

# Bayesian Statistics for Genetics Lecture 8: Meta-analysis

July, 2023

### Overview

The ability to combine information from multiple sources is a strength of Bayesian statistics;

- Use of prior information + study data
- Combining multiple studies' data, in a *meta-analysis*

Meta-analysis was briefly introduced in Session 7 (GLMs) – here we give a more general approach, and look at *mixed models*, which are also natural in Bayesian approaches.

### Overview



- Test association of disease (Y) with genotype (X = 0/1/2) is there a signal? (If so, learn new biology)
- Tiny effects, so combine multiple studies meta-analysis

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In medium-sized studies or larger, can approximate the data from study i well, as

$$\widehat{\beta}_i \sim N(\beta_i, \sigma_i^2),$$

where each study is big enough that uncertainty about  $\sigma_i$  is negligible.

How about across studies? One very simple model assumes homogeneity, i.e.

 $\beta_i = \beta_0$ 

and, with a flat prior on common parameter  $\beta_0$ , Session 4's results tell us that

$$\widehat{\beta}_{F} = \mathbb{E}[\beta_{0}|\text{data}] = \sum_{i=1}^{k} \frac{\frac{1}{\sigma_{i}^{2}}}{\sum_{i=1}^{k} \frac{1}{\sigma_{i}^{2}}} \widehat{\beta}_{i},$$
$$\text{Var}[\widehat{\beta}_{F}] = \text{Var}[\beta_{0}|\text{data}] = \frac{1}{\sum_{i=1}^{k} \frac{1}{\sigma_{i}^{2}}}.$$

This is known as the *fixed-effect* or *common-effect* approach, and  $\hat{\beta}_F$  is the *inverse-variance weighted* or *precision-weighted* estimate

- Under true homogeneity, just as efficient as pooling all the data and adjusting for study (Lin & Zeng, 2010)
- Under true homogeneity, Uniformly Most Powerful Unbiased (i.e. best) estimate of  $\beta_0$

But

- True homogeneity is not generally plausible perhaps in lab replicates, perhaps if all  $\beta_i = 0$
- Not learning about *heterogeneity* which may be important in practice

To help think about  $\beta_i \neq \beta_0$ , consider *data* from three studies;



Parameters those 3 studies are estimating;



Differences in means  $(\beta_i)$  and information per observation  $(\phi_i)$ 

One overall population we might learn about;



Mean difference, with each sub-population represented equally.

Another overall population we might learn about;



Weights here are 2/7/1, not 1/1/1 as before.

Another overall population we might learn about;



Still an average effect, but closer to  $\beta_2$  than before.

And another; (obviously, there are unlimited possibilities)



Weights here are 7/1/2.

And another; (obviously, there are unlimited possibilities)



Weights here are 7/1/2 – smaller average effect, closer to  $\beta_1$ 

With a flat prior, among all the weighted averages which has smallest posterior variance? The answer may look familiar;

$$\beta_F = \sum_{i=1}^k \frac{\frac{1}{\sigma_i^2}}{\sum_{i=1}^k \frac{1}{\sigma_i^2}} \beta_i$$

Its posterior mean and variance are the same as we saw for common effect  $\beta_0$ 

- Known as the *fixed-effectS* approach (note the plural) it assumes one fixed effect for each study, we estimate an average
- ... the average the data tells us most about

A single estimator can have more than one valid justification. If this applies to your estimator, state why *you* are using it.

Those justifications	Name:	Common effect	Fixed effect <b>S</b>	
once again;	Assumptions:			
		Effect size	Effect size	
		All $\beta_i = \beta_0$	$\beta_i$ unrestricted	
	Plausible?	Seldom	Often	
	$\widehat{\beta}_F$ estimates:	Single $\beta_0$	An average, $\beta_F$	
	Valid estimate?	Yes	Yes	
	Var[ $\widehat{eta}_F$ ] valid?	$pprox$ Yes $^*$	$pprox$ Yes $^*$	

- When testing, only care if **all**  $\beta_i = 0$ , when common-effect=fixed-effects
- This area is surprisingly controversial...
- \* Having negligible error in  $\sigma_i$  matters, but small-sample "fixes" are available

Q. Can I use  $\hat{\beta}_F$  under heterogeneity?

A. It depends who you ask (!)

... it is no longer an estimate of any parameter, nor can its standard error or associated confidence interval be found Whitehead & Whitehead, SiM

> The assumption should thus be viewed as a potentially useful approximation Greenland & Rothman, Modern Epi, pg 270

... it does **not**, however, implicitly assume that the true effect of treatment is the same in each trial Peto et al, e.g. Lancet, 1998

Default advice makes users reluctant to report  $\hat{\beta}_F$  alone under heterogeneity.

