

Meta-analysis of few small studies in small populations and rare diseases

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- Meta analysis
 - the random-effects model
 - frequentist approaches
 - the Bayesian approach
 - example
- Simulation study
 - heterogeneity estimation
 - effect estimation
- Conclusions

Meta analysis

The random effects model

- assume^{1,2}:

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

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

- ingredients:

Data:

- estimates y_i
- standard errors s_i

Parameters:

- true parameter value Θ
- heterogeneity τ

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- $\Theta \in \mathbb{R}$ of primary interest (“effect”)
- $\tau \in \mathbb{R}^+$ nuisance parameter (“between-trial heterogeneity”)

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Meta analysis

Frequentist approaches

- usual frequentist procedure:
 - (1) derive heterogeneity estimate $\hat{\tau}$
 - (2) conditional on $\tau = \hat{\tau}$, derive
 - estimate $\hat{\Theta}$
 - standard error $\hat{\sigma}_{\Theta}$

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$$\hat{\Theta} \pm \hat{\sigma}_{\Theta} z_{(1-\alpha/2)}$$

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- confidence interval via Normal approximation:

$$\hat{\Theta} \pm \hat{\sigma}_{\Theta} z_{(1-\alpha/2)}$$

- uncertainty in τ not accounted for
- Knapp-Hartung approach³:
 - compute

$$q := \frac{1}{k-1} \sum_i \frac{(y_i - \hat{\Theta})^2}{s_i^2 + \hat{\tau}^2}$$

- confidence interval via Student-*t* approximation:

$$\hat{\Theta} \pm \max\{\sqrt{q}, 1\} \hat{\sigma}_{\Theta} t_{(k-1);(1-\alpha/2)}$$

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Meta analysis

Bayesian approach

- Bayesian approach ⁴
 - set up model likelihood
 - specify prior information about unknowns (Θ, τ)
 - posterior results as \propto prior \times likelihood
 - marginal posterior $p(\Theta | \vec{y}, \vec{\sigma}) = \int p(\Theta, \tau | \vec{y}, \vec{\sigma}) d\tau \dots$

⁴A. J. Sutton, K. R. Abrams. *Bayesian methods in meta-analysis and evidence synthesis*. Statistical Methods in Medical Research, 10(4):277, 2001.

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 - marginal posterior $p(\Theta | \vec{y}, \vec{\sigma}) = \int p(\Theta, \tau | \vec{y}, \vec{\sigma}) d\tau \dots$
- Comments:
 - consideration of prior information
 - propagation of uncertainty
 - straightforward interpretation
 - computationally more expensive, usually done via stochastic integration (MCMC, BUGS)⁵
 - special case of simple random-effects MA may be solved semi-analytically (using `bmeta` R package)

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Meta analysis

Frequentist and Bayesian approaches

- many heterogeneity estimators available
- different prior specifications possible (should depend on context)

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Frequentist and Bayesian approaches

- many heterogeneity estimators available
(different answers *to the same question*)
- different prior specifications possible (should depend on context)
(different answers *to different questions*)

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- different prior specifications possible (should depend on context) (different answers *to different questions*)
- estimators for τ considered in the following:
 - DerSimonian-Laird estimator (DL)
 - restricted ML estimator (REML)⁶
 - Mandel-Paule estimator (MP)⁷
 - Bayes modal estimator (BM)⁸

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- estimators for τ considered in the following:
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- priors for τ considered in the following (where $\Theta = \log(\text{OR})$):
 - half-Normal ($\sigma = 0.5$)
 - half-Normal ($\sigma = 1.0$)
 - Uniform (0.0, 4.0)

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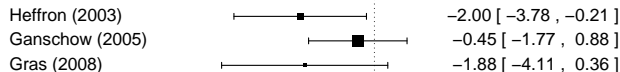
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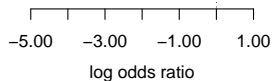
Example

