TESTING THE EQUALITY OF TWO COEFFICIENTS OF VARIATION: A NEW BAYESIAN APPROACH

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ABSTRACT. The use of testing procedures for comparing two coefficients of variation (CVs) of independent populations is not extensively explored in the Bayesian context. We propose to address this issue through a test based on a measure of evidence, the Bayesian Discrepancy Measure, recently introduced in the literature. Computing the Bayesian Discrepancy Measure is straightforward when the CVs depend on a single parameter of the distribution. In contrast, it becomes more difficult when this simplification does not occur since more parameters are involved, requiring often the use of MCMC methods. We derive the Bayesian Discrepancy Measure and the related test by considering a variety of distribution assumptions with multiparametric CVs and apply them to real datasets. As far as we know, some of the examined problems have not yet been covered in the literature.

1. INTRODUCTION

In many areas of applied statistics including medicine, biostatistics, anthropology, financial analysis, quality control and chemical experiments, the coefficient of variation (CV) is commonly used as a measure of dispersion and it is applied to compare relative variability of two or more independent populations. The problem of making inference on the equality of two CVs has been widely addressed in the literature in a frequentist perspective. The majority of statistical tests proposed are based on parametric models and require the determination of the limiting distribution of the sample CV which is often not easy to be derived. In the case of normal populations one of the most recent contributions is given in [1], where can also be found a quite exhaustive review of the related literature. Many of the proposals discussed are based on likelihood ratio statistics and their asymptotic properties. Various modified version of the standard likelihood ratio statistic have also been proposed. The different testing procedures in the literature consider either the difference or the ratio of the CVs. Usually it is assumed that the data follows symmetric distributions, however asymptotic tests for asymmetric distributions have also been discussed. For instance, the case of the lognormal distribution is considered in [2] and [3], and a most general assumption of asymmetry, with applications to the Beta and the Gamma distributions, has been considered in [4]. Nonparametric techniques, such as bootstrap, which free up the analysis from the parametric restrictive assumptions, have also alternatively been proposed (see [5] and [6]). Although being more flexible in terms of model assumptions required, such approaches still rely on the definition of an appropriate test statistic.

In the Bayesian framework few contributions to the use of tests for comparing CVs can be found and, as far as we know, they only refer to the case of normal distributions. In particular [7] proposed an approach based on the use of fractional Bayes factor, whereas

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Pereira and Stern \[8\] considered the application of a Bayesian measure of evidence for sharp null hypotheses (the so called Full Bayesian Significance Test).

In this paper, we propose to perform a test on the equality of two coefficients of variation (CVs) of independent populations through the Bayesian Discrepancy Measure (BDM), a Bayesian measure of evidence recently introduced in the literature (see \[9\]). To highlight the simplicity and the potential of this method, different cases and models have been considered and examples on real data are presented.

The structure of the paper is as follows. Section 2 provides a summary on the definition of the BDM and presents a general procedure to be followed to perform the comparison of parameter functions of two independent populations. Then, Section 3 deals with the comparison between two coefficients of variation and provides, on a case-by-case basis, the tools needed for that particular scenario, which are subsequently used in the related examples taken from the literature. Finally, the last section contains conclusions and guidelines to be followed for further research.

As far as we know, some of the tests analysed have not been investigated before in the literature, see Section 3.3 concerning the Skew-Normal case and 3.4 the Negative Binomial one.

2. DEFINING THE BAYESIAN DISCREPANCY MEASURE AND THE RELATED TEST

Let \( X \sim f(x|\theta) \) be a parametric model indexed by a scalar parameter \( \theta \in \Theta \), \( g(\theta) \) a prior density of \( \theta \) and \( x \) a sample of \( iid \) observations. We denote by \( g(\theta|x) \propto g(\theta) \cdot L(\theta|x) \) the posterior density of \( \theta \), where \( L(\theta|x) = \prod_{i=1}^{n} f(x_i|\theta) \) is the likelihood function. Let also \( G(\theta|x) \) be the corresponding distribution function and \( m_1 = G^{-1}(\frac{1}{2}|x) \) the posterior median.

