

# 1 Supplementary Note S1: Derivation of Bayes factors for a set of risk factors

Building on the 2-sample MR approach [1] our work is based on summarised data, where genetic variants are used as instrumental variables. For each genetic variant  $i = 1, \dots, n$  we observe the association of variant  $i$  with the risk factor  $X$  measured by the beta-coefficient  $\beta_{X_i}$  from a univariable regression where the genetic variant  $i$  is regressed on the risk factor  $X$ , and the association of variant  $i$  with the outcome  $Y$  measured by the beta-coefficient  $\beta_{Y_i}$  where the genetic variant  $i$  is regressed on the outcome  $Y$ , respectively. In fact, the beta-coefficients are estimates of the genetic association, but we omit the "hat" notation and treat the beta-coefficient as observations.

Multivariable MR [2] can be cast as a weighted linear regression model

$$\begin{aligned}\beta_Y &= \theta_1\beta_{X_1} + \dots + \theta_d\beta_{X_d} + \epsilon, \text{ weights} = se(\beta_Y)^{-2} \\ &= \beta_X\theta + \epsilon, \text{ weights} = se(\beta_Y)^{-2},\end{aligned}\tag{1}$$

where the dependent variable is the association with the outcome  $\beta_Y$  measured on  $i = 1, \dots, n$  instrumental variables and the predictors are the  $j = 1, \dots, d$  genetic associations with the  $d$  risk factors  $\beta_X = \{\beta_{X_1}, \dots, \beta_{X_d}\}$ , which is a matrix of dimension  $n \times d$  where  $d$  is the number of risk factors and  $n$  is the number of genetic variants. Again each individual element  $\beta_{X_{i,j}}$  of the predictor matrix is derived from a univariable regression where the genetic variant  $i$  is regressed on the risk factor  $X_j$ . In other words, the risk factors represent the variable space and the instrumental genetic variants are our observations. In practise, we standardise each observation of both,  $\beta_{Y_i}$  and  $\beta_{X_i}$  by dividing by  $se(\beta_{Y_i})$  before the analysis and we assume in the following derivations that  $\beta_Y$  and  $\beta_X$  are standardised.

We use Bayes factors [3] in order to quantify the evidence for a particular model. With model we refer to either one or a set of risk factors to have a causal effect on the outcome of interest. In order to formalise which risk factors are part of a specific model  $M_\gamma$  we introduce a binary indicator  $\gamma$  of length  $d$  that indicates which risk factors are selected and which ones are not

$$\gamma_j = \begin{cases} 1, & \text{if the } j\text{th risk factor is selected,} \\ 0 & \text{otherwise.} \end{cases}\tag{2}$$

The indicator  $\gamma$  encodes a specific regression model  $M_\gamma$  that includes the risk factors as indicated in  $\gamma$ . Accordingly, we define  $\beta_{X_\gamma}$  as the design matrix of the risk factors included and  $\theta_\gamma$  as the respective causal effects.

The computation of the Bayes factor for model  $M_\gamma$  against the Null model  $M_0$  as presented in the Methods section of the main article requires two ingredients: First the the marginal probability of  $\beta_Y$  given  $\beta_{X_\gamma}$  of model  $M_\gamma$  and second, the marginal probability of  $\beta_Y$  given the Null model  $M_0$ , which we derive as follows:

1.  $p_\gamma(\beta_Y | \beta_{X_\gamma})$ : the marginal probability of  $\beta_Y$  given  $\beta_{X_\gamma}$

In order to model the correlation between risk factors we base our likelihood on a multivariate Gaussian distribution

$$\beta_Y | \beta_{X_\gamma}, \theta_\gamma, \tau \sim N(\beta_{X_\gamma} \theta_\gamma, \frac{1}{\tau}). \quad (3)$$

Following Servin and Stephens'  $D_2$  prior [4] we use the following conjugate prior assumptions for the causal effects  $\theta$ , the residual  $\epsilon$  and the precision  $\tau$

$$\begin{aligned} \theta_\gamma | \tau &\sim N(0, \nu/\tau), \\ \epsilon &\sim N(0, \frac{1}{\tau}), \\ \tau &\sim \Gamma(\kappa/2, \lambda/2). \end{aligned} \quad (4)$$

