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Estimation of AUC of Bi-Generalized Half-Normal ROC Curve

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Abstract

In ROC literature, there are good number of Bi-distributional ROC curves which are developed to address the practical need and are based on normal and non-normal data. The most widely used ROC form is the Bi-Normal. However, the practical situations in diagnostic medicine and other life testing frameworks, data may not be attributed to make use of the Bi-Normal ROC curve. We have considered such situations using SAPS III dataset, where the data underpins Generalised Half-Normal distribution and not that of any existing bi-distributional ROC forms. The ROC and AUC expressions are derived and these are supported with SAPS III dataset and simulation. The present work is demonstrated by considering minimum (better case), moderate (moderate case) and maximum (worst case) overlapping scenarios at various sample sizes.

Key words: ROC curve; AUC; Non-normal data; Confidence intervals; Generalized Half-Normal distribution.

AMS Subject Classifications: 92B15, 62P10

1. Introduction

In classical statistics and machine learning, the problem of classifying an individual/ object/ image/ voice/ signal has grabbed the attention of researchers from diagnostic medicine, experimental psychology, finance and many more. The statistical tool that supports in explaining the performance of a classifier is the receiver operating characteristic (ROC) curve. Even though the tool originated in early 1950s to analyze the radar signals, researchers from the medical domain started using it in the early 1970s. The theoretical contributions started during mid 1970s wherein the mathematical frame work was proposed by by assuming the data of two populations follow a particular distribution, say 'normal'; hence the name '*binormal ROC model*' Egan (1975). However, basing on the practical need and situations, the theoretical development happened under non-normal data structures. Over the years, many researchers have attempted in proposing the bi-distributional ROC models by considering gamma (Hussain (2012)), logistic (Dorfman and Alf (1969)), half-normal (Vishnu and Kiruthika (2015)), exponential, and Weibull (Vishnu *et al.* (2012)) *etc.*

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A comprehensive coverage of such bi-distributional ROC models was made by Balaswamy and Vishnu (2016). In understanding the non-normal data, we are well aware that the shape and scale parameters play a crucial role in explaining the tail pattern and asymmetry.

Table 1: One sample KS test for some skewed distributions

Distribution	Status	Parameters	Estimates	KS test value	p-value
Normal	Alive	μ_0	25.53	0.9999	<2.2e-16
		σ_0	17.48		
	Dead	μ_1	33.82	0.9565	<4.44e-16
		σ_1	17.42		
Exponential	Alive	λ_0	0.04	0.1639	0.0575
	Dead	λ_1	0.03	0.2543	0.0059
GHN	Alive	α_0	1.18	0.1141	0.3563
		σ_0	32.66		
	Dead	α_1	1.21	0.1341	0.3936
		σ_1	42.04		

Let us consider a real data namely the Simplified Acute Physiology Score (SAPS) III, which helps in estimating the probability of mortality for ICU patients/subjects. SAPS III score and a status variable (Alive(0); Dead(1)) are the two characteristics recorded for each patient. Figure 1 depicts the density patterns of 'alive' and 'dead' patients indicating the deviation from symmetry. Further, goodness of fit criterion using the one-sample

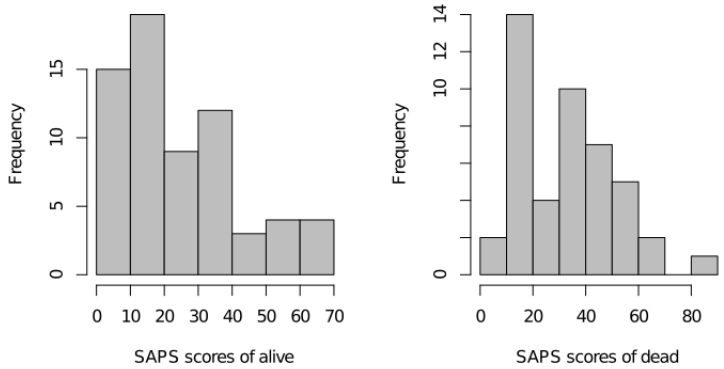

Figure 1: Histogram of SAPS III data

Kolmogorov-Smirnov (KS) test is performed to provide an evidence that the SAPS III data do not follow normality. Along with the normal distribution, exponential and generalised half-normal distribution (GHN) were also considered as competitor distributions. The results of the same are reported in Table 1, clearly indicating that the data is a good fit for GHN distribution. So, the existing bi-normal and bi-exponential ROC models do not support in defining a classifier that helps in classifier or allocating a subject into 'alive' or 'dead' classes of SAPS III data. Hence, the practical situation needs a classifier rule to be defined.

