as mean and variance in terms of incomplete sample. This research tries to overcome this drawback by discovering potential probability distributions under observations X_i (s) regardless of data incompleteness. Suppose we test on mean of normal distribution when variance known or unknown, so X_i (s) conforms $N(\mu, \Sigma)$ and the null hypothesis $H_0: \mu = \mu_0$ is in favor of alternative

hypothesis H_1 : no constraint on μ . Based on such potential distributions, the maximum likelihood of these hypotheses is determined.

Firstly, we estimate the number of potential probability distributions under observations X_i (s). Observations are classified into k classes following two conditions below.

1. Class c_1 represents observations whose components x_{ij} (s) are completed. Note that class c_1 may not exist.
2. Classes $c_2, c_3, \dots, c_k$ represent observations lacking the same components x_{ij} (s). For example, we have four observations $X_1 = \{x_{11}=1, x_{12}=2, x_{13}(\text{empty}), x_{14}(\text{empty})\}$, $X_2 = \{x_{21}=2, x_{22}=3, x_{23}(\text{empty}), x_{24}(\text{empty})\}$, $X_3 = \{x_{31}(\text{empty}), x_{32}(\text{empty}), x_{33}=1, x_{34}=2\}$ and $X_4 = \{x_{41}(\text{empty}), x_{42}(\text{empty}), x_{43}=2, x_{44}=3\}$. Thus, X_1 and X_2 belong to the same class (class 1); X_3 and X_4 belong to the same class (class 2) according to this condition. Note that empty value is considered as missing value. Two or many classes can overlap together. For example, if $X_5 = \{x_{11}=3, x_{12}(\text{empty}), x_{13}(\text{empty}), x_{14}(\text{empty})\}$ then X_5 belongs to different class – class 3, thus, class 1 and class 3 are overlapped.

The number of potential probability distributions is initialized to be k . Note that k should be much smaller than the size m of sample. Note that potential probability distribution is also called partial probability distribution. Let p_i be the potential probability distributions corresponding to class k . Suppose p_i conforms normal distribution $N(\mu_i, \Sigma_i)$ with mean μ_i and variance Σ_i . The probabilistic mixture model [2, p. 3] is defined as below.

$$P(x_i|\Theta) = \sum_{j=1}^k \alpha_j p_j(x_i|\theta_j) \quad (1)$$

Where p_j is the potential distribution and x_i is instance of variable X_i . Let $\Theta = \{\alpha_1, \alpha_2, \dots, \alpha_k, \theta_1, \theta_2, \dots, \theta_k\}$ and $\theta_j = \{\mu_j, \Sigma_j\}$ be probabilistic parameters of sample and potential distribution p_j , respectively. Equation (1)

indicates that the distribution of data point x_i is constituted of potential (or partial) distributions p_j (s). Each potential distribution p_j is weighted by the weight α_j such that $\sum_{j=1}^k \alpha_j = 1$. The weight α_j is the probability of p_j if we consider p_j as random variable. The weights α_j (s) are learned and updated from sample, which will be discussed later. The likelihood function of X is:

$$L(\Theta|X) = \prod_{i=1}^m P(x_i|\Theta) = \prod_{i=1}^m \sum_{j=1}^k \alpha_j p_j(x_i|\theta_j)$$

We take the logarithm of likelihood function so as to convert the repeated multiplication into repeated addition, so the log-likelihood function of X is [2, p. 3]:

$$\begin{aligned} \text{Log}L(\Theta|X) &= \log(L(\Theta|X)) \\ &= \sum_{i=1}^m \log\left(\sum_{j=1}^k \alpha_j p_j(x_i|\theta_j)\right) \end{aligned}$$

Let $Y_1, Y_2, \dots, Y_m$ be variables indicating that data point X_i comes from which potential distribution. The value of each Y_i ranges in $\{1, 2, 3, \dots, m\}$. Concretely, if $Y_i = y_i$ then data point X_i conforms distribution p_{y_i} . When $X = \{X_1, X_2, \dots, X_m\}$ is incomplete data, $Y = \{Y_1, Y_2, \dots, Y_m\}$ is observational data that let us exploit X . The probability of $Y_i = y_i$ is the prior probability of p_{y_i} which indicates that how weighted data point x_i comes from distribution p_{y_i} , so we have $P(y_i) = \alpha_{y_i}$. Similarly, the conditional probability of data point x_i given y_i is the partial probability p_j given x_i , so we have $P(x_i / y_i) = p_{y_i}(x_i|\theta_{y_i})$. Let (X, Y) be the complete data, the log-likelihood function is re-written as below [2, p. 3].

$$\begin{aligned} \text{Log}L(\Theta|X, Y) &= \log(L(\Theta|X, Y)) \\ &= \sum_{i=1}^m \log(P(x_i|y_i)P(y_i)) \end{aligned} \quad (2)$$

$$= \sum_{i=1}^m \log(\alpha_{y_i} p_{y_i}(x_i|\theta_{y_i}))$$

Our goal is to find out the optimal parameter $\Theta^* = \{\alpha_1^*, \alpha_2^*, \dots, \alpha_k^*, \theta_1^*, \theta_2^*, \dots, \theta_k^*\}$ that maximizes the log-likelihood function in (2). Expectation maximization (EM) algorithm being the iterative process is applied in order to find out Θ^* . Let $\Theta^t = \{\alpha_1^t, \alpha_2^t, \dots, \alpha_k^t, \theta_1^t, \theta_2^t, \dots, \theta_k^t\}$ be the optimal parameter at t^{th} iteration. Note that $\theta_j^t = \{\mu_j^t, \Sigma_j^t\}$ is the optimal parameter of partial probability p_j at t^{th} iteration. In general, starting with initial estimate Θ^0 , each iteration in EM algorithm has two steps [3, p. 8]:

- E-step: computing the conditional expectation based on the previous estimate Θ^t
 - M-step: finding out current estimate $\Theta^{t+1} = \Theta^*$ that maximizes such conditional expectation.
- Note that Θ^{t+1} is reserved for next iteration.

