Seed Science Research (2017) **27**, 321–327
doi:10.1017/S0960258517000228

SHORT COMMUNICATION

A note on the analysis of germination data from complex experimental designs

Signe M. Jensen[1], Christian Andreasen[1], Jens C. Streibig[1], Eshagh Keshtkar[2] and Christian Ritz[3]*

[1]Department of Plant and Environmental Sciences, Faculty of Science, University of Copenhagen, Højbakkegård Allé 13, DK-2630 Taastrup, Denmark; [2]Department of Agronomy, Faculty of Agriculture, Tarbiat Modares University, PO Box 14115-336, Tehran, Iran; [3]Department of Nutrition, Exercise and Sports, Faculty of Science, University of Copenhagen, Rolighedsvej 26, DK-1958 Frederiksberg C, Denmark

(Received 27 April 2017; accepted after revision 25 July 2017; first published online 18 September 2017)

Abstract

In recent years germination experiments have become more and more complex. Typically, they are replicated in time as independent runs and at each time point they involve hierarchical, often factorial experimental designs, which are now commonly analysed by means of linear mixed models. However, in order to characterize germination in response to time elapsed, specific event-time models are needed and mixed model extensions of these models are not readily available, neither in theory nor in practice. As a practical workaround we propose a two-step approach that combines and weighs together results from event-time models fitted separately to data from each germination test by means of meta-analytic random effects models. We show that this approach provides a more appropriate appreciation of the sources of variation in hierarchically structured germination experiments as both between- and within-experiment variation may be recovered from the data.

Keywords: between-experiment variation, *Gerbera hybrida*, log-logistic function, meta analysis, mixed model, randomized complete block design, time-to-event data

Introduction

Seed producers sometimes experience large differences in seed quality among different seed batches. The reason for this is difficult to unravel, but (typically unobserved) local environmental factors such as humidity, nutrients and water status during growth of the mother plants as well as the maturity and size of the harvested seed may play a role and render seemingly identical experiments very different (Carpenter *et al*., 1995). Such differences between seemingly identical experiments must be taken into account in the statistical analysis as they reflect variation in the physiological conditions. A single experiment is like a snapshot in time for a specific set of physiological conditions, which may change profoundly over time. Therefore, ideally, this variation should be captured by appropriate statistical models and be incorporated in estimated standard errors of the germination parameters to avoid misleading results.

Recently, Ritz *et al*. (2013) demonstrated that the current practice of analysing germination curves by means of non-linear regression techniques resulted in overly precise parameter estimates of, e.g., time to reach 50% germination (t_{50}), due to too small estimated standard errors. The authors suggested a more appropriate approach where germination data were modelled as event times, i.e. waiting times until germination was observed or germination became no longer possible (for instance due to termination of the experiment). This approach provided a more adequate statistical description of the type of response that resulted from germination experiments. This improved modelling approach, however, did still not allow accounting for dependencies between waiting times introduced as a consequence of the experimental design used. For instance, in a recent study of germination of *Gerbera hybrida* seeds, estimates and corresponding estimated standard errors were reported for two identical, but independently run experiments (Andreasen *et al*., 2014); we revisit this study below.

* Correspondence
Email: ritz@nexs.ku.dk

The aim of this short communication was to extend the methodology proposed by Ritz *et al*. (2013) to account for the variation often seen between independent germination experiments using a meta-analytic approach proposed by Jiang and Kopp-Schneider (2014) who showed that the meta-analytic approach is in most cases as efficient as a much more complex and cumbersome simultaneous non-linear mixed-effects model (for a continuous response). In the context of germination data no similar simultaneous mixed-effects model has been proposed to date.

