

BASE View Biomaterial LIMS Array LIMS Administrate Extensions Help

Experiments ▶ Temp\_Import\_Exp\_baselinePlate2and3

Properties **Bioassay sets** Overview

New root bioassay set... Delete Restore Columns... Export...

	Name	Tools	Spots/Values in db	Reporters in db
1	Mean signal			
2	root			
3	Illumina expression background correction			
4	Background corrected			
5	qQuantile normalization			
6	qQuantileNormalized bioassayset			
7	Illumina detection P-value calculation			
8	Detection P-value			
9	IlluminaDetectionPValue			
10	Filter: xtra('IlluminaDetectionPValue') < 0.05			
11	Filtered Detection P-value			

When running a plugin a help text is available in the initial pop-out window (see figure) . However, as soon as the user clicks 'Next' the help text is unavailable (although it can be accessed through the interface). It would be useful to have the possibility to open a separate window (directly from the Run analysis plugin dialogue, e.g., see figure) containing the help text in order to have it readily available when continuing and setting parameters.


Run analysis plugin

http://base.onk.lu.se/onk/common/plugin/index.jsp?ID=d2e9fadc2e3e024e&cmd=SelectP

Run analysis plugin

Please select the plugin and, optionally, the configuration to use.

Plugin: qQuantile normalization

 = required information

**qQuantile normalization**  
 The qQuantile normalization is inspired by the 'Cubic Spline' normalization in Illumina Beadstudio and the work by Workman et al., <http://www.pubmedcentral.nih.gov/articlerender.fcgi?tool=pubmed&pubmedid=12225587>

In qQuantile normalization, all assays (including the target) are sorted in increasing intensity. The sorted list of probe intensities are partitioned into q groups, and each of these q groups are adjusted (normalized) with the corresponding target group. After normalization the intensity distribution of each assay will be approximately the same as the target distribution. q is calculated as  $q = \max(10, \min(100, \text{target\_size}/10))$ . The program will stop if the number of well defined expression values in the target or any of the assays in the set is smaller than q.

The target is defined by selecting a subset of the assays in the bioassay set, and the target expression values are the medians of probe intensities over the bioassay set. Probes with no well defined measurements in the bioassay set are simply ignored in target calculation.

Since the normalization calculations are based on geometric means and performed in log space the intensities must be positive and larger than 0. Rather than executing the use of qQuantile normalization...

Next Cancel

Done

Button somewhere in window that opens separate dialogue with help text.