

Effect and shrinkage estimation in meta-analyses of two studies

Christian Röver

Department of Medical Statistics,
University Medical Center Göttingen,
Göttingen, Germany

December 2, 2016



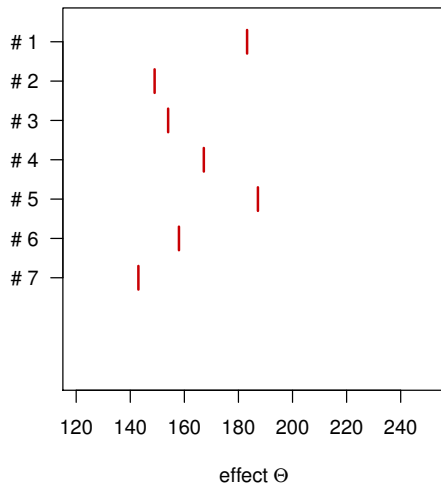
This project has received funding from the European Union's Seventh Framework Programme for research, technological development and demonstration under grant agreement number FP HEALTH 2013-602144.



- meta-analysis
- frequentist and Bayesian approaches
- two-study meta-analysis
- examples + simulations
- shrinkage estimation
- examples + simulations
- conclusions

Meta analysis

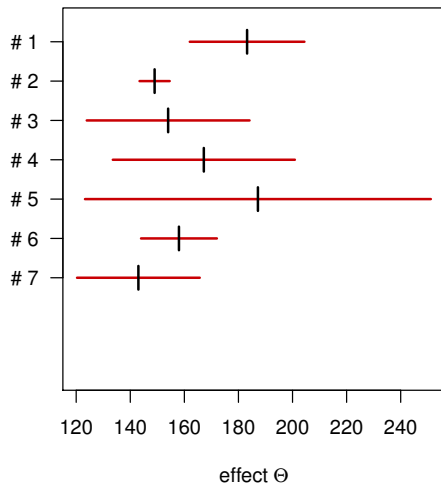
The random-effects model



- have:
 - estimates y_i
 - standard errors σ_i
- want:
 - combined estimate $\hat{\Theta}$
- nuisance parameter:
 - between-trial heterogeneity τ

Meta analysis

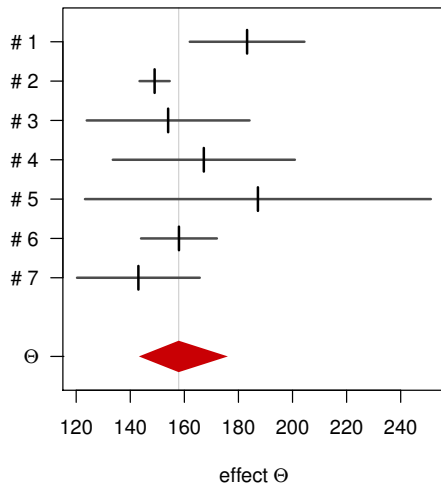
The random-effects model



- have:
 - estimates y_i
 - **standard errors** σ_i
- want:
 - combined estimate $\hat{\Theta}$
- nuisance parameter:
 - between-trial heterogeneity τ

Meta analysis

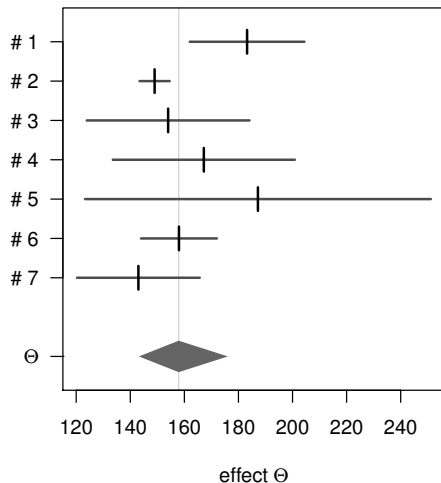
The random-effects model



- have:
 - estimates y_i
 - standard errors σ_i
- want:
 - combined estimate $\hat{\Theta}$
- nuisance parameter:
 - between-trial heterogeneity τ

Meta analysis

The random-effects model



- have:
 - estimates y_i
 - standard errors σ_i
- want:
 - combined estimate $\hat{\Theta}$
- nuisance parameter:
 - **between-trial heterogeneity τ**

Meta analysis

The random-effects model

- assume *normal-normal hierarchical model (NNHM)*

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

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

- model components:

Data:

- estimates y_i
- standard errors s_i

Parameters:

- effect Θ
- heterogeneity τ
- (study-specific effects θ_i)

Meta analysis

The random-effects model

- assume *normal-normal hierarchical model (NNHM)*

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

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

- model components:

Data:

- estimates y_i
- standard errors s_i

Parameters:

- effect Θ
- heterogeneity τ
- (study-specific effects θ_i)

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

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 $\hat{\sigma}_{\Theta}$

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

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

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 $\hat{\sigma}_{\Theta}$
- confidence interval via Normal approximation:

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

(uncertainty in τ not accounted for)

Meta analysis

Frequentist approaches

- Hartung-Knapp-Sidik-Jonkman approach (accounting for τ estimation uncertainty)¹:
 - 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:

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

¹G. Knapp, J. Hartung. Improved tests for a random effects meta-regression with a single covariate. *Statistics in Medicine* 22(17):2693–2710, 2003.

²C. Röver, G. Knapp, T. Friede. Hartung-Knapp-Sidik-Jonkman approach and its modification for random-effects meta-analysis with few studies. *BMC Medical Research Methodology* 15:99, 2015.

- Hartung-Knapp-Sidik-Jonkman approach (accounting for τ estimation uncertainty)¹:
 - 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:

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

- *modified* Knapp-Hartung approach²:
 - quadratic form q may turn out < 1 , confidence intervals may get shorter
 - truncate q to get more conservative interval:

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

¹G. Knapp, J. Hartung. Improved tests for a random effects meta-regression with a single covariate. *Statistics in Medicine* 22(17):2693–2710, 2003.

²C. Röver, G. Knapp, T. Friede. Hartung-Knapp-Sidik-Jonkman approach and its modification for random-effects meta-analysis with few studies. *BMC Medical Research Methodology* 15:99, 2015.

Meta analysis

Bayesian approach

- Bayesian approach ³
 - set up model likelihood (same as frequentist)
 - specify prior information about unknowns (Θ, τ)
 - posterior: \propto prior \times likelihood
 - inference requires integrals, e.g. $p(\Theta | y, \sigma) = \int p(\Theta, \tau | y, \sigma) d\tau \dots$
 - use numerical methods for integration (MCMC, `bayesmeta` R package⁴, ...)
- straightforward interpretation, no reliance on asymptotics, consideration of prior information, ...

