IDEAS®

Image Data Exploration and Analysis Software
User's Manual

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Technical Assistance

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CHAPTER 1

Preface

Welcome to the IDEAS version 4 application documentation. IDEAS 4.0 or later versions are required to open ImageStream^X data. Many new improvements have been added to the application.

HOW TO USE THIS MANUAL

This manual provides instruction for using the Amnis IDEAS® application to analyze data files from the Amnis ImageStream cell analysis system.

The intuitive user interface of the IDEAS application makes it easy for you to explore and analyze data. The application contains powerful algorithms that allow you to create an unlimited number of tailored features for a specific experiment. The application can quantify cellular activity by performing statistical analyses on thousands of events and, at the same time, permit visual confirmation of any individual event. Furthermore, you can operate the application in a batch processing mode and store specific analysis templates for either repeated use or sharing with colleagues.

The fastest way to put the IDEAS application to work is to first skim through this manual—becoming familiar with the application's structure, compensation, file types, and analysis tools—and then use the application wizards on some sample experimental data to begin exploring the power that the application provides. This manual has been integrated into the IDEAS application to provide searchable and context sensitive help. Typing F1 while in the application opens the help files.

What's New in IDEAS 4.0

IDEAS 4.0 is required to analyze data from the ImageStreamX and offers numerous improvements for analyzing data from any ImageStream instrument. Please refer to the our web site for the latest improvements and updates to this manual.

1 ImageStreamX
   - Data files collected on the ImageStreamX have new requirements that are built in to IDEAS 4.0 software.

2 General
   - Multiple files can be opened in a single instance of IDEAS.
   - Multiple window layouts can be displayed with resizable panels.
   - Open large data files that would not previously load due to memory constraints.
   - Drag and drop data files into an open instance of IDEAS.
   - Open data files containing up to 12 channels of imagery.
   - .daf files can be used as a template for loading data files.

3 Guided Analysis
   - New application wizards:
      — Open File
      — Display Properties
      — Apoptosis
      — Cell Cycle - Mitosis
      — Co-localization
      — Internalization
      — Nuclear localization
      — Shape change
   - New building blocks to generate graphs with recommended feature choices and default scaling:
      — Single cells
      — Focus
      — Fluorescence positives

4 Statistics and Reporting
   - View and export statistics for multiple populations or feature values for multiple objects in the statistics area.
   - New mean and median RD statistics available in the statistics area.
   - View and export graphs in the analysis area with a white (light mode) or dark (dark mode) background.

5 Image Display
   - Display settings accommodate 10 and 12 bit imagery as well as higher pixel intensities that result from EDF deconvolution.

- Multiple objects in an image are now separated into individual objects.
- Objects in the image gallery are vertically and horizontally centered.
- Object numbers appear in the upper left corner of an image and may be turned off for reporting.
- Zoom option to enlarge images in the image gallery and in the analysis area.
- Unlimited columns in Viewing modes in the image gallery.
- Any mask can be assigned to a column of a viewing mode, regardless of the image in that column.

6 Compensation

- Select any .cif, .daf, or .ctm file to obtain a compensation matrix.
- New compensation menu for viewing and editing compensation matrices and preview process for testing a matrix.
- Improved algorithm for selection of positive populations that eliminates saturated events and outliers.

7 Feature and Mask Improvements

Features

- Improved the Object per second and Objects/ml calculations.
- New Spot Intensity Max feature.
- New features:
  - Ensquared energy
  - Raw Centroid X
  - Raw Centroid Y
  - Shift X
  - Shift Y
  - XCorr

Masks

- The Spot mask's spot to cell background ratio has improved.
- Inspire mask is new.

CHAPTER 2

Setting Up the IDEAS® Application

This chapter describes the hardware and software requirements for the application, which includes the procedures for installing, removing, and upgrading the application. The following subsections cover this information:

Hardware and Software Requirements

This section states the minimum and the recommended hardware and software requirements for running the IDEAS application.

Hardware Requirements

The minimum hardware requirements are 512 MB of RAM and a 1-GHz processor. However, due to the large size of the image files that the ImageStream cell analysis system creates, a larger amount of RAM will prevent paging and thus increase performance.

Software Requirements

You must have Windows XP, Windows 2000, or a later version of the operating system installed on your computer. The latest service pack and any critical updates for the operating system must be included. You must also install the Microsoft .NET Framework 2.0, which requires Microsoft Internet Explorer 5.01 or later.

Important: If the software requirements are not met, Setup will not block installation nor provide any warnings. IDEAS is a 32 bit application and we strongly recommend running IDEAS on a computer with a 32 bit operating system. A 64 bit version of IDEAS is not available at this time.

