

# nQuery Advisor<sup>®</sup> Upgrade Comparison List

Features/Utilities	Version 5	Version 6	Version 7
<b>References</b> References for every sample size table are shown in a separate pane below the table and can be copied and pasted into reports.	✓	✓	✓
<b>Column names</b> You can assign names (e.g. Outcome A, Outcome B, or Low SD, High SD, etc.) to each column in a table. These names will display on the screen and in the plot legends, as well as in the printed or pasted tables.	✓	✓	✓
<b>RTF Copy and Paste with user font choice for tables and side-tables</b> You can copy and paste tables from nQuery Advisor into user documents using your selected font in Rich Text Format. The table structure, formatting, and Greek symbols are preserved.	✓	✓	✓
<b>RTF Copy and Paste with user font choice for statements, user notes, references and guides</b> You can copy nQuery Advisor statements, user notes, references and guides. Then you can paste them into user documents in your selected font using Rich Text Format. This process preserves formatting and Greek symbols.	✓	✓	✓
<b>Create randomization list (basic) for simple designs</b> You can create a randomization list for assignment of subjects to groups for designs with equal sample sizes. Simply specify the total sample size and the group names and click on the View List button.		✓	✓
<b>Create randomization list (advanced) for designs with strata, unequal n's</b> You can create a randomization list for assignment of subjects to groups for designs with unequal sample sizes, and/or randomization within strata. You can also specify randomization block sizes to use. Simply specify the design details and group and strata names and click on the View List button.		✓	✓
<b>Create randomization list (complex designs)</b> You can create a randomization list for assignment of subjects to groups for designs with unequal sample sizes, centers and strata, and have more user control over ID numbers. You can also specify randomization block sizes. Simply specify the design details and click on the View List button, then edit the default ID numbers if desired.			✓
<b>Random subset of cases</b> You can use this option to select a random subset of n cases from a total of N available cases.		✓	✓
<b>User control over number of decimal places displayed in table rows</b> You can specify the number of decimal places to display for each row in nQuery tables. These choices can be saved with the table and applied to other similar tables. They will also show in the printed copies of the tables.		✓	✓
<b>Expanded right click edit menus</b> You have more options in the right click edit menus.		✓	✓
<b>Standard Deviation Calculator</b> The Assistants menu option, Estimate SD, calculates the		✓	✓

pooled deviation from two independent samples.			
<b>The Help system.</b> When you choose the Help menu, you can now access the Help Topics in a PDF Help file if you prefer.			✓
<b>Sample Size Tables</b>			
<b>Two group Satterthwaite t-test of equal means (unequal variances) (equal and unequal n's) (MTT0uv, MTT0uvU)</b> Compute power and sample size for the two group t-test with <i>unequal variances</i> (Satterthwaite's t-test)	✓	✓	✓
<b>Two group t-test for fold change assuming log-normal distribution (equal and unequal n's) (MTT0cv, MTT0cvU)</b> Compute power and sample for detection of specified <i>fold-change</i> when the CV is specified (especially useful for planning <i>DNA microarray</i> studies)	✓	✓	✓
<b>Two group t-test of equal fold change with fold change threshold (equal and unequal n's) (MTT0fct, MTT0fct)</b> Compute probability of detection of specified fold-change when the CV is specified and the result must exceed a specified <i>foldchange threshold</i> (especially useful for planning <i>DNA microarray</i> studies)	✓	✓	✓
<b>t-test (ANOVA) for difference of means in 2 x 2 crossover design (MTT4)</b> Compute power and sample size for the 2 x 2 crossover design		✓	✓
<b>Two group <math>\chi^2</math> test of equal proportions – Compute one of two proportions (PTT0p)</b> For the two group Chi-square, you can now solve for the proportion which is detectably different from a specified proportion.	✓	✓	✓
<b>Two group continuity corrected <math>\chi^2</math> test of equal proportions – Compute one of two proportions (PTT1p)</b> For the two group continuity corrected Chi-square, you can now solve for the proportion which is detectably different from a specified proportion.	✓	✓	✓
<b>Confidence interval for relative risk (ratio of two proportions) (PTC3, PTC3U)</b> Compute sample size or confidence interval width for the relative risk (ratio of two independent proportions).		✓	✓
<b>Two-group t-tests (TOST) of equivalence in means (equal n's) (MTE1tg formerly MTE1)</b> Compute power and sample for equivalence in means (based on mean difference) for the two-group design.	✓	✓	✓
<b>t-tests (TOST) of equivalence in means for crossover design (MTE1co)</b> Compute power and sample for equivalence in means (based on mean difference) for the 2x2 crossover design.	✓	✓	✓
<b>Two-group t-tests (TOST) for ratio of means (using log scale) (equal n's) (MTE2tg, formerly MTE2)</b> Compute power and sample for equivalence in means (based on ratio of means) for the two-group design.	✓	✓	✓
<b>t-tests (TOST) of equivalence in ratio of means for crossover design (natural log scale) MTE2co)</b> Compute power and sample for equivalence in means (based on ratio of means) for the crossover design.	✓	✓	✓

<p><b>Calculation of the total number of required events for:</b></p> <p>Log-rank test for equality of survival curves (STT0)</p> <p>Test based on exponential survival, accrual period (STT1)</p> <p>Test based on exponential survival, accrual period, dropouts (STT2)</p> <p>Non-inferiority test for two exponential survival curves (STE0)</p>	✓	✓	✓
<p><b>Non-inferiority test for two exponential survival curves (STE0)</b></p> <p>Compute power or sample size for a noninferiority test of the hazard ratio for two exponential survival curves, allowing for an accrual period, and dropouts.</p>		✓	✓
<p><b>Confidence interval for intraclass correlation for k measurements (AOC3)</b></p> <p>Compute confidence interval width or sample size for the intraclass correlation.</p>		✓	✓
<p><b>Test and Confidence interval for intraclass correlation for k measurements (AOT2, AOC2)</b></p> <p>Compute sample size for test and confidence interval for Lin's concordance coefficient. (Updated formula for V(K) in side-tables.)</p>		✓	✓