³A. J. Sutton, K. R. Abrams. *Bayesian methods in meta-analysis and evidence synthesis*. Statistical Methods in Medical Research, 10(4):277, 2001.

⁴<http://cran.r-project.org/package=bayesmeta>

Meta analysis

The random-effects model

- *normal-normal hierarchical model (NNHM)* applicable for many endpoints: only need estimates and std. errors of some *effect measure*
- $k = 2$ to 3 studies is a common scenario: *majority* of meta analyses in Cochrane Database⁵
- frequentist methods run into problems for few studies (small k)
- two-study case: no satisfactory frequentist procedure⁶
- despite extreme setting, error control crucial⁷

⁵R.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.

⁶A. Gonnermann et al. No solution yet for combining two independent studies in the presence of heterogeneity. *Statistics in Medicine* 34(16):2476–2480, 2015

⁷European Medicines Agency (EMA). Guideline on clinical trials in small populations. CHMP/EWP/83561/2005, http://www.ema.europa.eu/docs/en_GB/document_library/Scientific_guideline/2009/09/WC500003615.pdf, 2006.

Examples

2-study meta analyses

- two examples of two-study meta-analyses^{8,9}
- binary endpoints (log-ORs)
- Bayesian analyses:
 - uniform effect (Θ) prior
 - half-normal heterogeneity (τ) priors with scales 0.5 and 1.0
- frequentist analyses:
 - normal approximation
 - Hartung-Knapp-Sidik-Jonkman (HKSJ) interval
 - modified Knapp-Hartung (mKH) interval
 - for $k = 2$ studies *DerSimonian-Laird*, *ML*, *REML* and *Paule-Mandel* heterogeneity estimates coincide¹⁰

⁸N.D. Crins et al. Interleukin-2 receptor antagonists for pediatric liver transplant recipients: A systematic review and meta-analysis of controlled studies. *Pediatric Transplantation* 18(8):839–850, 2014.

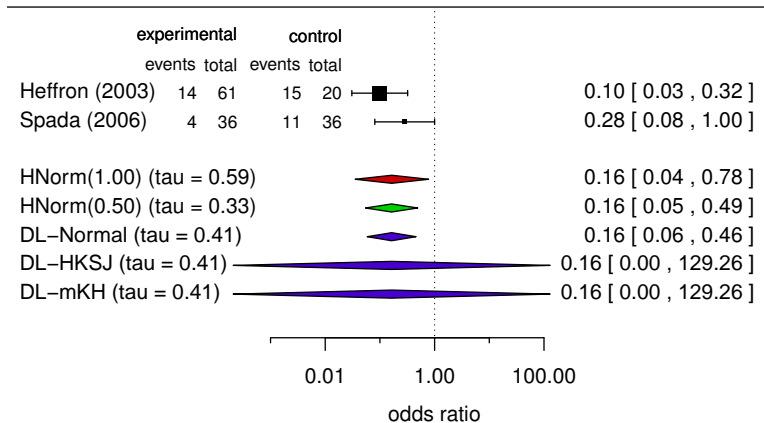
⁹R.C. Davi et al. KrystexxaTM (Pegloticase, PEG-uricase and puricase). Statistical Review and Evaluation STN 125293-0037, U.S. Department of Health and Human Services, Food and Drug Administration (FDA).

¹⁰A.L. Rukhin. Estimating common mean and heterogeneity variance in two study case meta-analysis. *Statistics & Probability Letters* 82(7):1318-1325, 2012.

Examples

2-study meta analyses

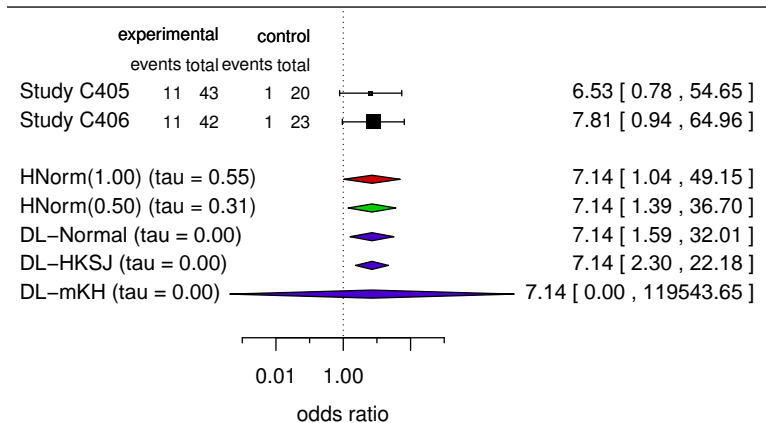
Crins et al. example: acute graft rejection



Examples

2-study meta analyses

Krystexxa example: infusion reaction



Simulation study

Setup

- How do methods compare in general?
- motivation: log-OR endpoint
- simulate data (according to NNHM) on log-OR scale
- consider combinations of studies of sizes $n_1, n_2 \in \{25, 100, 400\}$
(standard errors $\sigma_i = \frac{2}{\sqrt{n_i}}$)
- heterogeneity $\tau \in \{0.0, 0.1, 0.2, 0.5, 1.0\}$

Simulation study

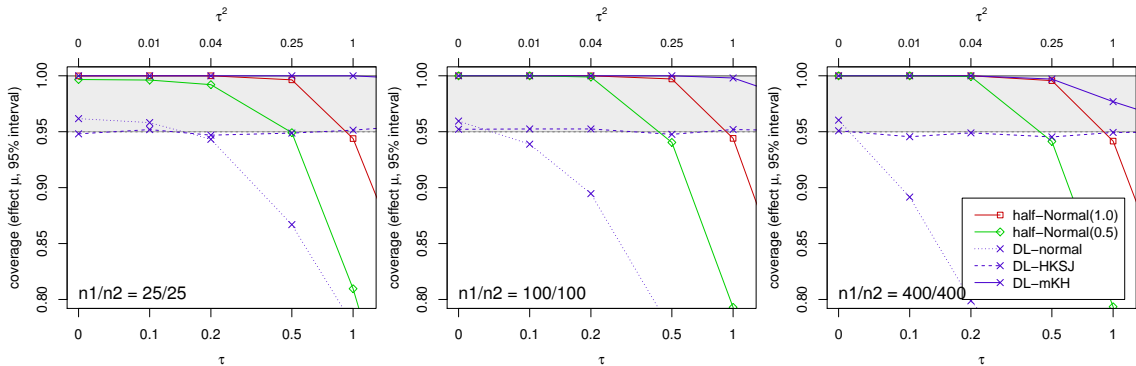
heterogeneity estimation: **zero estimates**

