Diversification practices reduce organic to conventional yield gap: A walkthrough of the anlaysis

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1 Overview

In our study Ponisio et al. 2015 we compared the yields or organic and conventional agriculture using a custom-build meta-analytic model. Here I explain the analytic differences between our study and others, example our modeling decisions, and walk through our code. Below is the output of the final meta-analytic model, which will be described in detail in this document.

```
print(out$bugs, dig=3)
```

```
## Inference for Bugs model at "model.jags", fit using jags,
##  3 chains, each with 1e+05 iterations (first 100 discarded), n.thin = 10
##  n.sims = 29970 iterations saved
##            mu.vect sd.vect      2.5%       25%       50%       75%
## cv.obs       1.154   0.134     0.909     1.061     1.149     1.241
## exp.mu       0.808   0.019     0.771     0.795     0.808     0.821
## sigma        0.189   0.023     0.145     0.172     0.188     0.204
## deviance -1293.537  36.474 -1362.740 -1318.528 -1294.309 -1269.421
##              97.5%  Rhat n.eff
## cv.obs       1.434 1.001  5100
## exp.mu       0.846 1.001 27000
## sigma        0.236 1.001  9400
## deviance -1219.532 1.001 20000
##
## For each parameter, n.eff is a crude measure of effective sample size,
## and Rhat is the potential scale reduction factor (at convergence, Rhat=1).
##
## DIC info (using the rule, pD = var(deviance)/2)
## pD = 665.1 and DIC = -628.4
## DIC is an estimate of expected predictive error (lower deviance is better).
```

2 Where it all began, Seufert et al. 2011

How organic agriculture may contribute to world food production has been subject to vigorous debate over the past decade. Early reviews comparing organic to conventional agriculture found yield gaps of $8-9\%$ in developed countries (Stanhill, 1990; Badgley *et al.*, 2007) but yield gains of as much as 180% in developing countries. Two recent meta-analyses, however, found organic yields to be $20-25\%$ lower than conventional yields (de Ponti *et al.*, 2012; Seufert *et al.*, 2012). These studies used different criteria for selecting the data to be included, but importantly each of the above studies used different analytical methods to combine the

data across the different sub-studies. The studies comparing organic and conventional yields systems often reported yields from multiple crops across several years. In addition, they tended to compare multiple treatments (usually organic) to one control treatment (usually conventional). For example from Denison *et al*. (2004):

```
samp
```

```
##       study   crop conv org year
## 100 study13  maize  CMT OMT 2001
## 101 study13  maize  CMT OMT 1999
## 102 study13 tomato  CWT OMT 2002
## 103 study13  maize  LMT OMT 2000
## 104 study13  maize  CMT OMT 1996
## 105 study13  maize  LMT OMT 2001
## 106 study13 tomato  LMT OMT 1999
## 107 study13  maize  CMT OMT 1997
## 108 study13 tomato  CMT OMT 2001
## 109 study13 tomato  CMT OMT 1995
## 110 study13 tomato  LMT OMT 1995
## 111 study13  maize  LMT OMT 1999
## 112 study13  maize  LMT OMT 2002
## 113 study13  maize  LMT OMT 1994
## 114 study13  maize  CMT OMT 1994
## 115 study13  maize  CMT OMT 2002
## 116 study13 tomato  LMT OMT 1998
## 117 study13 tomato  CMT OMT 1994
## 118 study13 tomato  CMT OMT 1999
## 119 study13 tomato  CWT OMT 1994
## 120 study13 tomato  CWT OMT 1995
## 121 study13 tomato  CMT OMT 1996
## 122 study13 tomato  LMT OMT 1996
## 123 study13 tomato  CWT OMT 1996
## 124 study13  maize  LMT OMT 1995
## 125 study13  maize  CMT OMT 1995
## 126 study13  maize  LMT OMT 1996
## 127 study13 tomato  LMT OMT 1994
## 128 study13 tomato  CWT OMT 1998
## 129 study13 tomato  CMT OMT 1998
## 130 study13 tomato  CMT OMT 1997
## 131 study13 tomato  LMT OMT 1997
## 132 study13 tomato  LMT OMT 2001
## 133 study13 tomato  CWT OMT 2001
## 134 study13 tomato  CWT OMT 1997
## 135 study13  maize  LMT OMT 1997
```

Using the organic to conventional yield comparisons without taking into account the underlying data structure can lead to potential pseudo-replication and an understated Type 1 error rate. We used a randomization test to estimate the Type I error rate of the Seufert et al. analysis. We forced the null hypothesis to be true by randomly re-assigning the 'organic' and 'conventional' labels for each study and then using the R package `Metafor` (Viechtbauer, 2010) to implement a random effects meta-analysis on each randomized dataset. Repeating this procedure 10^5 times enabled us to determine the Type I error rate (false rejection) resulting from not accounting for the hierarchical structure of the data. In over 50% of simulations, the null hypothesis was rejected using a nominal Type I error rate of 0.05 (Fig. 1). In other words, even if organic and conventional yields are known not to be different, applying the model used by Seufert *et al.* (2012) for these data would lead to the conclusion that they are significantly different in over 50% of cases. This

