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Analysis of dominance hierarchies using generalized mixed models

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Preface

This master's thesis has been done in the first half of 2011, from February to July. The author would like to thank his supervisor Jarle Tufto at Department of Mathematical Sciences at NTNU during this period for his help and advice.

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Abstract

This master's thesis investigates how well a generalized mixed model fits different dominance data sets. The data sets mainly represent disputes between individuals in a closed group, and the model to be used is an adjusted, intransitive extension of the Bradley-Terry model. Two approaches of model fitting are applied; a frequentist and a Bayesian one. The model is fitted to the data sets both with and without random effects (RE) added. The thesis investigates the relationship between the use of random effects and the accuracy, significance and reliability of the regression coefficients and whether or not the random effects affect the statistical significance of a term modelling intransitivity.

The results of the analysis in general suggest that models including random effects better explain the data than models without REs. In general, regression coefficients that appear to be significant in the model excluding REs, seem to remain significant when REs are taken into account. However the underlying variance of the regression coefficients have a clear tendency to increase as REs are included, indicating that the estimates obtained may be less reliable than what is obtained otherwise. Further, data sets fitting to transitive models without REs taken into account also, in general, seem to remain transitive when REs are taken into account.

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1 Introduction

1.1 Basic concepts

This project is concerned with paired comparisons between individuals interacting with each other within a closed group for a given period of time. These interactions are typically disputes between animals in contests about different kinds of needs and will be represented by data sets in the form of dominance matrices revealing how many disputes that have been won by individual i in contest with individual j for any pairs (i, j) of individuals within the group upon which the analysis is to be performed. The underlying assumption in this analysis is that the data sets have a hierarchical structure.

The data sets being analysed are matrices X in which element X_{ij} of the i -th row and the j -th column corresponds to the number of times individual i has won over individual j in interactions taking place within the period of time for which the data have been collected. A generalized mixed model will be fitted to this dominance matrix and different aspects of this model fitting will be analysed and investigated. Element X_{ij} is further assumed to have a binomial distribution with parameters p_{ij} and N_{ij} , the latter corresponding to element (i, j) of the symmetric matrix N containing the number of disputes between any pair of individuals (i, j) . p_{ij} is the probability that individual i wins over j in some dispute.

1.2 The Bradley-Terry model

1.2.1 Applications

In this project the Bradley-Terry (BT) model plays a major part. The BT model has several applications and is a very popular and frequently used tool to model the probabilities p_{ij} as described in the previous section in response to paired comparisons between individuals i and j . Further, several extensions and adjustments have been added to this model in order to handle draws, group comparisons and phenomena such as ties as well as home advantage effects for cases in which, for instance, sport teams are compared. Popular applications are multiclass classification, ranking of chess players and; as this project is concerned with; behaviour among the individuals in an animal group [1].

1.2.2 Model description

The BT model assumes that the outcome of a contest between two individuals is given by what is often referred to as strength parameters λ_i and λ_j indicating the relative strength of individual i and individual j , respectively [2]. The BT model assumes that the probability that individual i wins over j in some interaction is given by the ratio,

$$p_{ij} = \frac{\lambda_i}{\lambda_i + \lambda_j}. \quad (1)$$

From (1) the ratio $\frac{p_{ij}}{1-p_{ij}}$ can easily be found leading to

$$\log\left(\frac{p_{ij}}{1-p_{ij}}\right) = \log \lambda_i - \log \lambda_j, \quad (2)$$

Hence, using the re-parametrization $\log \lambda_i = \beta_i$ and $\log \lambda_j = \beta_j$ the BT model can be written on the form

$$\text{logit}(p_{ij}) = \beta_i - \beta_j. \quad (3)$$

The β_i and β_j parameters are often referred to as "absolute dominances", indicating the strength of the corresponding individual.

One aim of this project is to investigate how the dominance probabilities p_{ij} in (3) are explained by the traits of the individuals involved, traits that affect their interaction abilities, i.e. the abilities on which their dominance skills depend on. A common usage of the BT model is to let the absolute dominances be explained by these traits through a linear regression model. This can easily be incorporated in (3). If n different traits x_{i1}, \dots, x_{in} have been measured for the individuals $i = 1, \dots, N$ being evaluated, $\text{logit } p_{ij}$ may be expressed by the sum of the differences of all the corresponding traits between individual i and j . Further, each trait difference $x_{ik} - x_{jk}$ of the k -th trait of individual i and j may be scaled by some coefficient α_k indicating how heavily $\text{logit } p_{ij}$ depends on this particular trait. Hence we get the following linear regression model,

$$\text{logit}(p_{ij}) = \alpha_1(x_{i1} - x_{j1}) + \alpha_2(x_{i2} - x_{j2}) + \dots + \alpha_n(x_{in} - x_{jn}). \quad (4)$$

Comparing (3) by (4) we see that the latter is a Bradley-Terry model since all the elements of its right-hand side is a measure of the strength of either individual i or individual j of some kind. This again leads to

$$\begin{aligned} \beta_i &= \alpha_1 x_{i1} + \dots + \alpha_n x_{in}, \\ \beta_j &= \alpha_1 x_{j1} + \dots + \alpha_n x_{jn}. \end{aligned} \quad (5)$$

In all the analysis that this project is concerned with, the trait values measured for the individuals involved have been collected for a limited period of time. This is so one can assume these values and hence the regression coefficients $\alpha_1, \dots, \alpha_n$ to be approximately constant for this amount of time, which is important for the reliability of the generated results.

1.3 Regression

There are different ways to estimate the β_1, \dots, β_n parameters given in Section 1.2.2. One commonly used approach is the following: First, maximum likelihood estimation based on (3) is used to estimate the β_i value for individual $i = 1, \dots, N$. Next, the $\hat{\beta}_i$ estimates obtained are treated as response variables in a regression model in which the

x_{ij} -s are the explanatory variables and the α_i -s are the regression coefficients. In this way regression estimates of the α_i -s can be achieved.

However, this kind of model has certain disadvantages. One of these problems may arise if sparse data have been collected from the group being analysed. Then some of the β_i -s may be estimated to values of infinity. This can be seen from (1). For example, if all interactions between individual i and individual j that have been recorded are either interactions being won by i , or interactions in which i has lost against k and k has won over j , then p_{ij} will be estimated to 1. Hence, if all other interactions between i and the other individuals have one of these two kinds of outcomes, and unless the absolute dominance β_j of individual j is being estimated to 0, the strength parameter of i needs to be estimated to infinity to fulfil the criteria that $p_{ij} = 1$. This will not only cause the estimates \hat{x}_{ij} of the explanatory variables to be biased. In such cases, it is also obvious that the approximate asymptotic normal distribution of the $\hat{\beta}_i$ -s does not hold.

This is however not the only disadvantage related to the given estimation of the $\hat{\beta}_i$ parameters. Achieving the $\hat{\beta}_i$ -s only on basis of the p_{ij} -s before the regression is carried out probably gives less accurate estimate values than what would have been the case if the trait values had been included in the estimation as well. A different model approach is therefore to simply include both the dominance data X_{ij} and N_{ij} as well as the trait values x_{ij} in the estimation of the $\hat{\beta}_i$ -s and perform this estimation and the regression analysis in a single model. Then one should expect more correct values of the $\hat{\beta}_i$ parameters since more information is included in the estimation of them than what is the case in the other approach given above. Hence more correct estimates $\hat{\alpha}_{ij}$ of the regression coefficients are to be expected as well.

In this project the latter approach will be performed using generalized mixed models in two different ways: one frequentist approach and one Bayesian approach.

1.4 Intransitive models

A possible extension to the BT model, as suggested in [3], is to add one or more cross-product terms to (4) leading to an intransitive model,

$$\text{logit}(p_{ij}) = \sum_{k=1}^n \alpha_k (x_{ik} - x_{jk}) + \alpha_{uv} (x_{iu}x_{jv} - x_{iv}x_{ju}), \quad (6)$$

expressing the cross-product interaction effect of traits u and v between individuals i and j . This cross-product term $\alpha_{uv} (x_{iu}x_{jv} - x_{iv}x_{ju})$ models the correlative effect between trait u and v upon the dominance probability p_{ij} . This can intuitively be interpreted as the effect of two specific traits u and v working together, which significantly contributes to the outcome of an interaction, in addition to the isolated effects that the

traits u and v contribute with on each of their own. This way an intransitive model design is achieved.

The intransitive model differs from the transitive one in that the hierarchical dominance structure that it describes is allowed to be circular implying that individual i may be dominated by individual k even though i dominates j and j dominates k . It gets easier to get an understanding of this looking at the isolines of the trait space of (6). Let us consider a model of the form (6) in which two types of traits assigned '1' and '2' along with their cross-product effect are of interest. We then get

$$\text{logit}(p_{ij}) = \alpha_1(x_{i1} - x_{j1}) + \alpha_2(x_{i2} - x_{j2}) + \alpha_{12}(x_{i1}x_{j2} - x_{i2}x_{j1}). \quad (7)$$

Now, let us consider the trait space of (6) in which all possible combinations (x_{i1}, x_{i2}) of values for traits 1 and 2 exist. An isoline is achieved if a subspace within this trait space is constructed, in which all the belonging points $(x_{i1}, x_{i2})_{sub}$ give the same dominance for an individual. This can be found using (7) and solving it for the case in which individual i is equally dominant with individual j , that is, $p_{ij} = 1/2$. Solving for x_{i2} one gets, as shown in [3],

$$x_{i2} = \frac{\alpha_{12}x_{j2} + \alpha_1}{\alpha_{12}x_{j1} - \alpha_2}x_{i1} - \frac{\alpha_1x_{j1} + \alpha_2x_{j2}}{\alpha_{12}x_{j1} - \alpha_2}. \quad (8)$$

As can be seen from (8), all trait values for individual i making i equally dominant with some individual j , lie along one straight line with slope and intercept term dependent on the trait values (x_{j1}, x_{j2}) of individual j . Further, it can be shown [3] that all isolines within a trait space go through the same point $(x_1^*, x_2^*) = (\alpha_2/\alpha_{12}, -\alpha_1/\alpha_{12})$. Now, for a given point (x_{j1}, x_{j2}) in the trait space, the direction of the corresponding gradient vector gives the direction of which the dominance of an individual with these trait values increases at the fastest, and the magnitude of the vector is the respective amount of increment of this dominance. It can be shown [3] that this vector equals $(\alpha_1 + \alpha_{12}x_{j2}, \alpha_2 - \alpha_{12}x_{j1})$, and hence, given the expression for the intercept point (x_1^*, x_2^*) of the isolines given above, it can easily be found that the gradient vector is given by $(\alpha_{12}(-x_2^* + x_{j2}), \alpha_{12}(x_1^* - x_{j1}))$. Looking at this expression one can easily see that dominance increases the further away a set of trait values are with respect to (x_1^*, x_2^*) . It can also be shown that the direction of increasing dominance is clockwise when $\alpha_{12} > 0$ and anticlockwise when $\alpha_{12} < 0$.

This is where the circular property of the intransitive model comes in. Because of the increasing dominance around (x_1^*, x_2^*) in the clockwise or anticlockwise direction, a group of individuals whose traits were circularly distributed around (x_1^*, x_2^*) would have had an intransitive dominance structure in which individual k could dominate i even though i dominated j and j dominated k .

An interesting aspect is thus the properties of the model fittings of the data sets with respect to intransitivity and what differences the use of random effects might contribute

with. Further, the significance of α_{uv} and whether or not a significant α_{uv} will remain significant when random effects, as described in Section 2.2, are taken into account is also of interest. This thesis will investigate these questions.

1.5 The main purposes of this project

In the analysis being presented in this report an intransitive dominance model structure is fitted to several data sets by the use of the BT model with one or more cross-product terms in addition. The project will also use what is known as random effects (see section 2.2) included in some of its analysis. The report will take a closer look at how well this kind of model fits the data sets.

Certain traits that the investigated individuals possess have been chosen to be used in the analysis. The project will consider how significant each of the traits are with respect to the model, i.e. to which extent the outcomes of the contests between the individuals in the groups being analysed depend on these traits. This will be done through evaluation of the model coefficients α_k for traits $k = 1, \dots, n$ as given in (6). Of interest is also the coefficient α_{uv} as given in (6) related to the cross-product term for traits u and v . This report will investigate to which extent the use of random effects in the model affects this coefficient. Further, it will investigate whether or not an intransitive model interpretation fits the data. The effect that the use of random effects have on the nature of the estimates of the other model coefficients $\alpha_k, k = 1, \dots, n$ will also be investigated.

As mentioned in Section 1.3, the data sets will be fitted to the adjusted BT model in two different ways; one frequentist approach and one Bayesian approach. The report will evaluate prospective differences in the analysis performed by these two methods.

There are four data sets being evaluated in this project. Three of these are also evaluated in J. Tufto's article [3] from 1998 in which the cross-product term in (6) is suggested as a way to add an intransitive effect to the BT model. In [3] random effects are, however, not taken into account. Some of the purpose of this project is therefore to evaluate three of the same models; being referred to as Data set 1, 2 and 3 later in this report; considering random effects in addition to the cross-product term causing intransitivity in order to continue some of the analysis from [3].

2 Generalized mixed models

2.1 Generalized linear models

The generalized linear model (GLM) [4] is defined through a set of N independent random variables Y_1, \dots, Y_N , all coming from the same probability distribution in the exponential family. Some well-known probability distributions belonging to this family are the normal, the Poisson and the binomial distribution. A GLM is a generalization of least squares regression, relating the explanatory variables x_{i1}, \dots, x_{in} in the linear regression model to the random variables Y_i through a link function g applied to the expected value μ_i of the Y_i -s:

$$g(\mu_i) = \mathbf{x}_i^T \boldsymbol{\beta}. \quad (9)$$

Here \mathbf{x}_i is the $n \times 1$ vector containing the explanatory variables x_{i1}, \dots, x_{in} and $\boldsymbol{\beta}$ is the $n \times 1$ vector containing the regression coefficients β_1, \dots, β_n of the regression model.

Further, in our analysis we assume the number of successes X_{ij} for individual i in interactions with individual j to have a binomial distribution with the dominance probabilities p_{ij} and the number of interactions N_{ij} as parameters,

$$X_{ij} \sim \text{bin}(p_{ij}, N_{ij}). \quad (10)$$

Thus, comparing (9) by (4) we see that this applies to the BT model described in Section 1.2.2, $\text{logit}(p_{ij}) = \log\left(\frac{p_{ij}}{1-p_{ij}}\right)$ being the link function $g(\mu_i)$, p_{ij} the expected value μ_i and $\alpha_1, \dots, \alpha_n$ the model coefficients β_1, \dots, β_n .

However it often happens that the data being analysed violates the assumption given in (10). As mentioned in [3] this can occur when dependencies between the outcome of interactions are present or when the p_{ij} parameters have large stochastic variation. Both of these phenomena may cause larger variance in the X_{ij} parameters than what the binomial model indicates. This is known as overdispersion.

There are several ways to take overdispersion into account in the analysis. One approach which is frequently applied is the use a parameter ϕ to scale the variance of X_{ij} in (10),

$$\text{var}(X_{ij}) = \phi N_{ij} p_{ij} (1 - p_{ij}), \quad (11)$$

ϕ being estimated by

$$\hat{\phi} = \frac{D}{n - p}. \quad (12)$$

Here, D is the deviance of the model and $n - p$ is the corresponding residual degrees of freedom. This way ϕ is an indicator of the amount of overdispersion present in the

model fitting, and hence it indicates how well the data being analysed suit the binomial model. ϕ is often referred to as the dispersion parameter, and models based on (11) for which $\phi \neq 1$ are called quasi-likelihood models and one usually refer to them as being binomial with overdispersion or quasibinomial.

2.2 Mixed models

The trait coefficients $\alpha_1, \dots, \alpha_n$ given in (4) are often referred to as 'fixed effects' in order to distinguish them from something called 'random effects' as mentioned in Section 1.5. The use of random effects comes from the assumption often used in analysis of generalized models that the covariates x_{i1}, \dots, x_{in} and x_{j1}, \dots, x_{jn} in (4) not fully explains the variation in the response variable. The random effects are therefore often incorporated into generalized models to simulate the uncertainty in the choice of model and the choice of covariates.

Individual-specific random effects U_i and U_j related to individual i and j , respectively, can be used to model the uncertainty and the error that is caused by estimating the dominance probability p_{ij} by the chosen trait types. The difference $U_i - U_j$ between two of the random effects can be added as an extra term to the right-hand side expression of the BT model (4) or its intransitive extension (6). The random effects U_1, \dots, U_N are independent and identically distributed random variables assumed to come from a normal distribution with mean 0 and some standard deviation σ_a [5]. Fitting (6) with $U_i - U_j$ added to the right-hand side of the model to data and then investigating the nature of U_1, \dots, U_N we thus get an idea of to which extend the traits chosen for the model explain the data being analysed.

Of interest in this project is also the contest-specific random effect U_{ij} related to the interaction between individual i and j . Like the U_i -s, the U_{ij} -s are independent and identically distributed random variables assumed to come from a normal distribution with mean 0 and some standard deviation σ_b . Adding the random effect U_{ij} to the right-hand side expression of the BT model (4) or its intransitive extension (6), overdispersion as described in Section 2.1 is modelled. Hence, adding U_{ij} to the model one obtains an indication on how well the data actually fits the BT model. Generalized models including one or more random effects, and thus containing both fixed and random effects, are usually called generalized linear mixed models, or more generally generalized mixed models to include the possibility of non-linearity.

In the analysis of this project an intransitive generalized mixed model extension of the BT model (6), with and without both of the kinds of random effects described in this section, will be fitted to dominance data.

3 Methods

3.1 The frequentist approach

The data sets will be analysed in two different manners. The first one is a frequentist approach in which the `BTm{BradleyTerry2}` function for the software package *R* is used. This function fits the Bradley-Terry model to the given data set by logistic regression using either maximum likelihood, penalised quasi-likelihood if random effects are involved, or bias-reduced maximum likelihood [6].

R code for handling the analysis of data sets being fitted to the adjusted Bradley-Terry model (6) can be found in the Appendix of this report.

3.2 The Bayesian approach

The second approach is a hierarchical Bayesian approach performed by the software package *Winbugs*. The Bradley-Terry model along with the probability distribution of prospective random effects are manually specified. Prior distributions both for the trait coefficients being estimated as well as for the standard deviances of prospective random effects are also manually specified. On the basis of this input along with the dominance data *Winbugs* uses the most sufficient Markov chain Monte Carlo (MCMC) approach to fit the data to the specified model [7].

For the analysis presented in this report a Bayesian hierarchical model which structure is shown in Figure 1 is used. For all of the MCMC analysis a thinning factor of 50 is applied to avoid autocorrelation. For each data set 200.000 MCMC iterations are carried out, but when this is not sufficient in order to obtain convergence, even more iterations are used until convergence is reached. For prior distributions, all model coefficients are given the normal distribution with mean 0 and standard deviation $1.0e3$. This gives an approximately non-informative prior. All random effects have the normal distribution with mean 0 and a standard deviation σ , as discussed in Section 2.2. All analysis are carried out with a gamma prior distribution for the precision parameter $\tau = 1/\sigma^2$ of this normal distribution with scale and rate parameters fitting for the respective data set in order to obtain reliable results.

Winbugs implementation code for all of the analysis can be found in the Appendix of this report.

