

Supporting Information

February 3, 2026

S.1 Model

For each variant, we model its phenotypic effects as shown in Figure ???. We assume that the effect of the variant on a single endophenotype (E) determines its effects on a number of other traits (T_1, T_2, \dots, T_q). The effect on each trait T_i then determines its measured effect on that trait O_i . Furthermore, conditional on observing the true effects T_i on all traits, the observed trait effects O_i are conditionally independent. Finally, conditional on observing the effect on the endophenotype E , the true effects T_i are conditionally independent of each other. Dependencies among traits not captured by E could be added, but we omit these for now.

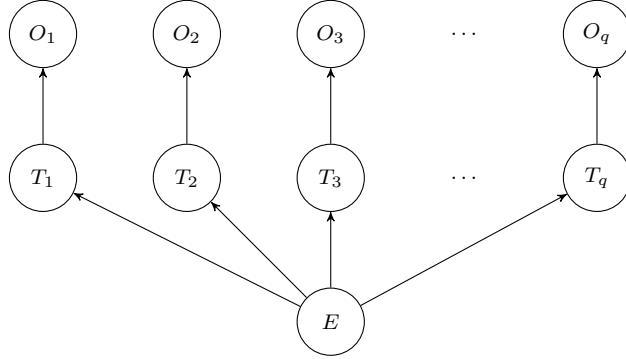


Figure 1: Model for phenotypic effects of a variant

We then specify conditional probability distributions as:

$$E \sim \mathcal{N}(\mu, \tau^2)$$

$$T_i \sim \mathcal{N}(\beta_i E, \sigma_i^2)$$

$$O_i \sim \mathcal{N}(T_i, s_i^2)$$

The intuition behind the parameters is as follows. The β_i control the relative values of the effects of the endophenotype on each of the traits, or in other words the “phenotypic profile”. They are relative values; if a variant has a two-fold effect on the endophenotype relative to another variant, it will have two-fold stronger effects on each of the traits, but the relative effects across traits will be the same between the two variants. The σ_i parameters control how important each trait is in the phenotypic profile; small values will insist that variants with the same endophenotype effects E have very similar effects on the trait, while larger values will allow variants with similar endophenotype effects to have discrepant trait effects.

μ and τ control the prior population distribution of E . Many times μ will be set to 0; however, in some cases (such as modeling variants from within a disease gene) it may be desirable to have $\mu \neq 0$. τ controls the “prevalence” of the endophenotype; small values of τ will bias more variants to have small effects E on the endophenotype.

The s_i values control the sampling distribution of the observed association statistics. They will depend on the frequency of the variant and the population in which it is tested for association.

Specification of these distribution allows us to answer several questions. For example:

1. **What is the posterior distribution of effects on one trait T_i , given observed effect on other traits $O_1, \dots, O_{i-1}, O_{i+1}, \dots, O_q$?** We would run the query $\Pr(T_i | O_2, \dots, O_q)$. The means of this posterior could be used for weights in an aggregate test, or the distributions could be used to filter variants for inclusion. Alternatively, this could be used as a prior in a Bayesian association analysis.
2. **What variants affect specified endophenotype?** For each variant, we would compute $\Pr(E | T_1, \dots, T_q)$.

Fitting the model

To use this model, we need to learn the parameters $\theta = \mu, \tau, \beta_i, \sigma_i$, and s_i .

For s_i , we assume that the variance of the observed coefficient O_i is equivalent under the null distribution ($T_i = 0$) and the alternate distribution. Thus, we can use the value of s_i fit under the null model, for example as determined by an association test. s_i will vary differ from variant to variant.

For fitting the remaining parameters, we consider two options. First, any number of the parameters θ could be externally specified. For example, to model an endophenotype based on lipodystrophy, relative values for β_i , as well as their variances in the population σ_i , could be measured epidemiologically.

Additionally, unspecified (or “unconstrained”) parameters can be fit given a collection of training variants $\hat{\mathbf{O}} = \hat{\mathbf{O}}^1, \dots, \hat{\mathbf{O}}^j$ where each training variant $\hat{\mathbf{O}}^j$ is a tuple of observed effect sizes $\hat{o}_1^j, \dots, \hat{o}_q^j$. The training algorithm will then learn values for unconstrained parameters such that the likelihood of the training variants is maximized. Specifically, we seek to maximize

$$L(\theta; \hat{\mathbf{O}}) = \int_{\hat{\mathbf{T}}^{\hat{E}}} L(\theta; \hat{\mathbf{O}}, \hat{\mathbf{T}}, \hat{E})$$

where $\hat{\mathbf{T}} = \hat{\mathbf{T}}^1, \dots, \hat{\mathbf{T}}^N$ and $\hat{E} = \hat{E}^1, \dots, \hat{E}^N$, or the values of T_i and E for each training sample j , are treated as unobserved latent data.

As is customary, we employ the EM algorithm. In the E-step, we estimate

$$\begin{aligned}
Q(\theta | \theta^{(t)}) &= \text{E}_{\hat{\mathbf{T}}, \hat{E} | \hat{\mathbf{O}}, \theta^{(t)}} \left[\log L(\theta; \hat{\mathbf{O}}, \hat{\mathbf{T}}, \hat{E}) \right] \\
&= \text{E}_{\hat{\mathbf{T}}, \hat{E} | \hat{\mathbf{O}}, \theta^{(t)}} \left[\log \left(\Pr(\hat{\mathbf{O}} | \hat{\mathbf{T}}) \Pr(\hat{\mathbf{T}} | \hat{E}) \Pr(\hat{E}) \right) \right] \\
&= \text{E}_{\hat{\mathbf{T}}, \hat{E} | \hat{\mathbf{O}}, \theta^{(t)}} \left[\log \Pr(\hat{\mathbf{O}} | \hat{\mathbf{T}}) + \log \Pr(\hat{\mathbf{T}} | \hat{E}) + \log \Pr(\hat{E}) \right] \\
&= \sum_j \text{E}_{\hat{\mathbf{T}}^j, \hat{E}^j | \hat{\mathbf{O}}^j, \theta^{(t)}} \left[\sum_i \log \left(\frac{1}{s_i^j \sqrt{2\pi}} e^{-\frac{(o_i^j - \hat{T}_i^j)^2}{2(s_i^j)^2}} \right) + \sum_i \log \left(\frac{1}{\sigma_i \sqrt{2\pi}} e^{-\frac{(\hat{T}_i^j - \beta_i \hat{E}^j)^2}{2\sigma_i^2}} \right) \right. \\
&\quad \left. + \log \left(\frac{1}{\tau \sqrt{2\pi}} e^{-\frac{(\hat{E}^j - \mu)^2}{2\tau^2}} \right) \right] \\
&= \sum_j \text{E}_{\hat{\mathbf{T}}^j, \hat{E}^j | \hat{\mathbf{O}}^j, \theta^{(t)}} \left[-\sum_i \frac{(o_i^j - T_i^j)^2}{2(s_i^j)^2} - \sum_i \frac{(T_i^j - \beta_i E^j)^2}{2\sigma_i^2} - \frac{(E^j - \mu)^2}{2\tau^2} \right. \\
&\quad \left. - \frac{1}{2} \sum_i \log \sigma_i^2 - \frac{1}{2} \log \tau^2 + C \right]
\end{aligned}$$

