Results

August 27, 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	2.851851851851852
ROS	2.5185185185173
VAE	2.4259259259259265
GAN	2.2037037037037033

Friedman statistic (distributed according to chi-square with 3 degrees of freedom: 3.5222222222221795. P-value computed by Friedman Test: 0.31789138961143547.

Iman and Davenport statistic (distributed according to F-distribution with 3 and 78 degrees of freedom: 1.18198766671445553. P-value computed by Iman and Daveport Test: 0.32209362196935565.

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

Algorithm	Ranking
SMOTE	70.00000000000001
ROS	54.55555555555557
VAE	51.38888888888889
GAN	42.05555555555564

Aligned Friedman statistic (distributed according to chi-square with 3 degrees of freedom: 21.893039624875573. P-value computed by Aligned Friedman Test: 6.866068820110538E-5.

Table 3: Average Rankings of the algorithms (Quade)

Algorithm	Ranking
SMOTE	3.1752645502645
ROS	2.5343915343915354
VAE	2.2956349206349205
GAN	1.9947089947089942

Quade statistic (distributed according to F-distribution with 3 and 78 degrees of freedom: 9.5153255960258². P-value computed by Quade Test: 1.986206218629327²E-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	1.8446619684315577	0.06508672649276634	0.016666666666666666	0.016952427508441503	0.016666666666666666	0.016952427508441503	0.024890039112340195
2	ROS	0.8959786703810385	0.3702641551795073	0.025	0.025320655519103666	0.025	0.03361747021845407	0.024890039112340195
1	VAE	0.6324555320336787	0.5270892568655363	0.05	0.050000000000000044	0.05	0.050000000000000044	0.05

Bonferroni-Dunn's procedure rejects those hypotheses that have a p-value $\leq 0.016666666666666666$.

Holm's procedure rejects those hypotheses that have a p-value $\leq 0.016666666666666666$.

Hommel's procedure rejects those hypotheses that have a p-value $\leq 0.016666666666666666$.

Holland's procedure rejects those hypotheses that have a p-value $\leq 0.016952427508441503$.

Finner's procedure rejects those hypotheses that have a p-value $\leq 0.016952427508441503$.

Li's procedure rejects those hypotheses that have a p-value $\leq 0.024890039112340195$.

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	3.2781427430325441	0.0010449254080749175	0.016666666666666666	0.0169524275084441503	0.016666666666666666	0.0169524275084441503	0.0382333352526417415
2	ROS	1.4663660381356829	0.14254859342114623	0.025	0.0253205655191103666	0.025	0.0336174702184521845407	0.0382333352526417415
1	VAE	1.0948866418080845	0.273566301998069925	0.05	0.0500000000000000044	0.05	0.0500000000000000044	0.05

Bonferroni-Dunn's procedure rejects those hypotheses that have a p-value ≤ 0.0166666666666666.

Holm's procedure rejects those hypotheses that have a p-value ≤ 0.025.

Hochberg's procedure rejects those hypotheses that have a p-value ≤ 0.0166666666666666.

Hommel's procedure rejects those hypotheses that have a p-value ≤ 0.025.

Holland's procedure rejects those hypotheses that have a p-value $\leq 0.0253205655191103666$.

Rom's procedure rejects those hypotheses that have a p-value ≤ 0.0166666666666666.

Finner's procedure rejects those hypotheses that have a p-value $\leq 0.0336174702184521845407$.

Li's procedure rejects those hypotheses that have a p-value $\leq 0.0382333352526417415$.

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/Holland/Hommel	Rom	Finner	Li
3	SMOTE	2.3973233179755065	0.016515343680903242	0.016666666666666666	0.016666666666666666	0.016952427508441503	0.024150262036368452
2	ROS	1.0959192310745174	0.27311412231156645	0.025	0.025	0.03361747021845407	0.024150262036368452
1	VAE	0.6110824143859142	0.5411450212999412	0.05	0.05	0.05000000000000044	0.05

Bonferroni-Dunn's procedure rejects those hypotheses that have a p-value $\leq 0.016666666666666666$.