Note that service packs and critical updates are available from the Microsoft Security Web Site.

Installing the IDEAS® Application

If the IDEAS application has previously been installed, the previous version will be removed during installation.

To install IDEAS software

1. Insert the CD or DVD that is labeled IDEAS application. Or download the application Setup file from your account at www.amnis.com.
2. View the contents in My Computer or Windows Explorer.
3. Double-click `Setup.exe`.
4. Follow the instructions until the installation process has completed.
5. An icon appears on the desktop and IDEAS Application appears on the All Programs menu.

Setting Your Computer to Run the IDEAS® Application

"Setting the Screen Resolution" on page 6

"Viewing File Name Extensions" on page 6

"Copying the Example Data Files" on page 7

Setting the Screen Resolution

Confirm that the screen resolution is adequate for the IDEAS application. To be able to view the entire application window, you must set the width of the screen resolution to a minimum of 1024 pixels.

To set the screen resolution

1. From the Start menu, select **Control Panel**, and then click **Display**.
2. Click the **Settings** tab to set the screen resolution.

Viewing File Name Extensions

When loading a file, the IDEAS application uses the file name extension to determine the file type. It will be easier for you to distinguish raw image files, compensated image files, and data analysis files from each other if Windows Explorer does not hide the extensions.

To view file name extensions

1. In Windows Explorer, go to **Tools** > **Folder Options**.
2. Click the **View** tab, and make sure that the Hide extensions for known file types check box is not selected.
3. Click **OK**.

Copying the Example Data Files

If the CD or DVD includes data files, copy them to a single directory on your hard drive. Sample data files are also available at www.amnis.com/login for customers with an Amnis account.

Note that the default data directory is installation directory\ImageStreamData, where installation directory is the directory that you installed the IDEAS application in. For example, the default data directory might be `C:\Program Files\AmnisCorporation\IDEAS\ImageStreamData`.

To copy the example data files

1 Copy the data files.

2 Right-click the directory that contains the data files, and click **Properties**.

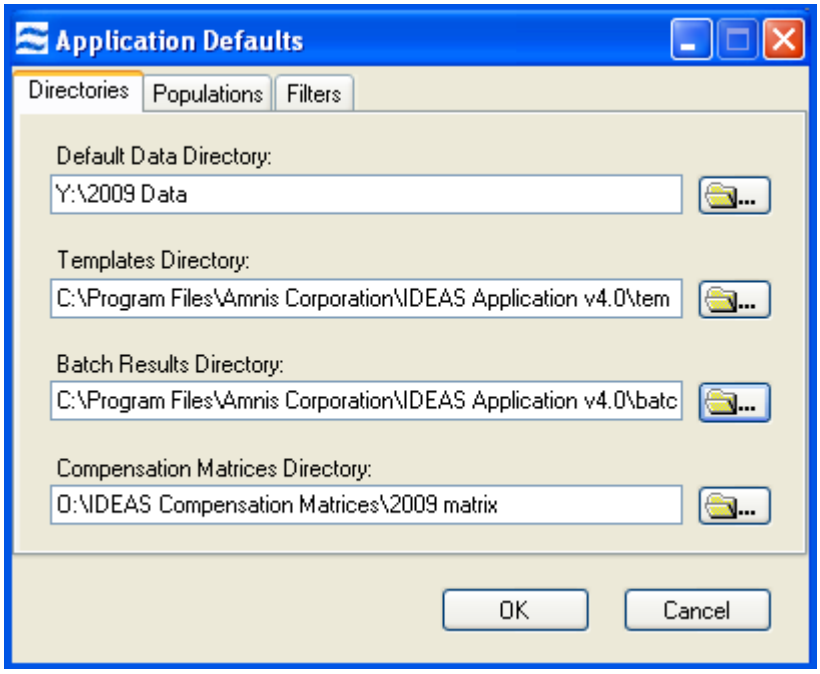
3 Clear the **Read-only** check box.

4 Click **OK**.

Viewing and Changing the Application Defaults

Files are automatically saved to the specified default directory.

- To view or change these defaults, click **Application Defaults** on the **Options** menu, and the **Directories** tab will be displayed, as shown in the following figure.
- To view or change the default color or symbol for populations, click the **Populations** tab.



CHAPTER 3

Overview of the IDEAS® Application

This chapter provides an overview of the IDEAS application user interface, the files that the IDEAS application creates and uses, the recommended directory organization and an overview of the workflow.

