

## **Feature Extraction 12.1 and CytoGenomics 5.0 Supplemental Release Note: Enhanced Gridding**

### **Feature Extraction 12.1 gridding enhancements:**

Feature Extraction (FE) 12.1 and CytoGenomics 5.0 software now includes an enhanced FE gridding algorithm for use with CGH arrays.

The enhanced gridding algorithm uses a new iterative method for determining array grid position, which helps to eliminate the occasional problems seen during auto-gridding of arrays. The updated algorithm reduces the number of CGH arrays failing auto-gridding, minimizing the need to manually grid those failed arrays.

The enhanced gridding algorithm is selected by default in the updated default CGH protocol in FE 12.1 and all default protocols in CytoGenomics 5.0. Those protocol names are listed below.

#### FE 12.1

CGH\_1201\_Sep17

#### CytoGenomics 5.0

CytoCGH\_0500\_1x\_Nov17

CytoCGH\_0500\_2x\_Nov17

CytoCGH\_0500\_4x\_Nov17

CytoCGH\_0500\_8x\_Nov17

CytoCGH\_0500\_SingleCell\_Nov17

### **Algorithm performance:**

While these enhancements improve the software's auto-gridding capabilities, they may result in small changes to the unprocessed raw results. Due to the small changes in grid placement, FE feature level data obtained with the new algorithm may vary slightly from that obtained with the previous algorithm. Consequently, in addition to fewer auto-gridding failures, small changes in FE QC metrics should be expected.

For arrays with low signal levels, there may be slight changes in results from CytoGenomics software. Marginal aberration calls may differ between the old and enhanced gridding algorithms.

Because of these potential changes, Agilent recommends that you revalidate any existing assay where there is a concern about continuity of results before you start using the enhanced gridding algorithm

### **Should I use the enhanced gridding algorithm?**

- Agilent recommends that customers without any historical CGH data use the new Enhanced Gridding CGH default protocols provided with FE 12.1 and CytoGenomics 5.0.
- Customers who have historical data, and have experienced failed auto-gridding on CGH arrays in the past, may choose to evaluate the new protocols by comparing their CytoGenomics results between the previous and enhanced gridding algorithms.
- Customers who have historical data and have not experienced auto-gridding failures may choose to continue using the previous gridding algorithm in the new FE 12.1 or CytoGenomics 5.0 software.

### **Verifying enhanced gridding algorithm:**

Note: When validating any software or protocol change, follow the processes established at your lab.

If you are upgrading from a previous version of the software to the latest version, Agilent recommends performing validation of the new gridding algorithm before switching to the new CGH protocols, just as you would whenever you begin working with a new software application.

As part of your validation, it may be necessary to compare results from arrays processed using both gridding algorithms. To facilitate this process Feature Extraction and CytoGenomics 5.0 allow you to easily automate the processing of arrays using multiple protocols.

As you define your verification 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 Gridding settings.
  - Compare Evaluation Metrics (Excellent, Good and Evaluate).
  - Compare Feature Outliers and Population.
- Compare processed (CNV) calls using false and true Enhanced Gridding setting.
  - Consider S/N values as you evaluate any changes between algorithms.

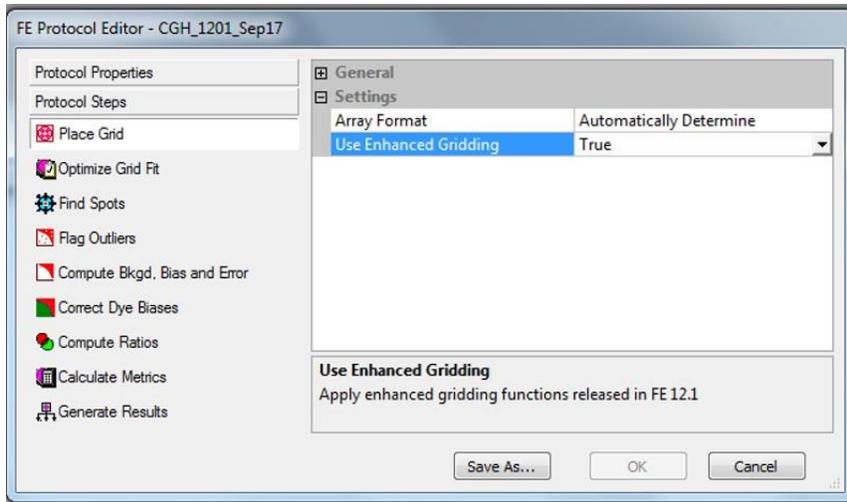
### **Editing protocols:**

In the default CGH protocols provided by Agilent, the enhanced gridding algorithm is set to “true”. Managing your protocols in FE and FE for CytoGenomics is easy and you can revert to the previous gridding algorithm at any time by using the Protocol Editor to change the Enhanced Gridding flag to “false” or by using a previous Agilent-provided CHG protocol.

Edit the enhance gridding flag to “False” - Save the default CGH protocol with a new name and then edit the protocol using the Protocol Editor. Set the “Use Enhanced Gridding” flag in the Protocol Editor to “False”.

Edit the enhance gridding flag to “True” for any imported protocol - By default, any imported protocol will be set to “False” for enhanced gridding. To change to “True”, edit the protocol using the Protocol Editor and set the “Use Enhanced Gridding” flag in the Protocol Editor to “True”.

For Research Use Only. Not for use in diagnostic procedures.



### Importing and exporting protocols

Note: For information regarding exporting and importing protocols, consult the Feature Extraction 12.1 User Guide (G4460-90058) or Feature Extraction for CytoGenomics 5.0 User Guide (G1662-90060).

It is important to remember that you must export any protocols that you would like to import into the new version of FE or FE for CytoGenomics **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 gridding 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)