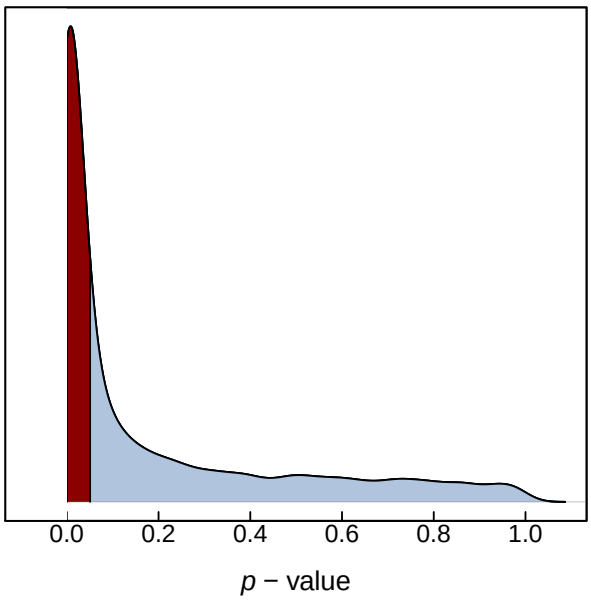


Figure 1: The distribution of p-values when the null hypothesis was forced to be true using the data and analysis type present in Seufert et al. Seufert *et al.* (2012). If the analysis procedure was valid for these data, the distribution of P-values should be uniform between 0 and 1. Instead it is sharply shifted toward low P-values. In over 50% of simulations, the null hypothesis was rejected using a nominal Type I error rate of 0.05 (red region above).

means that the actual Type I error rate is inflated relative to what was reported, leading to the following related statements: the significance levels were overstated; the confidence intervals were underestimated; the uncertainty was not fully accounted for.

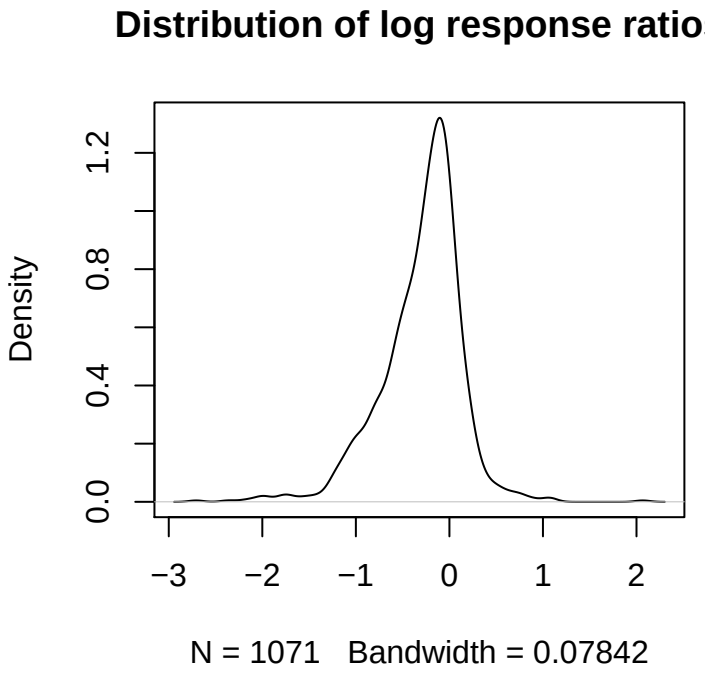
The de Ponti et al. (de Ponti *et al.*, 2012) study had similar issues with pseudo-replication. Additionally they did not account for the sampling variance within studies, which is the recommended practice to deal with unequal variances in the sample of studies (Gurevitch & Hedges, 1999).

Given these methodological and data-related critiques, a new study was needed to produce a more robust estimate of the gap between organic and conventional yields. We developed a hierarchical meta-analytic framework that overcomes the methodological pitfalls of previous studies by accounting for both the multi-level nature of the data and the yield variation within studies. Furthermore, via a literature search we compiled a more extensive and up-to-date meta-dataset, comprising 1071 organic to conventional yield comparisons from 115 studies — over three times the number of observations of any of the previous analyses. Our meta-dataset includes studies from 38 countries and 52 crop species over a span of 35 years.

3 Building our meta-analytic model

We built a hierarchical meta-analytic model to generate an estimate of the yield gap. Following standard practice, we compared the natural log of the ratios between organic and conventional yields (the "response ratio") across studies (Hedges *et al.*, 1999; Seufert *et al.*, 2012). The response ratio is more normally distributed than the raw ratio and independent of the units of measurement used within a study and, thus, comparable across studies (Hedges *et al.*, 1999).

```
plot(density(meta.dat$lnR), main="Distribution of log response ratios")
```



We constructed a hierarchical regression model to account for the dependencies in the yield data. We expanded on the traditional random effects model (Hedges & Olkin, 1985) by considering three additional sources of random variation (i.e., random effects): 1) between studies, 2) within a study between years, and 3) within a year between response ratios (e.g., across replicated trials of a crop planted at different times in the season). We also considered whether the variances of the random effect distributions for 2) and 3) were shared across studies, or study-specific.

