American Journal of Mathematics and Statistics 2015, 5(3): 111-122
DOI: 10.5923/j.ajms.20150503.02

Analysis of Gini’s Mean Difference for Randomized Block Design

Elsayed A. H. Elamir

Department of Statistics and Mathematics, Benha University, Egypt & Management & Marketing Department, College of Business, University of Bahrain, Kingdom of Bahrain

---

Abstract Analysis of Gini’s mean difference (ANOMD) for a randomized block design is derived where the total sum of difference (TSD) is partition into exact block sum of difference (BLSD), exact treatment sum of difference (TRSD) and within sum of difference (WSD). This exact partition is used for comparison of several mean and median values. The exact partitions are derived by getting rid of the absolute function from Gini’s mean difference (GMD) by using the idea of redefined the GMD as a weighted average of the data with sum of weights zero. ANOMD has advantages: offers meaningful measure of dispersion, does not square data, and the TSD does not depend on fixed location while BLSD, TRSD and WSD are depending on fixed location. Two ANOMD graphs are proposed. However, two tests for mean and median are proposed under the assumption of normal distribution. The ANOMD is compared with ANOVA and the effect sizes are shown that the percentage of explained variation based on ANOMD is more than the one based on ANOVA.

Keywords ANOVA, Effect sizes, Normal distribution, Gini’s cofficient

---

1. Introduction

Gini’s mean difference (GMD) depends on all pairwise distances rather than square of the data and has been used as an alternative to the standard deviation in many fields. The Gini’s coefficient is a most used measure of inequality; see, [1], [2] and [3]. It is known that the GMD has asymptotic relative efficiency of 98% at the normal distribution and more efficient than standard deviation if the normal distribution is contaminated by a small fraction; see, [8], [5] and [6]. It may also offer certain pedagogical advantages; see, [7]. For extensive discussion and comparisons; see [6] and [8] and the references therein.

The population GMD is defined as

$$\Delta = E|Y_1 - Y_2|$$

It can be estimated from the sample using many formulas such as

$$\delta = \frac{1}{n^2}\sum_{i=1}^{n}\sum_{j=1}^{n}|y_i - y_j| = \frac{2}{n(n-1)}\sum_{i=1}^{n-1}\sum_{j=i+1}^{n}|y_i - y_j|$$

See, for example, [8].

A random variable has a normal distribution with location parameter $-\infty < \mu < \infty$ and scale $\sigma > 0$ if its probability density function is

$$f(y) = \frac{1}{\sigma\sqrt{2\pi}}\exp\left(-\frac{(y-\mu)^2}{2\sigma^2}\right), \quad -\infty < y < \infty$$

The normal distribution has

$$E(Y) = \mu, \qquad V(Y) = \sigma^2 \text{ and } \Delta(Y) = 2\sigma/\sqrt{\pi}$$

Therefore,

$$\sigma = \Delta\sqrt{\pi}/2$$

This will be used later in simulation studies.

A randomized complete block design is a restricted randomization design in which the experimental units are first sorted into homogeneous rows, called blocks, and the groups (treatments) are then assigned at random within the blocks; see, [9]. The model for a randomized complete block design containing the comparison of no interaction effects, when both the block and treatment effects are fixed and there are B blocks (BL) and G groups (TR), is as

$$Y_{bg} = \mu + \rho_b + \tau_g + \varepsilon_{bg}$$

μ is a constant, ρ_b are constants for the block (row) effects, τ_g are constants for the group (column) effects and ε_{bg} are independent normally distributed with mean 0.

Analysis of Gini’s mean difference (ANOMD) for a randomized block design is derived where the total sum of difference (TSD) is partition into exact block sum of difference (BLSD), exact treatment sum of difference (TRSD) and within sum of difference (WSD). The exact partitions are derived by getting rid of the absolute function from Gini’s mean difference (GMD) by using the idea of redefined the GMD as a weighted average of the data with sum of weights zero. TSD does not depend on any fixed

---

* Corresponding author:
shabib40@gmail.com (Elsayed A. H. Elamir)

location and this is logic where TSD is the total of all pairwise distances while BLSD, TRSD and WSD are depending on any fixed location. This exact partition is used for comparison of several mean and median values. A simulation study is conducted to obtain the critical values for the ratios of mean BLSD to mean WSD and mean TRSD to mean WSD based on normal distribution. Two ANOMD graphs are proposed based on BLSD and WSD. However, two tests for means and medians are proposed under the assumption of normal distribution. The effect size measures are suggested under ANOMD. These measures are shown that the percentage of explained variation based on ANOMD is more than the percentage of explained variation based on ANOVA.

Representation of GMD as a weighted average is presented in Section 2. The partitions of TSD into exact BLSD and exact WSD are derived in Section 3. The critical values for ratios are obtained in Section 4. Two graphs are proposed in Section 5. ANOMD tests for mean and median with effect sizes are studied in Section 6. Section 7 is devoted to conclusion.

