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	2.85185185
ROS	2.51851851
VAE	2.42592592
GAN	2.20370370

Friedman statistic (distributed according to chi-square with 3 degrees of freedom: 3.52222222. P-value computed by Friedman Test: 0.31789138.

Iman and Davenport statistic (distributed according to F-distribution with 3 and 78 degrees of freedom: 1.18198766. P-value computed by Iman and Davenport Test: 0.322093621.

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

Algorithm	Ranking
SMOTE	70.000000
ROS	54.555555
VAE	51.388888
GAN	42.0555555

Aligned Friedman statistic (distributed according to chi-square with 3 degrees of freedom: 21.8930396. P-value computed by Aligned Friedman Test: 6.8660688E-5.

Table 3: Average Rankings of the algorithms (Quade)

Algorithm	Ranking
SMOTE	3.175264
ROS	2.5343915
VAE	2.29563492
GAN	1.99470899

Quade statistic (distributed according to F-distribution with 3 and 78 degrees of freedom: 9.515325. P-value computed by Quade Test: 1.98620621E-5.

Table 4: Contrast Estimation

	SMOTE	ROS	VAE	GAN
SMOTE	0,000	-0,001225	-0,001075	-0,002600
ROS	0,001225	0,000	0,0001500	-0,001375
VAE	0,001075	-0,0001500	0,000	-0,001525
GAN	0,002600	0,001375	0,001525	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	SMOTE	1.844661	0.065086	0.016666	0.016952	0.016666	0.016952	0.024890
2	ROS	0.895978	0.370264	0.025	0.025320	0.025	0.033617	0.024890
1	VAE	0.632455	0.527089	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 ≤ 0.024890.

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	SMOTE	3.278142	0.001044	0.016666	0.016952	0.016666	0.016952	0.038233
2	ROS	1.466366	0.142548	0.025	0.025320	0.025	0.033617	0.038233
1	VAE	1.094886	0.273566	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 ≤ 0.025.
Hochberg's procedure rejects those hypotheses that have a p-value ≤ 0.016666.
Hommel's procedure rejects those hypotheses that have a p-value ≤ 0.025.

Holland's procedure rejects those hypotheses that have a p-value ≤ 0.025320.
Rom's procedure rejects those hypotheses that have a p-value ≤ 0.016666.
Finner's procedure rejects those hypotheses that have a p-value ≤ 0.03361.
Li's procedure rejects those hypotheses that have a p-value ≤ 0.038233.

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	SMOTE	2.397323	0.016515	0.016666	0.016952	0.016666	0.016952	0.024150
2	ROS	1.095919	0.273114	0.025	0.025320	0.025	0.033617	0.024150
1	VAE	0.611082	0.541145	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 ≤ 0.025.
Hochberg's procedure rejects those hypotheses that have a p-value ≤ 0.016666.
Hommel's procedure rejects those hypotheses that have a p-value ≤ 0.025.
Holland's procedure rejects those hypotheses that have a p-value ≤ 0.025320.
Rom's procedure rejects those hypotheses that have a p-value ≤ 0.016666.
Finner's procedure rejects those hypotheses that have a p-value ≤ 0.03361.
Li's procedure rejects those hypotheses that have a p-value ≤ 0.024150.

Table 8: Adjusted p-values (FRIEDMAN)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Homm}
1	SMOTE	0.065086726	0.195260179	0.195260179	0.195260179	0.195260179
2	ROS	0.37026415	1.1107924	0.74052831	0.52708925	0.52708925
3	VAE	0.52708925	1.5812677	0.74052831	0.52708925	0.52708925

Table 9: Adjusted p-values (FRIEDMAN)

i	algorithm	unadjusted p	p_{Holl}	p_{Rom}	p_{Finn}	p_{Li}
1	SMOTE	0.065086726	0.182827059	0.195260179	0.182827059	0.120979614
2	ROS	0.37026415	0.60343276	0.52708925	0.5002674	0.439130903
3	VAE	0.52708925	0.60343276	0.52708925	0.52708925	0.52708925

Table 10: Adjusted p-values (ALIGNED FRIEDMAN)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Homm}
1	SMOTE	0.00104492540	0.00313477622	0.00313477622	0.00313477622	0.00313477622
2	ROS	0.142548593	0.42764578	0.285097186	0.273566301	0.273566301
3	VAE	0.273566301	0.82069890	0.285097186	0.273566301	0.273566301

Table 11: Adjusted p-values (ALIGNED FRIEDMAN)

i	algorithm	unadjusted p	p_{Holl}	p_{Rom}	p_{Finn}	p_{Li}
1	SMOTE	0.00104492540	0.00313150175	0.00313477622	0.00313150175	0.00143636579
2	ROS	0.142548593	0.264777085	0.273566301	0.206011384	0.16404
3	VAE	0.273566301	0.27356630	0.273566301	0.27356630	0.273566301

Table 12: Adjusted p-values (QUADE)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Homm}
1	SMOTE	0.0165153436	0.049546031	0.049546031	0.049546031	0.049546031
2	ROS	0.273114122	0.81934236	0.54622824	0.54114502	0.54114502
3	VAE	0.54114502	1.62343506	0.54622824	0.54114502	0.54114502

Table 13: Adjusted p-values (QUADE)

i	algorithm	unadjusted p	p_{Holl}	p_{Rom}	p_{Finn}	p_{Li}
1	SMOTE	0.0165153436	0.048732265	0.049546031	0.048732265	0.0347420587
2	ROS	0.273114122	0.47163692	0.54114502	0.38027452	0.373122474
3	VAE	0.54114502	0.54114502	0.54114502	0.54114502	0.54114502