EM algorithm stops when it meets the terminating condition, for example, the difference of previous estimate Θ^t and current estimate Θ^{t+1} is smaller than some pre-defined threshold ε , namely, $|\Theta^{t+1} - \Theta^t| < \varepsilon$. In E-step, the conditional expectation $Q(\Theta, \Theta^t)$ is determined as below [2, p. 4].

$$\begin{aligned} Q(\Theta, \Theta^t) &= \sum_{y \in \Psi} \text{Log} L(\Theta | X, y) P(y | X, \Theta^t) \\ &= \sum_{y \in \Psi} \sum_{i=1}^m \log(\alpha_{y_i} p_{y_i}(x_i | \theta_{y_i})) P(y | X, \Theta^t) \end{aligned} \quad (3)$$

Note that $Q(\Theta, \Theta^t)$ is the function of variable Θ and value Θ^t is known estimate in previous iteration. $Q(\Theta, \Theta^t)$ sums over all possible instances of $Y = \{Y_1, Y_2, \dots, Y_m\}$ and so Ψ denotes all combinational values over Y . Now we need to specify the probability of y given X and Θ^t , $P(y | X, \Theta^t)$. Note that $y = \{y_1, y_2, \dots, y_m\}$ is instance of observation variable data $Y = \{Y_1, Y_2, \dots, Y_m\}$. Applying Bayesian rule, we have [2, p. 3]:

$$\begin{aligned} P(y_j | x_j, \Theta^t) &= \frac{P(y_j | \Theta^t) P(x_j | y_j, \Theta^t)}{\sum_{h=1}^m P(y_h | \Theta^t) P(x_h | y_h, \Theta^t)} \\ &= \frac{\alpha_{y_j}^t p_{y_j}(x_j | \theta_{y_j}^t)}{\sum_{h=1}^m \alpha_{y_h}^t p_{y_h}(x_h | \theta_{y_h}^t)} \end{aligned} \quad (4)$$

Suppose $y_1, y_2, \dots$ and y_m are mutually independent, the probability of y given X is following product [2, p. 4].

$$P(y | X, \Theta^t) = \prod_{j=1}^m P(y_j | x_j, \Theta^t)$$

Consequently, the conditional expectation $Q(\Theta, \Theta^t)$ is expended as below [2, p. 4].

$$\begin{aligned} Q(\Theta, \Theta^t) &= \sum_{y \in \Psi} \sum_{i=1}^m \log(\alpha_{y_i} p_{y_i}(x_i | \theta_{y_i})) \prod_{j=1}^m P(y_j | x_j, \Theta^t) \\ &= \sum_{y_1=1}^k \sum_{y_2=1}^k \dots \sum_{y_m=1}^k \sum_{i=1}^m \log(\alpha_{y_i} p_{y_i}(x_i | \theta_{y_i})) * \\ &\quad \prod_{j=1}^m P(y_j | x_j, \Theta^t) \end{aligned}$$

(because Ψ denotes all combinational values over Y)

$$\begin{aligned} &= \sum_{y_1=1}^k \sum_{y_2=1}^k \dots \sum_{y_m=1}^k \sum_{i=1}^m \sum_{c=1}^k \delta_{c, y_i} \log(\alpha_c p_c(x_i | \theta_c)) * \\ &\quad \prod_{j=1}^m P(y_j | x_j, \Theta^t) \end{aligned}$$

(where $\delta_{c, y_i} = 1$ if and only if $y_i = c$ and where $c \in \{1, 2, \dots, k\}$ represents classes of potential probabilities

$$\begin{aligned} & p_c) \\ &= \sum_{c=1}^k \sum_{i=1}^m \log(\alpha_c p_c(x_i | \theta_c)) \sum_{y_1=1}^k \sum_{y_2=1}^k \dots \sum_{y_m=1}^k \delta_{c, y_i} * \\ &\quad \prod_{j=1}^m P(y_j | x_j, \Theta^t) \end{aligned}$$

$$\begin{aligned} &= \sum_{c=1}^k \sum_{i=1}^m \log(\alpha_c p_c(x_i | \theta_c)) * \\ &\quad \sum_{y_1=1}^k \sum_{y_2=1}^k \dots \sum_{y_m=1}^k \delta_{c, y_i} P(y_i | x_i, \Theta^t) \prod_{j=1, j \neq i}^m P(y_j | x_j, \Theta^t) \end{aligned}$$

$$\begin{aligned}
 &= \sum_{c=1}^k \sum_{i=1}^m \log(\alpha_c p_c(x_i | \theta_c)) P(y_i = c | x_i) * \\
 &\quad \sum_{y_1=1}^k \dots \sum_{y_{i-1}=1}^k \sum_{y_{i+1}=1}^k \dots \sum_{y_m=1}^k \prod_{j=1, j \neq i}^m P(y_j | x_j, \theta^t) \\
 &= \sum_{c=1}^k \sum_{i=1}^m \log(\alpha_c p_c(x_i | \theta_c)) P(y_i = c | x_i) * \\
 &\quad \prod_{j=1, j \neq i}^m \sum_{y_j=1}^k P(y_j | x_j, \theta^t) \\
 &= \sum_{c=1}^k \sum_{i=1}^m \log(\alpha_c p_c(x_i | \theta_c)) P(y_i = c | x_i) \quad (5) \\
 &\quad \left(\text{due to } \sum_{y_j=1}^k P(y_j | x_j, \theta^t) = 1 \right)
 \end{aligned}$$

In general, we have:

$$\begin{aligned}
 &Q(\Theta, \Theta^t) \\
 &= \sum_{c=1}^k \sum_{i=1}^m \log(\alpha_c p_c(x_i | \theta_c)) P(y_i = c | x_i) \quad (5)
 \end{aligned}$$

Note that $P(y_i = c | x_i)$ is computed following equation (4). Because equation (5) has two parameters α_c and $\theta_c = \{\mu_c, \Sigma_c\}$, the conditional expectation $Q(\Theta, \Theta^t)$ is split into two parts as below.

