CAMIS: Comparing Analysis Method Implementations in Software

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Background

The pharmaceutical industry has historically been limited to commercial software, such as SAS. Recently, the use of software such as R has gained momentum, due to its flexibility, far reaching capabilities, and open-source collaboration. However, there are knowledge gaps in understanding how certain statistical procedures are computed across different software.

Aim

To increase understanding of discrepancies, thereby helping the analyst to make informed choices on which software and method is best suited to their question.

Method

Analysis methods common to medical statistics were performed in both R and SAS. Where there were differences, the respective documentations were investigated.

Demonstrative Results

Conclusion

Discrepancies were generally found in default statistical output, and due to algorithmic variation – as seen in the results table. Additionally, parameterisation and reference levels must be considered between software for interpretation of results.

These results also point to the wider work of utilizing the availability of software tools, such as the R Validation Hub (creators of the Risk Assessment tool[1] used to score the epibasix package) as well as the CAMIS project. CAMIS is a PHUSE project collaboration to document in a GitHub repository, the similarities and differences between the implementation of statistical methods in software.

Call to Action!

As and when you discover differences in software – firstly check CAMIS (see QR code in header), as it may be documented and save you considerable time.

If not already documented, then you have the opportunity to contribute and help our community!

Getting different results for the same analysis depending on which software you use?

Me too! Here's why:

CAMIS

SAS Solutions	SAS Key Difference	SAS Code	Analysis Method	R Code	R Key Difference	R Solutions

Include "TIES=EFRON" in the MODEL statement to use the same tie-handling method as R.	Uses Breslow method[2] for handling ties, as default.	`proc phreg data=data1; class x1(ref=first); model time*event(0) = x1/rl; run;`	**Cox proportional hazards Regression**	`# survival::coxph`
				
				`mfit <- coxph(Surv(time, event) ~ x1, data=data1)`
				
				`summary(mfit)`
					Uses Efron method[3] for handling ties, as default.	Addition of argument "ties = 'breslow'" to coxph() produces a result using the same tie-handling method as SAS.

Include 'PARAM=GLM' in the CLASS statement to apply the same parameterisation as R.	Uses 'effect' parameterisation as default.	`proc logistic data=data2; class Sex(ref='F'); model Outcome=Sex; run;`	**Logistic Regression**	`# stats::glm`
				
				`z <- glm(Outcome ~ Sex,data=data2, family=binomial)`
				
				`summary(z)`
					Uses 'glm' parameterisation as default.	Option not found to use 'effect' parameterisation within function, to replicate SAS's default.

Code supplied on SAS Blog[4] to manually calculate McNemar's statistic using Edward's correction, if required.	Provides asymptotic (uncorrected) result with no option to use continuity correction.	`proc freq data=data3; tables before*after / agree; run;`	**McNemar's Test**	`# epibasix::mcNemar`
				
				`X<- table(data3$before, data3$after)`
				
				`summary(mcNemar(X))`
					Result uses Edward's continuity correction with no option to remove this.	Epibasix package categorised as 'High Risk' using the Risk Assessment Shiny App[1]. Advise use of a different package.

REFERENCES
[1] R Validation Hub. (2023). "The {riskassessment} application". https://github.com/pharmaR/riskassessment
[2] Breslow, N. E. (1974). Covariance Analysis of Censored Survival Data. Biometrics, 30, 89–99.
[3] Efron, B. (1977). The Efficiency of Cox's Likelihood Function for Censored Data. Journal of the American Statistical Association, 72, 557–565.
[4] Wicklin, R. (2022). "The McNemar test in SAS" *blogs.sas.com.* https://blogs.sas.com/content/iml/2022/04/18/mcnemar-test-sas.html

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