# **"Association Between Risk-of-Bias Assessments and Results of Randomized Trials in Cochrane Reviews: the ROBES Meta-Epidemiologic Study"**

## **Web Material**

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### <span id="page-1-0"></span>**Abbreviations**

(The) BRANDO study – study name (BRANDO - Bias in Randomized and Observational studies) (The) ROBES study – study name (ROBES -  $R$ isk of Bias in Evidence Synthesis)

### <span id="page-2-0"></span>**Web Appendix 1: Supplementary Methods**

#### <span id="page-2-1"></span>**Selection of eligible meta-analyses**

We carried out study selection using a combination of semi-automated queries and manual data categorization by the study team.

*Mapping of the risk of bias items*: Within the Review Manager software, authors of Cochrane reviews can amend the wording of standard risk of bias items or can add and exclude specific items. All verbatim 'non-standard' risk of bias domains were classified into categories to avoid loss of usable risk of bias data due to differences in wording. For example, if the user-defined bias domain was labelled 'randomization method' this was classified as 'sequence generation' domain. The vast majority of risk of bias tables did however contain the standard wording for domains.

*Exclusion of ineligible data*: From the initial dataset of 1399 reviews we excluded reviews that did not have all five recommended risk of bias items completed: sequence generation, allocation concealment, blinding (assessed just as 'blinding' without further descriptors or as blinding of specific, reviewer-defined, groups such as patients or assessors), incomplete outcome data and selective reporting. Having a completed 'Other bias' domain was not required as the use of this domain is recommended for potential topic- or design-specific biases that are not necessarily relevant to all types of studies. We further excluded meta-analyses that had fewer than 5 included trials and meta-analyses without a summary estimate, labelled 'non-estimable' in the supplied dataset (e.g. due to zero events in both intervention groups across all studies, or where review authors chose not to calculate a summary estimate (e.g. where meta-analysis was not considered appropriate)). We further excluded meta-analyses with continuous outcomes. The remaining metaanalyses were then scrutinized individually as follows.

*Selection of meta-analysis with primary outcomes*: In each of the remaining reviews, we tagged meta-analyses with outcome(s) that were described as primary outcomes in the text of the review. The first meta-analysis from each review to be included in our study (referred to as the 'selected' meta-analysis) was selected as follows: 1) If, having followed the exclusion process described above, only one meta-analysis in the review had a primary outcome then this was selected; 2) if there were multiple primary outcome meta-analyses available, the meta-analysis with the most included trials (and, if tied, that with most included participants) was selected from among these; and 3) if there were no primary outcome meta-analyses in the review, the meta-analysis with the most included trials (and, if tied, that with most included participants) was selected.

*Exclusion of overlapping meta-analyses*: For each review, we then examined whether there were any overlapping trials between the 'selected' meta-analysis and all other meta-analyses in that

review, in the order of decreasing size (number of trials, then number of participants), starting with meta-analyses with primary outcomes. The additional meta-analysis was included in the study only if it did not contain any trials already included in the selected meta-analysis. Any subsequent metaanalysis from the same review could only be included if it had no overlapping trials with any of the already included meta-analyses and so on.

*Dealing with meta-analyses' subgroups*: Meta-analyses that had no subgroups were taken whole and all related trial outcome level data were included. Of the meta-analyses that had subgroups, some had an overall estimate across all subgroups, while others only provided estimates for individual subgroups. In the case of the former, we treated such meta-analyses in the same way as those that did not have subgroups, ignoring the subgroups. In a small number of meta-analyses, results from one trial were recorded across 2 subgroups. We checked these to ensure that the same participants did not contribute to both estimates. If overlap was identified (e.g. 3-arm trial where the comparison group was used in both subgroup analyses), we removed one of the occurrences of a trial, at random. When only subgroup level estimates were provided, we assumed there was a justifiable rationale for not calculating an overall estimate (e.g. important clinical heterogeneity). In such cases we included only the largest subgroup, by number of included trials, if tied by number of participants, and if still tied, the subgroup that appeared first in the review.

Meta-analyses categorized as having an active comparison where it was not clear which intervention was experimental or novel were excluded. For the remaining meta-analyses comparing two active interventions, the newer or the more recently introduced intervention was coded as experimental intervention and the older or standard intervention was coded as a comparator in the analysis.