"Understanding the Data Analysis Workflow" on page 10

"Overview of compensation, analysis tools and file structure" on page 12

The ImageStream cell analysis system possesses unique capabilities that neither flow cytometry nor microscopy alone can deliver. Examples include the analysis of molecule co-localization and translocation, the analysis of cell-to-cell contact regions and signaling interactions, the detection of rare molecules and cells, and a comprehensive classification of large numbers of cells. The IDEAS application acquires data from INSPIRE™, compensates the images, and allows the user to evaluate the images with data analysis tools.

Understanding the Data Analysis Workflow

Data analysis in IDEAS begins with opening a raw image file (.rif) that was collected and saved using INSPIRE on the ImageStream. Then, an existing compensation matrix or a new compensation matrix is applied to the .rif file and two additional files are created, the .cif (compensated image file) and .daf (data analysis file).

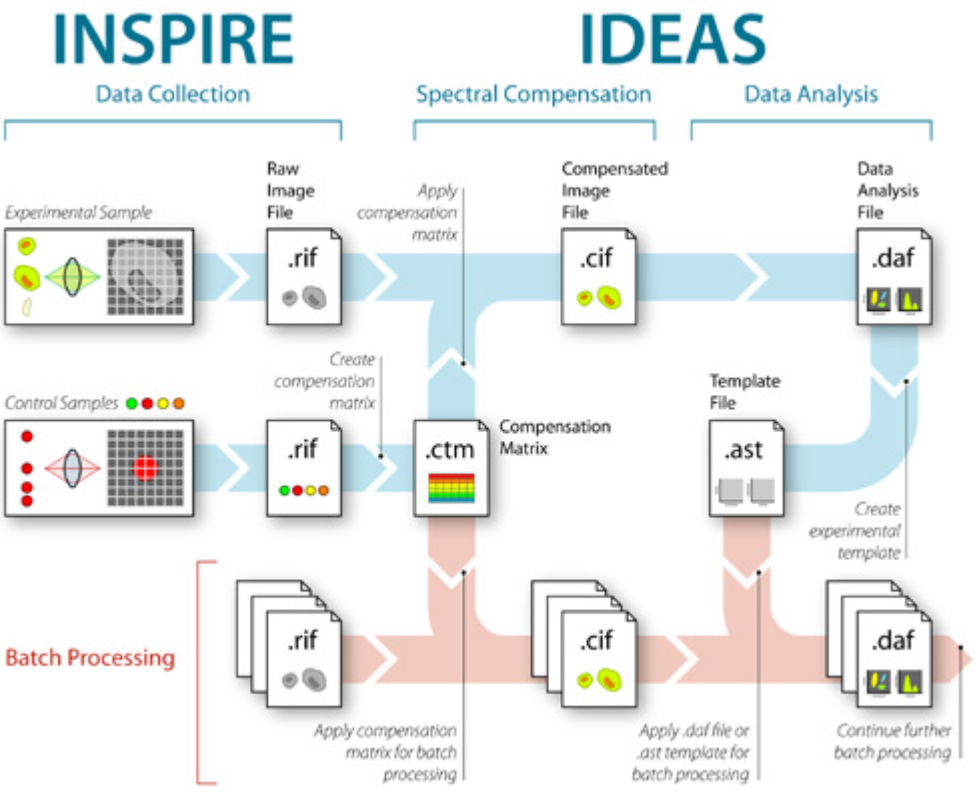
A compensation matrix performs fluorescence compensation, which removes fluorescence that leaks into other channels. See "Overview of Compensation" on page 38 for more information about compensation. A compensated image can accurately depict the correct amount of fluorescence in each cell image. Compensation is defined as the correction of the fluorescence crosstalk. When creating the .cif the IDEAS application also automatically performs corrections to the raw imagery using values saved from the instrument at the time of data collection. These corrections include flowspeed normalization, brightfield gains, and spatial registry.

A template is used to define the features, graphs, image display properties and analysis for the .daf. The default template includes over 200 calculated features per object. An expanded template is available that includes over 600 calculated features per object. Within the .daf file, the user can perform many analyses using the tools and wizards within the application and save the results as a template file (.ast).

The IDEAS application then calculates feature values and shows the data as specified by the selected template.

Once a data analysis file (.daf file) or compensated image file (.cif file) is saved, it can be opened directly for direct data analysis. You would only open a .cif if you wanted to change the template or a .rif file to change the compensation.

The diagram on the next page displays this workflow.



Overview of Data Analysis Workflow

1 Create a compensation matrix using the single color control files. Open an experimental .rif file or from the Compensation menu choose Create New Matrix.

2 A .cif and .daf file are automatically created. Analyze the experimental file using data analysis tools in the .daf file to create an analysis template.

3 Create a statistics report template within the .daf file and save the data file, and an anlaysis template.

Note: this is usually done on the positive and negative controls to create the appropriate analysis and then applied to the rest of the experimental files in the next step.

