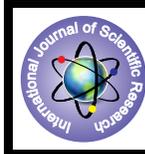


Parametric Test for Mean Using Maple Programme



Science

KEYWORDS : Parametric tests, Maple Programmes, Generalized lambda distribution.

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ABSTRACT

Here we present a general parametric method for testing the mean of any distribution using Maple Programme. By obtaining the first four central moments of the test statistics its distribution is fitted as a member in the Generalized Lambda Distribution (GLD) family under both the null and alternative hypotheses. To fit the distribution and to evaluate the power of the test, computer programmes in Maple language are provided. The method can be applied for any unimodal continuous distribution.

1. Introduction

Mean is the most important measure of location. Due to its primary role in statistical

decision making, test for mean plays a central role in statistical inference. The classical methods of testing the mean are known as the normal test and t-test. Both these tests are based on the important assumption that the available data belong to a normal distribution. When there are evidences of the distribution of the parent population deviating from normal, the test is still conducted using the classical procedures itself under the strength of the central limit theorem. Since, the central limit theorem is valid only for large sample sizes, practitioners found it very unreliable to depend on the test when there are explicit evidences of deviation from normal. Lack of normality is reflected through lack of symmetry or heavy tails for the distribution. Sophister (1928) had shown that the skewness in the population affects the distribution of t-statistics more than kurtosis. They had also shown that positive skewness in the population results in the negative skewness in the distribution of t and vice versa. Geary (1936) has shown that the skewness of the distribution of t is opposite in sign to the skewness of the population distribution. As a consequence, the sample mean should be more concentrated on the left side of the probability curve for a positively skewed distribution and on the right side of the probability curve for a negatively skewed distribution.

The GLD representations of almost all well known distributions are discussed in details in Karian and Dudewicz (2000). Also, numerical results reveal that the GLD representation of any unimodal continuous distribution almost agrees with the true distribution both in terms of cumulative distribution and probability distribution functions. In this article, we suggest a parametric test for population mean. The method is based on the GLD representation of the distribution of the test statistics. This method consists in fitting the distribution of the test statistics under both the null and alternative hypotheses and evaluation of power of the test. The method is more reliable as it utilizes maximum information from the sample and it can be used for all types of distributions. To apply this method, computer programmes in Maple language are provided. The most significant aspect of the method is that, by inputting the given set of observations in the programme, one can examine whether the observations are drawn from a population with the specified mean against any of the alternatives. A brief review of the GLD family is discussed in section 2. By deriving the first four central moments of the test statistics, the proposed test is described in section 3. The application of the method on real life data is also provided in this section.

2. Generalized Lambda Distributions (GLD) Family

The generalized lambda distribution (GLD) family is a four parameter family of distributions derived by Ramberg and Schmeiser (1974). Unlike most other four parameter family of distributions, GLD has no explicit expression for its pdf, instead,

members of the family are specified in terms of their quantile function. The quantile function of the four parameter GLD family is given by

$$Q(p) = \lambda_1 + [p^{\lambda_3} - (1-p)^{\lambda_4}] / \lambda_2$$

Here, λ_1 and λ_2 represent the location and scale parameters where as λ_3 and λ_4 represent the shape parameters of the distribution. The support of the random variable with the above distribution is $[\lambda_1 - 1/\lambda_2, \lambda_1 + 1/\lambda_2]$ when $\lambda_3 > 0$ and $\lambda_4 > 0$. The support is $(-\infty, \lambda_1 + 1/\lambda_2)$ when $\lambda_3 < 0$ and $\lambda_4 = 0$ and it is $(\lambda_1 - 1/\lambda_2, \infty)$ when $\lambda_3 = 0$ and $\lambda_4 < 0$.

