

# Prior distributions from meta-analytic predictions

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- the Bayesian hierarchical model
- estimating different quantities
- upstream priors and downstream likelihoods: the MAP prior
- investigating (prior) informativeness: ESS etc.
- being sceptical/conservative: anticipating prior-data conflict / robustification
- application areas:
  - predicting parameters
  - predicting data
  - predicting heterogeneity

# Meta-analysis modeling

Normal approximation for “effect measures”

- single study's outcome, often: **estimate  $\pm$  standard error**
- **normal approximation** (“Wald” CI) often appropriate (“large” sample size within study)
- (standard errors are assumed **known**, fixed!)
- sometimes **transformations** are used—
  - improved **normal approximation**
  - (later: implications for “between-study” modeling)
- examples:
  - means, mean differences, standardized mean differences
  - (log-) proportions, (log-) odds
  - (log-) risk ratios, (log-) odds ratios
  - (log-) rate ratios, (log-) hazard ratios
  - (Fisher-z transformed) correlation coefficients
  - ...

# Meta-analysis modeling

## Normal random effects

- variability (**heterogeneity**) between studies commonly anticipated
  - to reflect differing study characteristics
  - to implement stratification by study
  - to avoid overoptimism / naïve pooling
- especially for few studies (small  $k$ ), heterogeneity is hard to detect (tests have low power) <sup>1</sup>
- empirically: heterogeneity commonly present <sup>2</sup>
- some amount of **between-study heterogeneity** should be anticipated <sup>3</sup>  
(→ **random-effects** model)

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<sup>1</sup>R. J. Hardy, S. G. Thompson. [Detecting and describing heterogeneity in meta-analysis](#). *Statistics in Medicine*, **17**(8): 841–856, 1998.

<sup>2</sup>E. Kontopantelis, D. A. Springate, D. Reeves. [A re-analysis of the Cochrane Library data: The dangers of unobserved heterogeneity in meta-analyses](#). *PLoS ONE*, **8**(7):e69930, 2013.

<sup>3</sup>J. P. T. Higgins. [Commentary: Heterogeneity in meta-analysis should be expected and appropriately quantified](#). *International Journal of Epidemiology*, **37**(5):1158–1160, 2008.

# Meta-analysis modeling

The generic normal-normal hierarchical model (NNHM)

- the meta-analysis **data** set:
  - effect estimates  $y_i$  ( $i = 1, \dots, k$ )
  - ( standard errors  $s_i$  )
- model (likelihood):

$$y_i | \theta_i \sim \text{Normal}(\theta_i, s_i^2)$$
$$\theta_i | \mu, \tau \sim \text{Normal}(\mu, \tau^2)$$

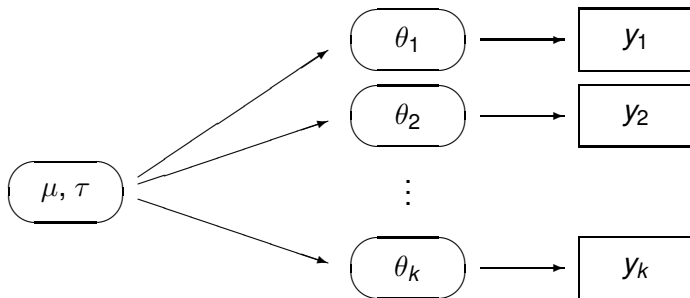
or (marginally):

$$y_i | \mu, \tau \sim \text{Normal}(\mu, \tau^2 + s_i^2)$$

- parameters:
  - “**study-specific effects**”  $\theta_i$
  - “**overall mean effect**”  $\mu$
  - “**heterogeneity**”  $\tau \geq 0$
- for  $\tau = 0$ , reduces to **common-effect** model ( $\tau = 0 \Rightarrow \theta_1 = \dots = \theta_k = \mu$ )

# Meta-analysis modeling

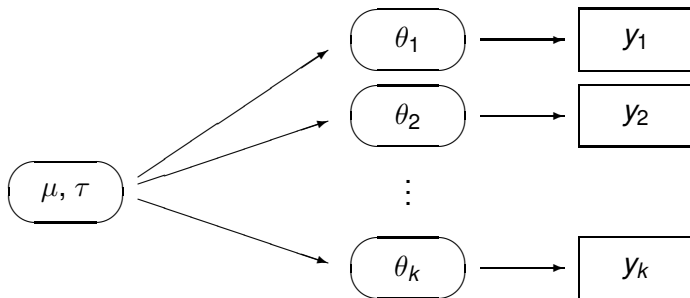
The generic normal-normal hierarchical model (NNHM)



- the NNHM as a *directed acyclic graph (DAG)*:  
overall parameters  $(\mu, \tau)$ , study-specific effects  $(\theta_i)$ , data  $(y_i)$

# Meta-analysis modeling

The generic normal-normal hierarchical model (NNHM)



- the NNHM as a *directed acyclic graph (DAG)*:  
overall parameters  $(\mu, \tau)$ , study-specific effects  $(\theta_i)$ , data  $(y_i)$ , standard errors  $(s_i)$

# Example

11 historical trials (Neuenschwander *et al.*, 2010)

