

A Short Review on Bayesian Estimation of a Common Coefficient of Variation from Inverse Gaussian Distributions

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SUMMARY

The coefficient of variation (CV) has been used in different disciplines with varied purpose related to variation in quantitative measurements. Statistical properties of CV have been studied by various researchers. Recently, a paper by the authors featuring an investigation of the posterior distribution of a common CV for inverse Gaussian populations with priors obtained through some empirical fitting procedure was presented by YPC at the 2022 ISBA World Meeting, June 26-July 1, 2022, held in Montreal, Canada. Some of these results along with other current developments by the authors on the topic were also reviewed during an invited presentation by MS in the honor of Dr. Daroga Singh at the 73rd Annual Conference of ISAS Conference held at the Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir, November 14-16, 2022. The purpose of this paper is to summarize and discuss three key papers on estimation and testing of CV from inverse Gaussian distribution focussed on – a common CV (from multiple populations under frequentist framework), CV for a single population with Bayesian framework and a common CV from multiple populations and Bayesian framework, reviewed at this conference.

Keywords: Common coefficient of variation; Inverse gaussian distribution; Bayesian inference; Conjugate priors; Lentil trials.

1. INTRODUCTION

The coefficient of variation (CV), a popular indicator for variability, follows the mean and standard deviation in the summary of a single variable for introductory lectures in statistics. CV is used for various purposes under different settings. It is used to measure heterogeneity, or thus, homogeneity of an experimental field, uniformity in seed quality testing (DUS: Distinctness, uniformity and stability), phenotypic stability of a genotype across environments (Lin *et al.*, (1986)), stability of income (Singh and Singh (1991)), precision and reproducibility of data in medical and biological science (Tian (2005)), among others. Its indirect uses include determining an optimal plot size (sample surveys - crop cutting sample surveys with which Dr. Daroga Singh and his team were

intensively involved), the sample size or the number of replications for an experiment, a Bayesian control chart for a common coefficient of variation (van Zyl & van der Merwe (2017)) among others.

In almost every field of investigation, researchers gather a large amount of data and their summaries over time and space. For instance in agricultural research, evaluation of crop genotypes/varieties is a continuous process leading to the availability of estimates of means and variances of genotypic performance. These estimates can be used as prior information to create a prior distribution in order to improve the estimates obtained from the current experiments. While the means and standard deviations of genotype yields are affected by environmental variables such as rainfall, temperature and various biotic stresses,

their ratio such as CV (standard deviation/mean) is likely to be more stable. Thus, one can form a more robust prior distribution for the CV relative to that for the components it is made of. Furthermore, in reality, most of the observations on variables of interest, such as agronomic traits and income etc., are positive and for such situations the inverse Gaussian distribution appears a worthy candidate. The availability of prior information enables an assessment under the Bayesian framework. Combining these two aspects, the inverse Gaussian distribution and prior information, the objective of this study is to review the selected work done in the area of estimation and testing of CV under Bayesian/frequentist frameworks in the contexts of single and multiple populations.

Coefficient of variation. In terms of the parameters of a distribution, the CV is defined as follows. Let a random variable $X \sim (\mu, \sigma^2)$, that is, X is distributed with mean μ and standard deviation σ , then the population CV δ is defined as

$$\delta = \sigma/\mu.$$

For a random sample X_1, X_2, \dots, X_n of size n , $X_i \sim (\mu, \sigma^2)$, the sample CV is given by

$$\hat{\delta} = \frac{S}{\bar{X}}$$

where

$$\bar{X} = \frac{\sum_{i=1}^n X_i}{n}, \text{ and } S = \sqrt{\frac{\sum_{i=1}^n (X_i - \bar{X})^2}{n-1}}$$

Sample CV has been widely studied in different contexts and for different statistical populations. In many real-world applications, data are non-negative, "thus, the populations" with non-negative observations are of obvious interest. The inverse Gaussian (IG) distribution (Folks and Chhikara (1978)) is one such distribution widely studied for modelling positive measurements. Chaubey *et al.* (2017) have explored the behavior of CV for IG distribution. This article reviews their research along the following three themes, organized into individual sections.