Let \( H : \theta = \theta_H \) be the sharp hypothesis that we want to test. The Bayesian Discrepancy Test (see \[9\]) is based on the measurement of the discrepancy between the posterior median \( m_1 \) and \( \theta_H \). This naturally leads to consider the intervals \( I_H \) (discrepancy interval) and \( I_E \) (external interval) defined, in case of \( \Theta = \mathbb{R} \), as

\[
I_H = \begin{cases} 
(m_1, \theta_H) & \text{if } m_1 < \theta_H, \\
\{m_1\} & \text{if } m_1 = \theta_H, \\
(\theta_H, m_1) & \text{if } m_1 > \theta_H.
\end{cases}
\]

\[
I_E = \begin{cases} 
(\theta_H, +\infty) & \text{if } m_1 < \theta_H, \\
(-\infty, \theta_H) & \text{if } \theta_H < m_1.
\end{cases}
\]

When \( m_1 = \theta_H \), the external interval \( I_E \) can be either \((-\infty, m_1)\) or \((m_1, +\infty)\). Note that \( \mathbb{P}(I_H \cup I_E) = \frac{1}{2} \). If the support of the posterior is a subset of \( \mathbb{R} \), the intervals \( I_H \) and \( I_E \) will be defined consequently.

The Bayesian Discrepancy Measure (BDM) is then defined as

\[
\delta_H = 2 \cdot \mathbb{P}(\theta \in I_H|x) = 2 \cdot \int_{I_H} dG(\theta|x) = 1 - 2 \cdot \int_{I_E} dG(\theta|x)
\]

\[
= 1 - 2 \cdot \min \{ \mathbb{P}(\theta > \theta_H|x), \mathbb{P}(\theta < \theta_H|x) \},
\]

the last formulation has the advantage of avoiding the computation of the posterior median.
The more $\theta_H$ is far from the median of the posterior distribution $G(\theta|x)$, the more $\delta_H$ is large and, in that case, $H$ is not conform to $G$. On the contrary, the smaller $\delta_H$ the stronger is the evidence in favour of $H$. The acceptance or rejection of $H$ depends on the value of $\delta_H$ and its comparison with a threshold $\omega \in \{0.95, 0.99, 0.995, 0.999, \ldots\}$. Notice that the BDM is invariant under one-to-one reparametrization.

The approach described previously can be extended to a more general case. Let $X \sim f(x|\theta)$, where $\theta = (\theta_1, \ldots, \theta_k) \in \Theta \subseteq \mathbb{R}^k$, $\varphi = \gamma(\theta)$ be the parameter of interest, where $\gamma : \Theta \to \Phi \subseteq \mathbb{R}$ is a known continuous function and there exists a one-to-one transformation from $\theta$ to $(\varphi, \zeta)$, where $\zeta$ is a noise parameter. It can happen that $\gamma(\theta) = \theta_j$, for some $j$. Let also

$$H : \varphi = \varphi_H$$

be the hypothesis that we want to test by means of the BDM. If it is possible to compute the marginal posterior of $\varphi$, i.e.

$$g_M(\varphi|x) = \int_{\gamma(\theta) = \varphi} g(\theta|x) \, d\theta, \quad \forall \varphi \in \Phi,$$

the BDM of the hypothesis (4) is reconducted to the univariate case, see formula (3). Since $\gamma$ induces a partition $\{\Theta_a, \Theta_H, \Theta_b\}$ of the parameter space $\Theta$, with

$$\Theta_H = \{\theta \in \Theta \mid \gamma(\theta) = \varphi_H\},$$

$$\Theta_a = \{\theta \in \Theta \mid \gamma(\theta) < \varphi_H\},$$

$$\Theta_b = \{\theta \in \Theta \mid \gamma(\theta) > \varphi_H\},$$

we can avoid the computation of $g_M(\varphi|x)$ and define, for the higher dimensional case, the BDM as

$$\delta_H = 1 - 2 \cdot \int_{I_E} dG(\theta|x)$$

$$= 1 - 2 \cdot \min_{a,b} \left\{ \mathbb{P}(\theta \in \Theta_a \mid x), \mathbb{P}(\theta \in \Theta_b \mid x) \right\},$$

where now the external set $I_E$ is given by

$$I_E = \arg\min_{a,b} \left\{ \mathbb{P}(\theta \in \Theta_a \mid x), \mathbb{P}(\theta \in \Theta_b \mid x) \right\}.$$

Methodological aspects of the Bayesian Discrepancy Test and similarities with Fisher’s pure significance test and Pereira and Stern’s FBST are discussed in [9].

