## Likelihood computation of regression for the time order determination

Based on the normality assumption, we have $\mathbf{y}_{i t} \sim \mathcal{N}\left(\mathbf{X}_{t} \mathbf{b}_{i}, \sigma_{M R i}^{2}\right), \mathbf{X}_{t}$ is the row of $\mathbf{X}$ at time $t$. Therefore the likelihood of the models in Equations 12 and 13 for the set of 12 i.i.d. samples $\mathcal{D}$ is:

$$
\mathcal{L}\left(\mathbf{b}_{i}, \sigma_{M R i}^{2} \mid \mathcal{D}\right)=\left(2 \pi \sigma_{M R i}^{2}\right)^{\frac{-12}{2}} \Pi_{0 \leq t \leq 32} \exp \left(-\frac{\left(\mathbf{y}_{i t}-\mathbf{X}_{t} \mathbf{b}_{i}\right)^{2}}{2 \sigma_{M R i}^{2}}\right)
$$

The corresponding log-likelihood is:

$$
\log \mathcal{L}\left(\mathbf{b}_{i}, \sigma_{M R i}^{2} \mid \mathcal{D}\right)=-\sum_{0 \leq t \leq 32}\left(\frac{\left(\mathbf{y}_{i t}-\mathbf{X}_{t} \mathbf{b}_{i}\right)^{2}}{2 \sigma_{M R i}^{2}}\right)-\frac{12}{2} \log \left(\sigma_{M R i}^{2}\right)-\frac{12}{2} \log (2 \pi)
$$

Parameters $\mathbf{b}_{i}$ and $\sigma_{M R i}^{2}$ are estimated by ordinary least squares:

$$
\begin{aligned}
& \hat{\mathbf{b}}_{i}=\left(\mathbf{X}^{T} \mathbf{X}\right)^{-1} \mathbf{X}^{T} \mathbf{y}_{i} \\
& \hat{\sigma}_{M R i}^{2}=\frac{\left(\mathbf{y}_{i}-\mathbf{X} \hat{\mathbf{b}}_{i}\right)^{T}\left(\mathbf{y}_{i}-\mathbf{X} \hat{\mathbf{b}}_{i}\right)}{12}
\end{aligned}
$$

Using the estimated parameters $\hat{\mathbf{b}}_{i}$ and $\hat{\sigma}_{M R i}^{2}$, we can formulate the log-likelihood such as:

$$
\log \mathcal{L}\left(\mathbf{b}_{i}, \sigma_{M R i}^{2} \mid \mathcal{D}\right)=-\frac{12}{2} \log \left(\frac{\left(\mathbf{y}_{i}-\mathbf{X} \hat{\mathbf{b}}_{i}\right)^{T}\left(\mathbf{y}_{i}-\mathbf{X} \hat{\mathbf{b}}_{i}\right)}{12}\right)+C
$$

where $C$ is a constant term and is the same for every gene.