1. Estimation and Testing of a Common Coefficient of Variation from Inverse Gaussian Distributions (Singh *et al.* (2021)),
2. Bayesian Inference for Inverse Gaussian Data with Emphasis on the Coefficient of Variation (Chaubey *et al.* (2021)), and

3. Bayesian Inference for a Common CV from Inverse Gaussian Distributions (Chaubey *et al.* (2022)).

Inverse Gaussian (IG) Distribution has an early introduction and details in Tweedie (1957, 1957), Chhikara and Folks (1977), Folks and Chhikara (1978), Chhikara and Folks (1989) among others. The probability density function (*pdf*) of an IG random variable X with mean μ and dispersion parameter λ , denoted by $IG(\mu, \lambda)$, is

$$f(x|\mu, \lambda) = \left\{ \frac{\lambda}{2\pi x^3} \right\}^{1/2} \exp \left\{ -\frac{\lambda}{2\mu^2 x} (x - \mu)^2 \right\};$$

$$x > 0, \mu > 0, \lambda > 0. \quad (1.1)$$

For the $IG(\mu, \lambda)$ distribution, the mean and variance are

$$E(X) = \mu, \text{ var}(X) = \mu^3/\lambda.$$

The population CV is thus given by

$$\delta = \sqrt{\mu/\lambda}.$$

Various other reparametrization normally found in the literature are those discussed by (i) Banerjee and Bhattacharyya: $(\mu, \lambda) \rightarrow (\psi = 1/\mu, \lambda)$

(ii) Betro and Rotondi [2]: $(\mu, \lambda) \rightarrow (\tau, \lambda)$ where $\tau = \lambda/\mu = 1/\delta^2$.

(iii) Chaubey *et al.*: $(\mu, \lambda) \rightarrow (\mu, \delta)$. In this case, the *pdf* of X is given by

$$f(x|\mu, \delta) = \left(\frac{\mu}{2\pi\delta^2 x^3} \right)^{1/2} \exp \left[-\frac{1}{2\delta^2} \left\{ \frac{(x - \mu)^2}{\mu x} \right\} \right]. \quad (1.2)$$

2. REVIEW OF ESTIMATION AND TESTING OF A COMMON COEFFICIENT OF VARIATION FROM INVERSE GAUSSIAN DISTRIBUTION

The crop improvement programs undertake the $G \times E$ interaction studies to compare genotypes for their phenotypic stability based on the positive valued agronomic traits such as crop yield. Thus, the statistical inference on a common CV across several IG populations is of interest.

Consider K inverse Gaussian populations with parameters (μ_i, δ_i) , $i = 1, 2, \dots, K$. The *pdf* of i^{th} population is given by

$$f(x|\mu_i, \delta_i) = \left\{ \frac{\mu_i}{2\pi\delta_i^2 x^3} \right\}^{1/2} \exp \left\{ -\frac{1}{2\delta_i^2} \frac{(x - \mu_i)^2}{\mu_i x} \right\};$$

$$x > 0, \mu_i > 0, \delta_i > 0. \quad (2.1)$$

This paper considers random samples $X_{ij}, j = 1, 2, \dots, n_i$, of size n_i be drawn from IG (μ_i, δ_i) $i = 1, 2, \dots, K$, and has proposed methods for:

(i) **Estimation of a common CV**, δ in terms of $\phi = \delta^2$. They proposed four estimators for the common CV, which in terms of their notations, are $\tilde{\phi}_{E_1}$: A simple **1-step iterative maximum likelihood estimator**, the mean of MLEs of $\phi_i = \delta_i^2$ weighted with the sample size but is not unbiased; $\tilde{\phi}_{E_2}$: **Maximum likelihood estimator**, which has unknown bias and requires an iterative solution of the maximum likelihood equations; $\tilde{\phi}_{E_3}$: **An unbiased estimator** constructed as a sample size weighted mean of the unbiased estimators of ϕ_i for a single population; and $\tilde{\phi}_{E_4}$: **A weighted estimator** based on $\hat{\phi}_i$ with weights inversely proportional to the estimated variance of $\hat{\phi}_i$.

(ii) **Test of homogeneity of the CVs**, i.e., $H_0: \delta_1 = \delta_2 = \dots = \delta_K$ vs. H_1 : at least two populations differ for δ . They proposed two tests: 1. **Likelihood Ratio Test** using the asymptotic distribution of $-2 \ln(\Lambda)$ (in common notations) as χ_{K-1}^2 under the null hypothesis; 2. **Test Based on the Weighted Sum of Squares (WSS)**. Using $\tilde{\phi}_{E_4}$ for the common CV, a test statistic based on the weighted sum of squares of $\hat{\phi}_{iS}$, analogous to the weighted analysis of variance test, which approximately has a chi-square distribution with $K - 1$ degrees of freedom under H_0 .

