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Research Article

Bayesian Credible Intervals for Maize Grain Yields of the Maintenance Varieties Evaluated in Sudan

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Abstract

Improved of maintenance crop varieties developed at agricultural research corporation, Wad median, Sudan is intended for seed foundation which is recently established. This study was undertaken to establish statistical investigation using Bayesian estimation for credible interval or posterior interval as a Bayesian strategy for a maintenance variety. Data on grain yield (kg/ha) on a maize crop variety were used. Bayesian posterior information can be annoying to investigate but are important in maintenance varieties that foundational claims are used to make general recommendations for practice. Half normal informative priors set of were used. The heritability of yield (varieties)) was (h = 0.75). Predicted posterior means of varieties were shown with a Bayesian interval for scientific inference in the maintenance maize grain yield. Bayesian approach is useful for reducing uncertainty on decisions based on economic evaluation of new maize varieties in Sudan, the use of credible intervals for grain yield allow for early decisions.

Keywords: Bayesian inference; maize; maintenance varieties; block design

Introduction

The maize crop plays an active role in the world economy and widely used for trade (Olson *et al.*, 2012). FAO (2007) reported that the demand of Maize in sub- Saharan Africa between increasing by 50% as worldwide and by 93% up to 2020. Also maize remains an important source of food with great potential to improve the livelihoods of most poor farmers in developing countries (Smale *et al.*, 2001). To maintain maize varieties will assess the farmers to be in level of adoption for determining the costs and technologies to be chosen and selected for variety development programs (Feder *et al.*, 1981). Prior information or identification of farmers' constraints and preferences is required in order to plan more appropriate, acceptable and cost effective development intervention programs for effective agricultural research and technology development, and their adoption (Thijssen *et al.*, 2008).

Nowadays, many crop yields can be affected by climatic factors such as precipitation, temperature and recent warming (Lobell and Burke, 2010). Also the impact of climate change may damage crop yields on a global scale

and lead to decreases in crop production (Chen *et al*., 2014). In rain-fed agricultural regions, also weather conditions have substantial impacts on crop productivity (Yu, 2011). The maintenance of forms can be managed through three phases of seed multiplication: breeder's seed, foundation seed, and certified seed. Therefore, we found the breeder's seed field should show the minimum variation for morphological traits to help guide quality control during multiplication, but not impede seed production and distribution (Rajhandari *et al*., 2001). Maintenance of varieties is preferred to be developing in the regions of their natural adaptation to minimize developmental shifts (NASA, 2000). Therefore, Bayesian approach can be very useful in maintenance varieties, seed production, because Bayesian credible information can help to understand the probability distribution over the parameters through rich statistical inferences of means (Omer *et al*., 2015). Bayesian approach in analysis crop variety trials have been discussed by many authors (Gelman *et al*., 2002): Theobald *et al*. (2002); Theobald and Talbot (2002); De los Campos *et al*. (2009); Forkman and Piepho (2013); de Oliveira *et al*., (2014); Omer *et al*. (2015) and Singh *et al*. (2015). Bayesian credible intervals based on Bayesian theories are conceptually different ways to quantify parametric and predictive uncertainties, because are always numerically identical when consistent prior information is used (Lu *et al*., 2012).

Objectives of the study
The purpose of this study is to use Bayesian approach for estimating posterior interval for maize grain yield of maintenance varieties and to estimate the heritability and genetic gain due to selection of maize varieties.

Materials and Methods

Plant Material and Growth Conditions
The field experiment was carried out during seasons 2014-2015 at Gezira Research Station in agricultural research corporation, Wad Medani, Sudan. The trial was designed as a randomized complete block design (RCBD) with 3 replications and the 16 new maize entries during 2015. Data on grain yield was used. To meet the objectives of this of objective, priors from past dataset will used. The performance of the methods developed will be evaluated using real maintenance variety data. Bayesian analysis will provide results from two types of priors' information for comparison of a differentiating characteristic, with the results analyzed separately using REML analysis. Bayesian evidences such credible interval is appropriate statistical information in this case that prevented the normal distribution and/or confidence of the data. However, Bayesian posterior means of genotypes has been compared with the frequentist means. In this paper, Bayesian estimation will based commonly used statistical tools such as coefficient of variation (CV%), predicted means of genotypes, with standard errors and confidence intervals,

average standard error of differences of predicted means, heritability, genetic gain due to selection, realized gain due to selection, and ranking of genotypes for selection. We ran the MCMC algorithm on three separate chains for 100000 iterations each, and we saved every fifth iteration among the last 5000 to form a posterior sample of size 1000 for each of the three chains.