Crins et al. (2014) data⁹

Liver transplant example: steroid-resistant rejection (SRR)



data: 3 estimates
(log ORs)
and standard errors



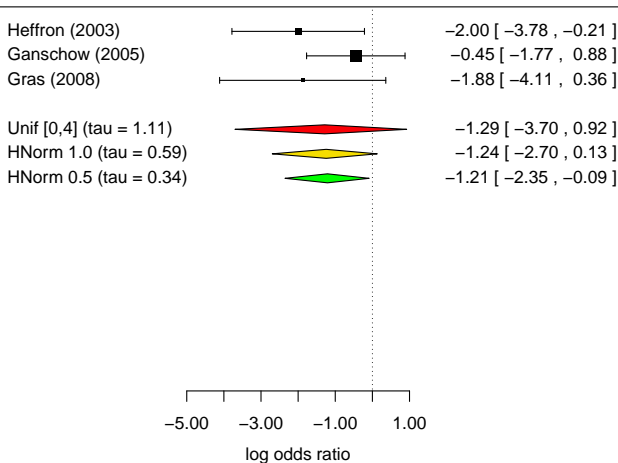
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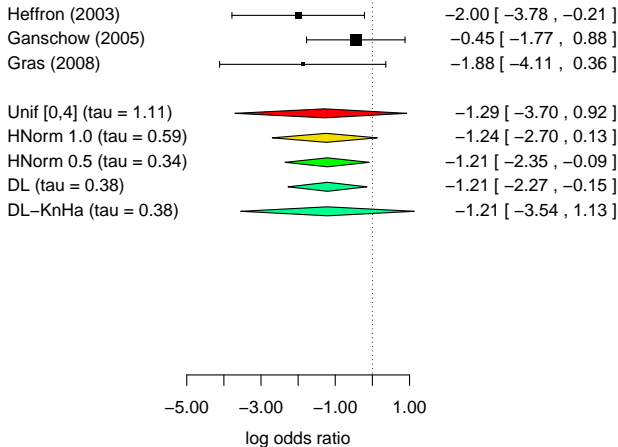
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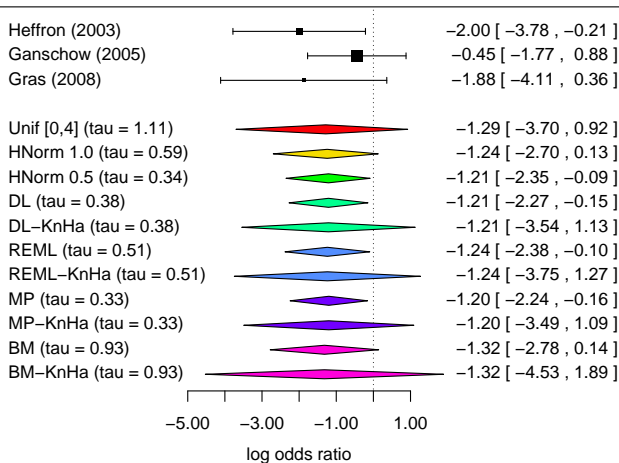
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Example

Crins et al. (2014) data

- different analyses yield different answers
- Bayesian and frequentist analyses answer different questions
- $k = 2$ to 3 studies is a common scenario
(*majority* of meta analyses in Cochrane Database¹⁰)

¹⁰R.M. Turner et al. Predicting the extent of heterogeneity in meta-analysis, using empirical data from the Cochrane Database of Systematic Reviews. *International Journal of Epidemiology* 41(3):818–827, 2012.

E. Kontopantelis et al. A re-analysis of the Cochrane Library data: The dangers of unobserved heterogeneity in meta-analyses. *PLoS ONE* 8(7):e69930, 2013.

Example

Crins et al. (2014) data

- different analyses yield different answers
- Bayesian and frequentist analyses answer different questions
- $k = 2$ to 3 studies is a common scenario
(*majority* of meta analyses in Cochrane Database¹⁰)
- how does performance compare **in general**, especially for few studies?

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Simulation study

Setup

- number of studies: $k \in \{3, 5, 10, 30\}$
- heterogeneity: $\tau^2 \in \{0.00, 0.01, 0.02, 0.05, 0.1, 0.2, 0.5, 1.0, 2.0\}$
($I^2 \in \{0.00, 0.06, 0.11, 0.23, 0.37, 0.54, 0.75, 0.85, 0.92\}$)
- standard errors s_i : truncated χ^2 -distribution¹¹
- 10'000 repetitions for each combination (k, τ^2)