(iii) **Test for a specified value of the common CV**, say δ_0 based on the approach in Chaubey *et al.* (2017) for an optimal power of $\hat{\phi}_i$ for symmetrizing its distribution extended to the case of several populations. The test statistic also requires cumulants of $\tilde{\phi}_{E_4}$ derived from the functions of the cumulants of $\hat{\phi}_i, i = 1, \dots, K$, which has a lengthy expression/computation.

2.1 Datasets

The studies in Singh *et al.* (2021) and Chaubey *et al.* use the data from a series of multi environment trials that were conducted by the International Center for Agricultural Research in the Dry Areas (ICARDA), Aleppo, Syria. Sarker *et al.* (2010) have reported several trials, however, this paper considered one multi-environment trial in 25 genotypes of small-seeded lentils from LIYT- S (Lentil International Yield Trials) evaluated in 5×5 triple lattices conducted on a total of 15 locations from six countries in 1998. The estimation of CV for yield in kg/ha was carried

out using the adjusted genotypic means. IG and other distributions were fitted using R (Ihaka and Gentleman (1996)). A reasonable goodness of fit tests/plots for IG distributions were found for three genotypes, labelled here as G2, G11, and G20.

The studies by Singh *et al.* (2021) and Chaubey *et al.* (2022) use the data from a series of multi-environment trials that were conducted by the International Center for Agricultural Research in the Dry Areas (ICARDA), Aleppo, Syria. More details on the genotypes and experimental design, the type of trials and the agro-ecological characterization of the environments where these trials were conducted are given in Sarker *et al.* (2010). Of the several trials, this paper considered one multi-environment trial in 25 genotypes of small-seeded lentils from LIYT- S (Lentil International Yield Trials) evaluated in 5×5 triple lattices conducted on a total of 15 locations from six countries in 1998. The estimation of CV for yield in kg/ha was carried out using the genotypic means adjusted for the incomplete block effects. Of the 24 test genotypes, the three genotypes labelled here as G2, G11 and G20 as mentioned in the multi-environment trials in Sarker *et al.* (2010), were used in these reviewed papers. The mean yield levels of these genotypes varied in the range 1492-1535 kg/ha and the sample CV in the range 0.48 to 0.60. IG and other distributions were fitted using R (Ihaka and Gentleman (1996)). A reasonable goodness of fit tests/plots for IG distributions were found for the three genotypes, and are available via link: https://doi.org/10.1007/978-3-030-86133-9_5 for Singh *et al.* (2021).

2.2 Highlights

The four estimators have been presented for a common CV from IG populations. These are based on maximum likelihood and method of moments for δ . The likelihood ratio test and a weighted sum of squares for homogeneity of CVs were studied. The power transformation of CV (Chaubey *et al.* (2017)) to test a specified value for the common CV has been presented using a large sample approximation. The simulation was used to study the properties of the estimators of the common CV and the Type I error rate of the tests.

Of the six tests, four for a specified value of common CV and two for their homogeneity, simulated error rates for the two tests (T_1 and Z_6 , in their notations) were found close to the target level. For example, with three IG populations with a $CV^2(\phi) = 0.25$ and samples

of sizes 10, 15 and 20, the simulated values Type I error rates, based on 100,000 simulations, corresponding to the true error rates 0.001, 0.01, 0.05 and 0.1 were essentially the same. They recommended: a) the use of chi-square distribution based on likelihood ratio test (T_1) for the equality of the CVs, b) a weighted estimator for estimation of the common CV $\tilde{\phi}_{E_4}$, (one of the four estimators), and c) power $h_0 = \frac{1}{5}$ of δ^2 :

3. REVIEW OF BAYESIAN INFERENCE FOR INVERSE GAUSSIAN DATA WITH EMPHASIS ON THE COEFFICIENT OF VARIATION

For a single IG population, this paper obtains, theoretically and numerically, the joint and marginal posterior distributions of μ and δ based on wide classes of joint priors. It derives Jeffrey’s non-informative prior for (μ, δ) and explores in greater detail the GIG (Generalized IG) (Joshi and Shah (1991)) and a conditional inverse gamma distribution as priors of μ and δ . A $GIG(q, a, b)$ random variable Z with parameters (q, a, b) has the *pdf* (see Jorgensen (1982))

$$f_Z(z) = \frac{1}{C_q(a, b)} z^{q-1} \exp\left[-\frac{1}{2}\left(az + \frac{b}{z}\right)\right] \quad (3.1)$$

where

$$C_q(a, b) = 2\left(\frac{b}{a}\right)^{q/2} K_q(\sqrt{ab}), \quad (3.2)$$

The entity $K_q(\cdot)$ is the modified Bessel function of second kind of order q (Glasser *et al.*), and has the following representation:

$$K_q(s) = \frac{1}{2} \int_0^\infty t^{q-1} \exp\left\{-\frac{s}{2}(t+t^{-1})\right\} dt.$$

