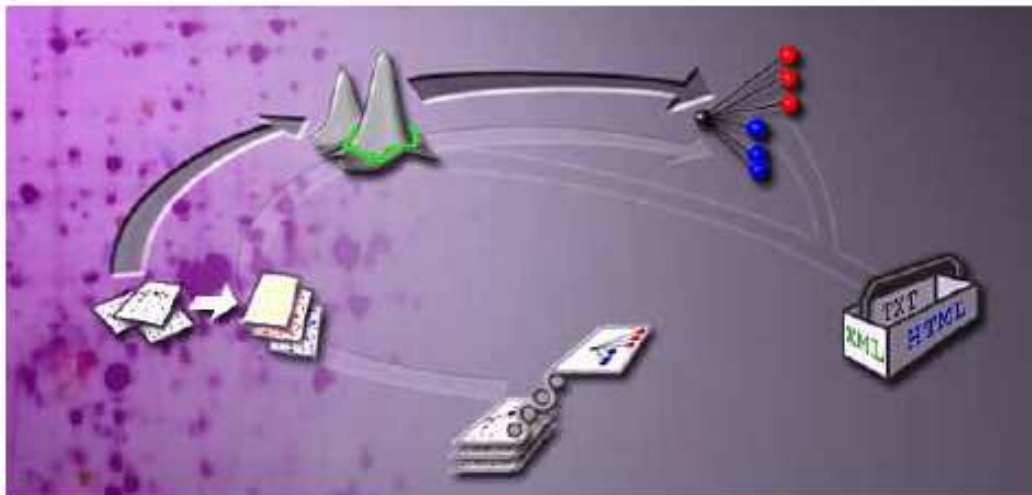


GE Healthcare

DeCyder 2D 6.5 Patch II

Software Change Description



Improvements in EDA normalization

The workspace normalization performed when an EDA workspace is created from two or more BVA workspaces using different internal standards, has now been improved.

The description below replaces p. 234 and 237: Sections A.2.1 and A.2.2 and figure A-1 in DeCyder™ Extended Data Analysis module, Version 1.0, User Manual.

An experimental group, for example a control group, common to all imported BVA workspaces can be used for normalization between the different BVA workspaces.

For each BVA workspace the mean of the log standard abundance values for each protein in the common group is calculated. The differences between the means in the reference workspace and the workspace(s) to normalize are determined per protein. These differences are then used to adjust all log standard abundance values for that protein in the BVA workspace(s) to normalize.

If a protein is missing in the common group in the reference workspace that protein is removed after normalization. The number of proteins available for further analysis can thus decrease after normalization.

It is recommended to use a common internal standard for all BVA workspaces whenever possible in order to minimize experimental variation.

Selection of spot detection algorithm in DIA

- It is now possible to perform spot detection with either the DeCyder 5 or the DeCyder 6 detection algorithm. See appendix for more information.

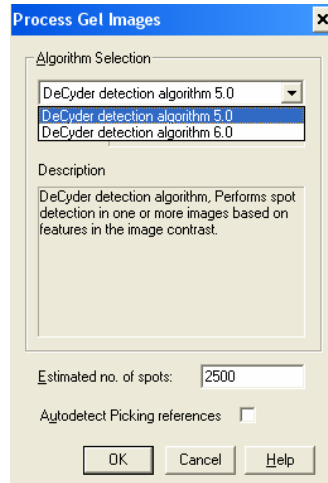
Corrections and improvements

- It is now possible to use a master spot map saved as template in one BVA as a master in a new BVA and link the two BVA workspaces in EDA.
- Import of EDA workspaces with new (added) conditions without values now works properly.
- In EDA partition clustering, the log standard abundance values of the curves are now based on the selected set rather than the entire set.
- In Image Loader the spot maps are now sorted in the order Cy™2, Cy3, Cy5 in the database to avoid rounding errors in the calculation of abundance values.
- Rank calculation in EDA Marker Selection has been improved.
- In BVA, the standard abundance values are now updated when moving a spot map from the standard group.
- In EDA, errors in the calculation of mean standard abundance values in partition cluster analysis and differential expression analysis graphs have been corrected.
- In very rare cases, after deletion of a database item, an exchange of images within a gel in a BVA workspace would occur. This issue has now been addressed.

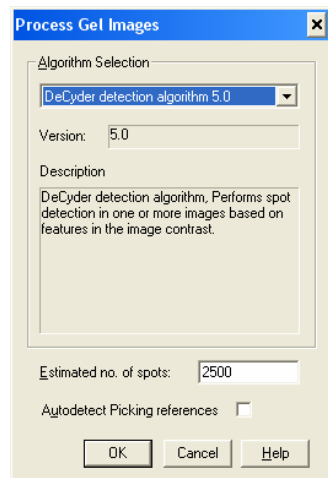
Appendix. Selection of Spot detection algorithm

In this version of DeCyder it is possible to also use the spot detection algorithm from DeCyder version 5 for detection of the spots in DIA and Batch Processor.