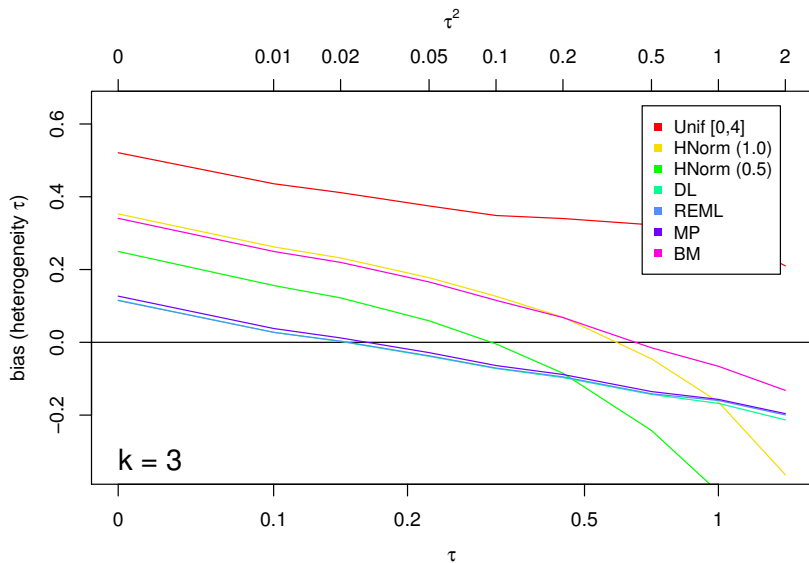
- compute Bayesian MAs (3 different priors)
- compute frequentist MAs (different τ estimators, Normal and Knapp-Hartung approximation)

¹¹S.E. Brockwell, I.R. Gordon. A comparison of statistical methods for meta-analysis. *Statistics in Medicine* 20(6):825–840, 2001.

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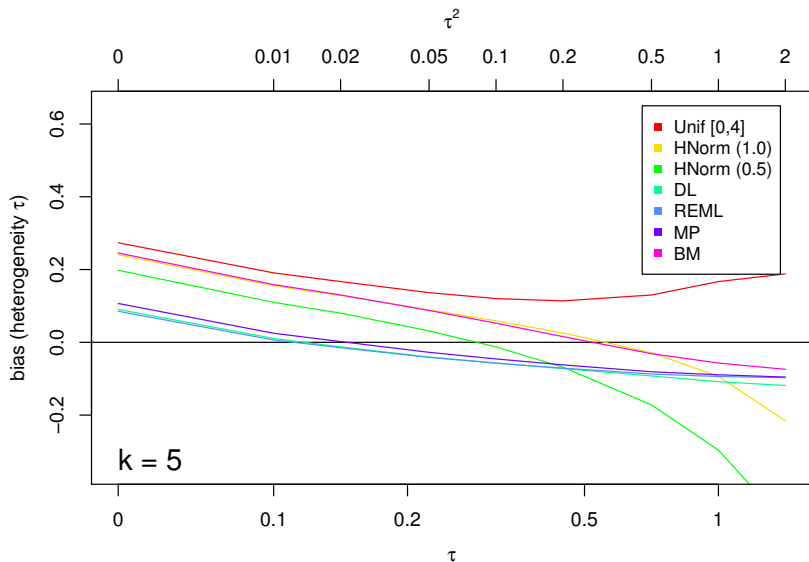
Simulation study