Materials and methods

Data

We revisited the germination experiments carried out by Andreasen *et al*. (2014) who investigated effects of fertilizer and calcium treatment on germination of *Gerbera hybrida* 'Gerbera Festival Rose', which is an ornamental plant of commercial interest. It is primarily propagated by seeds. The effect of increasing fertilizer dose in combination with foliar-applied calcium was investigated in two independent and identical experiments, carried out using different tables in the same greenhouse and initiated one week apart in July 2012. Plants for the experiments were delivered in a single batch to the University of Copenhagen in June 2012 as 5-week-old plants. Each plant was transplanted into a 2-litre pot (diameter 17 cm) with a low-nutrient peat soil mixture.

Both experiments were carried out as a randomized complete block design with three blocks (three adjacent tables in the greenhouse) and 10 treatments, which are described in detail below. In each of the two experiments, six plants per treatment were randomly placed on each of three tables. To avoid edge effects, 36 plants surrounded the 60 treated plants on each table. In total, 180 plants were used per experiment. For both experiments watering/fertilizing, spraying, pollination and seed harvesting and germination was carried out the same way by the same person as briefly detailed below; we refer to Andreasen *et al*. (2014) for additional details.

A 300-litre liquid stock solution of fertilizer containing 1.7 kg KNO_3, 2.1 kg NH_4NO_3, 1.95 kg $Ca(NO_3)_2$, 0.5 litres iron chelate (5.2%), 2.8 litres phosphoric acid (72%), and 4.5 litres Mikropioner (Azelis, Antwerp, Belgium) was diluted to five concentrations of nutrient solutions. The different solutions corresponded to electrical conductivities (EC) of 1.25, 2.50, 3.75, 5.00 and 6.25 mS·cm l^{-1}. The plants were usually watered manually with 300 ml fertilizer solution at intervals of 2–4 days. Each pot was placed on a plastic plate allowing excess water to be absorbed by the plants. Additionally, plants were sprayed three times, every other week, with a 0.5% foliar-applied calcium solution or deionized water. Thus each experiment involved a total of 10 fertilizer/calcium treatment combinations. Plants were treated once with a pesticide (to control larvae of *Bradysia* ssp.) and later on with two insecticides (to control various types of aphids).

Pollination was carried out manually using a brush. Pollen from one plant was used to pollinate another plant. Each flower was visited twice. Every 2–4 days plants were inspected and seeds harvested when they loosened up from the flower base. The seeds were harvested separately for each plant by hand and stored in paper bags, which were placed in a drying room at a temperature of 20°C and a relative humidity of 30%. Seeds were poo×led and portions of seeds sampled for the tests.

Seed germination tests of 50 seeds were carried out using a Jacobsen apparatus with trays kept at a temperature of 20°C with high humidity through covering and exposed to artificial daylight (e.g. Willan, 1985). For each experiment and table within the experiment and for all 10 treatment combinations four replicated germination tests (trays) were used, resulting in a total of $4 \times 10 \times 3 = 120$ trays per experiment. Thus the use of germination tests added another layer to the hierarchical structure of the experimental design such that each experiment consisted of three tables that again were sub-divided into 40 trays, which may be viewed as the basic sampling unit.

Statistical analysis

Germination data often exhibit the following two distinct features. First, germination need not be observed for all seeds. In other words, some seeds may be right-censored for various reasons, i.e. they may not be followed all the way until they germinate. Second, germination is usually monitored through a number of repeated inspections. Therefore, in the case of a seed germinating, the time of germination is not known exactly but bracketed by a monitoring interval. Typically, both features will imply a loss of information and hence they need to be addressed to avoid misleading conclusions (Ritz *et al*., 2013).