The full possible model, prior to model selection, with all sources of random variation is

$$\begin{aligned} y_{ijk} &= \mu + \alpha_i + \beta_{ij} + \eta_{ijk} + \epsilon_{ijk} \\ \alpha_i &\sim N(0, \sigma^2_\alpha) \\ \beta_{ij} &\sim N(0, \sigma^2_\beta[i]) \\ \eta_{ijk} &\sim N(0, \sigma^2_\eta[i]) \\ \epsilon_{ijk} &\sim N(0, S_{ijk}]) \\ \sigma^2_\beta[i] &\sim \Gamma(CV_\beta, scale_\beta) \\ \sigma^2_\eta[i] &\sim \Gamma(CV_\eta, scale_\eta) \end{aligned} \tag{1}$$

response ratio from the j^{th} year of the i^{th} study, μ is the mean response ratio across studies, α_i is the effect of i^{th} study, β_{ij} is the effect of j^{th} year of the i^{th} study, η_{ijk} is the effect of the k^{th} response ratio of the j^{th} year of i^{th} study, and ϵ_{ijk} is the residual. σ^2_α is the between study variance, $\sigma^2_\beta[i]$ is the between year variance of study i, $\sigma^2_\eta[i]$ is the within year, between response ratio variance of study i, and S_{ijk} is the variance of response ratio ijk as reported by its study. CV_β and CV_η and $scale_\beta$ and $scale_\eta$ are the coefficient of variation and scale parameters of the gamma distributions of the study-specific between- and within-year variances. When response ratios that shared a common control were combined, y_{ijk} corresponds to the aggregate within-study response ratio (Eq. 3, Lajeunesse, 2011) and S_{ijk} is its pooled variance (Eq. 8, Lajeunesse, 2011).

3.1 Parameter inclusion

To determine the levels of hierarchy supported by the data, we sequentially added random effects and examined the posteriors of the parameters to determine the support for their inclusion. We also confirmed our selection with Deviance Information Criterion (DIC). The DIC can be problematic for hierarchical models because the effective number of parameters is not clearly defined (Gelman & Hill, 2006; Kéry & Schaub, 2012). The DIC was therefore used in combination with a visual examination of the posterior distributions of the parameters to select the best supported model.

For the variance within and between year random effect distributions, we considered two parameterizations: 1) the variance terms, denoted σ^2_η and σ^2_β, respectively, were shared across all studies each with a Uniform(0,100) prior, and 2) the variance terms were study-specific (i.e., $\sigma^2_\eta[i]$ and $\sigma^2_\beta[i]$). In the latter case, the study-specific precision terms (1/variance) were assumed to be distributed according to a gamma distribution whose parameters were estimated. Uniform(0,100) priors were used for the coefficient of variation ($1/\sqrt{shape}$) and the square root of the scale.

We first added a random effect of study and examined the posterior for σ_α (the standard deviation of the common distribution from which the study effects are drawn). The posterior was clearly differentiated from zero (Fig. 2a). We next added random variation within a year and examined σ_η. We found it was also clearly different from zero (Fig. 2b). The DIC was also smaller than when only a random effect of study was included (Tab. 1). Next we allowed the within-year precisions to be study-specific and follow a gamma distribution. We examined the coefficient of variation of the gamma distribution and found it was clearly differentiated from zero (Fig. 2c). The DIC was also smaller than when a single within year effect was shared across studies (Tab. 1). Lastly, we added a between year random effect and examined σ_β. The posterior was concentrated at zero (Fig. 2d) so we concluded there was insufficient support for including it in the model. The estimate of the yield gap and its uncertainty did not differ substantially from when no between year effect was included (Fig. 3), the DIC, however, was marginally smaller then when no between year random effect was included (Tab. 1).