The Bayesian Discrepancy Test is suitable for comparing parameter functions of two independent populations $X_\ell \sim f(\cdot|\theta_\ell)$, $\ell = 1, 2$. Given a prior density $g_\ell(\theta_\ell)$ and $x_\ell = \{x_{\ell_1}, \ldots, x_{\ell_{n_\ell}}\}$ a sample of $n_\ell$ iid observations, the posterior density is then $g_\ell(\theta_\ell|x_\ell) \propto g_\ell(\theta_\ell) L_\ell(\theta_\ell|x_\ell)$.

We indicate with $\theta$ the joint parameter vector $\theta = (\theta_1, \theta_2) \in \Theta_1 \times \Theta_2 = \Theta$ of the two populations parameters. We have that $\Theta_\ell \subseteq \mathbb{R}^k$, where $k$ is the number of parameters in $\theta_\ell$ and $\ell = 1, 2$. Consequently, $\Theta \subseteq \mathbb{R}^k \times \mathbb{R}^k$.

We are interested in testing the hypothesis

$$H : \varphi_1 - \varphi_2 = 0,$$

which identifies the partition $\{\Theta_a, \Theta_H, \Theta_b\}$ of $\Theta$, where
The test can be performed by evaluating the BDM (as seen in (5)) that requires the computation of the minimum probability between \( \mathbb{P}(\Theta_a \mid x_1, x_2) \) and \( \mathbb{P}(\Theta_b \mid x_1, x_2) \), where

\[
\Theta_H = \{ \theta \in \Theta \mid \varphi_1 = \varphi_2 \},
\]
\[
\Theta_a = \{ \theta \in \Theta \mid \varphi_1 < \varphi_2 \},
\]
\[
\Theta_b = \{ \theta \in \Theta \mid \varphi_1 > \varphi_2 \}.
\]

The evaluation of these probabilities require the computation of multidimensional integrals that can not be solved in a closed form, which is why we proposed to approximate them using the Monte Carlo Integration method (the implemented R code is reported is available on Github at the address [https://github.com/maramanca/CVs_comparison/tree/main](https://github.com/maramanca/CVs_comparison/tree/main)).

3. Testing the equality of two CVs

Recall that the CV is an adimensional parameter defined as the ratio of the standard deviation to the absolute value of the expected value

\[
\varphi_\ell = \frac{\sqrt{\text{Var}(X_\ell)}}{|E(X_\ell)|}, \quad \ell = 1, 2.
\]

In some populations with several parameters, it may happen that the CV depends on only one of them, as is the case for the Log\(\text{N}(\cdot | \mu, \sigma^2)\) model where \( \text{CV} = \sqrt{e^{\sigma^2} - 1} \), but also for some other populations such as \( \text{Gamma}(\cdot | \alpha, \lambda) \), \( \text{Pareto}(\cdot | \alpha, \lambda) \) and \( \text{Weibull}(\cdot | \alpha, \lambda) \) where the CV depends solely on the shape parameter.

In what follows, we propose the analysis of several non-trivial cases in which the comparison involves the full parameter space.

3.1. The case of two independent Normal populations. Consider two independent Gaussian random variables \( X_\ell \sim N(x_\ell | \mu_\ell, \phi_\ell^{-1}) \), with \( X_\ell \in \mathbb{R} \) and \( (\mu_\ell, \phi_\ell) \in \mathbb{R} \times \mathbb{R}^+ \), for \( \ell = 1, 2 \). Assuming the non-informative priors

\[
(\mu_\ell, \phi_\ell) \sim \phi_\ell^{-1}, \quad \ell = 1, 2,
\]

and given \( n_\ell \) observations with sample means \( \bar{x}_\ell \) and sample standard deviations \( s_\ell \). It is known that the posterior distributions of the parameter vectors are Normal Gamma

\[
(\mu_\ell, \phi_\ell) \mid x \sim NG(\mu_\ell, \phi_\ell | \nu_\ell, \alpha_\ell, \beta_\ell), \quad \ell = 1, 2,
\]

with hyperparameters \( \eta_\ell = \bar{x}_\ell, \nu_\ell = n_\ell, \alpha_\ell = (n_\ell - 1)/2, \beta_\ell = n_\ell s_\ell^2/2 \).