Letting an average (e.g.  $\beta_F$ ) tell the whole story is the '*flaw* of averages';



- Average effect  $\beta_F$  answers one question
- This does not mean other questions aren't interesting!

An obvious measure of 'dispersion', i.e. spread;

$$\frac{1}{k}\sum_{i=1}^{k}(\beta_i-\beta_F)^2.$$

But we actually learn more about a weighted average of deviations around  $\beta_F$ ;

$$\zeta^2 = \frac{1}{\sum_{i=1}^k \eta_i \phi_i} \sum_{i=1}^k \eta_i \phi_i (\beta_i - \beta_F)^2.$$

An empirical estimate of this quantity can be written

$$\hat{\zeta}^2 = \frac{\sum_{i=1}^k \sigma_i^{-2} (\beta_i - \hat{\beta}_F)^2 - (k-1)}{\sum_{i=1}^k \sigma_i^{-2}} = \frac{Q - (k-1)}{\sum_{i=1}^k \sigma_i^{-2}}$$

where Q is a.k.a. Cochran's Q, and  $I^2 = 1 - (k-1)/Q$  (trunacted at zero) are standard non-Bayesian statistics for testing homogeneity.

#### Meta-analysis: exchangeability

As we've seen, no prior really describes lack of knowledge But for multiple parameters, we can (easily) state that knowledge about them is symmetric;

![](_page_18_Figure_2.jpeg)

The property  $p(\beta_1, \beta_2) = p(\beta_2, \beta_1)$  is called *exchangeability*.

#### Meta-analysis: exchangeability

Exchangeability is a weaker statement than  $p(\beta_1, \beta_2) = p(\beta_1)p(\beta_2)$ , a.k.a. *independence* (see previous slide) and a stronger statement than having identical distributions (see right).

![](_page_19_Figure_2.jpeg)

8.16

### Meta-analysis: partial exchangeability (\*)

An example with binary  $\{z_1, z_2, z_3\}$ ; (colors indicate probabilities) Are  $z_1, z_2, z_3$  identically distributed? Independent? Exchangeable?

![](_page_20_Figure_2.jpeg)

### Meta-analysis: partial exchangeability (\*)

Full exchangeability does not hold, but any two variables are exchangeable; (colors indicate probabilities again)

![](_page_21_Figure_2.jpeg)

The variables  $\{Y_1, Y_2, Y_3\}$  are 2-exchangeable; the concept can be generalized to *n*-exchangeability.

#### Meta-analysis: using exchangeability

In an exchangeable prior, there's no distinction between what we know about one  $\beta_i$  versus another. For example, a prior with exchangeable  $\beta_i$ , for meta-analysis;

$$egin{array}{rcl} \widehat{eta}_i &\sim & N(eta_i,\sigma_i^2) \ eta_i &\stackrel{i.i.d.}{\sim} & N(\mu, au^2) \end{array}$$

...for some  $\mu$ ,  $\tau^2$  – which may in turn have *hyperpriors*, describing uncertainty about the prior for the  $\beta_i$ .

This is a form of *hierarchical model* – more on these in later sessions.

Remarkably, it turns out that Bayesian hierarchical models and exchangeability are **equivalent** – this is *de Finetti's theorem*. If your beliefs on the  $\beta_i$  have exchangeability, they **must** correspond to  $\beta_i$  being random draws from some mixing distribution.

#### Meta-analysis: using exchangeability

In this hierarchical model, the default not-so-Bayesian estimate for  $\mu$  is *Der Simonian-Laird* (DSL);

$$\hat{\mu} = \frac{\sum_{i=1}^{k} \frac{1}{\sigma_i^2 + \hat{\tau}^2} \hat{\beta}_i}{\sum_{i=1}^{k} \frac{1}{\sigma_i^2 + \hat{\tau}^2}}, \quad \text{with } \operatorname{Var}[\hat{\beta}_F] = \frac{1}{\sum_{i=1}^{k} \frac{1}{\sigma_i^2 + \hat{\tau}^2}},$$
$$\text{and } \hat{\tau}^2 = \max\left(\frac{Q - (k - 1)}{\sum_{i=1}^{k} \sigma_i^{-2} - \sum_{i=1}^{k} \sigma_i^{-4}}, 0\right)$$

- DSL uses a method of moments plug-in for  $\tau^2$ , then fairly natural
- Gives  $\hat{\beta}_F$  when Q (heterogeneity) is below-average compared to homogeneity
- Estimates a weighted average of the  $\beta_i$  but where inverse-variance weights are 'moderated' by  $\tau^2$

Typical meta-analysis of 5 association studies;