Statistical Methods
Recently, Bayesian method has been widely applied in many different sciences for decision analyses, the feature Bayesian method is that priors are superior to frequentist approach (Lin, 2013). In agricultural experiments, the Bayesian analysis was carried out using data from previous trials (Besag *et al*., 1999). Some advantages of use Bayesian analysis are easy to interpret confidence intervals and p-values in direct way (Besag and Higdon, 1999). In other words, Bayesian interval has a 95% chance of containing the true parameter. The Benefits of Bayesian approaches that the prior information allows partial pooling of different data sources (Gelman, 2014).

Frequentist Confidence and Bayesian Credible Interval

The confidence interval provides a range that is highly likely (often 95% or 99%) to contain the true parameter that is being estimated. A confidence interval for the mean X from a normal population, can be written as

$$\bar{x} \pm t_{n-1} \times s.e.(\bar{x})$$

Where t_{n-1} is the appropriate percentage point of the t-distribution with (n–1) degrees of freedom. The 95% confidence interval is commonly used, for which t-values are 2.2, 2,1 and 2.0 for 10, 20 and 30 degrees of freedom. So we can usually write that the 95% confidence interval for the mean is roughly:

$$\bar{x} \pm 2 \times s.e.(\bar{x})$$

For example say variety-16 of maize crop gave $\bar{x}$ = 2221.5 tons with s.e. = 92.47 The 95% confidence interval for x is therefore about 2036.3 to 2406.19 kg/ha; and so we can say that that this range is likely to contain the population mean of maize grain yield. Therefore, exact 95% interval, which one can get from a statistical software package, is (2036.3 to 2406.19 kg/ha.). In other words, there is a 95% probability that the population mean is in the interval 2036.3 to 2406.19 kg/ha. More generally, for almost any estimate, whether it be a mean, or some other characteristic, and from almost any population distribution, we can write that the 95% confidence. A confidence interval does not contain 95% of the data in the sample that generated it; very approximately it called a prediction, or tolerance interval. In this an examples G16 mean with interval would say that most of the variety have yields in this range only. When the assumptions about the data may not be quite right, scientists

may feel they ought to abandon the ordinary confidence interval and use some different procedure altogether. In frequentist approach, the confidence interval is expressing an area around the sample mean. Therefore, the interpretation is less desirable performing inference about based on a single interval (Yang, 2006). There are various ways, including the mean, median, mode of parameters posterior distribution, in which one can summarize the distribution, mostly point estimation is conducted through reporting the posterior mean. In Bayesian approach the interval estimate for parameters of interest is called credible interval or posterior distribution (Jaynes, 1976). The differences between the frequentist and Bayesian conference intervals are that in the Frequentist approach, the confidence interval can claim that the region covers the true parameter, reflecting uncertainty in sampling procedure or implies the interval covers the true parameter among 95% of the experiments (Baklizi *et al.*, 1999). While Bayesian approach, credible Interval: a claim that the true parameter is inside the region with measurable probability (Box and Tiao, 1992). One can make a direct probability statement about parameters can implies the chance that the true parameter falls in (a, b) is 95% (Lin, 2013). A credible interval (or in general, a credible set) is the Bayesian analogue of a confidence interval. One advantage of the Bayesian procedures is the possibility of using the confidence limits (or credibility regions in the Bayesian context) as an alternative estimation of genetic parameters (Rodovalho *et al.*, 2014). Agresti and Min (2005) discussed Bayesian confidence intervals for association parameters. They argued that if one desires good coverage performance (in the frequentist sense) over the entire parameter space, it is best to use quite disuse priors. Even uniform priors are often too informative, and they recommended the Jeffrey's prior. In Bayesian approach the interval for parameters of interest (a) is called credible interval or posterior intervals. Any interval that has 95% posterior is called a 95% credible interval (CI). Given a posterior distribution interval $p(\theta|y)$, A is a credible set for θ if