The hypothesis \( H : \varphi_1 - \varphi_2 = 0 \), where \( \varphi_\ell = \frac{1}{|\mu_\ell|\sqrt{\phi_\ell}} \), identifies in the parameter space \( \Theta \) the subsets

\[
\Theta_a = \left\{ (\mu_1, \phi_1, \mu_2, \phi_2) \in \mathbb{R}^2 \times \mathbb{R}^2_+ \mid |\mu_1|\sqrt{\phi_1} > |\mu_2|\sqrt{\phi_2} \right\}
\]

and

\[
\Theta_b = \left\{ (\mu_1, \phi_1, \mu_2, \phi_2) \in \mathbb{R}^2 \times \mathbb{R}^2_+ \mid |\mu_1|\sqrt{\phi_1} < |\mu_2|\sqrt{\phi_2} \right\}.
\]
Table 1. Dispersion dimorphism in a set of anthropometric dimensions and relative BDM. Weight is expressed in kg; skinfolds in mm; all other measurements in cm.

|        | Men  | Women | \( \delta_H \) |
|--------|------|-------|-----------------|
|        | Mean | SD    | \( n_1 \) | CV  | Mean | SD    | \( n_2 \) | CV  |       |
| **Weight** | 67.22 | 8.46  | 140          | 0.126 | 53.71 | 7.59  | 140          | 0.141 | 0.812 |
| **Breadths** | | | | | | | | | |
| **Cephalic** | 15.10 | 0.64  | 141          | 0.042 | 14.53 | 0.58  | 172          | 0.040 | 0.550 |
| **Elbow** | 7.02  | 0.39  | 103          | 0.056 | 6.01  | 0.35  | 117          | 0.058 | 0.355 |
| **Circumferences** | | | | | | | | | |
| **Midarm relaxed** | 26.91 | 2.60  | 139          | 0.097 | 23.47 | 2.01  | 134          | 0.086 | 0.831 |
| **Midarm tensed** | 30.83 | 2.74  | 139          | 0.089 | 25.28 | 2.15  | 133          | 0.085 | 0.388 |
| **Skinfolds** | | | | | | | | | |
| **Biceps** | 4.10  | 1.79  | 137          | 0.437 | 6.08  | 2.51  | 133          | 0.413 | 0.420 |
| **Triceps** | 7.76  | 3.76  | 140          | 0.485 | 13.33 | 4.78  | 140          | 0.359 | 0.996 |
| **Subscapular** | 10.34 | 3.78  | 137          | 0.366 | 12.71 | 4.53  | 140          | 0.356 | 0.213 |
| **Suprailiac** | 9.23  | 4.34  | 140          | 0.470 | 10.21 | 4.48  | 140          | 0.439 | 0.507 |
| **Abdominal** | 12.15 | 6.52  | 97           | 0.537 | 12.77 | 5.74  | 111          | 0.449 | 0.848 |

The BDM (as seen in [5]) requires the computation of

\[
\mathbb{P}\left( (\mu_1, \phi_1, \mu_2, \phi_2) \in \Theta_j \mid x \right) = \int_{\Theta_j} \prod_{\ell=1}^{2} g(\mu_\ell, \phi_\ell | \eta_\ell, \nu_\ell, \alpha_\ell, \beta_\ell) \, d\mu_\ell \, d\phi_\ell,
\]

where \( j = a, b \) and \( g(\cdot) \) is the Normal Gamma density. We present now an application of this test using real data.

**Example 1. Anthropometric measures in Sardinian population**

We consider a set of anthropometric measures concerning the Sardinian population. The sample consists of 280 individuals of both sexes (140 males and 140 females) aged 20–25, that was collected between 1995–1998. We focus on the CVs comparisons among men and women. The same data were presented and analysed in [10], where the bootstrap test for the difference of CVs developed in [5] was applied to evaluate sexual dimorphism. Among the 20 measurements in the dataset, we applied the Bayesian Discrepancy Test to a subsample of 10 which can be assumed to be normally distributed. In Table 1 are reported the principal descriptive statistics together with the values of the discrepancy measure associated to each anthropometric dimension considered. Based on the BDM we conclude that only one hypothesis can be rejected, that is the equality between the coefficients of variation for men’s and women’s skinfolds triceps. The final conclusions go in the same direction as [10].
3.2. The case of two independent inverse Gaussian populations. Given two independent inverse Gaussian random variables $X_\ell \sim IG(x_\ell \mid \mu_\ell, \lambda_\ell)$ i.e.