This motivated us to come out with a newer version of ROC model wherein the data of two populations follow GHN distribution.

GHN is a special case of the three-parameter generalized gamma distribution. Even though the GHN distribution is a two-parameter distribution, the hazard rate function can form variety of shapes such as monotonically increasing, monotonically decreasing, and bath-tub shapes. Cooray and Ananda (2008) studied some properties of this family and examples are cited to compare with other commonly used failure time distributions such as Weibull, gamma, lognormal, and Birnbaum-Saunders. Moreover, there is difficulty in developing inference procedures with the generalized gamma distribution, particularly, the maximum likelihood estimation in which the iteration method such as Newton-Raphson fails. Even with samples of size 200 or 300, the algorithms do not converge (Hager and Bain (1970)). Some authors such as Parr and Webster (1965) and Stacy and Mihram (1965) faced problems with the maximum likelihood estimation. In addition, for interval estimation procedures also they faced difficulties. This prompted us to work on GHN with two parameters such as shape and scale and illustrated the features of parameters involved in it with the help of a real data called SAPS III. Simulation studies are also carried out to support the proposed methodology.

The probability density function and cumulative distribution function of GHN distribution are,

$$f(x) = \begin{cases} \sqrt{\frac{2}{\pi}} \left(\frac{\alpha}{x}\right) \left(\frac{x}{\sigma}\right)^{\alpha} exp\left(\frac{-1}{2}\left(\frac{x}{\sigma}\right)^{2\alpha}\right) & if\ x \geq 0 \\ 0 & if\ x < 0 \end{cases} \tag{1}$$

$$F(x) = 2\Phi\left[\left(\frac{x}{\theta}\right)^{\alpha}\right] \qquad x \geq 0,\ \theta, \alpha > 0 \tag{2}$$

where $\Phi(.)$ is the cumulative distribution function of standard normal deviate, α and σ are shape and scale parameters respectively. The expression given in (2) resembles the cumulative distribution function of the half-normal distribution, hence Cooray and Ananda (2008) named this distribution as GHN distribution. The density curves of GHN for different values of shape and scale parameters are shown in Figure 2. For fixed scale parameter, the GHN distribution will be positively skewed if $\alpha \in (0, 2.17)$; symmetric if $\alpha = 0$ and negatively skewed if $\alpha > 2.17$.

2. The Bi-generalised Half-Normal ROC curve

Let us assume that the scores or data points, say S={X,Y} in both populations 1 and 2 follow GHN distribution. Using the probabilistic definitions, the false positive rate (FPR) and true positive rate (TPR) of ROC curve at threshold 't' are given as

$$FPR = P(S > t/0) = 1 - \left[2\left(\Phi\left[\frac{t}{\sigma_0}\right]^{\alpha_0}\right) - 1\right] = 2\left[1 - \Phi\left(\frac{t}{\sigma_0}\right)^{\alpha_0}\right] \tag{3}$$

$$TPR = P(S > t/1) = 1 - \left[2\left(\Phi\left[\frac{t}{\sigma_1}\right]^{\alpha_1}\right) - 1\right] = 2\left[1 - \Phi\left(\frac{t}{\sigma_1}\right)^{\alpha_1}\right] \tag{4}$$