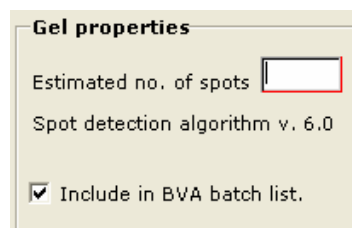
In DIA the selection of spot detection algorithm is done in the Process Gel Images dialogue.



Information on the detection algorithm used in a saved workspace is also displayed in this window.



In the Batch Processor the spot detection algorithm that will be used for the present batch is displayed in Gel Properties.

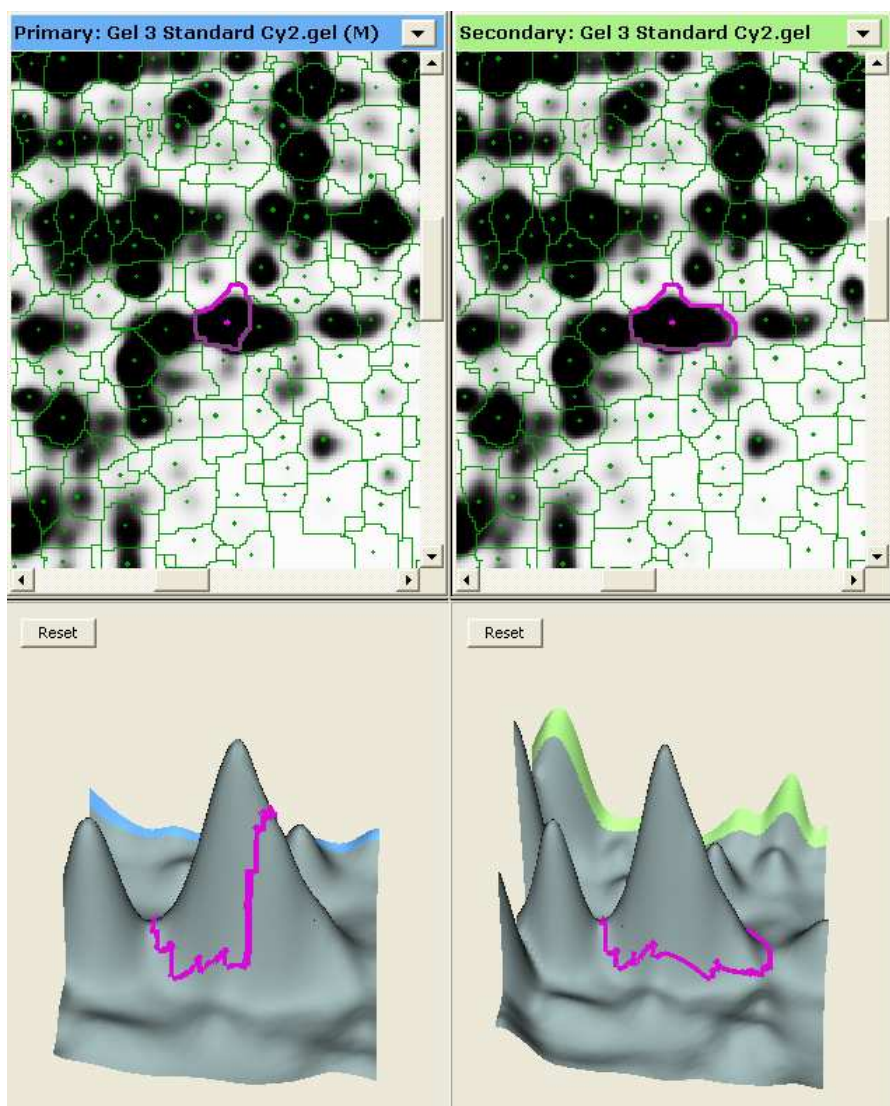


Change of spot detection algorithm in the Batch Processor must be done in DIA. The algorithm that was last used in a saved DIA workspace will be the one displayed in the Batch Processor. In order to change algorithm in the Batch Processor a DIA that has been processed with the desired algorithm can be opened, reprocessed with the same algorithm and saved. This setting is Windows® user specific.

The spot detection algorithms differ in splitting of the spots giving less spot splitting using the 6.0 algorithm.

Due to an improved loading of the images minor differences between the detection in DeCyder 5.0 and in DeCyder 6.0 with spot detection algorithm 5.0 can be obtained at the right edges of the images.

Example of results obtained with the different spot detection algorithms (spot detection algorithm 5.0 to the left and 6.0 to the right.)



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