In the M-step, we compute values for

$$\theta^{(t+1)} = (\beta_1^{(t+1)}, \dots, \beta_q^{(t+1)}, \sigma_1^{(t+1)}, \dots, \sigma_q^{(t+1)}, \mu^{(t+1)}, \tau^{(t+1)})$$

such that

$$\theta^{(t+1)} = \arg \max_{\theta} Q(\theta | \theta^{(t)})$$

Differentiating, we obtain the following equations:

$$\begin{aligned}
\beta_i &= \frac{\sum_j \text{E}[T_i^j E^j]}{\sum_j \text{E}[(E^j)^2]} \\
\sigma_i^2 &= \frac{1}{N} \sum_j \left(\text{E}\left[\left(T_i^j\right)^2\right] - 2\beta_i \text{E}[T_i^j E^j] + \beta_i^2 \text{E}[(E^j)^2] \right) \\
\mu &= \frac{\sum_j \text{E}[E^j]}{N} \\
\tau^2 &= \frac{1}{N} \sum_j \left(\text{E}\left[(E^j)^2\right] - 2\mu \text{E}[E^j] + N\mu^2 \right)
\end{aligned}$$

where all expectations are conditional upon the current parameter estimates $\theta^{(t)}$ and the observed data $\hat{\mathbf{O}}$. Thus, in order to update the parameters, we need to compute the sufficient statistics

$$\text{E}[E^j], \text{E}[(E^j)^2], \text{E}[T_i^j E^j], \text{E}\left[\left(T_i^j\right)^2\right]$$

which we can compute either analytically or via probabilistic inference in the Bayesian network using the current parameters $\theta^{(t)}$.

S.2 Analytic derivation of needed expectations

In the EM algorithm, the M-step updates require the sufficient statistics

$$\mathbb{E}[E^j], \quad \mathbb{E}[(E^j)^2], \quad \mathbb{E}[T_i^j E^j], \quad \mathbb{E}\left[\left(T_i^j\right)^2\right],$$

where all expectations are conditional on the observed data $\hat{\mathbf{O}}$ and on the current parameter estimates $\theta^{(t)}$. In this section we derive analytic expressions for these quantities for the single-endophenotype model without edges between traits.

For a fixed training variant j , recall the conditional distributions

$$E^j \sim \mathcal{N}(\mu, \tau^2), \quad T_i^j | E^j \sim \mathcal{N}(\beta_i E^j, \sigma_i^2), \quad O_i^j | T_i^j \sim \mathcal{N}\left(T_i^j, (s_i^j)^2\right).$$

We first collapse over T_i^j to obtain the marginal distribution of O_i^j given E^j :

$$O_i^j | E^j \sim \mathcal{N}\left(\beta_i E^j, \sigma_i^2 + (s_i^j)^2\right).$$

Define

$$v_i^j = \sigma_i^2 + (s_i^j)^2.$$

Then conditional on E^j , the observations O_1^j, \dots, O_q^j are independent with

$$\Pr\left(\hat{\mathbf{O}}^j = \mathbf{o}^j | E^j\right) = \prod_i \frac{1}{\sqrt{2\pi v_i^j}} \exp\left(-\frac{(o_i^j - \beta_i E^j)^2}{2v_i^j}\right).$$

Combining the Gaussian prior with this likelihood yields the conjugate posterior

$$E^j | \mathbf{o}^j \sim \mathcal{N}\left(m_E^j, V_E^j\right),$$

where

$$\begin{aligned} V_E^j &= \left(\frac{1}{\tau^2} + \sum_i \frac{\beta_i^2}{v_i^j}\right)^{-1} \\ m_E^j &= V_E^j \left(\frac{\mu}{\tau^2} + \sum_i \frac{\beta_i o_i^j}{v_i^j}\right). \end{aligned}$$

Therefore,

$$\mathbb{E}[E^j] = m_E^j, \quad \mathbb{E}[(E^j)^2] = V_E^j + (m_E^j)^2.$$

Next, for each trait i , the conditional posterior of T_i^j given E^j and o_i^j is also Gaussian:

$$T_i^j | E^j, o_i^j \sim \mathcal{N}\left(m_{T,i}^j(E^j), V_{T,i}^j\right),$$

with

$$\begin{aligned} V_{T,i}^j &= \left(\frac{1}{\sigma_i^2} + \frac{1}{(s_i^j)^2}\right)^{-1} = \frac{\sigma_i^2 (s_i^j)^2}{\sigma_i^2 + (s_i^j)^2} \\ m_{T,i}^j(E^j) &= V_{T,i}^j \left(\frac{\beta_i E^j}{\sigma_i^2} + \frac{o_i^j}{(s_i^j)^2}\right). \end{aligned}$$

Define the weights

$$a_i^j = \frac{\sigma_i^2}{\sigma_i^2 + (s_i^j)^2}, \quad b_i^j = \frac{(s_i^j)^2}{\sigma_i^2 + (s_i^j)^2} \beta_i,$$

so that $m_{T,i}^j(E^j) = a_i^j o_i^j + b_i^j E^j$.