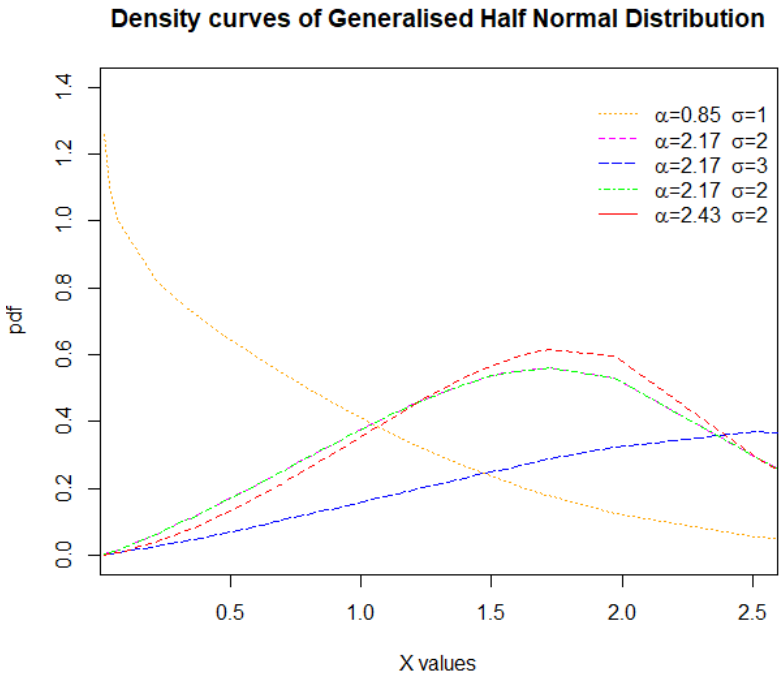

Figure 2: Density curves of GHN distribution

then from equation (3), the threshold can be expressed as,

$$t = \sigma_0 \left(\Phi^{-1} \left[1 - \frac{FPR}{2} \right]^{\frac{1}{\alpha_0}} \right) \tag{5}$$

The ROC expression given in equation (6) is the Bi-Generalised Half-Normal (Bi-GHN) ROC curve, where $\Phi^{-1}(.)$ is the inverse cumulative distribution function of standard normal deviate. Using equation (5) in equation (4), the ROC model is obtained and is given in equation (6).

$$ROC(t) = 2 \left[1 - \Phi \left(\frac{\sigma_H \left(\Phi^{-1} \left[1 - \frac{FPR}{2} \right]^{\frac{1}{\alpha_H}} \right)}{\sigma_D} \right)^{\alpha_D} \right] \tag{6}$$

where σ_0 and σ_1 are the scale parameters and α_0 and α_1 are the shape parameters of the '0' and '1' populations respectively. In next section, the expressions for the area under the curve (AUC) and Youden's index are given.

3. AUC of Bi-GHN ROC curve

The AUC can be interpreted as the average TPRs at all possible TNRs (TNR is the True Negative Rate, which is obtained from 1-FPR). Since ROC curve is only a graphical representation of a classifier it will be always better if we can summarize our findings by a single measure. Such a numerical summary measure of ROC curve is termed as AUC. AUC of an ROC curve explains the accuracy of a diagnostic test. The ability of the test

to discriminate between '1' and '0' groups can be explained by AUC measure. Higher the AUC value, better will be the discriminating power of the test. The value of AUC always lies between 0 and 1. The total area under the ROC curve is always unity because both TPR and TNR values lie between 0 and 1. The line connecting (0,0) and (1,1) in the ROC unit square plot is the diagonal line where the AUC will be equal to 0.5. A test for which AUC < 0.5 need not be considered at all. It means that the test has only 50 percentage or less chance of discriminating the subjects into '1' and '0' categories. Tests with AUC ≥ 0.5 will alone be considered for further classification. AUC of Bi-GHN ROC curve is,

$$AUC = \int_0^1 ROC(t)\, dt$$

$$AUC = \int_0^1 2\left[1 - \Phi\left(\frac{\sigma_0\left(\Phi^{-1}\left[1 - \frac{FPR}{2}\right]^{\frac{1}{\alpha_0}}\right)}{\sigma_1}\right)^{\alpha_1}\right] dt \tag{7}$$

If we consider $\sigma_1 = \sigma_0 = 1$, then it will reduce to one parameter Bi-GHN ROC curve and its AUC will take the following form.

Then the AUC of the one-parameter Bi-GHN can be obtained as

$$AUC = \int_0^1 2\left[1 - \left(1 - \frac{FPR}{2}\right)^{\frac{1}{\alpha_0}}\right]^{\alpha_1} dt$$

$$AUC = \frac{2^{(1-k)}\left[2^k(k-1)+1\right]}{k+1} \quad ; \quad \text{where} \quad k = \frac{\alpha_1}{\alpha_0} \tag{8}$$

In this paper we consider two parameter Bi-GHN distribution. Since, equation (7) does not have a closed form, we need to solve it using numerical integration. Variance of AUC can be obtained using bootstrap method which is described in following section. Another important summary measure of the ROC curve is Youden's index (J). The maximum value of 'J' is the value corresponding to the optimal threshold (cut-off) for the marker in the diagnostic test. The theoretical expression for Youden's index is

$$J = max\{TPR + TNR - 1\}$$

4. Parameter estimation under maximum likelihood method and their confidence intervals

Using the results of maximum likelihood estimates presented in the work of Cooray and Ananda (2008), the expressions for '0' and '1' populations are given in equations (9) and (10) respectively.