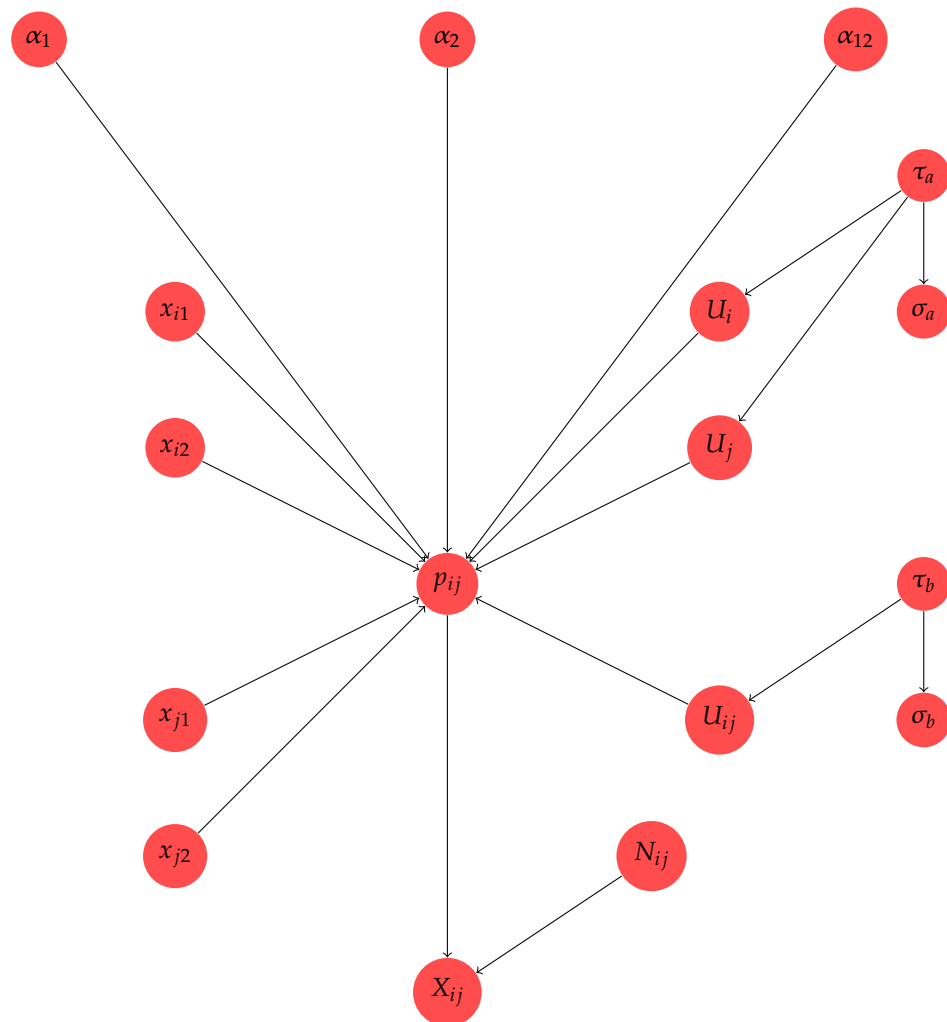


Figure 1: Illustration of the Bayesian hierarchical model used in the Bayesian approach as described in Section 3.2 in which both individual-specific and contest-specific random effects are included. In the model given above two kinds of traits denoted '1' and '2' are handled for individuals denoted i and j .

4 Data sets

4.1 General description

All data sets being analysed in this project are $N \times N$ sized dominance matrices \mathbf{X} , N being the number of individuals in the group being analysed and the elements $X_{i1}, X_{i2}, \dots, X_{i,i-1}, X_{i,i+1}, \dots, X_{iN}$ of the i -th row of \mathbf{X} corresponding to the number of interactions between individual i and, respectively, individual $1, 2, \dots, i-1, i+1, \dots, N$ in which i has won. For the first three data sets element (i, j) represents the number of contests in favour of individual i in interactions with individual j within a closed group of animals. The elements in the fourth and last data set represent the number of times 5 different newspapers cited each other for a given period of time.

4.2 Data set 1: Contests between male house sparrows in Denmark

The first data set is chosen from A.P. Møller's article [8] from 1987. The purpose of this article was to investigate the relationship between the badge size of house sparrows and their dominance pattern. The birds being investigated consisted of three separate flocks located at three different places in Denmark; Hollensted, Øster Brønderslev and Pandrup. The Hollensted flock was observed by a feeding stand from January to April 1984 and the two others were observed in two separate laboratory rooms from December 1984 to February 1985. Female house sparrows have a tendency to avoid contest interactions with male house sparrows in the winter season since the males are usually more dominant than the females at this time of the year. Therefore, only interactions between male house sparrows were recorded. In his article Møller concludes that in general the house sparrows with a larger badge seemed to dominate house sparrows with a smaller badge. In this report the age and the total badge size traits will be considered.

In the analysis of this project the dominance data of all of the three sparrow flocks are merged into one single dominance matrix as it may be considered reasonable to assume that the model coefficients $\alpha_1, \dots, \alpha_n$ as given in (6) do not differ from one subpopulation to the other. For all interactions between sparrows i and j from different flocks, the elements with coordinates (i, j) and (j, i) in the dominance matrix are simply given as 0. The dominance matrices correspond to Table I, II and III in [8], and the trait values used in the analysis of this project can also be found in these tables. The merged matrix is given in the Appendix of this report. In the analysis of this project covariate values of 1 and -1 are used for the age trait depending on whether the sparrows were adults or immature, respectively.

4.3 Data set 2: Contests between male house sparrows in Norway

The second data set is chosen from E. J. Solberg's and T. H. Ringsby's article [9] from 1997. Three separate groups of male house sparrows were observed at three different

farms situated at Storselsøy, Hestmona and Ytre-Kvarøy, all along the coast of northern Norway. Two of the traits registered for which values also are available in the article, were age (the sparrows were divided into one of two age categories: immatures and adults) and visible badge size. These are the two traits this project will consider in its analysis.

Like the data sets found in Møller's article [8], the dominance matrices for the three separate sparrow flocks described in Solberg's article [9] are in this project evaluated as one single dominance matrix generated the same way as for Data set 1. The dominance matrices correspond to Table 1, 2 and 3 in [9], and the trait values used in the analysis of this project can also be found in these tables. The merged matrix is given in the Appendix of this report. In the analysis of this project covariate values of 1 and -1 are used for the age trait depending on whether the sparrows were adults or immature, respectively. Missing trait values are registered as 'NA'.

4.4 Data set 3: Contests between woodland caribou in Canada

Interactions between woodland caribou were observed from September to May in the seasons of 1980/81 and 1981/82 in Parc des Grands-Jardins, a 310 km² big forest park situated 120 km north-east of the city center of Quebec, as described in an article from 1986 written by C. Barrette and D. Vandal [10]. Traits registered for the woodland caribou being analysed were sex, age and antler size. All these traits will be evaluated in this project.

The dominance matrix being analysed in this project corresponds to the one given in Table 3 in Barrette and Vandal's article [10]. This matrix is also given in the Appendix of this thesis. Trait values can be found in Table 1 in [10]. In the analysis given in this thesis the woodland caribou are given 1 and -1 as covariate values for the sex trait depending on whether they are males or females, respectively. As for the antler size trait, values 0, 1, 2, 3, and 4 are used for sizes 'none', 'small/15 cm spikes', 'medium', '1 large/large' and 'very large' as given in [10].

4.5 Data set 4: Citations among Norwegian newspapers

The fourth and last data set contains the number of times 5 of the biggest Norwegian newspapers cited each other during the year of 2010. These numbers were found using the media archive *Atekst* to be found on the web site <http://www.retriever.no/tjenester>. Through this page it is possible to access a database containing articles from Norwegian newspapers back to the year of 1945. The data achieved were obtained using names of newspapers as search quotes and then specifying as one of the search conditions from which newspaper the articles were to be accessed. The trait explanatory variables were chosen to be the readership and the circulation of the 5 evaluated newspapers for the period of time chosen (the year of 2010). These data were found at the web site <http://medienorge.uib.no/>. The page contains a search function for

which it is possible to look up these kinds of data for specific Norwegian newspapers for specific years.

The dominance matrix generated by the numbers found on <http://www.retriever.no/tjenester> are given along with the trait values found on <http://medienorge.uib.no/> in the Appendix of this thesis.

5 Results

5.1 General description

In the following subsections all relevant output diagnostics as generated by *R* and *Winbugs* are presented. In these subsections 'Case 1' refers to the case in which all random effects are omitted from the analysis. 'Case 2' refers to the case in which the random effects U_i and U_j related to individual i and j are included, whereas 'Case 3' refers to the case in which the contest-specific random effect U_{ij} is included in the model. Finally, 'Case 4' refers to the case in which all random effects, both $U_i - U_j$ as well as U_{ij} are included in the model. These are added as linear terms, as described in Section 2.2. All trait data except most of the categorical ones were standardized before the analysis was carried out. The categorical traits that were not standardized were the age trait in Data set 1 and 2, and the sex trait in Data set 3. Unfortunately, the *R* function used to analyse the data was not suitable for modelling the random effects U_{ij} and hence Case 3 and Case 4 were carried out by *Winbugs* only.

The output diagnostics from *R* and *Winbugs* for the model coefficients α_k and α_{uv} as given in (6) for Data set 1, 2, 3 and 4 can be found in Table 1, 3, 5 and 7, respectively. In these tables 'Mean' is the mean values of the posterior density distributions of α_k and α_{uv} , and 'SE' is their respective estimated standard deviations, i.e. the standard errors. $P_{post.}(\alpha > 0)$ is the probability that the respective model coefficient is non-negative, based on its posterior density distribution. The 'z value' in the output diagnostics from *R* is the asymptotic normally distributed estimator of the two-side z-test and corresponds to the ratio between the mean and the standard error. $P(Z > |z|)$ is the p-value for this test. 'DF' means degrees of freedom. 'Est. dispersion parameter' is the estimate $\hat{\phi}$ given in (12) of the dispersion parameter as described in Section 2.1. Further, 'MC error' is the Monte Carlo standard error of the mean for the MCMC approach used by *Winbugs*, and 'Median' is the median of the posterior density distribution of the respective model coefficient. 'Samples' is the number of samples from the posterior density distribution of the coefficient used to generate the output diagnostics from *Winbugs*.

Further, Figure 8, 15, 22, 23 and 30 show the trait spaces of the trait pair of Data set 1, 2, two of the three possible trait pairs of Data set 3, as well as the trait space of Data set 4, respectively, with the corresponding isolines as described in Section 1.4 and trait values for the individuals of the respective data sets.

The values in Table 2, 4 and 6 for Data set 2, 3 and 4, respectively, give the ratio between each of the estimated standard deviations σ_a and σ_b of the random effects, and the total variance in the response $\text{logit}(p_{ij})$ for all cases in which random effects are included. Unfortunately Data set 1 had to be let out of this analysis since *Winbugs* could not handle the model in which the total variance was estimated for this data set. For the standard deviations of the individual- and the contests-specific random effects σ_a and

σ_b , the ratios mentioned are given by, respectively, $\left(\frac{2\sigma_a^2}{n}\right) \sum_{i \neq j} (\text{logit}(\hat{p}_{ij}) - \text{logit}(\bar{p}))^2$ and $\left(\frac{\sigma_b^2}{n}\right) \sum_{i \neq j} (\text{logit}(\hat{p}_{ij}) - \text{logit}(\bar{p}))^2$. Here, n is the number of estimated \hat{p}_{ij} -s, and \bar{p} is the mean of all estimated dominance probabilities \hat{p}_{ij} (which means that $\text{logit}(\bar{p}) = 0$ in our case). The way this is implemented in *Winbugs* can be seen in the Appendix of this thesis for the model implementation of Case 2 of Data set 2.

In all tables the symbol '-' means that the given kind of information was chosen not to be evaluated for the given parameter. '*' means that the given software or software function being applied was not able to generate the given kind of information.

5.2 Data set 1

In this section output diagnostics for the analysis of the data sets given in the article written by Møller are presented. The estimations of the model coefficients, as generated by *R* and *Winbugs*, are presented in Table 1 and the output diagnostics of the most slowly converging parameter in the Bayesian analysis of *Winbugs* are presented in Figure 2, 3, 4 and 5 for Case 1, 2, 3 and 4, respectively. In the table and the figures the parameters of the age and the total badge size trait along with the interaction parameter between the two of these are referred to as 'Age', 'Total badge size' and 'Age \times Total badge size', respectively. Density plots of the estimated standard deviations of the random effects for Case 2, 3 and 4 can be found in Figure 6 and 7.

Unfortunately the penalised quasi-likelihood method of *R* generated extremely large ($\sim 10^{14}$) estimates of the model coefficients, and other output diagnostics also explicitly confirmed that the method did not converge. Hence, Case 2 of Data set 1 has not been evaluated by *R* in this thesis.

Software	Case						
R	1	Model coef. α	Mean \pm SE	z value	$P(Z > z)$	$P_{post.}(\alpha > 0)$	DF
		Age	0.35341 \pm 0.05652	6.253	4.03e-10	1	1
		Total badge size	2.41327 \pm 0.12617	19.128	< 2e-16	1	1
		Age \times Total badge size	-0.26378 \pm 0.06356	-4.150	3.33e-05	0	1
		Est. dispersion parameter	6.91				
Winbugs	1	Model coef. α	Mean \pm SE	MC Error	Median	$P_{post.}(\alpha > 0)$	Samples
		Age	0.3554 \pm 0.05761	0.001163	0.3566	1.0	2000
		Total badge size	2.423 \pm 0.1263	0.002843	2.418	1.0	2000
		Age \times Total badge size	-0.2653 \pm 0.06382	0.001273	-0.2646	0.0	2000
	2						
		Age	0.0382 \pm 1.183	0.02778	0.06844	0.5235	10000
		Total badge size	5.582 \pm 1.69	0.04898	5.42	1.0	10000
		Age \times Total badge size	-0.7536 \pm 0.1814	0.001693	-0.7463	0.0	10000
		SE $\hat{\sigma}_a$ of U_i and U_j	6.429 \pm 1.576	0.03076	6.174	-	10000
	3						
		Age	0.442 \pm 0.8163	0.0287	0.4273	0.713	2000
		Total badge size	8.511 \pm 1.935	0.09218	8.229	1.0	2000
		Age \times Total badge size	-0.7577 \pm 0.8299	0.03214	-0.7297	0.175	2000
		SE $\hat{\sigma}_a$ of U_{ij}	9.981 \pm 2.087	0.08266	9.759	-	2000
	4						
		Age	0.4097 \pm 1.102	0.03626	0.4078	0.646	2000
		Total badge size	6.953 \pm 1.886	0.1014	6.735	1.0	2000
		Age \times Total badge size	-0.3582 \pm 0.7022	0.01852	-0.3489	0.3035	2000
		SE $\hat{\sigma}_a$ of U_i and U_j	5.134 \pm 1.054	0.0589	4.959	-	2000
		SE $\hat{\sigma}_a$ of U_{ij}	1.731 \pm 2.033	0.0516	1.235	-	2000

Table 1: Diagnostics for Data set 1. Estimations of the parameters based on the data sets from the Møller article for Case 1 and 2, as generated by R and Winbugs, and Case 3 and 4, as generated by Winbugs.

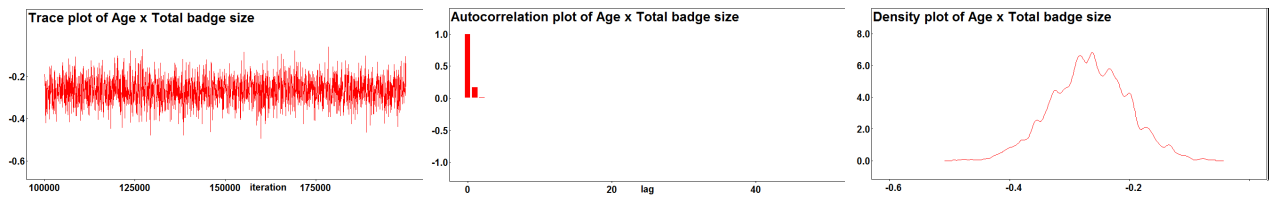


Figure 2: Diagnostics for Data set 1, Case 1. Final trace, autocorrelation and kernel density plots of Age \times Total badge size, the most slowly converging parameter, as generated by Winbugs.

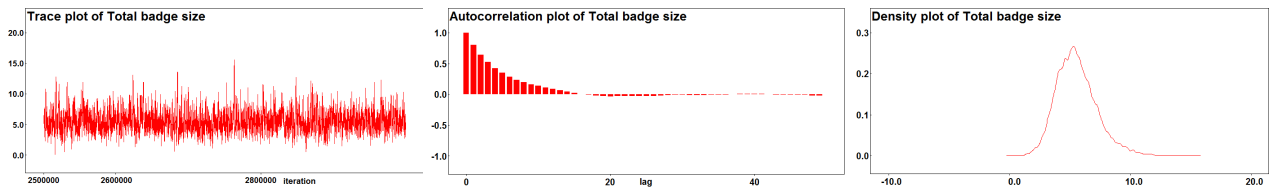


Figure 3: Diagnostics for Data set 1, Case 2. Final trace, autocorrelation and kernel density plots of Total badge size, the most slowly converging parameter, as generated by Winbugs.

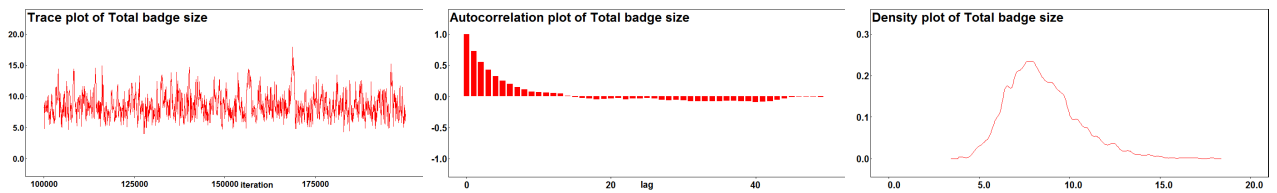


Figure 4: Diagnostics for Data set 1, Case 3. Final trace, autocorrelation and kernel density plots of Total badge size, the most slowly converging parameter, as generated by Winbugs.

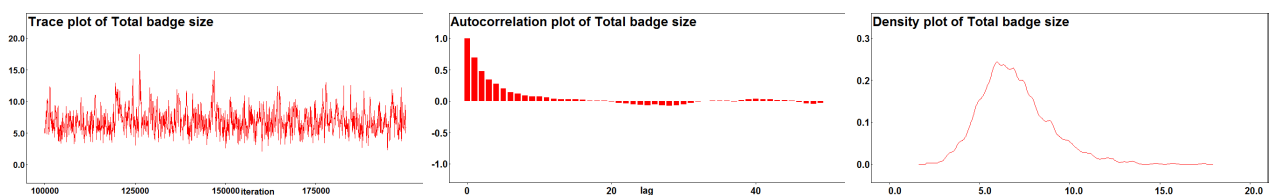


Figure 5: Diagnostics for Data set 1, Case 4. Final trace, autocorrelation and kernel density plots of Total badge size, the most slowly converging parameter, as generated by Winbugs.

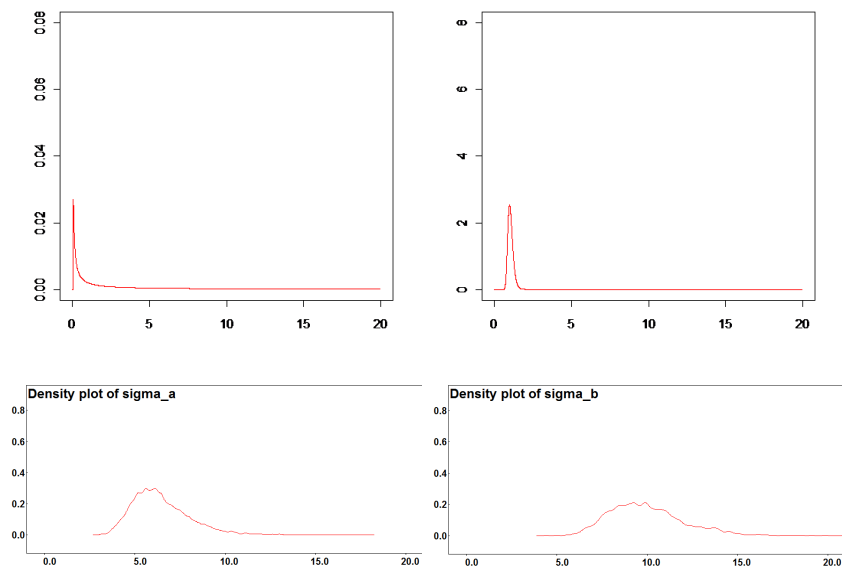


Figure 6: Prior density plots (top row, as generated by *R*), and kernel density plots (bottom row, as generated by *Winbugs*) of the SE $\hat{\sigma}_a$ of U_i, U_j for Case 2 and the SE $\hat{\sigma}_b$ of U_{ij} for Case 3, respectively, for Data set 1. Note the differences in the scaling of the y-axes.

