Chapter 21. 경험적 베이즈 추정 전략(Empirical Bayes Estimation Strategies) 2019-07-31 신재혁

21.1 베이즈 디컨볼루션(Bayes Deconvolution)

1) 컨볼루션(Convolution)?

정의 [편집]

두 개의 함수 f와 g가 있을 때, 두 함수의 합성곱을 수학 기호로는 f*g와 같이 표시한다.

합성곱 연산은 두 함수 f, g 가운데 하나의 함수를 반전(reverse), 전이(shift)시킨 다음, 다른 하나의 함수와 곱한 결과를 적분하는 것을 의미한다. 이를 수학 기호로 표시하면 다음과 같다.

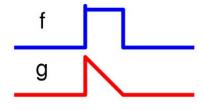
$$(f*g)(t) = \int_{-\infty}^{\infty} f(\tau)g(t-\tau) d\tau$$

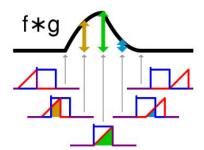
또한 g 함수 대신에 f 함수를 반전, 전이 시키는 경우 다음과 같이 표시할 수도 있다. 이 두 연산은 형태는 다르지만 같은 결과값을 갖는다.

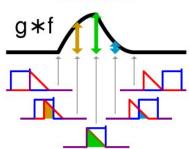
$$(f*g)(t) = \int_{-\infty}^{\infty} f(t-\tau)g(\tau) d\tau$$

위의 적분에서 적분 구간은 함수 f와 g가 정의된 범위에 따라서 달라진다.

Convolution







2) 베이즈 디컨볼루션(Bayes Deconvolution)?

prior:
$$\Theta_i \stackrel{\text{iid}}{\sim} g(\theta), \qquad i = 1, 2, \dots, N$$

evidence= observable random vriable:
$$X_i \stackrel{\mathrm{ind}}{\sim} p_i(X_i | \Theta_i)$$

$$f_i(X_i) = \int_{\mathcal{T}} p_i(X_i|\theta_i)g(\theta_i) d\theta_i$$

marginal distribution of X_i:

이러한 설정에서 *관측된 X를 토대로 미지의 사전분포 g에 대해서 추정하고 싶다.*

 $p_i(X_i|\Theta_i)$ $=\mathcal{N}(\Theta_i,\sigma^2)$ 와 같이 theta에 대해 간단한 분포로 표현된다면,

$$f_i(X_i) = \int_{\mathcal{T}} p_i(X_i|\theta_i)g(\theta_i) d\theta_i$$

= $g * \mathcal{N}(0,\sigma^2)$ 으로 표현할 수 있다.

따라서, g를 구하는 문제는 위 합성곱 효과를 제거하면, 즉 디컨볼루션(Deconvolution)을 하면 구할 수 있다. 이러한 문제를 베이즈 디컨볼루션(Bayes Deconvolution)이라고 한다.

3) 왜 g를 알고 싶은가?

: 베이즈 사후 기댓값을 추정하길 원하거나, 사후 밀도를 그리길 원하는 등 다양한 이유가 있을 수 있다. 추후 예제로 설명.

4) 베이즈 디컨볼루션(Baves Deconvolution)의 방법? 크게 q-모델링과 f-모델링으로 나뉜다.

21.6 디컨볼루션과 f-모델링(Deconvolution and f-Modeling)

1) f-Modeling이란?

$$f_i(X_i) = \int_{\mathcal{T}} p_i(X_i|\theta_i)g(\theta_i) d\theta_i$$

marginal distribution of X i =

를, 관측 표본 X1, X2, ..., Xn을 통해 직접 적합화 한 후, 원하는 대답을 f항으로 직접 표현하는 공식을 찾아 적용하는 방법이다.

예를 들어

- 로빈의 공식(6.5)

$$E\{\theta|x\} = (x+1)f(x+1)/f(x).$$

- 지역 거짓 발견율(15.38)

$$fdr(z) = \pi_0 f_0(z)/f(z)$$

- 트위디의 공식(20.37)

$$E\{\mu|z\} = z + \sigma^2 l'(z) \qquad \text{with } l'(z) = \frac{d}{dz} \log f(z)$$

등이 있다.

그러나 베이즈 사후 기댓값이나 사후 분포가 아닌, g, 즉 사전분포를 알고자 할 때는 문제가 생긴다.

그럼에도 불구하고, 사전분포 g를 추정하는 f-Modeling 기법이 존재한다.

2) 푸리에 변환(Fourier Transform)?