- example: *treatment failure* in transplantation;  
data from 11 “historical” **control groups** (930 patients) to support **new trial** <sup>4</sup>

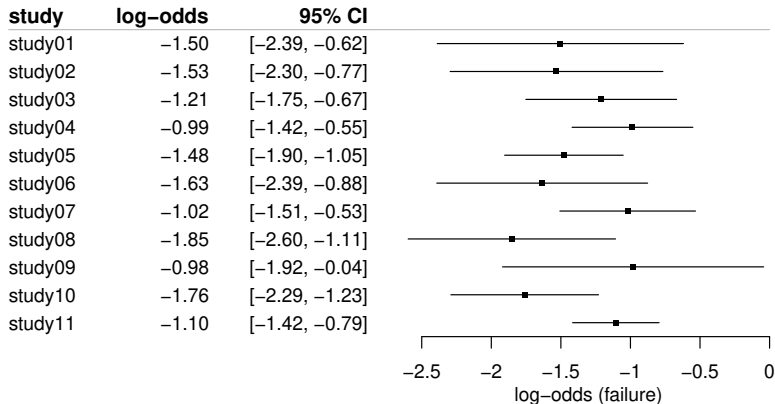
$i$	events	proportion (%)	odds	log-odds $y_i (s_i)$
1	6 / 33	18.2	0.222	-1.50 (0.45)
2	8 / 45	17.8	0.216	-1.53 (0.39)
3	17 / 74	23.0	0.298	-1.21 (0.28)
4	28 / 103	27.2	0.373	-0.99 (0.22)
5	26 / 140	18.6	0.228	-1.48 (0.22)
6	8 / 49	16.3	0.195	-1.63 (0.39)
7	22 / 83	26.5	0.361	-1.02 (0.25)
8	8 / 59	13.6	0.157	-1.85 (0.38)
9	6 / 22	27.3	0.375	-0.98 (0.48)
10	16 / 109	14.7	0.172	-1.76 (0.27)
11	53 / 213	24.9	0.331	-1.10 (0.16)

<sup>4</sup>B. Neuenschwander, G. Capkun-Niggli, A. Branson, D. J. Spiegelhalter. Summarizing historical information on controls in clinical trials. *Clinical Trials*, 7(1):5–18, 2010.



# Example

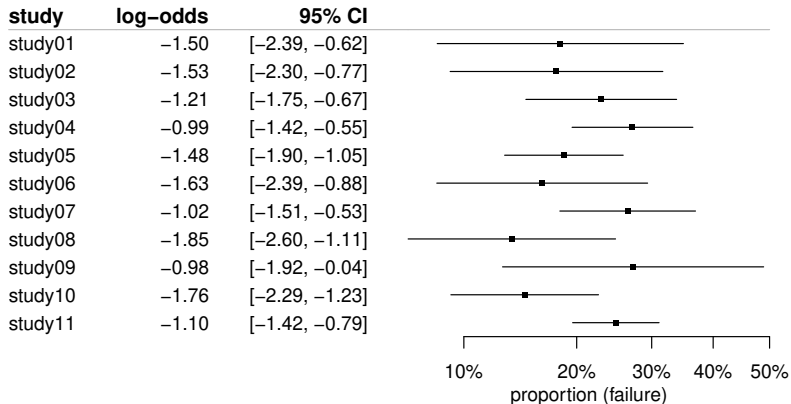
11 historical trials (Neuenschwander *et al.*, 2010)



- analysis on **log-odds** scale

# Example

11 historical trials (Neuenschwander *et al.*, 2010)



- analysis on **log-odds** scale (proportions  $\approx$  10–30%)

# Example

## Meta-analysis

- analyze using NNHM
- prior settings
  - (non-informative) uniform effect ( $\mu$ ) prior <sup>5</sup>
  - (weakly informative) half-Normal(1.0) heterogeneity ( $\tau$ ) prior <sup>6</sup>
- `bayesmeta` R package<sup>7</sup>

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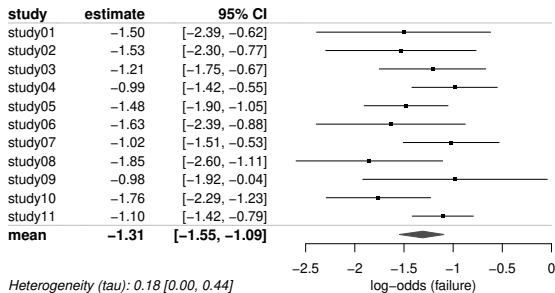
<sup>5</sup>C. Röver. Bayesian random-effects meta-analysis using the `bayesmeta` R package. *Journal of Statistical Software*, **93**(6), 2020.

<sup>6</sup>C. Röver, R. Bender, S. Dias, C. H. Schmid, H. Schmidli, S. Sturtz, S. Weber, T. Friede. On weakly informative prior distributions for the heterogeneity parameter in Bayesian random-effects meta-analysis. *Research Synthesis Methods*, **12**(4):448–474, 2021.