Using the law of total expectation and the posterior moments of E^j derived above, we obtain

$$\begin{aligned} \mathbb{E}[T_i^j E^j] &= \mathbb{E}\left[\mathbb{E}\left[T_i^j | E^j, o_i^j\right] E^j\right] \\ &= \mathbb{E}\left[\left(a_i^j o_i^j + b_i^j E^j\right) E^j\right] \\ &= a_i^j o_i^j \mathbb{E}[E^j] + b_i^j \mathbb{E}\left[(E^j)^2\right] \\ &= a_i^j o_i^j m_E^j + b_i^j \left(V_E^j + (m_E^j)^2\right). \end{aligned}$$

Similarly,

$$\begin{aligned} \mathbb{E}\left[\left(T_i^j\right)^2\right] &= \mathbb{E}\left[\text{Var}\left(T_i^j | E^j, o_i^j\right)\right] + \mathbb{E}\left[\left(\mathbb{E}\left[T_i^j | E^j, o_i^j\right]\right)^2\right] \\ &= V_{T,i}^j + \mathbb{E}\left[\left(a_i^j o_i^j + b_i^j E^j\right)^2\right] \\ &= V_{T,i}^j + \left(a_i^j o_i^j\right)^2 + 2a_i^j o_i^j b_i^j \mathbb{E}[E^j] + \left(b_i^j\right)^2 \mathbb{E}\left[(E^j)^2\right] \\ &= V_{T,i}^j + \left(a_i^j o_i^j\right)^2 + 2a_i^j o_i^j b_i^j m_E^j + \left(b_i^j\right)^2 \left(V_E^j + (m_E^j)^2\right). \end{aligned}$$

These expressions provide the analytic sufficient statistics needed in the M-step equations derived in the previous section.

S.3 Extension to multiple endophenotypes

We can generalize the model to allow each variant to act on multiple endophenotypes. Let there be K endophenotypes E_1, \dots, E_K . For variant j , let E_k^j denote its effect on endophenotype k , and let $\mathbf{E}^j = (E_1^j, \dots, E_K^j)^T$ denote the vector of endophenotype effects. The corresponding graphical model is shown in Figure ??.

We assume the K endophenotype effects are independent *a priori* (and note that a full covariance prior could be substituted without changing the inference strategy). We specify conditional probability distributions as:

$$E_k \sim \mathcal{N}(\mu_k, \tau_k^2) \quad (k = 1, \dots, K)$$

$$T_i \sim \mathcal{N}\left(\sum_{k=1}^K \beta_{ik} E_k, \sigma_i^2\right) \quad (i = 1, \dots, q)$$

$$O_i \sim \mathcal{N}(T_i, s_i^2) \quad (i = 1, \dots, q)$$

Here, β_{ik} is the contribution of endophenotype k to trait i ; equivalently, it is the strength of the edge $E_k \rightarrow T_i$. In an implementation, the structure (which edges are permitted) can be specified in a configuration file; if the edge $E_k \rightarrow T_i$ is absent, we fix $\beta_{ik} = 0$. As before, the σ_i control how

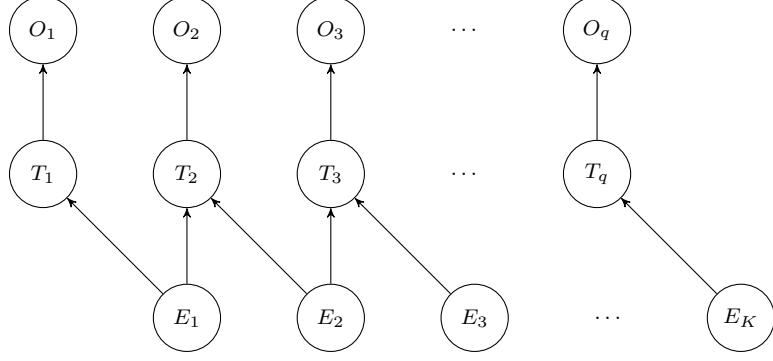


Figure 2: Model for phenotypic effects of a variant with multiple endophenotypes

tightly trait T_i follows the endophenotype-driven profile, and s_i controls the sampling distribution of the observed association statistics. The parameters μ_k and τ_k describe the prior population distribution of endophenotype k .

For convenience, define the $q \times K$ matrix $\mathbf{B} = (\beta_{ik})$, the prior mean vector $\mu = (\mu_1, \dots, \mu_K)^T$, and the prior covariance $\Sigma_E = \text{diag}(\tau_1^2, \dots, \tau_K^2)$. For each variant j , let $\mathbf{o}^j = (o_1^j, \dots, o_q^j)^T$ denote the observed effects. Collapsing over T_i as before yields

$$O_i^j \mid \mathbf{E}^j \sim \mathcal{N}\left(\mathbf{b}_i^T \mathbf{E}^j, \sigma_i^2 + (s_i^j)^2\right),$$

where \mathbf{b}_i^T is the i th row of \mathbf{B} , and s_i^j is the (variant-specific) standard error for O_i^j .

Let $v_i^j = \sigma_i^2 + (s_i^j)^2$ and define the diagonal weight matrix

$$\mathbf{W}^j = \text{diag}\left(\frac{1}{v_1^j}, \dots, \frac{1}{v_q^j}\right).$$

Then the posterior distribution of \mathbf{E}^j given the observations \mathbf{o}^j is multivariate normal:

$$\begin{aligned} \mathbf{E}^j \mid \mathbf{o}^j &\sim \mathcal{N}\left(\mathbf{m}_E^j, \mathbf{V}_E^j\right) \\ \mathbf{V}_E^j &= (\Sigma_E^{-1} + \mathbf{B}^T \mathbf{W}^j \mathbf{B})^{-1} \\ \mathbf{m}_E^j &= \mathbf{V}_E^j (\Sigma_E^{-1} \mu + \mathbf{B}^T \mathbf{W}^j \mathbf{o}^j). \end{aligned}$$

For fitting the model using EM, the M-step requires expectations with respect to the posterior. The basic sufficient statistics for variant j are

$$E[\mathbf{E}^j], \quad E[\mathbf{E}^j (\mathbf{E}^j)^T], \quad E[T_i^j \mathbf{E}^j], \quad E[(T_i^j)^2].$$

From the posterior above,

$$E[\mathbf{E}^j] = \mathbf{m}_E^j, \quad E[\mathbf{E}^j (\mathbf{E}^j)^T] = \mathbf{V}_E^j + \mathbf{m}_E^j (\mathbf{m}_E^j)^T.$$