Below, we describe a two-step analysis. Firstly, separate event-time models, as proposed by Ritz *et al*. (2013), were fitted to data from each independent sub-experiment within the experiments, e.g. trays in the motivating example with *Gerbera hybrida*. Subsequently, estimates of parameters of interest from these models were used as response in a meta-analytic random effects model, which is a special case of a linear mixed model where the residual standard deviation is not estimated but explicitly specified using weights. In the context of analysis of dose–response toxicological data, Jiang and Kopp-Schneider (2014) proposed this two-step analysis.

https://doi.org/10.1017/S0960258517000228 Published online by Cambridge University Press

Step 1

Initially, we assume that the mean trend in the germination data observed in each tray may be described by a (cumulative) germination curve that is based on the three-parameter log-logistic model:

$$F(t) = \frac{d}{1 + \exp[b(\{\log(t) - \log(t_{50})\}]}, \quad (1)$$

where $F(t)$ denotes the fraction of seeds germinating between the onset of the experiment (at time 0) and time t. The upper limit d denotes the maximal germination and is thus a function of the quality of the seed. However, we know that if some seeds are dormant, the germination curve might only show the upper limit in the experiment as a temporary plateau. The parameter t_{50} defines the time it takes for 50% (relative to the upper limit d) of the seeds in the test to germinate. Consequently, t_{50} and d are biologically meaningful and important parameters for describing the initial germination speed and the maximum germination. Finally, the parameter b reflects the steepness of the germination curve at time t_{50}: the larger the absolute value of the slope, the steeper the slope is.

As pointed out by Ritz *et al*. (2013) a number of alternatives for F are available. In principle the models fitted to data from different trays need not be the same as long as the parameter of interest may be estimated. For instance, whenever all seeds germinate, the parameter d (maximum germination) may be fixed at 1, and a two-parameter log-logistic model should instead be fitted to data.

So, as a first step, the three-parameter log-logistic model [Eqn (1)] was fitted to the germination data of each replication (each tray) according to the event-time approach described by Ritz *et al*. (2013) to extract estimates of relevant parameters (e.g. t_{50}) and corresponding standard errors.

Step 2

The meta-analytic random effects model specified below allows explicit specification of the hierarchical structure of the experimental design while incorporating standard errors of estimates to allow more precise estimates to contribute more to the analysis than less precise estimates. In this step the parameter estimates (e.g. t_{50}) obtained from the fitted event-time models in Step 1 are then arranged in a new data file (see the Appendix for an example).

Specifically, for the motivating example we specify the following meta-analytic random effects model assuming an interaction between calcium application and fertilizer dose:

$$\text{Estimated } t_{50,\mathrm{i}} = \mu(\text{calcium}_\mathrm{i}, \text{fertilizer}_\mathrm{i}) + A(\text{table}_\mathrm{i}) + B\big(\text{experiment}_\mathrm{i}\big) + \theta_\mathrm{i} + \varepsilon_\mathrm{i}, \quad (2)$$

where i refers to the cluster, the μ values denote the parameters signifying the mean t_{50} levels for the treatment combinations of the interaction; A and B are random effects capturing differences between tables and between experiments; θ is the random effect explaining the heterogeneity between trays; and ε_i is the residual error. Random effects and residual errors are assumed to be mutually independent and normally distributed with mean 0. The standard deviations of the random effects are denoted σ_{table}, $\sigma_{\text{experiment}}$ and σ_{tray}. These standard deviations are unknown and have to be estimated from data. Following the meta-analytic approach by Jiang and Kopp-Schneider (2014) the standard deviations of the residual errors are assumed to be known and equal to the estimated standard errors of the estimates. This means that the smaller the standard error obtained in a tray-specific analysis in Step 1, the larger the weight of the corresponding estimate in the meta-analytic model fit.

An additive model where absence of an interaction is assumed may be specified in a similar manner:

$$\text{Estimated } t_{50,\mathrm{i}} = \mu_1(\text{calcium}_\mathrm{i}) + \mu_2(\text{fertilizer}_\mathrm{i}) + A\big(\text{table}_i\big) + B\big(\text{experiment}_i\big) + \theta_\mathrm{i} + \varepsilon_\mathrm{i}, \quad (3)$$

where the parameters μ_1 and μ_2 denote the main effects parameters of calcium application and fertilizer dose, respectively.