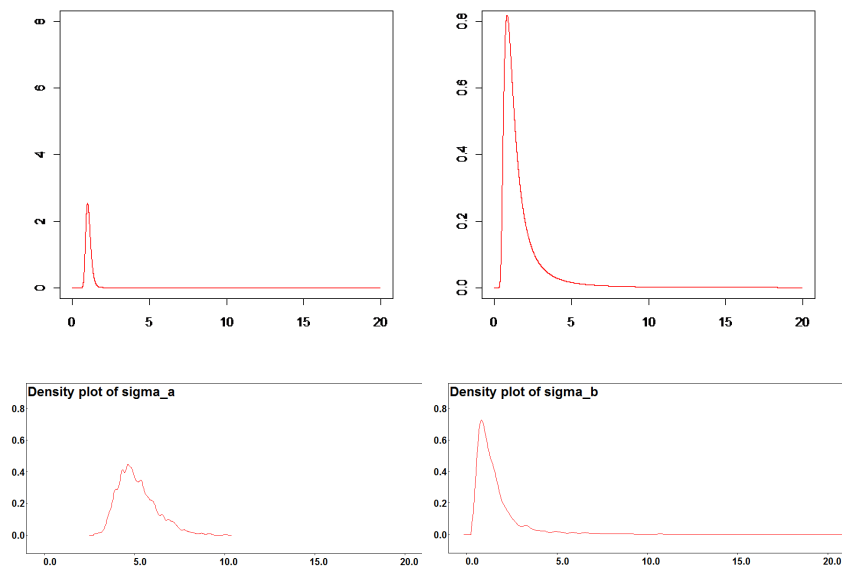


Figure 7: Prior density plots (top row, as generated by *R*), and kernel density plots (bottom row, as generated by *Winbugs*) of the SE $\hat{\sigma}_a$ of U_i, U_j and the SE $\hat{\sigma}_b$ of U_{ij} , respectively from Case 4 of for Data set 1. Note the differences in the scaling of the y-axes.

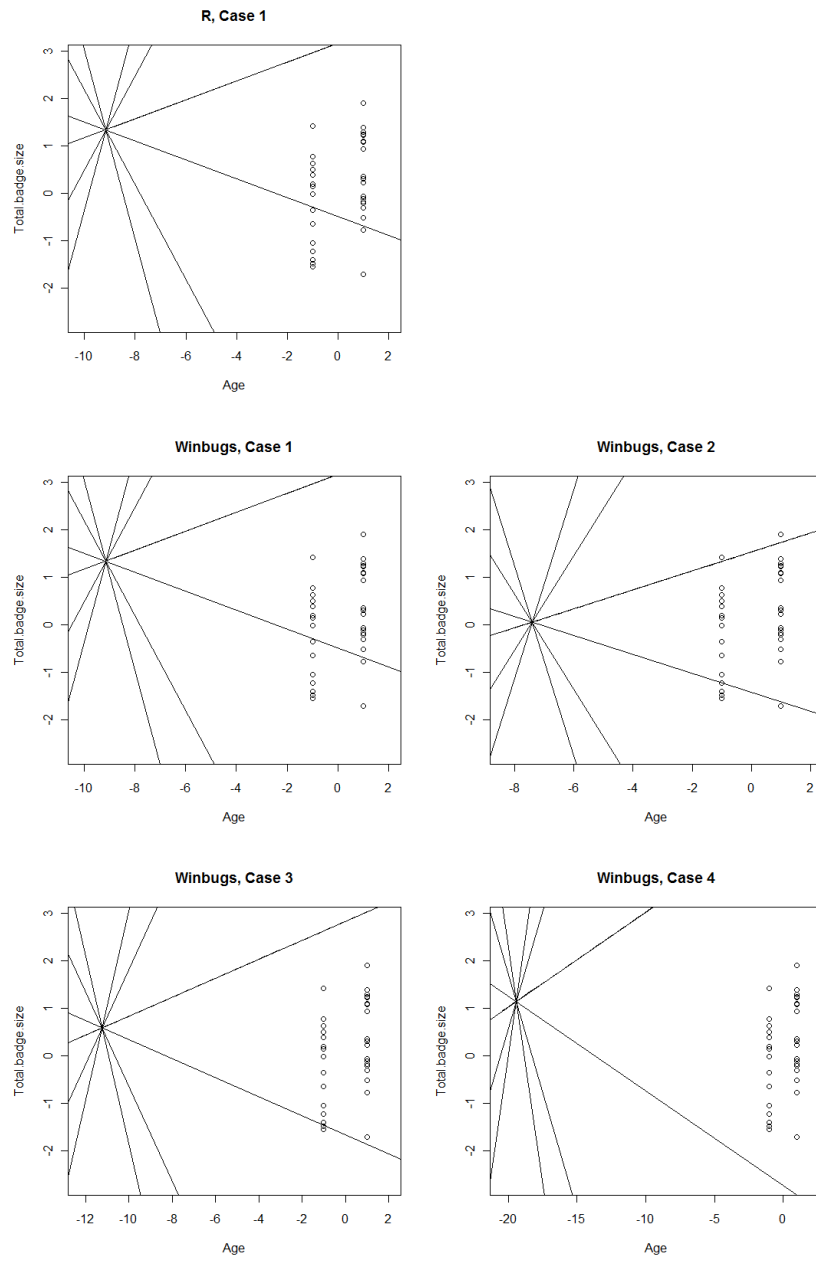


Figure 8: Isolines in the trait space of Data set 1 along with trait values for the individuals (marked as dots).

5.3 Data set 2

In this section output diagnostics for the analysis of the data sets given in the article written by Solberg are presented. The estimations of the model coefficients, as generated by *R* and *Winbugs*, are presented in Table 3 and the output diagnostics of the the slowest converging parameter in the Bayesian analysis of *Winbugs* are presented in Figure 9, 10, 11 and 12 for Case 1, 2, 3 and 4, respectively. In the table and the figures the parameters of the age and the visible badge size trait along with the interaction parameter between the two of these are referred to as 'Age', 'Visible badge size' and 'Age \times Visible badge size', respectively. Density plots of the estimated standard deviations of the random effects for Case 2, 3 and 4 can be found in Figure 13 and 14.

		Case		
Software	Std. dev. of the RE	2	3	4
<i>R</i>	σ_a	96.1368%	*	*
<i>Winbugs</i>	σ_a	82.99439%	-	57.83203%
	σ_b	-	55.34066%	14.53856%

Table 2: Diagnostics for Data set 2. The ratio between the standard deviation of the random effect and the total variance in the response variable $\text{logit}(p_{ij})$ for Case 2, as generated by *R* and *Winbugs* and for Case 3 and 4 as generated by *Winbugs* only.

Software	Case						
<i>R</i>	1	Model coef. α	Mean \pm SE	z value	$P(Z > z)$	$P_{post.}(\alpha > 0)$	DF
		Age	-0.06164 ± 0.07094	-0.869	0.385	0.19353	1
		Visible badge size	0.15671 ± 0.12478	1.256	0.209	0.89712	1
		Age \times Visible badge size	0.16003 ± 0.12405	1.290	0.197	0.90249	1
		Est. dispersion parameter	3.66				
	2						
		Age	-0.1866 ± 0.2816	-0.663	0.508	0.25217	1
		Visible badge size	0.4134 ± 0.3564	1.160	0.246	0.87802	1
		Age \times Visible badge size	0.1356 ± 0.1902	0.713	0.476	0.76313	1
		SE $\hat{\sigma}_a$ of U_i and U_j	0.9295 ± 0.1968	4.723	2.32e-06	-	1
<i>Winbugs</i>	1	Model coef. α	Mean \pm SE	MC Error	Median	$P_{post.}(\alpha > 0)$	Samples
		Age	-0.06024 ± 0.072	0.001475	-0.05957	0.1935	2000
		Visible badge size	0.1573 ± 0.1253	0.003066	0.1547	0.899	2000
		Age \times Visible badge size	0.1625 ± 0.1206	0.002716	0.1637	0.9035	2000
	2						
		Age	-0.1717 ± 0.3308	0.009138	-0.1759	0.2765	2000
		Visible badge size	0.4376 ± 0.4209	0.01007	0.4411	0.8765	2000
		Age \times Visible badge size	0.1519 ± 0.2003	0.004882	0.1564	0.785	2000
		SE $\hat{\sigma}_a$ of U_i and U_j	1.081 ± 0.2981	0.007512	1.031	-	2000
	3						
		Age	-0.2946 ± 0.2086	0.005435	-0.2819	0.065	2000
		Visible badge size	0.6978 ± 0.3232	0.007203	0.6844	0.9875	2000
		Age \times Visible badge size	-0.2366 ± 0.3171	0.006219	-0.2212	0.214	2000
		SE $\hat{\sigma}_a$ of U_{ij}	1.477 ± 0.2922	0.005487	1.447	-	2000
	4						
		Age	-0.23 ± 0.3446	0.007577	-0.2315	0.248	2000
		Visible badge size	0.5603 ± 0.4519	0.009053	0.5611	0.9025	2000
		Age \times Visible badge size	$-1.023E-4 \pm 0.3004$	0.006884	0.005352	0.508	2000
		SE $\hat{\sigma}_a$ of U_i and U_j	1.069 ± 0.3241	0.007896	1.029	-	2000
		SE $\hat{\sigma}_a$ of U_{ij}	0.758 ± 0.2778	0.009824	0.7578	-	2000

Table 3: Diagnostics for Data set 2. Estimations of the parameters based on the data sets from the Solberg article for Case 1 and 2, as generated by *R* and *Winbugs*, and Case 3 and 4, as generated by *Winbugs*.

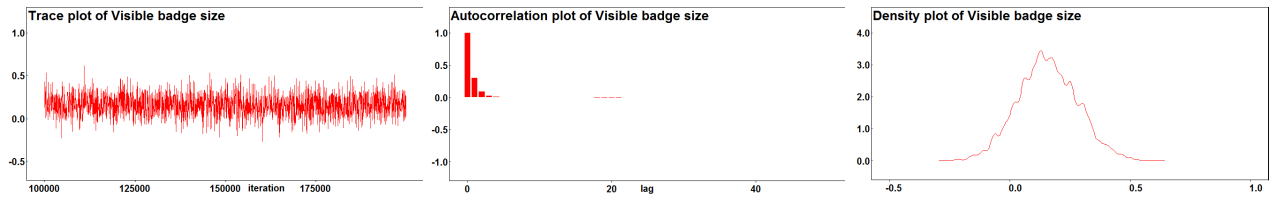


Figure 9: Diagnostics for Data set 2, Case 1. Final trace, autocorrelation and kernel density plots of Visible badge size, the most slowly converging parameter, as generated by Winbugs.

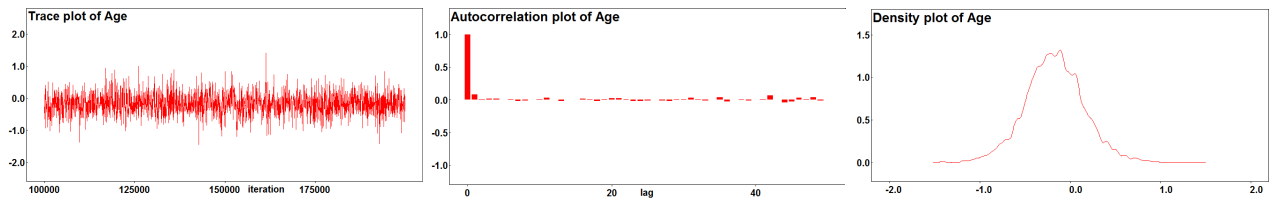


Figure 10: Diagnostics for Data set 2, Case 2. Final trace, autocorrelation and kernel density plots of Age, the most slowly converging parameter, as generated by Winbugs.

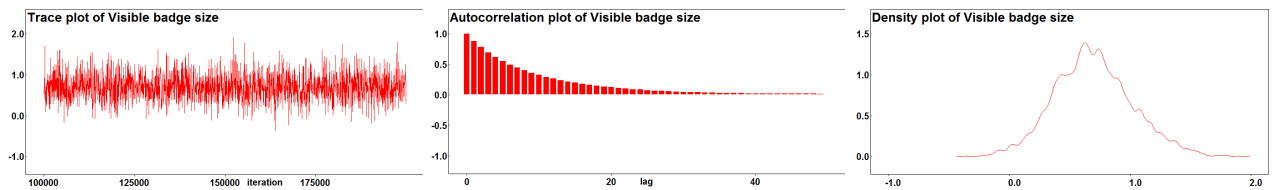


Figure 11: Diagnostics for Data set 2, Case 3. Final trace, autocorrelation and kernel density plots of Visible badge size, the most slowly converging parameter, as generated by Winbugs.

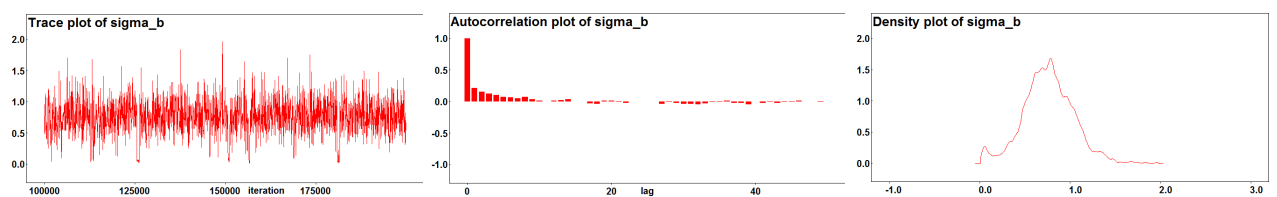


Figure 12: Diagnostics for Data set 2, Case 4. Final trace, autocorrelation and kernel density plots of the SE $\hat{\sigma}_b$ of U_{ij} , the slowest converging parameter, as generated by Winbugs.

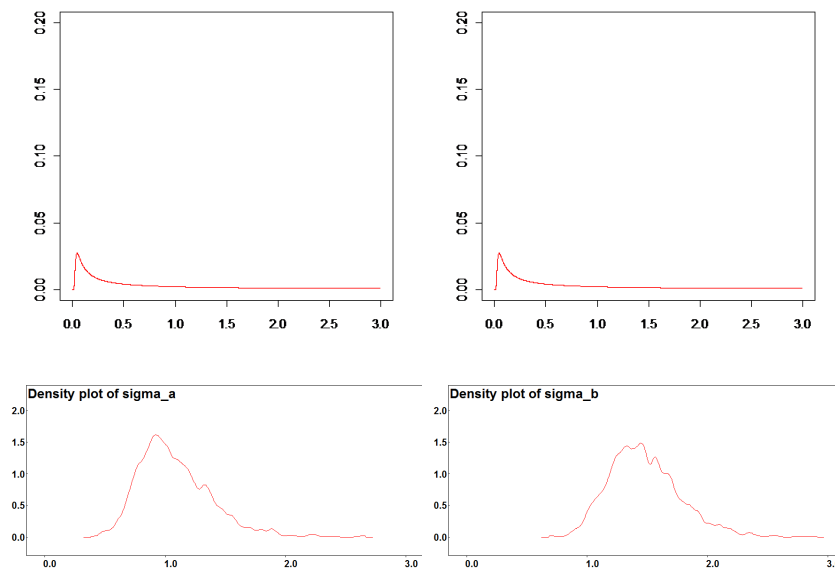


Figure 13: Prior density plots (top row, as generated by *R*), and kernel density plots (bottom row, as generated by *Winbugs*) of the SE $\hat{\sigma}_a$ of U_i, U_j for Case 2 and the SE $\hat{\sigma}_b$ of U_{ij} for Case 3, respectively, for Data set 2. Note the differences in the scaling of the y-axes.

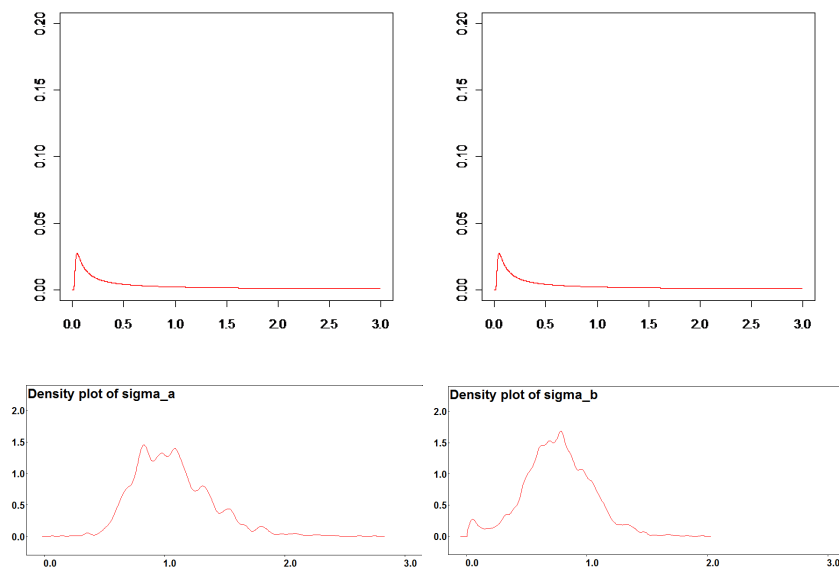


Figure 14: Prior density plots (top row, as generated by *R*), and kernel density plots (bottom row, as generated by *Winbugs*) of the SE $\hat{\sigma}_a$ of U_i, U_j and the SE $\hat{\sigma}_b$ of U_{ij} , respectively from Case 4 of for Data set 2. Note the differences in the scaling of the y-axes.