$$\frac{n_0}{\widehat{\alpha}_0} + \sum_{i=1}^{n_0} log(x_i) - n_0\left(\sum_{i=1}^{n_0} x_i^{2\widehat{\alpha}_0} log(x_i)\right)\left(\sum_{i=1}^{n_0} x_i^{2\widehat{\alpha}_0}\right)^{-1} \tag{9}$$

$$\frac{n_1}{\widehat{\alpha}_1} + \sum_{j=1}^{n_1} log(y_j) - n_1 \left(\sum_{j=1}^{n_1} y_j^{2\widehat{\alpha}_1} log(y_j) \right) \left(\sum_{j=1}^{n_1} y_j^{2\widehat{\alpha}_1} \right)^{-1} \tag{10}$$

since $\hat{\alpha}_0$ and $\hat{\alpha}_1$ are fixed point solutions of the above non-linear equations, it can be obtained by using a simple iterative scheme as follows: $h(\alpha_{(j)}) = \alpha_{(j+1)}$ where $\lambda_{(j)}$ is the j^{th} iterate of $\hat{\alpha}$. The iteration procedure should be stopped when α_j less than α_{j+1} is sufficiently small. Once we obtain $\widehat{\alpha}_0$ and $\widehat{\alpha}_1$, we can obtain $\widehat{\sigma}_0$ and $\widehat{\sigma}_1$ from below expressions.

$$\widehat{\sigma}_0 = \left(\frac{1}{n_0} \sum_{i=1}^{n_0} x_i^{2\widehat{\alpha}_0} \right)^{\frac{1}{2\widehat{\alpha}_0}} \tag{11}$$

$$\widehat{\sigma}_1 = \left(\frac{1}{n_1} \sum_{j=1}^{n_1} y_j^{2\widehat{\alpha}_1} \right)^{\frac{1}{2\widehat{\alpha}_1}} \tag{12}$$

The $(1-\delta)$ confidence interval for $\widehat{\sigma}_0$ and $\widehat{\sigma}_1$ can be written as

$$\widehat{\sigma}_0 \pm Z_{\frac{\delta}{2}} \sqrt{\frac{(\frac{\pi}{2}) - 2 + (2 - log(2) - \gamma)^2}{n_0(\pi^2 - 4)}}$$

and

$$\widehat{\sigma}_1 \pm Z_{(\frac{\delta}{2})} \sqrt{\frac{(\frac{\pi}{2}) - 2 + (2 - log(2) - \gamma)^2}{n_1(\pi^2 - 4)}}$$

where γ is the Euler's constant (=0.5772156649).

The $(1-\delta)$ confidence interval for $\widehat{\alpha}_0$ and $\widehat{\alpha}_1$ can be written as

$$\widehat{\alpha}_0 \pm Z_{(\frac{\delta}{2})} \frac{2\widehat{\alpha}_0}{\sqrt{n_0(\pi^2 - 4)}}$$

$$\widehat{\alpha}_1 \pm Z_{(\frac{\delta}{2})} \frac{2\widehat{\alpha}_1}{\sqrt{n_1(\pi^2 - 4)}}$$

5. Numerical illustrations

To illustrate the proposed methodology, SAPS III dataset is used. Out of the 111 subjects, 66 (59.46%) belong to alive population and the remaining are of dead population. Table 2 report the parameter estimates along with their confidence limits for both alive and dead populations. Using the expression given in equation (7) the AUC value turns out to be 0.5793. Since the AUC expression do not have the closed form, the $V(\widehat{AUC})$ is obtained using bootstrap method. Upon performing 100 bootstraps, the $\widehat{AUC}_{Boot}$= 0.5629 and its variance is 0.0014. The bootstrap expressions for AUC and its variance are given below.

$$\widehat{AUC}_B = \frac{1}{B} \sum_{b=1}^{B} AUC_b \tag{13}$$

Table 2: The parameters estimates and confidence limits of Bi-GHN ROC curve

n_0	n_1	$\hat{\theta}_0$	$\hat{\theta}_1$	$\hat{\lambda}_0$	$\hat{\lambda}_1$
		(L_0,U_0)	(L_1,U_1)	(L_0,U_0)	(L_1,U_1)
66	45	1.2070	1.2071	32.2297	39.8010
		(0.9666,1.4474)	(0.9158,1.4982)	(32.1977,32.2617)	(39.7623,39.8397)