heterogeneity estimation: **bias**



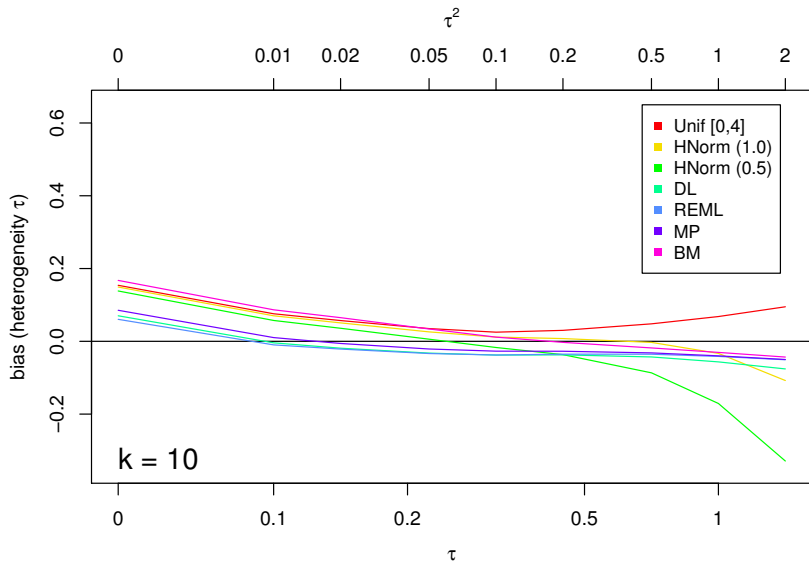
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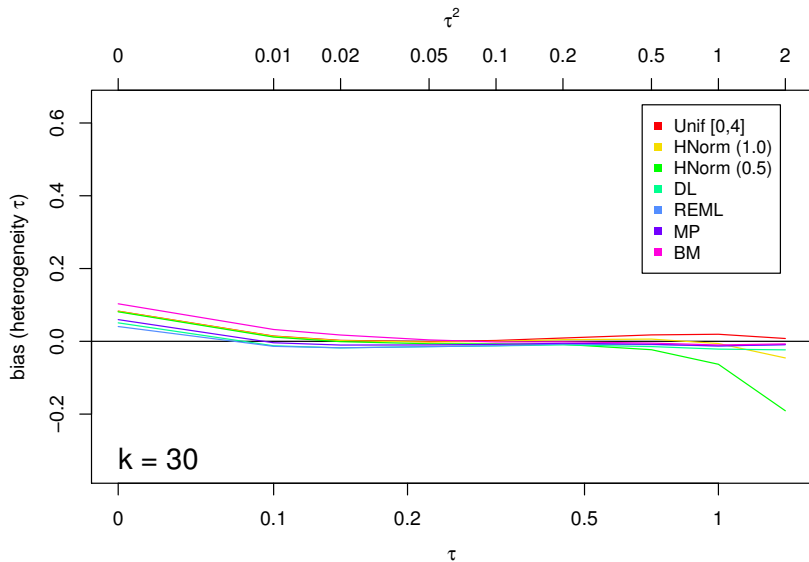
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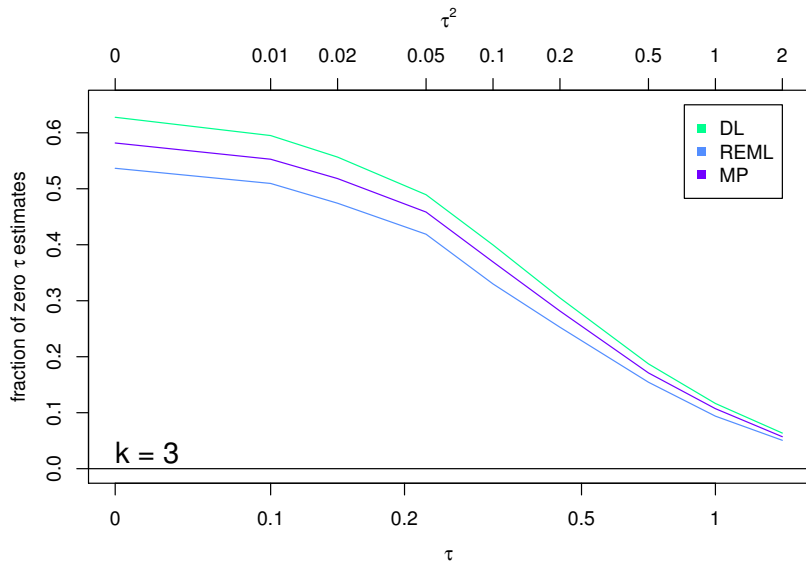
Simulation study

heterogeneity estimation: **bias**

- frequentist estimators similar
- Bayes estimators: positive/negative bias (“shrinkage”), depending on prior
- *Bayes Modal* (penalized likelihood) estimator in between