<sup>7</sup><http://cran.r-project.org/package=bayesmeta>

# Example

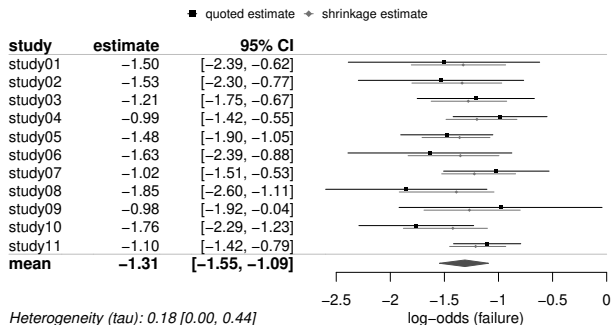
## Meta-analysis: overall parameters



- **overall mean** ( $\mu$ ) estimate: -1.31 [-1.55, -1.09]  
heterogeneity ( $\tau$ ): 0.18 [0.00, 0.44]
- proportion ( $\text{logit}^{-1}(\mu)$ ): 21% [18%, 25%]

# Example

## Meta-analysis: shrinkage estimates

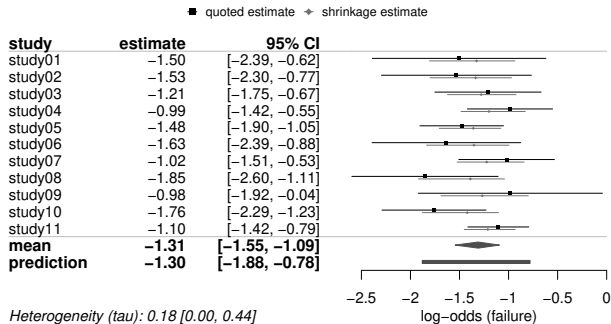


- **shrinkage estimates** (study-specific effects  $\theta_j$ )
- joint analysis useful to support individual trials <sup>8</sup>

<sup>8</sup>S. Wandel, B. Neuenschwander, C. Röver, T. Friede. [Using phase II data for the analysis of phase III studies: an application in rare diseases](#). *Clinical Trials*, **14**(3):277–285, 2017.

# Example

## Meta-analysis: prediction

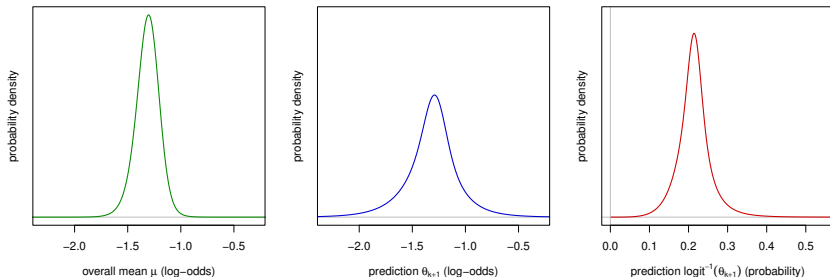


- **prediction**: effect in a new (“future”) trial ( $\theta_{k+1}$ )  
( $\text{logit}^{-1}(\theta_{k+1})$ : 21% [13%, 31%])
- useful e.g. for trial design<sup>9</sup>

<sup>9</sup>H. Schmidli, B. Neuenschwander, T. Friede. *Meta-analytic-predictive use of historical variance data for the design and analysis of clinical trials*. *Computational Statistics and Data Analysis*, **113**:100–110, 2017.

# Example

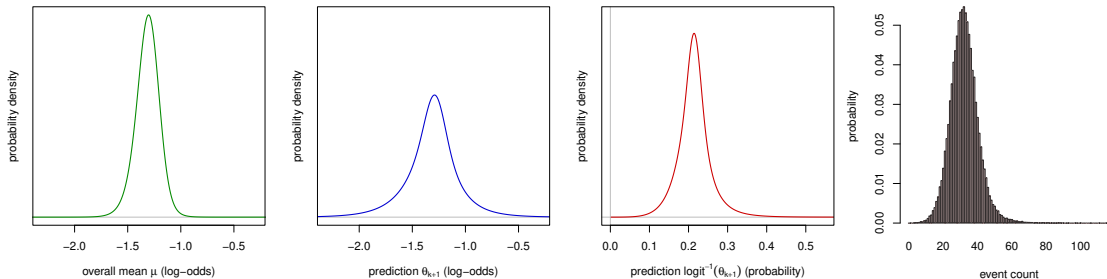
## Meta-analysis: predicting data



- predictions  $\theta_{k+1}$  imply predicted probabilities  $\text{logit}^{-1}(\theta_{k+1})$

# Example

## Meta-analysis: predicting data



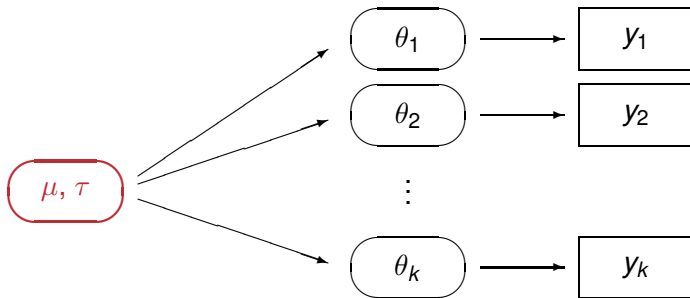
- predictions  $\theta_{k+1}$  imply predicted probabilities  $\text{logit}^{-1}(\theta_{k+1})$
- for a specific trial scenario (e.g. sample size  $N_{k+1} = 150$ ), may derive **predicted data** (event counts)
- useful for checking consistency with historical data <sup>10</sup>

<sup>10</sup>F. M. Kluxen, K. Weber, C. Strupp, S. M. Jensen, L. A. Hothorn, J.-C. Garcin, T. Hofmann. [Using historical control data in bioassays for regulatory toxicology](#). *Regulatory Toxicology and Pharmacology*, **126**:105024, 2021.