### <span id="page-4-0"></span>**Web Appendix 2: Analysis Details, Model Specification and WinBUGS Code**

#### <span id="page-4-1"></span>**Illustration of the analysis on a single meta-analysis example**

The underlying idea of the analysis is illustrated in Web Figure 1, for a single meta-analysis of antihypertensive medication for prevention of cardiovascular mortality and morbidity in the elderly.(3) In this example, the overall odds ratio in studies assessed as at high or unclear risk of bias for sequence generation was 0.69 (95% confidence interval 0.61, 0.78), while the corresponding odds ratio for studies at low risk of bias was 0.87 (95% confidence interval 0.65, 1.16). The ratio of odds ratios comparing studies at high/unclear with low risk of bias measures the difference in effect size in the two sets of trials, and was  $0.79$  (=0.69/0.87) with 95% confidence interval 0.60 to 1.02 (estimated using meta-regression in Stata 14). This process is then repeated for each included metaanalysis and average ratio of odds ratio is estimated across all meta-analyses and measures of how bias varies across meta-analyses.

<span id="page-5-1"></span>**Web Figure 1**. Example Meta-analysis, Depicting the Ratio of Odds Ratios Comparing the Overall Intervention Effect in Studies at High or Unclear Risk of Bias With That in Studies at Low Risk of Bias for Sequence Generation



Random-effects meta-analysis of antihypertensive medication (vs placebo or no treatment) for cardiovascular mortality and morbidity, stratified by risk of bias for sequence generation. Odds ratios smaller than 1 favor antihypertensive medication and larger than 1 favor placebo or no treatment. The solid line represents "no difference" between treatments, and the dashed lines represent the estimates from the subgroup meta-analyses of studies with high or unclear risk of bias (top panel) and studies with low risk of bias (lower panel) for sequence generation. The double arrow shows the difference between the subgroup estimates, which is quantified using meta-regression to calculate a ratio of odds ratios and its confidence interval. CI, confidence interval.

#### <span id="page-5-0"></span>**Statistical analysis details**

Datasets for main analyses were prepared, and the analyses of correlations between risk of bias domains were carried out using Stata 14 statistical software. Bayesian hierarchical models were fitted in WinBUGS, using two chains run for 500,000 iterations after a burn-in of 50,000 iterations, with the exception of multivariable analyses with interactions, for which two chains were run for 100,000 iterations following a burn-in of 100,000 iterations.

In all models, we assumed that the observed number of events  $r_{im0}$ ,  $r_{im1}$  in each treatment arm of trial *i* in meta-analysis *m* has a binomial distribution:

 $r_{imo} \sim Binomial(\pi_{imo}, n_{imo})$ 

 $r_{im1} \sim Binomial(\pi_{im1}, n_{im1})$ 

 $logit(\pi_{im0}) = \mu_{im}$ 

 $logit(\pi_{im1}) = \mu_{im} + \theta_{im}$ 

In the univariable analyses, the underlying log-odds ratio  $\theta_{im}$  in trial *i* in meta-analysis *m* was assumed equal to

$$
\theta_{im} = \delta_{im} + \beta_{im} C_{im}
$$
 [Model A, univariate analysis]

where  $C_{im} = 1$  for trials with high or unclear risk of bias and  $C_{im} = 0$  for trials with low risk of bias for each bias domain. The parameter  $\delta_{im}$  represents the intervention effect in trials with low risk of bias. These are assumed to be randomly distributed within each meta-analysis *m:*

$$
\delta_{im} \sim Normal(d_m, \tau_m^2) \tag{i}
$$

Parameter  $\beta_{im}$  quantifies the potential bias associated with the study design characteristic of interest in trial *i* within meta-analysis *m*. We assumed the following model structure, which allows the bias to vary within each meta-analysis and also allows average bias  $b_m$  to vary across metaanalyses:

$$
\beta_{im} \sim Normal(b_m, \kappa^2) \tag{ii}
$$

$$
b_m \sim Normal(b_0, \varphi^2)
$$

For all location parameters (overall mean bias  $b_0$ , trial baseline response rates  $\mu_{im}$ , average intervention effects  $d_m$ ), vague Normal(0,1000) or Normal(0,100) priors were assumed. A generic informative prior was declared for the between-trial heterogeneity variances (based on external empirical data) (15):  $log(\tau_m^2) \sim Normal(-2.56, 1.74^2)$ . Modified inverse gamma(0.001,0.001) priors were declared for  $\kappa$  and  $\varphi$ , as used in the BRANDO study (16).