2.1 Estimation of Parameters and Fitting of GLD

The popular method of fitting GLD to a data set is the method of moments due to

Ramberg et al. (1979). In this method the parameters λ_3 and λ_4 are first derived by solving the equations $\alpha_3 = a_3$ and $\alpha_4 = a_4$, where α_3 and α_4 are the coefficients of skewness and kurtosis of the distribution and a_3 and a_4 are their sample estimates. These systems of equations are too complex, so that to obtain the solutions computer programme in Maple language is provided. By solving the equations $\alpha_1 = a_1$, $\alpha_2 = a_2$ and using the estimated values of λ_3 and λ_4 , the values of λ_1 and λ_2 were determined. It may be noted that skewness and kurtosis are independent of location and scale parameters and moments of all orders exist if λ_3 and λ_4 are of same sign. Since corresponding to every admissible pair of skewness and kurtosis measures GLD family contains a member, a wide variety of densities with different tail shapes are available in the family. This family was used for Monte-Carlo simulation studies of robustness of statistical procedures and for sensitivity analysis. The family contains unimodal, U-shaped, J-shaped, symmetric and asymmetric distributions. One of the important advantages of this family is that all its members can be represented by a single quantile function and almost all known distributions can be represented as its member.

3. Test for Mean

Here we propose a general parametric test for the mean of any population with unknown distribution. The main features of the proposed test is that the sampling distribution of the test statistics is estimated as a member in the four parameter GLD family based on its first four moments. The critical region of the test is determined directly using the fitted GLD. Power of the test can also be evaluated under this method. In order to simplify the analysis, computer programmes in Maple language are provided.

Let X be a random variable with mean μ_1' , variance μ_2' , skewness $\sqrt{\beta_1}$ and kurtosis β_2' . For a given sample of n observations, x_1, x_2, \dots, x_n , let m_1' denote the mean and m_r denote the rth order sample central moments, $r = 1, 2, 3, \dots$. To test $H_0 : \mu_1' = \mu_0$, the test statistics is the sample mean m_1' . Under the null hypothesis, the estimates of mean, variance, skewness and kurtosis of the test statistics are obtained as

$$a_1 = \mu_0 \tag{3.1}$$

$$a_2 = m_2 / n \tag{3.2}$$

$$a_3 = m_3 / (\sqrt{n} m_2^{3/2}) \tag{3.3}$$

$$a_4 = [m_4 + 3(n-1)m_2^3] / nm_2^2 \tag{3.4}$$

The values of (a_1, a_2, a_3, a_4) can be evaluated using the following programme.

3.1 Programme-P₁

Procedure to determine the values of (a_1, a_2, a_3, a_4) -test for mean- via observations

Function: Findalphas via observations

Purpose:- Compute a-values of sample mean

Arguments: X -list of data

Findalphas:= Proc(X::list)

Local n, i, m₁, m₂, m₃, m₄, S, S1, S2, a₁, a₂, a₃, a₄;

n := nops(X);

m₁ := evalf(convert(X, '+')/n);

S := [seq((X[i] - m₁)², i = 1..n)];

m₂ := evalf(convert(S, '+')/n);

S1 := [seq((X[i] - m₁)³, i = 1..n)];

m₃ := evalf(convert(S1, '+')/n);

S2 := [seq((X[i] - m₁)⁴, i = 1..n)];

m₄ := evalf(convert(S2, '+')/n);

a₁ := μ₀, under H₀;

a₂ := evalf(m₂/n);

a₃ := evalf(m₃/(sqrt(n)*m₂^{3/2}));

a₄ := evalf((m₄+3(n-1)*m₂³)/n*m₂²);

Ah := (a₁, a₂, a₃, a₄);

end;

Using these values of (a_1, a_2, a_3, a_4) as arguments in the following programme, the GLD parameters of the distribution of the test statistics and the percentile points can be evaluated.

3.2 Programme-P₂

Procedure to determine lambdas and the percentile points from sample Ah-values

#Function: Findlambdas

#Purpose: Estimation of GLD parameters by Newton's approx.

#Arguments: Ah-list of a1, a2, a3, a4;

I3, I4-Initial approx. of λ3 and λ4

Findlambdas := Proc(Ah::list, I3::Numeric, I4::Numeric)

Local A, B, C, D1, D2, D, α1, α2, α3, α4, F, a1, a2, a3, a4, V, J, err3, err4, Fk, Jk, Y, Eq3, Eq4, A1, A2, L, FirstL, SecondL, I, R1, R2, R3, R4, R5, R6, R7, R8;

with(linalg, vector, matrix, jacobian, linsolve);

a1 := 0; a2 := 1; a3 := evalf(Ah[3]); a4 := evalf(Ah[4]); L3 := I3; L4 := I4;

$$A := [1/(1 + \lambda_3)] - [1/(1 + \lambda_4)];$$

$$B := [1/(1 + 2*\lambda_3)] + [1/(1 + 2*\lambda_4)] - 2 * Beta(1 + \lambda_3, 1 + \lambda_4);$$