# The NNHM

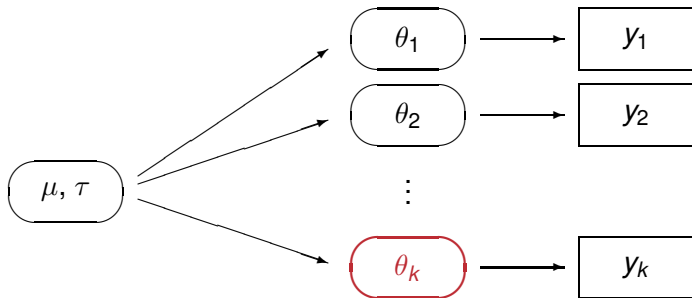
## Aims of analysis



- overall mean  $(\mu, \tau)$

# The NNHM

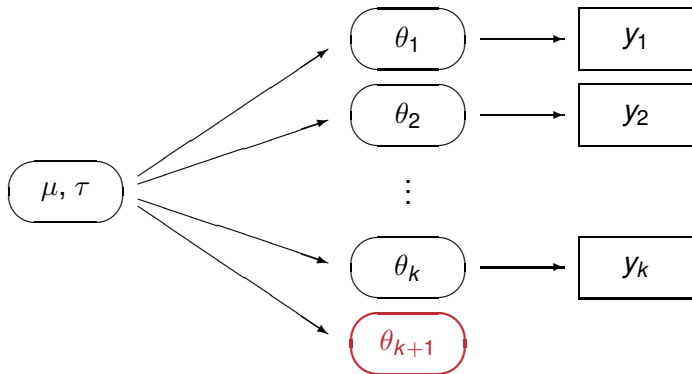
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- overall mean ( $\mu, \tau$ )
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# The NNHM

## Aims of analysis



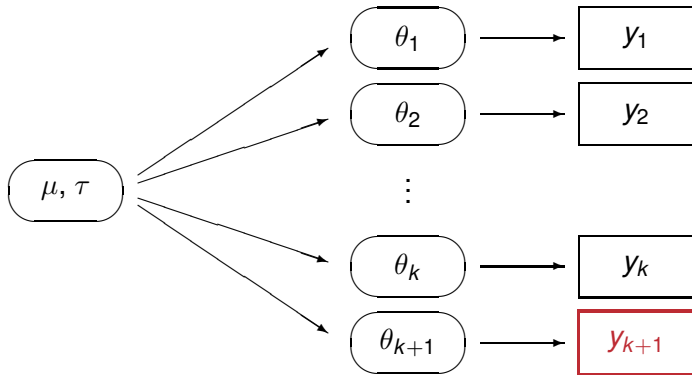
- overall mean ( $\mu, \tau$ )

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- prediction ( $\theta_{k+1}$ )

# The NNHM

## Aims of analysis



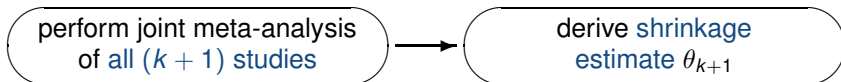
- overall mean ( $\mu, \tau$ )
- shrinkage estimation ( $\theta_i$ )
- prediction (parameter  $\theta_{k+1}$ )
- prediction (data  $y_{k+1}$ )

# Meta-analysis of historical data

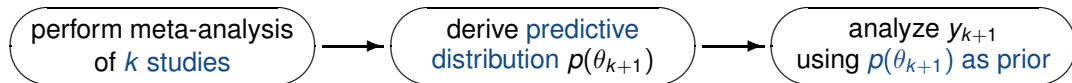
## MAP vs. MAC

- suppose  $k$  “historical” + 1 current studies are given, interest is in new  $(k+1)$ th study (data  $y_{k+1}$ , effect  $\theta_{k+1}$ )
- two possibilities:

**meta-analytic-combined (MAC)** approach:



**meta-analytic-predictive (MAP)** approach:

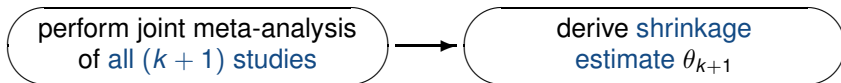


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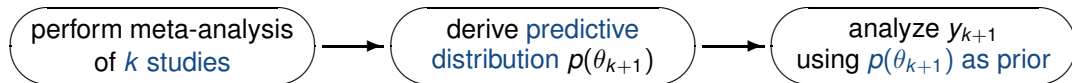
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- two possibilities:

**meta-analytic-combined (MAC)** approach:



**meta-analytic-predictive (MAP)** approach:



(which is preferable?)