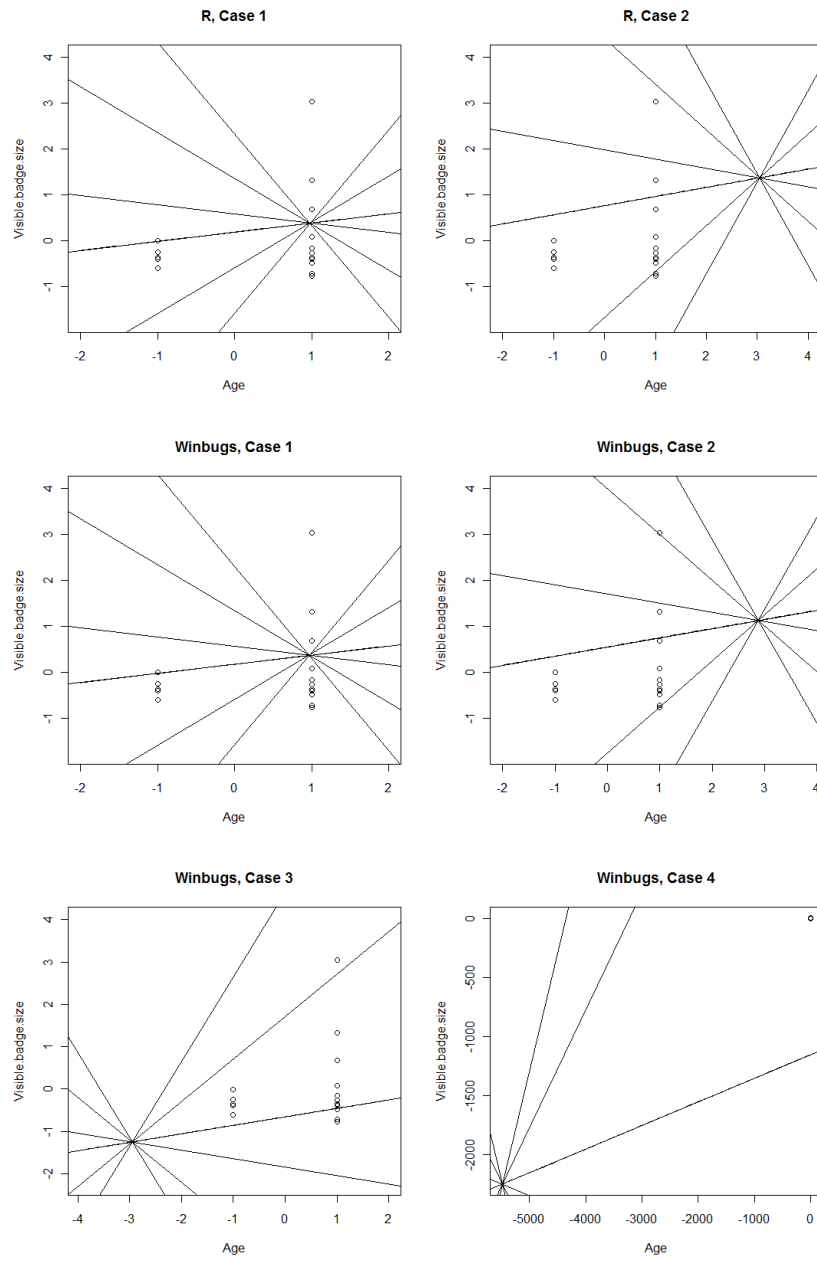


Figure 15: Isolines in the trait space of Data set 2 along with trait values for the individuals (marked as dots).

5.4 Data set 3

In this section output diagnostics for the analysis of the data set given in the article written by Barette and Vandall are presented. The estimations of the model coefficients, as generated by *R* and *Winbugs*, are presented in Table 5 and the output diagnostics of the the most slowly converging parameter in the Bayesian analysis of *Winbugs* are presented in Figure 16, 17, 18 and 19 for Case 1, 2, 3 and 4, respectively. In the table and the figures the parameters of the sex, age and the antler size trait along with the interaction parameter between sex and age as well as sex and antler size are referred to as 'Sex', 'Age', 'Antler size', 'Sex \times Age' and 'Sex \times Antler size', respectively. Density plots of the estimated standard deviations of the random effects for Case 2, 3 and 4 can be found in Figure 20 and 21.

Software	Std. dev. of the RE	Case		
		2	3	4
<i>R</i>	σ_a	25.23867%	*	*
<i>Winbugs</i>	σ_a	24.67561%	-	11.31489%
	σ_b	-	21.95006%	35.42440%

Table 4: Diagnostics for Data set 3. The ratio between the standard deviation of the random effect and the total variance in the response variable $\text{logit}(p_{ij})$ for Case 2, as generated by *R* and *Winbugs* and for Case 3 and 4 as generated by *Winbugs* only.

Software	Case						
R	1	Model coef. α	Mean \pm SE	z value	$P(Z > z)$	$P_{post.}(\alpha > 0)$	DF
		Sex	0.98213 \pm 0.03439	28.56	<2e-16	1	1
		Age	0.55721 \pm 0.03250	17.14	<2e-16	1	1
		Antler size	1.19526 \pm 0.04149	28.81	<2e-16	1	1
		Sex \times Age	-0.42398 \pm 0.03247	-13.06	<2e-16	0	1
		Sex \times Antler size	0.45156 \pm 0.03505	12.88	<2e-16	1	1
		Est. dispersion parameter	20.34				
	2						
		Sex	1.47493 \pm 0.31876	4.627	3.71e-06	0.99999	1
		Age	1.00316 \pm 0.34437	2.913	0.00358	0.99809	1
		Antler size	1.68790 \pm 0.32408	5.208	1.91e-07	1.00000	1
		Sex \times Age	-0.36751 \pm 0.03928	-9.357	< 2e-16	0.00000	1
		Sex \times Antler size	0.47470 \pm 0.04310	11.013	< 2e-16	1.00000	1
		SE $\hat{\sigma}_a$ of U_i and U_j	1.3119 \pm 0.2348	5.588	2.29e-08	-	1
Winbugs	1	Model coef. α	Mean \pm SE	MC Error	Median	$P_{post.}(\alpha > 0)$	Samples
		Sex	0.9835 \pm 0.03598	8.375E-4	0.9844	1.0	2000
		Age	0.5584 \pm 0.03257	7.289E-4	0.5578	1.0	2000
		Antler size	1.196 \pm 0.042	9.735E-4	1.195	1.0	2000
		Sex \times Age	-0.4239 \pm 0.03229	7.694E-4	-0.4229	0.0	2000
		Sex \times Antler size	0.4519 \pm 0.03564	7.218E-4	0.4519	1.0	2000
	2						
		Sex	1.479 \pm 0.351	0.01176	1.472	1.0	4000
		Age	0.9863 \pm 0.3612	0.01157	0.9895	0.997	4000
		Antler size	1.712 \pm 0.3429	0.01146	1.706	1.0	4000
		Sex \times Age	-0.3695 \pm 0.03912	6.095E-4	-0.3688	0.0	4000
		Sex \times Antler size	0.4769 \pm 0.04382	8.199E-4	0.476	1.0	4000
		SE $\hat{\sigma}_a$ of U_i and U_j	1.386 \pm 0.2682	0.005412	1.347	-	4000
	3						
		Sex	1.179 \pm 0.1398	0.003133	1.175	1.0	2000
		Age	1.164 \pm 0.1706	0.004379	1.159	1.0	2000
		Antler size	1.654 \pm 0.1495	0.003714	1.657	1.0	2000
		Sex \times Age	0.272 \pm 0.1625	0.003781	0.2673	0.9625	2000
		Sex \times Antler size	0.3732 \pm 0.1399	0.003179	0.3721	0.994	2000
		SE $\hat{\sigma}_a$ of U_{ij}	2.071 \pm 0.109	0.002413	2.067	-	2000
	4						
		Sex	1.495 \pm 0.4578	0.01727	1.492	0.999	2000
		Age	1.62 \pm 0.496	0.01839	1.617	0.9955	2000
		Antler size	2.213 \pm 0.4806	0.01859	2.189	1.0	2000
		Sex \times Age	0.3826 \pm 0.2907	0.007783	0.3818	0.909	2000
		Sex \times Antler size	0.3732 \pm 0.1399	0.003179	0.3721	0.975	2000
		SE $\hat{\sigma}_a$ of U_i and U_j	1.515 \pm 0.4665	0.01335	1.478	-	2000
		SE $\hat{\sigma}_b$ of U_{ij}	3.791 \pm 0.3561	0.008257	3.766	-	2000

Table 5: Diagnostics for Data set 3. Estimations of the parameters based on the data sets from the Barrette and Vandal article for Case 1 and 2, as generated by R and Winbugs, and Case 3 and 4, as generated by Winbugs.

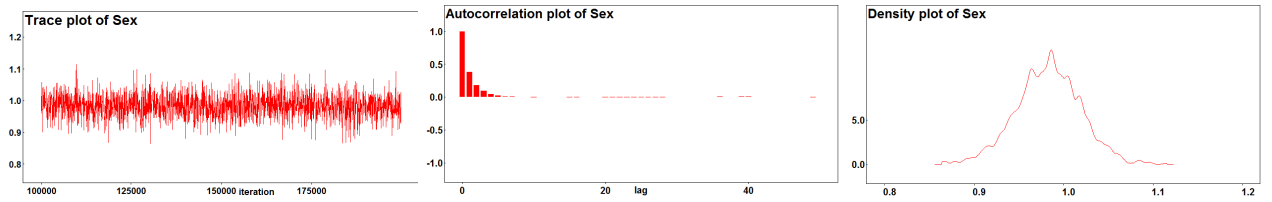


Figure 16: Diagnostics for Data set 3, Case 1. Final trace, autocorrelation and kernel density plots of Sex, the most slowly converging parameter, as generated by Winbugs.

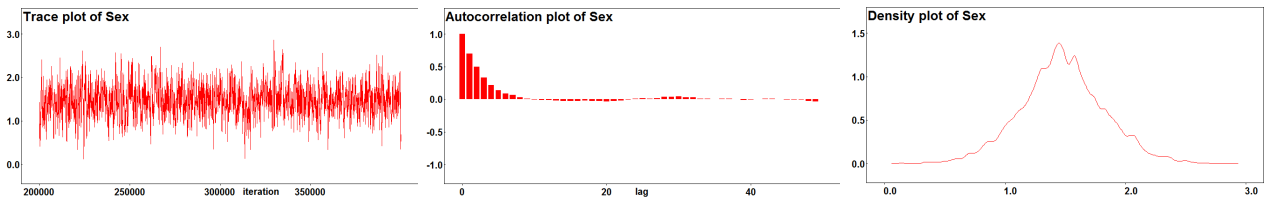


Figure 17: Diagnostics for Data set 3, Case 2. Final trace, autocorrelation and kernel density plots of Sex, the most slowly converging parameter, as generated by Winbugs.

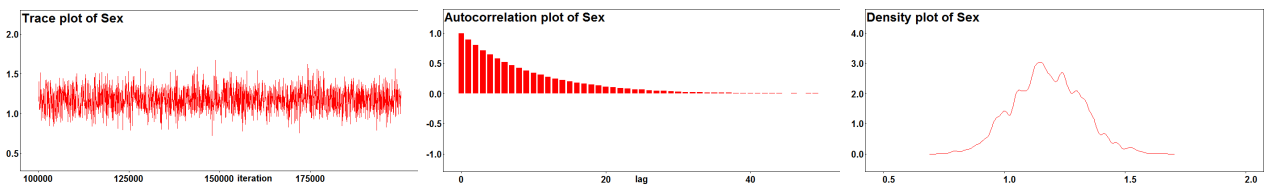


Figure 18: Diagnostics for Data set 3, Case 3. Final trace, autocorrelation and kernel density plots of Sex, the most slowly converging parameter, as generated by Winbugs.

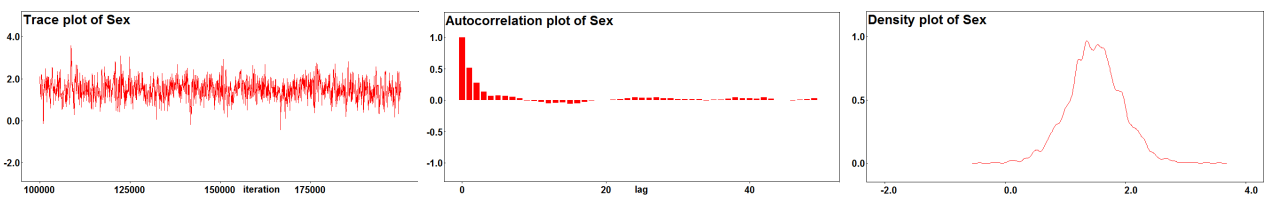


Figure 19: Diagnostics for Data set 3, Case 4. Final trace, autocorrelation and kernel density plots of Sex, the most slowly converging parameter, as generated by Winbugs.

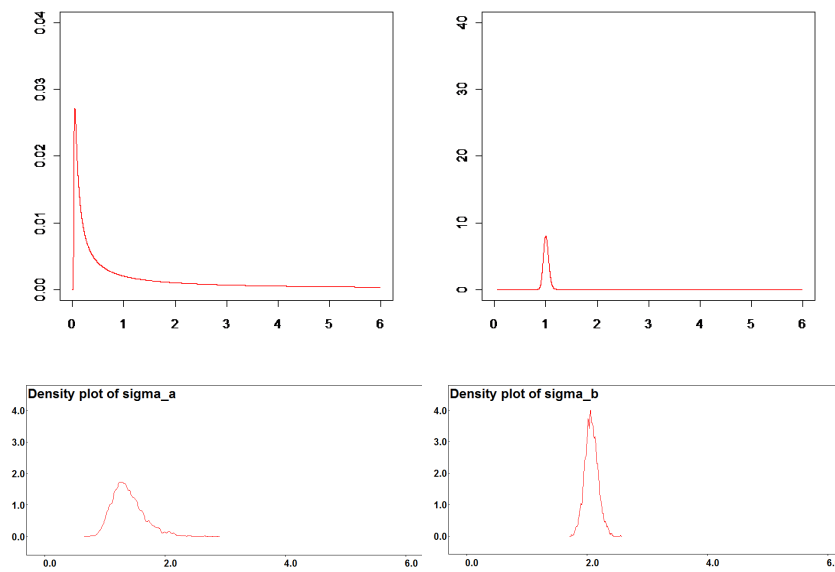


Figure 20: Prior density plots (top row, as generated by *R*), and kernel density plots (bottom row, as generated by *Winbugs*) of the SE $\hat{\sigma}_a$ of U_i, U_j for Case 2 and the SE $\hat{\sigma}_b$ of U_{ij} for Case 3, respectively, for Data set 3. Note the differences in the scaling of the y-axes.

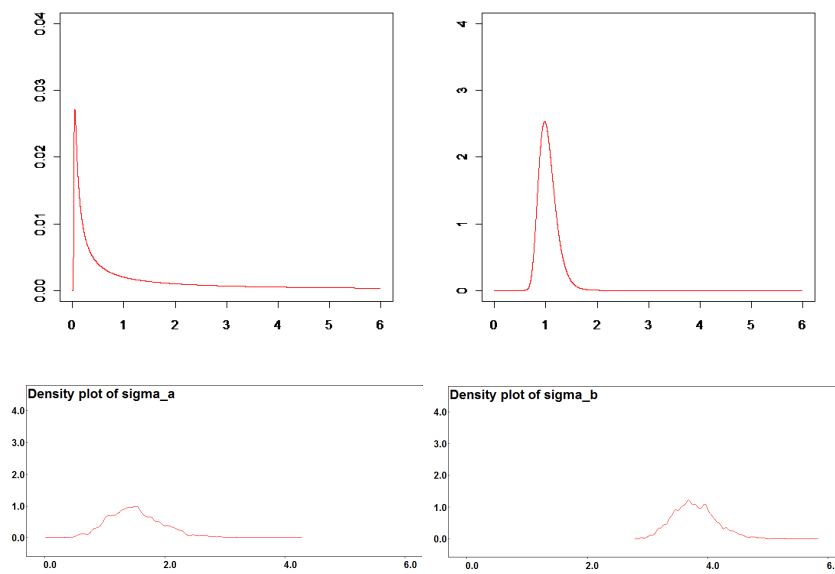


Figure 21: Prior density plots (top row, as generated by *R*), and kernel density plots (bottom row, as generated by *Winbugs*) of the SE $\hat{\sigma}_a$ of U_i, U_j and the SE $\hat{\sigma}_b$ of U_{ij} , respectively from Case 4 of for Data set 3. Note the differences in the scaling of the y-axes.

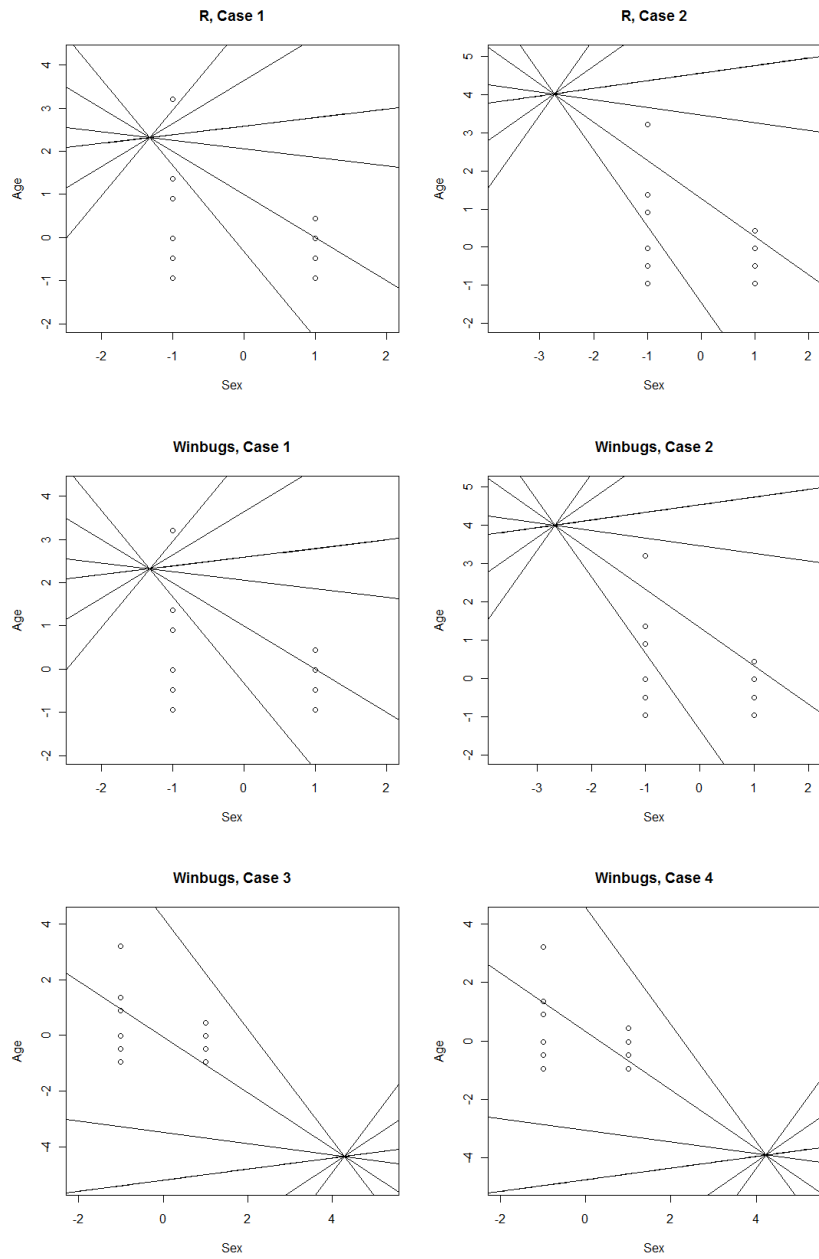


Figure 22: Isolines in the 'Sex vs. Age' trait space of Data set 3 along with the individuals (marked as dots).