For multivariable analyses without interactions, we specified Model B for the underlying log odds ratio  $\theta_{im}$ :

$$
\theta_{im} = \delta_{im} + \beta_{1im}C_{1im} + \beta_{2im}C_{2im} + \beta_{3im}C_{3im} + \beta_{4im}C_{4im}
$$
 [Model B, multivariable analysis]

where  $C_{1im}$  to  $C_{4im}$  refer to bias domains: sequence generation, allocation concealment, blinding and incomplete outcome data; and  $\beta_{1im}$  to  $\beta_{4im}$  quantify the corresponding potential biases associated with high or unclear risk of bias judgements for these domains. The  $\delta_{im}$  were assumed randomly distributed within each meta-analysis, as in (i), and a separate model of the form (ii) was assumed for each bias parameter  $\beta_{1im}$  to  $\beta_{4im}$ .

For multivariable analyses with interaction terms, allowing for interactions between sequence generation, allocation concealment and blinding, we specified Model C for the underlying log odds ratio  $\theta_{im}$ :

 $\theta_{im} = \delta_{im} + \beta_{1im}C_{1im} + \beta_{2im}C_{2im} + \beta_{3im}C_{3im} + \beta_{4im}C_{4im} + \gamma_{1im}C_{2im}C_{3im} + \gamma_{2im}C_{1im}C_{2im} +$  $\gamma_{3im} C_{1im} C_{3im}$  [Model C, multivariable analysis with interactions]

where parameters  $\gamma_{1im}$  to  $\gamma_{3im}$  quantify the interactions between: allocation concealment and blinding, sequence generation and allocation concealment, and sequence generation and blinding, respectively, when both domains within their respective interaction pairs are at high or unclear risk of bias. The  $\delta_{im}$  were assumed randomly distributed within each meta-analysis, as in (i), and a separate model of the form (ii) was assumed for each bias parameter  $\beta_{1im}$  to  $\beta_{4im}$  and for each interaction parameter  $\gamma_{1im}$  to  $\gamma_{3im}$ .

Priors for all location parameters and for between-trial heterogeneity variances  $\tau_m^2$  were identical to those used in the univariable models. In the multivariable models, we used narrower modified inverse gamma(0.01,0.01) priors for the  $\kappa$  and  $\varphi$  parameters. This change was made because of convergence difficulties with the inverse gamma(0.001,0.001) priors.

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#### **WinBUGS code for univariable analyses (Model A) for estimation of average bias and between and within meta-analysis heterogeneity**

```
model{
        for (i in 1:N) {
        r[i] \sim \text{dbin}(p[i], n[i]) # likelihood
        logit(p[i]) < - muf[s[i]] + treat[i]*(delta[i] + beta[i]*C1[i]) # model<br>beta[i]~dnorm(b[ma[i]],p.k2[ma[i]])l(-10,10) # between
                                                                      # between study, within meta-analysis, variation in bias #RE for treatment effect within meta-analysis
          delta[i]~dnorm(d[ma[i]],p.d[ma[i]])I(-10,10)rhat[i] \leftarrow p[i] \leftarrow n[i] \leftarrow n[i]
    dev[i] <- 2 * (r[i] * (log(r[i])-log(rhat[i])) + (n[i]-r[i]) * (log(n[i]-r[i]) - log(n[i]-rhat[i])))
     redundant[i] <- C0[i]
                 }
                resdev <- sum(dev[])
        for (i in 1:N trial) {m}u[j] ~ dnorm(0,.01)} \qquad \qquad # priors for study baseline effects - unrelated
        for (m in 1:N_ma) \{<br>dlml ~ dnorm(0..01)
         d[m] ~ dnorm(0,.01) \qquad # priors for true fixed (unrelated) treatment effects<br>blml ~ dnorm(b0.p.phi) \qquad +between meta-analysis variation in mean
                - dnorm(b0,p.phi)<br>var d[m]~dlnorm(-2.56,0.33) # qeneric informative prior for between-trial variances
                                                          # generic informative prior for between-trial variances
                p.d[m] <- 1/var_d[m]
                p.k2[m] <- p.k*equals(kappa_ok[m],1) + cut(p.k)*equals(kappa_ok[m],0)
        } 
        b0 \sim dnorm(0,,001) \longrightarrow \quad \longrightarrow \quad \longrightarrow \rightarrow vague prior for overall mean bias
   p.k1 ~ dgamma(.001,.001) # vague prior for between study variation in bias
        kappa \lt- pow(p.k,-0.5)
   p.k <- p.k1/(1-patom.k)
  patom.k \sim dbeta(1,1)
        p.phi1 ~ dgamma(.001,.001) #vague prior for between meta-analysis variation in mean bias
        phi <- pow(p.phi,-0.5)
        p.phi <- p.phi1/(1-patom.phi)
        patom.phi \sim dbeta(1.1)
```
#### # Parameters to monitor q[1] <- b0 q[2] <- exp(b0) q[3] <- kappa q[4] <- phi