Additionally, conditional on \mathbf{E}^j , the posterior of T_i^j given o_i^j remains univariate normal:

$$\begin{aligned} T_i^j \mid \mathbf{E}^j, o_i^j &\sim \mathcal{N}\left(m_{T,i}^j(\mathbf{E}^j), V_{T,i}^j\right) \\ V_{T,i}^j &= \left(\frac{1}{\sigma_i^2} + \frac{1}{(s_i^j)^2}\right)^{-1} = \frac{\sigma_i^2(s_i^j)^2}{\sigma_i^2 + (s_i^j)^2} \\ m_{T,i}^j(\mathbf{E}^j) &= V_{T,i}^j \left(\frac{\mathbf{b}_i^T \mathbf{E}^j}{\sigma_i^2} + \frac{o_i^j}{(s_i^j)^2}\right). \end{aligned}$$

Define

$$a_i^j = \frac{\sigma_i^2}{\sigma_i^2 + (s_i^j)^2}, \quad b_i^j = \frac{(s_i^j)^2}{\sigma_i^2 + (s_i^j)^2}.$$

Then $m_{T,i}^j(\mathbf{E}^j) = a_i^j o_i^j + b_i^j \mathbf{b}_i^T \mathbf{E}^j$. Using the law of total expectation, we obtain

$$\begin{aligned} \mathbb{E}\left[T_i^j \mathbf{E}^j\right] &= a_i^j o_i^j \mathbf{m}_E^j + b_i^j \left(\mathbf{V}_E^j + \mathbf{m}_E^j \left(\mathbf{m}_E^j\right)^T\right) \mathbf{b}_i \\ \mathbb{E}\left[\left(T_i^j\right)^2\right] &= V_{T,i}^j + \left(a_i^j o_i^j\right)^2 + 2a_i^j o_i^j b_i^j \mathbf{b}_i^T \mathbf{m}_E^j + \left(b_i^j\right)^2 \mathbf{b}_i^T \left(\mathbf{V}_E^j + \mathbf{m}_E^j \left(\mathbf{m}_E^j\right)^T\right) \mathbf{b}_i. \end{aligned}$$

Differentiating the expected complete-data log-likelihood yields M-step updates analogous to the single-endophenotype case. In particular, the update for the K -vector of coefficients for trait i , \mathbf{b}_i , is

$$\mathbf{b}_i = \left(\sum_j \mathbb{E}\left[\mathbf{E}^j (\mathbf{E}^j)^T\right]\right)^{-1} \left(\sum_j \mathbb{E}\left[T_i^j \mathbf{E}^j\right]\right),$$

with the understanding that if the configuration fixes certain entries of \mathbf{b}_i to zero, the corresponding rows/columns should be removed from the linear system and the fixed entries restored after solving. The update for σ_i^2 is

$$\sigma_i^2 = \frac{1}{N} \sum_j \mathbb{E}\left[\left(T_i^j - \mathbf{b}_i^T \mathbf{E}^j\right)^2\right],$$

and the updates for μ_k and τ_k^2 are

$$\mu_k = \frac{1}{N} \sum_j \mathbb{E}\left[E_k^j\right], \quad \tau_k^2 = \frac{1}{N} \sum_j \mathbb{E}\left[\left(E_k^j - \mu_k\right)^2\right].$$

Finally, we note that inference can also be performed by Gibbs sampling. In a Gibbs sampler, we alternate sampling $T_i^j \mid \mathbf{E}^j, o_i^j$ using the univariate normal conditional above, and sampling $\mathbf{E}^j \mid \mathbf{T}^j$ using the multivariate normal conditional

$$\mathbf{E}^j \mid \mathbf{T}^j \sim \mathcal{N}\left(\mathbf{m}_{E|T}^j, \mathbf{V}_{E|T}\right),$$

where

$$\mathbf{V}_{E|T} = \left(\boldsymbol{\Sigma}_E^{-1} + \mathbf{B}^T \text{diag}\left(\frac{1}{\sigma_1^2}, \dots, \frac{1}{\sigma_q^2}\right) \mathbf{B}\right)^{-1}, \quad \mathbf{m}_{E|T}^j = \mathbf{V}_{E|T} \left(\boldsymbol{\Sigma}_E^{-1} \mu + \mathbf{B}^T \text{diag}\left(\frac{1}{\sigma_1^2}, \dots, \frac{1}{\sigma_q^2}\right) \mathbf{t}^j\right).$$

S.4 Extension to allow edges between traits

We can extend the model to allow dependencies among traits not captured by the endophenotypes by adding directed edges between the true trait effects T_1, \dots, T_q . Let $\text{Pa}(i)$ denote the set of parent traits of T_i in a user-specified directed acyclic graph (DAG). For each directed edge $T_p \rightarrow T_i$, introduce a coefficient α_{ip} which captures the contribution of the true effect on trait p to the true effect on trait i , beyond what is explained by the endophenotypes. If an edge $T_p \rightarrow T_i$ is absent from the graph, we fix $\alpha_{ip} = 0$. The resulting graphical model is shown in Figure ??.

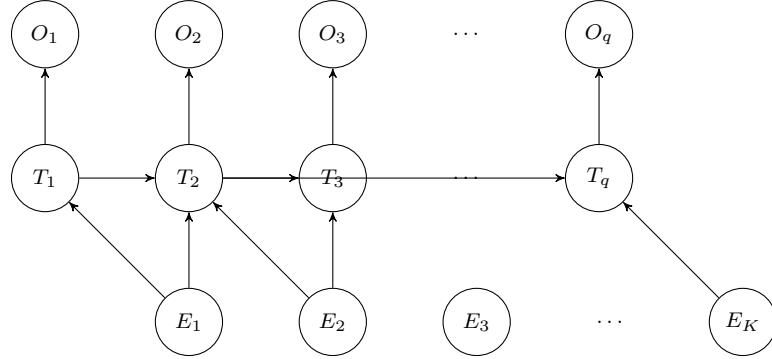


Figure 3: Model for phenotypic effects of a variant with multiple endophenotypes and directed edges between traits

We then specify

$$T_i \sim \mathcal{N} \left(\mathbf{b}_i^T \mathbf{E} + \sum_{p \in \text{Pa}(i)} \alpha_{ip} T_p, \sigma_i^2 \right), \quad O_i \sim \mathcal{N} (T_i, s_i^2),$$

together with the prior on \mathbf{E} from the previous section. Because the trait graph is required to be a DAG, there exists a topological ordering of traits under which each trait depends only on traits earlier in the ordering; if a cycle is present, the model does not define a valid Bayesian network and inference should be refused.