$$f(x_\ell \mid \mu_\ell, \lambda_\ell) = \left(\frac{\lambda_\ell}{2\pi x_\ell^2}\right) \exp\left\{-\frac{1}{2\lambda_\ell} \left(\frac{x_\ell - \mu_\ell}{\mu_\ell\sqrt{2\lambda_\ell}}\right)^2\right\},$$

with $X_\ell \in \mathbb{R}^+$ and $(\mu_\ell, \lambda_\ell) \in \mathbb{R}^+ \times \mathbb{R}^+$ for $\ell = 1, 2$.

Assuming the Jeffreys non-informative priors

$$g(\mu_\ell, \lambda_\ell) \propto \frac{1}{\sqrt{\mu_\ell^3 \lambda_\ell}}, \quad \ell = 1, 2$$

and given $n_\ell$ observations, the posterior distribution of the parameter vector is

$$g_\ell(\mu_\ell, \lambda_\ell \mid x_\ell) \propto \sqrt{\frac{\lambda_\ell^{n_\ell-1}}{\mu_\ell}} \exp\left\{-\frac{n_\ell \lambda_\ell}{2} \left(\frac{\bar{x}_\ell - 2}{\mu_\ell} + \frac{1}{a_\ell}\right)\right\}, \quad \ell = 1, 2$$

where $\bar{x}_\ell$ and $a_\ell$ are the arithmetic and harmonic means respectively.

The hypothesis $H : \varphi_1 - \varphi_2 = 0$, where $\varphi_\ell = \sqrt{\frac{a_\ell}{\lambda_\ell}}$, identifies on the parameter space $\Theta$ the subsets

$$\Theta_a = \left\{(\mu_1, \lambda_1, \mu_2, \lambda_2) \in \mathbb{R}^4_+ \mid \mu_1 \lambda_2 < \mu_2 \lambda_1\right\}$$

and

$$\Theta_b = \left\{(\mu_1, \lambda_1, \mu_2, \lambda_2) \in \mathbb{R}^4_+ \mid \mu_1 \lambda_2 > \mu_2 \lambda_1\right\}.$$ 

The evaluation of the probabilities

$$\mathbb{P}\left((\mu_1, \lambda_1, \mu_2, \lambda_2) \in \Theta_j \mid x_1, x_2\right) = \int_{\Theta_j} \prod_{\ell=1}^2 g_\ell(\mu_\ell, \lambda_\ell \mid x_\ell) \, d\mu_\ell \, d\lambda_\ell, \quad j = a, b$$

allows us to compute the BDM.

It is worth to notice that, in this case, the measure of skewness is three times the coefficient of variation. A test on the comparison of two skewness indices is then equivalent to testing the equality of two coefficients of variation.

**Example 2.** Hodgkin’s disease plasma bradykininogen levels

We consider a study on the Hodgkin’s disease in which plasma bradykininogen levels were measured for two groups of patients with active and inactive Hodgkin’s disease. The outcome variable is measured in micrograms of bradykininogen per milliliter of plasma. This dataset was analyzed in [11] where it was shown that the data fit an inverse Gaussian distribution. In the group of patients with active disease we have that $n_1 = 17$ and $\varphi_1 = 0.2889$ while in second group, with inactive Hodgkin’s disease, $n_2 = 28$ and $\varphi_2 = 0.2810$.

The computation of $\delta_H$ is linked to the evaluation of two four-dimensional integrals (see (9)). We approximate the integrals by means of the Monte Carlo integration. Since the posterior distribution is known up to a normalizing constant, it is not possible to sample directly from it. We, therefore, applied the random walk Metropolis-Hasting algorithm using a bivariate Normal proposal distribution. In order to obtain a chain that converges to the target distribution, $10^6$ samples were employed and reduced to $2 \cdot 10^5$ after considering a burn-in period and a chain thinning.