}

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#### **WinBUGS code for multivariable analyses (Model B) for estimation of average bias and between and within meta-analysis heterogeneity**

```
model{
           for (i in 1:N) \{ r[i] ~ dbin(p[i],n[i]) # likelihood
           logit(p[i]) <- mu[s[i]] + treat[i]*(delta[i] + beta1[i]*seq1[i] + beta2[i]*alloc1[i] + beta3[i]*blind1[i] + beta4[i]*incomp1[i]) # model
             beta1[i]~dnorm(b1[ma[i]],p.ka1[ma[i]])I(-10,10) # between study, within MA, variation in bias beta2[i]-dnorm(b2[ma[i]],p.ka2[ma[i]])I(-10,10) # between study, within MA, variation in bias
             beta2[i]~dnorm(b2[ma[i]],p.ka2[ma[i]])I(-10,10) # between study, within MA, variation in bias beta3[i]-dnorm(b3[ma[i]],p.ka3[ma[i]])I(-10,10) # between study, within MA, variation in bias
             beta3[i]~dnorm(b3[ma[i]],p.ka3[ma[i]])I(-10,10) # between study, within MA, variation in bias<br>beta4[i]~dnorm(b4[ma[i]],p.ka4[ma[i]])I(-10,10) # between study, within MA, variation in bias
             beta4[i]~\text{-}dnorm(b4[mail], p.ka4[mail])[(-10, 10)]delta[i]~dnorm(d[ma[i]],p.d[ma[i]])I(-10,10) # RE for treatment effect within meta-analysis
       rhat[i] <- p[i] * n[i] \rightarrow p[i] * n[i] \rightarrow France \dev[i] \langle -2 \times (r[i] \times (log(r[i]) - log(rhat[i])) + (n[i] - r[i]) \times (log(n[i] - r[i])) - log(n[i] - rhat[i])) \rangle}
                      resdev <- sum(dev[])
           for (j in 1:N trial) {m}u[j] ~ dnorm(0,.01)} \qquad \qquad # priors for study baseline effects - unrelated
           for (m in 1:N_ma) {<br>d[m] \sim dnorm(0..01)
                      d[m] \sim \text{dnorm}(0, 01) # priors for true fixed (unrelated) treatment effects<br>b1[m] ~ dnorm(b01,p.phi1) # between meta-analysis variation in mean bias
                      b1[m] \sim \text{dnorm}(b01, p. \text{phi1}) # between meta-analysis variation in mean bias b2[m] \sim \text{dnorm}(b02, p. \text{phi2}) # between meta-analysis variation in mean bias
                                                                              # between meta-analysis variation in mean bias
                      b3[m] \sim dnorm(b03,p.phi3) # between meta-analysis variation in mean bias
       b4[m] ~ dnorm(b04,p.phi4) \qquad \qquad b4[m] ~ dnorm(b04,p.phi4) \qquad \qquad \qquad \qquad # between meta-analysis variation in mean bias var d[m]~dlnorm(-2.56,0.33) \qquad \qquad \qquad \qquad \qquad \qquad \qquad \qquad \qquad \qquad# generic informative prior for between-trial variances
                      p.d[m]<- 1/var_d[m]
                      p.ka1[m] \leq p.k1*equals(kappa_ok1[m],1) + cut(p.k1)*equals(kappa_ok1[m],0)
            p.ka2[m] <- p.k2*equals(kappa_ok2[m],1) + cut(p.k2)*equals(kappa_ok2[m],0)
                      p.ka3[m] <- p.k3*equals(kappa_ok3[m],1) + cut(p.k3)*equals(kappa_ok3[m],0)
                      p.ka4[m] < p.k4*equals(kappa_ok4[m],1) + cut(p.k4)*equals(kappa_ok4[m],0)
           }
```
p.kz1~dgamma(.01,.01) kappa1 <- pow(p.k1,-0.5) p.k1<-p.kz1/(1-patom.k1) patom.k1~dbeta(1,1) p.kz2~dgamma(.01,.01) kappa2 <- pow(p.k2,-0.5) p.k2<-p.kz2/(1-patom.k2) patom.k2~dbeta(1,1) p.kz3~dgamma(.01,.01) kappa3 <- pow(p.k3,-0.5) p.k3<-p.kz3/(1-patom.k3) patom.k3~dbeta(1,1) p.kz4~dgamma(.01,.01)  $kappa4 <$ - pow(p.k4,-0.5) p.k4<-p.kz4/(1-patom.k4) patom.k4~dbeta(1,1) p.phiz1~dgamma(.01,.01)  $phi1 < -pow(p.phi1,-0.5)$ p.phi1<-p.phiz1/(1-patom.phi1) patom.phi1~dbeta(1,1) p.phiz2~dgamma(.01,.01) phi2 <- pow(p.phi2,-0.5) p.phi2<-p.phiz2/(1-patom.phi2) patom.phi2~dbeta(1,1)