$$\begin{aligned}
 &Q(\Theta, \Theta^t) \\
 &= \sum_{c=1}^k \sum_{i=1}^m \log(\alpha_c) P(y_i = c | x_i) \\
 &+ \sum_{c=1}^k \sum_{i=1}^m \log(p_c(x_i | \theta_c)) P(y_i = c | x_i) \quad (6)
 \end{aligned}$$

Let

$$\begin{aligned}
 G(\alpha_c) &= \sum_{i=1}^m \log(\alpha_c) P(y_i = c | x_i) \\
 H(\theta_c) &= \sum_{i=1}^m \log(p_c(x_i | \theta_c)) P(y_i = c | x_i)
 \end{aligned}$$

It is easy to recognize that both $G(\alpha_c)$ and $H(\theta_c)$ are less than or equal to 0 because of $0 \leq \alpha_c, p_c(x_i | \theta_c) \leq 1$. Hence, the expectation $Q(\Theta, \Theta^t)$ is maximal if and only if both $G(\alpha_c)$ and $H(\theta_c)$ are minimal. In other words, we find out extreme points α_c^* and $\theta_c^* = \{\mu_c^*, \Sigma_c^*\}$ that minimize both $G(\alpha_c)$ and $H(\mu_c, \Sigma_c)$ when $Q(\Theta, \Theta^t)$ is considered as function of variables α_c and $\theta_c = \{\mu_c, \Sigma_c\}$.

Applying Lagrange function into $G(\alpha_c)$ with constraint $\sum_{c=1}^k \alpha_c = 1$, extreme point α_c^* is the solution of the equation formed by setting first-order derivative of sum of $G(\alpha_c)$ and Lagrange constraint to be zero.

$$\frac{\partial}{\partial \alpha_c} \left(G(\alpha_c) + \lambda \left(\sum_{c=1}^k \alpha_c - 1 \right) \right) = 0$$

(where λ is Lagrange multiplier)

$$\begin{aligned}
 &\Leftrightarrow \sum_{i=1}^m \frac{k}{\alpha_c} P(y_i = c | x_i) + k\lambda = 0 \\
 &\Leftrightarrow \sum_{i=1}^m P(y_i = c | x_i) + \alpha_c \lambda = 0
 \end{aligned}$$

We have equation (7) to determine λ .

$$\sum_{i=1}^m P(y_i = c | x_i) + \alpha_c \lambda = 0 \quad (7)$$

Summing (7) over k classes $\{1, 2, \dots, k\}$, we have [2, p. 5]:

$$\begin{aligned}
 &\sum_{i=1}^m \sum_{c=1}^k P(y_i = c | x_i) + \lambda \sum_{c=1}^k \alpha_c = 0 \\
 &\Leftrightarrow m + \lambda = 0
 \end{aligned}$$

$$\left(\text{due to } \sum_{c=1}^k P(y_i = c | x_i) = 1 \text{ and } \sum_{c=1}^k \alpha_c = 1 \right)$$

$$\Leftrightarrow \lambda = -m$$

Substituting $\lambda = -m$ into equation (7), extreme point α_c^* is totally determined.

$$\alpha_c^* = \frac{1}{m} \sum_{i=1}^m P(y_i = c | x_i)$$

Where $P(y_i = c | x_i)$ is calculated following equation (4). Now we find out another extreme point $\theta_c^* = \{\mu_c^*, \Sigma_c^*\}$. Suppose potential distribution $p_c(x_i | \theta_c)$ is normal, it is expended as below.

$$p_c(x_i | \theta_c) = |2\pi\Sigma_c|^{-\frac{1}{2}} e^{-\frac{1}{2}(x_i - \mu_c)^T \Sigma_c^{-1} (x_i - \mu_c)}$$

It implies that

$$H(\mu_c, \Sigma_c) = \sum_{i=1}^m \left(-\frac{n}{2} \log(2\pi) - \frac{1}{2} \log|\Sigma_c| - \frac{1}{2} (x_i - \mu_c)^T \Sigma_c^{-1} (x_i - \mu_c) \right) P(y_i = c | x_i)$$

(where n is the dimension of sample space X)

The first-order partial derivative of $H(\mu_c, \Sigma_c)$ with respect to μ_c is [4, p. 35]:

$$\begin{aligned} \frac{\partial H(\mu_c, \Sigma_c)}{\partial \mu_c} &= \sum_{i=1}^m 2\Sigma_c^{-1} (x_i - \mu_c) P(y_i = c | x_i) \\ &\left(\text{due to } \frac{\partial (x_i - \mu_c)^T \Sigma_c^{-1} (x_i - \mu_c)}{\partial \mu_c} = 2\Sigma_c^{-1} (x_i - \mu_c) \text{ when } \Sigma_c \text{ is symmetric} \right) \end{aligned}$$

The optimal μ_c^* maximizing $H(\mu_c, \Sigma_c)$ is the solution of equation created by setting partial derivatives of $H(\mu_c, \Sigma_c)$ with regard to mean μ_c to be zero. Note that $\emptyset$ denotes zero vector $(0, 0, \dots, 0)$.

$$\begin{aligned} \frac{\partial H(\mu_c, \Sigma_c)}{\partial \mu_c} &= \emptyset \\ \Leftrightarrow \sum_{i=1}^m 2\Sigma_c^{-1} (x_i - \mu_c) P(y_i = c | x_i) &= \emptyset \\ \Leftrightarrow \sum_{i=1}^m (x_i - \mu_c) P(y_i = c | x_i) &= \emptyset \end{aligned}$$

$$\Leftrightarrow \mu_c^* = \frac{\sum_{i=1}^m x_i P(y_i = c | x_i)}{\sum_{i=1}^m P(y_i = c | x_i)}$$

The first-order partial derivative of $H(\mu_c, \Sigma_c)$ with respect to Σ_c is:

$$\begin{aligned} \frac{\partial H(\mu_c, \Sigma_c)}{\partial \Sigma_c} &= \sum_{i=1}^n \left(-\frac{1}{2} \Sigma_c^{-1} + \frac{1}{2} \Sigma_c^{-1} (x_i - \mu_c)(x_i - \mu_c)^T \Sigma_c^{-1} \right) P(y_i = c | x_i) \end{aligned}$$

Due to:

$$\frac{\partial \log(|\Sigma_c|)}{\partial \Sigma_c} = \Sigma_c^{-1}$$

And

$$\begin{aligned} \frac{\partial (x_i - \mu)^T \Sigma_c^{-1} (x_i - \mu)}{\partial \Sigma_c} &= \frac{\partial \text{tr}((x_i - \mu)(x_i - \mu)^T \Sigma_c^{-1})}{\partial \Sigma_c} \end{aligned}$$

Because author [2, p. 5] mentioned:

$(x_i - \mu)^T \Sigma_c^{-1} (x_i - \mu) = \text{tr}((x_i - \mu)(x_i - \mu)^T \Sigma_c^{-1})$
Where $\text{tr}(A)$ is trace operator which takes sum of diagonal elements of matrix $\text{tr}(A) = \sum_i a_{ii}$.