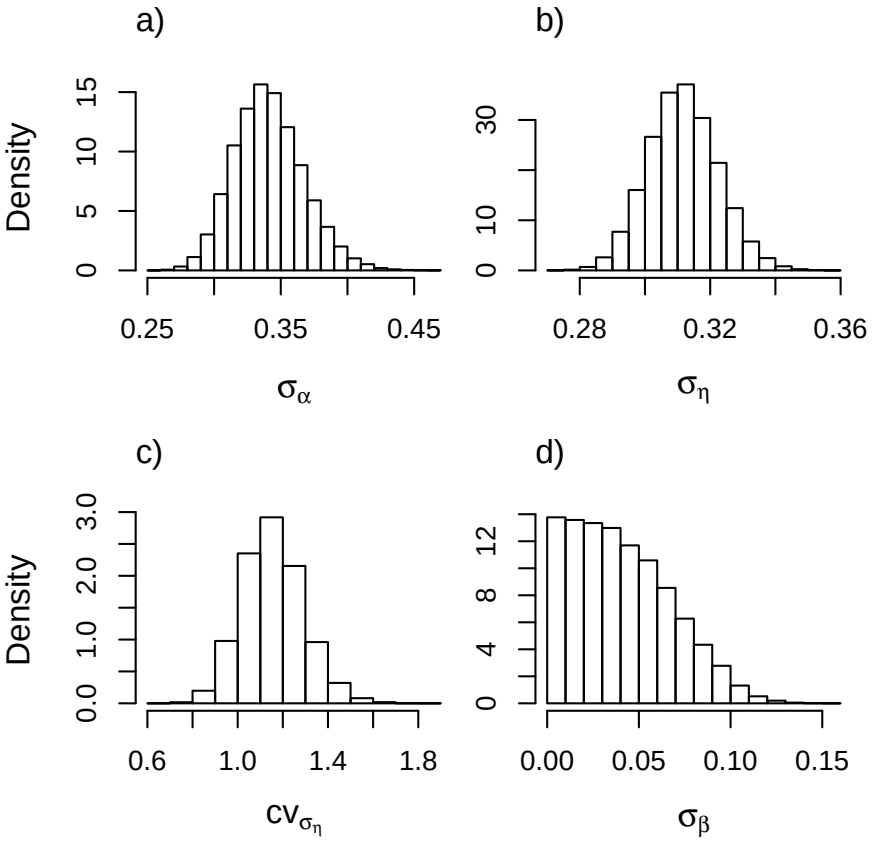


Figure 2: The posterior distributions for the random effect of a) study (σ_α); b) response ratios within a year (σ_η); c) response ratios within a year where the within year variance is study-specific, CV_{σ_η} is the coefficient of variation ($1/\sqrt{shape}$) of the gamma distribution (this model is most supported by the data); and d) between year (σ_β). Including a between-year variance term was not supported by the data (the posterior for (σ_β is not differentiated from zero).

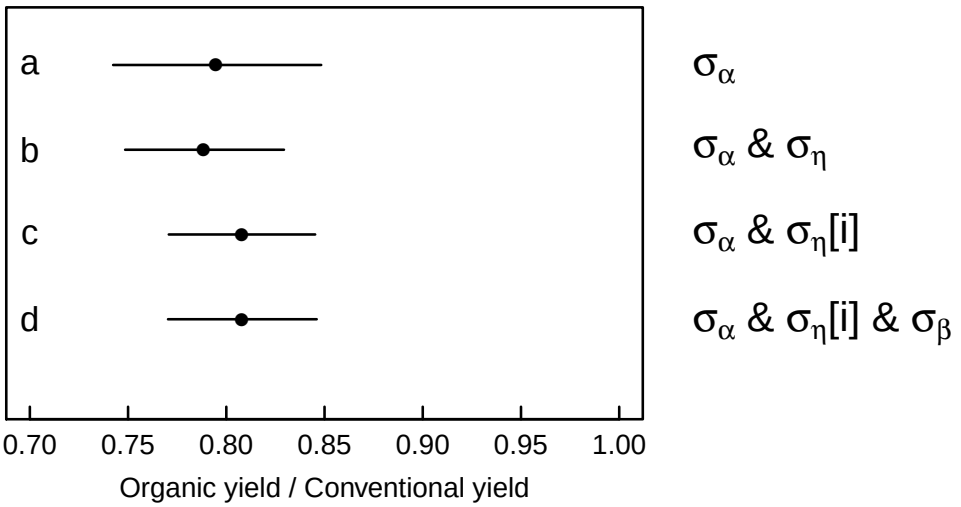


Figure 3: The sensitivity of the yield gap to including different levels of hierarchy in the model. The random effects included in the model are: a) study (σ_α); b) study and response ratios within a year (σ_η); c) study and response ratios within a year where the within year variance is study-specific ($\sigma_\eta[i]$) (this model is most supported by the data); and d) study, study-specific within-year variance, and between year (σ_β). Including a between-year variance term was not supported by the data (the posterior for (σ_β is not differentiated from zero). Values are the posterior mean with 95% credible intervals.

Table 1: Parameter posteriors for models without explanatory variables. μ is the true mean response ratio across years and studies, σ_α is the standard deviation of the distribution from which the study random effects are drawn; σ_η is the standard deviation of the distribution from which the within year random effects are drawn; CV_{σ_η} is the coefficient of variation of the gamma from which the study-specific within-year variance are drawn; and σ_β is the standard deviation of the distribution of random between year effects. Values of Rhat < 1.1 indicate convergence. Lower Deviance Information Criterion (DIC) indicates better model fit to the data.

Parameter	Posterior mean	Posterior standard deviation	95% CI	Rhat
Study random effect, DIC=1684.8				
μ	0.795	0.027	$0.742 - 0.848$	1.001
σ_α	0.341	0.026	$0.294 - 0.396$	1.001
Study and within year random effects, DIC= -565.9				
μ	0.788	0.021	$0.749 - 0.829$	1.001
σ_α	0.188	0.024	$0.144 - 0.239$	1.001
σ_η	0.312	0.011	$0.291 - 0.333$	1.001
Study and study-specific within year random effects, DIC= -618.0				
μ	0.808	0.019	$0.771 - 0.845$	1.001
σ_α	0.189	0.023	$0.145 - 0.237$	1.001
CV_{σ_η}	1.155	0.135	$0.907 - 1.436$	1.001
Study, study-specific within year, and between year random effects, DIC= -621.2				
μ	0.808	0.019	$0.770 - 0.846$	1.001
σ_α	0.186	0.024	$0.142 - 0.234$	1.001
CV_{σ_η}	1.157	0.136	$0.907 - 1.440$	1.001
σ_β	0.041	0.027	$0.002 - 0.098$	1.001