G=1		G=0							
N	Mean	SD	N	Mean	SD			Μ	lean Difference, 95% Cl
33	12.1	9.8	30	7.7	9.8	F			4.40 [ -0.45 , 9.25 ]
52	4.4	1.4	49	5.1	2.8	⊢∎∹			–0.70 [ –1.57 ,0.17 ]
25	4.5	1.6	23	8.1	1.8	⊨∎→			–3.60 [ –4.57 , –2.63 ]
25	4	1.04	25	7.12	1.26	H <b>ar</b> t			–3.12 [ –3.76 , –2.48 ]
68	6.89	3.35	71	7.55	3.96	<b>⊢</b> ∎ <u>∔</u>			-0.66 [ -1.88 , 0.56 ]
72	7.9	4.25	71	7.55	3.96	<b>⊢</b> ∎1			0.35 [ -1.00 ,1.70 ]
Fixed effects (not hierarchical)				•			-2.04 [ -2.45 , -1.64 ]		
Hie	rarchical	(DerSir	nonia	n–Laird)	)	-			–1.21 [ –2.69 , 0.28 ]
						-5.00 0.00	5.00	10.00	
	Mean Difference								

Using full Bayes, we can introduce priors on the hyper-parameters;

$$\begin{aligned} \hat{\beta}_i &\sim N(\beta_i, \sigma_i^2) \\ \beta_i &\stackrel{i.i.d.}{\sim} N(\mu, \tau^2) \\ \mu &\sim N(0, \psi^2) \\ \tau^2 &\sim p(\tau^2) \end{aligned}$$

![](_page_25_Figure_1.jpeg)

- Try  $\psi^2$  at 0.1, 1, 1000
- Try  $\tau^2$  fixed at 1/4, 1, 25, 100 and a selection from Lambert (2005);  $L_1 : \tau^{-2} \sim \Gamma(0.001, 0.001); L_3 : \log(\tau^2) \sim U(-10, 10); L_5 : \tau^{-2} \sim U(1/1000, 1000); L_7 : \tau^{-2} \sim Par(1, 0.001);$  $L_9 : \tau \sim U(0, 100); L_{11} : \tau \sim N(0, 100), \tau > 0$
- Priors matter for  $\mu$ , not  $\beta_F$

For the priors with fixed  $\psi, \tau^2$ ;

![](_page_26_Figure_2.jpeg)

Similarly, precision-weighted 'spread'  $\zeta^2$  is more stable than  $\tau^2$ 

![](_page_27_Figure_2.jpeg)

- Not as stable as for  $\beta_F$  as data tell us less about  $\zeta^2$  than overall location
- Just reporting the original-data forest plot is a sane summary

And for priors with fixed  $\psi^2$ ,  $\tau^2$  – the same story;

![](_page_28_Figure_2.jpeg)

### More on sensitivity

Why, in these models, does the prior on  $\tau^2$  matter so much?

Recall our example; what values of  $\tau$  are plausible?

![](_page_29_Figure_3.jpeg)

### More on sensitivity

Homogeneity (i.e.  $\tau =$ 0) isn't ruled out by data – but low  $\tau$  values **are**, under  $\Gamma$  priors. This can't be entirely avoided, expect to think carefully about the prior.

![](_page_30_Figure_2.jpeg)

Exchangeability is a strong justification for using hierarchical models (see e.g. Higgins & Spiegelhalter 2009). But the 'classical' motivation looks like this;

![](_page_31_Figure_2.jpeg)

Randomly-sampled effect-sizes have mean  $\mu$ , variance  $\tau^2$  – parameters of the random effects distribution.

![](_page_32_Figure_1.jpeg)

- In RE model,  $\psi$  is the standard deviation of the prior on average study effect  $\mu$ ;  $\tau$  is the standard deviation of the study effects
- An assumption of i.i.d. effects is often hard to justify; typically, later studies' designs depend on earlier studies' results – e.g. replication studies
- But random effects models are needed for prediction what  $\beta_i$  might we see in the next study?

Q. So will *this* upset people? A. Again (!) it depends who you ask

Random-effects models are unpopular with some...

![](_page_33_Picture_3.jpeg)

I'll not let the random differences between different trials contribute to my final p-value or contribute to my final estimate of the magnitude of the effect or to the confidence intervals that I'll put about it.

The random effects analysis says, look, we've got a lot of different trial results, here. What's the mean and what's the scatter of the different trials results? I don't think that this is actually wholly wrong [...] I think it does answer a question. But it's a very abstruse and uninteresting question

Richard Peto, Statistics in Medicine, 1987

It's worth noting that random-effects models do **not** provide intervals that 'reflect heterogeneity';

![](_page_34_Figure_2.jpeg)

Recall that  $\mu$  and its posterior describe the mean of the population of study effects you might ever see, not necessarily the set of effects in the observed studies.