It implies [4, p. 45]

$$\begin{aligned} \frac{\partial (x_i - \mu)^T \Sigma_c^{-1} (x_i - \mu)}{\partial \Sigma_c} &= -\Sigma_c^{-1} (x_i - \mu)(x_i - \mu)^T \Sigma_c^{-1} \end{aligned}$$

Where Σ_c is symmetric and invertible matrix.

The optimal Σ_c^* maximizing $H(\mu_c, \Sigma_c)$ is the solution of equation created by setting partial derivatives of $H(\mu_c, \Sigma_c)$ with regard to mean Σ_c to zero.

Note that $[0]$ denotes zero matrix $\begin{bmatrix} 0 & \dots & 0 \\ \vdots & \ddots & \vdots \\ 0 & \dots & 0 \end{bmatrix}$, we

have:

$$\frac{\partial H(\mu_c, \Sigma_c)}{\partial \Sigma_c} = [0]$$

$$\Leftrightarrow \sum_{i=1}^m \left(-\frac{1}{2} \Sigma_c^{-1} + \frac{1}{2} \Sigma_c^{-1} (x_i - \mu_c)(x_i - \mu_c)^T \Sigma_c^{-1} \right) P(y_i = c | x_i) = [0]$$

$$\Leftrightarrow \sum_{i=1}^m (-\Sigma_c + (x_i - \mu_c)(x_i - \mu_c)^T) P(y_i = c | x_i) = [0]$$

$$\Leftrightarrow \sum_{i=1}^m ((x_i - \mu_c)(x_i - \mu_c)^T) P(y_i = c | x_i) - \Sigma_c \sum_{i=1}^m P(y_i = c | x_i) = [0]$$

$$\Leftrightarrow \Sigma_c^* = \frac{\sum_{i=1}^m (x_i - \mu_c)(x_i - \mu_c)^T P(y_i = c | x_i)}{\sum_{i=1}^m P(y_i = c | x_i)}$$

In general, the optimal parameters α_c^* and $\theta_c^* = \{\mu_c^*, \Sigma_c^*\}$ for each potential (partial) probability p_c form a following triple shown as equation (8). Note that $P(y_i = c | x_i)$ is computed following equation (4).

$$\left\{ \begin{array}{l} \alpha_c^* = \frac{1}{m} \sum_{i=1}^m P(y_i = c | x_i) \\ \mu_c^* = \frac{\sum_{i=1}^m x_i P(y_i = c | x_i)}{\sum_{i=1}^m P(y_i = c | x_i)} \\ \Sigma_c^* = \frac{\sum_{i=1}^m (x_i - \mu_c^*)(x_i - \mu_c^*)^T P(y_i = c | x_i)}{\sum_{i=1}^m P(y_i = c | x_i)} \end{array} \right. \quad (8)$$

Of course, we have k groups $(\alpha_1^*, \theta_1^*), (\alpha_2^*, \theta_2^*), \dots$ and (α_k^*, θ_k^*) like (8) and so the global optimal parameter $\Theta^* = \{\alpha_1^*, \alpha_2^*, \dots, \alpha_k^*, \theta_1^*, \theta_2^*, \dots, \theta_k^*\}$ in M-step of EM algorithm is totally specified. The basic idea is to divide the global optimal parameter Θ^* into k groups of partial parameters (α_j^*, θ_j^*) and find out such partial parameters in particular.

Back the test on mean of normal distribution when the null hypothesis $H_0: \mu = \mu_0$ is in flavor of alternative hypothesis H_1 : no constraint on μ . The likelihood ratio $R(X)$ is defined as the ratio of the maximum likelihood of null hypothesis to the maximum likelihood of alternative hypothesis.

$$R = \frac{L_0^*(X)}{L_1^*(X)}$$

Where $L_0^*(X)$ and $L_1^*(X)$ are maximum likelihoods of null hypothesis and alternative hypothesis, respectively.

This research proposes a 4-step testing process based on mixture model in order to test on mean of normal distribution in case of incomplete data.

1. Specifying k classes and k respective partial probabilities $p_c(x_c | \theta_c)$ with $c = \overline{1, k}$ and $\theta_c = \{\mu_c, \Sigma_c\}$. The weights α_c (s) of partial probabilities p_c (s) are initialized by the ratio of the number X_i (s) belonging to class c to m , the number of total X_i (s),

$$\alpha_c = \frac{\text{The number of } X_i(s) \text{ belonging to class } c}{m}$$

- a. Class c_1 represents observations whose components x_{ij} (s) are completed. Note that class c_1 may not exist.

- b. Classes $c_2, c_3, \dots, c_k$ represent observations lacking the same components x_{ij} (s).

2. Specifying the likelihood functions of null hypothesis and alternative hypothesis such as $L_0(X)$ and $L_1(X)$.

$$\text{a. } L_0(\Theta | X) = \prod_{i=1}^m P(x_i | \Theta) = \prod_{i=1}^m \sum_{c=1}^k \alpha_c p_c(x_i | \theta_c)$$

Where parameter $\theta_c = \{\mu_c, \Sigma_c\}$ is constant and is assigned by sample mean μ_0 and known covariance matrix Σ (or sample covariance matrix S).

$$\text{b. } L_1(\Theta | X) = \prod_{i=1}^m P(x_i | \Theta) = \prod_{i=1}^m \sum_{c=1}^k \alpha_c p_c(x_i | \theta_c).$$

3. Applying EM algorithm into find out optimal parameters α_c^* and $\theta_c^* = \{\mu_c^*, \Sigma_c^*\}$ for each potential (partial) probability p_c .