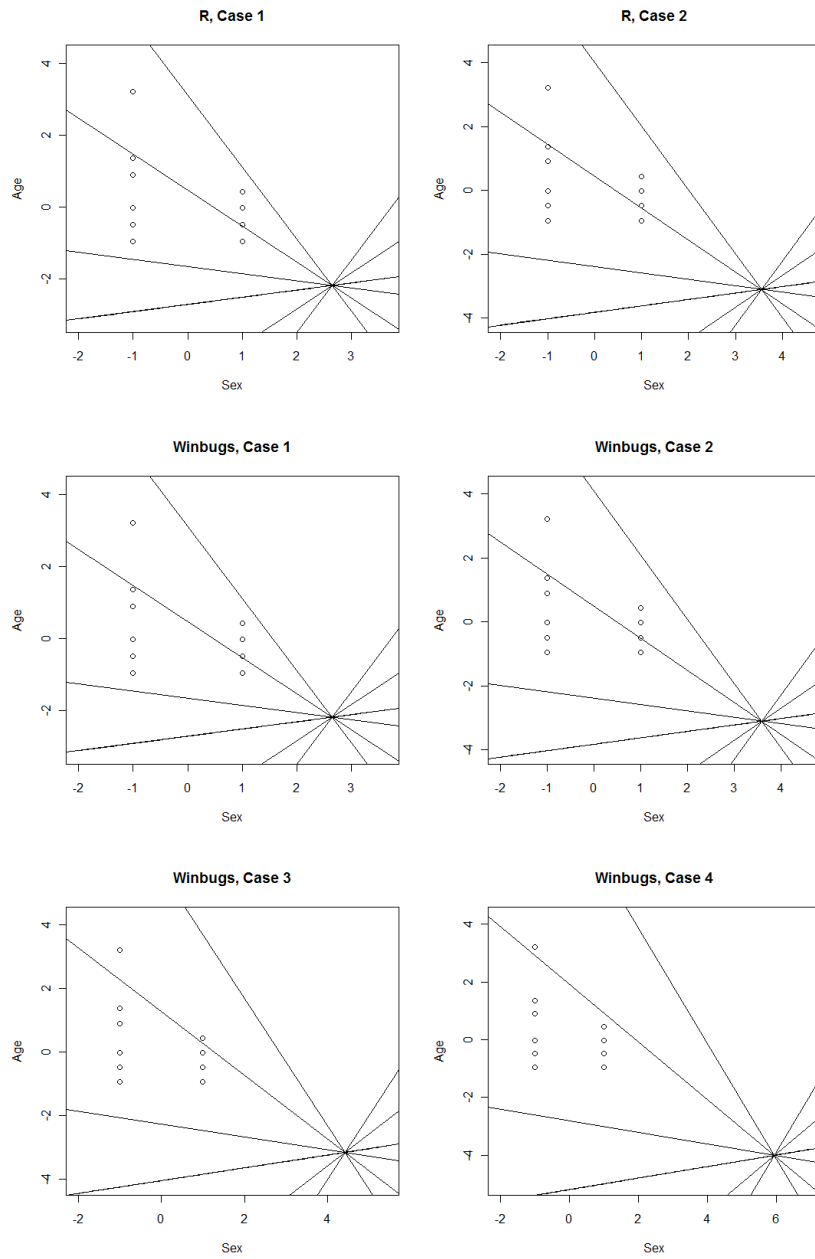


Figure 23: Isolines in the 'Sex vs. Antler size' trait space of Data set 3 along with trait values for the individuals (marked as dots).

5.5 Data set 4

In this section output diagnostics for the analysis of the newspaper citations are presented. The estimations of the model coefficients, as generated by *R* and *Winbugs*, are presented in Table 7 and the output diagnostics of the the most slowly converging parameter in the Bayesian analysis of *Winbugs* are presented in Figure 24, 25, 26 and 27 for Case 1, 2, 3 and 4, respectively. In the table and the figures the parameters of the readership and the circulation trait along with the interaction parameter between the two of these are referred to as 'Readership', 'Circulation' and 'Readership \times Circulation', respectively. Density plots of the estimated standard deviations of the random effects for Case 2, 3 and 4 can be found in Figure 28 and 29.

		Case		
Software	Std. dev. of the RE	2	3	4
<i>R</i>	σ_a	10.31155%	*	*
<i>Winbugs</i>	σ_a	23.98898%	-	17.83186%
	σ_b	-	16.12637%	8.120731%

Table 6: Diagnostics for Data set 4. The ratio between the standard deviation of the random effect and the total variance in the response variable $\text{logit}(p_{ij})$ for Case 2, as generated by *R* and *Winbugs* and for Case 3 and 4 as generated by *Winbugs* only.

Software	Case						
R	1	Model coef. α	Mean \pm SE	z value	$P(Z > z)$	$P_{post.}(\alpha > 0)$	DF
		Readership	0.166156 \pm 0.011349	14.641	< 2e-16	1	1
		Circulation	-0.392013 \pm 0.022410	-17.492	< 2e-16	0	1
		Readership \times Circulation	-0.036143 \pm 0.006741	-5.362	8.23e-08	0	1
		Est. dispersion parameter	18.59				
	2						
		Readership	0.173342 \pm 0.040112	4.321	1.55e-05	1.00000	1
		Circulation	-0.396321 \pm 0.105131	-3.770	0.000163	0.00012	1
		Readership \times Circulation	-0.036387 \pm 0.006795	-5.355	8.56e-08	0.00000	1
		SE $\hat{\sigma}_a$ of U_i and U_j	0.1999 \pm 0.1026	1.948	0.0514	-	1
Winbugs	1	Model coef. α	Mean \pm SE	MC Error	Median	$P_{post.}(\alpha > 0)$	Samples
		Readership	0.1663 \pm 0.0115	2.325E-4	0.1663	1.0	2000
		Circulation	-0.393 \pm 0.02164	4.263E-4	-0.3931	0.0	2000
		Readership \times Circulation	-0.03627 \pm 0.006731	1.463E-4	-0.036	0.0	2000
	2						
		Readership	0.1769 \pm 0.06723	0.004673	0.1741	0.9915	2000
		Circulation	-0.3976 \pm 0.1654	0.00883	-0.3968	0.0315	2000
		Readership \times Circulation	-0.03631 \pm 0.006832	1.276E-4	-0.0362	0.0	2000
		SE $\hat{\sigma}_a$ of U_i and U_j	0.3054 \pm 0.2294	0.01145	0.2356	-	2000
	3						
		Readership	0.1798 \pm 0.05739	0.002791	0.179	0.9985	2000
		Circulation	-0.4289 \pm 0.09964	0.003207	-0.4302	0.0	2000
		Readership \times Circulation	-0.036 \pm 0.0304	0.001629	-0.03602	0.1125	2000
		SE $\hat{\sigma}_b$ of U_{ij}	0.3718 \pm 0.1196	0.003481	0.3477	-	2000
	4						
		Readership	0.1852 \pm 0.07229	0.004936	0.1811	0.9965	2000
		Circulation	-0.4429 \pm 0.1701	0.008695	-0.4339	0.0105	2000
		Readership \times Circulation	-0.03708 \pm 0.02374	9.188E-4	-0.03753	0.0575	2000
		SE $\hat{\sigma}_a$ of U_i and U_j	0.2761 \pm 0.2712	0.01712	0.2034	-	2000
		SE $\hat{\sigma}_b$ of U_{ij}	0.2635 \pm 0.1122	0.002976	0.24	-	2000

Table 7: Diagnostics for Data set 4. Estimations of the parameters based on the data from 2010 regarding the 5 biggest Norwegian newspapers, for Case 1 and 2, as generated by R and Winbugs, and Case 3 and 4, as generated by Winbugs.

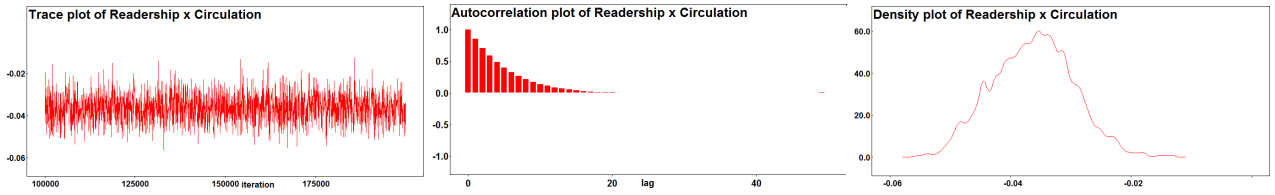


Figure 24: Diagnostics for Data set 4, Case 1. Final trace, autocorrelation and kernel density plots of Readership \times Circulation, the most slowly converging parameter, as generated by Winbugs.

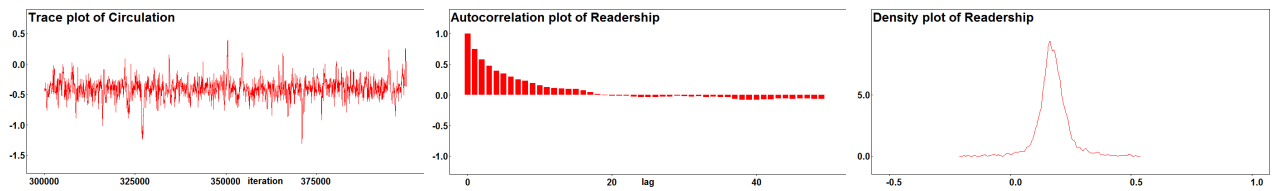


Figure 25: Diagnostics for Data set 4, Case 2. Final trace, autocorrelation and kernel density plots of Readership, the most slowly converging parameter, as generated by Winbugs.

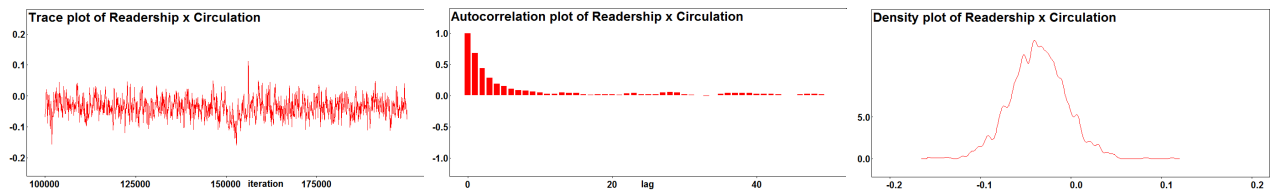


Figure 26: Diagnostics for Data set 4, Case 3. Final trace, autocorrelation and kernel density plots of Readership \times Circulation, the most slowly converging parameter, as generated by Winbugs.

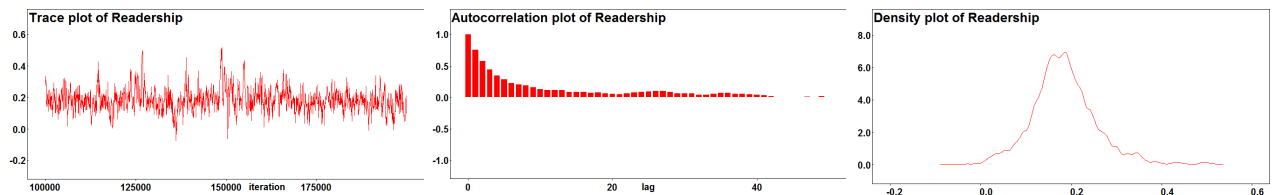


Figure 27: Diagnostics for Data set 4, Case 4. Final trace, autocorrelation and kernel density plots of Age, the most slowly converging parameter, as generated by Winbugs.

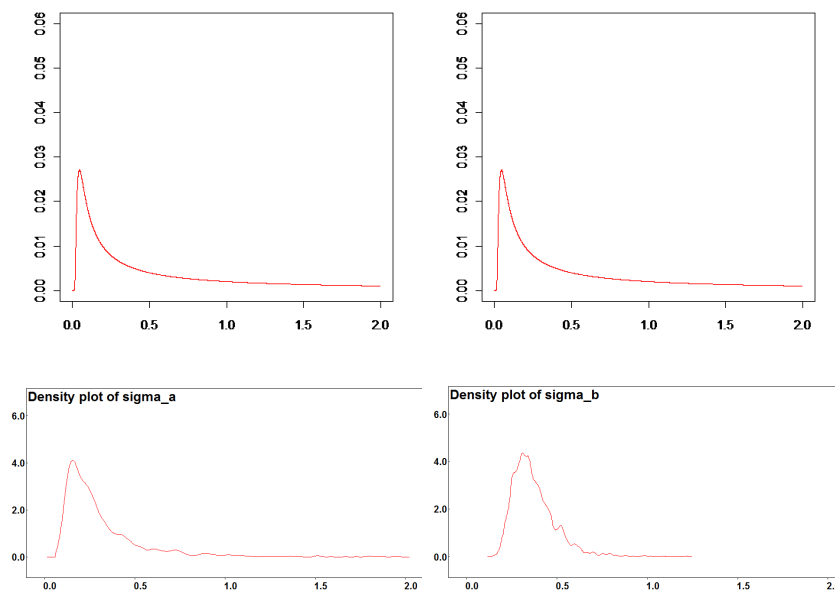


Figure 28: Prior density plots (top row, as generated by *R*), and kernel density plots (bottom row, as generated by *Winbugs*) of the SE $\hat{\sigma}_a$ of U_i, U_j for Case 2 and the SE $\hat{\sigma}_b$ of U_{ij} for Case 3, respectively, for Data set 4. Note the differences in the scaling of the y-axes.

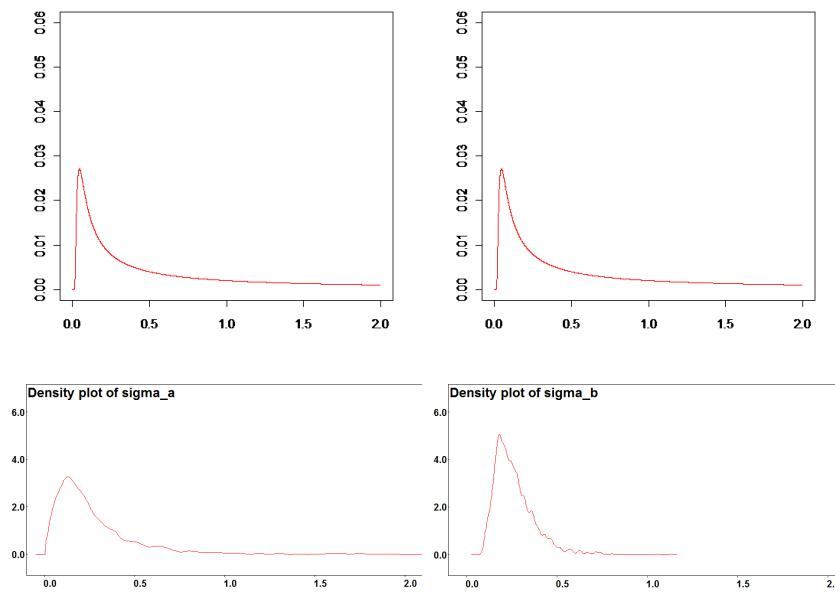


Figure 29: Prior density plots (top row, as generated by R), and kernel density plots (bottom row, as generated by $Winbugs$) of the SE $\hat{\sigma}_a$ of U_i, U_j and the SE $\hat{\sigma}_b$ of U_{ij} , respectively fro Case 4 of for Data set 4. Note the differences in the scaling of the y-axes.

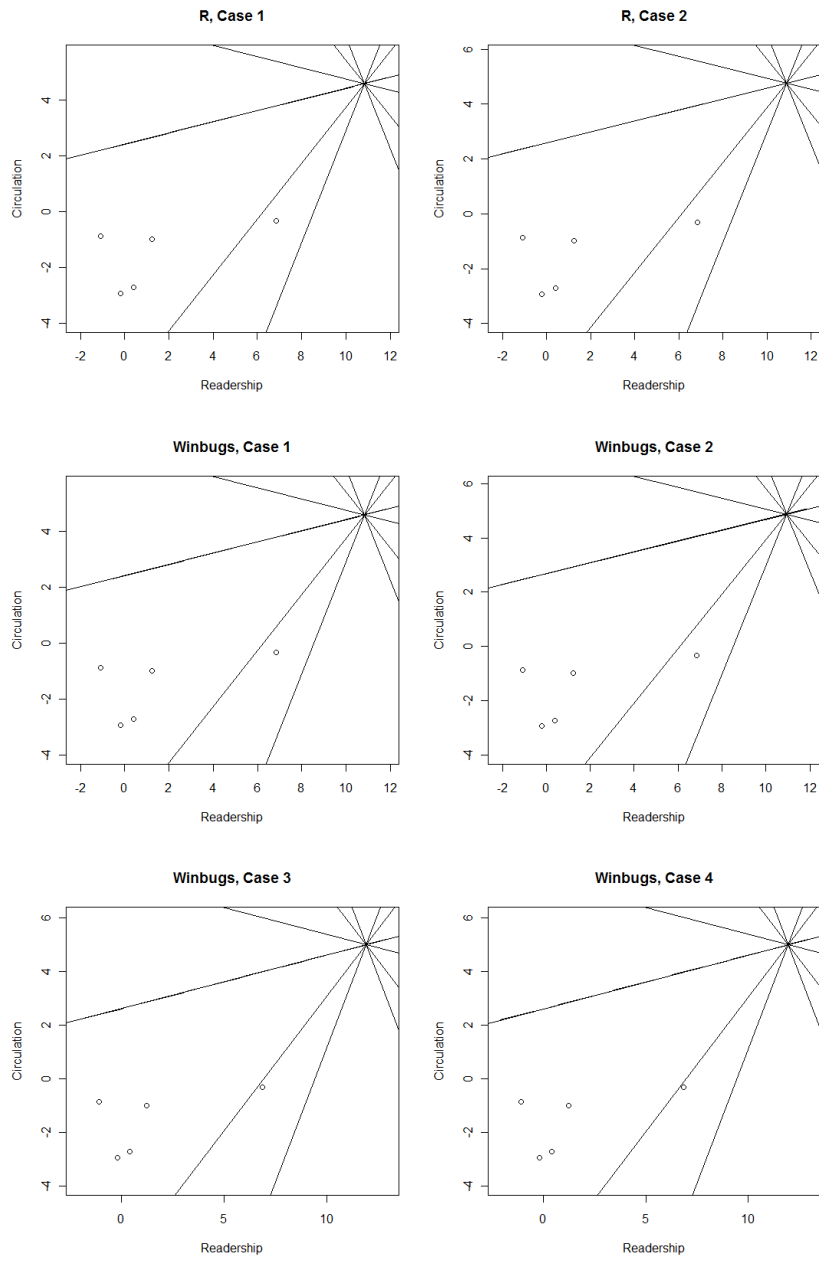


Figure 30: Isolines in the trait space of Data set 4 along with trait values for the individuals (marked as dots).

6 Discussion

As one can see from the tables in Section 5, the estimates of the model coefficients generated by the frequentist and the Bayesian approach in general seem to be very similar. The standard errors (SE) also tend to get similar values. Further, as far as the Bayesian approach is concerned, all trace and autocorrelation plots in Section 5 along with the low values of the MC errors; in general being 5% or less of the respective SEs; indicate that convergence of the MCMC algorithms being used by *Winbugs* has been reached.

The SEs of the model coefficients for the cases in which random effects (RE) of some kind were included in the model, tend to be bigger than for Case 1 in which no REs were present. This is what to be expected. The use of individual-specific REs U_i , U_j implies the presence of overdispersion as described in Section 2.1 and is a measure for how well the chosen traits describe the data given the choice of model (in this case the adjusted Bradley-Terry (BT) model (6)). Hence, the use of it implies that the chosen traits not necessarily give a satisfactory description, and the values of the model coefficients α_k might be estimated to have larger variance, i.e. be more uncertain, than what is to be expected when no REs are considered. On the other hand the contest-specific REs U_{ij} are measures for how well the adjusted BT model (6) fits the data. Hence the use of these implies that (6) might not necessarily describe the nature of the data satisfactory, giving more uncertainty and hence, more variance in the estimates.

Further, one can also notice that no 'single trait' coefficients α_k were estimated to be close to 0, except possibly the age trait coefficient for Case 2 of Data set 1. The values of the posterior probabilities, referred to as $P_{post.}(\alpha > 0)$ in the tables in Section 5, in general suggest the coefficient estimates to be significant, mainly suggesting that no traits were redundant. Using these posterior probability values it also seems like the cross-product coefficients; except for one exception; appear to be significant. The one exception is the estimate of the 'Age \times Visible badge size' coefficient for Case 4 of Data set 2 as shown in Table 3. The estimate itself is obviously close to 0 and $P_{post.}(\alpha > 0)$ lies close to 1/2. This is further confirmed by the corresponding isoline plot in Figure 15. One can see that all trait pairs for the respective individuals are distributed far away from (x_1^*, x_2^*) , the intercept point of the isolines. Hence the sparrows for this case in general all lie on the same side of a large amount of isolines, indicating a strongly transitive model. From that point of view it is not surprising that the cross-product coefficient gets as small as it does. This can also be seen more or less directly from the coordinates values $(\alpha_2/\alpha_{12}, -\alpha_1/\alpha_{12})$ of (x_1^*, x_2^*) as given in Section 1.4; the smaller the cross-product coefficient α_{12} gets, the bigger the absolute values of the coordinate values will be.