Table 3: Bootstrap estimates of measures of Bi-GHN ROC curve

$\widehat{AUC}_{Boot}$	$V(\widehat{AUC}_{Boot})$	$\widehat{FPR}_{Boot}$	$\widehat{TPR}_{Boot}$	$\widehat{c}$	$\widehat{J}$
0.5629	0.0014	0.2736	0.4857	36	0.1226

Table 4: Parameter combinations

Scenario	α_0	α_1	σ_0	σ_1
Better	0.75	2.20	0.99	2.11
Moderate	0.53	0.91	0.92	2.61
Worst	1.21	1.52	2.28	2.52

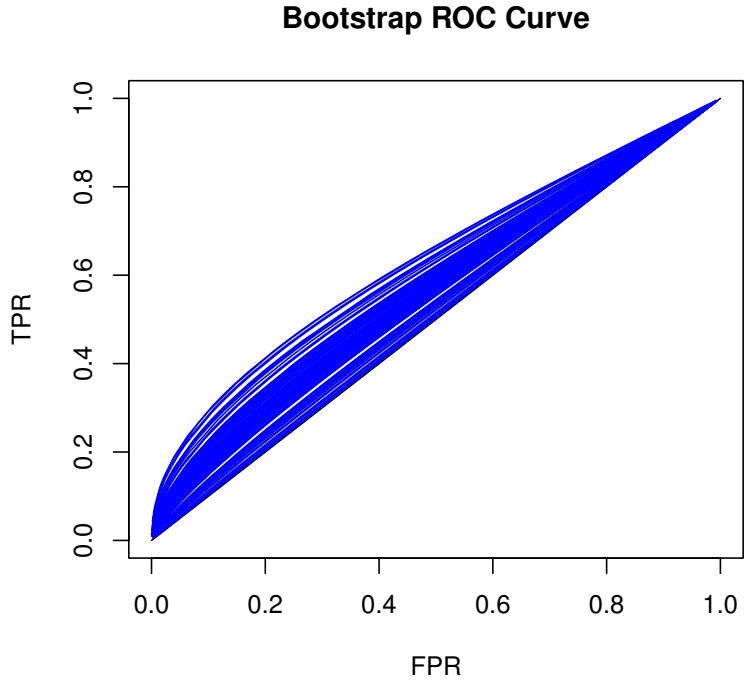

Figure 3: Bootstrap ROC curves for SAPS III dataset

$$V(\widehat{AUC}_B) = \frac{1}{B-1}\sum_{b=1}^{B}(AUC_b - \widehat{AUC}_B)^2 \tag{14}$$

Using the Youden's index, the optimal theshold is determined, that is, t= 36. At this cutoff, the FPR and TPR are observed to be 0.2736 and 0.4857 respectively. The obtained threshold is able to correctly classify 57 subjects out of 100 subjects. It is also noticed that this threshold generates 27% of false positives and truely detects the subject status upto 48% only. Figure 3 depicts the ROC curves generated at each bootstrap.

5.1. Simulation Studies

Further, to give a generalized view on the working methodology of the proposed Bi-GHN ROC curve, sizeable simulations are carried out with various parameter combinations at different sample sizes n= {25, 50, 100, 150, 200, 500}. Three different parameter combinations are considered to illustrate the *better, moderate* and *worst* case scenarios.

The parameter estimates and their confidence intervals of populations '0' and '1' for the combinations (Table 4) at different sample sizes are reported in Tables 5, 7 and 9 respectively. Accordingly, the estimated values of the measures of the proposed ROC curve are reported in Tables 6, 8 and 10 respectively.