In general, arbitrary factorial designs may be analysed and, in particular, the usual inferential procedures of model reduction using the likelihood ratio test, i.e. approximate chi-square tests (e.g. test for interaction) as well as pairwise comparisons based on an approximate Wald-type U-test may be used; regression-type models may also be fitted (Konstantopoulos, 2011). Additionally, the meta-analytic approach provides insights on how the total variation in the germination data may be decomposed into contributions corresponding to the different sources of variation present due to the design of the experiment (through estimated standard deviations). Moreover, on a practical note, the meta-analytic approach is computationally very fast as simple models are fitted to smaller data sets; lack of convergence of some of these simple models may occur and it may be dealt with by assuming missing values or, in some cases, censoring.

For the example with *Gerbera hybrida* the test of interaction, i.e. for simplification from the model in Eqn (2) to the model in Eqn (3), was carried out

https://doi.org/10.1017/S0960258517000228 Published online by Cambridge University Press

initially. Subsequently appropriate pairwise comparisons were calculated.

For the sake of comparison we also did the original, separate statistical analyses for the data from the two experiments, denoted A and B, as described by Andreasen *et al.* (2014). Each of these analyses involved fitting a joint event-time model including all treatment combinations, i.e. fitting a total of 10 germination curves simultaneously in the same model. Again three-parameter log-logistic models (Eqn (1)) with parameters depending on the treatment combination were used. These separate analyses did not include any effects for capturing between-table and between-tray variation in estimated standard errors of the parameter estimates.

Statistical analyses were carried out using the statistical environment R (R Core Team, 2016) with the add-on packages 'drc' (Ritz *et al.*, 2015), 'multcomp' (Hothorn *et al.*, 2008), and, in particular, 'metafor' (Viechtbauer, 2010) for event-time models, multiple comparisons, and the meta-analytic approach, respectively. The R script used for the two-step analysis is provided in the Appendix.

Results

The results are shown in Fig. 1: increased fertilizer dose led to slower germination. There was a significant interaction between calcium application and fertilizer dose ($P = 0.04$), implying that the improved nutritional status of the mother plants affected the germination ability of the produced seeds differently, depending on presence or absence of treatment with foliar-applied calcium. Specifically, it was for the highest fertilizer dose only that there was a significant difference between effects with and without foliar-applied calcium treatment. This finding tentatively suggests that there are different non-linear dose–response relationships between time to germination and fertilizer dose depending on absence or presence of calcium treatment.

Table 1 shows estimates of t_{50} with corresponding standard errors for each of the 10 treatment combinations. Although the estimates agree reasonably between experiments A and B, the differences between the pairs of estimates for the same treatment combination were generally large compared with the standard errors of the estimates. Thus seemingly identical experiments still exhibit substantial differences.

The meta-analytic random effects model approach (A+B) resulted in standard errors that were larger by a factor between 1.3 and 3.4, compared with the separate models. The estimated standard deviations for the experiment- and table-specific random effects were 0 and 4.0 days, respectively, while the standard deviation for the tray-specific random effect was 4.0 days.