Looking at the tables in Section 5 one can see that the 'Est. dispersion parameter' output from *R* confirm that overdispersion in some amount is present in all data sets. Further, this confirms the need for including the individual-specific REs in the model as they, as

mentioned in Section 2.1, simulate overdispersion.

Comparing the SEs of the estimated \hat{p}_{ij} -s for the non-RE Case 1 with the other RE Cases 2, 3 and 4 there is no doubt that the REs do make a difference to the model fitting of the data; the SEs get significantly larger when REs of some kind are taken into account. This is also confirmed in the tables of Section 5 in which none of the REs are estimated to be non-significant. Output diagnostics for some of the \hat{p}_{ij} -s for all data sets and cases can be found in the very last part of the Appendix of this report. Here one can clearly see that the underlying variance in the \hat{p}_{ij} parameters increase when REs are used in the model. Also, comparing the plots of the prior density distribution of the standard deviations σ_a of U_i , U_j and σ_b for U_{ij} as given in Section 5 along with the corresponding kernel density plots, these figures also confirm that the REs in general do make a difference to the model fitting compared to the non-RE case. We see that for most of the cases the kernel density plots differs considerably from their respective prior plots. This would have not been the case if the REs did not contribute with relevant information about the data sets with respect to the given model fitting. Further, for the three data sets evaluated in Table 2, 4 and 6 it can be seen that a substantial part of the total variance in $\text{logit}(p_{ij})$ comes from the variance in the REs in all cases.

When it comes to intransitivity we observe from the isoline plots that all data sets in all cases; except for one exception discussed below; are evaluated to have a transitive dominance structure. In transitive cases the trait values of the individuals are not distributed around the intercept point (x_1^*, x_2^*) as described in Section 1.4. From the description of the circular property of the intransitive model and the changing of dominance magnitude along successive isolines as described in Section 1.4 it follows that an individual along an isoline will dominate all individuals distributed on the "less-dominant" side of the isoline. Hence if all individuals are distributed on one side of an isoline it is impossible to obtain the circular effect described in Section 1.4, and the underlying dominance structure of the model fitting is transitive.

According to this one can observe from the isoline plots that the dominance structure of all data sets seem to be transitive, except for Case 1 of Data set 2. In this exception, we can clearly see that both the individual-specific and the contest-specific REs make a difference; excluding them gives an intransitive model, including them gives a transitive model. For Data set 2 one can also observe that all model fittings excluding the contest-specific RE U_{ij} predict the dominance of juvenile sparrows to be more dependent on the badge size than the adult sparrows, since juveniles are distributed further away from the isoline intercept and hence, the value of the gradient vector $(\alpha_{12}(-x_2^* + x_{j2}), \alpha_{12}(x_1^* - x_{j1}))$ indicating change in dominance, gets bigger. Intuitively this observation may be regarded as sensible as one could assume the juveniles to use the badge size to compensate for lack of age in disputes with older sparrows. On the other hand, including U_{ij} , the situation is the opposite; now the adults are the ones being more dependent on the badge size. This phenomenon, that a subgroup within the

group of individuals being evaluated with the same value for a categorical trait (in this case age), changes from being more to less dependent on the second trait type in the model than the other subgroup(s) when U_{ij} is taken into account, is also observed in the 'Sex vs. Age' evaluation of Data set 3 as displayed in Figure 22.

As one can see from above, the use of REs in generalized mixed models contribute to the model fitting in several ways. In general they contribute with more information to the model fitting and hence more variance to the parameters being estimated, and from this thesis one can see some of the possible effects of this, as for example for Data set 2 in which the use of REs seemed to change the model suggested for the data set from being apparently intransitive to transitive. The use of contests-specific REs may also change to which extent a subgroup's dominance, as described above, depends on a certain trait. Hence, when fitting generalized mixed models to data sets these potential effects should be considered.

7 References

References

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The dominance matrices for Data set 3 and 4, respectively.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
1	NA	65	27	38	24	14	30	28	13	28	14	12	24	19	26	17	14	5	2	5
2	3	NA	29	72	26	18	17	56	6	16	16	15	17	14	30	15	12	12	7	4
3	5	7	NA	0	2	112	41	25	26	19	4	32	27	20	43	18	23	12	4	6
4	0	0	35	NA	21	16	31	43	13	27	25	38	38	22	23	20	19	19	13	12
5	9	0	33	3	NA	14	36	2	18	46	38	33	32	26	16	22	19	34	13	8
6	6	12	2	5	0	NA	51	4	29	14	12	31	36	22	34	19	24	14	11	6
7	4	9	0	1	1	0	NA	2	28	24	21	39	38	38	7	22	22	25	16	7
8	2	0	0	0	12	10	20	NA	11	26	10	20	14	8	33	6	16	5	8	0
9	1	0	0	1	0	0	0	2	NA	91	0	2	40	0	1	12	0	19	21	7
10	2	0	0	0	2	1	1	1	1	NA	43	86	61	39	0	67	32	33	21	10
11	0	1	0	1	3	0	1	1	25	2	NA	50	30	47	0	39	24	31	36	28
12	6	3	1	0	0	1	1	2	39	6	0	NA	52	23	24	23	43	9	24	7
13	1	1	1	0	0	0	0	2	0	0	0	1	NA	1	8	35	32	23	36	18
14	0	3	0	0	0	0	0	1	21	1	0	1	43	NA	14	0	23	16	24	9
15	0	0	0	0	0	2	1	1	23	17	7	0	2	2	NA	9	18	0	6	3
16	1	3	0	3	0	0	1	0	0	1	0	0	0	140	0	NA	27	0	68	8
17	3	6	0	2	0	0	0	0	128	0	0	0	0	0	0	1	NA	0	99	32
18	0	0	0	1	0	0	0	1	0	0	0	0	1	1	6	16	20	NA	37	0
19	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	3	0	NA	29
20	1	1	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	137	7	NA

	Aftenposten	VG	Dagbladet	BT	DN
Aftenposten	NA	543	564	903	330
VG	1134	NA	612	670	410
Dagbladet	672	313	NA	596	349
BT	458	154	119	NA	89
DN	394	176	172	256	NA

Explanatory variables for Data set 4.

	Readership	Circulation
Aftenposten	663000	239831
VG	884000	233295
Dagbladet	431000	98130
BT	232000	82432
DN	266000	80559

Winbugs implementation code for the model along with corresponding initial values for the MCMC algorithm of the Bayesian approach for Data set 1, Case 1, 2, 3 and 4, respectively.

Case 1

```
model
{
  for(i in 2:n){
    for(j in 1:(i-1)){
      X[i,j] ~ dbin(p[i,j], N[i,j])
      logit(p[i,j]) <- Age*(x[i,1] - x[j,1]) + Total.badge.size*(x[i,2] - x[j,2])
        + Int_AgeTotal.badge.size*(x[i,1] * x[j,2] - x[j,1] * x[i,2])
    }
  }

  Age ~ dnorm(0.0,1.0E-6);
  Total.badge.size ~ dnorm(0.0,1.0E-6);
  Int_AgeTotal.badge.size ~ dnorm(0.0,1.0E-6);

  p.Age <- step(Age)
  p.TBS <- step(Total.badge.size)
  p.Int <- step(Int_AgeTotal.badge.size)
}

```

```
list(Age = 0,
     Total.badge.size = 0,
     Int_AgeTotal.badge.size = 0)

```

Case 2

```
model
{
  U[1] ~ dnorm(0.0, tau)
  for(i in 2:n){
    U[i] ~ dnorm(0.0, tau)
    for(j in 1:(i-1)){
      X[i,j] ~ dbin(p[i,j], N[i,j])
      logit(p[i,j]) <- Age*(x[i,1] - x[j,1]) + Total.badge.size*(x[i,2] - x[j,2])
        + Int_AgeTotal.badge.size*(x[i,1] * x[j,2] - x[j,1] * x[i,2])
        + U[i] - U[j]
    }
  }

  Age ~ dnorm(0.0,1.0E-6);
  Total.badge.size ~ dnorm(0.0,1.0E-6);
  Int_AgeTotal.badge.size ~ dnorm(0.0,1.0E-6);
  tau ~ dgamma(1.0E-3,1.0E-3); # 1/sigma^2
  sigma <- 1.0/sqrt(tau);

  p.Age <- step(Age)
  p.TBS <- step(Total.badge.size)
  p.Int <- step(Int_AgeTotal.badge.size)
}

```

```
list(Age = 0,
     Total.badge.size = 0,
     Int_AgeTotal.badge.size = 0, tau = 10)

```

Case 3

```
model
{
  for(i in 2:n){
    for(j in 1:(i-1)){
      U[i,j] ~ dnorm(0.0, tau)
      X[i,j] ~ dbin(p[i,j], N[i,j])
      logit(p[i,j]) <- Age*(x[i,1] - x[j,1]) + Total.badge.size*(x[i,2] - x[j,2])
        + Int_AgeTotal.badge.size*(x[i,1] * x[j,2] - x[j,1] * x[i,2])
        + U[i,j]
    }
  }

  Age ~ dnorm(0.0,1.0E-6);
  Total.badge.size ~ dnorm(0.0,1.0E-6);
  Int_AgeTotal.badge.size ~ dnorm(0.0,1.0E-6);
  tau ~ dgamma(1.0E1,1.0E1); # 1/sigma^2
}

```

```

sigma <- 1.0/sqrt(tau);

p.Age <- step(Age)
p.TBS <- step(Total.badge.size)
p.Int <- step(Int_AgeTotal.badge.size)
}

list(Age = 0,
      Total.badge.size = 0,
      Int_AgeTotal.badge.size = 0, tau = 10)

Case 4

model
{
  U[1] ~ dnorm(0.0, tau)
  for(i in 2:n){
    U[i] ~ dnorm(0.0, tau)
    for(j in 1:(i-1)){
      U2[i,j] ~ dnorm(0.0, tau)
      X[i,j] ~ dbin(p[i,j], N[i,j])
      logit(p[i,j]) <- Age*(x[i,1] - x[j,1]) + Total.badge.size*(x[i,2] - x[j,2]) + Int_AgeTotal.badge.size*(x[i,1] + x[j,2]
        + U[i] - U[j] + U2[i,j])
    }
  }

  Age ~ dnorm(0.0,1.0E-6);
  Total.badge.size ~ dnorm(0.0,1.0E-6);
  Int_AgeTotal.badge.size ~ dnorm(0.0,1.0E-6);
  tau ~ dgamma(1.0E1,1.0E1); # 1/sigma^2
  sigma <- 1.0/sqrt(tau);
  tau2 ~ dgamma(1.0E0,1.0E0);
  sigma2 <- 1.0/sqrt(tau2);

  p.Age <- step(Age)
  p.TBS <- step(Total.badge.size)
  p.Int <- step(Int_AgeTotal.badge.size)
}

list(Age = 0,
      Total.badge.size = 0,
      Int_AgeTotal.badge.size = 0, tau = 10, tau2 = 10)

```

Winbugs implementation code for the model along with corresponding initial values for the MCMC algorithm of the Bayesian approach for Data set 2, Case 1, 2, 3 and 4, respectively.

```

Case 1

model
{
  for(i in 2:n){
    for(j in 1:(i-1)){
      X[i,j] ~ dbin(p[i,j], N[i,j])
      logit(p[i,j]) <- Age*(x[i,1] - x[j,1]) + Visible.badge.size*(x[i,2] - x[j,2])
        + Int_AgeVisible.badge.size*(x[i,1] * x[j,2] - x[j,1] * x[i,2])
    }
  }

  Age ~ dnorm(0.0,1.0E-6);
  Visible.badge.size ~ dnorm(0.0,1.0E-6);
  Int_AgeVisible.badge.size ~ dnorm(0.0,1.0E-6);
  p.Age <- step(Age)
  p.VBS <- step(Visible.badge.size)
  p.Int <- step(Int_AgeVisible.badge.size)
}

list(Age = 0,
      Visible.badge.size = 0,
      Int_AgeVisible.badge.size = 0)

Case 2

model
{
  U[1] ~ dnorm(0.0, tau)
  for(i in 2:n){
    U[i] ~ dnorm(0.0, tau)
    for(j in 1:(i-1)){
      X[i,j] ~ dbin(p[i,j], N[i,j])
      logit(p[i,j]) <- Age*(x[i,1] - x[j,1]) + Visible.badge.size*(x[i,2] - x[j,2]) + Int_AgeVisible.badge.size*(x[i,1] * x
+ U[i] - U[j])
    }
  }

  Age ~ dnorm(0.0,1.0E-6);
  Visible.badge.size ~ dnorm(0.0,1.0E-6);
  Int_AgeVisible.badge.size ~ dnorm(0.0,1.0E-6);
  tau ~ dgamma(1.0E-3,1.0E-3); # 1/sigma^2
  sigma <- 1.0/sqrt(tau);

##### Estimating the total variance of logit(p[i,j])
  for(i in 1:(n-1)){
    for(j in (i+1):n){
      p[i,j]<- 1-p[j,i]
    }
  }
  for(i in 1:n){
    logit(p[i,i]) <- 0
  }

  for(i in 1:n){
    for(j in 1:n){
      l[i,j] <- (logit(p[i,j]))*(logit(p[i,j]))
    }
  }

  s <- sum(l[,,])/(n*(n-1))

#####

  p.Age <- step(Age)
  p.VBS <- step(Visible.badge.size)
  p.Int <- step(Int_AgeVisible.badge.size)
}

list(Age = 0,
      Visible.badge.size = 0,
      Int_AgeVisible.badge.size = 0
      , tau = 10)

```

```

Case 3

model
{
  for(i in 2:n){
    for(j in 1:(i-1)){
      U[i,j] ~ dnorm(0.0, tau)
      X[i,j] ~ dbin(p[i,j], N[i,j])
      logit(p[i,j]) <- Age*(x[i,1] - x[j,1]) + Visible.badge.size*(x[i,2] - x[j,2]) + Int_AgeVisible.badge.size*(x[i,1] * x
+ U[i,j]
    }
  }

  Age ~ dnorm(0.0,1.0E-6);
  Visible.badge.size ~ dnorm(0.0,1.0E-6);
  Int_AgeVisible.badge.size ~ dnorm(0.0,1.0E-6);
  tau ~ dgamma(1.0E-3,1.0E-3); # 1/sigma^2
  sigma <- 1.0/sqrt(tau);

  p.Age <- step(Age)
  p.VBS <- step(Visible.badge.size)
  p.Int <- step(Int_AgeVisible.badge.size)
}

list(Age = 0,
      Visible.badge.size = 0,
      Int_AgeVisible.badge.size = 0
, tau = 10)

Case 4

model
{
  U[1] ~ dnorm(0.0, tau)
  for(i in 2:n){
    U[i] ~ dnorm(0.0, tau)
    for(j in 1:(i-1)){
      U2[i,j] ~ dnorm(0.0, tau2)
      X[i,j] ~ dbin(p[i,j], N[i,j])
      logit(p[i,j]) <- Age*(x[i,1] - x[j,1]) + Visible.badge.size*(x[i,2] - x[j,2]) + Int_AgeVisible.badge.size*(x[i,1] * x
+ U[i] - U[j] + U2[i,j]
    }
  }

  Age ~ dnorm(0.0,1.0E-6);
  Visible.badge.size ~ dnorm(0.0,1.0E-6);
  Int_AgeVisible.badge.size ~ dnorm(0.0,1.0E-6);
  tau ~ dgamma(1.0E-3,1.0E-3); # 1/sigma^2
  tau2 ~ dgamma(1.0E-3,1.0E-3);
  sigma <- 1.0/sqrt(tau);
  sigma2 <- 1.0/sqrt(tau2);

  p.Age <- step(Age)
  p.VBS <- step(Visible.badge.size)
  p.Int <- step(Int_AgeVisible.badge.size)
}

list(Age = 0,
      Visible.badge.size = 0,
      Int_AgeVisible.badge.size = 0
, tau = 10
, tau2 = 10)

```

Winbugs implementation code for the model along with corresponding initial values for the MCMC algorithm of the Bayesian approach for Data set 3, Case 1, 2, 3 and 4, respectively.

Case 1

```

model
{
  for(i in 2:n){
    for(j in 1:(i-1)){
      X[i,j] ~ dbin(p[i,j], N[i,j])
      logit(p[i,j]) <- Sex*(x[i,1] - x[j,1]) + Age*(x[i,2] - x[j,2]) + Antler.size*(x[i,3] - x[j,3])
      + Int_SexAge*(x[i,1] * x[j,2] - x[j,1] * x[i,2]) + Int_SexAntler.size*(x[i,1] * x[j,3] - x[j,1] * x[i,3])
    }
  }

  Sex ~ dnorm(0.0,1.0E-6);
  Age ~ dnorm(0.0,1.0E-6);
  Antler.size ~ dnorm(0.0,1.0E-6);
  Int_SexAge ~ dnorm(0.0,1.0E-6);
  Int_SexAntler.size ~ dnorm(0.0,1.0E-6);

  p.Sex <- step(Sex)
  p.Age <- step(Age)
  p.AS <- step(Antler.size)
  p.Int1 <- step(Int_SexAge)
  p.Int2 <- step(Int_SexAntler.size)
}

list(Sex = 0, Age = 0, Antler.size = 0, Int_SexAge = 0, Int_SexAntler.size = 0)

```

Case 2

```

model
{
  U[1] ~ dnorm(0.0, tau)
  for(i in 2:n){
    U[i] ~ dnorm(0.0, tau)
    for(j in 1:(i-1)){
      X[i,j] ~ dbin(p[i,j], N[i,j])
      logit(p[i,j]) <- Sex*(x[i,1] - x[j,1]) + Age*(x[i,2] - x[j,2]) + Antler.size*(x[i,3] - x[j,3])
      + Int_SexAge*(x[i,1] * x[j,2] - x[j,1] * x[i,2]) + Int_SexAntler.size*(x[i,1] * x[j,3] - x[j,1] * x[i,3])
      + U[i] - U[j]
    }
  }

  Sex ~ dnorm(0.0,1.0E-6);
  Age ~ dnorm(0.0,1.0E-6);
  Antler.size ~ dnorm(0.0,1.0E-6);
  Int_SexAge ~ dnorm(0.0,1.0E-6);
  Int_SexAntler.size ~ dnorm(0.0,1.0E-6);
  tau ~ dgamma(1.0E-3,1.0E-3); # 1/sigma^2
  sigma <- 1.0/sqrt(tau);

  p.Sex <- step(Sex)
  p.Age <- step(Age)
  p.AS <- step(Antler.size)
  p.Int1 <- step(Int_SexAge)
  p.Int2 <- step(Int_SexAntler.size)
}

list(Sex = 0, Age = 0, Antler.size = 0, Int_SexAge = 0, Int_SexAntler.size = 0, tau = 10)

```

Case 3

```

model
{
  for(i in 2:n){
    for(j in 1:(i-1)){
      U[i,j] ~ dnorm(0.0, tau)
      X[i,j] ~ dbin(p[i,j], N[i,j])
      logit(p[i,j]) <- Sex*(x[i,1] - x[j,1]) + Age*(x[i,2] - x[j,2]) + Antler.size*(x[i,3] - x[j,3])
      + Int_SexAge*(x[i,1] * x[j,2] - x[j,1] * x[i,2]) + Int_SexAntler.size*(x[i,1] * x[j,3] - x[j,1] * x[i,3]) + U[i,j]
    }
  }
}