- a. Optimal parameters α_c^* with respect to null hypothesis: $\alpha_c^* = \frac{1}{m} \sum_{i=1}^m P(y_i = c | x_i)$. Note that $\theta_c = \{\mu_c, \Sigma_c\}$ is constant.

- b. Optimal parameters α_c^* and $\theta_c^* = \{\mu_c^*, \Sigma_c^*\}$ with respect to alternative hypothesis:

$$\alpha_c^* = \frac{1}{m} \sum_{i=1}^m P(y_i = c | x_i)$$

$$\mu_c^* = \frac{\sum_{i=1}^m x_i P(y_i = c | x_i)}{\sum_{i=1}^m P(y_i = c | x_i)}$$

$$\Sigma_c^* = \frac{\sum_{i=1}^m (x_i - \mu_c^*)(x_i - \mu_c^*)^T P(y_i = c | x_i)}{\sum_{i=1}^m P(y_i = c | x_i)}$$

4. Substituting α_c^* and $\theta_c^* = \{\mu_c^*, \Sigma_c^*\}$ into likelihood functions $L_0(X)$ and $L_1(X)$ so that the likelihood ratio is totally determined. It is proved that $-2\log(R)$ is approximate to chi-square distribution χ^2 with n degrees of freedom when population covariance Σ is known; so H_0 is rejected in favor of H_1 if $-2\log(R) > \chi^2_{\alpha, n}$ with significant level α .

Please pay attention to step 1 and step 3 because it is slightly complicated. Suppose data sample is n -dimension vector space X , which contains m observation vectors $X_1, X_2, \dots, X_m$ where $X_i = \{x_{i1}, x_{i2}, \dots, x_{in}\}$. Thus, $X = \{X_1, X_2, \dots, X_m\}$ compose a matrix whose each row is observation X_i . Suppose X_i (s) conforms $N(\mu, \Sigma)$. If class c is composed of u non-empty components $a_{c_1}, a_{c_2}, \dots, a_{c_u}$ where $c_u = \overline{1, n}$, then the mean μ_c contains only $c_1^{th}, c_2^{th}, \dots, c_u^{th}$ components which correspond with $c_1^{th}, c_2^{th}, \dots, c_u^{th}$ columns in matrix X . Similarly, the covariance matrix Σ_c contains only variances among $c_1^{th}, c_2^{th}, \dots, c_u^{th}$ components which correspond with $c_1^{th}, c_2^{th}, \dots, c_u^{th}$ columns in matrix X . All arithmetical operators in step 3 are performed based on such u non-empty components $a_{c_1}, a_{c_2}, \dots, a_{c_u}$. This important thing is the tip of this research. The mean μ_c in the likelihood function of null hypothesis is constant and is assigned by $c_1^{th}, c_2^{th}, \dots, c_u^{th}$ components of sample mean μ_0 . The covariance matrix Σ_c in the likelihood function of null hypothesis is constant and is assigned by $c_1^{th}, c_2^{th}, \dots, c_u^{th}$ components of population covariance Σ or sample covariance S in case of unknown Σ . It means that it is not necessary to computed the optimal parameters μ_c^* and Σ_c^* with respect to likelihood function of null hypothesis $L_0(X)$.

For example, sample X has four observations $X_1 = \{x_{11}=1, x_{12}=2, x_{13} \text{ (empty)}, x_{14} \text{ (empty)}\}$, $X_2 = \{x_{21}=2, x_{22}=3, x_{23} \text{ (empty)}, x_{24} \text{ (empty)}\}$, $X_3 = \{x_{31} \text{ (empty)}, x_{32} \text{ (empty)}, x_{33}=1, x_{34}=2\}$ and $X_4 = \{x_{41} \text{ (empty)}, x_{42} \text{ (empty)}, x_{43}=2, x_{44}=3\}$. These observations formed a 4x4 matrix shown in table 1.

X_1	$x_{11} = 1$	$x_{12} = 2$	$x_{13} = ?$	$x_{14} = ?$
X_2	$x_{21} = 2$	$x_{22} = 3$	$x_{23} = ?$	$x_{24} = ?$
X_3	$x_{31} = ?$	$x_{32} = ?$	$x_{33} = 1$	$x_{34} = 2$
X_4	$x_{41} = ?$	$x_{42} = ?$	$x_{43} = 2$	$x_{44} = 3$

Table 1. An example of incomplete sample X where question mark (?) denotes missing value (or empty value).

Suppose we test on mean of normal distribution and so X_i (s) conforms $N(\mu, \Sigma)$ and the null hypothesis $H_0: \mu = \mu_0 = (0, 0, 0, 0)^T$ and H_1 : no constraint on μ .

Suppose variance is known, $\Sigma = \begin{bmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \end{bmatrix}$.

Sample X is classified into two classes such as class 1 containing X_1, X_2 and class 2 containing X_3, X_4 . Let p_1 and p_2 are partial probabilities attaching to class 1 and class 2, respectively. Both p_1 and p_2 conform normal distribution, $p_1 \sim N(\mu_1, \Sigma_1)$ and $p_2 \sim N(\mu_2, \Sigma_2)$. Let $Y = \{Y_1, Y_2, Y_3, Y_4\}$ be the set of observations where Y_i indicates X_i belongs to which class (1 or 2). Because X_1, X_2 belong to class 1 and X_3, X_4 belong to class 2, we have $Y = \{Y_1 = 1, Y_2 = 1, Y_3 = 2, Y_4 = 2\}$, $p_1(x_1) = 0.5$, $p_1(x_2) = 0.5$, $p_1(x_3) = 0$, $p_1(x_4) = 0$, $p_2(x_1) = 0$, $p_2(x_2) = 0$, $p_2(x_3) = 0.5$ and $p_2(x_4) = 0.5$.