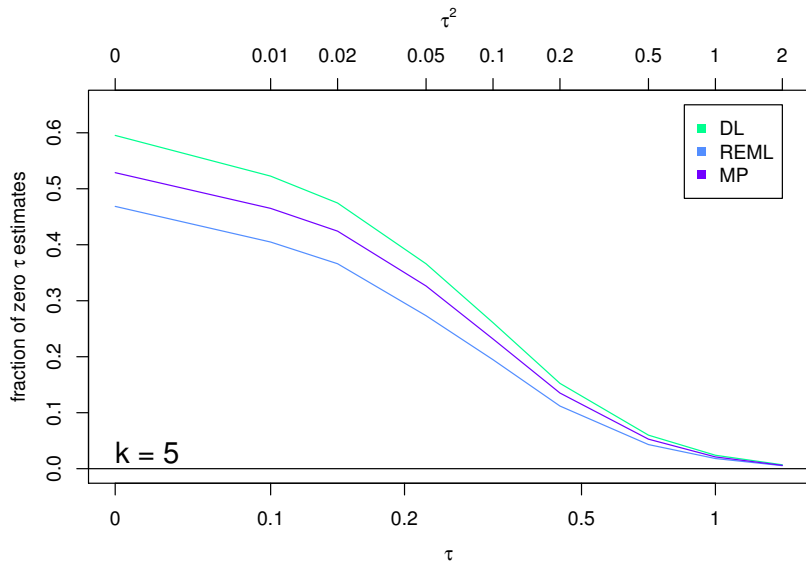
Simulation study

heterogeneity estimation: **zero estimates**



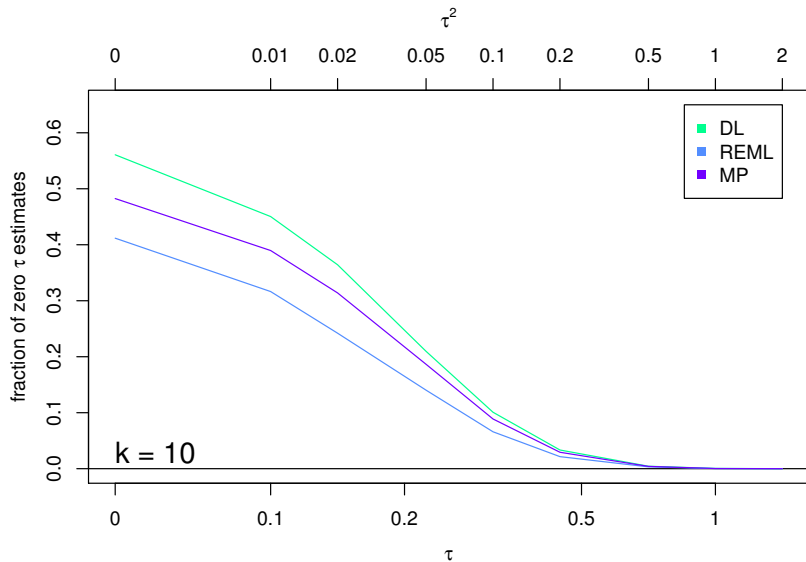
Simulation study

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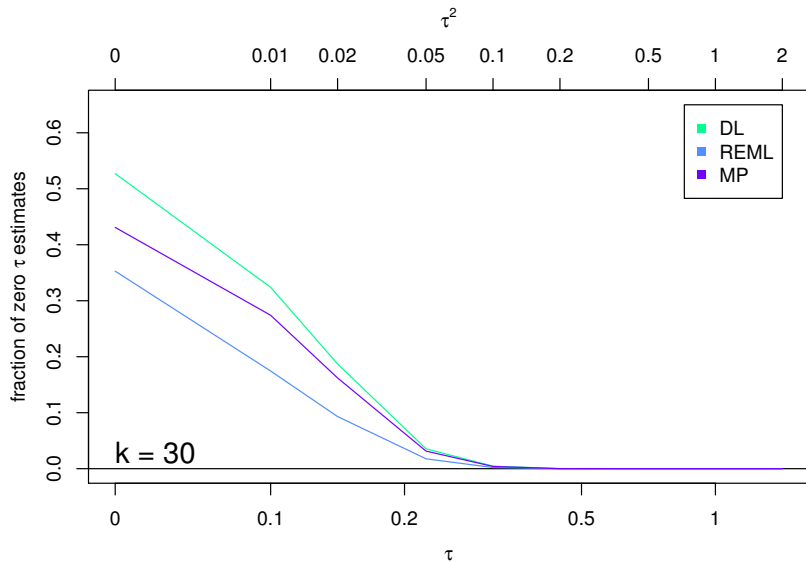
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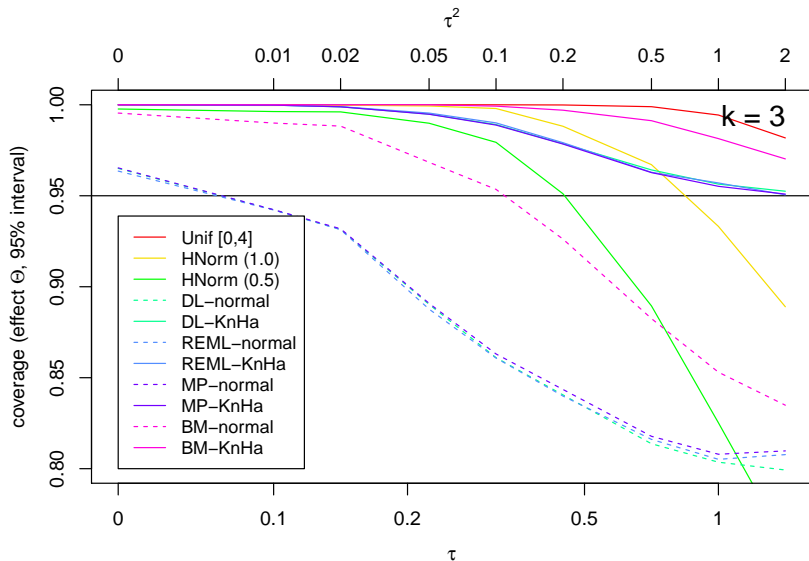
Simulation study

heterogeneity estimation: **zero estimates**

- surprisingly large fraction of zero estimates, even for 'large' true τ values (leading to *fixed effects* model)