- Percentages of zero heterogeneity estimates (effectively *fixed-effect* analyses):

n_1 / n_2	true heterogeneity τ				
	0.0	0.1	0.2	0.5	1.0
25 / 25	68	67	62	47	29
100 / 100	68	63	52	29	15
400 / 400	68	53	34	16	8
25 / 100	68	65	60	41	23
100 / 400	68	61	46	24	13
25 / 400	68	65	59	39	22

Simulation study

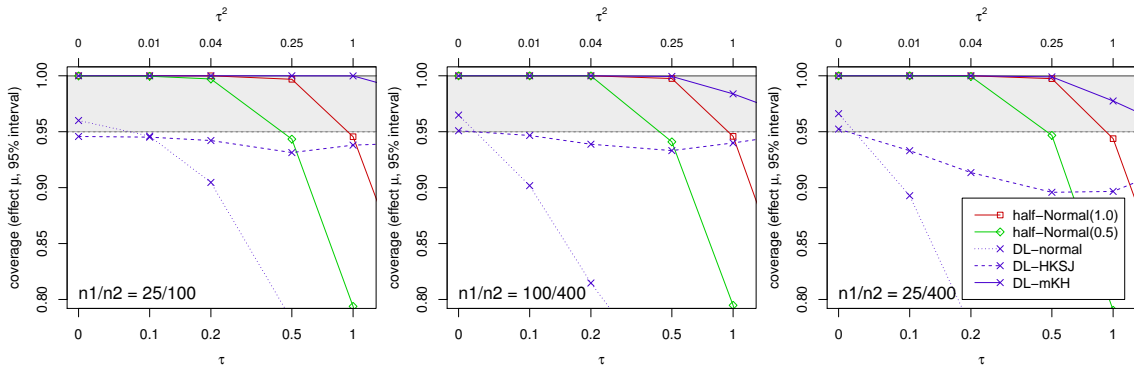
effect CI coverage (two equal-sized studies)



- undercoverage for normal approx.

Simulation study

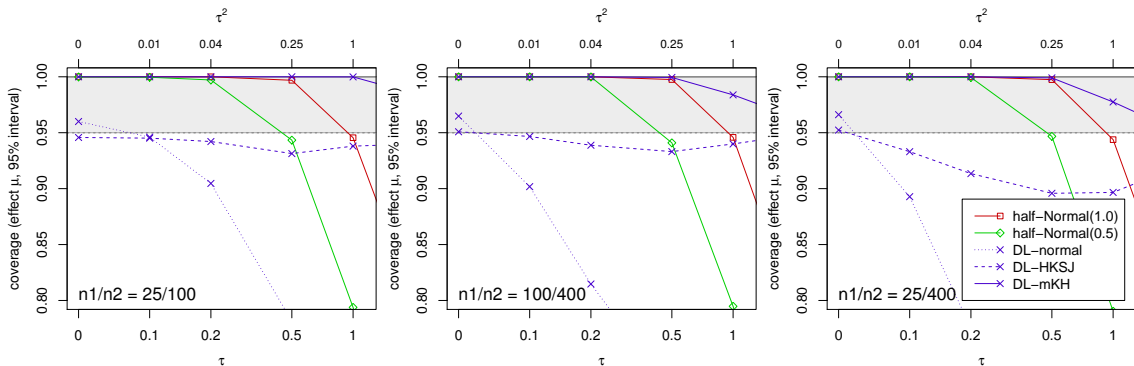
effect CI coverage (two unequal-sized studies)



- undercoverage for normal approx.
- undercoverage for HKSJ at unequal sizes

Simulation study

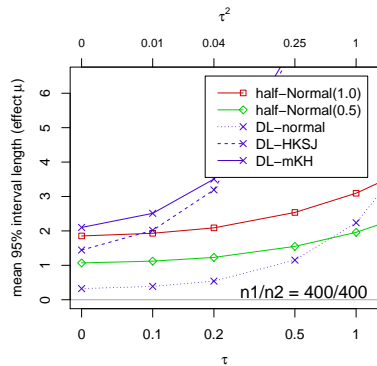
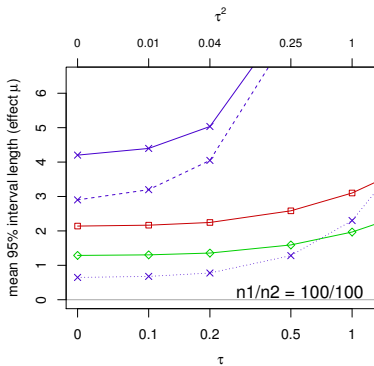
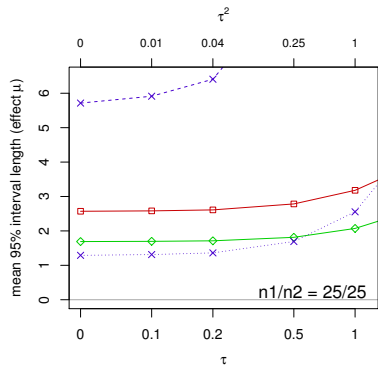
effect CI coverage (two unequal-sized studies)



- undercoverage for normal approx.
- undercoverage for HKSJ at unequal sizes
- Bayesian intervals as expected
- mKH very conservative

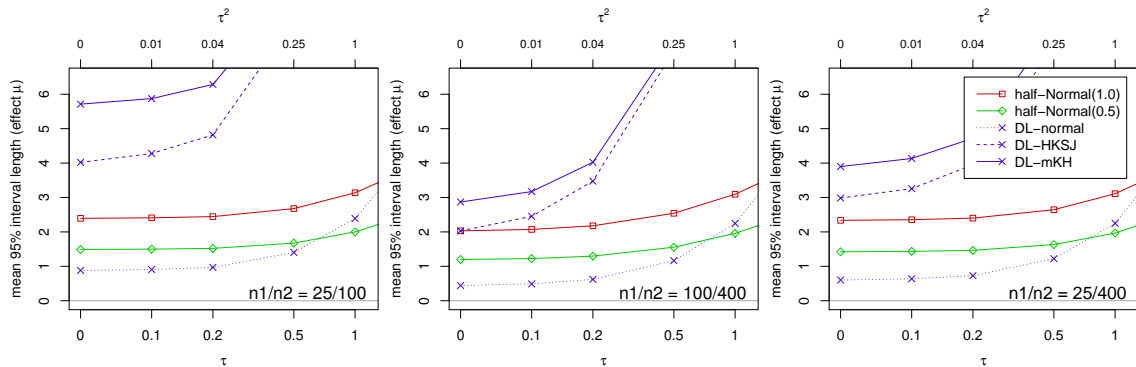
Simulation study

effect CI length (two equal-sized studies)