$$C := [1/(1 + 3*\lambda_3)] - [1/(1 + 3*\lambda_4)] + 3 * Beta(1 + 2*\lambda_3, 1 + \lambda_4) + 3 * Beta(1 + \lambda_3, 1 + 2*\lambda_4);$$

$$D1 := [1/(1 + 4*\lambda_3)] + [1/(1 + 4*\lambda_4)] + 6 * Beta(1 + 2*\lambda_3, 1 + 2*\lambda_4);$$

$$D2 := -4 * Beta(1 + 3 * \lambda_3, 1 + \lambda_4) - 4 * Beta(1 + \lambda_3, 1 + 3 * \lambda_4); D := D1 + D2;$$

$$\alpha 1 := \lambda 1 + A / \lambda 2; \alpha 2 := \text{abs}(B - A^2) / \lambda 2^2;$$

$$\alpha 3 := (C - 3 * A * B + 2 * A^3) / \text{abs}((B - A^2)^{3/2});$$

$$\alpha 4 := (d - 4 * A * C + 6 * B * A^2 - 3 * A^4) / (B - A^2)^2;$$

$$\text{Eq3} := \alpha 3 - a3; \text{Eq4} := \alpha 4 - a4;$$

F := vector([Eq3,Eq4]); V := vector([λ3, λ4]);

j := evalf(jacobian(F, V)); err3 := 1; err4 := 1;

while (err3 > .0001 or err4 > .0001) do

Fk := vector([evalf(subs(λ3 = L3, λ4 = L4, -Eq3)), evalf(subs(λ3 = L3, λ4 = L4, -Eq4))]);

Jk := matrix([[subs(λ3 = L3, λ4 = L4, j[1, 1]), subs(λ3 = L3, λ4 = L4, j[1, 2])], [subs(λ3 = L3, λ4 = L4, j[2, 1]), subs(λ3 = L3, λ4 = L4, j[2, 2])]);

[subs(λ3 = L3, λ4 = L4, j[2, 1]), subs(λ3 = L3, λ4 = L4, j[2, 2])]);

Y := linsolve(Jk, Fk); L3 := L3 + Y [1];

L3 := L3 + Y [1]; L4 := L4 + Y [2];

err3 := evalf(abs(subs(λ3 = L3, λ4 = L4, Eq3)));

err4 := evalf(abs(subs(λ3 = L3, λ4 = L4, Eq4)));

od;

print(L3, L4, err3, err4);

A1 := evalf(subs(λ 3 = L3, λ4 = L4,A));

A2 := evalf(subs(λ3 = L3, λ4 = L4,B));

L2 := abs(sqrt(((A2 - A1²)/a2)));

L1 := a1 - A1/L2;

FirstL := [L1, L2, L3, L4];

if L3 < 0 then SecondL := [-FirstL[1], FirstL[2], FirstL[4],

FirstL[3]] else SecondL :=

FirstL fi;

if evalf(Ah[3]) < 0 then L := [-SecondL[1], SecondL[2], SecondL[4], SecondL[3]] else

L := SecondL fi ;

l := [L[1] * sqrt(Ah[2]) + Ah[1], (L[2])/(sqrt(Ah[2])), L[3], L[4]];

t0.05 := l[1] + ((0.05)^{|l3|-}(0.95)^{|l4|})/l[2] ;

t0.95 := l[1] + ((0.95)^{|l3|-}(0.05)^{|l4|})/l[2] ;

t0.025 := l[1] + ((0.025)^{|l3|-}(0.975)^{|l4|})/l[2] ;

t0.975 := l[1] + ((0.975)^{|l3|-}(0.025)^{|l4|})/l[2] ;

t0.01 := l[1] + ((0.01)^{|l3|-}(0.99)^{|l4|})/l[2] ;

t0.99 := l[1] + ((0.99)^{|l3|-}(0.01)^{|l4|})/l[2] ;

t0.005 := l[1] + ((0.005)^{|l3|-}(0.995)^{|l4|})/l[2] ;

t0.995 := l[1] + ((0.995)^{|l3|-}(0.005)^{|l4|})/l[2] ;

end;

For a given level of significance, the power of the test can be evaluated based on the following programme

