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	2.259259259259259
ROS	2.685185185185186
VAE	2.4629629629629629
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	61.7592592592596
VAE	55.0
GAN	51.74074074074075

Aligned Friedman statistic (distributed according to chi-square with 3 degrees of freedom: 21.8228771388385037. P-value computed by Aligned Friedman Test: 7.100731656650705E-5.

Table 3: Average Rankings of the algorithms (Quade)

Algorithm	Ranking
SMOTE	2.314814814815
ROS	2.7711640211164021
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: 0.0015753474626343.

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	1.21220436397815	0.22543333830507435	0.0166666666666666	0.0169524275084441503	0.0166666666666666666	0.0169524275084441503	0.0230482836823449906
2	GAN	0.948683298050142	0.3427817111479111	0.025	0.0253205655191103666	0.025	0.0336174702184547	0.0230482836823449906
1	VAE	0.579750904364203	0.5620826100354468	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 ≤ 0.0166666666666666.

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

Holland's procedure rejects those hypotheses that have a p-value $\leq 0.0169524275084441503$.

Finner's procedure rejects those hypotheses that have a p-value $\leq 0.0169524275084441503$.

Li's procedure rejects those hypotheses that have a p-value $\leq 0.0230482836823449906$.

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	1.4381249144383983	0.1503986146853170	0.0166666666666666	0.016952427508441503	0.0166666666666666	0.016952427508441503	0.01091269858640415
2	VAE	0.6452010567797652	0.5187969014526351	0.025	0.025320655519103666	0.025	0.033617470218458407	0.01091269858640415
1	GAN	0.2628596897991649	0.7926587268583212	0.05	0.05000000000000044	0.05	0.05000000000000044	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 ≤ 0.0166666666666666.

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

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 ≤ 0.01091269858640415.

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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	0.9535571740996699	0.3403078423889078	0.016666666666666666	0.016952427508441503	0.016666666666666666	0.016952427508441503	0.0011278533242860224
2	VAE	0.6312279848546548	0.5278914640746286	0.025	0.025320655519103666	0.025	0.033617470218445407	0.0011278533242860224
1	SMOTE	0.0268607654675122 8	0.9785707868385656	0.05	0.05000000000000044	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 $\leq 0.016666666666666666$.

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 $\leq 0.0011278533242860224$.

Table 8: Adjusted p-values (FRIEDMAN)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Homm}
1	ROS	0.22543336830507435	0.6763001049152231	0.6763001049152231	0.5620826100354468	0.5141725667218666
2	GAN	0.3427817111479111	1.0283451334437332	0.6855634222958222	0.5620826100354468	0.5620826100354468
3	VAE	0.5620826100354468	1.6862478301063404	0.6855634222958222	0.5620826100354468	0.5620826100354468

Table 9: Adjusted p-values (FRIEDMAN)

i	algorithm	unadjusted p	p_{Holl}	p_{Rom}	p_{Finn}	p_{Li}
1	ROS	0.22543336830507435	0.5352960639422917	0.5620826100354468	0.5352960639422917	0.3398403717712251
2	GAN	0.3427817111479111	0.5680641207983322	0.5620826100354468	0.5352960639422917	0.4390702008743972 4
3	VAE	0.5620826100354468	0.5680641207983322	0.5620826100354468	0.5620826100354468	0.5620826100354468

Table 10: Adjusted p-values (ALIGNED FRIEDMAN)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Homm}
1	ROS	0.15039861468531707	0.45119584405595512	0.45119584405595512	0.45119584405595512	0.45119584405595512
2	VAE	0.5187969014526351	1.5563907043579053	1.0375938029052703	0.7926587268583212	0.7926587268583212
3	GAN	0.7926587268583212	2.3779761805749633	1.0375938029052703	0.7926587268583212	0.7926587268583212

Table 11: Adjusted p-values (ALIGNED FRIEDMAN)

i	algorithm	unadjusted p	p_{Holl}	p_{Rom}	p_{Finn}	p_{Li}
1	ROS	0.15039861468531707	0.3867385922149047	0.45119584405595512	0.3867385922149047	0.42041332208962473
2	VAE	0.5187969014526351	0.7684435779484151	0.7926587268583212	0.6661951651342299	0.7144603046692617
3	GAN	0.7926587268583212	0.7926587268583212	0.7926587268583212	0.7926587268583212	0.7926587268583212

Table 12: Adjusted p-values (QUADE)

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	p_{Hoch}	p_{Homm}
1	ROS	0.34030784223889078	1.0209235271667234	1.0209235271667234	0.9785707868385656	0.7918371961119429
2	VAE	0.5278914640746286	1.5836743922238858	1.0557829281492572	0.9785707868385656	0.9785707868385656
3	SMOTE	0.9785707868385656	2.935712360515697	1.0557829281492572	0.9785707868385656	0.9785707868385656

Table 13: Adjusted p-values (QUADE)

i	algorithm	unadjusted p	p_{Holl}	p_{Rom}	p_{Finn}	p_{Li}
1	ROS	0.34030784223889078	0.7129061008244639	0.9785707868385656	0.7129061008244639	0.9407602488254007
2	VAE	0.5278914640746286	0.7771135303064023	0.9785707868385656	0.7129061008244639	0.9609896112608455
3	SMOTE	0.9785707868385656	0.9785707868385656	0.9785707868385656	0.9785707868385656	0.9785707868385656