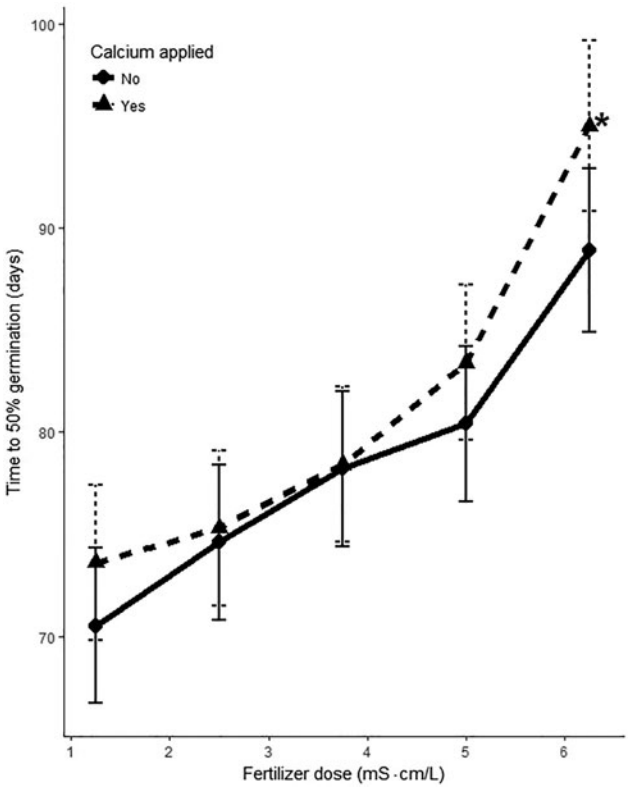

Figure 1. Parameter estimates of t_{50} with corresponding 95% confidence intervals based on the two-step analysis where tray-specific log-logistic models (Eqn (1)) were fitted and combined using a meta-analytic approach. A significant difference between applying and not applying calcium within a fertilizer dose is indicated by the asterisk.

This is not surprising as in the present example there was much more information to estimate variation between 240 trays and six tables than between only two experiments, which did not allow recovering any between-experiment variation. It is also noteworthy that if the experiment-specific effects had been included as a fixed effect rather than random effects in the meta-analytic approach, then the estimated standard errors would have increased additionally by around 18% (data not shown).

Discussion

In the example with *Gerbera hybrida* we found that variation between two seemingly identical experiments still led to increased standard errors of estimated t_{50} values (up to a factor of 3) compared with the corresponding results from within-experiment analyses. This finding suggests that ignoring the between-experiment will lead to unrealistically precise estimates, reinforcing that results from a single experiment will often be overly optimistic. In other words, the assumption of physiological determinants of seed

https://doi.org/10.1017/S0960258517000228 Published online by Cambridge University Press

Table 1. Parameter estimates of t_{50} with corresponding standard errors in parentheses were obtained by fitting an event-time model to each experiment (A and B) separately and by using the proposed meta-analytic approach to each experiment separately

Treatment combination		Original analysis (for each experiment)		Meta-analytic approach (for experiments combined)
Calcium	Fertilizer dose	A	B	A + B
No	1.25	70.9 (0.6)	70.0 (0.6)	70.5 (1.9)
	2.5	75.8 (0.7)	72.8 (0.6)	74.6 (1.9)
	3.75	79.4 (0.8)	76.6 (0.7)	78.2 (1.9)
	5	84.5 (0.8)	75.9 (0.8)	80.4 (1.9)
	6.25	87.4 (1.1)	91.4 (1.4)	88.9 (2.0)
Yes	1.25	73.7 (0.6)	73.7 (0.7)	73.6 (1.9)
	2.5	78.1 (0.7)	71.7 (0.6)	75.3 (1.9)
	3.75	79.5 (0.7	77.3 (0.8)	78.4 (1.9)
	5	84.1 (0.8)	83.2 (0.8)	83.4 (1.9)
	6.25	93.6 (1.2)	97.0 (1.6)	95.0 (2.1)

In both cases germination was assumed to be described by the three-parameter log-logistic model defined by Eqn (1).

germination being constant across experiments, even if they are carried out very close in time and in many ways under seemingly similar conditions, is not tenable. For the present example with *Gerbera hybrida* we tentatively speculate that the absence of tight control of light and temperature in the greenhouse might be part of the explanation why two experiments run one week apart showed sizeable differences.

We showed how to apply the two-step analysis with the parameter of interest being t_{50}. Similar analyses may be carried out for any other relevant parameter. It should be noted that the proposed two-step analysis has to be carried out separately for each parameter of interest. Simultaneous inference for several parameters such b, d and t_{50} in Eqn (1) is also possible using the meta-analytic approach in Step 2 (e.g. Pipper *et al*., 2012). Such extensions could be useful in case estimated mean germination curves with corresponding confidence bands are of interest.