Further we can derive analytically the joint posterior distribution for  $\theta_\gamma$  and  $\tau$  as

$$\begin{aligned} \tau | \beta_Y, \beta_{X_\gamma} &\sim \Gamma((n + \kappa)/2, 1/2(\beta_Y^t \beta_Y - \Theta^t \Omega^{-1} \Theta + \lambda)), \\ \theta_\gamma | \beta_Y, \beta_{X_\gamma}, \tau &\sim N(\Theta, \frac{1}{\tau} \Omega), \end{aligned}$$

where

$$\underbrace{\Theta}_{d \times 1} = \underbrace{\Omega}_{d \times d} \underbrace{\beta_{X_\gamma}^t}_{d \times n} \underbrace{\beta_Y}_{n \times 1}, \quad (5)$$

$$\Omega = \underbrace{(\nu^{-1} + \beta_{X_\gamma}^t \beta_{X_\gamma})^{-1}}_{d \times d}. \quad (6)$$

Next we integrate out the causal effects  $\theta_\gamma$ . To begin with we sort the equation so that the integral contains only terms dependent on  $\theta_\gamma$

$$\begin{aligned} p_\gamma(\beta_Y | \beta_{X_\gamma}, \tau) &= \int_{-\text{inf}}^{\text{inf}} \frac{p_\gamma(\beta_Y | \beta_{X_\gamma}, \theta_\gamma, \tau) p_\gamma(\theta_\gamma | \tau)}{p_\gamma(\theta_\gamma | \beta_Y, \beta_{X_\gamma}, \tau)} \delta \theta_\gamma \\ &= \int_{-\text{inf}}^{\text{inf}} \frac{(2\pi)^{-\frac{n}{2}} \tau^{\frac{n}{2}} \exp(-\frac{\tau}{2}(\beta_Y - \beta_{X_\gamma} \theta_\gamma)^t (\beta_Y - \beta_{X_\gamma} \theta_\gamma))}{(2\pi)^{-\frac{1}{2}} \frac{|\Omega|^{-1/2}}{|\tau|^{-1/2}} \exp(-\frac{\tau}{2}(\theta_\gamma - \Theta)^t \Omega^{-1}(\theta_\gamma - \Theta))} \\ &\quad \times (2\pi)^{-\frac{1}{2}} \frac{|\nu|^{-1/2}}{|\tau|^{-1/2}} \exp\left(-\frac{\tau}{2\nu} \theta_\gamma^t \theta_\gamma\right) \delta \theta_\gamma \\ &= (2\pi)^{-\frac{n}{2}} \tau^{\frac{n}{2}} \frac{|\Omega|^{1/2}}{|\nu|^{1/2}} \exp\left(-\frac{1}{2}(\beta_Y^t \beta_Y - \Theta^t \Omega^{-1} \Theta) \tau\right) \\ &\quad \int_{-\text{inf}}^{\text{inf}} \exp\left(-\frac{1}{2}(2\theta_\gamma^t \beta_{X_\gamma}^t \beta_Y + \theta_\gamma^t \beta_{X_\gamma}^t \beta_{X_\gamma} \theta_\gamma - \frac{1}{\nu} \theta_\gamma^t \theta_\gamma - \theta_\gamma^t \Omega^{-1} \theta_\gamma + 2\theta_\gamma^t \Omega^{-1} \Theta) \tau\right) \delta \theta_\gamma. \end{aligned}$$

By completing the square and integrating out  $\theta_\gamma$  this simplifies to

$$p_\gamma(\beta_Y | \beta_{X_\gamma}, \tau) = (2\pi)^{-\frac{n}{2}} \tau^{\frac{n}{2}} \frac{|\Omega|^{1/2}}{|\nu|^{1/2}} \exp\left(-\frac{1}{2}(\beta_Y^t \beta_Y - \Theta^t \Omega^{-1} \Theta) \tau\right) \quad (7)$$

Next we integrate out the precision  $\tau$

$$\begin{aligned} p_\gamma(\beta_Y | \beta_{X_\gamma}) &= \int_0^{\text{inf}} p_\gamma(\beta_Y | \beta_{X_\gamma}, \tau) p(\tau) \delta\tau \quad (8) \\ &= (2\pi)^{-\frac{n}{2}} \frac{|\Omega|^{1/2}}{|\nu|^{1/2}} \times \\ &\quad \int_0^{\text{inf}} \tau^{\frac{(n+\kappa)}{2}-1} \exp\left(-\frac{1}{2}(\beta_Y^t \beta_Y - \Theta^t \Omega^{-1} \Theta + \lambda) \tau\right) \delta\tau. \end{aligned}$$