Definition [edit]

The Fourier transform of a function f is traditionally denoted \hat{f} , by adding a circumflex to the symbol of the function. There are several common conventions for defining the Fourier transform of an integrable function $f: \mathbb{R} \to \mathbb{C}$. [1][2] One of them is

$$\hat{f}\left(\xi
ight)=\int_{-\infty}^{\infty}f(x)\;e^{-2\pi ix\xi}\;dx, \quad ext{ (Eq. 1)}$$

for any real number ξ.

When the independent variable x represents time, the transform variable ξ represents frequency (e.g. if time is measured in seconds, then frequency is in hertz). Under suitable conditions, f is determined by \hat{f} via the inverse transform:

$$f(x) = \int_{-\infty}^{\infty} \hat{f}\left(\xi
ight) e^{2\pi i x \xi} \, d\xi, \quad ext{ (Eq.2)}$$

for any real number x.

Convolution theorem [edit]

Main article: Convolution theorem

The Fourier transform translates between convolution and multiplication of functions. If f(x) and g(x) are integrable functions with Fourier transforms $\hat{f}(\xi)$ and $\hat{g}(\xi)$ respectively, then the Fourier transform of the convolution is given by the product of the Fourier transforms $\hat{f}(\xi)$ and $\hat{g}(\xi)$ (under other conventions for the definition of the Fourier transform a constant factor may appear).



This means that if:

$$h(x)=(f*g)(x)=\int_{-\infty}^{\infty}f(y)g(x-y)\,dy,$$

where * denotes the convolution operation, then:

$$\hat{h}(\xi) = \hat{f}(\xi) \cdot \hat{g}(\xi).$$

3) 푸리에 변환을 이용한 f-modeling과 g의 추정 위의 Convolution Thm에 의해,

$$f = g * N(0,0^2) \longrightarrow \hat{f} = \hat{g} \cdot \hat{N}(0,0^2)$$
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따라서, (21.60)이 성립한다.

next. A function f(x) and its Fourier transform $\phi(t)$ are related by

$$\phi(t) = \int_{-\infty}^{\infty} f(x)e^{itx} dx$$
 and $f(x) = \frac{1}{2\pi} \int_{-\infty}^{\infty} \phi(t)e^{-itx} dt$. (21.59)

For the *normal case* where $X_i = \Theta_i + Z_i$ with $Z_i \sim \mathcal{N}(0, 1)$, the Fourier transform of f(x) is a multiple of that for $g(\theta)$,

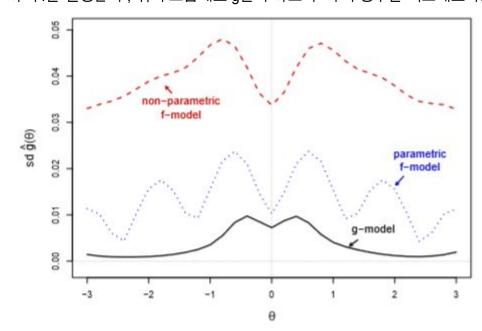
$$\phi_f(t) = \phi_g(t)e^{-t^2/2},$$
(21.60)

따라서 특별히 위의 경우에는 f-modeling을 통해 g를 추정할 수 있게 된다. 아래의 흐름을 따른다.

- 1. 관측 표본 X1, X2, ... , Xn을 통해 marginal distribution f를 직접 적합화하여 추정한다.
- 2. f의 푸리에 변환 f hat을 계산한다.
- 3. $f hat*exp(t^2 / 2) = g hat을 역 푸리에 변환하여 g를 구한다.$

여기에서,

- (1) 비모수적 모델: 각 관측 값 Xi에 1/N 확률을 할 당하는 경험적 밀도 f를 사용
- (2) 모수적 모델: 관측 표본 X1, X2, ..., Xn 에 포아송 회귀를 사용해 밀도 f를 추정 하여 f를 설정한 후, 위의 흐름대로 g를 구하고 두 가지 경우를 비교해보자.



21.2 g-모델링과 추정(g-Modeling and Estimation)

1) g-Modeling이란?

theta에 대한 직접적인 Modeling을 통해 g를 추정하는 방법. 일반적으로 g를 p-모수적 지수 패밀리(p-parameter exponential family)라고 가정한다. 그러면 g를 다음과 같이 쓸 수 있다.

$$g = g(\alpha) = e^{Q\alpha - \psi(\alpha)}$$

2) 데이터 생성 Process

책에서는 간단한 설명을 위해. 몇 가지 가정을 한다.