The best supported model, coded in JAGS, is

```
## model {
##      for(study in 1:Nstudy) {
##        for(year in 1:Nyear[study]) {
##          for(obs in 1:Nobs[study,year]) {
##            P[study,year,obs] <- 1/V[study,year,obs]
##            RR[study,year,obs] ~ dnorm(mu.RR[study,year,obs],
##                                       P[study,year,obs])
##            mu.RR[study,year,obs] ~ dnorm(mu.study[study],
##                                      tau.yr.obs[study])
##          }
##        }
##        mu.study[study] ~ dnorm(mu, tau)
##        tau.yr.obs[study] ~ dgamma(shape.obs, scale.obs)
##      }
##
##      mu ~ dnorm(0, 1e-4)
##      exp.mu <- exp(mu)
##      tau <- 1 / (sigma * sigma)
##      sigma ~ dunif(0, 100)
##
##      shape.obs <- (1/cv.obs)^2
##      cv.obs ~ dunif(0, 100)
##      scale.obs <- (1/in.scale.obs)^2
##      in.scale.obs ~ dunif(0, 100)
##    }
```

Where the parameters names match the notation in Equ. 1.

4 Analysis

After deciding on the model parameterization, the most difficult part of running a model in JAGS in getting tha data in the right format (in my opinion). Our situation was particularly difficult because we needed to build in flexibility to pool different combinations of response ratios using the method presented in Lajeunesse Lajeunesse (2011) depending on the explanatory variable being considered (when response ratios that share a control split between different levels of an explanatory variable, they can be left un-pooled). Below I focus on the best supported model without explanatory variables.

First we have a function to calculate pooled RR and their variances

```
## applies the Lajeunesse (2011) method for combining RR with shared
## controls. Returns a pooled RR and variance
poolCommonControl <- function(dd) {

  ## function to make covariance matrix:
  covMat <- function(x){
    ## case 1: organic is repeated
    if(all(diff(as.numeric(x[,"mean.org"]))==0))
      vals <- as.numeric(x[1, c("sd.org", "n.organic", "mean.org")])
    if(all(diff(as.numeric(x[,"mean.conv"]))==0))
      vals <- as.numeric(x[1, c("sd.conv", "n.conv", "mean.conv")])

    m <- matrix(vals[1]^2/(vals[2]*vals[3]^2),
```

```
                ncol=nrow(dd), nrow=nrow(dd))
    diag(m) <- as.numeric(x[,"varlnR"])
    m
  }

  ## covariance matrix and its inverse:
  V <- covMat(dd)
  V.inv <- solve(V)

  X <- matrix(1, nrow(V))
  E <- matrix(dd[,"lnR"], nrow(V))
  ## compute and return RR_bar and variance(RR_bar), as defined in
  ## Eq. 3 and subsequent text in Lajeunesse (2011):
  return(c(obs=dd$obs[1],
           lnR=as.numeric(solve(t(X) %*% V.inv %*% X) %*%
                          (t(X) %*% V.inv %*% E)),
           varlnR=as.numeric(solve(t(X) %*% V.inv %*% X))))
}
```

Which is called by this function which combines the meta-data based on keys

```
## takes raw meta-data and a vector of covariates and combines data
## using lajeunesse (2011). Returns a dataframe with keys, the
## observation number, the pooled RR and its variance

poolRR <- function(D, covariates) {
  ## first split the data up into relevant groups:
  if(length(covariates) == 1) {
    dd <- split(D, paste(D$study,
                         D[,covariates],
                         D$year_conv,
                         D$mult_yrs,
                         D$duplicate_trt_dat,
                         sep=';'))
  }
  if(length(covariates) > 1) {
    dd <- split(D, paste(D$study,
                         apply(D[,covariates], 1, paste, collapse=':'),
                         D$year_conv,
                         D$mult_yrs,
                         D$duplicate_trt_dat,
                         sep=';'))
  }

  ## combine response ratios for studies that share treatments using
  ## the method given in Lajeunesse (2011):
  share.trts <- which(sapply(strsplit(names(dd), split=';'),
                             function(x) rev(x)[[1]]) == 'yes')

  dd[share.trts] <- lapply(dd[share.trts],
                           poolCommonControl)

  dd[-share.trts] <-
    lapply(dd[-share.trts], function(x) x[,c('obs', 'lnR', 'varlnR')])
```

```
  return(do.call(rbind, dd))
}
```