2. Representation of GMD as a Weighted Average

Let $Y_1, Y_2, \dots, Y_n$ be a random sample from a continuous distribution with, density function $f(y)$, quantile function $y(F) = F^{-1}(y) = Q(F)$, $0 < F < 1$, cumulative distribution function $F(y) = F$ and $Y_{1:n}, \dots, Y_{n:n}$ the order statistics. There is a relationship between the second L-moment and GMD where the second L-moment is a half GMD, therefore

$$\lambda_2 = \frac{1}{2} E(Y_{2:2} - Y_{1:2})$$

Hence,

$$\Delta = E(Y_{2:2} - Y_{1:2})$$

From [9] and [10] this can be estimated as

$$\delta = \frac{2}{n(n-1)} \sum_{i=1}^{n} (2i - n - 1) Y_{i:n} = \frac{1}{n} \sum_{i=1}^{n} \frac{2(2i - n - 1)}{(n-1)} Y_{i:n}$$

3. Exact GMD Partitions about Mean and Median

Assume there are G different groups (treatments) with individuals in each group y_{bg}, with block $b = 1,2,\dots,B$, and $n = BG$. Let $y_{bg} - \bar{y}$ is the total deviation ($\bar{y} = \sum_g^G \sum_b^B y_{bg} / n$), $\bar{y}_g - \bar{y}$ is the deviation of group mean ($\bar{y}_g = \sum_{b=1}^{B} y_{bg} / B$) around total mean, $\bar{y}_b - \bar{y}$ is the deviation of block mean ($\bar{y}_b = \sum_{g=1}^{G} y_{bg} / G$) around total mean and $y_{bg} - \bar{y}_b - \bar{y}_g + \bar{y}$ is the error or within.

The sample GMD is

$$\delta = \frac{1}{n} \sum_{i=1}^{n} \frac{2(2i - n - 1)}{(n-1)} y_{i:n}$$

This can be rewritten without order and taking the rank of y as

$$\delta = \frac{1}{n} \sum_{i=1}^{n} \frac{2(2\ \mathrm{rank}(y) - n - 1)}{(n-1)} Y_i = \frac{1}{n} \sum_{i=1}^{n} w_i Y_i$$

This is a weighted average form where

$$w_i = \frac{2(2\ \mathrm{rank}(y) - n - 1)}{(n-1)}$$

Note that,

$$\sum_{i=1}^{n} w_i = 0$$

Therefore, the total sum of differences (TSD) is considered as

$$TSD = \sum_{i=1}^{n} w_i Y_i$$

This is the most important equation to obtain the exact analysis of total differences as follows.

Theorem 1

In a randomized complete block design the total sum of differences about mean is partitions as

$$TSD = BLSD + TRSD + WSD$$

where

$$TSD = \sum_{g=1}^{G}\sum_{b=1}^{B} w_{bg}\left(Y_{bg} - \bar{Y}\right),$$

$$BLSD = \sum_{g=1}^{G}\sum_{b=1}^{B} w_{bg}\ (\bar{Y}_b - \bar{Y}),$$

$$TRSD = \sum_{g=1}^{G}\sum_{b=1}^{B} w_{bg}\ \left(\bar{Y}_g - \bar{Y}\right)$$

$$WSD = \sum_{g=1}^{G}\sum_{b=1}^{B} w_{bg}\left(Y_{bg} - \bar{Y}_b - \bar{Y}_g + \bar{Y}\right)$$

and

$$w_{bg} = \frac{2(2\ \mathrm{rank}(y_{bg}) - n - 1)}{(n-1)}$$

Proof:

Where $\sum w = 0$, the total sum of differences is

$$TSD = \sum_{i=1}^{n} w_i Y_i = \sum_{i=1}^{n} w_i (Y_i - \bar{Y})$$

By adding and subtracting $\bar{Y}_b$, $\bar{Y}_g$ and $\bar{Y}$ and taking the summation over both g and b then

$$TSD = \sum_{g=1}^{G}\sum_{i=1}^{B} w_{bg}\left(Y_{bg} - \bar{Y}_b + \bar{Y}_b - \bar{Y}_g + \bar{Y}_g - \bar{Y} + \bar{Y} - \bar{Y}\right)$$

Therefore,

$$\sum_{g=1}^{G}\sum_{b=1}^{B} w_{bg}\left(Y_{bg} - \bar{Y}\right) = \sum_{g=1}^{G}\sum_{b=1}^{B} w_{bg}\ (\bar{Y}_b - \bar{Y}) + \sum_{g=1}^{G}\sum_{b=1}^{B} w_{bg}\ \left(\bar{Y}_g - \bar{Y}\right) + \sum_{g=1}^{G}\sum_{b=1}^{B} w_{bg}\left(Y_{bg} - \bar{Y}_b - \bar{Y}_g + \bar{Y}\right)$$

Theorem 2

In a randomized complete block design the total sum of differences about median is partitions as

$$TSD = BLSD + BSD + WSD$$

where

$$TSD = \sum_{g=1}^{G}\sum_{b=1}^{B} w_{bg}\left(Y_{bg} - \tilde{Y}\right),$$

$$BLSD = \sum_{g=1}^{G}\sum_{b=1}^{B} w_{bg}\ \left(\tilde{Y}_b - \check{Y}\right),$$

$$TRSD = \sum_{g=1}^{G}\sum_{b=1}^{B} w_{bg}\ \left(\tilde{Y}_g - \tilde{Y}\right)$$

$$WSD = \sum_{g=1}^{G}\sum_{b=1}^{B} w_{bg}\left(Y_{bg} - \tilde{Y}_b - \tilde{Y}_g + \tilde{Y}\right)$$

Proof: same as mean.

