Results

August 29, 2023

1 Tables of Friedman, Aligned Friedman, Bonferroni-Dunn, Holm, Hochberg and Hommel Tests

Table 1: Average Rankings of the algorithms (Friedman)

Algorithm	Ranking
SMOTE	2.259259259259259
ROS	2.685185185185186
VAE	2.462962962962963
GAN	2.5925925925925926

Friedman statistic (distributed according to chi-square with 3 degrees of freedom: 1.6555555555556003. P-value computed by Friedman Test: 0.6468595851395035.

Iman and Davenport statistic (distributed according to F-distribution with 3 and 78 degrees of freedom: 0.5425010502730859. P-value computed by Iman and Daveport Test: 0.6546355580526126.

Table 2: Average Rankings of the algorithms (Aligned Friedman)

Algorithm	Ranking
SMOTE	49.49999999999999
ROS	61.75925925925926
VAE	55.0
GAN	51.74074074074075

Aligned Friedman statistic (distributed according to chi-square with 3 degrees of freedom: 21.822877138885037. P-value computed by Aligned Friedman Test: 7.100731656650705E-5.

Table 3: Average Rankings of the algorithms (Quade)

Algorithm	Ranking
SMOTE	2.314814814814815
ROS	2.771164021164021
VAE	2.6124338624338628
GAN	2.301587301587302

Quade statistic (distributed according to F-distribution with 3 and 78 degrees of freedom: 5.597037521993534. P-value computed by Quade Test: 0.0015753474746236343.

Table 4: Contrast Estimation

	SMOTE	ROS	VAE	GAN
SMOTE	0,000	0,0006000	0,0003750	0,0005250
ROS	-0,0006000	0,000	-0,0002250	-7,500e-05
VAE	-0,0003750	0,0002250	0,000	0,0001500
GAN	-0,0005250	7,500e-05	-0,0001500	0,000

Table 5: Holm / Hochberg / Holland / Rom / Finner / Li Table for $\alpha = 0.05$ (FRIEDMAN)

i	algorithm	$z = (R_0 - R_i)/SE$	p	Holm/Hochberg/Hommel	Holland	Rom	Finner	Li
3	ROS	1.212206	0.2254333	0.01666666	0.01695242	0.016666	0.016952	0.023048
2	GAN	0.948683	0.342781	0.025	0.025320	0.025	0.033617	0.023048
1	VAE	0.57975	0.562082	0.05	0.050000	0.05	0.050000	0.05

Bonferroni-Dunn's procedure rejects those hypotheses that have a p-value ≤ 0.016666.
Holm's procedure rejects those hypotheses that have a p-value ≤ 0.016666.
Hommel's procedure rejects those hypotheses that have a p-value ≤ 0.016666.
Holland's procedure rejects those hypotheses that have a p-value ≤ 0.016952.
Finner's procedure rejects those hypotheses that have a p-value ≤ 0.016952.
Li's procedure rejects those hypotheses that have a p-value ≤ 0.023048.

Table 6: Holm / Hochberg / Holland / Rom / Finner / Li Table for $\alpha = 0.05$ (ALIGNED FRIEDMAN)

i	algorithm	$z = (R_0 - R_i)/SE$	p	Holm/Hochberg/Hommel	Holland	Rom	Finner	Li
3	ROS	1.438124	0.150398	0.016666	0.016952	0.016666	0.016952	0.010912
2	VAE	0.645201	0.518796	0.025	0.025320	0.025	0.033617	0.010912
1	GAN	0.262859	0.792658	0.05	0.050000	0.05	0.050000	0.05

Bonferroni-Dunn's procedure rejects those hypotheses that have a p-value $\leq$ 0.016666.
Holm's procedure rejects those hypotheses that have a p-value ≤ 0.016666.

Hommel's procedure rejects those hypotheses that have a p-value ≤ 0.016666.
Holland's procedure rejects those hypotheses that have a p-value ≤ 0.016952.
Finner's procedure rejects those hypotheses that have a p-value ≤ 0.016952.
Li's procedure rejects those hypotheses that have a p-value ≤ 0.010912.

Table 7: Holm / Hochberg / Holland / Rom / Finner / Li Table for $\alpha = 0.05$ (QUADE)

i	algorithm	$z = (R_0 - R_i)/SE$	p	Holm/Hochberg/Hommel	Holland	Rom	Finner	Li
3	ROS	0.95355	0.340307	0.016666	0.016952	0.016666	0.016952	0.001127
2	VAE	0.63122	0.527891	0.025	0.025320	0.025	0.033617	0.001127
1	SMOTE	0.026860	0.978570	0.05	0.050000	0.05	0.050000	0.05

Bonferroni-Dunn's procedure rejects those hypotheses that have a p-value ≤ 0.016666.
Holm's procedure rejects those hypotheses that have a p-value ≤ 0.016666.
Hommel's procedure rejects those hypotheses that have a p-value ≤ 0.016666.
Holland's procedure rejects those hypotheses that have a p-value ≤ 0.016952.
Finner's procedure rejects those hypotheses that have a p-value ≤ 0.016952.
Li's procedure rejects those hypotheses that have a p-value ≤ 0.001127.

Table 8: Adjusted p-values (FRIEDMAN)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Homm}
1	ROS	0.225433	0.676300	0.676300	0.562082	0.514172
2	GAN	0.342781	1.028345	0.685563	0.562082	0.562082
3	VAE	0.562082	1.686247	0.685563	0.562082	0.562082

Table 9: Adjusted p-values (FRIEDMAN)

i	algorithm	unadjusted p	p_{Holl}	p_{Rom}	p_{Finn}	p_{Li}
1	ROS	0.225433	0.535296	0.562082	0.535296	0.339840
2	GAN	0.342781	0.568064	0.562082	0.535296	0.439070
3	VAE	0.562082	0.568064	0.562082	0.562082	0.562082

Table 10: Adjusted p-values (ALIGNED FRIEDMAN)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Homm}
1	ROS	0.150398	0.451195	0.451195	0.451195	0.451195
2	VAE	0.518796	1.556390	1.037593	0.792658	0.792658
3	GAN	0.792658	2.377976	1.037593	0.792658	0.792658

Table 11: Adjusted p-values (ALIGNED FRIEDMAN)

i	algorithm	unadjusted p	p_{Holl}	p_{Rom}	p_{Finn}	p_{Li}
1	ROS	0.150398	0.386738	0.451195	0.386738	0.420413
2	VAE	0.518796	0.768443	0.792658	0.666195	0.714460
3	GAN	0.792658	0.792658	0.792658	0.792658	0.792658

Table 12: Adjusted p-values (QUADE)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Homm}
1	ROS	0.340307	1.020923	1.020923	0.978570	0.791837
2	VAE	0.527891	1.583674	1.055782	0.978570	0.978570
3	SMOTE	0.978570	2.935712	1.055782	0.978570	0.978570

Table 13: Adjusted p-values (QUADE)

i	algorithm	unadjusted p	p_{Holl}	p_{Rom}	p_{Finn}	p_{Li}
1	ROS	0.340307	0.712906	0.978570	0.712906	0.940760
2	VAE	0.527891	0.777113	0.978570	0.712906	0.960989
3	SMOTE	0.978570	0.978570	0.978570	0.978570	0.978570

4