```

```

}

Sex ~ dnorm(0.0,1.0E-6);
Age ~ dnorm(0.0,1.0E-6);
Antler.size ~ dnorm(0.0,1.0E-6);
Int_SexAge ~ dnorm(0.0,1.0E-6);
Int_SexAntler.size ~ dnorm(0.0,1.0E-6);
tau ~ dgamma(1.0E2,1.0E2); # 1/sigma^2
sigma <- 1.0/sqrt(tau);

p.Sex <- step(Sex)
p.Age <- step(Age)
p.AS <- step(Antler.size)
p.Int1 <- step(Int_SexAge)
p.Int2 <- step(Int_SexAntler.size)
}

list(Sex = 0, Age = 0, Antler.size = 0, Int_SexAge = 0, Int_SexAntler.size = 0, tau = 10)

Case 4

model
{
  U[1] ~ dnorm(0.0, tau)
  for(i in 2:n){
    U[i] ~ dnorm(0.0, tau)
    for(j in 1:(i-1)){
      U2[i,j] ~ dnorm(0.0, tau2)
      X[i,j] ~ dbin(p[i,j], N[i,j])
      logit(p[i,j]) <- Sex*(x[i,1] - x[j,1]) + Age*(x[i,2] - x[j,2]) + Antler.size*(x[i,3] - x[j,3])
      + Int_SexAge*(x[i,1] * x[j,2] - x[j,1] * x[i,2]) + Int_SexAntler.size*(x[i,1] * x[j,3] - x[j,1] * x[i,3])
      + U[i] - U[j] + U2[i,j]
    }
  }

  Sex ~ dnorm(0.0,1.0E-6);
  Age ~ dnorm(0.0,1.0E-6);
  Antler.size ~ dnorm(0.0,1.0E-6);
  Int_SexAge ~ dnorm(0.0,1.0E-6);
  Int_SexAntler.size ~ dnorm(0.0,1.0E-6);
  tau ~ dgamma(1.0E-3,1.0E-3); # 1/sigma^2
  tau2 ~ dgamma(1.0E1,1.0E1)
  sigma <- 1.0/sqrt(tau);
  sigma2 <- 1.0/sqrt(tau2);

  p.Sex <- step(Sex)
  p.Age <- step(Age)
  p.AS <- step(Antler.size)
  p.Int1 <- step(Int_SexAge)
  p.Int2 <- step(Int_SexAntler.size)
}

list(Sex = 0, Age = 0, Antler.size = 0, Int_SexAge = 0, Int_SexAntler.size = 0, tau = 10, tau2 = 10)

```

Winbugs implementation code for the model along with corresponding initial values for the MCMC algorithm of the Bayesian approach for Data set 4, Case 1, 2, 3 and 4, respectively.

```

Case 1
model
{
  for(i in 2:n){
    for(j in 1:(i-1)){
      X[i,j] ~ dbin(p[i,j], N[i,j])
      logit(p[i,j]) <- Readership*(x[i,1] - x[j,1]) + Circulation*(x[i,2] - x[j,2])
      + Int_ReadershipCirculation*(x[i,1] * x[j,2] - x[j,1] * x[i,2])
    }
  }
  Readership ~ dnorm(0.0,1.0E-6);
  Circulation ~ dnorm(0.0,1.0E-6);
  Int_ReadershipCirculation ~ dnorm(0.0,1.0E-6);

  p.R <- step(Readership)
  p.C <- step(Circulation)
  p.Int <- step(Int_ReadershipCirculation)
}

list(Readership = 0,
     Circulation = 0,
     Int_ReadershipCirculation = 0)

Case 2
model
{
  U[1] ~ dnorm(0.0, tau)
  for(i in 2:n){
    U[i] ~ dnorm(0.0, tau)
    for(j in 1:(i-1)){
      X[i,j] ~ dbin(p[i,j], N[i,j])
      logit(p[i,j]) <- Readership*(x[i,1] - x[j,1]) + Circulation*(x[i,2] - x[j,2]) + Int_ReadershipCirculation*(x[i,1] * x[j,2] - x[j,1] * x[i,2])
      + U[i] - U[j]
    }
  }
  Readership ~ dnorm(0.0,1.0E-6);
  Circulation ~ dnorm(0.0,1.0E-6);
  Int_ReadershipCirculation ~ dnorm(0.0,1.0E-6);
  tau ~ dgamma(1.0E-3,1.0E-3); # 1/sigma^2
  sigma <- 1.0/sqrt(tau);

  p.R <- step(Readership)
  p.C <- step(Circulation)
  p.Int <- step(Int_ReadershipCirculation)
}

list(Readership = 0,
     Circulation = 0,
     Int_ReadershipCirculation = 0,
     tau = 10)

Case 3
model
{
  for(i in 2:n){
    for(j in 1:(i-1)){
      U[i,j] ~ dnorm(0.0, tau)
      X[i,j] ~ dbin(p[i,j], N[i,j])
      logit(p[i,j]) <- Readership*(x[i,1] - x[j,1]) + Circulation*(x[i,2] - x[j,2]) + Int_ReadershipCirculation*(x[i,1] * x[j,2] - x[j,1] * x[i,2])
      + U[i,j]
    }
  }
  Readership ~ dnorm(0.0,1.0E-6);
  Circulation ~ dnorm(0.0,1.0E-6);
}

```



```

    Int_ReadershipCirculation ~ dnorm(0.0,1.0E-6);
    tau ~ dgamma(1.0E-3,1.0E-3); # 1/sigma^2
    sigma <- 1.0/sqrt(tau);

    p.R <- step(Readership)
    p.C <- step(Circulation)
    p.Int <- step(Int_ReadershipCirculation)
  }

list(Readership = 0,
     Circulation = 0,
     Int_ReadershipCirculation = 0,
     tau = 10)

Case 4
model
{
  U[1] ~ dnorm(0.0, tau)
  for(i in 2:n){
    U[i] ~ dnorm(0.0, tau)
    for(j in 1:(i-1)){
      U2[i,j] ~ dnorm(0.0, tau2)
      X[i,j] ~ dbin(p[i,j], N[i,j])
      logit(p[i,j]) <- Readership*(x[i,1] - x[j,1]) + Circulation*(x[i,2] - x[j,2]) + Int_ReadershipCirculation*(x[i,1] * x
      + U[i] - U[j] + U2[i,j]
    }
  }

  Readership ~ dnorm(0.0,1.0E-6);
  Circulation ~ dnorm(0.0,1.0E-6);
  Int_ReadershipCirculation ~ dnorm(0.0,1.0E-6);
  tau ~ dgamma(1.0E-3,1.0E-3); # 1/sigma^2
  sigma <- 1.0/sqrt(tau);
  tau2 ~ dgamma(1.0E-3,1.0E-3); # 1/sigma^2
  sigma2 <- 1.0/sqrt(tau2);

  p.R <- step(Readership)
  p.C <- step(Circulation)
  p.Int <- step(Int_ReadershipCirculation)
}

list(Readership = 0,
     Circulation = 0,
     Int_ReadershipCirculation = 0,
     tau = 10,
     tau2 = 10)

```

Winbugs implementation code for the dominance matrices of Data set 1, 2, 3 and 4, respectively.

```
list(X = structure(.Data = c(NA, 6, 11, 1, 3, 4, 4, 10, 4,
7, 8, 6, 27, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, 0, NA, NA, 1,
3, NA, NA, 5, 12, 3, 7, 4, 25, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
0, NA, NA, 7, 13, 9, NA, 7, NA, 1, 10, 1, 14, NA, NA, NA, NA,
NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA, NA, NA, 0, 0, 0, NA, 5, 8, 2, 6, 2, NA, NA, 3, 4, NA,
NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA, NA, NA, NA, NA, NA, NA, 0, 0, 0, 0, NA, NA, NA, NA, 2, NA,
NA, 3, 3, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, 0, NA, 0, 0, NA,
NA, NA, 3, 8, NA, 4, 1, 18, NA, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, 0,
NA, NA, 0, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, 8, NA, NA, NA, NA,
NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA, NA, NA, 0, 0, 0, 0, NA, 0, NA, NA, NA, 2, 7, 1, 27, NA,
NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA, NA, NA, NA, NA, NA, NA, 0, 0, NA, 0, 0, 0, NA, NA, NA, NA,
1, 3, 33, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, 0, 0, 0, NA, NA,
NA, NA, 0, NA, NA, NA, NA, NA, NA, 13, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
0, 0, 0, NA, NA, 0, NA, 0, 0, NA, NA, NA, 12, NA, NA, NA, NA,
NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA, NA, NA, 0, 0, 0, 0, 0, 0, NA, 0, 0, NA, NA, NA, 21, NA,
NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA, NA, NA, NA, NA, NA, NA, 14, 2, 0, 0, 0, 0, 0, 0, 0, 0,
0, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA, NA, NA, NA, NA, NA, NA, NA, 7, 13, 1, 14, 6, 2, 7, 4, 13,
NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, 0, NA, 17, 2, 56,
32, 25, 25, 3, 25, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
0, 0, NA, 2, 33, 8, 12, 12, 4, 18, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA, NA, NA, 0, 0, 0, NA, 6, NA, 1, 6, NA, 9, NA, NA, NA,
NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA, NA, NA, NA, NA, NA, NA, 0, 0, 6, 0, NA, 25, 25, 25, 12,
41, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, 0, 0, 0, NA,
0, NA, 8, 17, 3, 18, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
NA, 0, 0, 0, 0, 4, 0, NA, 31, 3, 9, NA, NA, NA, NA, NA, NA, NA,
NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA, NA, NA, 0, 0, 0, 0, 0, 0, 0, NA, 6, 69, NA, NA, NA, NA,
NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA, NA, NA, NA, NA, NA, 0, 0, 0, NA, 0, 0, 0, 0, NA, 12,
NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, 0, 0, 0, 0, 0,
0, 13, 0, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
19, 46, 23, 34, 2, 25, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, 0, NA,
16, NA, 5, 2, 2, 18, 7, 7, 14, 11, NA, 9, NA, NA, NA, NA, NA,
NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA, 0, 0, NA, NA, 11, 16, NA, 5, 9, NA, 12, NA, 7, 2, NA,
NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA, NA, NA, NA, NA, 0, NA, NA, NA, 2, NA, 5, 9, NA, 14, 12,
7, NA, 4, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, 0, 0, 0, 0, NA, 3, 11,
NA, 12, 4, NA, 5, 4, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, 0, 0,
0, NA, 0, NA, 1, NA, NA, NA, NA, 5, NA, NA, NA, NA, NA, NA, NA,
NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA, 0, 0, NA, 0, 0, 0, NA, 2, NA, NA, 12, 2, NA, 4, NA, NA,
NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA, NA, NA, NA, 0, 0, 0, 0, NA, NA, 0, NA, 12, 4, 2, NA,
NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, 0, NA, NA, 0,
NA, 2, NA, 5, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, 0, 0, NA,
0, 0, NA, NA, 0, 0, NA, NA, NA, 1, NA, NA, NA, NA, NA, NA, NA,
NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
NA, 0, 0, 0, 0, NA, NA, 0, 0, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
```

```

NA, NA, NA, NA, NA, 0, 0, NA, 0, 0, 0, 0, NA, 0, NA, NA, NA,
NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA, NA, NA, NA, NA, NA, NA, NA, 0, NA, 0, NA, 0, NA, NA,
NA, NA, 0, NA, NA, NA, 1, NA, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, 0,
0, 0, NA, NA, 0, NA, NA, NA, NA, 0, NA), .Dim = c(37,37)),
N = structure(.Data = c(1, 6, 11, 1, 3, 4, 4, 10, 4, 7, 8, 6, 41,
1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
1, 1, 1, 6, 1, 1, 1, 3, 1, 1, 5, 12, 3, 7, 4, 27, 1, 1, 1, 1,
1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 11,
1, 1, 7, 13, 9, 1, 7, 1, 1, 10, 1, 14, 1, 1, 1, 1, 1, 1, 1, 1,
1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 7, 1, 5,
8, 2, 6, 2, 1, 1, 3, 4, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 3, 3, 13, 5, 1, 1, 1, 2,
1, 1, 3, 3, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
1, 1, 1, 1, 1, 1, 1, 4, 1, 9, 8, 1, 1, 1, 3, 8, 1, 4, 1, 18,
1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
1, 1, 1, 4, 1, 1, 2, 1, 1, 1, 1, 1, 1, 1, 1, 8, 1, 1, 1, 1, 1,
1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 10,
5, 7, 6, 1, 3, 1, 1, 1, 2, 7, 1, 27, 1, 1, 1, 1, 1, 1, 1, 1,
1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 4, 12, 1, 2,
2, 8, 1, 1, 1, 1, 1, 3, 33, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 7, 3, 1, 1, 1, 1, 2,
1, 1, 1, 1, 13, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
1, 1, 1, 1, 1, 1, 1, 1, 1, 8, 7, 10, 1, 1, 4, 1, 7, 1, 1, 1,
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1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 7, 1, 17, 2, 56, 32, 25, 25, 3,
25, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
1, 1, 1, 1, 1, 1, 1, 1, 13, 17, 1, 2, 39, 8, 12, 12, 4, 18, 1,
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14, 56, 39, 6, 1, 25, 29, 25, 12, 41, 1, 1, 1, 1, 1, 1, 1, 1,
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8, 1, 25, 1, 8, 17, 3, 18, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 25, 12, 1, 29,
8, 1, 31, 3, 9, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 7, 25, 12, 6, 25, 17, 31,
1, 6, 82, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
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1, 1, 1, 1, 1, 1, 13, 25, 18, 9, 41, 18, 9, 82, 12, 1, 1, 1,
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41, 19, 46, 23, 34, 2, 25, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 28, 1, 16, 1, 5, 2, 2, 18,
7, 7, 14, 11, 1, 9, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
1, 1, 1, 1, 1, 1, 1, 1, 1, 23, 16, 1, 1, 11, 16, 1, 5, 9, 1,
12, 1, 7, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
1, 1, 1, 1, 1, 1, 30, 1, 1, 1, 2, 1, 5, 9, 1, 14, 12, 7, 1,
4, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
1, 1, 1, 5, 5, 11, 2, 1, 3, 11, 1, 12, 4, 1, 5, 4, 1, 1, 1, 1,
1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 4,
2, 16, 1, 3, 1, 1, 1, 1, 1, 5, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 41, 2, 1, 5,
11, 1, 1, 2, 1, 1, 12, 2, 1, 4, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 19, 18, 5, 9, 1, 1, 2,
1, 12, 4, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
1, 1, 1, 1, 1, 1, 1, 1, 1, 46, 7, 9, 1, 12, 1, 1, 12, 1, 2,
1, 5, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
1, 1, 1, 1, 1, 1, 23, 7, 1, 14, 4, 1, 1, 4, 2, 1, 1, 1, 1, 1,
1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
1, 1, 34, 14, 12, 12, 1, 1, 12, 2, 1, 1, 1, 1, 1, 1, 1, 1,
1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2,
11, 1, 7, 5, 5, 2, 1, 5, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 25, 1, 7, 1,
4, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 9, 2, 4, 1, 1, 4, 1, 1,
1, 1, 1, 1, 1), .Dim = c(37,37)), x = structure(.Data = c(-1, 0.196334737626553,
-1, -1.49663641097529, -1, 1.41219583525878, 1, -1.71210546625189,
1, 1.2428987203986, 1, -0.773276011118138, -1, -1.40429253014246,
1, -1.71210546625189, -1, -1.23499541528228, 1, -0.511635015425126,
-1, -1.05030765361662, -1, -0.650150836674368, -1, -1.55819899819717,
1, 1.90469653303387, 1, 1.22750807359313, 1, 1.10438289914936,
1, 0.935085784289175, -1, 0.76578866942899, -1, 0.627272848179749,
1, 0.304069265264852, -1, -0.0191343176500451, 1, -0.173040785704758,
-1, -0.357728547370413, 1, 1.38141454164784, 1, 1.28907066081501,

```



```
1361, 824, 715, 1, 345, 724, 586, 521, 345, 1), .Dim = c(5,5)),
x = structure(.Data = c(1.23793068897421, -0.987599731889648, 6.847751184396,
-0.317576409654443, 0.398104187346705, -2.71118012801022, -1.08285211600846,
-0.863691692046816, -0.199186212517686, -2.92490502155532), .Dim = c(5,
2)), n = 5)
```

R functions made by the author of this report.

```
intransitiveModel3 = function(dominanceMatrix, covariateMatrix, interactionVector = 0, randomEffect = 1){
# This function uses the BIm[Bradley-Terry2] function to fit data sets to an intransitive extension (optional)
# of the Bradley-Terry model including individual-specific random effects (optional).

# interactionVector is as vector containing the indices of the covariates for which the interaction parameter
# is to be computed. # I.e., if interactionVector = c(i,j,i,k), the interaction parameter between the i-th
# and the j-th as well as the i-th and the k-th # covariate value columns (from left to right) in covariateMatrix
# are computed.

  nInteractions = 0

  playerNames = c("Ind1","Ind2")

  covNames = colnames(covariateMatrix)

  pred = covariateMatrix
  nCovariates = dim(pred)[2]

  contests = countsToBinomial(dominanceMatrix)
  names(contests)[1:2] = playerNames

  if(length(interactionVector) > 1){
    p1 = contests[,1]
    p2 = contests[,2]
    interactions1 = matrix(NA,length(p1),length(interactionVector)/2)
    interactions2 = matrix(NA,length(p2),length(interactionVector)/2)

    intLength = dim(interactions1)[1]
    nInteractions = dim(interactions1)[2]

    for(i in 1:nInteractions){

      interactions1[,i] = pred[p1[1:intLength], interactionVector[2*i-1]]*pred[p2[1:intLength], interactionVector[2*i]]
      interactions2[,i] = pred[p2[1:intLength], interactionVector[2*i-1]]*pred[p1[1:intLength], interactionVector[2*i]]

    }

    contests = data.frame(contests)

    interactionNames = matrix('', 1, nInteractions)
    for(i in 1:nInteractions){
      interactionNames[i] = paste('Int_', covNames[interactionVector[2*i-1]], covNames[interactionVector[2*i]], sep = '')
    }

    contestsIndCmds = matrix('', 1, 2)
    contestsIndCmds[1] = 'contests$Ind1 = data.frame(Individual = contests$Ind1, '
    contestsIndCmds[2] = 'contests$Ind2 = data.frame(Individual = contests$Ind2, '
    for(i in 1:nInteractions){
      contestsIndCmds[1] = paste(contestsIndCmds[1], interactionNames[i], ' = interactions1[,', i, ']', sep = '')
      contestsIndCmds[2] = paste(contestsIndCmds[2], interactionNames[i], ' = interactions2[,', i, ']', sep = '')
    }
    contestsIndCmds = substr(contestsIndCmds, 1, nchar(contestsIndCmds)-1)
    contestsIndCmds = paste(contestsIndCmds, ')', sep = '')

    contests$Ind1 = eval(parse(text=contestsIndCmds[1]))
    contests$Ind2 = eval(parse(text=contestsIndCmds[2]))
  }

  Individual = matrix(1:dim(pred)[1],dim(pred)[1],1)
  colnames(Individual) = 'Individual'
  pred = data.frame(cbind(Individual, pred))

  data = list(contests, pred)
  names(data) = c('contests','predictions')

  formula = ''
  for(i in 1:nCovariates){
    formula = paste(formula,covNames[i],'[Individual]+',sep='')
  }

  if(nInteractions == 1){
    formula = paste(formula, interactionNames, '+',sep='')
  }
}
```

```

    if(nInteractions > 1){
      for(i in 1:nInteractions){
        formula = paste(formula, interactionNames[i], '+', sep='')
      }
    }
    if(randomEffect){
      formula = paste(formula, '(1|Individual)', sep='')
    } else{
      formula = substr(formula, 1, nchar(formula)-1)
    }

    modelCommand = paste('model = BIm(cbind(win1,win2), Ind1, Ind2, ~', formula, ', data=data, id="Individual")')
    model = eval(parse(text=modelCommand))

    return(list(data = data, model = model, summary = summary(model)))
  }

sigmaDist = function(a,b, values){
# This function returns prior distribution values for the sigma parameter, sigma being the standard deviation of the random effects.
  return(((2)*(b^a)/gamma(a))*(values^(-(2*a+1)))*exp(-b*values^(-2)))
}

isolines = function(a, b, c, covariateMatrix, traitIndices, filename, main, type = 'png'){
# Plots the isolines of a data set in the trait space as given by the vector traitIndices giving the indices of the columns of covariateMatrix
# which the specified trait are to be subtracted. a, b and c are model coefficients.
  X = covariateMatrix[,traitIndices[1]]
  Y = covariateMatrix[,traitIndices[2]]
  A = c(0.2, 1, 2, -0.2, -1, -2)
  B = -a/c - A*(b/c)

  curve(A[1]*x + B[1], xlim = c(min(X, b/c)-1, max(X, b/c)+1), ylim = c(min(Y, -a/c)-1, max(Y, -a/c)+1),
        xlab = colnames(covariateMatrix)[traitIndices[1]], ylab = colnames(covariateMatrix)[traitIndices[2]],
        main = main)

  points(X, Y)

  for(i in 1:length(A)){
    abline(B[i], A[i])
  }

  savePlot(filename, type)
}

```

Output diagnostics for 10 of the first estimated p_{ij} for each case of each data set.