Comparison with ANOVA

The analysis of variance (ANOVA) for a randomized complete block design is

$$\sum_{g=1}^{G}\sum_{b=1}^{B}\left(Y_{bg}-\bar{Y}\right)^2=\sum_{g=1}^{G}\sum_{b=1}^{B}(\bar{Y}_b-\bar{Y})^2+\sum_{g=1}^{G}\sum_{b=1}^{B}\left(\bar{Y}_g-\bar{Y}\right)^2+\sum_{g=1}^{G}\sum_{b=1}^{B}\left(Y_{bg}-\bar{Y}_b-\bar{Y}_g+\bar{Y}\right)^2$$

See; for example, [12].

The analysis of Gini's mean difference (ANOMD) for a randomized complete block design is

$$\sum_{g=1}^{G}\sum_{b=1}^{B}w_{bg}\left(Y_{bg}-\bar{Y}\right)=\sum_{g=1}^{G}\sum_{b=1}^{B}w_{bg}\,(\bar{Y}_b-\bar{Y})+\sum_{g=1}^{G}\sum_{b=1}^{B}w_{bg}\,\left(\bar{Y}_g-\bar{Y}\right)+\sum_{g=1}^{G}\sum_{b=1}^{B}w_{bg}\left(Y_{bg}-\bar{Y}_b-\bar{Y}_g+\bar{Y}\right)$$

Note that:

1. ANOMD replaces the square in ANOVA by weights and that ensures stability in statistical inferences.
2. ANOMD can be extended to any measure of location (median) easily where TSD does not depend on any fixed location and this is logic where TSD is the sum of all pairwise distances.

Illustrative example

To have an idea on how the method work. Table 1 shows TSD partition for a hypothetical data. Note that, $TSA = 39.5$, $BLSD = 9$, $TRSD = 14$ and $WSD = 16.5$ and the total is 39.5 that gives exact partitions.

Table 1. TSD partition into $BLSD$, $TRSD$ and WSD for a hypothetical data

y	w	wy	$w(\bar{y}_b-\bar{y})$	$w(\bar{y}_g-\bar{y})$	$w(y-\bar{y}_g-\bar{y}_b+\bar{y})$
Group 1					
5	-1.5	-7.5	1	0.5	3.5
12	1.5	18	3	-0.5	3
7	-0.5	-3.5	0.67	0.17	-0.17
Group 2					
15	2	30	-1.33	2.53	9.33
10	1	10	2	2.67	-3.00
8	0	0	0	0	0
Group 3					
3	-2	-6	1.33	4.67	4.67
9	0.5	4.5	1	-1.17	0.50
6	-1	-6	1.33	2.33	-1.33
Total		39.5	9	14	16.5

3.1. Divisors and ANOMD Tables

ANOMD is introduced and used to test for population means and medians under the following assumptions.

1. The observations are random and independent samples from the populations.
2. The distributions of the populations from which the samples are selected are normal.
3. The Δ's of the distributions in the populations are equals.

A simulation study is conducted to compute the suitable divisors for scaled BLSD, TRSD and WSD using the following steps:

1. For selected design simulate data from normal distribution using a very large number N.
2. Compute $BLSD/\Delta$, $TRSD/\Delta$, and WSD/Δ for each G and B.
3. Compute the average for each one.

Table 2. Simulated averages for $BLSD/\Delta$, $TRSD/\Delta$ and WSD/Δ with different values of G and B from normal distribution and the number of replications is 10000

G	3	5	7	10	3	5	7	10	3	5	7	10
B	BL				TR				W			
					for mean							
5	4.166	4.11	4.08	4.07	2.15	4.15	6.18	9.24	8.45	16.45	24.50	36.54
10	9.230	9.19	9.07	9.03	2.05	4.09	6.11	9.11	18.50	36.60	54.68	81.75
15	14.11	14.15	14.08	14.02	2.06	4.08	6.05	9.06	28.57	56.80	84.76	126.7
20	19.30	19.20	19.11	19.12	1.98	4.05	6.02	9.07	38.52	76.88	114.8	171.5
30	29.37	29.17	29.12	29.09	2.05	4.01	6.02	8.99	58.72	116.8	174.8	261.8
50	49.40	49.12	49.13	49.07	2.03	3.99	6.02	8.99	98.70	197.0	294.8	441.6
100	99.34	99.12	99.15	99.11	2.01	4.01	5.95	9.02	198.7	397.2	594.5	892.1
					for median							
5	4.48	4.50	4.48	4.47	2.27	4.47	6.61	9.82	8.22	16.01	23.90	35.73
10	9.89	9.82	9.91	9.90	2.23	4.39	6.60	9.85	17.96	35.76	53.53	80.27
15	15.20	15.31	15.33	15.3	2.25	4.41	6.62	9.92	27.55	55.30	83.12	124.7
20	20.31	20.55	20.72	20.8	2.28	4.41	6.57	9.92	37.41	74.80	112.5	169.3
30	30.88	31.36	31.54	31.6	2.20	4.42	6.60	9.94	56.99	114.2	171.9	258.4
50	51.79	52.78	53.18	53.4	2.22	4.43	6.60	9.96	95.74	192.7	290.2	436.4
100	104.7	106.4	106.7	106.9	2.20	4.51	6.60	9.96	193.0	389.1	586.1	882.2

From the simulation results in Table 2, the proposed ANOMD table about mean is summarized in Table 3.