This is all brought together by this long, unwieldy function that returns the data structure necessary for the JAGS model including the indexes for looping and arrays of RR, variances and covariates is applicable

```
## makes data arrays for Bayesian analysis; takes the raw
## meta-data set, whether to apply the lajeunesse method to combine RR
## with shared controls, and a vector of explanatory variables. The
## default for covariates is "Crop.species" so RR are never combined
## between crop species. Returns a list of the number of studies
## (Nstudy), the number of years for each study (Nyear), a matrix
## (study, year) of the number of observations in each year (Nobs),
## and an array (study, year, observation) of the RR and their
## variances, and an array of covariates if applicable

makeData <- function(meta.dat,
                     lajeunesse = TRUE,
                     covariates=c('Crop.species')) {

  convert2Int <- function(x) seq_along(x)[match(x, unique(x))]

  if(lajeunesse) {
    dd <- poolRR(meta.dat,
                 covariates=covariates)
    keys.split <- sapply(rownames(dd), strsplit, split=';')
    get <- function(i) as.vector(sapply(keys.split, function(x) x[i]))
    study <- get(1)
    year <- get(3)
  } else {
    dd <- meta.dat
    study <- as.character(meta.dat$study)
    year <- meta.dat$year_conv
  }

  ## make study index
  ind.study <- convert2Int(study)

  ## make year index
  ind.year <- rep(NA, nrow(dd))
  for(i in unique(ind.study))
    ind.year[ind.study==i] <- convert2Int(year[ind.study==i])

  ## make obs index
  ind.obs <- rep(NA, nrow(dd))
  for(i in unique(ind.study))
    for(j in unique(ind.year[ind.study==i]))
      ind.obs[ind.year==j & ind.study==i] <-
        seq_len(sum(ind.year==j & ind.study==i))

  ## make response ratio and vi matrices
  makeMat <- function(d.vec) {
    mat <- array(NA, dim=c(max(ind.study),
```

```
                          max(ind.year),
                          max(ind.obs)))
    mat[cbind(ind.study, ind.year, ind.obs)] <- d.vec
    return(mat)
  }
  RR.mat <- makeMat(dd$lnR)
  vi.mat <- makeMat(dd$varlnR)

  ## make index bounds
  nstudy <- max(ind.study)
  nyear  <- apply(RR.mat[,,1],  1, function(x) sum(!is.na(x)))
  nobs   <- apply(RR.mat[,,], 1:2, function(x) sum(!is.na(x)))

  covs <- NA
  num.cats <- NA
  ## covariates (only for lajeunesse)
  if(lajeunesse) {
    num.covs <- length(covariates)
    if(num.covs > 1) {
      covs <- sapply(get(2), strsplit, split=':')
      getCov <- function(cov)
        as.numeric(as.factor(sapply(covs, function(x) x[cov])))
      covs <- lapply(1:num.covs, function(cov)
        make.mat(getCov(cov)))
      names(covs) <- covariates
      num.cats <- sapply(covs, max, na.rm=TRUE)
    }
  }

  return(list(Nstudy=nstudy,
              Nyear=nyear,
              Nobs=nobs,
              V=vi.mat,
              RR=RR.mat,
              covariates=covs,
              num.cats=num.cats))
}
```

We then pacakges everything up in a function that also passes the JAGS parameters (init values, thinning rate etc.) and runs the model.

```
## takes preped data and a scale parameter and packages the data and
## parameters for JAGS, then runs the analysis. Returns the JAGS
## summary output
runAnalysis <- function(dd, scale) {

  my.inits <- function() {
    list()
  }
  my.params <- get.params()

  dd <- list(data=dd, inits=my.inits, params=get.params())

  bugs <- run.model(dd,
```

```
                    n.thin=scale,
                    n.iter=(1e4)*scale,
                    n.burnin=1e1*scale,
                    n.chains=3)

  return(list(data=dd,
       bugs=bugs,
       summary=bugs$BUGSoutput$summary))
}
```

```
print(out$bugs, dig=3)
```