Since the resulting discrepancy measure is $\delta_H = 0.2532$, we do not have enough evidence to reject the null hypothesis of CVs equality. The same dataset has been recently analysed in the frequentist frame in [12], where the authors have considered four different versions.
of confidence intervals for the difference of CVs. The methods used were the Generalized Confidence Interval, the Adjusted Generalized Confidence Interval ([13], [14]), the Method of Variance Estimation Recovery (MOVER) ([15]) and bootstrap percentiles. Exception made for the bootstrap percentiles, the remaining methods are based on the determination of pivotal quantities specific to the distribution assumed and require asymptotic approximations. Our method leads to the same conclusions as [12].

3.3. The case of two independent Skew Normal populations. Consider two independent Skew Normal random variables $X_\ell \in \mathbb{R}, \ell = 1, 2$, with density

$$f(x_\ell | \mu_\ell, \sigma_\ell, \lambda_\ell) = \frac{2}{\sigma_\ell} \phi \left( \frac{x_\ell - \mu_\ell}{\sigma_\ell} \right) \Phi \left( \frac{\lambda_\ell (x_\ell - \mu_\ell)}{\sigma_\ell} \right) = \frac{2}{\sigma_\ell \sqrt{2\pi}} e^{-\frac{(x_\ell - \mu_\ell)^2}{2\sigma_\ell^2}} \int_{-\infty}^{\lambda_\ell (x_\ell - \mu_\ell)/\sigma_\ell} \frac{1}{\sqrt{2\pi}} e^{-t^2} dt,$$

where the location, the scale and the shape parameters are $(\mu_\ell, \sigma_\ell, \lambda_\ell) \in \mathbb{R} \times \mathbb{R}^+ \times \mathbb{R}$. Given $\delta_\ell = \frac{\lambda_\ell}{\sqrt{\lambda_\ell^2 + 1}}$, the expected value, variance and coefficient of variation can be expressed as

$$E(X_\ell) = \mu_\ell + \sigma_\ell \delta_\ell \sqrt{\frac{2}{\pi}},$$
$$Var(X_\ell) = \sigma_\ell^2 \left( 1 - \frac{2\delta_\ell^2}{\pi} \right),$$
$$CV(X_\ell) = \varphi_\ell = \frac{\sqrt{\sigma_\ell^2 \left( 1 - \frac{2\delta_\ell^2}{\pi} \right)}}{|\mu_\ell + \sigma_\ell \delta_\ell \sqrt{\frac{2}{\pi}}|}.$$

The Jeffreys priors can be approximated as

$$g_\ell(\mu_\ell, \sigma_\ell, \lambda_\ell) \propto \frac{1}{\sigma_\ell} g_\ell(\lambda_\ell),$$

where $g_\ell(\lambda_\ell)$, the prior distribution of the shape parameter, is a generalized t-Student distribution with location parameter $\mu_\ell = 0$, scale parameter $\sigma_\ell = \pi/2$ and degrees of freedom $\nu_\ell = 1/2$ (see [16]), i.e.

$$g_\ell(\lambda_\ell) = \frac{1}{B(\nu_\ell/2, \frac{1}{2})} \sqrt{\frac{\sigma_\ell}{\nu_\ell}} \left( 1 + \frac{\sigma_\ell (\lambda_\ell - \mu_\ell)^2}{\nu_\ell} \right)^{-\frac{\nu_\ell + 1}{2}}.$$

The posterior distributions of the parameter vectors are then

$$g_\ell(\mu_\ell, \sigma_\ell, \lambda_\ell | x_\ell) \propto \frac{2^{\nu_\ell}}{\sigma_\ell^{\nu_\ell+1}} g_\ell(\lambda_\ell) \prod_{i=1}^{\nu_\ell} \phi \left( \frac{x_i - \mu_\ell}{\sigma_\ell} \right) \Phi \left( \frac{\lambda_\ell (x_i - \mu_\ell)}{\sigma_\ell} \right).$$