1. 가능한 theta의 값의 공간이 유한하다

$$\mathcal{T} = \{\theta_{(1)}, \theta_{(2)}, \dots, \theta_{(m)}\}\$$

2. 커널 $p_i(\cdot|\cdot)$ 이 i에 종속되지 않는다

ex1)
$$X_i \sim \operatorname{Poi}(\Theta_i)$$
 ex2) $X_i \sim \mathcal{N}(\Theta_i, \sigma^2)$

counter ex) $X_i \sim \text{Bi}(n_i, \Theta_i)$

3. X i 관측치의 표본공간이 유한하고 이산이다

$$\mathcal{X} = \{x_{(1)}, x_{(2)}, \dots, x_{(n)}\}\$$

이러한 가정에서 다음과 같이 수식을 전개할 수 있다.

A p-parameter exponential family (5.50) for g can be written as

$$g = g(\alpha) = e^{\mathbf{Q}\alpha - \psi(\alpha)}, \tag{21.11}$$

where the p-vector α is the natural parameter and Q is a known $m \times p$ structure matrix. Notation (21.11) means that the j th component of $g(\alpha)$ is

$$g_j(\alpha) = e^{Q'_j \alpha - \psi(\alpha)}, \tag{21.12}$$

with Q'_j the j th row of Q; the function $\psi(\alpha)$ is the normalizer that makes $g(\alpha)$ sum to 1,

$$\psi(\alpha) = \log\left(\sum_{j=1}^{m} e^{Q'_{j}\alpha}\right). \tag{21.13}$$

Define

$$p_{kj} = \Pr\{X_i = x_{(k)} | \Theta_i = \theta_{(j)}\},$$
 (21.16)

for k = 1, 2, ..., n and j = 1, 2, ..., m, and the corresponding $n \times m$ matrix

$$P = (p_{ki}),$$
 (21.17)

having kth row $P_k = (p_{k1}, p_{k2}, \dots, p_{km})'$. The convolution-type formula (21.6) for the marginal density f(x) now reduces to an inner product,

$$f_k(\alpha) = \Pr_{\alpha} \{ X_i = x_{(k)} \} = \sum_{j=1}^m p_{kj} g_j(\alpha)$$

= $P'_k g(\alpha)$. (21.18)

In fact we can write the entire marginal density $f(\alpha) = (f_1(\alpha), f_2(\alpha), ..., f_n(\alpha))'$ in terms of matrix multiplication,

$$f(\alpha) = Pg(\alpha). \tag{21.19}$$

The vector of counts $y = (y_1, y_2, ..., y_n)$, with

$$y_k = \#\{X_i = x_{(k)}\},$$
 (21.20)

is a sufficient statistic in the iid situation. It has a multinomial distribution (5.38),

$$y \sim \text{Mult}_n(N, f(\alpha)),$$
 (21.21)

이러한 수식 전개는 g-modeling의 데이터 생성 Process를 다음과 같이 기술할 수 있도록 해준다. (정확하게는 X가 아니라 y)

$$\alpha \to g(\alpha) = e^{Q\alpha - \psi(\alpha)} \to f(\alpha) = Pg(\alpha) \to y \sim \operatorname{Mult}_n(N, f(\alpha))$$

3) g-Modeling Estimation

추론은 데이터 생성 Process의 역방향으로 진행된다.

$$y \to \hat{\alpha} \to f(\hat{\alpha}) \to g(\hat{\alpha}) = e^{Q\hat{\alpha} - \psi(\hat{\alpha})}$$

사실, 가운데의 f(alpha hat)을 구하는 것은 불필요하다. alpha의 값만 추정하면 바로 g(alpha hat)으로 계산할 수 있다.

일반적으로 alpha는

$$l_y(\alpha) = \log \left(\prod_{k=1}^n f_k(\alpha)^{y_k} \right) = \sum_{k=1}^n y_k \log f_k(\alpha).$$
 에 MLE를 적용해서 추정한다.

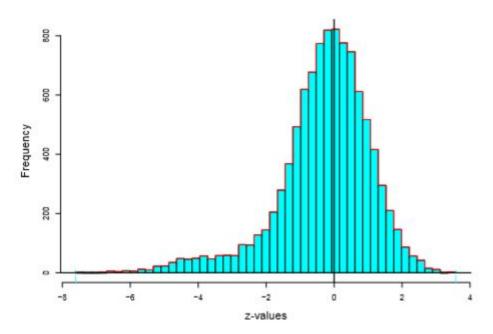
21.4. 예제 1: 인공적 미세배열(9000개의 mu는 0, 1000개의 mu는 N(-3, 1))

