Goal

Does local ancestry affect the gene network?

Two nodes and their correlations

Consider two genes k_1 , k_2 and the corresponding gene expression vector of y_{k_1} and y_{k_2} , each of length n where n is the number of subjects. We also have two local ancestry vectors x_{k_1} and x_{k_2} . The temporary question of interest is whether the correlation between y_{k_1} and y_{k_2} is driven by either x_{k_1} or x_{k_2} .

Without loss of generality, let's see how much the correlation between the two expression levels changes with respect to the values of x_{k_1} . Each element of the local ancestry vector x takes one of three values : 0, 1, or 2. When we divide the n samples into three groups based on local ancestry each with size n_0 , n_1 , n_2 , we can observe three correlation coefficients: ρ_0 , ρ_1 , and ρ_2 . Using Fisher's transformation, we consider three normally distributed z values for each group : z_0 , z_1 , and z_2 .

$$z_{i} = \frac{1}{2} ln\left(\frac{1+\rho_{i}}{1-\rho_{i}}\right) \sim N\left(\frac{1}{2} ln\left(\frac{1+\tilde{\rho}_{i}}{1-\tilde{\rho}_{i}}\right), \frac{1}{\sqrt{n_{i}-3}}\right)$$

where $\tilde{\rho}_i$ is the underlying true correlation coefficient for the group with local ancestry i.

We assume that z_0 , z_1 , and z_2 have linear relationship. We formulate the model like below.

$$\begin{bmatrix} z_0 \\ z_1 \\ z_2 \end{bmatrix} \sim MVN \left(\begin{bmatrix} \mu \\ \mu + \beta \\ \mu + 2\beta \end{bmatrix}, \begin{bmatrix} \frac{1}{n_0 - 3} & 0 & 0 \\ 0 & \frac{1}{n_1 - 3} & 0 \\ 0 & 0 & \frac{1}{n_2 - 3} \end{bmatrix} \right)$$

with hypotheses

$$H_0:\beta=0$$

$$H_A: \beta \neq 0$$

For notational convenience, we define the following matrix and vectors.

$$\Sigma = \begin{bmatrix} \frac{1}{n_0 - 3} & 0 & 0\\ 0 & \frac{1}{n_1 - 3} & 0\\ 0 & 0 & \frac{1}{n_2 - 3} \end{bmatrix} = \begin{bmatrix} \sigma_0^2 & 0 & 0\\ 0 & \sigma_1^2 & 0\\ 0 & 0 & \sigma_2^2 \end{bmatrix}$$

$$oldsymbol{\mu} = egin{bmatrix} \mu \ \mu \ \mu \end{bmatrix}, \quad oldsymbol{\mu}_{oldsymbol{eta}} = egin{bmatrix} \mu \ \mu + eta \ \mu + 2eta \end{bmatrix}, \quad oldsymbol{z} = egin{bmatrix} z_0 \ z_1 \ z_2 \end{bmatrix}$$

Also for notational convenience, we introduce Φ and Λ

$$\Phi = \sigma_0^2 \sigma_1^2 + \sigma_1^2 \sigma_2^2 + \sigma_2^2 \sigma_0^2$$

$$\Lambda = \sigma_1^2 \sigma_2^2 z_0 + \sigma_0^2 \sigma_2^2 z_1 + \sigma_0^2 \sigma_1^2 z_2$$

Now, we set up the log likelihood of the two cases: when β is 0 and when β is the MLE estimator.

$$\ell_{\beta=0} = -\frac{1}{2}log|2\pi\Sigma| - \frac{1}{2}((\boldsymbol{z} - \boldsymbol{\mu})^T \Sigma^{-1}(\boldsymbol{z} - \boldsymbol{\mu}))$$
(1)

$$\frac{\partial \ell_{\beta=0}}{\partial \mu} = \frac{z_0 - \mu}{\sigma_0^2} + \frac{z_1 - \mu}{\sigma_1^2} + \frac{z_2 - \mu}{\sigma_2^2} = 0 \tag{2}$$

$$\Rightarrow \hat{\mu}_{0,MLE} = \frac{\sigma_1^2 \sigma_2^2 z_0 + \sigma_2^2 \sigma_0^2 z_1 + \sigma_0^2 \sigma_1^2 z_2}{\sigma_0^2 \sigma_1^2 + \sigma_1^2 \sigma_2^2 + \sigma_2^2 + \sigma_0^2} = \frac{\Lambda}{\Phi}$$
 (3)

is the MLE estimator for the μ under the null hypothesis.