- both (MAP and MAC) approaches are **equivalent**:<sup>11</sup>
  - analysis of  $(k+1)$ th study (estimation of  $\theta_{k+1}$  using  $y_{k+1}$ ) based on MAP prior may be interpreted as shrinkage estimation in a joint meta-analysis
  - information of remaining studies contributed to  $(k+1)$ th shrinkage estimate is expressed through MAP prior (predictive distribution) from  $k$  studies
- example of **logical consistency** of Bayesian methods — posterior may be factored:

$$\underbrace{p(\theta_{k+1} | y_1, \dots, y_{k+1})}_{\text{MAC posterior}} \propto \underbrace{p(y_{k+1} | \theta_{k+1})}_{\text{likelihood}} \times \underbrace{p(\theta_{k+1} | y_1, \dots, y_k)}_{\text{MAP prior}}$$

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<sup>11</sup>H. Schmidli *et al.* Robust meta-analytic-predictive priors in clinical trials with historical control information. *Biometrics*, 70(4):1023–1032, 2014.

# Example

## Historical and current data

- *new* trial yields  $x_c = 29$  events in a control group of size  $N_c = 150$  ( $\frac{x_c}{N_c} = 0.19$ )
- new study consistent with historical studies?

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<sup>12</sup>A. Gelman, J. B. Carlin, H. Stern, D. B. Dunson, A. Vehtari, D. B. Rubin. *Bayesian data analysis*. Chapman & Hall / CRC, 2014.

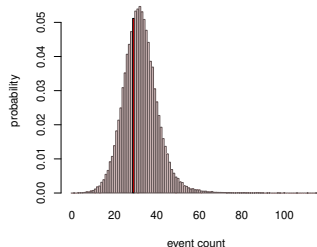
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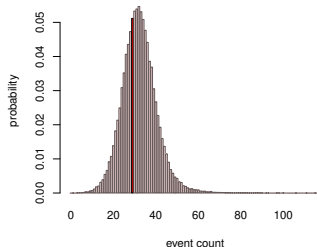
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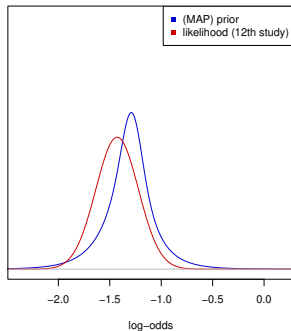
- in terms of MAP prior: a “**prior predictive check**”<sup>12</sup>
- may be turned into a (prior predictive) *p*-value<sup>13</sup> (here:  $p = 0.78$ )

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# Example

## Historical and current data

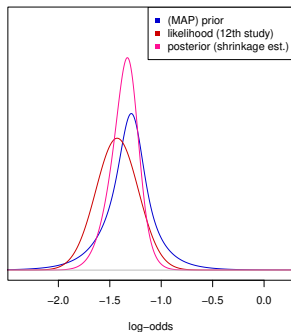


- MAP prior and estimate  $(y_{12}, s_{12})$  combine to form shrinkage estimate.  
(probability: 0.19 [0.14, 0.26])

<sup>14</sup>B. Neuenschwander, S. Weber, H. Schmidli, A. O'Hagan. Predictively consistent prior effective sample sizes. *Biometrics*, **76**(2):578.587, 2020.

# Example

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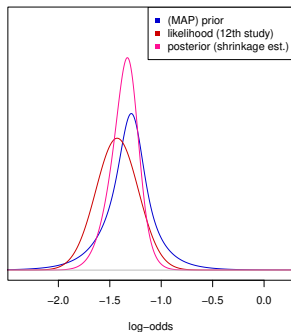


- MAP prior and estimate ( $y_{12}, s_{12}$ ) combine to form shrinkage estimate.  
(probability: 0.19 [0.14, 0.26]  $\rightarrow$  0.21 [0.16, 0.25])

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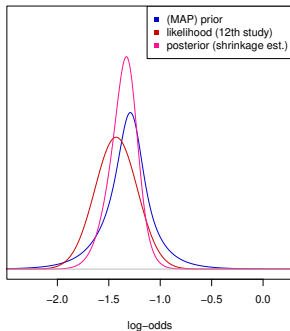


- MAP prior and estimate  $(y_{12}, s_{12})$  combine to form shrinkage estimate.  
(probability: 0.19 [0.14, 0.26]  $\rightarrow$  0.21 [0.16, 0.25])
- substantial precision gain: posterior std.dev. only  $0.7 \times s_{12}$
- would otherwise require 104% increase in sample size (“156 additional patients”)

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- more generally: **(MAP) prior** associated with “**effective sample size**”<sup>14</sup>  
(here:  $ESS_{ELIR} = 153$ )

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# Example

## Historical and current data

- new trial yields  $x_c = 29$  events in a **control** group of size  $N_c = 150$  ( $\frac{x_c}{N_c} = 0.19$ )
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- combine “plain” estimates / combine active with control + historical

	events		log-odds		log-OR	
	control	treatment	control	treatment	estimate	95% CI
RCT only	29/150	40/300	-1.43 (0.21)	-1.87 (0.17)	-0.44 (0.27)	[-0.97, 0.08]