$$p(\theta \in A|y) = \int_A p(\theta|y)d\theta.$$

For example the two sided 95% CI for: θ: $p(\theta L < \theta < \theta U|\text{data}) = 0.95$ or $p(\theta \geq \theta U \text{ or } \theta \leq \theta L|\text{data}) = 0.05$, The credible can be construct using equal trails, where equal tai area interval divide the portability of the complements in two equal area: $p(\theta \leq \theta_L|\text{data}) = p(\theta \geq \theta_U|\text{data}) = 0.025$; another frequently used Bayesian credible set is called the Highest Posterior Density (HPD) Intervals (Lin, 2013). A HPD interval is a region that contains parameters with highest posterior density values (Hashemi *et al.*, 1997).

Prior Distribution
A prior distribution of a parameter is the probability distribution that represents one's belief or associated uncertainty (Gelman, 2006). In Bayesian statistics, a prior

distribution for μ with density p(μ) is chosen that reflects a researcher's knowledge and uncertainty about μ. For an example in a maize crop trial, suppose that a researcher has estimated that 5% of the genotypes are reliable and the researcher is 95% sure that the actual variation in genotypes means was no larger than 25% (Finley *et al.*, 2011). In order to estimate the average of grain yield for maize crop based on a given sample size of 16 genotypes, the priors on means and variance of genotypic response may be collected using the data from past trials. A Bayesian statistician could then estimate that, given the prior knowledge of distribution of means, the mean response for the maize crop is normally distributed with a mean of, say 150 kg/ha and a standard deviation of, say 25 kg/ha. When the sample of say, 16 genotypes is collected, it is approximately normally distributed as the Bayesian inference or the posterior probability distribution considers both the prior probabilities and the data (Yi *et al.*, 2013).

A- Priori distributions
In Bayesian context, one uses precision parameter τ, where $\tau = 1/\sigma^2$ (inverse of variance), instead of variance of normal distribution. This prior, using the WinBUGS code, is expressed as $\sigma_g \sim N(0, \tau) * I(0.)$ where *I(0,)* restricts the generated values of $\sigma_g \sim N(0, \sigma^2)$ in the positive range. Five sets of half normal distribution priors evaluated in this study. To be specific, we chose the following classes of priors:

P_1: the priors for the standard deviation components: σ_r, σ_g and σ_e follow half-normal distribution $N(100, \tau^{-1} = 500) * I(0,)$

P_2: the priors for the standard deviation components: σ_r, σ_g and σ_e follow half-normal distribution $N(100, \tau^{-1} = 1000) * I(0,)$

P_3: the priors for the standard deviation components: σ_r, σ_g and σ_e follow half-normal distribution $N(500, \tau^{-1} = 1000) * I(0,).$

P_4: the priors for the standard deviation components: σ_r, σ_g and σ_e follow half-normal distribution $N(1000, \tau^{-1} = 500) * I(0,).$

P_5: the priors for the standard deviation components: σ_r, σ_g and σ_e follow half-normal distribution $N(1000, \tau^{-1} = 1000) * I(0,)$, using Gelman *et al.* (2009) notation. Here, τ is precision parameter, $\tau = \sigma^{-2}$ given as inverse of variance.

Results and Discussion
Bayesian information is presented here and found that there was a statistical significant of genotypes means. Bayesian estimation of predicted crop yields reflected the trend of the observed yields the estimated using classical approach, which Bayesian interference give wide inference of

posterior. The choice of priors for Bayesian analysis was made from the statistics for RCBD models. The estimates of variance components and heritability and genetic gain using Bayesian approach are presented in Table 2. The posterior mean yield of the maintenances varieties, ranks, conference /creditable intervals are presented in Table 3 and 4.