When class 1 lacks columns (components) 3 and 4 and relates only X_1 and X_2 , the mean μ_1 receives two first components of μ and the covariance Σ_1 containing variances between X_1 and X_2 is the sub-matrix of Σ . Similarly, the mean μ_2 receives two last components of μ and the covariance Σ_2 is the sub-matrix of Σ which contains variances between X_3 and X_4 . We have:

$$\mu_1^0 = \begin{bmatrix} 0 \\ 0 \end{bmatrix}, \Sigma_1^0 = \begin{bmatrix} 1 & 0 \\ 0 & 1 \end{bmatrix}, \mu_2^0 = \begin{bmatrix} 0 \\ 0 \end{bmatrix}, \Sigma_2^0 = \begin{bmatrix} 1 & 0 \\ 0 & 1 \end{bmatrix}$$

Let α_1 and α_2 be the weights of partial probabilities p_1 and p_2 , respectively. Hence, α_i is initialized as the number of X_i (s) belonging to class i . We have:

$$\alpha_1^0 = \frac{2}{4} = 0.5, \alpha_2^0 = \frac{2}{4} = 0.5$$

At the first iteration of EM algorithm, the probability of y given X denoted $P(y_i | x_i)$ is calculated according to equation (4), for example:

$$P(y_1 = 1 | x_1) = \frac{\alpha_{y_1}^0 p_{y_1}(x_1)}{P(x_i)} = \frac{\alpha_1^0 p_1(x_1)}{P(x_i)} = \frac{0.5 * 0.5}{\frac{1}{4}} = 1$$

In the similar way, we have:

- $P(y_1 = 1 | x_1) = 1, P(y_1 = 1 | x_2) = 1, P(y_1 = 1 | x_3) = 0, P(y_1 = 1 | x_4) = 0, P(y_1 = 2 | x_1) = 0, P(y_1 = 2 | x_2) = 0, P(y_1 = 2 | x_3) = 1, P(y_1 = 2 | x_4) = 1.$
- $P(y_2 = 1 | x_1) = 1, P(y_2 = 1 | x_2) = 1, P(y_2 = 1 | x_3) = 0, P(y_2 = 1 | x_4) = 0, P(y_2 = 2 | x_1) = 0, P(y_2 = 2 | x_2) = 0, P(y_2 = 2 | x_3) = 1, P(y_2 = 2 | x_4) = 1.$
- $P(y_3 = 1 | x_1) = 1, P(y_3 = 1 | x_2) = 1, P(y_3 = 1 | x_3) = 0, P(y_3 = 1 | x_4) = 0, P(y_3 = 2 | x_1) = 0, P(y_3 = 2 | x_2) = 0, P(y_3 = 2 | x_3) = 1, P(y_3 = 2 | x_4) = 1.$
- $P(y_4 = 1 | x_1) = 1, P(y_4 = 1 | x_2) = 1, P(y_4 = 1 | x_3) = 0, P(y_4 = 1 | x_4) = 0, P(y_4 = 2 | x_1) = 0, P(y_4 = 2 | x_2) = 0, P(y_4 = 2 | x_3) = 1, P(y_4 = 2 | x_4) = 1.$

Parameters $\mu_1, \Sigma_1, \mu_2, \Sigma_2, \alpha_1$ and α_2 are re-calculated according to equation (8).

$$\begin{aligned} \alpha_1^* &= \frac{1}{4} \sum_{i=1}^m P(y_i = 1 | x_i) \\ &= \frac{1}{4} (P(y_1 = 1 | x_1) + P(y_2 = 1 | x_2) \\ &\quad + P(y_3 = 1 | x_3) + P(y_4 = 1 | x_4)) \\ &= 0.5 \\ \alpha_2^* &= \frac{1}{4} \sum_{i=1}^m P(y_i = 2 | x_i) \\ &= \frac{1}{4} (P(y_1 = 2 | x_1) + P(y_2 = 2 | x_2) \\ &\quad + P(y_3 = 2 | x_3) + P(y_4 = 2 | x_4)) \\ &= 0.5 \end{aligned}$$

$$\mu_1^* = \frac{\sum_{i=1}^2 x_i P(y_i = 1 | x_i)}{\sum_{i=1}^2 P(y_i = 1 | x_i)} = \frac{\begin{bmatrix} 1 \\ 2 \end{bmatrix} 1 + \begin{bmatrix} 2 \\ 3 \end{bmatrix} 1}{1 + 1} = \begin{bmatrix} 1.5 \\ 2.5 \end{bmatrix}$$

$$\mu_2^* = \frac{\sum_{i=3}^4 x_i P(y_i = 2 | x_i)}{\sum_{i=3}^4 P(y_i = 2 | x_i)} = \frac{\begin{bmatrix} 1 \\ 2 \end{bmatrix} 1 + \begin{bmatrix} 2 \\ 3 \end{bmatrix} 1}{1 + 1} = \begin{bmatrix} 1.5 \\ 2.5 \end{bmatrix}$$

$$\begin{aligned} \Sigma_1^* &= \frac{\sum_{i=1}^2 (x_i - \begin{bmatrix} 1.5 \\ 2.5 \end{bmatrix}) (x_i - \begin{bmatrix} 1.5 \\ 2.5 \end{bmatrix})^T P(y_i = 1 | x_i)}{\sum_{i=1}^2 P(y_i = 1 | x_i)} \\ &= \begin{bmatrix} 0.25 & 0.25 \\ 0.25 & 0.25 \end{bmatrix} \end{aligned}$$

$$\begin{aligned} \Sigma_2^* &= \frac{\sum_{i=3}^4 (x_i - \begin{bmatrix} 1.5 \\ 2.5 \end{bmatrix}) (x_i - \begin{bmatrix} 1.5 \\ 2.5 \end{bmatrix})^T P(y_i = 2 | x_i)}{\sum_{i=3}^4 P(y_i = 2 | x_i)} \\ &= \begin{bmatrix} 0.25 & 0.25 \\ 0.25 & 0.25 \end{bmatrix} \end{aligned}$$

