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## **Feature Extraction 12.2.0 Supplemental Release Note: Enhanced Spot Finding**

### **Feature Extraction 12.2.0 spot finding enhancements:**

Feature Extraction (FE) 12.2.0 software now includes an enhanced spot finding algorithm for use with CGH arrays and protocols.

The enhanced spot finding algorithm provides an additional data processing path to optimize the expected window from which to look for pixels associated with each spot (feature) and remove any pixels within the increased window size attributable to neighboring spots. Depending upon the nature of the array data, this additional processing path will automatically verify if it can more accurately determine the centroid location and provide the same or better results with a reduced number of “no-uniform” features.

Enhanced Spot Finding is an “opt-in” feature selection and is enabled by creating a custom CGH protocol (CGH\_1201\_Sep17) and selecting “true” for Enhanced Spot Finding. The Enhanced Spot Finding algorithm is only available when the Enhanced Gridding algorithm is also selected.

Note: Enhanced Spot Finding is not currently available in CytoGenomics software.

### **Algorithm performance:**

These enhancements are designed to improve the software’s ability to determine the centroid of the feature and improve the accuracy of the pixels integrated into the feature result. The results obtained with protocols that use enhanced spot finding may vary slightly from results obtained without spot finding (e.g., fewer non-uniform features). Array formats that may benefit from Enhanced Spot Finding include: 1x1m and 2x400k arrays per slide, although it may be used with any Agilent array format. Note that array processing time may increase when using the Enhanced Spot Finding algorithm.

As with any new version of software, Agilent recommends the user complete the appropriate validation processes when switching to CGH protocols that use enhanced spot finding.

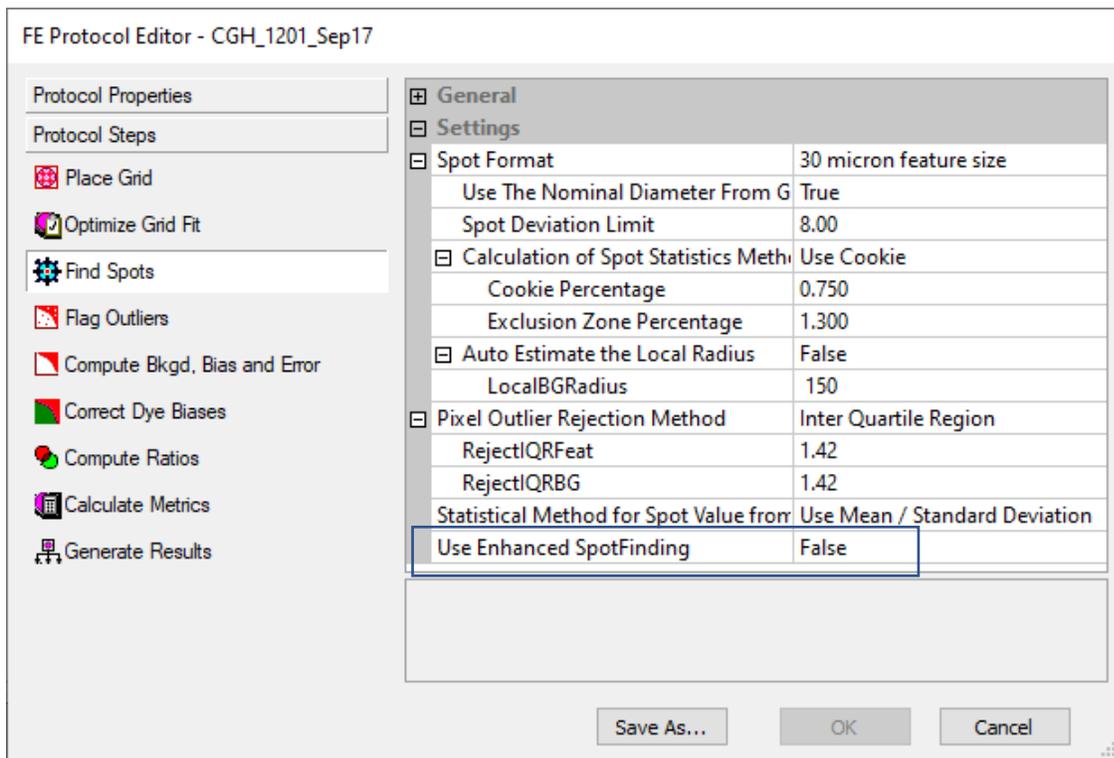
### **Validating enhance spot finding algorithm performance:**

When validating any software or protocol change, follow the processes established at your laboratory. If you are upgrading from a previous version of Feature Extraction to version 12.2, Agilent recommends performing validation of any new functionality before incorporating the change into your standard workflow. As part of your validation, it may be necessary to compare results from arrays processed using both the current and the enhance spot finding algorithms. To facilitate this process Feature Extraction allows you to easily automate the processing of arrays using multiple protocols. As you define your validation plan, you may consider the following to complement your local validation processes. Keep in mind that you know your assay the best.

- Compare FE QC Chart results for arrays processed using *false* and *true* Enhanced Spot Finding settings.
- Compare Evaluation Metrics (Excellent, Good and Evaluate).
- Compare Feature Outliers and Population.
- Compare processed (CNV) calls using false and true Enhanced Spot Finding.
- Consider S/N values as you evaluate any changes between algorithms.

### Editing protocols:

In the default CGH protocols provided by Agilent, the enhanced spot finding algorithm is set to “false”. To change the flag to “true”, save the default CGH protocol with a new name and then edit the protocol using the Protocol Editor. Set the “Use Enhanced Spot Finding” flag in the Protocol Editor to “true”. Managing your protocols in FE is easy and you can revert to the previous gridding algorithm at any time by using the Protocol Editor to change the Enhanced Spot Finding flag to “false” or by using a previous Agilent-provided CHG protocol.



### Importing and exporting protocols

Note: For information regarding exporting and importing protocols, consult the Feature Extraction 12.2 User Guide (G4460-90058). It is important to remember that you must export any protocols that you would like to import into the new version of FE **before** uninstalling the previous version of software. Exported protocols may be manually imported into the new version of the software, or you may use the “Migration Tool” to migrate the protocols from the previous version to the new version. All imported protocols will have the enhanced spot finding flag set to “False” by default.

If you have any questions about the new gridding algorithm or concerns on how best to proceed, please contact Agilent: [genomics@agilent.com](mailto:genomics@agilent.com)