It is convenient to write this extension in matrix form. Let \mathbf{A} be the $q \times q$ matrix with entries $(\mathbf{A})_{ip} = \alpha_{ip}$, and define $\mathbf{L} = \mathbf{I} - \mathbf{A}$. Under the DAG assumption, \mathbf{L} is invertible. Let $\mathbf{D} = \text{diag}(\sigma_1^2, \dots, \sigma_q^2)$. Then the trait model can be written as the linear structural equation

$$\mathbf{LT}^j = \mathbf{BE}^j + \boldsymbol{\varepsilon}^j, \quad \boldsymbol{\varepsilon}^j \sim \mathcal{N} (\mathbf{0}, \mathbf{D}),$$

and hence

$$\begin{aligned} \mathbf{T}^j | \mathbf{E}^j &\sim \mathcal{N} (\mathbf{ME}^j, \Sigma_T) \\ \mathbf{M} &= \mathbf{L}^{-1} \mathbf{B} \\ \Sigma_T &= \mathbf{L}^{-1} \mathbf{D} (\mathbf{L}^{-1})^T. \end{aligned}$$

The observation model remains conditionally independent given \mathbf{T}^j . Let $\mathbf{S}^j = \text{diag}((s_1^j)^2, \dots, (s_q^j)^2)$. Then, collapsing over \mathbf{T}^j yields

$$\mathbf{O}^j | \mathbf{E}^j \sim \mathcal{N} (\mathbf{ME}^j, \mathbf{V}^j), \quad \mathbf{V}^j = \Sigma_T + \mathbf{S}^j.$$

As above, the posterior distribution of \mathbf{E}^j given \mathbf{o}^j is multivariate normal:

$$\begin{aligned}\mathbf{E}^j | \mathbf{o}^j &\sim \mathcal{N} \left(\mathbf{m}_E^j, \mathbf{V}_E^j \right) \\ \mathbf{V}_E^j &= \left(\boldsymbol{\Sigma}_E^{-1} + \mathbf{M}^T (\mathbf{V}^j)^{-1} \mathbf{M} \right)^{-1} \\ \mathbf{m}_E^j &= \mathbf{V}_E^j \left(\boldsymbol{\Sigma}_E^{-1} \mu + \mathbf{M}^T (\mathbf{V}^j)^{-1} \mathbf{o}^j \right).\end{aligned}$$

In addition, the posterior mean of the true trait effects can be computed in closed form. Since $\mathbf{T}^j | \mathbf{E}^j$ and $\mathbf{O}^j | \mathbf{T}^j$ are both multivariate normal, we have

$$\mathbb{E} [\mathbf{T}^j | \mathbf{o}^j] = \mathbf{M} \mathbf{m}_E^j + \boldsymbol{\Sigma}_T (\mathbf{V}^j)^{-1} \left(\mathbf{o}^j - \mathbf{M} \mathbf{m}_E^j \right).$$

For fitting the model using EM, the sufficient statistics can be obtained from the joint multivariate normal posterior of $(\mathbf{E}^j, \mathbf{T}^j) | \mathbf{o}^j$, and the M-step updates for $(\mathbf{b}_i, \{\alpha_{ip}\}_{p \in \text{Pa}(i)})$ correspond to a linear regression of T_i on the predictors $(\mathbf{E}, \mathbf{T}_{\text{Pa}(i)})$ using posterior expected cross-products.

As in the previous section, inference can also be performed by Gibbs sampling. One convenient Gibbs scheme alternates the block updates

$$\mathbf{T}^j | \mathbf{E}^j, \mathbf{o}^j \sim \mathcal{N} \left(\mathbf{m}_{T|E}^j, \boldsymbol{\Sigma}_{T|E}^j \right), \quad \mathbf{E}^j | \mathbf{T}^j \sim \mathcal{N} \left(\mathbf{m}_{E|T}^j, \mathbf{V}_{E|T} \right),$$

where

$$\begin{aligned}\mathbf{m}_{T|E}^j &= \mathbf{M} \mathbf{E}^j + \boldsymbol{\Sigma}_T (\mathbf{V}^j)^{-1} (\mathbf{o}^j - \mathbf{M} \mathbf{E}^j) \\ \boldsymbol{\Sigma}_{T|E}^j &= \boldsymbol{\Sigma}_T - \boldsymbol{\Sigma}_T (\mathbf{V}^j)^{-1} \boldsymbol{\Sigma}_T.\end{aligned}$$

For the $\mathbf{E}^j | \mathbf{T}^j$ update, define $\mathbf{y}^j = \mathbf{L} \mathbf{T}^j$. Then $\mathbf{y}^j | \mathbf{E}^j \sim \mathcal{N}(\mathbf{B} \mathbf{E}^j, \mathbf{D})$, and hence

$$\begin{aligned}\mathbf{V}_{E|T} &= (\boldsymbol{\Sigma}_E^{-1} + \mathbf{B}^T \mathbf{D}^{-1} \mathbf{B})^{-1} \\ \mathbf{m}_{E|T}^j &= \mathbf{V}_{E|T} (\boldsymbol{\Sigma}_E^{-1} \mu + \mathbf{B}^T \mathbf{D}^{-1} \mathbf{y}^j).\end{aligned}$$

Alternatively, one can update the trait nodes T_i one-at-a-time using their Markov blanket in the trait DAG; the resulting full conditionals are univariate normal.

S.5 Control for outlier traits

A practical failure mode of the base model is that a single trait with an extremely strong observed association can force the posterior endophenotype \mathbf{E}^j to be large, because the model has no other mechanism to explain a highly unlikely observation. In applications where we seek variants that match a coherent multi-trait pattern (rather than variants driven by a single trait), this behavior is undesirable.

We address this by introducing, for each trait i and variant j , a binary indicator $Z_i^j \in \{0, 1\}$ which controls an inflation of the residual variance in the trait layer. Intuitively, when $Z_i^j = 1$ trait i is treated as an “outlier” for variant j and is given less influence on the inferred endophenotypes.

Model definition

Let $\kappa > 1$ denote a variance inflation factor. Let $\pi_i \in (0, 1)$ be the prior probability that trait i is an outlier for a randomly chosen variant. (In many applications we will impose $\pi_i \equiv \pi$ for all traits for stability and interpretability.)

