

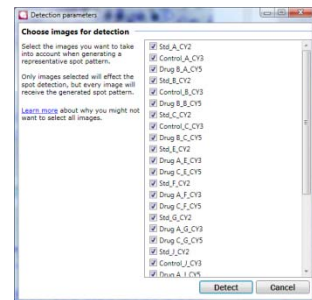
Progenesis SameSpots v4.0 – new features in the latest release

Version 4.0 of Progenesis SameSpots is now available with a wide range of new features developed in response to feedback from our rapidly expanding customer base. There is a new experiment design option and there has also been a focus on providing more features to help with the assessment and improvement of quality control within your proteomics experiments. Progenesis SameSpots v4.0 supports Microsoft Windows 7.

Feature highlights include:

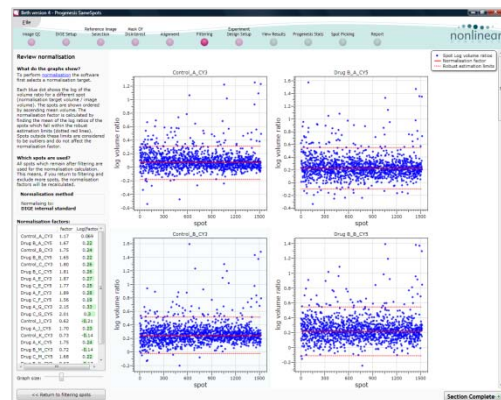
Increased control over generation of the SameSpots outline map

You can select the images that contribute to the generation of the SameSpots outline map – all of these images still have the final SameSpots outlines passed to them and are measured as part of the experiment. This puts you in control of the detection process and gives you the option to remove images from this part of the process should you wish.



Visualisation of normalisation across your images

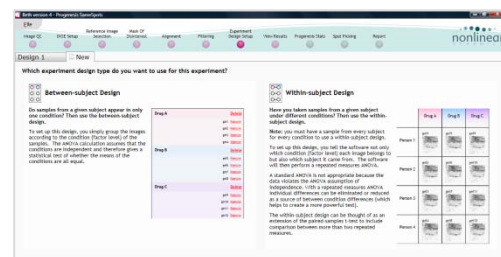
It had previously been very difficult to assess the quality of normalisation of measures in your experiment. You can now visualise the results of normalisation on a scatter plot and the normalisation factor for each image. You can then take corrective action to ensure experimental quality is maintained.



You now have the option not to use any normalisation in your experiment (non-DIGE only). For example in a dilution series experiment you would not want to use normalised volumes.

Increased flexibility in the type of experiment design you can analyse

The addition of a second experiment design option allows the comparison of different samples from the same subjects, under different conditions. The software then performs a repeated measures ANOVA – the appropriate statistical test for this type of experiment. An example of where you would use this type of experiment design is for the analysis of a time-course experiment.



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