Table 5: Parameter estimates at equal sample sizes (*Better case*)

n_0	n_1	$\widehat{\alpha}_0$ (L_0, U_0)	$\widehat{\alpha}_1$ (L_1, U_1)	$\widehat{\sigma}_0$ (L_0, U_0)	$\widehat{\sigma}_1$ (L_1, U_1)
25	25	0.7503	2.1000	0.9823	2.1026
		(0.5086,0.9274)	(1.4215,2.7817)	(0.7363,1.3569)	(2.0499,2.5524)
50	50	0.7499	2.1008	0.9926	2.1078
		(0.6553,0.8586)	(1.5638,2.5805)	(0.8894,1.2258)	(2.0616,2.2741)
100	100	0.7501	2.1016	0.9931	2.1102
		(0.6609,0.8234)	(1.6195,2.4398)	(0.9093,1.1403)	(2.0897,2.2362)
150	150	0.7482	2.1017	0.9936	2.1062
		(0.6642,0.8387)	(1.7602,2.3742)	(0.9247,1.0979)	(2.0924,2.2114)
200	200	0.7499	2.1018	0.9963	2.1115
		(0.6745,0.8049)	(1.8604,2.3484)	(0.9325,1.0089)	(2.0943,2.1940)
500	500	0.7524	2.1021	0.9991	2.1129
		(0.6996,0.7816)	(1.9496,2.3011)	(0.9269,1.0018)	(2.0995,2.1689)

With respect to better case, the following observations can be seen. For n= 100, the optimal cutoff is 1.1563, which is determined at the maximum value of Youden's index $\widehat{J}$= 0.5639. The classification of an individual can be in the following way: An individual is classified into Population '1', if S $>$ 1.1563 and Population '0', if S $\leq$ 1.1563. The optimal cutoff is able to detect around 82.92% of true positive cases with 29.63% of false positives.

Table 6: Accuracy cum intrinsic measures of Bi-GHN ROC (*Better case*)

n_0	n_1	$\widehat{AUC}$	$\widehat{FPR}$	$\widehat{TPR}$	$\hat{c}$	$\hat{J}$	$V(\widehat{AUC})$
25	25	0.9160	0.3282	0.8233	0.9789	0.5111	0.0029
50	50	0.9187	0.3062	0.8265	1.0048	0.5173	0.0132
100	100	0.9218	0.2963	0.8292	1.1563	0.5639	0.0147
150	150	0.9253	0.2923	0.8238	1.0353	0.5315	0.0142
200	200	0.9268	0.2871	0.8226	1.0675	0.5355	0.0068
500	500	0.9283	0.2745	0.8337	0.9992	0.5391	0.0018

The $\widehat{AUC}$ is observed to be 0.9218 which means that, the cutoff will be able to classify the individuals with 92.18% of accuracy. The ROC curves for this situation are shown in Figure 4 with a maximum coverage of area in the unit square plot. Interpretation can be given for the remaining sample sizes in similar manner.

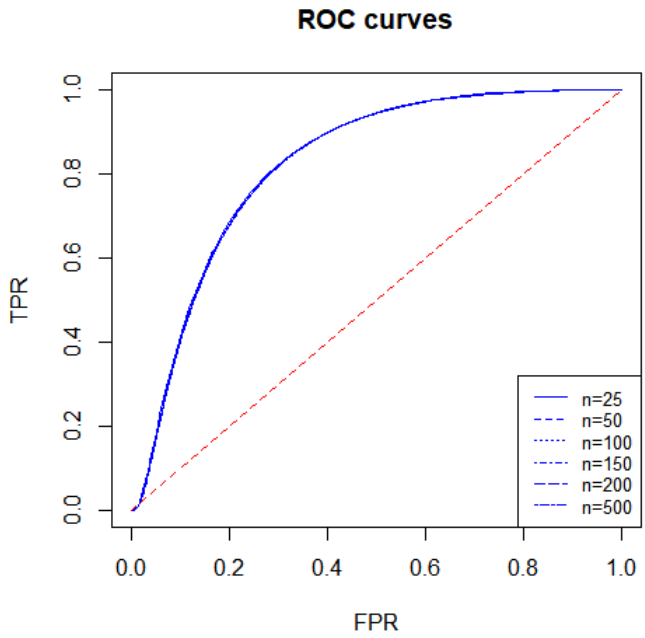

Figure 4: Better case

Now, let us consider the results of moderate case that are reported in Tables 7 and 8. For better understanding, let us consider a sample size from the results reported in Table 8. At $n = 150$, $\widehat{J}$= 0.3526 and the optimal cutoff ($\widehat{c}$) is 0.8886. At this $\widehat{c}$, we can observe 71.44% of true positives and 38.64% of false positives. The $\widehat{AUC}$= 0.7583, which can be interpreted