Table 3. Summary of ANOMD table for mean

Variation	Sum of absolute	Divisor	MD estimate	R
Block	$BLSD$	$d1 \cong (B-1)+\frac{1}{G}$	$MBL=\frac{BLSD}{d1}$	$R_1=\frac{MBL}{MW}$
Treatment	$TRSD$	$d2 \cong (G-1)+\frac{1}{B}$	$MTR=\frac{TRSD}{d2}$	$R_2=\frac{MTR}{MW}$
Within	WSD	$d3 \cong (B-1)(G-1)+\frac{G+B}{GB}$	$MW=\frac{WSD}{d3}$	
Total	TSD			

Also, from the simulation results in Table 2, the proposed ANOMD table about median is summarized in Table 4.

Table 4. Summary of ANOMD table for median

Variation	Sum of absolute	Divisor	MD estimate	R
Block	$BLSD$	$d1 \cong 1.05B-0.5$	$MBL=\frac{BLSD}{d1}$	$R_3=\frac{MBL}{MW}$
Treatment	$TRSD$	$d2 \cong 1.1(G-1)$	$MTR=\frac{TRSD}{d2}$	$R_4=\frac{MTR}{MW}$
Within	WSD	$d3 \cong (B-1)(G-1)-.01n$	$MW=\frac{WSD}{d3}$	
Total	TSA			

4. Simulation Approach for Critical Values

The following steps are used to obtain the critical values:

1. For any given design simulate data from normal distribution using large number N.
2. Compute R for each N.
3. Use quantile function in software R to obtain the required quantile for R.

Table 5. Simulated critical values for R_1 and R_2 using normal distribution for different B and G and the number of replications is 10000

$1-\alpha=0.95$										
G	3	4	5	8	10	3	4	5	8	10
B			R_1					R_2		
10	2.54	2.24	2.15	2.04	2.01	3.61	2.93	2.68	2.16	2.00
15	2.10	1.95	1.87	1.79	1.76	3.37	2.80	2.57	2.14	1.98
20	1.86	1.78	1.74	1.65	1.65	3.30	2.79	2.50	2.06	1.95
25	1.73	1.69	1.61	1.58	1.56	3.27	2.71	2.47	2.15	1.93
30	1.65	1.60	1.56	1.53	1.51	3.10	2.69	2.45	2.12	1.93
50	1.47	1.45	1.42	1.39	1.37	3.09	2.67	2.42	2.05	1.92
100	1.33	1.30	1.29	1.27	1.26	3.09	2.64	2.40	2.04	1.89
$1-\alpha=0.99$										
10	3.73	3.20	3.03	2.72	2.69	6.28	4.68	3.99	3.08	2.65
15	2.95	2.57	2.41	2.30	2.24	5.51	4.25	3.63	2.85	2.58
20	2.41	2.28	2.15	2.02	2.01	5.17	4.12	3.53	2.79	2.56
25	2.18	2.08	2.00	1.89	1.86	5.10	4.09	3.50	2.74	2.51
30	2.03	1.95	1.88	1.81	1.78	4.95	4.05	3.50	2.74	2.51
50	1.74	1.71	1.62	1.58	1.56	4.80	3.95	3.48	2.72	2.50
100	1.50	1.45	1.43	1.40	1.40	4.80	3.82	3.47	2.72	2.38

Table 6. Simulated critical values for R_3 and R_4 using normal distribution for different B and G and the number of replications is 10000

$1-\alpha=0.95$										
G	3	4	5	8	10	3	4	5	8	10
B			R_3					R_4		
10	2.54	2.17	2.15	2.01	1.96	3.95	3.18	2.80	2.20	2.04
15	2.09	1.89	1.88	1.76	1.75	3.78	3.04	2.72	2.23	2.03
20	1.87	1.77	1.74	1.64	1.63	3.49	2.96	2.68	2.18	2.01
25	1.76	1.61	1.65	1.57	1.55	3.46	2.92	2.64	2.16	1.98
30	1.68	1.58	1.57	1.51	1.50	3.39	2.84	2.62	2.15	1.98
50	1.50	1.45	1.43	1.38	1.37	3.37	2.83	2.57	2.14	1.97
100	1.33	1.31	1.30	1.27	1.27	3.26	2.77	2.51	2.11	1.97
$1-\alpha=0.99$										
10	4.02	3.07	2.97	2.67	2.59	7.17	4.90	4.35	3.02	2.78
15	2.96	2.49	2.47	2.21	2.18	6.51	4.82	4.18	3.01	2.69
20	2.48	2.24	2.20	2.03	1.99	5.73	4.52	3.79	2.98	2.66
25	2.27	2.02	2.01	1.91	1.87	5.64	4.43	3.76	2.90	2.65
30	2.09	1.91	1.89	1.82	1.79	5.32	4.23	3.75	2.86	2.59
50	1.79	1.71	1.67	1.59	1.57	5.16	4.22	3.70	2.83	2.56
100	1.51	1.45	1.44	1.41	1.40	5.14	4.21	3.58	2.78	2.54

Tables 5 and 6 give the simulated critical values for R_1, R_2, R_3 and R_4 based on normal distribution for different values of B and G.