Holm's procedure rejects those hypotheses that have a p-value ≤ 0.025.

Hochberg's procedure rejects those hypotheses that have a p-value $\leq 0.016666666666666666$.

Hommel's procedure rejects those hypotheses that have a p-value ≤ 0.025.

Holland's procedure rejects those hypotheses that have a p-value $\leq 0.025320565519103666$.

Rom's procedure rejects those hypotheses that have a p-value $\leq 0.016666666666666666$.

Finner's procedure rejects those hypotheses that have a p-value ≤ 0.03361747021845407.

Li's procedure rejects those hypotheses that have a p-value $\leq 0.024150262036368452$.

7

Table 8: Adjusted p-values (FRIEDMAN)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Homm}
1	SMOTE	0.0650867264927634	0.195260179478299902	0.195260179478299902	0.195260179478299902	0.195260179478299902
2	ROS	0.37026415517950073	1.1107924655538522	0.7405283103590146	0.527089256865363	0.527089256865363
3	VAE	0.527089256865363	1.581267770596609	0.7405283103590146	0.527089256865363	0.527089256865363

Table 9: Adjusted p-values (FRIEDMAN)

i	algorithm	unadjusted p	p_{Holl}	p_{Rom}	p_{Finn}	p_{Li}
1	SMOTE	0.0650867264927634	0.182827059307730414	0.195260179478299902	0.182827059307730414	0.120979614528417589
2	ROS	0.37026415517950073	0.6034327657482204	0.527089256865363	0.5002674692501129	0.4391309038254 0415
3	VAE	0.527089256865363	0.6034327657482204	0.527089256865363	0.527089256865363	0.527089256865363

Table 10: Adjusted p-values (ALIGNED FRIEDMAN)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Homm}
1	SMOTE	0.0010449254080749175	0.0031347762242247526	0.0031347762242247526	0.0031347762242247526	0.0031347762242247526
2	ROS	0.1425485934211462 3	0.4276457802634387	0.285097186842229246	0.27356630199806925	0.27356630199806925
3	VAE	0.27356630199806925	0.8206989059942078	0.285097186842229246	0.27356630199806925	0.27356630199806925

Table 11: Adjusted p-values (ALIGNED FRIEDMAN)

i	algorithm	unadjusted p	p_{Holl}	p_{Rom}	p_{Finn}	p_{Li}
1	SMOTE	0.0010449254080749175	0.0031315017578210647	0.0031347762242247526	0.0031315017578210647	0.0014363657906220008
2	ROS	0.1425485934211462 3	0.26477708535594524	0.27356630199806925	0.20601138401703178	0.1640408496561
3	VAE	0.27356630199806925	0.27356630199806692	0.27356630199806925	0.27356630199806692	0.27356630199806925

Table 12: Adjusted p-values (QUADE)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Homm}
1	SMOTE	0.0165153436809032342	0.04954603104270973	0.04954603104270973	0.04954603104270973	0.04954603104270973
2	ROS	0.273114122311566645	0.8193423669346993	0.5462282446231329	0.5411450212999412	0.5411450212999412
3	VAE	0.5411450212999412	1.6234350638998238	0.5462282446231329	0.5411450212999412	0.5411450212999412

Table 13: Adjusted p-values (QUADE)

i	algorithm	unadjusted p	p_{Holl}	p_{Rom}	p_{Finn}	p_{Li}
1	SMOTE	0.0165153436809032342	0.0487322659806234 1	0.04954603104270973	0.0487322659806234 1	0.034742058776794725
2	ROS	0.273114122311566645	0.4716369208171157	0.5411450212999412	0.3802745280771379	0.3731224746155354 4
3	VAE	0.5411450212999412	0.5411450212999412	0.5411450212999412	0.5411450212999412	0.5411450212999414