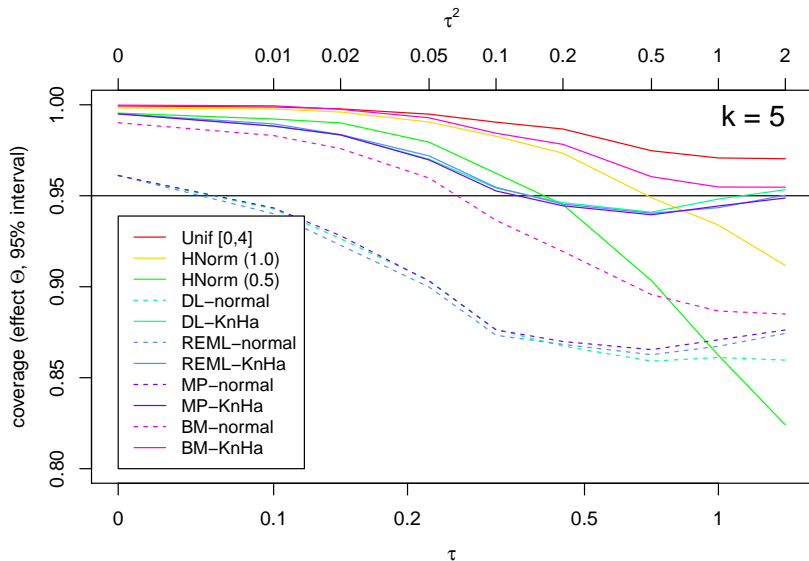
Simulation study

effect estimation: 95% CI coverage



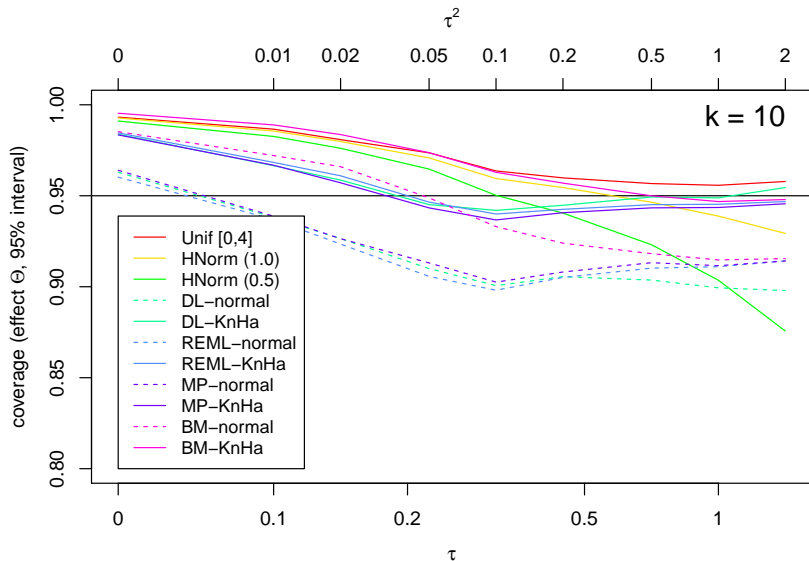
Simulation study

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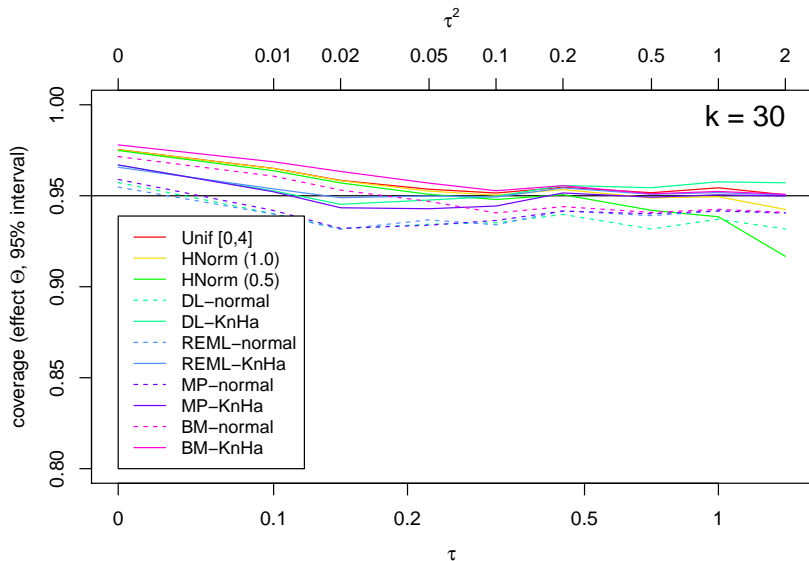
Simulation study