Selection of Priors

The choices of priors for Bayesian analysis were made from the statistics given in Table 1 for maize data. The five prior sets of half normal distributions ($P_1 – P_5$) were used. The priors set derived from informative priors were used to build more suitable priors for maintenances varieties in the future. The values of DIC are different to each other for priors sets, however, the prior set P_3 seems to have numerically lowest

value of DIC (764.28).Therefore, the prior P_3 was chosen for predicting performance of the genotypes, genetic parameters and credible intervals as presented in Table 3.

Table 2 shows the estimates of genetic gain (family selection) considering three selection rates (5% , 10% and 20%) calculated according to the predicted Bayesian values of popcorn families (posterior mode). Genetic gains were of 40%, 34% and 28% respectively for grain yield. The significant genetic variability among genotypes was 22.51% of the grain yield. Furthermore, the heritability value that we obtained was high expected for grain yield. Calculation of heritability and Genetic Gain showed that the heritability in the Genetic Gain with higher heritability tended to show higher prediction accuracies.

Table 1: Discrepancy statistics values for selection of the priors for data on maize maintainers varieties for grain yield based on half-normal distribution.

Priors	$\bar{D}$	$\hat{D}$	p_D	DIC	CV
P_1	1824.07	1809.80	14.27	1838.34	4.50
P_2	1823.92	1809.77	14.15	1838.07	4.50
P_3	750.14	735.99	14.14	764.28	22.51
P_4	778.33	764.18	14.15	792.48	45.02
P_5	778.36	764.22	14.14	792.51	45.02

$\bar{D}$ =posterior mean of (- 2 × log-likelihood). $\hat{D}$ = - 2 × log-likelihood at posterior means of parameters.

p_D = effective number of parameters, DIC = Deviance information criterion.

Priors set are:

P_1: σ_r , σ_g and σ_e independently $\sim$ positive Half $-$ normal $(100, 500)$.

P_2: σ_r , σ_g and σ_e independently $\sim$ positive Half $-$ normal $(100, 1000)$.

P_3: σ_r , σ_g and σ_e independently $\sim$ positive Half $-$ normal $(500, 1000)$.

P_4: σ_r , σ_g and σ_e independently $\sim$ positive Half $-$ normal $(1000, 500)$.

P_4: σ_r , σ_g and σ_e independently $\sim$ positive Half $-$ normal $(1000, 1000)$.

Table 2: Bayesian estimation of heritability and genetic gain for grain yield using half-normal prior (500, 1000).

Parameters	mean	SD	MC error	2.50%	median	97.50%
CVpc	22.51	0.0014	0.000021	22.51	22.51	22.51
GA10	34.21	0.0028	0.000039	34.2	34.21	34.22
GA20	27.29	0.0022	0.000032	27.29	27.29	27.29
GA5	40.21	0.00325	0.000047	40.21	40.21	40.22
h2	0.75	0.00034	0.0000048	0.7499	0.75	0.7501

Table 3: Predicted values of the genotypes means, credible intervals and their ranks for a Bayesian approach for maintainers varieties for grain yield based on Half-normal Distribution.

Genotypes	mean	Rank	Mean	Rank	SD	MC error	Percentile			Rank		
							2.50%	50%	97.50%	2.50%	50%	97.50%
G1	2803	2	2747	2	375	6.158	1982	2748	3479	2	2	2
G2	2174	9	1986	10	371.3	6.266	1244	1988	2705	11	10	11
G3	2171	10	1992	9	373	5.369	1247	1992	2723	10	9	9
G4	2138	12	1947	12	376.9	6.275	1202	1946	2689	12	12	12
G5	2063	14	1851	14	374.8	6.362	1097	1855	2567	14	14	14
G6	2164	11	1978	11	373.1	5.593	1254	1979	2710	9	11	10
G7	2093	13	1896	13	372.3	5.497	1176	1897	2636	13	13	13
G8	2278	8	2118	8	377.8	6.065	1377	2107	2858	8	8	8
G9	2304	7	2149	7	375.8	6.134	1395	2147	2881	7	7	7
G10	2314	6	2163	6	378.6	5.612	1410	2164	2897	6	6	6
G11	1424	16	1091	16	371.4	5.358	353.9	1087	1820	16	16	16
G12	2392	4	2259	4	380.5	6.095	1503	2264	2999	4	4	4
G13	1531	15	1221	15	376.3	5.673	483.3	1223	1970	15	15	15
G14	2431	3	2300	3	378	5.857	1561	2299	3022	3	3	3
G15	2386	5	2240	5	374.1	5.982	1499	2246	2973	5	5	5
G16	2874	1	2838	1	372.8	6.179	2120	2844	3568	1	1	1
Mean		304	2020		307.1	5.265	1411	2020	2614			