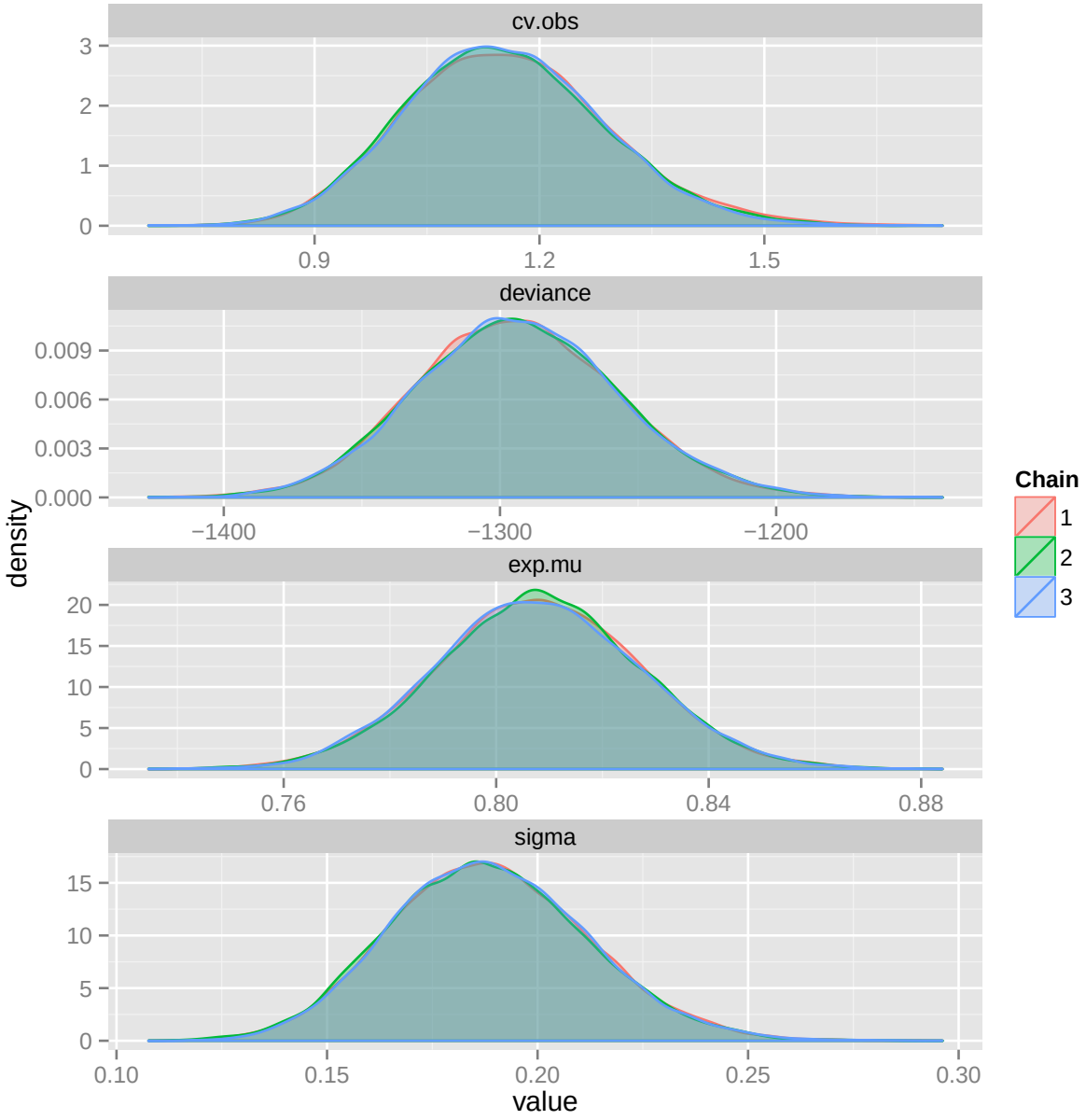
```
## Inference for Bugs model at "model.jags", fit using jags,
##  3 chains, each with 1e+05 iterations (first 100 discarded), n.thin = 10
##  n.sims = 29970 iterations saved
##            mu.vect sd.vect      2.5%       25%       50%       75%
## cv.obs       1.154   0.134     0.909     1.061     1.149     1.241
## exp.mu       0.808   0.019     0.771     0.795     0.808     0.821
## sigma        0.189   0.023     0.145     0.172     0.188     0.204
## deviance -1293.537  36.474 -1362.740 -1318.528 -1294.309 -1269.421
##              97.5%  Rhat n.eff
## cv.obs       1.434 1.001  5100
## exp.mu       0.846 1.001 27000
## sigma        0.236 1.001  9400
## deviance -1219.532 1.001 20000
##
## For each parameter, n.eff is a crude measure of effective sample size,
## and Rhat is the potential scale reduction factor (at convergence, Rhat=1).
##
## DIC info (using the rule, pD = var(deviance)/2)
## pD = 665.1 and DIC = -628.4
## DIC is an estimate of expected predictive error (lower deviance is better).
```

exp.mu is the mean ratio of organic and conventional yields, which is around 80.1% with 95% credible intervals ranging from around $77 - -85\%$

Sigma is the between study variance, and cv.obs is the coefficient of variation of γ distribution the within-study variance parameters are drawn from.