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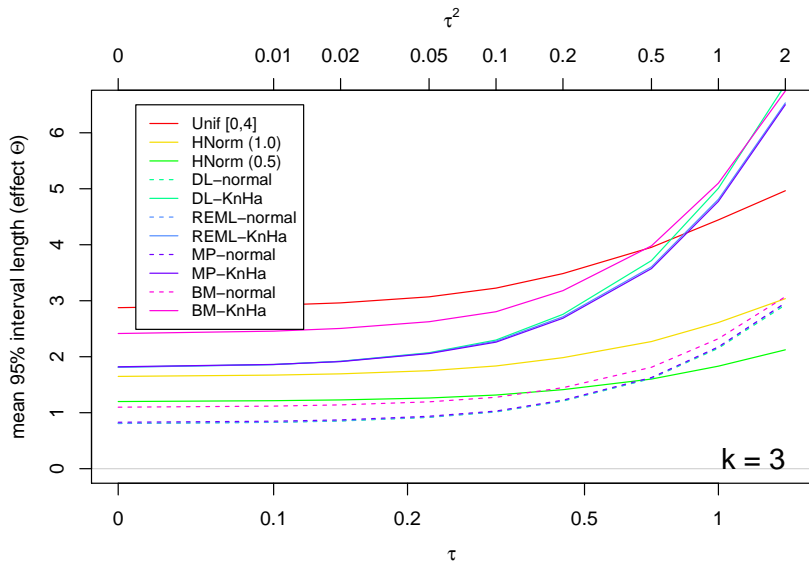
Simulation study

effect estimation: **95% CI coverage**

- poor coverage using normal approximation, Knapp-Hartung adjustment crucial
- little difference between different frequentist methods