The above integral is the normalisation constant of a Gamma distribution with shape  $\alpha = \frac{(n+\kappa)}{2}$  and rate  $\beta = \frac{1}{2}(\beta_Y^t \beta_Y - \Theta^t \Omega^{-1} \Theta + \lambda)$ . Thus the above simplifies to

$$p_\gamma(\beta_Y | \beta_{X_\gamma}) = (2\pi)^{-\frac{n}{2}} \frac{|\Omega|^{1/2}}{|\nu|^{1/2}} \left(\frac{\lambda}{2}\right)^{\frac{\kappa}{2}} \frac{\Gamma(\frac{n+\kappa}{2})}{\Gamma(\frac{\kappa}{2})} \left(\frac{1}{2}(\beta_Y^t \beta_Y - \Theta^t \Omega^{-1} \Theta + \lambda)\right)^{-\frac{(n+\kappa)}{2}}. \quad (9)$$

2.  $p_0(\beta_Y)$ : the marginal probability of  $\beta_Y$  given the Null model  $M_0$

Next, we derive the marginal probability of the Null model, i.e. where no risk factor and no intercept is included. Under the Null we assume

$$\beta_Y | \frac{1}{\tau} \sim N\left(0, \frac{1}{\tau}\right) \quad (10)$$

with an expectation fixed at zero, which is a consequence of the missing intercept.

First, we integrate out the precision  $\tau$

$$\begin{aligned} p_0(\beta_Y) &= \int_0^{\text{inf}} p_0(\beta_Y | \tau) p(\tau) \delta\tau \\ &= (2\pi)^{-\frac{n}{2}} \int_0^{\text{inf}} \tau^{\frac{(n+\kappa)}{2}-1} \exp\left(-\frac{1}{2}(\beta_Y^t \beta_Y + \lambda) \tau\right) \delta\tau. \quad (11) \end{aligned}$$

Again the above integral is the normalisation constant of a Gamma distribution with shape  $\alpha = \frac{(n+\kappa)}{2}$  and rate  $\beta_0 = \frac{1}{2}(\beta_Y^t \beta_Y + \lambda)$ . Thus the above simplifies to

$$p_0(\beta_Y) = (2\pi)^{-\frac{n}{2}} \left(\frac{\lambda}{2}\right)^{\frac{\kappa}{2}} \frac{\Gamma(\frac{n+\kappa}{2})}{\Gamma(\frac{\kappa}{2})} \left(\frac{1}{2}(\beta_Y^t \beta_Y + \lambda)\right)^{-\frac{(n+\kappa)}{2}}. \quad (12)$$

The Bayes factor for model  $M_\gamma$  against  $M_0$  is defined as the ratio of the marginal probability of  $\beta_Y$  given model  $M_\gamma$  (9) over the marginal probability of  $\beta_Y$  given the Null model (12)

$$\begin{aligned}
BF(M_\gamma) &= \frac{p_\gamma(\beta_Y \mid \beta_{X_\gamma})}{p_0(\beta_Y)} \\
&= \frac{\frac{|\Omega|^{1/2}}{|\nu|^{1/2}} \left(\frac{1}{2}(\beta_Y^t \beta_Y - \Theta^t \Omega^{-1} \Theta + \lambda)\right)^{-(n+\kappa)/2}}{\left(\frac{1}{2}(\beta_Y^t \beta_Y + \lambda)\right)^{-(n+\kappa)/2}} \\
&= \frac{|\Omega|^{1/2}}{|\nu|^{1/2}} \left(\frac{\beta_Y^t \beta_Y - \Theta^t \Omega^{-1} \Theta + \lambda}{\beta_Y^t \beta_Y + \lambda}\right)^{-(n+\kappa)/2}. \tag{13}
\end{aligned}$$

In limit  $\kappa$  and  $\lambda \rightarrow 0$  the Bayes Factor simplifies to the following closed form expression

$$BF(M_\gamma) = \frac{|\Omega|^{1/2}}{|\nu|^{1/2}} \left(\frac{\beta_Y^t \beta_Y - \Theta^t \Omega^{-1} \Theta}{\beta_Y^t \beta_Y}\right)^{-n/2}. \tag{14}$$

## References

- [1] Pierce, B. L. and Burgess, S. (2013). Efficient design for mendelian randomization studies: Subsample and 2-sample instrumental variable estimators. *American Journal of Epidemiology* *178*, 1177–1184.
- [2] Burgess, S. and Thompson, S. G. (2015). Multivariable mendelian randomization: the use of pleiotropic genetic variants to estimate causal effects. *Am J Epidemiol* *181*, 251–60.
- [3] Kass, R. E. and Raftery, A. E. (1995). Bayes factors. *Journal of the American Statistical Association* *90*, 773–795.
- [4] Servin, B. and Stephens, M. (2007). Imputation-based analysis of association studies: candidate regions and quantitative traits. *PLoS Genet* *3*, e114.