

Detailed description and R script of `b.pair` function for two-sided bootstrap pairwise test with unequal sample sizes

The null hypothesis of the bootstrap pairwise test is that, with the probability β , the difference between the means of two samples is lower than the difference of two means randomly generated from the combination of the two distributions. In order to test this null hypothesis for a pair of samples with n and m replicates, the following steps are conducted to generate 9999 bootstrap resamples: n values are randomly sampled with replacement from the first sample of the tested pair and m values are randomly sampled with replacement from the second sample of the tested pair. These are then merged to a list of $n + m$ values. From this list, two samples of the sizes n and m are sampled with replacement and the difference between their means is calculated. After generating the 9999 bootstrap resamples, the test statistic is calculated as follows (Efron and Tibshirani, 1993):

$$p(\hat{\tau}) = \frac{1}{B} \cdot \sum_{j=1}^B I(|\tau_j| > |\hat{\tau}|),$$

$p(\hat{\tau})$ is the significance level, B is the number of bootstrap samples, τ_j is the difference of the random means calculated for each of the bootstrap resamples and $\hat{\tau}$ is the difference between the mean of the two samples. I is an indicator function, which is 1 if $\tau_j > \hat{\tau}$ or 0, if this is not the case.

References

Efron, B. and Tibshirani, R.: An Introduction to the Bootstrap, Chapman & Hall/CRC, 1993