5. Graphic Presentation

5.1. ANOMD General Plot

This plot is for all groups to detect shifts in means or medians. The $X-$axis contains the index of the groups and the $Y-$axis contains the heights for the sum of $h_1 = w(\bar{y}_g - \bar{y})/(((g-1))\Delta)$, and $h_2 = w(y - \bar{y}_g - \bar{y}_b + \bar{y})/((b-1)(g-1)\Delta)$ for each group. Note that mean is used as an example. Separate curves are drawn for sum of h_1 and h_2. The points on each curve are connected by lines. This graph should reflect the heights, shifts, and patterns among all groups.

5.2. ANOMAD Individual Plot

This plot is for each group to detect shifts inside the group. The $X-$axis contains the index of the data for each group $(1,2,\dots,n_g, g=1,2,..,G)$ and the $Y-$axis contains the heights, $h_3 = w(\bar{y}_g - \bar{y})/((g-1)\Delta)$ and $h_4 = w(y - \bar{y}_g - \bar{y}_b + \bar{y})/((b-1)(g-1))\Delta$ for each value. Separate curves are drawn h_3 and h_4. The points on each curve are connected by lines. This graph should reflect the heights, shifts and patterns in each group.

Figures 1, 2 and 3 show that:

1. When means or medians are equals the two lines will be near from each other and most likely that there will be interference among them or the treatment line may be down the within line; see, Figures 1 and 2 a0. In this case it will not be clear pattern in each group and the heights will be almost the same for on each group; see, Figures 1 and 2 a1, a2 and a3. This may be indicating a strong evidence for no shifts in means or medians.
2. When mean(s) or median(s) are not equals the treatment line will start to go up until it may be separated from the within line; see, Figure 3 a0. In this case it will be clear pattern in group(s) with clear different gaps or heights; see, Figure 3 a1, a2 and a3. It is clear that the second group has a different pattern from others. This may give a strong evidence for shift (s) in mean(s) or median(s).

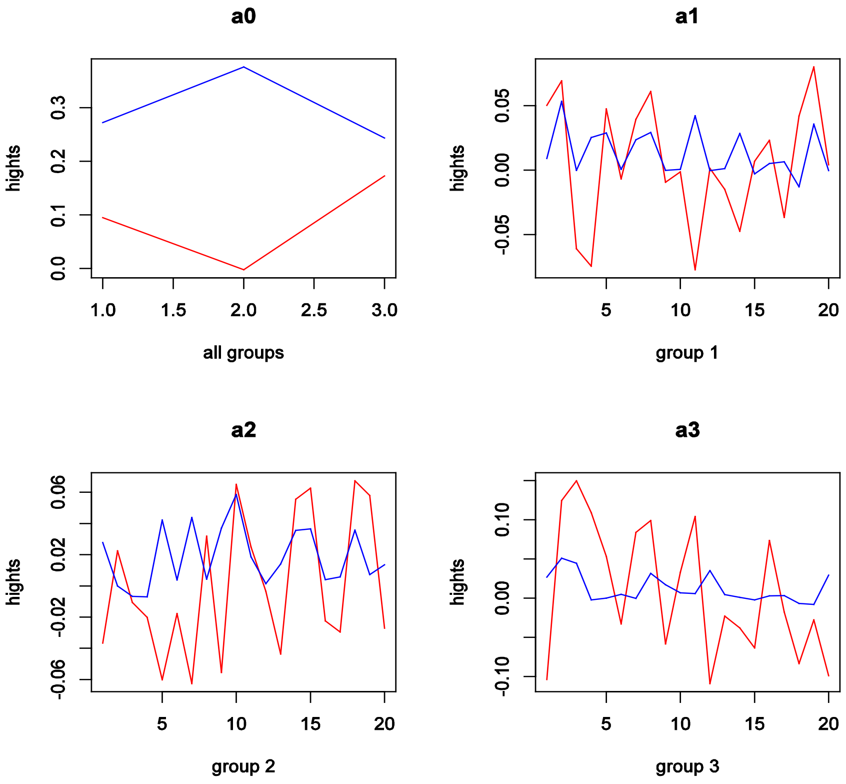

Figure 1. ANOMD plot for simulated data from $N(10,1)$: (a0) all groups and (a1), (a2) and (a3) for each group and $G = 3$, $n = 60$. Red line is treatment and blue line is within