Simulation study

effect CI length (two unequal-sized studies)



- substantially shorter intervals for Bayesian methods

Conclusions I

Meta-analysis of 2 studies

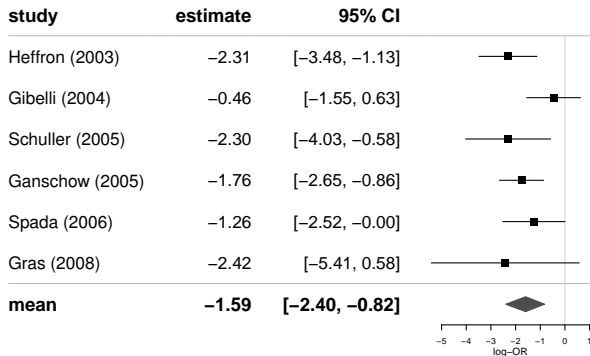
- two-study meta-analysis is a common scenario
- common frequentist methods tend to be either very conservative or too liberal
- small k technically not a problem for Bayesian approach
(no reliance on asymptotics)
- w.r.t. long-run performance, Bayesian meta-analysis provides a middle ground
- interpretation is straightforward

- paper to appear¹¹

¹¹T. Friede, C. Röver, S. Wandel, B. Neuenschwander. Meta-analysis of two studies in the presence of heterogeneity with applications in rare diseases. *Biometrical Journal*, (in press), 2016. URL: <http://dx.doi.org/10.1002/bimj.201500236>.

Shrinkage estimation

Introduction

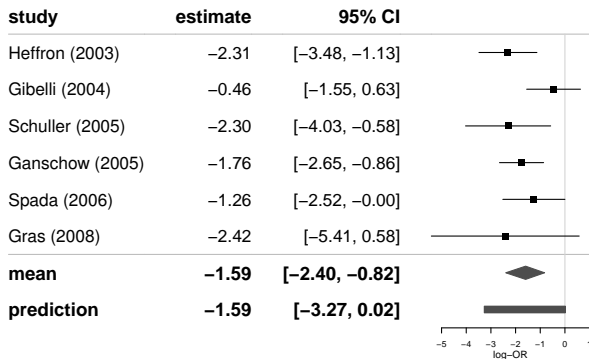


different aims of meta analysis:

- overall mean of studies?
→ **effect estimation** (Θ)

Shrinkage estimation

Introduction



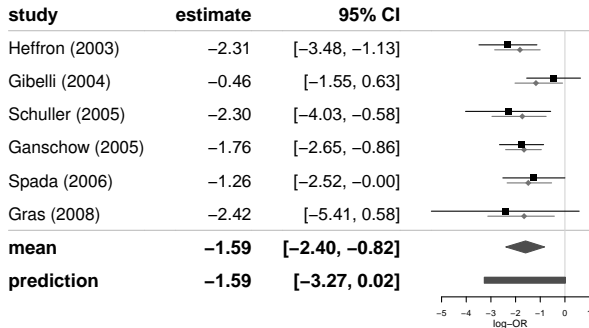
different aims of meta analysis:

- overall mean of studies?
→ **effect estimation** (Θ)
- future studies?
→ **prediction** (θ_{k+1})

Shrinkage estimation

Introduction

■ quoted estimate ◆ shrinkage estimate



different aims of meta analysis:

- overall mean of studies?
→ **effect estimation** (Θ)
- future studies?
→ **prediction** (θ_{k+1})
- individual studies?
→ **shrinkage estimation** (θ_i)

Shrinkage estimation

Introduction

shrinkage estimation:

- specific for the i th study
- estimate of study's specific mean θ_i
- based on all estimates $(y_1, \dots, y_k, \sigma_1, \dots, \sigma_k)$
- (more or less) “shrunk” towards the overall mean Θ
- joint analysis informs hyperprior $p(\Theta, \tau)$ and prior $p(\theta_i|\Theta, \tau)$
→ more informative posterior based on data y_i .

Shrinkage estimation

The MAP / MAC connection

- two ways to analyze i th estimate:
 - **Meta-analytic-combined (MAC)** approach:
perform joint meta-analysis of all studies,
determine i th shrinkage estimate
 - **Meta-analytic-predictive (MAP)** approach:
meta-analyze all but i th study;
resulting posterior yields *meta-analytic predictive (MAP) prior*,
use MAP prior and data y_i to infer θ_i
- both approaches yield identical results¹²

¹²H. Schmidli, et al. Robust meta-analytic-predictive priors in clinical trials with historical control information. *Biometrics* 70(4):1023–1032, 2014.

Shrinkage estimation

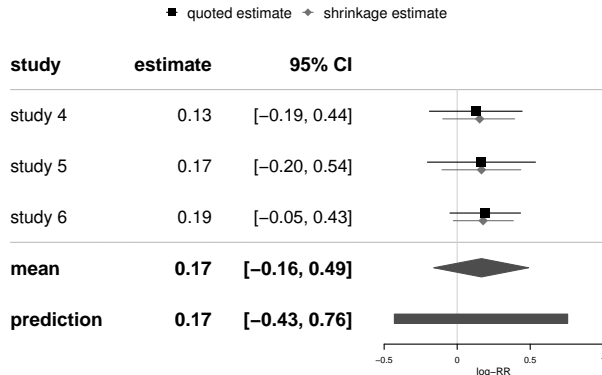
Inference for single trials

- often of primary interest: a particular study (-outcome)
(**not** a more general evidence synthesis)
- example:
 - phase III studies
 - additional information: studies from earlier phases
- aim is not a synthesis of all available data,
but use of MAP prior may be readily motivated¹³
- separate consideration of (*MAP*) *prior* and *data* yields a transparent analysis
- allows to consider external information when data are sparse
(e.g. rare diseases)

¹³S. Wandel, B. Neuenschwander, C. Röver, T. Friede. Using phase II data for the analysis of phase III studies: an application in rare diseases. (*submitted for publication*), 2016. Preprint: <http://arxiv.org/abs/1609.03367>.