b01 ~ dnorm(0,.001) # vague prior for overall mean bias b02 ~ dnorm(0,.001) # vague prior for overall mean bias b03 ~ dnorm(0,.001) # vague prior for overall mean bias # vague prior for overall mean bias



}

**WinBUGS code for multivariable analyses with interaction terms (Model C), allowing for interactions between sequence generation, allocation concealment and blinding** 

```
model{
    for (i in 1:N) {
     r[i] ~ dbin(p[i],n[i]) # likelihood
#model 
    logit(p[i]) <- mu[s[i]] + treat[i]*(delta[i] + beta1[i]*seq1[i] + beta2[i]*alloc1[i] + beta3[i]*blind1[i] + beta4[i]*incomp1[i] +
gamma[i,1]*alloc1[i]*blind1[i] + gamma[i,2]*alloc1[i]*seq1[i] + gamma[i,3]*blind1[i]*seq1[i]) 
      beta1[i]~dnorm(b1[ma[i]],p.ka1[ma[i]])I(-10,10) # between study, within MA, variation in bias<br>beta2[i]~dnorm(b2[ma[i]],p.ka2[ma[i]])I(-10,10) # between study, within MA, variation in bias
      beta2[i]~dnorm(b2[ma[i]],p.ka2[ma[i]])I(-10,10) # between study, within MA, variation in bias beta3[i]~dnorm(b3[ma[i]],p.ka3[ma[i]])I(-10,10) # between study, within MA, variation in bias
      beta3[i]~dom(b3[maj][p.ka3[maj][n]](-10,10)
       beta4[i]~dnorm(b4[ma[i]],p.ka4[ma[i]])I(-10,10) # between study, within MA, variation in bias
    for(z \in \{1:3\}gamma[i,z]~dnorm(bi[ma[i],z], pi.ka[ma[i],z])I(-10,10)
            }
      delta[i]~dnorm(d[ma[i]],p.d[ma[i]])I(-10,10) # RE for treatment effect within meta-analysis
     rhat[i] <- p[i] * n[i] \blacksquare and the state residual deviance in the state residual deviance
     dev[i] \langle -2 \times (r[i] \times (log(r[i]) - log(rhat[i])) + (n[i] - r[i]) \times (log(n[i] - r[i])) - log(n[i] - rhat[i])) \rangle}
             resdev <- sum(dev[])
    for (i in 1:N trial) {m}u[j] ~ dnorm(0,.01)} \qquad \qquad \qquad # priors for study baseline effects - unrelated
    for (m in 1:N_ma) {<br>d[m] ~ dnorm(0..01)
             d[m] ~ dnorm(0,.01) \downarrow # priors for true fixed (unrelated) treatment effects<br>b1[m] ~ dnorm(b01.p.phi1) \downarrow between meta-analysis variation in mean bias
             b1[m] ~ dnorm(b01,p.phi1) # between meta-analysis variation in mean bias
             b2[m] ~ dnorm(b02,p.phi2) # between meta-analysis variation in mean bias
                                                                 # between meta-analysis variation in mean bias