Table 7: Parameter estimates at equal sample sizes (*Moderate case*)

n_0	n_1	$\widehat{\alpha}_0$ (L_0, U_0)	$\widehat{\alpha}_1$ (L_1, U_1)	$\widehat{\sigma}_0$ (L_0, U_0)	$\widehat{\sigma}_1$ (L_1, U_1)
25	25	0.5314 (0.3618,0.7080)	0.9100 (0.6155,1.2044)	1.2429 (1.1210,1.3487)	2.4724 (2.3095,2.8732)
50	50	0.5348 (0.4086,0.6720)	0.9112 (0.6986,1.1408)	1.2497 (1.1807,1.3414)	2.4775 (2.3338,2.8453)
100	100	0.5365 (0.4099,0.6522)	0.9127 (0.7198,1.1361)	1.2538 (1.2357,1.3301)	2.4798 (2.3546,2.7881)
150	150	0.5397 (0.4286,0.6492)	0.9162 (0.7122,1.1289)	1.2606 (1.2312,1.3283)	2.4805 (2.3645,2.6754)
200	200	0.5329 (0.4319,0.6434)	0.9113 (0.7035,1.1152)	1.2644 (1.2376,1.3242)	2.4844 (2.3938,2.6072)
500	500	0.5222 (0.4691,0.6218)	0.9275 (0.6829,1.1008)	1.2667 (1.2456,1.3091)	2.4881 (2.4123,2.5697)

Table 8: Accuracy cum intrinsic measures of Bi-GHN ROC (*Moderate case*)

n_0	n_1	$\widehat{AUC}$	$\widehat{FPR}$	$\widehat{TPR}$	$\widehat{c}$	$\hat{J}$	$V(\widehat{AUC})$
25	25	0.7508	0.4057	0.7068	0.8338	0.3041	0.0166
50	50	0.7536	0.4044	0.7086	0.8563	0.3519	0.0189
100	100	0.7547	0.3927	0.7104	0.8598	0.3539	0.0251
150	150	0.7583	0.3864	0.7144	0.8886	0.3526	0.0310
200	200	0.7599	0.3514	0.7187	0.8837	0.3571	0.0035
500	500	0.7615	0.3554	0.7198	0.8503	0.3609	0.0012

as, $\widehat{c}$ has the ability to classify the individuals with 75.83% of accuracy. The ROC curves for the moderate case are depicted in Figure 5. Next, we consider the results pertaining to

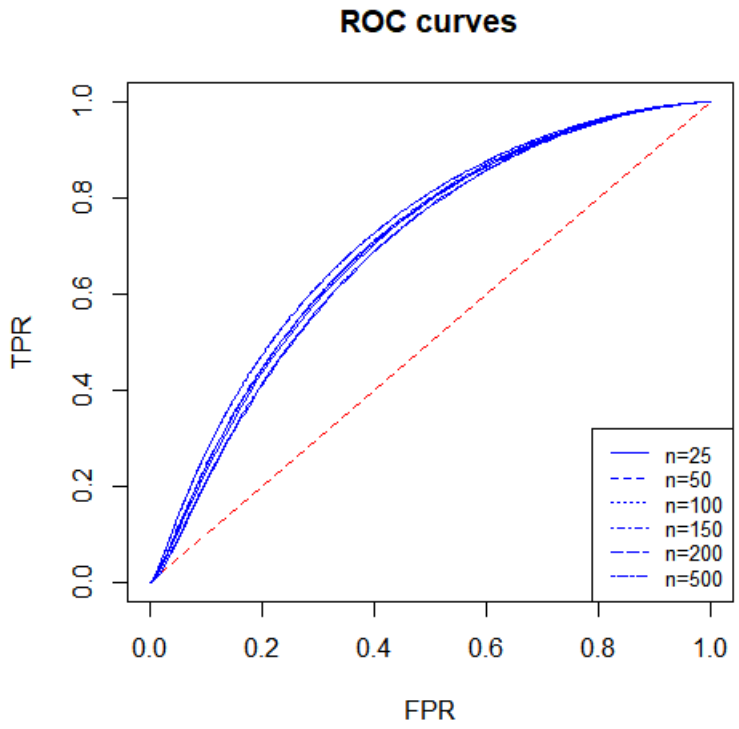

Figure 5: Moderate case

worst classification scenario presented in Tables 9 and 10. The $\widehat{AUC}$ is around 54%. So, this lower $\widehat{AUC}$ will have a maximum overlapping area between the populations '0' and '1'.