Where $\mu_1^*, \Sigma_1^*, \mu_2^*, \Sigma_2^*, \alpha_1^*$ and α_2^* are optimal parameters that maximizing log-likelihood function. Because the deviation between α_1^* and α_1^0 is zero and the deviation between α_2^* and α_2^0 is zero, algorithm is stopped at the first iteration. Let $R(X)$ be the likelihood ratio.

$$R = \frac{L_0^*(X)}{L_1^*(X)}$$

(where $L_0^*(X)$ and $L_1^*(X)$ are maximum likelihoods of null hypothesis and alternative hypothesis, respective)

$$\Leftrightarrow -2\log R = 2(\log L_1^* - \log L_0^*)$$

(where $\log L_0^*(X)$ and $\log L_1^*(X)$ are maximum likelihoods of null hypothesis and alternative hypothesis, respective)

$$\begin{aligned} \Leftrightarrow -2\log R &= 2 \left(\sum_{i=1}^m \log (\alpha_{y_i}^* p_{y_i}(x_i | \theta_{y_i})) \right. \\ &\quad \left. - \sum_{i=1}^m \log (\alpha_{y_i}^0 p_{y_i}(x_i | \theta_{y_i})) \right) \end{aligned}$$

$$\Leftrightarrow -2\log R = 0 \text{ (due to } \alpha_{y_i}^* = \alpha_{y_i}^0 = 0.5, \forall y_i)$$

Thus, hypothesis $H_0: \mu_0 = (0, 0, 0, 0)^T$ cannot be rejected in favor of H_1 : no constraint at significant level 0.05% because $-2\log R = 0 < 9.49 = \chi_{0.05,4}^2$.

3. Mixture model vs. filling missing values

Filling missing values method is to try to estimate missing values (or empty values) so as to transform incomplete data into complete data and after that, hypothesis testing is done on complete data as usual. We discuss some methods of filling missing values and compare them with mixture model. Suppose data sample is n -dimension vector space, which contains m observation vectors $X_1, X_2, \dots, X_m$ where $X_i = \{x_{i1}, x_{i2}, \dots, x_{in}\}$. Thus, $X = \{X_1, X_2, \dots, X_m\}$ composes a matrix whose each row is observation X_i . In case of incomplete data, X is sparse matrix and observation X_i is not always complete vector when it can lack some components x_{ij} (s). Table 2 is an example of sample X .

	v = 1	v = 2	v = 3	v = 4
u = 1	$x_{11} = 1$	$x_{12} = 2$	$x_{13} = ?$	$x_{14} = ?$
u = 2	$x_{21} = 2$	$x_{22} = 3$	$x_{23} = ?$	$x_{24} = ?$
u = 3	$x_{31} = ?$	$x_{32} = ?$	$x_{33} = 1$	$x_{34} = 2$
u = 4	$x_{41} = ?$	$x_{42} = ?$	$x_{43} = 2$	$x_{44} = 3$

Table 2. Incomplete sample where question mark (?) denotes missing value (or empty value), u denotes row index and v denotes column index.

In the easiest way, if each column is considered as random variable, the missing value will be estimated as the mean of column vector. This way is called average method.

$$x_{ij} = \frac{1}{K} \sum_k x_{kj}$$

(Where K is the number of non – empty values)

According to average method, we have $x_{31} = x_{41} = (1+2) / 2 = 1.5$, $x_{32} = x_{42} = (2+3) / 2 = 2.5$, $x_{13} = x_{23} = (1+2) / 2 = 1.5$, $x_{14} = x_{24} = (2+3) / 2 = 2.5$. The strong point of average method is easy to calculated mean value and its cost is low but it is based on the assumption that column is random variable but this thing is not totally exact because the null hypothesis requires that only X_i (s) being row vectors are random variables. On the contrary, mixture model approach follow hard on the requirement of null hypothesis.

Another way to predict empty values is to use Bayesian rule as estimation tool. It is better than average method because it takes advantage of

probability distribution under 2-dimension data. Let $z = x_{uv}$ be the random variable that are dependent on row index u and column index v which, in turn, are random variables. According to Bayesian rule, the probability of z given u and v is:

$$P(z = z_0 | u, v) = \frac{P(u, v | z_0)P(z_0)}{\sum_z P(u, v | z)P(z)}$$

Assuming that u and v are mutually independent given z , $P(z / u, v)$ is re-written.

$$P(z = z_0 | u, v) = \frac{P(u | z_0)P(v | z_0)P(z_0)}{\sum_z P(u | z)P(v | z)P(z)}$$

Let $\theta = P(z) = \{\theta_1, \theta_2, \dots, \theta_k\}$ be the parameter of $P(z / u, v)$ where θ_i corresponds with the i^{th} value of z , we have:

$$P(z = z_0 | u, v) = \frac{P(u | z_0)P(v | z_0)\theta_0}{\sum_z P(u | z)P(v | z)\theta}$$

The goal of Bayesian estimate method is to determine $P(z / u, v)$ via finding out optimal parameter θ . This method is iterative process whose iteration includes two steps: calculating $P(z / u, v)$ based on θ and re-calculating θ . Let t and θ^t denotes t^{th} iteration and the estimate of parameter θ at t^{th} iteration. Note that θ^0 can be initialized by 0.5. These two steps are described as below.

1. The current probability $P(z / x, y)$ is calculated based on previous estimate of parameter θ^{t-1} .

$$P(z = z_0 | u, v) = \frac{P(u | z_0)P(v | z_0)\theta_0^{t-1}}{\sum_z P(u | z)P(v | z)\theta^{t-1}}$$

2. Assigning current $P(z / x, y)$ to current estimate of parameter θ^t .

$$\theta^t = P(z | u, v)$$

If the deviation $|\theta^t - \theta^{t-1}|$ is less than a threshold ε , then algorithm is stopped; otherwise go back step 1.