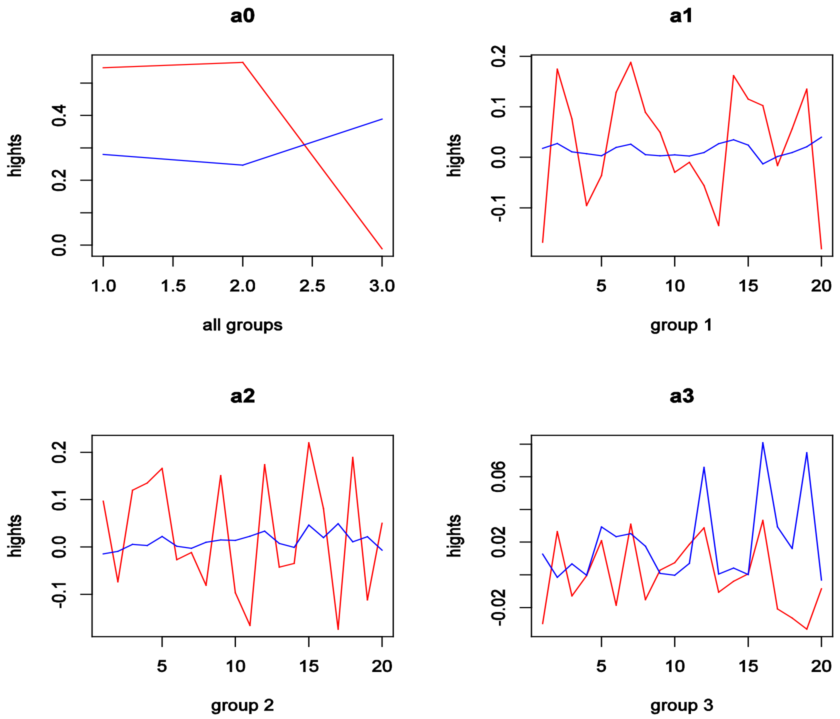

Figure 2. ANOMD plot for simulated four groups $N(10,1)$ and one group $N(10.5,1)$: (a0) all groups and (a1), (a2), and (a3) for each group and $G = 3$, $n = 20$. Red line is treatment and blue line is within

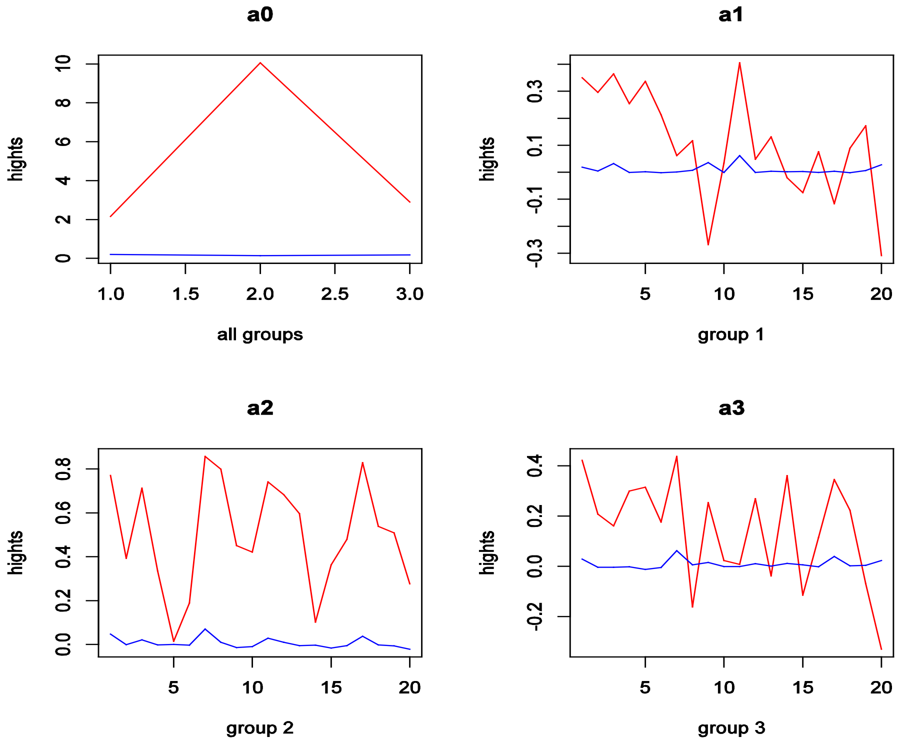

Figure 3. ANOMD plot for simulated four groups $N(10,1)$ and one group $N(12,1)$: (a0) all groups and (a1), (a2), and (a3) for each group and $G = 3$, $n = 60$. Red line is treatment and blue line is within

6. Test for Mean and Median

For mean the null hypothesis H_0 is that
Blocks

$$H_0\colon \mu_1 = \mu_2 = \mu_3 = \cdots = \mu_B$$

Treatments

$$H_0\colon \mu_1 = \mu_2 = \mu_3 = \cdots = \mu_G$$

For median the null hypothesis is that
Blocks

$$H_0\colon \nu_1 = \nu_2 = \nu_3 = \cdots = \nu_B$$

Treatments

$$H_0\colon \nu_1 = \nu_2 = \nu_3 = \cdots = \nu_G$$

Fresh & fun is a food chain with three outlets; see, [12]. The owner is interested in testing the average service quality at the three outlets. Fourteen people are selected and they asked to eat at each of the three outlets. The order of visits to the three outlets was randomized, but each customer visited each outlet one time. After each visit, each customer rated the service on a scale of 1 to 100. The data is given in Table 7.

To test for the assumption of normal distribution, the function *shapiro.test()* in *R-software* is used. Table 7 gives the sample data with means, medians, MD and Shapiro-wilk test for normal distribution. The results for the three groups are given in Table 7 where p-values more than 0.01, 0.05 and 0.10, therefore, the assumption of normal cannot be rejected. Because the maximum MD to minimum MD is 1.4, the assumption of homogeneity of Δ's may not be rejected.