Maize Predicted Means under Bayesian Approach

The *a posteriori* means of the genotypes, 95% confidence intervals and their *a posteriori* ranks from alternative ways are presented in Table 3. The precision of the means under Bayesian approach is different than that of the frequentist approach (average SE of 0.375 vs 0.304. Correlation between the predicted values under the two approaches was 0.999 (p<0.001). The performance of the genotypes under Bayesian approach has been given also in terms of the percentiles of the predicted values and of their ranks. This has been possible due to availability of a large number of simulated values under the Bayesian model. Denoting the genotype numbered 1 to 16 by G1 to G16, the top 4 genotypes were G16, G1, G14, and G12 using Bayesian approach, which were also selected under frequentist approach. Selection based on quantiles of ranks of the genotypes appears quite desirable, instead of using only means, which is possible due to the availability of distribution of ranks from the computation process. When selecting the genotypes based on distribution of ranks, the top 4 genotypes using the *a posteriori* mean ranks and or median of the ranks were also G16, G1, G14, and G12. While the selection of the genotypes would be based on *a posteriori* mean rank or mean value, the distribution of ranks at the extreme quantiles also could be useful.
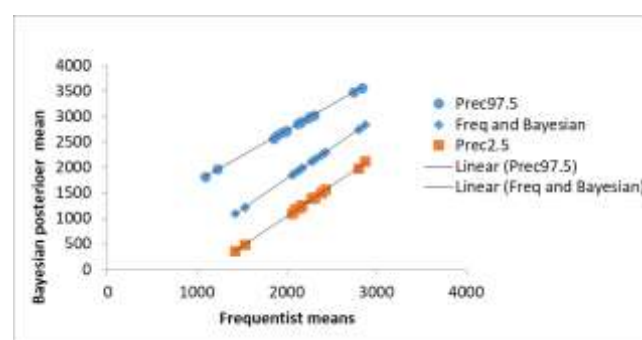

Fig. 1: Scatterplot of predicted means of grain yield (kg/ha) of the 16 maize genotypes for comparing frequentist mean, Bayesian posterior mean and Bayesian credible bands using 95% credible interval values for individual genotypes.

The Fig. 1 indicates comparison of Bayesian and frequentist estimates of predicted mean of each genotypes, The correlation between frequentist and Bayesian approaches was highly significantly positive (0.99, P<0.001). The Bayesian and frequentist approaches for maize yield performance prediction were evaluated, which mostly

differed in mean predicted and their ranks. These results were to explore the extent and pattern of confidante intervals of grain yield. The present investigation revealed that there was wide chance of containing the true means for the top majority of desired genotypes. Overall the results emphasize that investigating a maintenance varieties for adaptation using Bayesian approach should consider in future work. The necessary codes of the WinBUGS (Spiegelhalter *et al.*, 2003) and R-package (R Development Core Team, 2009) will obtained from first author.

Conclusions

Bayesian analysis was used to assess the maintenance of varieties on the predication genotypes of interest and to be undertaken to adjust for any genotype estimation. The results of this experiment could be used for further statistical information for Bayesian inferences, the variance components will saved as prior information for more investigation for other varieties. Bayesian confidence / credible interval seem to be on of importance strategies for statistical information for seed and yield production based on maintenance of varieties. The additional information obtained in the proposed method, successfully evaluation rich statistical information like posterior information in detailed understanding of maintenance of varieties distributions.

Acknowledgments

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