3.2 Programme-P₃

Procedure to determine the power values of the test for mean

Function: Power via iteration

Purpose: Compute power values of GLD test for mean

Arguments: l-list of lambda values

M0, M1- mean values under H0, H1

P0-initial approx. of power

#K-percentile point corr. to the test

FindPower:= Proc(l: list,M0::Numeric, M1::Numeric, P0::Numeric, K::Numeric)

Local l1, Q, E, err, P, p;

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I1 := evalf(I[1] +M1 -M0);
Q := I1 + ( p[3]-(1-p)[4])/I[2] ;
P := P - 0;E := K - Q; err := 0.5;
while (err > .00001) do P := P + .0002; err := evalf(subs(p = P,E)); od;
if the test is lower tailed then print(P,err) else print(1-P,err) fi;
end:
    
```

3.3 Illustration

Extensive numerical study is made to compare this method with the existing methods

in all type of distributions and found that this method give more powerful tests in the case of all type of distributions. Some of the results are given below.

Example-1: Death time (in weeks) of patients with cancer of the tongue with mean survival time μ , are given below

1, 3, 4, 5, 5, 8, 12, 13, 18, 23, 26, 27, 30, 42, 56, 62, 69, 104, 104, 112, 129, 181.

Do the data support the assumption of a mean survival time of 65 weeks against the alternative that the mean survival time is below 65 weeks.

Solution: The hypothesis to be tested in this case is $H_0 : \mu_1' = 65$ against $H_1 : \mu_1' < 65$. For this sample, the mean, variance, skewness and kurtosis are $m_1' = 47$, $m_2 = 2368$, $\sqrt{b_1} = 1.1854$ and

$b_2 = 3.4968$. To fit a GLD to the distribution of m_1' , using programme P1 the values of

$(\alpha_1, \alpha_2, \alpha_3, \alpha_4)$ are estimated as (65, 107.6364, .2527, 3.0226) and using programme P2, the corresponding GLD parameters are obtained as $\lambda_1 = 61.9498$, $\lambda_2 = 0.0187$, $\lambda_3 = 0.0975$, $\lambda_4 = 0.1712$. For the level of significance $\alpha = 0.05$, the critical region of the test is $m_1' < t_{0.05}$, where $t_{0.05} = 48.8722$. Since the observed value of m_1' (47) falls in the critical region, the test leads to the rejection of the null hypothesis.

Example 2: Rahnster (1981) investigated histopathological changes due to different levels of metal concentrations in horse kidneys. We list below a part of their data dealing with the average cadmium concentrations in the kidney cortex of horses.

11.9, 16.7, 23.4, 25.8, 25.9, 27.5, 28.5, 31.1, 32.5, 35.4, 38.3, 38.5, 41.8, 42.9,

50.7, 52.3, 52.5, 52.6, 54.5, 54.7, 56.6, 56.7, 58.0, 60.8, 61.8, 62.3, 62.5, 62.6,

63.0, 67.7, 68.5, 69.7. Do the data indicate the average cadmium concentrations in the horse kidney is 50 against the alternative that it is above 50.

Solution: The hypothesis to be tested in this case is $H_0 : \mu_1' = 50$ against $H_1 : \mu_1' > 50$. For this sample, the mean, variance, skewness and kurtosis are $m_1' = 46.49$, $m_2 = 263.147$, $\sqrt{b_1} = -0.4245$ and $b_2 = 1.978$, which is a negatively skewed leptokurtic distribution. To fit a GLD to the distribution of m_1' , the estimated values of $(\alpha_1, \alpha_2, \alpha_3, \alpha_4)$ are (50, 8.2233, -0.075, 2.9678) and the corresponding GLD parameters are $\lambda_1 = 49.7363$, $\lambda_2 = 0.0713$, $\lambda_3 = 0.1289$, $\lambda_4 = 0.1534$. For the level of significance $\alpha = 0.05$, the critical region for the test is $m_1' > t_{0.95}$, where $t_{0.95} = 54.82$. Since the observed value of m_1' (46.49) doesn't fall in the critical region, the test leads to the acceptance of the null hypothesis. For this example, by applying the classical t-test, the critical region is obtained as $m_1' \geq 54.942$, which leads to the acceptance of the null hypothesis. At

$\mu_1' = 55$, the power of the proposed test as 0.52, while for the t-test the power is 0.507.

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