Recently, a related two-step analysis has been successfully applied in the analysis of other types of agricultural data from hierarchical experimental designs such as randomized complete block and split-plot designs (e.g. Mennan *et al*., 2012; Altop *et al*., 2014). This approach involves fitting a linear (mixed) model with weights proportional to the reciprocal estimated standard errors, implying estimation of an additional parameter, namely the residual standard deviation. This approach, however, implies the additional, but not necessarily realistic assumption that estimates have standard errors proportional to the estimated standard errors. The meta-analytic approach instead assumes that estimates retain the standard errors they were found to have in Step 1, from the separate analyses. This is also the reason that meta-analyses in general differ from weighted analyses (Chen and Peace, 2013). In practice the two approaches may occasionally lead to similar results (as was the case in the example with *Gerbera hybrida*; data not shown). Finally, it should be noted that the two-step analysis may not optimally utilize germination data from individual germination tests which were not run for long enough time to characterize the entire germination curve. In such cases a mixed-model analysis, if it were available, would allow borrowing of strength between germination curves, leading to improved inference.

Acknowledgements

We would like to thank Andrius Hansen Kemezys and Renate Müller for providing data for the motivating example. We would also like to thank the editor for his patience and one reviewer for two rounds of helpful comments and suggestions.

References

Altop, E.K., Mennan, H., Streibig, J. C., Budak, U. and Ritz, C. (2014) Detecting ALS and ACCase herbicide tolerant accession of *Echinochloa oryzoides* (Ard.) Fritsch. in rice (*Oryza sativa* L.) fields. *Crop Protection* **65**, 202–206.

Andreasen, C., Kemezys, A.H. and Müller, R. (2014) The effect of fertilizer level and foliar-applied calcium on seed production and germination of *Gerbera hybrida*. *HortScience* **49**, 538–543.

Carpenter, W.J., Ostmark, E.R. and Cornell, J.A. (1995) Temperature and seed moisture govern germination and storage of *Gerbera* seed. *HortScience* **30**, 98–101.

Chen, D.-G. and Peace, K. E. (2013) *Applied Meta-Analysis with R*. CRC Press, Boca Raton.

Hothorn, T., Bretz, F. and Westfall, P. (2008) Simultaneous inference in general parametric models. *Biometrical Journal* **50**, 346–363.

Jiang, X. and Kopp-Schneider, A. (2014) Summarizing EC_{50} estimates from multiple dose-response experiments: A

https://doi.org/10.1017/S0960258517000228 Published online by Cambridge University Press

comparison of a meta-analysis strategy to a mixed-effects model approach. *Biometrical Journal* **56**, 493–512.

Konstantopoulos, S. (2011) Fixed effects and variance components estimation in three-level meta-analysis. *Research Synthesis Methods* **2**, 61–76.

Mennan, H., Streibig, J.C., Ngouajio, M. and Kaya, E. (2012) Tolerance of two *Bifora radians* Bieb populations to ALS inhibitors in winter wheat. *Pest Management Science* **68**, 116–122.

Pipper, C.B., Ritz, C. and Bisgaard, H. (2012) A versatile method for confirmatory evaluation of the effects of a covariate in multiple models. *Applied Statistics* **61**, 315–326.

R Core Team (2016) *R: A Language and Environment for Statistical Computing*. R Foundation for Statistical Computing, Vienna, Austria.

Ritz, C., Pipper, C.B. and Streibig, J.C. (2013) Analysis of germination data from agricultural experiments. *European Journal of Agronomy* **45**, 1–6.

Ritz, C., Baty, F., Streibig, J.C. and Gerhard, D. (2015). Dose-response analysis using R. *PLOS ONE* **10**, e0146021.

Willan, R.L. (1985) A guide to forest seed handling – with special reference to the tropics. *FAO Forestry Paper* 20/2.

Viechtbauer, W. (2010) Conducting meta-analyses in R with the metafor package. *Journal of Statistical Software* **36**, 1–48.