To obtain the likelihood of the sample, let X_1, X_2, \dots, X_n be *i.i.d.* $\sim IG(\mu, \delta)$, with summary statistics given as

$$\bar{x} = n^{-1} \sum x_i, \bar{x}_r = n^{-1} \sum \frac{1}{x_i} \text{ and } V = \frac{1}{n} \sum \left(\frac{1}{x_i} - \frac{1}{\bar{x}}\right).$$

For each of the two sets of joint informative priors for (μ, δ) , GIG-GIG and GIG - conditional inverse Gamma (cIGm), the paper obtains theoretical expressions and simulated results on their joint posterior and marginal posteriors.

a. **GIG-GIG Prior:** The joint prior for (μ, δ) is given by

$$p(\mu, \delta) = p_1(\mu)p_2(\delta) \quad (3.3)$$

where $p_1(\mu)$ is obtained by assuming $\mu \sim GIG(q_1, a, b)$ and $p_2(\delta)$ is obtained by assuming $\delta^2 \sim GIG(q_2, u, v)$. The posterior distribution of δ , for large n , is then approximated by

$$p(\delta | X) \propto \frac{1}{C_{q_0}(u, v_0)} \left(\frac{1}{\delta^2}\right)^{\frac{n}{2}-q_2} \exp\left[-\frac{1}{2}\left\{u\delta^2 + \frac{v_0}{\delta^2}\right\}\right] \quad (3.4)$$

where $q_0 = \frac{n}{2} - q_2 + 1$ and $v_0 = v + n\bar{x}V$.

That is, approximately for large n , $\delta^2 | X \sim GIG(q_0, u, v_0)$. Thus, it concludes that GIG is a conjugate prior for δ for large n .

b. **GIG - conditional inverse Gamma (cIGm) Prior.** Here, the joint prior for (μ, δ) is given by

$$p(\mu, \delta) = p_1(\mu)p_2(\delta|\mu),$$

where $p_1(\mu)$ is obtained by assuming $\mu \sim GIG(q_1, a, b)$ and $p_2(\delta|\mu)$ is obtained by assuming $\mu/\delta^2 \sim Gamma(\alpha, \beta)$. Thus, the posterior distribution δ is given by

$$p(\delta | X) \propto \delta^{-(n+2\alpha+1)} \exp\left\{\frac{n}{\delta^2}\right\} 2\left\{\frac{v(\delta; X)}{u(\delta; X)}\right\}^{\frac{q\delta}{2}} K_{q\delta}\left(\sqrt{u(\delta; X)v(\delta; X)}\right)$$

where

$$u(\delta; X) = \left(a + \frac{2}{\beta\delta^2} + \frac{n\bar{x}_r}{\delta^2}\right), v(\delta; X) = \left(b + \frac{n\bar{x}}{\delta^2}\right), q_\delta = \frac{n}{2} + q_1 + \alpha.$$

The above posterior approximates, for large n , to

$$p(\delta | X) \propto \delta^{-(n+2\alpha)} \exp\left[-\frac{n\bar{x}V}{2\delta^2}\right]$$

and we conclude that the approximate posterior of δ^2 is inverse Gamma distribution. The performance of these two priors for estimation of mean active repair time (Folks and Chhikara (1978)) were tabulated for ten sets of the parameters (q_1, a, b, q_2, u, v) keeping the prior means of the CV around 1. OpenBUGS worked well considering the complex nature of the posteriors. They used OpenBUGS with 66667 iterations for simulating the posterior, with the number of simulated samples being 100002. For obtaining credible intervals, 1024 points were taken to smooth the density.

