**One sequence**

The differences , , on natural log-scale of a measurement on the one treatment versus on the other treatment have variances , where is the within-subject standard deviation on log-scale (which is assumed the same under treatment and ).

The measurements on original scale are assumed from now on log-normally distributed. Thus, this is related to the coefficient of variation (of the within-subject variation) on the original scale as

The variance of the average difference  is , and

the distribution of the   is

where is the systematic difference between treatment and . Otherwise stated:

where standard normally distributed.

An confidence interval for   is thus

This confidence interval will be between margins and with probability

with the standard normal cumulative distribution function.

To account for small samples, t-distributions may be used instead of the normal distribution and the probability becomes:

Examples:

For an , (80%-125% equivalence margins on the original scale), two-sided 90%-CI and assuming only a small systematic difference (ratio 1.05 on original scale), 17 subjects give at least 90% power to detect a two-sided 90%-CI within the equivalence margins.

For an , (80%-125% equivalence margins on the original scale), two-sided 90%-CI and assuming only a small systematic difference (ratio 1.05 on original scale), 50 subjects give at least 80% power to detect a two-sided 90%-CI within the equivalence margins.

For an , (75%-133% equivalence margins on the original scale), two-sided 90%-CI and assuming no systematic difference (ratio 1.00 on original scale), 25 subjects give at least 80% power to detect a two-sided 90%-CI within the equivalence margins.

For an , (75%-133% equivalence margins on the original scale), two-sided 90%-CI and assuming no systematic difference (ratio 1.05 on original scale), 28 subjects give at least 80% power to detect a two-sided 90%-CI within the equivalence margins.

**Two sequences (two groups-two periods)**

Similar idea. In each sequence, , (so and )there is an average difference   and then make:

as the estimator, so with the number in each sequence:

(Note that if we take 2 sequences of each , then we have subjects in total and

so the same standard error as taking subjects in total in one sequence. However, now difference in carry-over (if present can be estimated).)