Table 7. Service quality score for three outlets and normal test

		Outlets						
Customer	O1	O2	O3	Means	Med.			
1	830	647	630	702.33	647	Shapiro-Wilk test		
2	743	840	786	789.67	786		p-value	δ
3	652	747	730	709.67	730	O1	0.73	89.18
4	885	639	617	713.67	639	O2	0.15	128.12
5	814	943	632	796.33	814	O3	0.27	112.28
6	733	916	410	686.33	733			
7	770	923	727	806.67	770			
8	829	903	726	819.33	829			
9	847	760	648	751.67	760			
10	878	856	668	800.67	856			
11	728	878	670	758.67	728			
12	693	990	825	836.00	825			
13	807	871	564	747.33	807			
14	901	980	719	866.67	901			
Means	793.57	849.5	668	770.36				
Med.	810.5	874.5	669		765			

From Table 8, since $R_1 = 0.81 < 2.25$ the null hypothesis could not be reject, .i.e., blocking is not effective while $R_2 = 13.06 > 3.44$, therefore, the outlets are different in averages.

Table 8. ANOMD for testing means for quality service

Variation	Sum of absolute	Divisor	MD estimate	R	$qSim^*_{0.95}$
Block	982.68	13.33	73.72	0.81	2.15
Treatment	2455.599	2.07	1186.28	13.06	3.44
Within	2398.059	26.40	90.83		
Total	5836.341				

*This value from simulation study

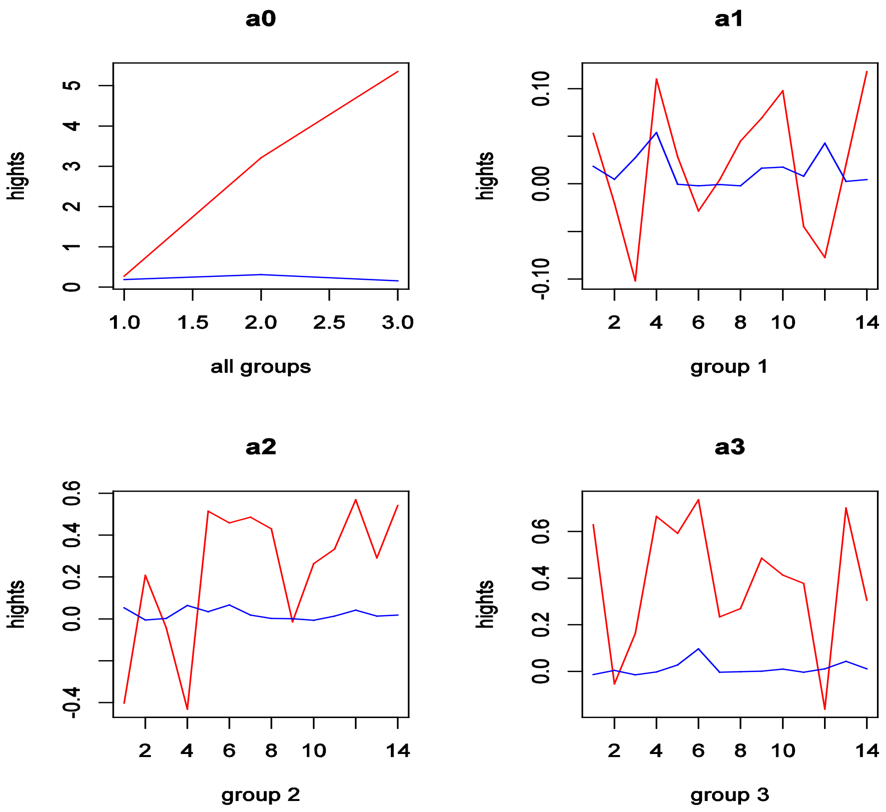

Figure 4. ANOMD plots for the service quality data for three outlets

Figure 4 shows that

1. Most of the points of treatment line are above the within line with a big gap. This might give a visual evidence of shift in average; see, Figure 4 a0.
2. The first group is stable while the second and third groups have big shifts. The second group has pattern near from third group but the gaps or heights are much more than the other groups. This may indicate that the third group is different from others; see, Figure 4 a1, a2 and a3.

Table 9. ANOMD for testing medians for quality service

Variation	Sum of absolute	Divisor	MD estimate	R	$qSim^*_{0.95}$
Block	1270	14.347	88.52	1.26	2.14
Treatment	2778.098	2.200	1262.77	18.06	3.79
Within	1788.244	25.58	69.91		
Total	5836.341				

*This value from simulation

Table 9 shows that the block is not significance while the treatment is significance for testing medians. The ANOVA table for the above data is given in Table 10.