For each variant j and trait i , define

$$Z_i^j \sim \text{Bernoulli}(\pi_i), \quad c(Z_i^j) = \begin{cases} 1, & Z_i^j = 0 \\ \kappa^2, & Z_i^j = 1. \end{cases}$$

We extend the trait layer to

$$T_i^j \mid \mathbf{E}^j, \mathbf{T}_{\text{Pa}(i)}^j, Z_i^j \sim \mathcal{N} \left(\mathbf{b}_i^T \mathbf{E}^j + \sum_{p \in \text{Pa}(i)} \alpha_{ip} T_p^j, \sigma_i^2 c(Z_i^j) \right),$$

and retain the observation model

$$O_i^j \mid T_i^j \sim \mathcal{N} \left(T_i^j, (s_i^j)^2 \right).$$

When $Z_i^j = 1$, the increased variance $\kappa^2 \sigma_i^2$ reduces the leverage of trait i on \mathbf{E}^j and on the fitted loadings, providing a mechanism to “soak up” trait-specific signals that do not align with the multi-trait pattern.

It is convenient to write this in matrix form (as in the trait-edge extension). Let \mathbf{A} be the matrix of trait-edge coefficients, and let $\mathbf{L} = \mathbf{I} - \mathbf{A}$. For each variant j , define the diagonal matrix

$$\mathbf{D}^j(\mathbf{Z}^j) = \text{diag} \left(\sigma_1^2 c(Z_1^j), \dots, \sigma_q^2 c(Z_q^j) \right).$$

Conditional on $\mathbf{Z}^j = (Z_1^j, \dots, Z_q^j)$, the trait layer becomes

$$\mathbf{LT}^j = \mathbf{BE}^j + \boldsymbol{\varepsilon}^j, \quad \boldsymbol{\varepsilon}^j \sim \mathcal{N} (\mathbf{0}, \mathbf{D}^j(\mathbf{Z}^j)).$$

Therefore

$$\begin{aligned} \mathbf{T}^j \mid \mathbf{E}^j, \mathbf{Z}^j &\sim \mathcal{N} \left(\mathbf{ME}^j, \Sigma_T^j(\mathbf{Z}^j) \right) \\ \mathbf{M} &= \mathbf{L}^{-1} \mathbf{B} \\ \Sigma_T^j(\mathbf{Z}^j) &= \mathbf{L}^{-1} \mathbf{D}^j(\mathbf{Z}^j) (\mathbf{L}^{-1})^T. \end{aligned}$$

Let $\mathbf{S}^j = \text{diag} \left((s_1^j)^2, \dots, (s_q^j)^2 \right)$. Collapsing over \mathbf{T}^j yields

$$\mathbf{O}^j \mid \mathbf{E}^j, \mathbf{Z}^j \sim \mathcal{N} \left(\mathbf{ME}^j, \mathbf{V}^j(\mathbf{Z}^j) \right), \quad \mathbf{V}^j(\mathbf{Z}^j) = \Sigma_T^j(\mathbf{Z}^j) + \mathbf{S}^j.$$

Estimation: analytic (exact) E-step by enumerating \mathbf{Z}^j

Conditional on \mathbf{Z}^j , the model remains linear-Gaussian, so the posterior of \mathbf{E}^j given \mathbf{o}^j and \mathbf{Z}^j is multivariate normal:

$$\begin{aligned} \mathbf{E}^j \mid \mathbf{o}^j, \mathbf{Z}^j &\sim \mathcal{N} \left(\mathbf{m}_E^j(\mathbf{Z}^j), \mathbf{V}_E^j(\mathbf{Z}^j) \right) \\ \mathbf{V}_E^j(\mathbf{Z}^j) &= \left(\Sigma_E^{-1} + \mathbf{M}^T (\mathbf{V}^j(\mathbf{Z}^j))^{-1} \mathbf{M} \right)^{-1} \\ \mathbf{m}_E^j(\mathbf{Z}^j) &= \mathbf{V}_E^j(\mathbf{Z}^j) \left(\Sigma_E^{-1} \mu + \mathbf{M}^T (\mathbf{V}^j(\mathbf{Z}^j))^{-1} \mathbf{o}^j \right). \end{aligned}$$

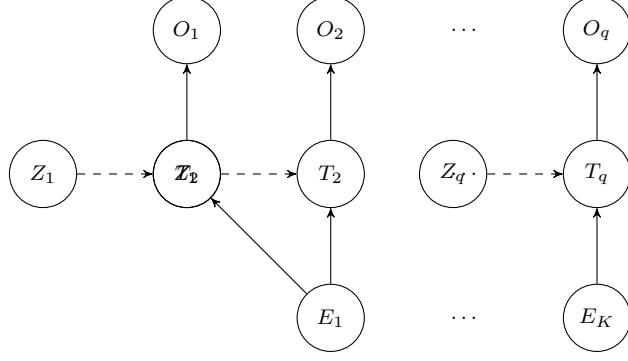


Figure 4: Adding per-trait outlier indicators Z_i that inflate the residual variance in the trait layer by a factor κ^2 when $Z_i = 1$

Similarly, the posterior mean of \mathbf{T}^j conditional on \mathbf{Z}^j is

$$\mathbb{E} [\mathbf{T}^j | \mathbf{o}^j, \mathbf{Z}^j] = \mathbf{Mm}_E^j(\mathbf{Z}^j) + \Sigma_T^j(\mathbf{Z}^j) (\mathbf{V}^j(\mathbf{Z}^j))^{-1} \left(\mathbf{o}^j - \mathbf{Mm}_E^j(\mathbf{Z}^j) \right).$$

To obtain the unconditional posterior, we marginalize over $\mathbf{Z}^j \in \{0, 1\}^q$:

$$\Pr(\mathbf{Z}^j = \mathbf{z}) = \prod_{i=1}^q \pi_i^{z_i} (1 - \pi_i)^{1-z_i}, \quad \Pr(\mathbf{Z}^j = \mathbf{z} | \mathbf{o}^j) \propto \Pr(\mathbf{Z}^j = \mathbf{z}) \Pr(\mathbf{o}^j | \mathbf{Z}^j = \mathbf{z}).$$

Since $\mathbf{o}^j | \mathbf{Z}^j$ is Gaussian after integrating out \mathbf{E}^j , $\Pr(\mathbf{o}^j | \mathbf{Z}^j = \mathbf{z})$ can be computed in closed form, and the posterior over \mathbf{Z}^j can be normalized by summing over all 2^q configurations.