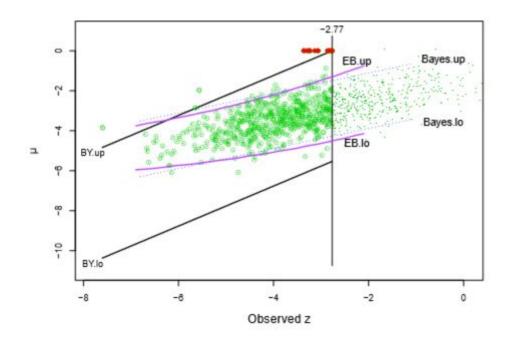
N = 10,000 independent observations

$$z_i \stackrel{\text{ind}}{\sim} \mathcal{N}(\mu_i, 1), \qquad i = 1, 2, \dots, N = 10,000,$$

with

$$\mu_i \sim \begin{cases}
0 & \text{for } i = 1, 2, \dots, 9000 \\
\mathcal{N}(-3, 1) & \text{for } i = 9001, \dots, 10,000.
\end{cases}$$





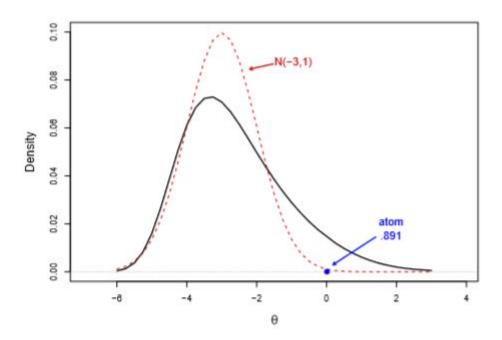


Figure 21.6 The heavy black curve is the g-modeling estimate of $g(\mu)$ for $\mu \neq 0$ in the artificial microarray example, suppressing the atom at zero, $\hat{g}(0) = 0.891$. It is only a rough estimate of the actual nonzero density $\mathcal{N}(-3, 1)$.

21.4. 예제 2: 전립선 연구 데이터(암환자 52명, 정상 50명, N=6033 유전자 활동성)

n=102 men, 52 prostate cancer patients and 50 normal controls. Each man's gene expression levels were measured on a panel of N=6033 genes, yielding a 6033×102 matrix of measurements x_{ij} ,

$$x_{ij} = \text{activity of } i \text{ th gene for } j \text{ th man.}$$
 (15.1)

For each gene, a two-sample t statistic (2.17) t_i was computed comparing gene i's expression levels for the 52 patients with those for the 50 controls. Under the null hypothesis H_{0i} that the patients' and the controls' responses come from the same normal distribution of gene i expression levels, t_i will follow a standard Student t distribution with 100 degrees of freedom, t_{100} . The transformation

$$z_i = \Phi^{-1}(F_{100}(t_i)),$$
 (15.2)

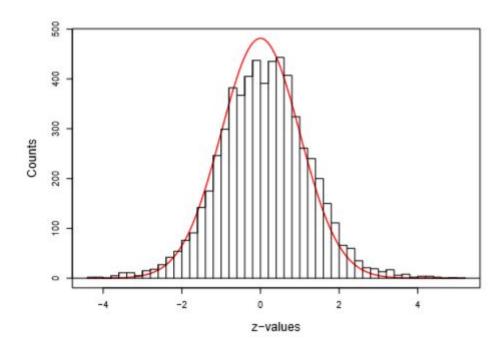
where F_{100} is the cdf of a t_{100} distribution and Φ^{-1} the inverse function of a standard normal cdf, makes z_i standard normal under the null hypothesis:

$$H_{0i}: z_i \sim \mathcal{N}(0, 1).$$
 (15.3)

Of course the investigators were hoping to spot some *non-null* genes, ones for which the patients and controls respond differently. It can be shown that a reasonable model for both null and non-null genes is^{2†}

$$z_i \sim \mathcal{N}(\mu_i, 1),$$
 (15.4)

 μ_i being the effect size for gene i. Null genes have $\mu_i = 0$, while the



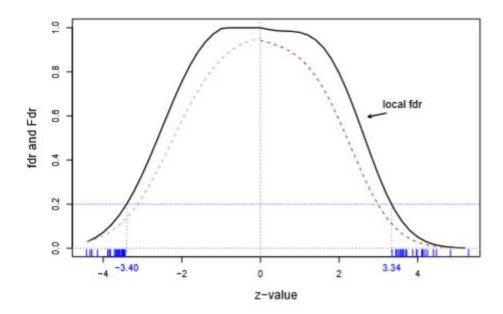


Figure 15.5 Local false-discovery rate estimate $\widehat{\text{fdr}}(z)$ (15.39) for prostate study of Figure 15.1; 27 genes on the right and 25 on the left, indicated by dashes, have $\widehat{\text{fdr}}(z_i) \leq 0.2$; light dashed curves are the left and right tail-area estimates $\widehat{\text{Fdr}}(z)$ (15.26).