    b4[m] ~ dnorm(b04,p.phi4) \# between meta-analysis variation in mean bias
```

```
for(z in 1:3)\{bi[m, z] \sim dnorm(bi0[z], pi.phi[z])
}
```

```
 var_d[m]~dlnorm(-2.56,0.33) # generic informative prior for between-trial variances
          p.d[m] < -1/\text{var} d[m]
          p.ka1[m] <- p.k1*equals(kappa_ok1[m],1) + cut(p.k1)*equals(kappa_ok1[m],0)
    p.ka2[m] <- p.k2*equals(kappa_ok2[m],1) + cut(p.k2)*equals(kappa_ok2[m],0)
          p.ka3[m] \leq p.k3*equals(kappa_ok3[m],1) + cut(p.k3)*equals(kappa_ok3[m],0)
          p.ka4[m] < p.k4*equals(kappa_ok4[m],1) + cut(p.k4)*equals(kappa_ok4[m],0)
   # Only informative if both interacting variables informative
          pi.ka[m,1]<-pi.k[1]*equals(kappa_ok2[m],1)*equals(kappa_ok3[m],1) + cut(pi.k[1])*(1-
(equals(kappa ok2[m],1)*equals(kappa ok3[m],1))pi.ka[m,2]<-pi.k[2]*equals(kappa_ok2[m],1)*equals(kappa_ok1[m],1) + cut(pi.k[2])*(1-
(equals(kappa_0k2[ml,1)*equals(kappa_0k1[ml,1)])pi.ka[m,3]<-pi.k[3]*equals(kappa_ok3[m],1)*equals(kappa_ok1[m],1) + cut(pi.k[3])*(1-
(equals(kappa_ok3[m],1)*equals(kappa_ok1[m],1)))
```
#### }

```
b01 ~ dnorm(0,.001) # vague prior for overall mean bias
b02 \sim \text{dnorm}(0,001) \qquad \qquad \qquad \# \text{ vague prior for overall mean bias}<br>b03 \sim \text{dnorm}(0,001) \qquad \qquad \# \text{value prior for overall mean bias}b03 \sim \text{dnorm}(0,001) \qquad \qquad \qquad \# \text{ vague prior for overall mean bias}<br>b04 \sim \text{dnorm}(0,001) \qquad \qquad \# \text{value prior for overall mean bias}# vague prior for overall mean bias
for(z in 1:3)\{bi0[z] \sim \text{dnorm}(0,001)}
p.kz1~dgamma(.01,.01)
kappa1 <- pow(p.k1,-0.5)
p.k1<-p.kz1/(1-patom.k1)
patom.k1~dbeta(1,1)
p.kz2~dgamma(.01,.01)
```
### kappa2 < - pow(p.k2, -0.5) p.k2< -p.kz2/(1 -patom.k2) patom.k2~dbeta(1,1) p.kz3~dgamma(.01,.01) kappa3 < - pow(p.k3, -0.5) p.k3< -p.kz3/(1 -patom.k3) patom.k3~dbeta(1,1) p.kz4~dgamma(.01,.01) kappa4 < - pow(p.k4, -0.5) p.k4< -p.kz4/(1 -patom.k4) patom.k4~dbeta(1,1) for( $z$  in 1:3) $\{$ pi.kz[z]~dgamma(.01,.01) kappai[z]< -pow(pi.k[z], -0.5) pi.k[z]< -pi.kz[z]/(1 -i.patom.k[z]) i.patom.k[z]~dbeta(1,1) }

#### p.phiz1~dgamma(.01,.01) phi1 < - pow(p.phi1, -0.5) p.phi1< -p.phiz1/(1 -patom.phi1) patom.phi1~dbeta(1,1)

p.phiz2~dgamma(.01,.01) phi2 < - pow(p.phi2, -0.5) p.phi2< -p.phiz2/(1 -patom.phi2) patom.phi2~dbeta(1,1)