Let $\gamma^j(\mathbf{z}) = \Pr(\mathbf{Z}^j = \mathbf{z} | \mathbf{o}^j)$. Then posterior expectations are mixture averages, for example

$$\mathbb{E} [\mathbf{E}^j | \mathbf{o}^j] = \sum_{\mathbf{z}} \gamma^j(\mathbf{z}) \mathbf{m}_E^j(\mathbf{z}), \quad \mathbb{E} [\mathbf{E}^j (\mathbf{E}^j)^T | \mathbf{o}^j] = \sum_{\mathbf{z}} \gamma^j(\mathbf{z}) \left(\mathbf{V}_E^j(\mathbf{z}) + \mathbf{m}_E^j(\mathbf{z}) \mathbf{m}_E^j(\mathbf{z})^T \right).$$

The outlier responsibility for trait i at variant j is

$$\phi_i^j \equiv \Pr(Z_i^j = 1 | \mathbf{o}^j) = \sum_{\mathbf{z}} \gamma^j(\mathbf{z}) z_i.$$

For EM training with fixed (κ, π_i) , the M-step updates for the trait coefficients become weighted least squares. Define the regression residual

$$r_i^j = T_i^j - \mathbf{b}_i^T \mathbf{E}^j - \sum_{p \in \text{Pa}(i)} \alpha_{ip} T_p^j.$$

Then, using the expected complete-data log-likelihood, the variance update is

$$\sigma_i^2 = \frac{1}{\sum_j w_j} \sum_j w_j \mathbb{E} \left[\frac{(r_i^j)^2}{c(Z_i^j)} \mid \hat{\mathbf{O}} \right],$$

and the coefficient updates for $(\mathbf{b}_i, \{\alpha_{ip}\})$ correspond to solving the normal equations formed from the weighted cross-products $\mathbb{E} \left[(\mathbf{E}^j, \mathbf{T}_{\text{Pa}(i)}^j) (\mathbf{E}^j, \mathbf{T}_{\text{Pa}(i)}^j)^T / c(Z_i^j) \right]$ and $\mathbb{E} \left[T_i^j (\mathbf{E}^j, \mathbf{T}_{\text{Pa}(i)}^j)^T / c(Z_i^j) \right]$.

This analytic approach is exact, but its cost grows as $O(2^q)$ per variant and is only practical for small numbers of traits.

Estimation: variational approximation

For larger q , we can approximate the posterior with a mean-field family

$$q(\mathbf{E}^j, \mathbf{T}^j, \mathbf{Z}^j) = q(\mathbf{E}^j, \mathbf{T}^j) \prod_{i=1}^q q(Z_i^j), \quad q(Z_i^j = 1) = \phi_i^j.$$

Define

$$\alpha_i^j \equiv \mathbb{E}_q \left[\frac{1}{c(Z_i^j)} \right] = (1 - \phi_i^j) + \frac{\phi_i^j}{\kappa^2}.$$

A standard coordinate ascent update yields $q(\mathbf{E}^j, \mathbf{T}^j)$ as a Gaussian distribution obtained by replacing the diagonal residual covariance $\mathbf{D}^j(\mathbf{Z}^j)$ with an effective covariance

$$\tilde{\mathbf{D}}^j \equiv \text{diag} \left(\frac{\sigma_1^2}{\alpha_1^j}, \dots, \frac{\sigma_q^2}{\alpha_q^j} \right), \quad \tilde{\Sigma}_T^j = \mathbf{L}^{-1} \tilde{\mathbf{D}}^j (\mathbf{L}^{-1})^T, \quad \tilde{\mathbf{V}}^j = \tilde{\Sigma}_T^j + \mathbf{S}^j.$$

Thus the approximate posterior of \mathbf{E}^j is

$$\begin{aligned} q(\mathbf{E}^j) &= \mathcal{N} \left(\tilde{\mathbf{m}}_E^j, \tilde{\mathbf{V}}_E^j \right) \\ \tilde{\mathbf{V}}_E^j &= \left(\Sigma_E^{-1} + \mathbf{M}^T \left(\tilde{\mathbf{V}}^j \right)^{-1} \mathbf{M} \right)^{-1} \\ \tilde{\mathbf{m}}_E^j &= \tilde{\mathbf{V}}_E^j \left(\Sigma_E^{-1} \mu + \mathbf{M}^T \left(\tilde{\mathbf{V}}^j \right)^{-1} \mathbf{o}^j \right). \end{aligned}$$

The Bernoulli factors update via the log-odds

$$\log \frac{\phi_i^j}{1 - \phi_i^j} = \log \frac{\pi_i}{1 - \pi_i} - \frac{1}{2} \log \kappa^2 + \frac{1}{2} \left(1 - \frac{1}{\kappa^2} \right) \frac{\mathbb{E}_q \left[(\epsilon_i^j)^2 \right]}{\sigma_i^2},$$

where $\epsilon^j = \mathbf{LT}^j - \mathbf{BE}^j$. Because ϵ^j is linear in $(\mathbf{T}^j, \mathbf{E}^j)$ and $q(\mathbf{T}^j, \mathbf{E}^j)$ is Gaussian, the moment $\mathbb{E}_q[(\epsilon_i^j)^2]$ can be computed from the posterior mean and covariance. Iterating these updates yields a scalable approximation which avoids the 2^q enumeration, at the cost of a mean-field approximation that typically underestimates posterior uncertainty.

For EM training, the M-step uses the same weighted least squares form as above, with the replacement $\mathbb{E}[1/c(Z_i^j)] \approx \alpha_i^j$ and $\mathbb{E}[(r_i^j)^2/c(Z_i^j)] \approx \alpha_i^j \mathbb{E}_q[(r_i^j)^2]$.

Estimation: Gibbs sampling

Finally, we can sample from the posterior by extending the existing Gibbs sampler with updates for \mathbf{Z}^j .