### Summary – for inference

![](_page_35_Picture_1.jpeg)

![](_page_35_Figure_2.jpeg)

Assumptions of exchangeability provide attractive shrinkage and 'borrowing strength', when there's no reason to distinguish  $\beta_i$ . But, at least in genetic association work, ancestry may suggest which  $\beta_i$  may be similar;

Right: dendrogram illustrating mean MAF similarities/differences between African American, European American, Latinos, Japanese Americans & Native Hawaiians; data from the Type 2 Diabetes (T2D) consortium.

![](_page_36_Figure_3.jpeg)

The Meta-ANalysis of Transethnic Association studies (MANTRA) method (Morris, 2011) exploits the MAF information (or  $F_{ST}$ ) to cluster effects in sub-populations. Conceptually;

![](_page_37_Figure_2.jpeg)

Within each cluster, there is a single 'center' effect selected from the study effects  $\beta_1, \beta_2, \dots, \beta_k$  – each study is equally likely to be such a center, *a priori*, and each non-center study gets assigned to its 'nearest' center.

Within-cluster, the center effect size has prior

$$egin{array}{rl} eta_c &\sim & N(\mu, au^2) \ au^2 &\sim & Exp(1) \ \mu &\sim & {
m flat.} \end{array}$$

The number of clusters C has prior

$$\mathbb{P}[C=c] = \begin{cases} \frac{1}{2}, & c=1\\ \frac{1}{2^c} \frac{2^{k-1}}{2^{k-1}-1}, & c=2, \dots, k, \end{cases}$$

i.e. homogeneity has 50% prior support, then it 'tails off'.

MANTRA is implemented with reversible jump MCMC – somewhat like Gibbs Sampling, but allowing center effects  $\beta_c$  to enter/leave the model. It is run twice, with all  $\beta_i = 0$  (i.e. the null) and the model above (alternative).

Its output;

- Bayes Factor comparing the null with the clustered, non-zero  $\beta_i$
- Posterior probability of C > 1 under the alternative
- Posterior probabilities of cluster-membership, for each study, under the alternative

The computational effort required is non-trivial (e.g. 10 mins per SNP) but can be parallelized; 32 processors for 1 week enables GWAS with 2.5M SNPs.

Output for T2D association, at rs7754840 in the (known) CDKAL1 locus;

![](_page_40_Figure_2.jpeg)

Compared to the null, get BF = 8.9 for C = 1, but BF = 11.0 for unconstrained model – and 99.2% posterior probability that C > 1.

Showing the posterior probability of cluster memberships;

![](_page_41_Figure_2.jpeg)

The big Bayes Factor occurs as the data suggest differences between group as well as a non-zero average effect. **Both** violate the null – that **all**  $\beta_i = 0$ .

Heterogeneity and average effect in the fixed-effects analysis; writing

$$Z_i^2 = \hat{\beta}_i^2 / \sigma_i^2$$

$$Z_F^2 = \hat{\beta}_F / \text{Var}[\hat{\beta}_F],$$
then  $Z^2 = \sum_{i=1}^k Z_i^2$ 

$$= Z_F^2 + \sum_{i=1}^k \sigma_i^{-2} (\hat{\beta}_i - \hat{\beta}_F)^2$$

$$= Z_F^2 + Q,$$

i.e. the signal-to-noise over all studies is the signal-to-noise for the average effect  $\beta_F$  plus the heterogeneity – Cochran's Q.

GWAS usually only examines  $\beta_F$  – but there's no need to restrict like this. See also the ASSET method, looking at differences by disease subtype.

## Summary

- Meta-analysis is natural in a Bayesian framework
- Summarizing what You know is still a challenge
- Questions of heterogeneity are of interest, but often more sensitive to modeling assumptions; prior information matters

### **Obligatory XKCD** cartoon

#### And finally;

MANY MELA-ANALYSIS SIUDIES INCLUDE THE PHRASE "WE SEARCHED MEDLINE, EMBASE, AND COCHRANE FOR STUDIES ... " THIS HAS LED TO META-META-ANALYSES COMPARING META-ANALYSIS METHODS. eg. M SAMPSON (2003), PL ROYLE (2005) E LEE (2011), AR LEMESHOW (2005) VE PERFORMED A META-META-META-ANALYSIS OF THESE META-META-ANALYSES. METHODS: WE SEARCHED MEDLINE, EMBASE, AND COCHRANE FOR THE PHRASE "WE SEARCHED MEDLINE, EMBASE, AND COCHRANE FOR THE PHRASE "LIE SEARCHED MEDILINE EMBASE AND LIFE GOAL #28: GET A PAPER REJECTED WITH THE COMMENT "TOO META"

The meta-*meta* analyses are real!