Table 10. ANOVA for quality service data

Variation	SS	df	MS	F-ratio	critical
Block	116605.0	13	8969.6	0.91	2.15
Treatment	241912.7	2	120956.4	12.28	3.40
Within	256123.9	26	9850.9		
Total	614641.6				

6.1. Effect Sizes

Effect sizes (ES) provide another measure of the magnitude of the difference expressed in standard variation units in the original measurement. Thus, with the test of statistical significance and the interpretation of the effect size (*ES*), the researcher can address issues of both statistical significance and practical importance. The most direct one is

$$\eta^2 = \frac{SS_{effect}}{SS_{Total}}$$

where SS is the sum of squares. η^2 measures the proportion of the variation in Y that is associated with membership of the different groups defined by X. η^2 is an uncorrected effect size estimate that estimates the amount of variance explained based on the sample, and not based on the entire population. ω^2 has been suggested to correct for this bias as

$$\omega^2 = \frac{df_{effect}\left(MS_{effect} - MS_{error}\right)}{SS_{Total} + MS_{error}}$$

See; for example, [13], [14], [15], [16] and [17].

These two measures could be extended to ANOMD as

$$\eta_{MD} = \frac{SD_{effect}}{SD_{Total}}$$

and

$$\omega_{MD} = \frac{Divisor_{effect}\left(MSD_{effect} - MSD_{error}\right)}{SD_{Total} + MSD_{error}}$$

Where η_{MD} measures the proportion of mean differences in Y that is associated with membership of the different groups defined by X. For the above data, Table 11 gives the computations of these measures.

Table 11. The effect sizes for ANOMD and ANOVA tests

	Using mean		Using median		ANVOA	
	η_{MD}	ω_{MD}	η_{MD}	ω_{MD}	η	ω
Block	0.17	0.04*	0.22	0.05	0.19	0.02*
Treatment	0.44	0.38	0.48	0.44	0.39	0.35

Note that: *absolute value

From Table 11, it is interesting to note that the percentage of explained variation using ANOMD for treatment is 44% (η) and 38% (ω) while the percentage of explained variation using ANOVA for treatment is 39% and 35%, respectively.

7. Conclusions

The ANOMD for a randomized complete block was derived by partition the total sum of differences into exact between sum of differences and exact within sum of differences. It had been shown that the TSD had been expressed as a linear combination of the data instead of square.

The ANOMD had important information about the shifts in means and medians that studied by finding the ratios R_1, R_2, R_3 and R_4 and tested for equal means or medians. Also, it offered a very effective way to find out the shifts in means and medians graphically. Actually, the graph is a very strong point if one can obtain the right conclusion from it. Two effect size measures are extended to ANOMD. These measures are showed that the percentage of explained variation based on ANOMD is more than the percentage of explained variation based on ANOVA.

Also, it is shown that the TSD had not depended on any fixed location and this may make basis for comparisons between more than location measures.

REFERENCES

[1] Cowell, F.A., 1995, *Measuring Inquality.* (2nd edition). Harvester Wheatsheaf, Hamel Hempstead.

[2] Champernowne, D.G., and Cowell, F.A., 1998), *Economics inequality and income distribution*. Combridge University Press, Cambridge, UK.

[3] Barrett, G.F., and Donald, S.G, 2009, Statistical inference with generalized Gini indices of inequality, poverty, and welfare. *Journal of Business and Economic Statistics*, 20, 1-17.

[4] David, H. A., 1968, Gini's mean difference rediscovered. *Biometrika*, 55, 573-575.

[5] Gerstenberger, C. and Vogel, D., 2014, On the efficiency of Gini's mean difference. Cornel University Library, arxiv.org/abs/1405.5027.

[6] Gerstenkorn, T. and Gerstenkorn, J., 2003, Gini’s mean difference in the theory and application. *Statistica*, IXIII, 469-488.

[7] Algina, J., Keselman, H.J., & Penfield, R.D., 2005, An alternative to Cohen’s standardized mean difference effect size: A robust parameter and confidence interval in the two independent group’s case. *Psychological Methods,10,* 317-328.

[8] Yitzhaki, S., 2003, Gini's mean difference: A superior measure of variability for non-normal distributions. *Metron*, 61, 285-316.

[9] Neter, J., Kutner, H., Nachtsheim, C. and Wasserman, W., 1996, *Applied linear statistical models*. 4th ed., McGraw-Hill.

[10] Elamir, E.A.H. and Seheult, H., 2003, Trimmed L-moments. *Computational Statistics & Data Analysis*, 4, 299-314.

[11] Elamir, E.A.H and Seheult, H., 2004, Exact variance structure of sample L-moments. *Journal of Statistical Planning and Inference*, 124, 337-359.

[12] Groebner, F.D., Shannon, P.W., Fry, P. C. and Smith, K.D., 2001, *Business Statistics: A decision making approach*. 6th ed., Prenhall.

[13] Cohen, J., 1988, *Statistical power analysis for the behavioral sciences(2nd ed.)*. Hillsdale, NJ: Erlbaum.

[14] Cohen, J., 1994, The earth is round (p < .05). *American Psychologist, 49*, 997-1003.

[15] Olejnik, S., and Algina, J., 2000, Measures of effect size for comparative studies: applications, interpretations, and limitations. *Contemporary Educational Psychology,* 25, 241–286.

[16] Bakeman, R., 2005, Recommended effect size statistics for repeated measures designs. B*ehavior Research Methods,* 37, 379–384.

[17] Lakens, D., 2013, Calculating and reporting effect sizes to facilitate cumulative science: a practical primer for *t*-tests and ANOVAs. *Frontiers in Psychology*, 4, 1-12.