Shrinkage estimation

The HSV example



HSV example

(cure rate endpoint, non-inferiority)^a:

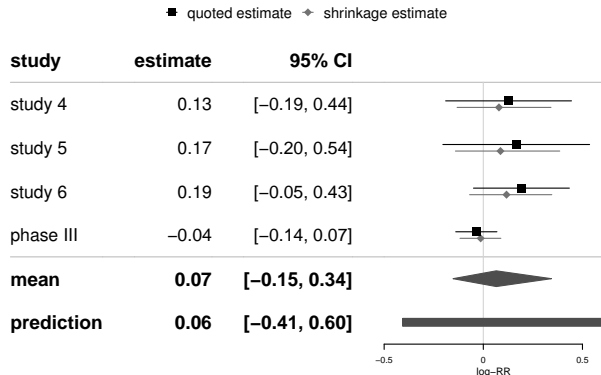
- end of phase II:
3 studies available,
prediction interval constitutes
prior for planned phase III study

^aS. Wandel, B. Neuenschwander, C. Röver, T. Friede. Using phase II data for the analysis of phase III studies: an application in rare diseases. (submitted for publication), 2016.

Preprint: <http://arxiv.org/abs/1609.03367>.

Shrinkage estimation

The HSV example



HSV example

(cure rate endpoint, non-inferiority)^a:

- end of phase II:
3 studies available,
prediction interval constitutes
prior for planned phase III study
- phase III:
new trial's **shrinkage interval**
summarizes trial considering
informative "phase II" prior

^aS. Wandel, B. Neuenschwander, C. Röver, T. Friede. Using phase II data for the analysis of phase III studies: an application in rare diseases. (submitted for publication), 2016.

Preprint: <http://arxiv.org/abs/1609.03367>.

Shrinkage estimation

in 2-study meta-analysis

- common case:
inference on a **single** study
- consideration of external information / data (**single** estimate)
- consideration of potential heterogeneity
- → use NNHM framework and shrinkage estimate

Shrinkage estimation

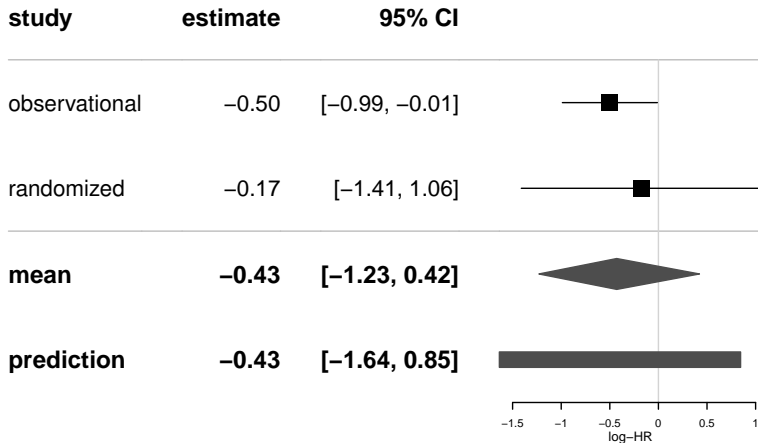
The Creutzfeld-Jakob disease (CJD) example

- Creutzfeld-Jakob disease (CJD) is a **rare disease**
- A small **randomized trial** on the use of Doxycycline was conducted, external **registry data** was considered in addition¹⁴
- heterogeneity suspected between randomized and observational evidence
- both (randomized and observational) estimates were meta-analyzed using NNHM
- originally, interest was in overall effect (Θ)

¹⁴D. Vargas et al. Doxycycline in early CJD – a double-blinded randomized phase II and observational study. *General Neurology* (accepted for publication).

Shrinkage estimation

The Creutzfeld-Jakob disease (CJD) example



Shrinkage estimation

two-study scenario

- consider: primary interest in randomized trial outcome
(no “breaking of randomization” by pooled analysis)
- does it make sense to consider shrinkage estimates from a 2-study meta-analysis?
- how do shrinkage estimates behave in general?

Shrinkage estimation

two-study scenario

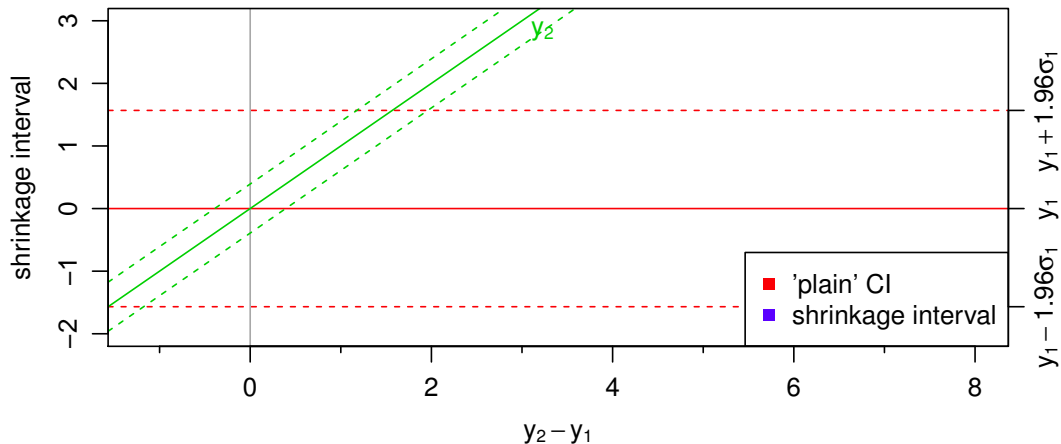
- consider: primary interest in randomized trial outcome
(no “breaking of randomization” by pooled analysis)
- does it make sense to consider shrinkage estimates from a 2-study meta-analysis?
- how do shrinkage estimates behave in general?