Appendix

```
library(drc)

library(metafor)

library(multcomp)

library(plyr)

## Step 1

## Fitting models separately for each tray (name of the data set: "germination")

## to obtain biologically meaningful parameters such as t50 and/or d
fitFct <- function(dataSet)

{drm(obs~start+end, data=dataSet, type="event", fct=LL.3())}
fitRes <- dlply(germination, .(Tray), fitFct)

# Note: automated fitting in a loop as above only works if the same model

# is applicable to all replicates


## Note that the following lines are just one way to arrange data for step 2

## (it could also be done in e.g., Excel)

## Estimating t50 from the fits
EDfct <- function(fitObj){ED(fitObj, 50, display=FALSE)[1:2]}
EDMat <- ldply(fitRes, EDfct)

## Collecting information on the design also to be used in the meta analysis

dRes <- ddply(germination, .(Tray), function(dataSet){as.character(dataSet[["Dose"]][1])})

cRes <- ddply(germination, .(Tray), function(dataSet){as.character(dataSet[["Ca"]][1])})

cdRes<-ddply(germination,.(Tray),function(dataSet){as.character(dataSet[["CaDose"]][1])})

tRes<-ddply(germination,.(Tray),function(dataSet){as.character(dataSet[["Table"]][1])})

# Note: "CaDose" is the variable corresponding to the treatment combinations

step2Data <- as.data.frame(cbind(EDMat, dRes, cRes, cdRes, tRes,
rep(c("A", "B"), c(120, 120))))[, -c(4, 6, 8, 10)]

names(step2Data) <- c("Tray", "Est", "SE", "Dose", "Ca", "CaDose", "Table", "Exp")
## Data resulting from step 1 head(step2Data)
```

https://doi.org/10.1017/S0960258517000228 Published online by Cambridge University Press

```
# Output
#    Tray       Est        SE Dose Ca CaDose Table Exp
# 1 A1a1 66.18263 1.851040 1.25 0 0.1.25       1    A
# 2 A1a2 64.16946 1.951942 1.25 0 0.1.25       1    A
# 3 A1a3 60.65752 1.534325 1.25 0 0.1.25       1    A
# 4 A1a4 65.44839 2.142873 1.25 0 0.1.25       1    A
# 5 A1b1 65.87644 1.857532 2.5 0 0.2.5         1    A
# 6 A1b2 68.11249 1.833385 2.5 0 0.2.5         1    A


## Step 2
## Fitting the meta analytic random-effects model
## Joint model for both experiments
ts.mm1 <-rma.mv(Est, (SE)^2, mods=~ Dose*Ca, random=~ 1|Exp/Table/Tray, data=step2Data)
## Note the Exp/Table/Tray to ensure that tray is nested within table nested within
experiment.
## REML estimation is used (default method)


## Testing for interaction
ts.mm1.ml <-rma.mv(Est, (SE)^2, mods=~ Dose*Ca, random=~ 1|Exp/Table/Tray, data=step2Data,
method="ML")
ts.mm2.ml <-rma.mv(Est, (SE)^2, mods=~ Dose+Ca, random=~ 1|Exp/Table/Tray, data=step2Data,
method="ML")
anova(ts.mm1.ml, ts.mm2.ml)


## Estimating t_50 for each treatment combination
ts.mm <-rma.mv(Est, (SE)^2, mods=~ CaDose-1, random=~ 1|Exp/Table/Tray, data=step2Data)
coef(summary(ts.mm))


## Defining contrast matrix
allPairWiseComp <- contrMat(table(step2Data[["CaDose"]]), "Tukey")


## Obtaining pairwise comparisons
beta <- coef(summary(ts.mm))[, "estimate"]
names(beta) <- rownames(coef(summary(ts.mm)))
Sigma <- ts.mm[['vb']]
summary(glht(parm(beta, Sigma, 0), linfct=allPairWiseComp))
# Reported in Table 1 (multiplicity adjusted!)
```

https://doi.org/10.1017/S0960258517000228 Published online by Cambridge University Press