Data set 1

Case 1

```

node mean sd MC error 2.5% median 97.5% start sample
p[2,1] 0.02577 0.0053 1.04E-4 0.01687 0.02497 0.03762 100000 2000
p[3,1] 0.9318 0.009577 1.868E-4 0.9112 0.9329 0.9488 100000 2000
p[3,2] 0.998 7.415E-4 1.479E-5 0.9962 0.9982 0.9991 100000 2000
p[4,1] 0.03007 0.007967 1.611E-4 0.0175 0.0289 0.04761 100000 2000
p[4,2] 0.738 0.04701 0.001158 0.6375 0.7409 0.821 100000 2000
p[4,3] 0.001232 5.236E-4 1.036E-5 5.211E-4 0.001123 0.002602 100000 2000
p[5,1] 0.9457 0.00833 1.985E-4 0.9279 0.9465 0.9604 100000 2000
p[5,2] 0.9994 2.43E-4 5.725E-6 0.9988 0.9994 0.9997 100000 2000
p[5,3] 0.4012 0.04289 9.141E-4 0.3166 0.4014 0.4846 100000 2000
p[5,4] 0.9996 1.884E-4 4.281E-6 0.9991 0.9996 0.9999 100000 2000

```

Case 2

node mean sd MC error 2.5% median 97.5% start sample
 p[2,1] 0.6152 0.1255 0.002827 0.3552 0.621 0.8405 100000 2000
 p[3,1] 0.4288 0.1179 0.002521 0.2155 0.4235 0.6725 100000 2000
 p[3,2] 0.325 0.1397 0.003302 0.1026 0.3098 0.6393 100000 2000
 p[4,1] 0.6795 0.1369 0.003623 0.382 0.6934 0.9049 100000 2000
 p[4,2] 0.9219 0.06994 0.00162 0.7249 0.9428 0.9924 100000 2000
 p[4,3] 0.3492 0.126 0.002952 0.1338 0.3375 0.6147 100000 2000
 p[5,1] 0.03138 0.02843 5.995E-4 0.004294 0.02334 0.1065 100000 2000
 p[5,2] 0.1699 0.0968 0.002125 0.03847 0.1505 0.4116 100000 2000
 p[5,3] 0.009012 0.01117 2.568E-4 5.699E-4 0.005218 0.04179 100000 2000
 p[5,4] 0.4567 0.1644 0.00398 0.1561 0.4531 0.775 100000 2000

Case 3

node mean sd MC error 2.5% median 97.5% start sample
 p[2,1] 0.004705 0.02359 4.72E-4 1.813E-16 4.293E-7 0.05484 100000 2000
 p[3,1] 0.01687 0.03636 8.898E-4 4.287E-9 0.001774 0.1323 100000 2000
 p[3,2] 0.98 0.1201 0.002288 0.7864 1.0 1.0 100000 2000
 p[4,1] 0.01922 0.08624 0.002189 9.725E-17 3.725E-7 0.2693 100000 2000
 p[4,2] 0.08793 0.1872 0.004665 4.453E-11 0.002724 0.7285 100000 2000
 p[4,3] 5.793E-4 0.005815 1.464E-4 0.0 1.441E-11 0.0013 100000 2000
 p[5,1] 0.0549 0.1078 0.002396 1.673E-8 0.006063 0.3799 100000 2000
 p[5,2] 0.09719 0.1459 0.00352 2.336E-6 0.02863 0.52 100000 2000
 p[5,3] 0.007166 0.02085 4.522E-4 1.611E-12 7.704E-5 0.06987 100000 2000
 p[5,4] 0.06906 0.1036 0.002385 5.146E-6 0.02557 0.3761 100000 2000

Case 4

node mean sd MC error 2.5% median 97.5% start sample
 p[2,1] 0.01744 0.04513 0.001049 3.966E-9 7.561E-4 0.1553 100000 2000
 p[3,1] 0.0286 0.0477 9.726E-4 1.264E-6 0.007987 0.1678 100000 2000
 p[3,2] 0.8472 0.3071 0.005956 0.002914 0.9993 1.0 100000 2000
 p[4,1] 0.0665 0.1569 0.003729 7.845E-9 0.002077 0.6502 100000 2000
 p[4,2] 0.1783 0.2534 0.004913 4.609E-6 0.04921 0.9004 100000 2000
 p[4,3] 0.00974 0.0333 8.004E-4 7.406E-11 1.091E-4 0.09691 100000 2000
 p[5,1] 0.02254 0.06366 0.001382 2.747E-9 5.49E-4 0.2344 100000 2000
 p[5,2] 0.06215 0.1117 0.002291 9.555E-7 0.01248 0.4171 100000 2000
 p[5,3] 0.004745 0.01644 3.808E-4 9.015E-12 4.608E-5 0.04778 100000 2000
 p[5,4] 0.04867 0.08486 0.001856 1.08E-6 0.01137 0.322 100000 2000

Data set 2

Case 1

node mean sd MC error 2.5% median 97.5% start sample
 p[2,1] 0.4304 0.04036 8.123E-4 0.3483 0.4311 0.5079 100000 2000
 p[3,1] 0.4673 0.02003 4.078E-4 0.4263 0.4677 0.5048 100000 2000
 p[3,2] 0.5351 0.02037 4.075E-4 0.4965 0.5346 0.5773 100000 2000
 p[4,1] 0.4558 0.03564 7.705E-4 0.3843 0.4561 0.5246 100000 2000
 p[4,2] 0.4998 0.01683 3.911E-4 0.4667 0.5 0.532 100000 2000
 p[4,3] 0.4777 0.02051 4.571E-4 0.4362 0.4781 0.5174 100000 2000
 p[5,1] 0.4375 0.03886 7.958E-4 0.3598 0.4379 0.5114 100000 2000
 p[5,2] 0.5 0.004737 1.101E-4 0.4906 0.5 0.509 100000 2000
 p[5,3] 0.4685 0.01992 4.095E-4 0.4279 0.4688 0.5062 100000 2000
 p[5,4] 0.5001 0.0121 2.813E-4 0.477 0.5 0.5241 100000 2000

Case 2

node mean sd MC error 2.5% median 97.5% start sample
 p[2,1] 0.2315 0.05503 0.001197 0.132 0.2279 0.3529 100000 2000
 p[3,1] 0.322 0.2129 0.004284 0.02987 0.2769 0.8106 100000 2000
 p[3,2] 0.5518 0.232 0.004535 0.09147 0.5583 0.9345 100000 2000
 p[4,1] 0.4757 0.08244 0.001612 0.3163 0.4752 0.6364 100000 2000
 p[4,2] 0.7322 0.05551 0.001348 0.6131 0.7349 0.8345 100000 2000
 p[4,3] 0.6527 0.2195 0.004227 0.1646 0.7001 0.9671 100000 2000
 p[5,1] 0.2462 0.06494 0.00147 0.1305 0.241 0.3856 100000 2000
 p[5,2] 0.5114 0.07099 0.001544 0.3687 0.5144 0.6432 100000 2000
 p[5,3] 0.46 0.2326 0.00426 0.0717 0.459 0.9127 100000 2000
 p[5,4] 0.2783 0.06599 0.001913 0.1575 0.2755 0.4173 100000 2000

Case 3

node mean sd MC error 2.5% median 97.5% start sample
 p[2,1] 0.1279 0.06407 0.00146 0.03273 0.1185 0.2782 100000 2000
 p[3,1] 0.4627 0.269 0.006475 0.03099 0.4499 0.9388 100000 2000
 p[3,2] 0.5457 0.2646 0.00543 0.07084 0.5625 0.9638 100000 2000
 p[4,1] 0.3625 0.1055 0.002194 0.1669 0.3629 0.5742 100000 2000
 p[4,2] 0.7866 0.07093 0.001341 0.6316 0.7934 0.9062 100000 2000
 p[4,3] 0.4999 0.2674 0.005612 0.04224 0.5048 0.947 100000 2000
 p[5,1] 0.3012 0.1064 0.00206 0.1162 0.2902 0.5221 100000 2000
 p[5,2] 0.2198 0.09287 0.001948 0.07352 0.2082 0.4248 100000 2000

p[5,3] 0.4704 0.2684 0.007193 0.03375 0.4607 0.9381 100000 2000
 p[5,4] 0.4926 0.1346 0.00349 0.2297 0.4935 0.7529 100000 2000

Case 4

node mean sd MC error 2.5% median 97.5% start sample
 p[2,1] 0.1557 0.06878 0.001819 0.04747 0.1472 0.3151 100000 2000
 p[3,1] 0.3739 0.252 0.004517 0.02741 0.3247 0.9071 100000 2000
 p[3,2] 0.5633 0.2558 0.006081 0.0676 0.5867 0.9649 100000 2000
 p[4,1] 0.4045 0.1035 0.002621 0.2119 0.4024 0.6035 100000 2000
 p[4,2] 0.7792 0.0682 0.001565 0.6306 0.7846 0.8969 100000 2000
 p[4,3] 0.6267 0.2528 0.005901 0.09617 0.6882 0.9751 100000 2000
 p[5,1] 0.2887 0.1013 0.002479 0.1214 0.2786 0.5134 100000 2000
 p[5,2] 0.3082 0.1109 0.003557 0.1188 0.302 0.5443 100000 2000
 p[5,3] 0.4721 0.2615 0.005875 0.03903 0.4674 0.9448 100000 2000
 p[5,4] 0.4075 0.1288 0.003235 0.1804 0.397 0.6786 100000 2000

Data set 3

Case 1

node mean sd MC error 2.5% median 97.5% start sample
 p[2,1] 0.5 0.0 2.236E-12 0.5 0.5 0.5 100000 2000
 p[3,1] 0.1117 0.01047 2.154E-4 0.09226 0.1112 0.1331 100000 2000
 p[3,2] 0.1117 0.01047 2.154E-4 0.09226 0.1112 0.1331 100000 2000
 p[4,1] 0.5279 0.00982 2.116E-4 0.509 0.5277 0.5472 100000 2000
 p[4,2] 0.5279 0.00982 2.116E-4 0.509 0.5277 0.5472 100000 2000
 p[4,3] 0.9631 0.00519 1.192E-4 0.9523 0.9634 0.9724 100000 2000
 p[5,1] 0.2651 0.007621 1.734E-4 0.2508 0.2651 0.2803 100000 2000
 p[5,2] 0.2651 0.007621 1.734E-4 0.2508 0.2651 0.2803 100000 2000
 p[5,3] 0.6818 0.01674 3.317E-4 0.6478 0.6821 0.714 100000 2000
 p[5,4] 0.244 0.01139 2.353E-4 0.2228 0.2441 0.2673 100000 2000

Case 2

node mean sd MC error 2.5% median 97.5% start sample
 p[2,1] 0.3113 0.03955 7.458E-4 0.2377 0.3103 0.3904 200000 4000
 p[3,1] 0.1259 0.02444 4.655E-4 0.08225 0.1242 0.1776 200000 4000
 p[3,2] 0.2413 0.03582 5.307E-4 0.1771 0.2398 0.3186 200000 4000
 p[4,1] 0.1734 0.02921 4.591E-4 0.1201 0.1714 0.2346 200000 4000
 p[4,2] 0.3165 0.03582 5.472E-4 0.2479 0.3155 0.3899 200000 4000
 p[4,3] 0.807 0.03539 6.387E-4 0.7333 0.8092 0.8695 200000 4000
 p[5,1] 0.2046 0.03465 6.64E-4 0.1419 0.2029 0.2777 200000 4000
 p[5,2] 0.3623 0.04411 7.066E-4 0.2794 0.3615 0.4545 200000 4000
 p[5,3] 0.55 0.04882 7.811E-4 0.4516 0.5501 0.6467 200000 4000
 p[5,4] 0.5505 0.04753 7.655E-4 0.456 0.5507 0.6422 200000 4000

Case 3

node mean sd MC error 2.5% median 97.5% start sample
 p[2,1] 0.0542 0.02665 5.696E-4 0.01543 0.05011 0.1177 100000 2000
 p[3,1] 0.1513 0.06055 0.001444 0.05196 0.145 0.2834 100000 2000
 p[3,2] 0.188 0.06144 0.001243 0.08467 0.1816 0.3219 100000 2000
 p[4,1] 0.02863 0.02491 5.902E-4 0.002003 0.02152 0.09487 100000 2000
 p[4,2] 0.01659 0.01369 2.916E-4 0.001533 0.01299 0.05258 100000 2000
 p[4,3] 0.9871 0.01573 3.92E-4 0.9426 0.9926 0.9997 100000 2000
 p[5,1] 0.2716 0.07584 0.001851 0.1398 0.2654 0.4365 100000 2000
 p[5,2] 0.02507 0.02598 5.947E-4 0.001042 0.01707 0.09739 100000 2000
 p[5,3] 0.9256 0.04264 0.001043 0.816 0.9341 0.9853 100000 2000
 p[5,4] 0.1278 0.06544 0.001367 0.03262 0.1159 0.2875 100000 2000

Case 4

node mean sd MC error 2.5% median 97.5% start sample
 p[2,1] 0.04813 0.02511 5.635E-4 0.01262 0.04408 0.105 100000 2000
 p[3,1] 0.1609 0.06142 0.001218 0.05998 0.1541 0.3013 100000 2000
 p[3,2] 0.1975 0.06438 0.001541 0.08615 0.1925 0.3365 100000 2000
 p[4,1] 0.01076 0.01496 3.47E-4 2.389E-5 0.004951 0.05217 100000 2000
 p[4,2] 0.005885 0.008182 1.471E-4 2.387E-5 0.002795 0.02889 100000 2000
 p[4,3] 0.991 0.01362 2.71E-4 0.9538 0.9966 1.0 100000 2000
 p[5,1] 0.2777 0.07574 0.001789 0.1434 0.2728 0.4346 100000 2000
 p[5,2] 0.01566 0.02261 4.233E-4 3.307E-5 0.006975 0.08056 100000 2000
 p[5,3] 0.9384 0.03897 8.874E-4 0.8417 0.9462 0.9897 100000 2000
 p[5,4] 0.1345 0.06633 0.001307 0.03173 0.1259 0.2854 100000 2000

Data set 4

Case 1

node mean sd MC error 2.5% median 97.5% start sample
 p[2,1] 0.711 0.007451 1.48E-4 0.6968 0.711 0.7262 100000 2000
 p[3,1] 0.6059 0.007077 1.314E-4 0.592 0.606 0.6197 100000 2000
 p[3,2] 0.31 0.01137 2.451E-4 0.2877 0.31 0.333 100000 2000

```

p[4,1] 0.3747 0.004172 8.234E-5 0.3663 0.3746 0.3827 100000 2000
p[4,2] 0.2091 0.01013 1.991E-4 0.1894 0.209 0.2296 100000 2000
p[4,3] 0.2515 0.009396 1.913E-4 0.2335 0.2514 0.2705 100000 2000
p[5,1] 0.5948 0.007826 1.455E-4 0.5795 0.5948 0.6097 100000 2000
p[5,2] 0.2942 0.01201 2.588E-4 0.2707 0.2941 0.3186 100000 2000
p[5,3] 0.4807 0.001229 2.667E-5 0.4783 0.4807 0.4831 100000 2000
p[5,4] 0.7436 0.01042 2.127E-4 0.7223 0.7436 0.7634 100000 2000

```

Case 2

```

node mean sd MC error 2.5% median 97.5% start sample
p[2,1] 0.6707 0.009517 2.224E-4 0.6519 0.6706 0.6896 100000 2000
p[3,1] 0.5973 0.01018 2.021E-4 0.5772 0.5976 0.6171 100000 2000
p[3,2] 0.3431 0.01276 2.462E-4 0.3185 0.3431 0.3678 100000 2000
p[4,1] 0.3104 0.009524 2.176E-4 0.2914 0.3106 0.3287 100000 2000
p[4,2] 0.1936 0.00959 2.155E-4 0.1755 0.1933 0.2127 100000 2000
p[4,3] 0.2072 0.009873 2.054E-4 0.189 0.2072 0.2278 100000 2000
p[5,1] 0.5156 0.01282 2.711E-4 0.4912 0.516 0.5413 100000 2000
p[5,2] 0.267 0.01213 2.43E-4 0.2425 0.267 0.2913 100000 2000
p[5,3] 0.4103 0.01316 3.067E-4 0.3854 0.4104 0.4366 100000 2000
p[5,4] 0.7371 0.01363 3.255E-4 0.71 0.7372 0.7632 100000 2000

```

Case 3

```

node mean sd MC error 2.5% median 97.5% start sample
p[2,1] 0.6776 0.01123 2.686E-4 0.656 0.6774 0.6999 100000 2000
p[3,1] 0.5459 0.01438 3.072E-4 0.5176 0.5457 0.5736 100000 2000
p[3,2] 0.3373 0.01522 4.056E-4 0.3088 0.337 0.3674 100000 2000
p[4,1] 0.3376 0.0128 2.875E-4 0.3133 0.3377 0.3627 100000 2000
p[4,2] 0.1877 0.01335 2.606E-4 0.1612 0.1875 0.215 100000 2000
p[4,3] 0.1707 0.01363 3.109E-4 0.1454 0.1702 0.1976 100000 2000
p[5,1] 0.5471 0.01831 4.01E-4 0.5108 0.5473 0.5826 100000 2000
p[5,2] 0.3002 0.01884 4.942E-4 0.2648 0.3001 0.3393 100000 2000
p[5,3] 0.3402 0.02085 4.957E-4 0.2998 0.3399 0.3829 100000 2000
p[5,4] 0.7446 0.02213 4.59E-4 0.6992 0.7456 0.7865 100000 2000

```

Case 4

```

node mean sd MC error 2.5% median 97.5% start sample
p[2,1] 0.6764 0.01129 2.476E-4 0.655 0.6766 0.6988 100000 2000
p[3,1] 0.549 0.01452 2.962E-4 0.5203 0.5489 0.5774 100000 2000
p[3,2] 0.3389 0.01521 3.06E-4 0.3095 0.3388 0.3684 100000 2000
p[4,1] 0.3355 0.01278 2.387E-4 0.3101 0.3351 0.3597 100000 2000
p[4,2] 0.1875 0.01329 3.318E-4 0.1624 0.1871 0.2132 100000 2000
p[4,3] 0.1718 0.01351 2.831E-4 0.1456 0.1718 0.1979 100000 2000
p[5,1] 0.5436 0.01827 3.54E-4 0.5071 0.544 0.5789 100000 2000
p[5,2] 0.2962 0.01858 4.488E-4 0.2607 0.2956 0.3335 100000 2000
p[5,3] 0.3419 0.02094 3.765E-4 0.3012 0.3422 0.3842 100000 2000
p[5,4] 0.7427 0.02202 4.498E-4 0.6966 0.7435 0.7835 100000 2000

```