For the alternative hypothesis,

$$\begin{split} \ell_{\beta \neq 0} &= -\frac{1}{2} log |2\pi \Sigma| - \frac{1}{2} ((\boldsymbol{z} - \boldsymbol{\mu}_{\beta})^T \Sigma^{-1} (\boldsymbol{z} - \boldsymbol{\mu}_{\beta})) \\ \frac{\partial \ell_{\beta \neq 0}}{\partial \mu} &= \frac{z_0 - \mu}{\sigma_0^2} + \frac{z_1 - \mu - \beta}{\sigma_1^2} + \frac{z_2 - \mu - 2\beta}{\sigma_2^2} \\ &\Rightarrow \hat{\mu}_{A,MLE} = \frac{\sigma_1^2 \sigma_2^2 z_0 + \sigma_2^2 \sigma_0^2 (z_1 - \beta) + \sigma_0^2 \sigma_1^2 (z_2 - 2\beta)}{\sigma_0^2 \sigma_1^2 + \sigma_1^2 \sigma_2^2 + \sigma_2^2 \sigma_0^2} = \frac{\Lambda - \sigma_2^2 \sigma_0^2 \beta - 2\sigma_0^2 \sigma_1^2 \beta}{\Phi} \end{split}$$

is the MLE estimator for μ under the alternative hypothesis. Now we plug in the above to get the MLE estimator for β .

$$\begin{split} \frac{\partial \ell_{\beta \neq 0}}{\partial \beta} &= \frac{z_1 - \mu - \beta}{\sigma_1^2} + \frac{2(z_2 - \mu - 2\beta)}{\sigma_2^2} \\ &\Rightarrow \sigma_2^2(z_1 - \hat{\mu}_{A,MLE} - \hat{\beta}_{A,MLE}) + 2\sigma_1^2(z_2 - \hat{\mu}_{A,MLE} - 2\hat{\beta}_{A,MLE}) = 0 \\ &\Rightarrow \frac{\Phi z_1 - \Lambda + (\sigma_0^2 \sigma_2^2 + 2\sigma_0^2 \sigma_1^2 - \Phi)\hat{\beta}_{A,MLE}}{\Phi \sigma_1^2} + \frac{2(\Phi z_2 - \Lambda + (\sigma_0^2 \sigma_2^2 + 2\sigma_0^2 \sigma_1^2 - 2\Phi)\hat{\beta}_{A,MLE})}{\Phi \sigma_2^2} = 0 \\ &\Rightarrow \hat{\beta}_{A,MLE} = \frac{(\sigma_2^2 + 2\sigma_1^2)\Lambda - (\sigma_2^2 z_1 + 2\sigma_1^2 z_2)\Phi}{(\sigma_2^2 + 2\sigma_1^2)(\sigma_0^2 \sigma_2^2 + 2\sigma_0^2 \sigma_1^2 - 2\Phi)} \end{split}$$

Now we can perform the likelihood ratio test and see if β is significantly different from 0. Under the null,

$$-2log\left(\frac{N_3(\boldsymbol{z}; \hat{\boldsymbol{\mu}}, \boldsymbol{\Sigma})}{N_3(\boldsymbol{z}; \hat{\boldsymbol{\mu}}_{\boldsymbol{\beta}}, \boldsymbol{\Sigma})}\right) \sim \chi_1^2$$

and we can compute the corresponding p-value.