p.phiz3~dgamma(.01,.01) phi3 < - pow(p.phi3, -0.5) p.phi3< -p.phiz3/(1 -patom.phi3) patom.phi3~dbeta(1,1)

```
p.phiz4~dgamma(.01,.01)
phi4 < pow(p.phi4,-0.5)p.phi4<-p.phiz4/(1-patom.phi4)
patom.phi4~dbeta(1,1)
for(z in 1:3)\{pi.phiz[z]~dgamma(.01,.01)
       i.phi[z]<-pow(pi.phi[z],-0.5)
       pi.phi[z]<-pi.phiz[z]/(1-i.patom.phi[z])
       i.patom.phi[z]~dbeta(1,1)
}
# Parameters to monitor
qf[1] <- b01
qf[2] <- b02
qf[3] < b03qf[4] < b04qf[5] <- exp(b01)
qf[6] < \exp(b02)qf[7] <- exp(b03)
qf[8] <- exp(b04)
for(z \in \{1:3\})exp.bi0[z]<-exp(bi0[z])
}
bias.alloc.blind<-b02+b03+bi0[1]
bias.alloc.seq<-b02+b03+bi0[2]
bias.blind.seq<-b03+b01+bi0[3]
ror.bias.alloc.blind<-exp(bias.alloc.blind)
ror.bias.alloc.seq<-exp(bias.alloc.seq)
ror.bias.blind.seq<-exp(bias.blind.seq)
qr[1] <- kappa1
qr[2] <- kappa2
qr[3] <- kappa3
```
qr[4] <- kappa4 qr[5] <- phi1 qr[6] <- phi2 qr[7] <- phi3 qr[8] <- phi4

}

# **Web Appendix 3: Included Reviews and Meta-Analyses**

<span id="page-19-0"></span>















and high dose of EPO)















\* Meta-analysis number within the review (the first number refers to the comparison number and the second is the meta-analysis number within the comparison)

<span id="page-34-0"></span>**Web Figure 2**. Number of Trials With Each Combination of the Four Risk of Bias Domain Judgements by Type of Outcome Measure



 $\checkmark$  = Low risk of bias;  $\star$  = High or unclear risk of bias; SG = Sequence generation; AC = Allocation concealment; Blind = Blinding; IOD = Incomplete outcome data. \* Semi-objective outcomes are those that are thought to be accurately assessed but potentially influenced by clinician/patient judgment (e.g. hospital admissions, duration of hospitalization, withdrawals, caesarian section etc.)

<span id="page-35-0"></span>**Web Figure 3**. Estimated Ratios of Odds Ratios and Effects on Heterogeneity Associated With Risk of Bias Judgements for Each Domain Independently, According to Type of Outcome Measure: Univariable Analyses (Model A)



This figure corresponds to Table 4 in the main paper. Objective outcomes and semi-objective outcomes combined. ROR = ratio of risk ratios; CrI = credible interval; κ – measure of within meta-analysis heterogeneity; φ – measure of between meta-analysis heterogeneity.

<span id="page-36-0"></span>**Web Figure 4**. Estimated Ratios of Odds Ratios and Effects on Heterogeneity From Multivariable Analyses of Associations With Risk of Bias Judgements for Each Domain, Adjusted for the Effect of the Other Three Domains (Model B)



This figure corresponds to Table 5 in the main paper. Objective outcomes and semi-objective outcomes combined. Analyses for each bias domain were adjusted for risk of bas judgements for the other three domains. ROR = ratio of risk ratios; CrI = credible interval; κ – measure of within meta-analysis heterogeneity; φ – measure of between metaanalysis heterogeneity.

**Web Table 1**. Estimated Ratios of Odds Ratios and Between-Meta-Analysis Heterogeneity in Mean Bias Associated With Risk of Bias Judgements, According to Type of Outcome Measure: Univariable Sensitivity Analyses for High Risk of Bias Compared to Low or Unclear Risk of Bias



<span id="page-37-0"></span>ROR = ratio of odds ratios; CrI = credible interval.

**Web Table 2**. Estimated Ratios of Odds Ratios and Between-Meta-Analysis Heterogeneity in Mean Bias Associated With Risk of Bias Judgements, According to Type of Outcome Measure: Univariable Sensitivity Analyses for Meta-Analyses With Other Objective and Semi-Objective Outcomes and for High Risk of Bias Compared to Low Or Unclear Risk of Bias



<span id="page-38-0"></span> $ROR =$  ratio of odds ratios;  $Crl =$  credible interval.

<span id="page-39-0"></span>**Web Table 3**. Estimated Ratios of Odds Ratios and Between-Meta-Analysis Heterogeneity in Mean Bias Associated With Risk of Bias Judgments, According to Type of Outcome Measure: Multivariable Analyses With Interactions



Number of contributing meta-analyses (trials): all outcomes 222 (2403); mortality 42 (429); Other objective/semiobjective 54 (568); Subjective/mixed 126 (1406). ROR = ratio of odds ratios; CrI = credible interval.