For $n = 100$, the $\widehat{AUC}$= 0.5466, where the ROC curve is quite closer to the chance diagonal line indicating random classification. The $\widehat{c} = 1.3878$ is able to detect 66.53% of true positives and 58.57% of false positives. The ROC curves for this case are presented in Figure 6. Since the curves obtained here are closer to the chance diagonal, the classifier fails to classify the subjects into one of the populations with better accuracy.

6. Summary

In this paper, Bi-GHN ROC curve is proposed and accordingly the expressions for AUC, FPR and TPR are derived. Since AUC does not have closed form expression, its variance is obtained using bootstrap. The proposed work is supported with SAPS III dataset and simulations. Better, moderate and worst case scenarios are considered at different sample sizes. For the SAPS III dataset, the optimal threshold is observed to be 36 and $\widehat{AUC}$= 0.5793. The obtained threshold is able to classify the subjects in alive and dead population with 57.93% of accuracy only.

Table 9: Parameter estimates at equal sample sizes (*Worst case*)

n_0	n_1	$\widehat{\alpha}_0$ (L_0, U_0)	$\widehat{\alpha}_1$ (L_1, U_1)	$\widehat{\sigma}_0$ (L_0, U_0)	$\widehat{\sigma}_1$ (L_1, U_1)
25	25	1.2085 (0.8174,1.5996)	1.5200 (1.1281,2.0119)	2.3239 (2.1519,2.5725)	2.6336 (2.4423,2.7656)
50	50	1.2100 (0.9331,1.4868)	1.5183 (1.1609,1.8657)	2.3120 (2.1703,2.5484)	2.6323 (2.4542,2.7614)
100	100	1.2143 (1.0142,1.4014)	1.5169 (1.2072,1.7967)	2.2970 (2.1754,2.5086)	2.5177 (2.4631,2.7547)
150	150	1.2214 (1.0331,1.3857)	1.5210 (1.2740,1.6959)	2.3106 (2.1987,2.4906)	2.6287 (2.4782,2.7512)
200	200	1.2150 (1.1198,1.3241)	1.5200 (1.3461,1.6345)	2.3056 (2.2172,2.4239)	2.6269 (2.5006,2.7154)
500	500	1.2321 (1.1501,1.3098)	1.5288 (1.4378,1.6190)	2.2917 (2.2562,2.3778)	2.6261 (2.5311,2.6921)

Table 10: Accuracy cum intrinsic measures of Bi-GHN ROC (*Worst case*)

n_0	n_1	$\widehat{AUC}$	$\widehat{FPR}$	$\widehat{TPR}$	$\widehat{c}$	$\hat{J}$	$V(\widehat{AUC})$
25	25	0.5319	0.5341	0.6431	1.6358	0.1090	0.0103
50	50	0.5354	0.6101	0.6543	1.3252	0.0908	0.0052
100	100	0.5466	0.5857	0.6653	1.3878	0.0996	0.0050
150	150	0.5490	0.5774	0.6786	1.4026	0.1011	0.0030
200	200	0.5584	0.5540	0.6822	1.5101	0.1082	0.0012
500	500	0.5665	0.5390	0.6909	1.4756	0.1152	0.0003

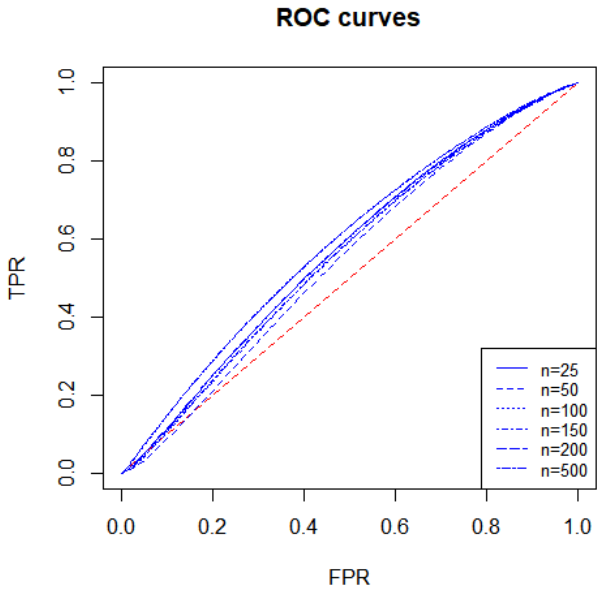

Figure 6: Worst case

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