The hypothesis $H : \varphi_1 - \varphi_2 = 0$ identifies in the parameter space $\Theta$ the subsets

$$\Theta_a = \left\{ (\mu_1, \sigma_1, \lambda_1, \mu_2, \sigma_2, \lambda_2) \in \mathbb{R}^4 \times \mathbb{R}^2_+ \mid \varphi_1 < \varphi_2 \right\}$$

and

$$\Theta_b = \left\{ (\mu_1, \sigma_1, \lambda_1, \mu_2, \sigma_2, \lambda_2) \in \mathbb{R}^4 \times \mathbb{R}^2_+ \mid \varphi_1 > \varphi_2 \right\}.$$
Table 2. Three differentially expressed miRNAs in the colon cancer study.

| miRNA     | Tumor tissue Mean | SD  | CV  | Healthy tissue Mean | SD  | CV  | δ_H |
|-----------|------------------|-----|-----|---------------------|-----|-----|-----|
| miR-182   | 13.9             | 0.59| 0.04| 13.32               | 0.32| 0.02| 0.9997 |
| miR-183   | 13.17            | 0.72| 0.05| 12.32               | 0.43| 0.04| 0.9964 |
| miR-96    | 10.75            | 0.85| 0.08| 10.19               | 0.41| 0.04| 1    |

To compute BDM we evaluate the probabilities

\[ P\left(\left\{\mu_1, \sigma_1, \lambda_1, \mu_2, \sigma_2, \lambda_2\right\} \in \Theta_j \mid x_1, x_2\right), \quad j = a, b. \]

Example 3. Differential expression in colon cancer genes

In the framework of genetic studies, microRNA (miRNA) levels are often used as diagnostic tools for cancer detection. Comparisons between two disease conditions, such as the presence or absence of cancer cells, often result in determining the presence of differentially expressed genes. A gene is said differentially expressed if there is a difference in its expression levels (abundance of miRNA) between two conditions. Usually such differences are investigated by applying pair comparison statistical tests which rely on the assumption of normality distribution for gene’s expression, and different transformations and normalizations of the original variable are applied in order to guarantee such condition.

Instead, in a recent study [17] was proposed to assume a Skew Normal distribution for the gene’s expression, since it helps to overcome the presence of possible asymmetries. Following these suggestions we considered a study on colon cancer, analysed in [17], and compared the CVs of a selection of genes in healthy and tumor tissues. The aim of the original work was to determine which miRNAs were differentially expressed between the two sets of samples collected during surgery from 145 subjects (116 with colon cancer and 29 healthy). Data is available from the public genomics data repository Gene Expression Omnibus (GEO) and accessible through GEO Series accession number GSE18392. In this analysis we consider a small selection of 3 miRNAs among those which were found to be differentially expressed (see [18]).

Given that we only know the posterior distribution up to a normalising constant, the application of MCMC methods is necessary in order to calculate the probabilities (10). In particular, following the literature on Bayesian inference for a Skew-Normal distribution (see [16]), a Gibbs-sampler has been used. Chains convergence was reached with \(6 \cdot 10^5\) samples, that were reduced to \(3 \cdot 10^4\) after considering a burn-in period and a chain thinning. In Table 2 are reported the principal descriptive statistics and the discrepancy measure values. According to the \(\delta_H\) obtained all the hypothesis can be rejected, confirming a difference in the two tissue samples also in terms of their CVs.

3.4. The case of two independent Negative Binomial populations. Let us consider two discrete Negative Binomial populations. It is known that, given \(X_\ell|\lambda_\ell \sim \text{Poiss}(x_\ell \mid \lambda_\ell)\) with \(\lambda_\ell \sim \text{Gamma}(\lambda_\ell \mid \alpha_\ell, \beta_\ell)\), then the unconditional random variables \(X_\ell\) follow a Negative Binomial distribution