# Example

## Historical and current data

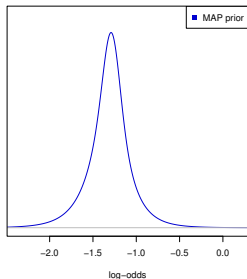
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	control	treatment	control	treatment	estimate	95% CI
RCT only	29/150	40/300	-1.43 (0.21)	-1.87 (0.17)	-0.44 (0.27)	[-0.97, 0.08]
RCT + MAP	$\frac{29+198}{150+930}$	40/300	-1.35 (0.14)	-1.87 (0.17)	-0.52 (0.22)	[-0.96, -0.09]

- historical controls:
  - more precise control group + effect estimates
  - fewer control patients

# The MAP prior

## Practical issues: simplification



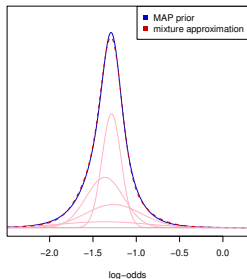
- for practical application (communication, pre-specification, ...):  
“simple” summary of MAP prior required

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<sup>15</sup>S. Weber, Y. Yi, J. W. Seaman, T. Kakizume, H. Schmidli. [Applying meta-analytic-predictive priors with the R Bayesian evidence synthesis tools](#). *Journal of Statistical Software*, **100**(19):1–32, 2021.

# The MAP prior

## Practical issues: simplification



	weight	mean	std.dev.
1	0.37	-1.29	0.11
2	0.32	-1.36	0.22
3	0.22	-1.26	0.32
4	0.09	-1.37	0.50

- for practical application (communication, pre-specification, ...):  
“simple” summary of MAP prior required
- idea: approximate by **mixture distribution** of few components<sup>15</sup>  
(implemented in `RBeST`; here: 4 normal components)

<sup>15</sup>S. Weber, Y. Yi, J. W. Seaman, T. Kakizume, H. Schmidli. [Applying meta-analytic-predictive priors with the R Bayesian evidence synthesis tools](#). *Journal of Statistical Software*, **100**(19):1–32, 2021.

# The MAP prior

## Practical issues: robustification

- concern: analysis hinges on **exchangeability** of historical and current trials.
- pooling of control rates challenges **randomization**
- **consistency check** may be implemented (e.g., prior predictive  $p$ -value)  
— but probably with **little “power”**
- to safeguard against assumption violation: anticipate potential **prior/data conflict**
- **“robustification”** ideas:
  - “more conservative” priors (heavier tails, greater variance, . . .)
  - include possibility of alternative models → **mixture prior**

$$p(\theta) = \begin{cases} \text{informative (MAP)} & \text{with probability } (1 - w_R) \\ \text{non-informative (vague)} & \text{with probability } w_R \end{cases}$$

- latter solution commonly preferred (easily motivated, elicited, . . .)
- ESS considerations etc. may again be applied

# Other MAP prior applications

## Treatment effect estimation

- shrinkage estimation also useful for **treatment effects** (e.g., MAP prior from earlier-phase data)<sup>16</sup>

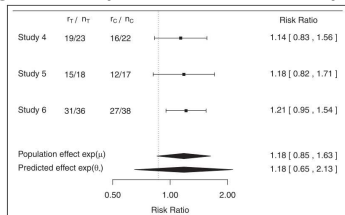


Figure 1. Data and results at end-of-phase II meeting.

<sup>16</sup>S. Wandel, B. Neuenschwander, C. Röver, T. Friede. Using phase II data for the analysis of phase III studies: an application in rare diseases. *Clinical Trials*, **14**(3):277–285, 2017.

<sup>17</sup>C. Röver, T. Friede. Dynamically borrowing strength from another study through shrinkage estimation. *Statistical Methods in Medical Research*, **29**(1):293–308, 2020.

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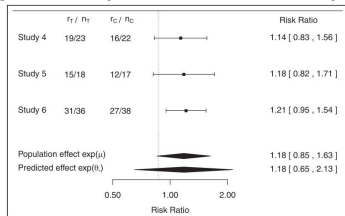


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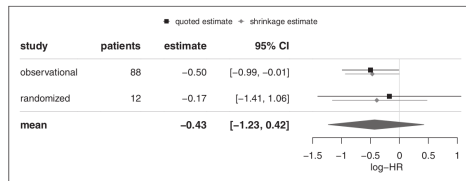


Figure 2. Forest plot for the CJD example (log-HR outcome). The shrinkage interval for the log-HR based on randomized evidence here is  $[-1.16, 0.48]$ , spanning only two-thirds of the original confidence interval width.

- borrowing of information also for a (heterogeneous) **pair of estimates** (i.e.,  $k = 2$ )<sup>17</sup> (focus on **shrinkage estimate**  $\theta_2$ , not overall mean  $\mu$ )

<sup>16</sup>S. Wandel, B. Neuenschwander, C. Röver, T. Friede. [Using phase II data for the analysis of phase III studies: an application in rare diseases](#). *Clinical Trials*, **14**(3):277–285, 2017.

<sup>17</sup>C. Röver, T. Friede. [Dynamically borrowing strength from another study through shrinkage estimation](#). *Statistical Methods in Medical Research*, **29**(1):293–308, 2020.