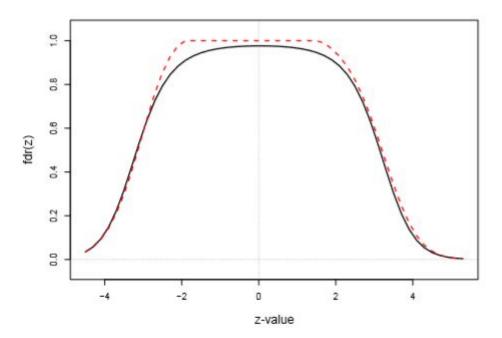


Figure 21.9 The black curve is the empirical Bayes estimated false-discovery rate $\widehat{\Pr}\{\mu=0|z\}$ from g-modeling. For large values of |z| it nearly matches the locfdr f-modeling estimate fdr(z), red curve.

Appendix. Mathematics in g-modeling

$$l_{y}(\alpha) = \log \left(\prod_{k=1}^{n} f_{k}(\alpha)^{y_{k}} \right) = \sum_{k=1}^{n} y_{k} \log f_{k}(\alpha).$$
 (21.25)

Its score function $l_y(\alpha)$, the vector of partial derivatives $\partial l_y(\alpha)/\partial \alpha_h$ for $h=1,2,\ldots,p$, determines the MLE $\hat{\alpha}$ according to $l_y(\hat{\alpha})=0$. The $p\times p$ matrix of second derivatives $\ddot{l}_y(\alpha)=(\partial^2 l_y(\alpha)/\partial \alpha_h\partial \alpha_l)$ gives the Fisher information matrix (5.26)

$$\mathcal{I}(\alpha) = E\{-\ddot{l}_{\nu}(\alpha)\}. \tag{21.26}$$

The exponential family model (21.11) yields simple expressions for $l_y(\alpha)$ and $\mathcal{I}(\alpha)$. Define

$$w_{kj} = g_j(\alpha) \left(\frac{p_{kj}}{f_k(\alpha)} - 1 \right)$$
 (21.27)

and the corresponding m-vector

$$W_k(\alpha) = (w_{k1}(\alpha), w_{k2}(\alpha), \dots, w_{km}(\alpha))'.$$
 (21.28)

Lemma 21.1 The score function $l_y(\alpha)$ under model (21.22) is

$$\dot{l}_{y}(\alpha) = QW_{+}(\alpha), \quad \text{where } W_{+}(\alpha) = \sum_{k=1}^{n} W_{k}(\alpha)y_{k}$$
 (21.29)

and Q is the $m \times p$ structure matrix in (21.11).

Lemma 21.2 The Fisher information matrix $\mathcal{I}(\alpha)$, evaluated at $\alpha = \hat{\alpha}$, is

$$\mathcal{I}(\hat{\alpha}) = Q' \left\{ \sum_{k=1}^{n} W_k(\hat{\alpha}) N f_k(\hat{\alpha}) W_k(\hat{\alpha})' \right\} Q, \qquad (21.30)$$

where $N = \sum_{1}^{n} y_k$ is the sample size in the empirical Bayes model (21.1)–(21.2).

Lemma 21.3 †The maximizer $\hat{\alpha}$ of $m(\alpha)$ has approximate bias vector and covariance matrix

$$\operatorname{Bias}(\hat{\alpha}) = -\left(\mathcal{I}(\hat{\alpha}) + \ddot{s}(\hat{\alpha})\right)^{-1} \dot{s}(\hat{\alpha})$$
and
$$\operatorname{Var}(\hat{\alpha}) = \left(\mathcal{I}(\hat{\alpha}) + \ddot{s}(\hat{\alpha})\right)^{-1} \mathcal{I}(\hat{\alpha}) \left(\mathcal{I}(\hat{\alpha}) + \ddot{s}(\hat{\alpha})\right)^{-1},$$
(21.33)

where $\mathcal{I}(\hat{\alpha})$ is given in (21.30).

Theorem 21.4 The penalized maximum likelihood estimate $\hat{g} = g(\hat{\alpha})$ has estimated bias vector and covariance matrix

$$Bias(\hat{g}) = D(\hat{\alpha})QBias(\hat{\alpha})$$
and
$$Var(\hat{g}) = D(\hat{\alpha})QVar(\hat{\alpha})Q'D(\hat{\alpha})$$
(21.38)

with $Bias(\hat{\alpha})$ and $Var(\hat{\alpha})$ as in (21.33).³