Given $(\mathbf{E}^j, \mathbf{T}^j)$, each Z_i^j is conditionally independent with

$$\Pr(Z_i^j = 1 | \mathbf{E}^j, \mathbf{T}^j, \mathbf{o}^j) = \frac{\pi_i \mathcal{N}(\epsilon_i^j; 0, \kappa^2 \sigma_i^2)}{\pi_i \mathcal{N}(\epsilon_i^j; 0, \kappa^2 \sigma_i^2) + (1 - \pi_i) \mathcal{N}(\epsilon_i^j; 0, \sigma_i^2)},$$

where $\epsilon^j = \mathbf{LT}^j - \mathbf{BE}^j$. Thus Z_i^j can be drawn by a Bernoulli step using the above probability.

Conditional on \mathbf{Z}^j , the updates for \mathbf{E}^j and \mathbf{T}^j remain Gaussian. For example,

$$\mathbf{E}^j \mid \mathbf{T}^j, \mathbf{Z}^j \sim \mathcal{N}\left(\mathbf{m}_{E|T}^j, \mathbf{V}_{E|T}^j\right), \quad \mathbf{V}_{E|T}^j = \left(\boldsymbol{\Sigma}_E^{-1} + \mathbf{B}^T (\mathbf{D}^j(\mathbf{Z}^j))^{-1} \mathbf{B}\right)^{-1},$$

and $\mathbf{m}_{E|T}^j$ follows by conjugacy using $\mathbf{L}\mathbf{T}^j$ as the Gaussian observation for $\mathbf{B}\mathbf{E}^j$.

The conditional for each T_i^j can be updated as in the trait-edge Gibbs scheme, except that each occurrence of σ_i^2 is replaced by $\sigma_i^2 c(Z_i^j)$, and child contributions use the corresponding child variance $\sigma_c^2 c(Z_c^j)$.

Gibbs sampling is asymptotically exact and can handle large numbers of traits and complex trait graphs, but it can be slower and requires burn-in and convergence diagnostics. In contrast, analytic enumeration is exact but only feasible for small q , and the variational approximation is scalable and fast but approximate. When q is small, the analytic approach dominates. For moderate or large q without requiring exact posterior uncertainty, the variational approximation is usually preferred. Gibbs sampling is most appropriate when exactness is important or when the variational approximation is unstable, at the cost of runtime.

S.6 Determining κ and π

The hyperparameters κ and π_i control how aggressively the model downweights trait-specific outliers. These parameters are not reliably identified from positives alone, and in many applications we choose them to optimize separation between a curated positive set and a large background set of variants. We therefore recommend selecting (κ, π) by cross-validation with an objective that emphasizes the extreme tail of the ranked list, which is the relevant regime for genome-wide screening.

Scoring function

For each variant j , inference under a fixed (κ, π) yields a posterior mean and covariance for \mathbf{E}^j , denoted $(\mathbf{m}_E^j, \mathbf{V}_E^j)$ (using analytic, variational, or Gibbs inference). We define an endophenotype evidence score

$$S^j \equiv \left(\mathbf{m}_E^j\right)^T \left(\mathbf{V}_E^j\right)^{-1} \mathbf{m}_E^j,$$

which is the squared Mahalanobis norm of the posterior mean. In the single-endophenotype case this reduces to the squared posterior z -score $(m_E^j / \sqrt{V_E^j})^2$. This score increases when the data support a coherent endophenotype signal with small posterior uncertainty, and it decreases when the signal is explained instead by one or more outlier indicators Z_i^j .

Composite cross-validation metric

Let \mathcal{P} denote the curated positive set. Let \mathcal{B} denote a large background set (e.g., random variants from the genome-wide set excluding \mathcal{P}). Optionally, let \mathcal{H} denote a “hard negative” set (e.g., variants significant for one trait but not others).

For a target background false positive rate α (e.g., $\alpha = 10^{-3}$ or 10^{-4}), define the threshold t_α as the $(1 - \alpha)$ empirical quantile of S^j over \mathcal{B} . Define

$$\text{TPR}_\alpha = \frac{1}{|\mathcal{P}|} \sum_{j \in \mathcal{P}} \mathbf{1}\{S^j \geq t_\alpha\}, \quad \text{FPR}_{\alpha, \text{hard}} = \frac{1}{|\mathcal{H}|} \sum_{j \in \mathcal{H}} \mathbf{1}\{S^j \geq t_\alpha\}.$$

We propose the composite metric

$$\text{Score}(\kappa, \pi) = \frac{1}{|\mathcal{A}|} \sum_{\alpha \in \mathcal{A}} (\text{TPR}_\alpha - \lambda \text{FPR}_{\alpha, \text{hard}}),$$

where \mathcal{A} is a small set of tail operating points (e.g., $\{10^{-3}, 10^{-4}\}$) and $\lambda \geq 0$ is a penalty weight (e.g., $\lambda = 1$). If no hard-negative set is available, we set $\lambda = 0$.

This metric directly targets performance in the extreme tail while guarding against trivial improvements that simply inflate scores for many single-trait signals.

Cross-validation procedure

We recommend selecting (κ, π) over a grid (typically log-spaced for π and a small set of κ values). Let \mathcal{P} be split into K folds $\mathcal{P}_1, \dots, \mathcal{P}_K$. For each grid point (κ, π) , we repeat:

1. For each fold k :
 - (a) Train model parameters θ on $\mathcal{P} \setminus \mathcal{P}_k$ using EM (with the chosen inference method holding (κ, π) fixed).
 - (b) Compute scores S^j for $j \in \mathcal{P}_k$, and for sampled sets from \mathcal{B} (and \mathcal{H} , if used).
 - (c) Compute the composite metric for fold k .
2. Average the fold metrics to obtain $\text{Score}(\kappa, \pi)$.

Select the grid point with the largest score, then retrain θ on the full positive set \mathcal{P} using the selected (κ, π) .

Fast abbreviated option

The procedure above is statistically clean but can be expensive because EM is nested inside the cross-validation loop. A faster approximation is:

1. Train θ once on all positives using a reasonable default (κ, π) (or with $\pi = 0$ as a baseline).
2. Holding θ fixed, choose (κ, π) by cross-validation using only the inference step and the scoring metric above.
3. Optionally run a final EM training pass using the selected (κ, π) .

This abbreviated procedure is appropriate when the fitted structural parameters θ are relatively stable across plausible choices of (κ, π) , which is often the case when κ and π primarily modulate how outliers are downweighted rather than changing the coherent multi-trait signal.