\[ X_\ell \sim NB\left(x_\ell \mid \frac{\beta_\ell}{\beta_\ell + 1}, \alpha_\ell\right), \quad \ell = 1, 2 \]
with \((\alpha_\ell, \beta_\ell) \in \mathbb{R}^+ \times \mathbb{R}^+\). Its expected value, variance and coefficient of variation are
\[
E(X_\ell) = \frac{\alpha_\ell}{\beta_\ell},
\]
\[
Var(X_\ell) = \frac{\alpha_\ell(\beta_\ell + 1)}{\beta_\ell^2},
\]
\[
CV(X_\ell) = \varphi_\ell = \sqrt{\frac{\beta_\ell + 1}{\alpha_\ell}}.
\]
Assuming the Jeffreys priors for \(\lambda_\ell\) (see [19])
\[
g_\ell(\alpha_\ell, \beta_\ell) \propto \frac{1}{\beta_\ell} \sqrt{\alpha_\ell \psi_1(\alpha_\ell)} - 1, \quad \ell = 1, 2
\]
where \(\psi_1(\alpha_\ell) = \sum_{j=0}^{\infty} (\alpha_\ell + j)^{-2}\) is the PolyGamma function. The posterior distributions of the parameter vectors take the expressions
\[
g_\ell(\alpha_\ell, \beta_\ell | x_\ell) \propto \prod_i \frac{(x_i + \alpha_\ell - 1)!}{(\alpha_\ell - 1)!^{n_i}} \left[\frac{\beta_\ell^{n_i}}{(\beta_\ell + 1)^{\alpha_\ell + n_i}}\right]^n \frac{1}{\beta_\ell} \sqrt{\alpha_\ell \psi_1(\alpha_\ell)} - 1.
\]
The hypothesis \(H: \varphi_1 - \varphi_2 = 0\) identifies on the parameter space \(\Theta\) the subsets
\[
\Theta_a = \left\{(\alpha_1, \beta_1, \alpha_2, \beta_2) \in \mathbb{R}_+^2 \times \mathbb{R}_+^2 \mid \alpha_2(\beta_1 + 1) < \alpha_1(\beta_2 + 1)\right\}
\]
and
\[
\Theta_b = \left\{(\alpha_1, \beta_1, \alpha_2, \beta_2) \in \mathbb{R}_+^2 \times \mathbb{R}_+^2 \mid \alpha_2(\beta_1 + 1) < \alpha_1(\beta_2 + 1)\right\},
\]
for which we have to compute the probabilities
\[
(11) \quad \mathbb{P}\left((\alpha_1, \beta_1, \alpha_2, \beta_2) \in \Theta_j \mid x_1, x_2\right), \quad j = a, b.
\]

**Example 4.** Superspreading of COVID-19 infections

In the epidemiology context, when investigating the spreading dynamics of an infectious disease, it is often of interest to model the number of new infections (second cases) generated by an infectious subject. This kind of variable, in cases of individual variability in the transmission patterns, is overdispersed and right skewed (see [20]), therefore the negative binomial distribution is often considered for its analysis. During the Sars-Cov-2 (COVID-19) pandemic many national health systems have collected such kind of information considering contact tracing data to try their best in catching the diffusion pathways of the disease and the behaviours leading to its increase. In particular, differences in individual contact patterns were a symptom of a superspreading phenomenon as was observed that a small number of infected could causes most of the secondary infections. Looking at the recent literature we used two published data on secondary cases of COVID-19 and compared their CVs through the BDM. The first dataset considered comes from data tracing in two Indian states (see [21]) from March to July 2020. It is a large dataset containing the offspring distribution for 88,527 cases, with sample mean 0.48 and variance 1.15 that leads to a CV of 2.218. The second one contains 290 cases from Hong Kong (see [22]) recorded from January to April 2020. In this case the observed mean is 0.58 whereas the variance 1.29 leading to a sample CV of 2.217. This two coefficients of variation are extremely close between each other and, as expected, we get to a small BDM of \(\delta_H = 0.00972\). We therefore can not reject the hypothesis on the coefficients of variation equality between the India and the Hong Kong samples.
Also for this last model, the application of Metropolis-Hasting algorithms was required for the evaluation of probabilities. In order to obtain a chain that converged to the target distribution, \(1.3 \times 10^5\) samples were employed and reduced to \(10^5\) after considering a burn-in period.

4. Discussion and Conclusions

In this paper we have proposed a new Bayesian approach to test the equality of the coefficients of variation of two independent populations. The procedure presented is general and it does not require “ad hoc” techniques such as those proposed to solve similar problems in the frequentist settings, which are usually applicable only to particular cases.

Furthermore, as far as we know, the cases of the Skew Normal populations and Negative Binomial ones are completely original and they have not been addressed before in the literature.

The method outlined here has a more general validity as it can be extended to comparisons between parameters of two independent populations and/or their functions. This is feasible without making use of any asymptotic technique. Extensions include comparisons between skewness and kurtosis coefficients, regression coefficients, etc.

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