Package SSDDA : Sample Size Determination and Data Analysis in the context of continuous co-primary endpoints in clinical trials.

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Nowadays, in clinical research, in order to capture a multi-factorial effect of some product, it is increasingly common to define multiple co-primary endpoints and then testing simultaneously a finite number of associated null hypotheses denoted $\mathcal{H}_0^k$, $k = 1, \ldots, m$. In this context where many hypotheses are tested, and each individual test has a specified Type I error probability, the probability that at least some Type I errors (false rejections or false positives) are committed increases with the number of hypotheses. Multiple hypothesis testing methods have been proposed for dealing with this problem. The most common one in clinical trials is undoubtedly the single step Bonferroni procedure. That could be explain by its ease of use and also for its control of the familywise error rate (FWER), which is defined as the probability of one or more false rejection among the family of the m hypotheses $\mathcal{H}_0^k$. This procedure is conservative (lead to wrongly "accepting" the null hypothesis) and might lead to biased test decisions, as information about correlations of the end points is not exploited.
In the context of "at least one win" continuous co-primary endpoints the aim of the work [1] is to provide sample size calculation methods, as well as corrections for Type-I errors probabilities based on a global method with a multivariate linear model or on an individual method involving a union-intersection procedure which controls the FWER and takes into account correlations among endpoints.
In the context of "at least r win" continuous co-primary endpoints, no procedures of sample size computation are developed. Therefore the aim of this work consists in providing a method which permits the sample size computation for single step (e.g. Bonferroni) and stepwise (e.g. Holm and Hochberg) procedures commonly used in clinical research. This choice will allow to seamlessly integrate this work within current clinical practice.
To facilitate the use of all these methods we have developed an R package SSDDA, which we

will present.

References

[1] Lafaye de Micheaux, P., Liquet, B., Marque, S., Riou, J. (2013). Power and sample size determination in clinical trials with multiple primary continuous correlated end points. To appear in *Journal of Biopharmaceutical Statistics*.