- investigate example cases
- investigate long-run behaviour

- consider again pairs of studies
($n_1, n_2 \in \{25, 100, 400\}$, $p(\tau) = \text{HN}(0.5), \dots$)

Shrinkage estimation

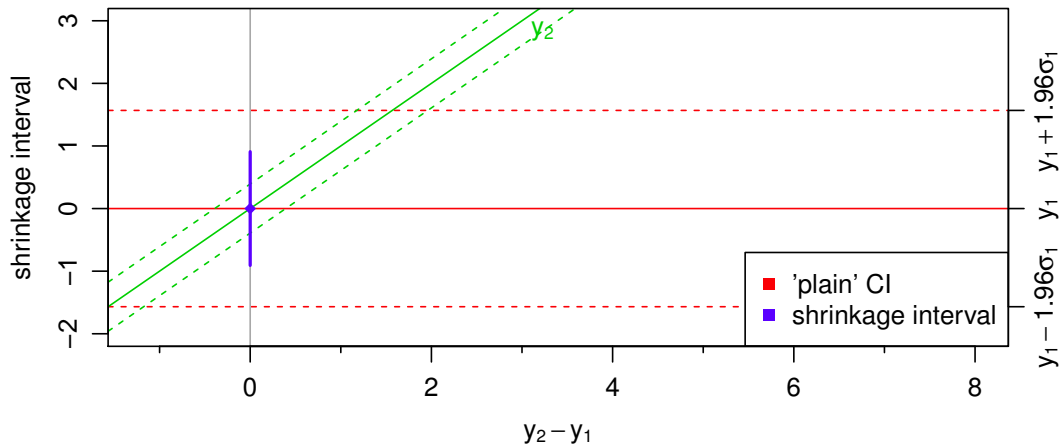
two-study scenario



- $n_1 = 25$, $n_2 = 400$, $p(\tau) = \text{HN}(0.5)$, interested in θ_1

Shrinkage estimation

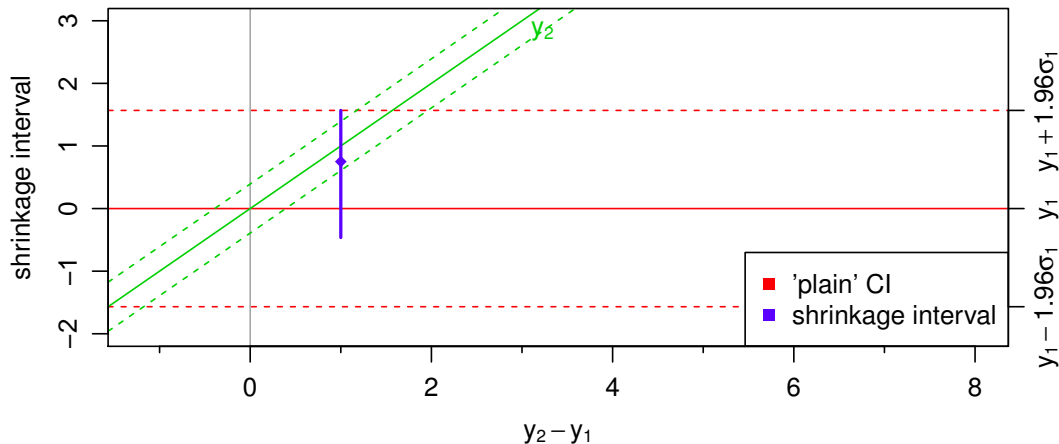
two-study scenario



- $n_1 = 25$, $n_2 = 400$, $p(\tau) = \text{HN}(0.5)$, interested in θ_1

Shrinkage estimation

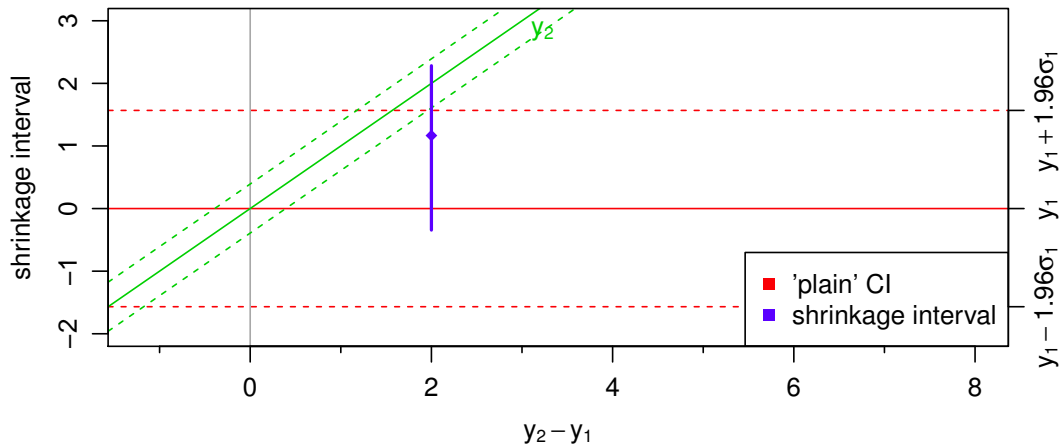
two-study scenario



- $n_1 = 25$, $n_2 = 400$, $p(\tau) = \text{HN}(0.5)$, interested in θ_1

Shrinkage estimation

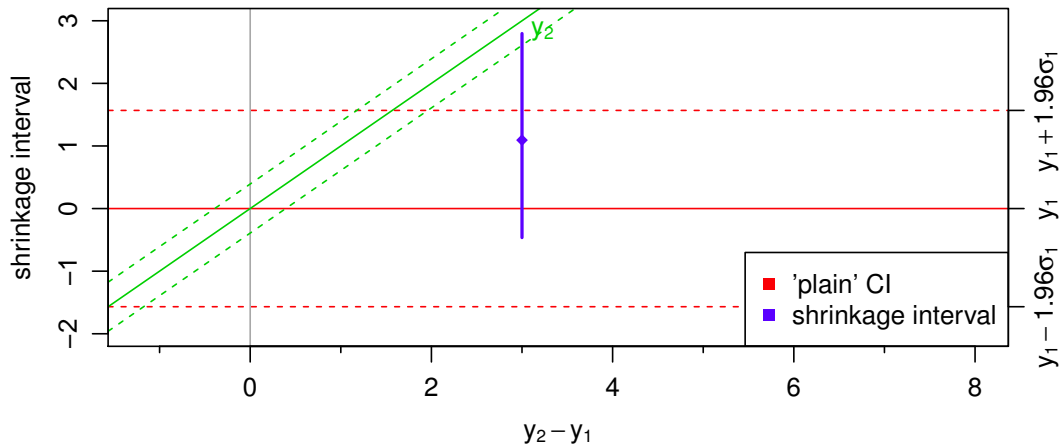
two-study scenario



- $n_1 = 25$, $n_2 = 400$, $p(\tau) = \text{HN}(0.5)$, interested in θ_1

Shrinkage estimation

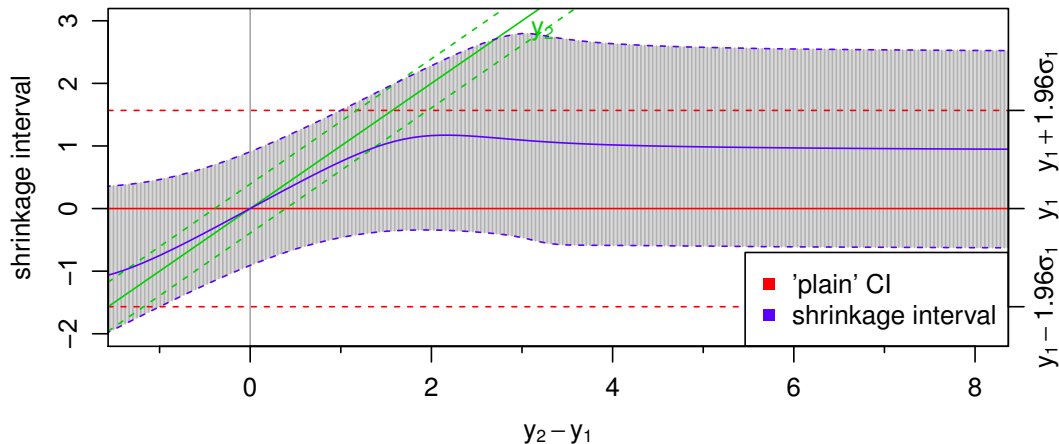
two-study scenario



- $n_1 = 25$, $n_2 = 400$, $p(\tau) = \text{HN}(0.5)$, interested in θ_1

Shrinkage estimation

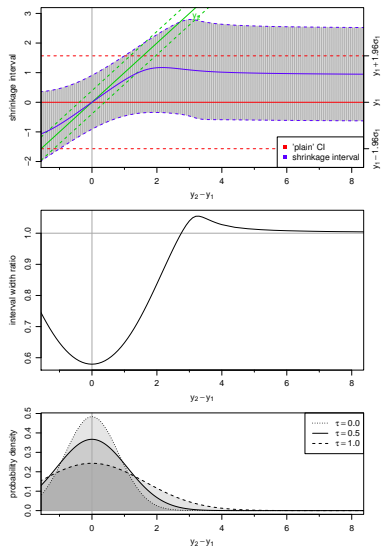
two-study scenario



- $n_1 = 25$, $n_2 = 400$, $p(\tau) = \text{HN}(0.5)$, interested in θ_1

Shrinkage estimation

two-study scenario



- 'robust' behaviour
- ratio of CI widths:
gain may be substantial
- probability density of $(y_2 - y_1)$:
unlikely to exceed $|y_2 - y_1| = 5$

Shrinkage estimation

two-study simulations

- how do shrinkage intervals behave *on average*?
- what gain can we expect (if any)?
- investigate:
 - coverage
 - interval width
- may translate shortened intervals into *sample size gain* (assuming standard errors scale approximately with $\frac{1}{\sqrt{n}}$), e.g.:
relative interval width of 90% corresponds to a $(0.90^{-2} - 1) = 26\%$ gain in sample size

Shrinkage estimation