3.1 Highlights

The posteriors found were well behaved, as no computational problems arose. The exact computations were quite fast, so no need for creating an approximation for the posterior was considered necessary. The simulated values matched very well with the exact values. To quote a few selected cases to estimate CV from the Active Repair Time Data (Folks and Chhikara (1978)), we notice for GIG-GIG priors with values $(q_1, a, b, q_2, u, v) = (-0.5, 4, 4, -0.5, 1, 1)$: the exact and simulated means of δ up to 3 decimals were 1.348 and 1.349 respectively, while the 95% credible intervals were, exact: (1.061, 1.661) and simulated: (1.060, 1.665). For the joint priors, GIG-cIGm with parameters $(q_1, a, b, \alpha, \beta) = (-.5, 4, 4, 3, 2)$, the posterior mean of the CV was 1.362 (exact) and 1.338 (simulated), and the 95% credible intervals were, Exact: (1.055, 1.702) and simulated: (1.046, 1.656).

4. REVIEW OF BAYESIAN INFERENCE FOR A COMMON CV FROM INVERSE GAUSSIAN DISTRIBUTIONS

This study (Chaubey *et al.* (2022)) reports the mean and credible intervals from the posterior distribution of the common CV of the three genotypes G2, G11 and G20 as mentioned in the multi-environment trials in Sarker *et al.* (2010). Some summary statistics of the multi-environment international yield trials in small-seeded lentils from the 21 genotypes are: genotype means in the range: 1347 – 1633 kg/ha and CV = 0.49 – 0.56 (across 15 environments, other than G2, G11, G20). There was one local check, thus these averages and ranges are based on $25 - 1 - 3 = 21$ genotypes. The prior distributions and their parameters were estimated from $G \times E$ lentil trials data for the remaining (21) genotypes, thus they used empirical priors based on five distributions: Normal, Lognormal, IG, Weibull, Gamma, for genotypic means and CV. We also fitted four other distributions, namely, Chisquare, inverse χ^2 , F and Gumbel, but their performance, in terms of goodness-of-fit statistic (Kolmogorov-Smirnov, Cramer-von Mises, Anderson-Darling) and goodness-of-fit Criterion (Akaike's Information Criterion, Bayesian Information Criterion), were no better than the preceding five distributions and, therefore, were not pursued further. Some of the key R functions such as `fitdistr()`, R2WinBUGS and an HPD computing function from Chaubey *et al.* (2021) were used in the computation. For posterior distributions, they used

R2WinBUGS with 3 chains, 100,000 iterations, and 50000 burn-ins for each chain. The posterior means using the simulations were tabulated for δ for the eight combinations of the joint priors with parameters estimated by fitting the distributions on the rest of the genotypes. These eight priors were the combinations of IG and Gamma, the two priors for δ , and Truncated normal, lognormal, IG and Gamma, the four priors for μ .

4.1 Highlights - Posteriors of Common CV

The genotypes, G2, G11 and in the range G20 had means (over 15 locations) in the range 1492-1535, sample CV in the range 0.48-0.60 and the CV estimated as maximum likelihood estimates (MLEs) from IG distributions in the range 0.55-0.80. The frequentist estimates of the common CV of these three genotypes were: 0.54 (obtained as the mean of sample CV) and 0.652 (the mean of the MLEs of CV from IG distributions), while the average of the posterior means over the eight priors investigated was 0.634. The 95% credible intervals were also close, for instance, (0.548, 0.723) for the IG-IG prior for (δ, μ) and (0.548, 0.722) for the Gamma - Gamma prior. The posterior mean is within reasonable closeness to the likelihood estimates. Considering various families of priors, the posterior distributions were found to be reasonably robust for the estimation of the common CV for the three selected genotypes.

5. IG DISTRIBUTIONS IN ROUTINE DATA ANALYSIS AND CONCLUSION

The three papers on estimation and tests of hypothesis on the CV from a single population, and a common CV from multi-populations using the frequentist and Bayesian approaches were reviewed and some main features were described. An IG distribution suited for modelling the positive values in routine data analysis has potential but is not popular in the analysis of designed experiments. Looking into the usefulness of IG distribution and availability of large datasets to feed in the prior distributions, the authors are of the view to encourage the use of IG under the Bayesian framework for the models including $y_{ij} \sim IG(\mu_{ij}, \sigma_{ij}^2)$, where, $\mu_{ij} = \mu + \tau_i + \beta_j$ (say in a randomized complete block design), and compare with a normal distribution model: $y_{ij} \sim N(\mu_{ij}, \sigma^2)$. The priors for μ_{ij} , σ_{ij} and σ^2 could be drawn from a large class of distributions with parameter estimates from prior experiments.

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Conflict of Interest Statement

On behalf of all authors, the corresponding author states that there is no conflict of interest.

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