# Other MAP prior applications

## Heterogeneity estimation

- important for meta-analysis: **heterogeneity prior** specification (especially for few studies)
- general guidance available for **non-informative**<sup>18</sup> or **weakly informative** priors<sup>19</sup>
- important aspect: **empirical information** — *what can we learn from past analyses?*

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<sup>18</sup>C. Röver. **Bayesian random-effects meta-analysis using the `bayesmeta` R package**. *Journal of Statistical Software*, **93**(6), 2020.

<sup>19</sup>C. Röver, R. Bender, S. Dias, C. H. Schmid, H. Schmidli, S. Sturtz, S. Weber, T. Friede. **On weakly informative prior distributions for the heterogeneity parameter in Bayesian random-effects meta-analysis**. *Research Synthesis Methods*, **12**(4):448–474, 2021.

# Other MAP prior applications

## Heterogeneity estimation

- important for meta-analysis: **heterogeneity prior** specification (especially for few studies)
- general guidance available for **non-informative** <sup>18</sup> or **weakly informative** priors <sup>19</sup>
- important aspect: **empirical information** — *what can we learn from past analyses?*
- pooling of heterogeneity *estimates* tricky: hard to summarize / model
- need: joint model for “historical” meta-analyses

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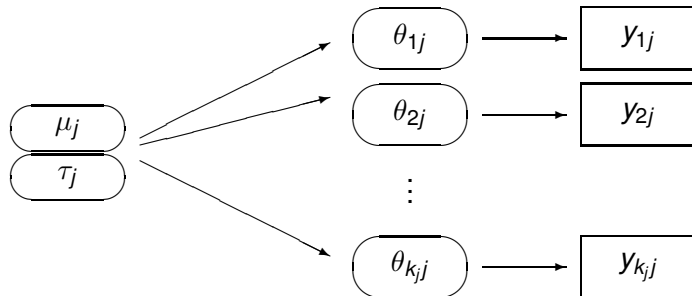
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# Other MAP prior applications

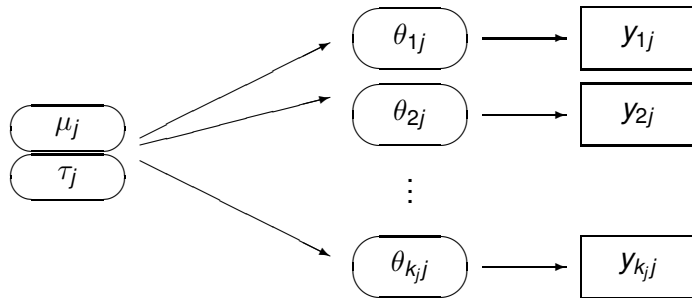
Heterogeneity prediction: the model



- model DAG for  $j$ th meta-analysis

# Other MAP prior applications

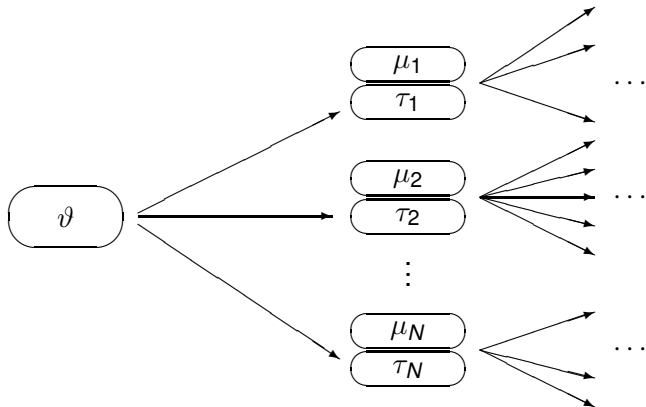
Heterogeneity prediction: the model



- model DAG for  $j$ th meta-analysis (out of several)
- idea: combine  $(j = 1, \dots, N)$  meta-analyses, infer  $\tau$  distribution

# Other MAP prior applications

Heterogeneity prediction: the model



- additional overarching layer, combining  $N$  meta-analyses
- common heterogeneity distribution for  $\tau_1, \dots, \tau_N$  (e.g., half-Normal( $\vartheta$ ))

# Other MAP prior applications

## Heterogeneity prediction: the model

- **data**:  $N$  meta-analyses, each involving  $k_j$  studies, effect estimates  $y_{ij}$ , standard errors  $s_{ij}$  ( $i = 1, \dots, k_j, j = 1, \dots, N$ ),
- assume:

$$y_{ij} | \mu_j, \tau_j, s_{ij} \sim \text{Normal}(\mu_j, s_{ij}^2 + \tau_j^2)$$
$$\mu_j | \mu_p, \sigma_p \sim \text{Normal}(\mu_p, \sigma_p^2)$$

for fixed “neutral”  $\mu_p$  and “large”  $\sigma_p$  ( $\rightarrow$  stratification, no pooling)

- **heterogeneity stage**:

$$\tau_j | \vartheta \sim P(\vartheta)$$

for some “heterogeneity distribution”  $P(\vartheta)$

- **parameters**:  $N$  means  $\mu_j$  and heterogeneities  $\tau_j$ ; “distribution” parameter(s)  $\vartheta$
- (hyper-) **prior** required for  $\vartheta$
- **aim**: prediction  $\tau^*$