two-study simulations: coverage (%)

τ prior:		HN(0.5)							HN(1.0)						
n_1/n_2	τ :	0.0	0.1	0.2	0.5	1.0	2.0	*	0.0	0.1	0.2	0.5	1.0	2.0	*
25/400		99.8	99.5	99.0	93.4	84.1	79.4	94.7	99.4	99.2	99.1	96.6	92.6	90.8	95.1
25/100		98.7	98.8	98.3	93.6	86.1	79.9	95.1	98.3	98.7	98.5	96.3	93.2	90.4	94.4
100/400		98.5	98.1	97.2	93.3	90.7	90.6	94.9	98.0	97.6	97.3	95.1	93.5	93.6	95.3
25/25		96.7	96.8	96.1	94.6	90.4	84.5	95.0	97.1	97.1	96.6	95.8	94.1	92.1	94.9
100/100		96.8	96.7	96.4	94.0	91.3	91.0	95.7	96.7	96.6	96.8	95.3	93.8	93.8	94.9
400/400		96.9	96.7	95.0	93.9	93.9	94.1	95.0	96.6	96.6	95.0	94.7	94.9	95.0	95.0
100/25		96.0	95.8	95.1	94.8	93.9	92.6	94.7	96.0	95.9	95.4	95.2	94.8	94.4	94.8
400/100		95.2	95.8	95.2	94.8	93.7	93.8	95.1	95.4	95.7	95.3	95.1	94.4	94.6	95.1
400/25		95.2	94.9	95.3	94.7	94.8	94.5	95.3	95.1	94.9	95.3	94.8	94.9	95.2	95.2

*: heterogeneity τ drawn from prior distribution

Shrinkage estimation

two-study simulations: relative interval width (%)

τ prior:		HN(0.5)							HN(1.0)						
n_1/n_2	τ :	0.0	0.1	0.2	0.5	1.0	2.0	*	0.0	0.1	0.2	0.5	1.0	2.0	*
25/400		62.3	62.7	63.0	65.6	72.1	83.1	65.1	75.6	75.9	76.2	78.6	83.8	90.9	81.5
25/100		67.5	67.4	67.9	69.8	75.2	84.2	69.5	78.5	78.4	78.8	80.8	85.2	91.4	83.2
100/400		78.5	78.7	79.9	85.2	91.4	95.9	83.4	85.7	85.9	86.9	90.9	95.1	97.8	92.1
25/25		78.9	79.0	79.0	79.7	81.8	86.8	79.7	85.2	85.2	85.3	86.2	88.3	92.4	87.6
100/100		85.1	85.4	85.7	88.5	92.5	96.2	87.5	89.9	90.1	90.4	92.7	95.6	97.9	93.9
400/400		89.9	90.5	91.9	95.5	97.8	99.0	93.7	93.0	93.4	94.5	97.2	98.7	99.5	97.3
100/25		92.9	92.9	93.0	93.4	94.6	96.6	93.3	95.0	95.0	95.1	95.6	96.7	98.1	96.1
400/100		95.0	95.1	95.4	96.7	98.1	99.1	96.2	96.5	96.6	96.9	97.9	98.9	99.5	98.2
400/25		98.0	98.0	98.1	98.2	98.6	99.2	98.2	98.6	98.6	98.6	98.8	99.1	99.5	99.0