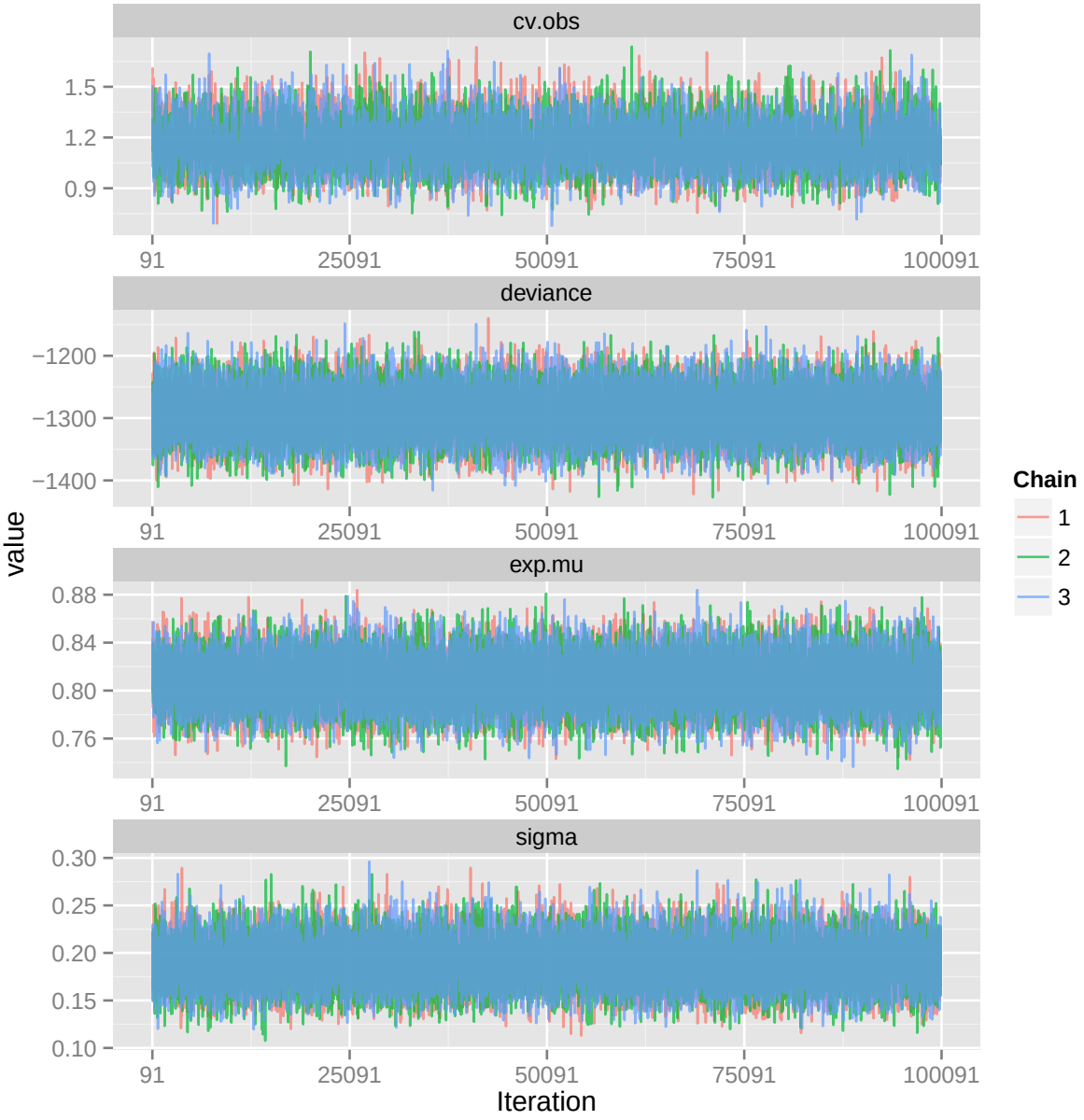
Values of Rhat ¡ 1.1 indicate convergence, whcih we We can see from inspecting the posteriors

```
ggs_density(inspect.out)
```



The chains look wonderfully grassy

```
ggs_traceplot(inspect.out)
```



5 Explanatory variables

We also extended this model in order to accommodate analyses of study characteristics such as crop type and management practices. We analyze these additional explanatory variables one at a time because not all studies reported all explanatory variables. In these analyses, for cases where multiple organic treatments represented different categories for a specific explanatory variable, they could not be combined using Lajeunesse's method (Lajeunesse, 2011). The potential bias resulting from non-independence of the response ratios in these cases, however, would be minimized by the fact that they are not pooled together in the analysis (Lajeunesse, 2011).

Letting h index the categories for a particular explanatory variable (e.g., crop species), we then have:

$$y_{hijk} = \mu + \gamma_h + \alpha_i + \eta_{ijk} + \beta_{ij} + \epsilon_{ijk} \tag{2}$$

where γ_h is the effect of the h^{th} category, and the rest of the model parallels that given in Eq. 1.

The model including explanatory variables in JAGS is

```
## model {
##     for(study in 1:Nstudy) {
##       for(year in 1:Nyear[study]) {
##         for(obs in 1:Nobs[study,year]) {
##           P[study,year,obs] <- 1/V[study,year,obs]
##           RR[study,year,obs] ~ dnorm(mu.RR[study,year,obs], P[study,year,obs])
##           mu.RR[study,year,obs] ~ dnorm(mu.study[study,year,obs],
##                                         tau.obs[study])
##           mu.study[study,year,obs] ~ dnorm(mu[cov[study,year,obs]], tau)
##         }
##       }
##       tau.obs[study] ~ dgamma(shape.obs, scale.obs)
##     }
##
##     ## set priors on covariates
##     for(covs in 1:Ncov) {
##       mu[covs] ~ dnorm(0, 1E-3)
##       exp.mu[covs] <- exp(mu[covs])
##     }
##     tau <- 1 / (sigma * sigma)
##     sigma ~ dunif(0, 100)
##
##     shape.obs <- (1/cv)^2
##     cv ~ dunif(0, 100)
##     scale.obs <- (1/in.scale)^2
##     in.scale ~ dunif(0, 100)
##
##   }
```

Where the parameters names match the notation in Equ. 1 and cov is a matrix of explanatory variables assiciated with each response ratio.

To re-run the models with explanatory variables, we just added each variable one-by-one to the covariates argument of the makeData() function.

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