# Other MAP prior applications

## Heterogeneity prediction: the model

- **data**:  $N$  meta-analyses, each involving  $k_j$  studies, effect estimates  $y_{ij}$ , standard errors  $s_{ij}$  ( $i = 1, \dots, k_j, j = 1, \dots, N$ ),
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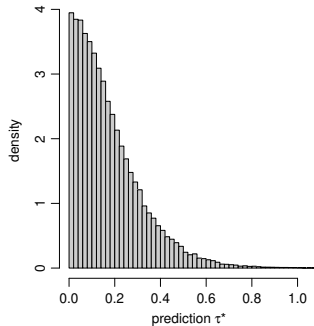
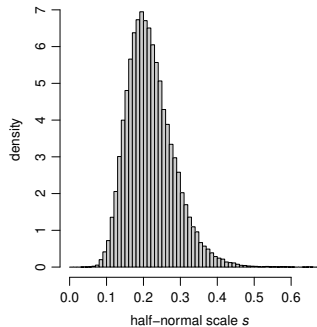
(e.g.:  $\tau_j | \vartheta \sim \text{half-Normal}(\vartheta)$ )

- **parameters**:  $N$  means  $\mu_j$  and heterogeneities  $\tau_j$ ; “distribution” parameter(s)  $\vartheta$
- (hyper-) **prior** required for  $\vartheta$  (half-normal scale  $\vartheta$ )
- **aim**: prediction  $\tau^*$

# Other MAP prior applications

## Heterogeneity prediction

- posterior: scale parameter  $s$
- posterior predictive:  $\tau^* | s \sim \text{half-Normal}(s)$



(figures from an example application)

- **posterior predictive** serves as **“MAP” prior** for new  $((N+1)$ th) analysis

# Other MAP prior applications

Heterogeneity prediction: simplification, “robustification”

- simplification:
  - **posterior predictive** is a **mixture distribution**  
( $\tau^*|\vartheta \sim \text{half-Normal}(\vartheta)$ , with uncertain  $\vartheta$ )
  - half-normal example — obvious parametric approximation:  
by **half-normal**, or **half-normal mixture**  
(e.g., **half-Student- $t$**  distribution)
- robustification:
  - rather “**conservatization**” (?)
  - generally: **larger**  $\tau$  value yields “**more conservative**” meta-analysis  
(less shrinkage, wider intervals, ...)
  - **stochastically larger** or **heavier-tailed** prior  
usually considered a *conservative* choice

# Other MAP prior applications

Heterogeneity prediction: simplification, “robustification”

- original idea and first implementation: Rhodes *et al.* (2015)<sup>20</sup> and Turner *et al.* (2015)<sup>21</sup>
- general approach detailed<sup>22</sup>

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<sup>20</sup>K.M. Rhodes *et al.* Predictive distributions were developed for the extent of heterogeneity in meta-analyses of continuous outcome data. *Journal of Clinical Epidemiology*, **68**(1):52–60, 2015.

<sup>21</sup>R.M. Turner *et al.* Predictive distributions for between-study heterogeneity and simple methods for their application in Bayesian meta-analysis. *Statistics in Medicine*, **34**(6):984–998, 2015.

<sup>22</sup>C. Röver, S. Sturtz, J. Lilienthal, R. Bender, T. Friede. Summarizing empirical information on between-study heterogeneity for Bayesian random-effects meta-analysis. *Statistics in Medicine*, **42**(14):2439–2454, 2023.

<sup>23</sup>J. Lilienthal, S. Sturtz, C. Schürmann, M. Maiworm, C. Röver, T. Friede, R. Bender. Bayesian random-effects meta-analysis with empirical heterogeneity priors for application in health technology assessment with very few studies. *Research Synthesis Methods*, **15**(2):275–287, 2024.



# Other MAP prior applications

Heterogeneity prediction: simplification, “robustification”

- original idea and first implementation: Rhodes *et al.* (2015)<sup>20</sup> and Turner *et al.* (2015)<sup>21</sup>
- general approach detailed<sup>22</sup>
- applied to IQWiG data<sup>23</sup> to help pre-specifying analyses in regulatory context

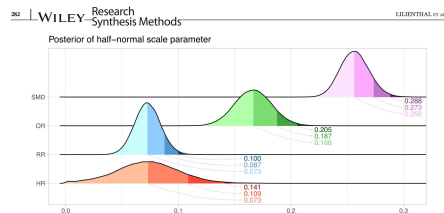


FIGURE 7 Posterior distributions of the half-normal scale parameter for different effect measures. Different color shades and the given numerical values indicate the 90%, 90%, and 99% quantiles, respectively.

<sup>20</sup>K.M. Rhodes *et al.* Predictive distributions were developed for the extent of heterogeneity in meta-analyses of continuous outcome data. *Journal of Clinical Epidemiology*, **68**(1):52–60, 2015.

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# Prior distributions from meta-analytic predictions

## Summary

- **hierarchical models** established for meta-analysis
- **Bayesian** models advantageous for sparse data and advanced applications
- besides **main effect**: **shrinkage, prediction**
- **MAP priors** as data-informed priors
- useful in many contexts (**controls, effects, nuisance parameters, ...**)
- option to implement scepticism via **robustification**
- analogous “MAP” approach for empirically motivated **heterogeneity priors**