With example in table 2, suppose ranges of u , v and z are $\{1, 2, 3, 4\}$, $\{1, 2, 3, 4\}$ and $\{1, 2, 3\}$, the conditional probabilities $P(u / z)$ and $P(v / z)$ are calculated and shown in table 3.

	z = 1	z = 2	z = 3
u = 1	0.5	0.25	0

u = 2	0	0.25	0.5
u = 3	0.5	0.25	0
u = 4	0	0.25	0.5
v = 1	0.5	0.25	0
v = 2	0	0.25	0.5
v = 3	0.5	0.25	0
v = 4	0	0.25	0.5

Table 3. Conditional probabilities $P(u/z)$ and $P(v/z)$

Suppose the parameter is initialized by 0.5, we have $\theta^0 = P^0(z/u, v) = 0.5$. It means that the prior probabilities of z is 0.5. It is easy to calculate the posterior probabilities $P(z/u, v)$, for example:

$$\begin{aligned}
 &P(z = 1|u = 1, v = 1) \\
 &= \frac{P(u = 1|z = 1)P(v = 1|z = 1)\theta_1^0}{P(u = 1|z = 1)P(v = 1|z = 1)\theta_1^0 + P(u = 1|z = 2)P(v = 1|z = 2)\theta_1^0 + P(u = 1|z = 3)P(v = 1|z = 3)\theta_1^0} \\
 &= \frac{0.5 * 0.5 * 0.5}{0.5 * 0.5 * 0.5 + 0.25 * 0.25 * 0.5 + 0 * 0 * 0.5} \\
 &= 0.8
 \end{aligned}$$

By the similar way, the probabilities $P(z/u, v)$, at the first iteration, over all values of u, v and z are calculated and shown in table 4.

	z = 1	z = 2	z = 3
u=1, v=1	0.8	0.2	0
u=1, v=2	0	1	0
u=1, v=3	0.8	0.2	0
u=1, v=4	0	1	0
u=2, v=1	0	1	0
u=2, v=2	0	0.2	0.8
u=2, v=3	0	1	0
u=2, v=4	0	0.2	0.8
u=3, v=1	0.8	0.2	0
u=3, v=2	0	1	0
u=3, v=3	0.8	0.2	0
u=3, v=4	0	1	0
u=4, v=1	0	1	0
u=4, v=2	0	0.2	0.8
u=4, v=3	0	1	0
u=4, v=4	0	1	0

Table 4. Posterior probabilities of $z, P(z/u, v)$

At next iteration posterior probabilities $z, P(z/u, v)$ are computed by similar way except that the parameter θ is assigned by values in table 3. In other words, the parameter for next iteration is assigned as current posterior probabilities $z, P(z/u, v)$. Now we estimate missing values such as $x_{31}, x_{41}, x_{32}, x_{42}, x_{13}, x_{23}, x_{14}$ and x_{24} . The posterior probabilities for $x_{31} = 1, x_{31} = 2, x_{31} = 4$ are $P(z = 1|u = 3, v = 1) = 0.8, P(z = 2|u = 3, v = 1) = 0.2$ and $P(z = 3|u = 3, v = 1) = 0$, respectively. Because $P(z = 1|u = 3, v = 1) = 0.8$ is maximal, x_{31} receives value 1, $x_{31} = 1$. By the similar way, we have $x_{41} = 2, x_{32} = 2, x_{42} = 3, x_{13} = 1, x_{23} = 2, x_{14} = 2$ and $x_{24} = 3$. These estimates are much better than ones resulted from average method even if the algorithm have just come over one iteration. Table 5 shows the complete sample whose missing values are estimated.

	v = 1	v = 2	v = 3	v = 4
u = 1	$x_{11} = 1$	$x_{12} = 2$	$x_{13} = 1$	$x_{14} = 2$
u = 2	$x_{21} = 2$	$x_{22} = 3$	$x_{23} = 2$	$x_{24} = 3$
u = 3	$x_{31} = 1$	$x_{32} = 2$	$x_{33} = 1$	$x_{34} = 2$
u = 4	$x_{41} = 2$	$x_{42} = 3$	$x_{43} = 2$	$x_{44} = 3$

Table 5. Complete sample whose missing values are estimated by Bayesian method.

However, the drawback of Bayesian estimate method in hypothesis testing is that it gives three assumptions as below.

- Sample scalar values x_{ij} (s) are considered as random values while vector X_i (s) are random variables in null hypothesis. Scalar distribution is different from vector distribution with regard to the modality of data. When the modality of data is transformed, the meaning of data is changed unpredictably.
- Row index u and column index v are also considered as random variables but this assumption doesn't exist in null hypothesis.
- Row variable u and column variable v are mutually independent given sample value x_{ij} .

In general, mixture model approach is better than filling missing values approaches in flavor of hypothesis testing because it does not give any

additional assumption about sample space except assumptions that null hypothesis issues such as the normality of sample data. In other words, it conserves attributes of sample data.

4. Conclusions

The basic idea of this research is to analyze the global distribution as a set of partial (or potential) distributions. Because it is impossible to apply the global distribution into incomplete sample, the research applies each partial distribution into a sub-sample of incomplete sample where sub-sample is defined as a piece of incomplete sample so that such sub-sample contains complete observation vectors. Partial distributions are unified into a mixture model and expectation maximization (EM) algorithm is used to find out optimal parameters of mixture model such that these optimal parameters maximize the likelihood function. The ratio of the maximum likelihood of null hypothesis to the maximum likelihood of alternative hypothesis is totally determined based on these optimal parameters. Consequently, this ratio is used to test null hypothesis in favor of alternative hypothesis by the normal way that is to take advantage of chi-square distribution. The excellent of this research is that there is no requirement of filling missing values existing in incomplete sample. When missing values are replaced by estimated values, inherent attributes of sample data changed or disturbed even if such estimated values are considered as the best-predicted values. In other words, this method maintains inherent attributes of sample data. Moreover, the higher the density of missing

values is, the more effective this research is. Especially, if the data incompleteness occurs frequently or conforms a particular period or rule in process of collecting samples, then the corporation of partial distributions and likelihood ratio test delivers the best result. However if missing values occur randomly such as pepper-and-salt noise, this approach is not good choice for test because pepper-and-salt noise data has no inherent features and so partial distributions cannot be specified and estimated precisely.

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