*: heterogeneity τ drawn from prior distribution

Shrinkage estimation

two-study simulations: relative sample size gain (%)

τ prior:		HN(0.5)							HN(1.0)						
n_1/n_2	τ :	0.0	0.1	0.2	0.5	1.0	2.0	*	0.0	0.1	0.2	0.5	1.0	2.0	*
25/400		162	160	158	144	113	68.4	147	77.8	76.5	75.4	67.1	50.5	28.8	58.3
25/100		123	123	121	111	89.6	56.3	113	64.8	65.0	63.6	57.1	43.5	25.6	50.0
100/400		64.5	64.0	60.0	43.8	25.7	12.7	49.4	37.4	37.1	34.3	23.9	13.3	6.2	20.7
25/25		61.2	60.9	60.7	58.4	51.8	36.9	58.7	38.7	38.5	38.1	35.8	30.0	19.6	32.2
100/100		38.8	38.1	37.1	29.6	19.4	10.1	32.3	24.4	23.8	23.0	17.4	10.7	5.3	14.8
400/400		24.2	22.9	19.4	11.0	5.5	2.4	15.1	16.1	15.1	12.5	6.6	3.1	1.3	6.3
100/25		15.9	16.0	15.8	14.8	11.9	7.5	14.9	10.9	10.9	10.7	9.6	7.2	4.2	8.4
400/100		11.0	10.7	10.0	7.3	4.2	2.0	8.3	7.4	7.2	6.6	4.5	2.5	1.1	3.9
400/25		4.1	4.1	4.0	3.7	2.9	1.7	3.7	2.9	2.8	2.8	2.5	1.8	1.0	2.1

*: heterogeneity τ drawn from prior distribution

Shrinkage estimation

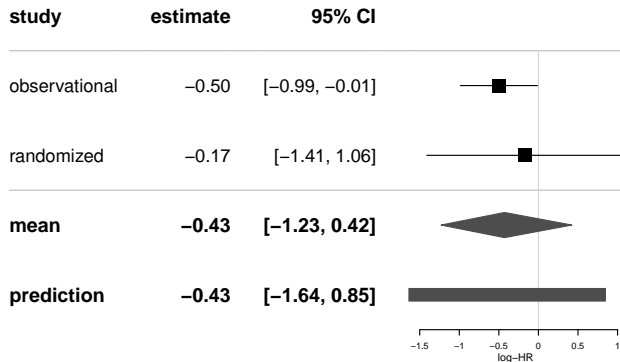
two-study simulations: fraction of shortened intervals (%)

τ prior:		HN(0.5)							HN(1.0)						
n_1/n_2	τ :	0.0	0.1	0.2	0.5	1.0	2.0	*	0.0	0.1	0.2	0.5	1.0	2.0	*
25/25		100.0	99.9	100.0	99.7	97.4	81.9	99.5	99.4	99.1	99.1	97.7	91.1	68.8	91.4
25/100		99.9	99.9	99.9	99.1	92.3	68.6	98.6	99.2	99.3	98.9	96.4	83.9	57.4	86.9
25/400		99.9	99.9	99.9	98.8	90.7	64.0	98.1	99.3	99.3	99.1	95.8	82.3	53.9	85.8
100/25		99.7	99.8	99.7	98.7	89.9	65.3	98.1	98.2	98.1	97.9	94.6	80.3	53.8	85.2
100/100		99.3	98.9	98.5	90.9	68.6	39.7	91.5	97.6	96.6	95.6	83.7	59.8	33.5	71.3
100/400		99.2	98.7	97.3	84.2	56.9	31.1	87.2	97.5	96.8	94.5	77.0	50.1	26.9	65.4
400/25		99.6	99.8	99.5	97.6	86.7	58.9	96.9	98.1	98.1	97.1	93.0	76.3	48.7	82.3
400/100		98.7	98.2	95.8	80.4	54.4	29.5	84.7	96.1	95.1	91.6	72.4	47.0	24.9	62.3
400/400		97.6	96.0	88.5	60.3	34.1	17.7	72.0	95.1	92.6	83.0	54.2	30.4	15.5	48.6

*: heterogeneity τ drawn from prior distribution

Shrinkage estimation

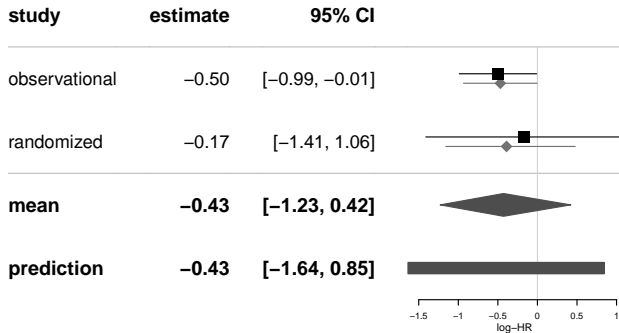
The Creutzfeld-Jakob disease (CJD) example



Shrinkage estimation

The Creutzfeld-Jakob disease (CJD) example

■ quoted estimate ◆ shrinkage estimate



- shrinkage interval width: 66%,
129% gain in sample size
(≈ 27 instead of 12 patients)

Conclusions II

Shrinkage estimates for 2 studies

- readily motivated
- robust behaviour
- potentially substantial gain despite 'pathological' setting ($k = 2$)
- especially if $\sigma_2 \leq \sigma_1$
- good coverage

Conclusions II

Shrinkage estimates for 2 studies

- readily motivated
 - robust behaviour
 - potentially substantial gain despite 'pathological' setting ($k = 2$)
 - especially if $\sigma_2 \leq \sigma_1$
 - good coverage
-
- `install.packages("bayesmeta")`
`library("bayesmeta")`

+++ additional slides +++

CJD example

R code

```
cjd <- cbind.data.frame("study"      = c("observational", "randomized"),
                        "logHR"      = c(-0.49948, -0.17344),
                        "logHR.se"   = c(0.2493, 0.6312), stringsAsFactors=FALSE)

# analyze:
require("bayesmeta")
bm <- bayesmeta(y          = cjd$logHR,
                sigma      = cjd$logHR.se,
                labels     = cjd$study,
                tau.prior  = function(t){dhalfnormal(t, scale=0.5)})

# show results:
print(bm)

# show forest plot:
forestplot(bm, xlab="log-HR")
forestplot(bm, exponentiate=TRUE, xlog=TRUE, xlab="hazard ratio")

# show shrinkage estimates:
print(bm$theta)
```