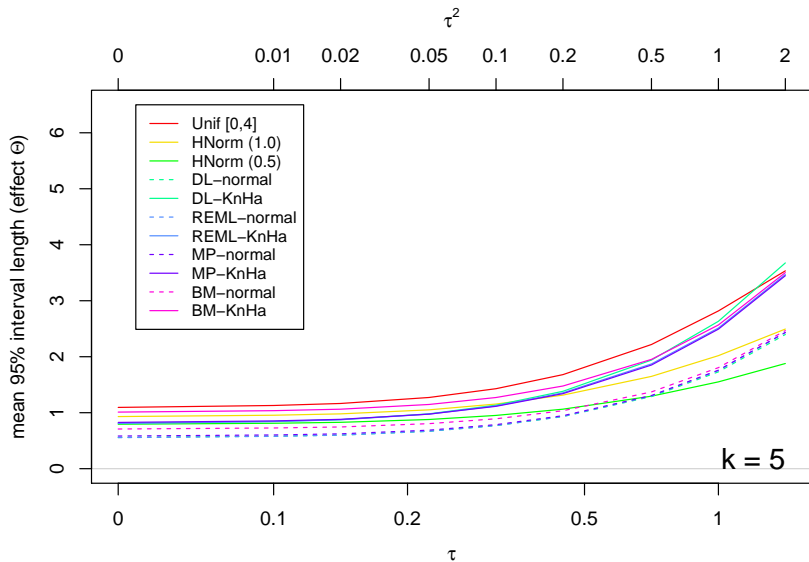
Simulation study

effect estimation: **95% CI length**



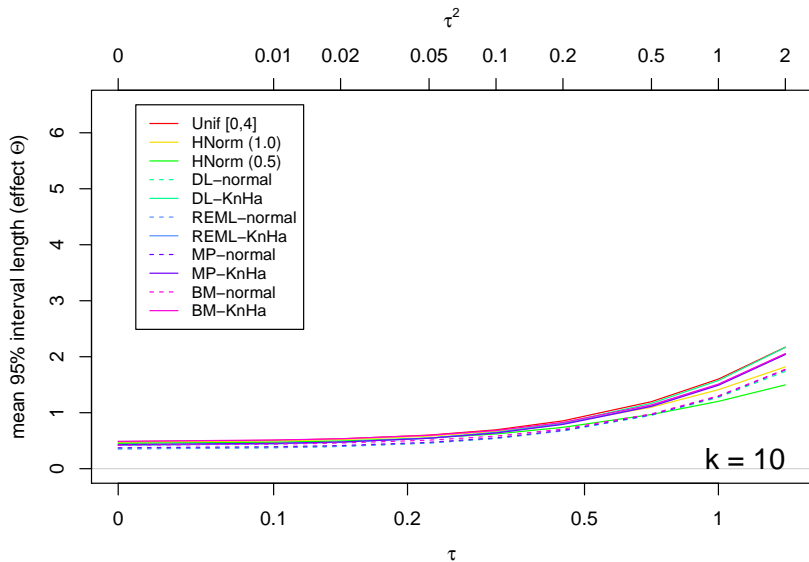
Simulation study

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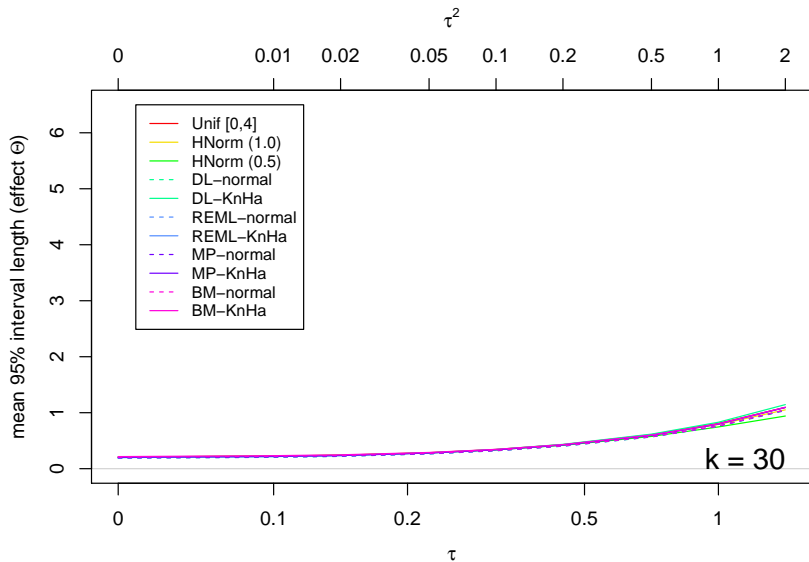
Simulation study

effect estimation: **95% CI length**



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effect estimation: **95% CI length**



Simulation study

effect estimation: **95% CI length**

- Knapp-Hartung CIs substantially longer than normal CIs, especially for small k
- Bayesian intervals (with realistic priors) shorter

Conclusions

- small differences between different frequentist methods
- differences most pronounced in (common!) case of few studies
- consideration of estimation uncertainty:
undercoverage with normal approximation,
application of Knapp-Hartung adjustment crucial for nominal level
- surprisingly many zero τ estimates
- Bayesian methods behave as expected:
conservative / anticonservative for “small” / “large” τ
 (“Mean coverage” (calibration) accurate *by construction*)
- Bayesian methods allow to utilize external information
(effect and heterogeneity, e.g.¹²)
- `bmeta` R package to appear on CRAN soon
- ACKNOWLEDGMENT:
funded by the EU through InSPiRe (FP HEALTH 2013 - 602144)

¹²R.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.

+++ additional slides +++

Implementation

bmeta R package under development

```
> cochran01 <- bmeta(Cochran1954[,"mean"], sqrt(Cochran1954[,"se2"]))
> cochran02 <- bmeta(Cochran1954[,"mean"], sqrt(Cochran1954[,"se2"]),
+                   mu.prior.mean=150, mu.prior.sd=100,
+                   tau.prior=function(x){return(dexp(x, rate=0.05))})
>
> cochran01$summary
      tau      mu  mu.pred
mode   10.303255 156.504954 154.16345
median 12.888735 157.896520 157.33321
mean   14.844457 158.547999 158.54800
sd      9.950631  8.358115  19.70028
95% lower 0.000000 143.180913 119.77459
95% upper 32.665117 176.106158 200.12309
>
> # compute posterior quantiles:
> cochran01$dposterior(mu.p=c(0.005, 0.995))
[1] 135.0429 187.3122
>
> # plot posterior density:
> x <- seq(from=130, to=190, length=100)
> plot(x, cochran02$dposterior(mu=x), type="l")
> lines(x, cochran01$dposterior(mu=x))
```