Note: all parameters, including ϕ, g , are on log scale.

Suppose that ϕ_{ij} follows a normal distribution with mean ϕ_i and standard deviation σ : $\phi_{ij} \sim N(\phi_i, \sigma^2)$, and ϕ_i 's are i.i.d. from $N(\hat{\phi}, \hat{\sigma}^2)$, where $1 \leq i \leq n$ and $1 \leq j \leq m$. In our case, n = 106 and m = 3.

$$P(\phi_{ij}|\hat{\phi},\hat{\sigma},\sigma) = \int P(\phi_{ij},\phi_i|\hat{\phi},\hat{\sigma})dF(\phi_i)$$
$$= \int_{-\infty}^{\infty} \phi(\phi_{ij}|\phi_i,\sigma)\phi(\phi_i|\hat{\phi},\hat{\sigma})d\phi_i$$

where $\phi(x|\mu,\sigma)$ is the probability density function for normal distribution with mean μ and variance σ^2 . Here if σ and $\hat{\sigma}$ are switched, the probability will stay the same, and the variance of ϕ_{ij} 's is roughly $\sigma^2 + \hat{\sigma}^2$. With the likelihood of observing ϕ_{ij} given parameter values for $\hat{\phi}, \hat{\sigma}$ and σ , we can find the maximum likelihood estimates for the 3 parameters with constraints $\sigma \geq \hat{\sigma}$.

Suppose there is a linear relationship between g and ϕ : $g_i = a + b\phi_i$, then it follows that $g_i + \phi_i = a + (b+1)\phi_i + \epsilon_i$, for $1 \le i \le n$ where ϵ_i is the noise in the estimators/observations for gene i, and $\epsilon_i \sim N(0, \sigma_e^2)$. Since $\phi_i \sim N(\hat{\phi}, \hat{\sigma}^2)$, we have $g_i + \phi_i \sim N(a + (b+1)\hat{\phi}, (b+1)^2\hat{\sigma}^2 + \sigma_e^2)$. With the values for $g_i + \phi_i$, the sufficient statistics (mean and variance) can be found which will provide estimators of $a + (b+1)\hat{\phi}$ and $b + 1)^2\hat{\sigma}^2 + \sigma_e^2$. However there are 3 parameters $(a, b \text{ and } \sigma_e)$, which means they are not all identifiable from data. (more than 1 set of parameters can give the maximum likelihood).