4 Perform batch processing, applying compensation and template files created above.

Overview of compensation, analysis tools and file structure

Data Acquisition and Compensation

Data are first acquired from the ImageStream using the Amnis INSPIRE™ instrument-control application. Next, the IDEAS application processes and analyzes the image data. The IDEAS application contains the algorithms and tools that are needed to analyze the imagery. Preprocessing algorithms and tools correct for instrument biases, including flowspeed variations, spatial alignments, illumination irregularities, and camera background. Compensation for spectral crosstalk is calculated from control files and applied to experimental files.

After the preprocessing completes, the IDEAS application allows for the interrogation of the image data, segmenting out cells, nuclei, cytoplasm, FISH spots, beads, and other objects of interest. Using a default template, the application calculates the values for over 200 standard features per object, to be used in subsequent analyses. Guided analysis for many common applications is available through the use of wizards. Finally, the application displays imagery and feature-calculation results, and it defines cell populations in a host of plots and histograms.

Data Analysis Tools

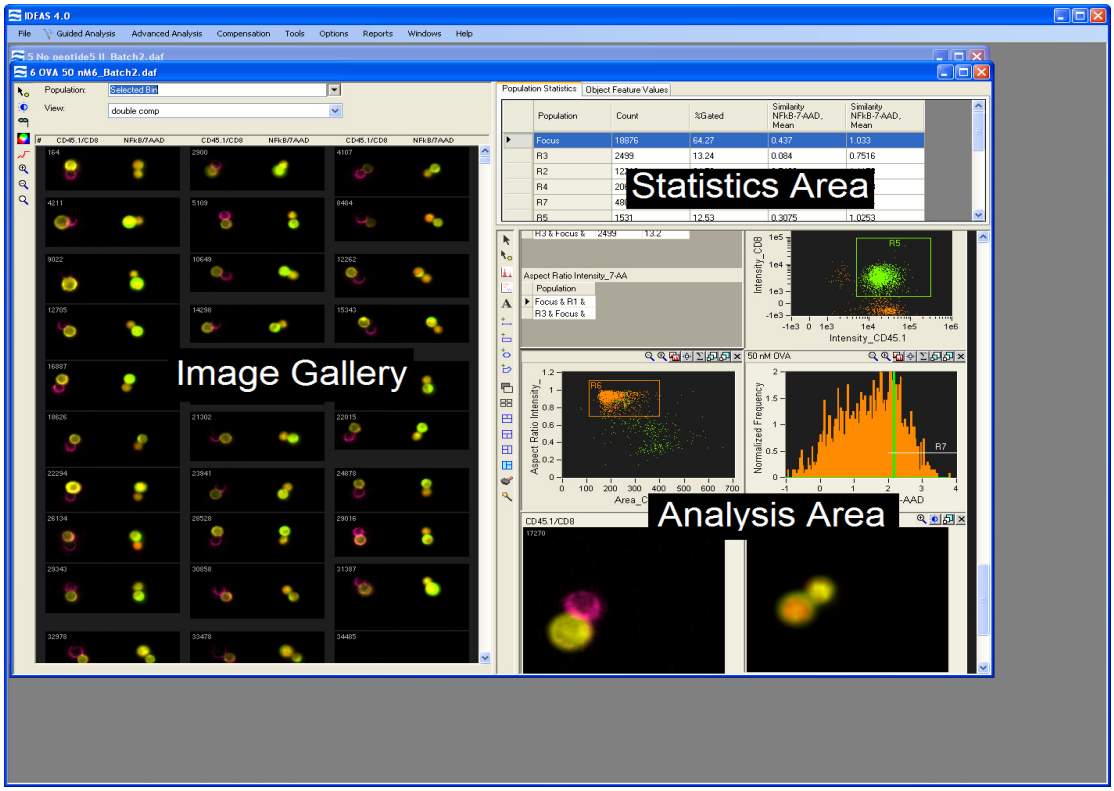
Data in the IDEAS application can be further explored by using the data analysis tools. For example, populations of cells can be identified by drawing regions on histograms or scatter plots, or by tagging individual objects. The IDEAS application provides standard distribution statistics for all defined populations. In addition, users can further define images by creating features—a mathematical expression that contains quantitative and positional information about the image.

The application also contains tools that allow you to view grayscale and pseudocolor images, to apply gains and thresholds, and to build composite images. For individual images, tools are available to examine pixel intensities, create line profiles of pixel intensities, and compute the distribution statistics of the pixels in a region of an image. Both morphological measurements and intensity information are available for calculating feature values and for building classifiers. Histograms and scatter plots display feature data graphically and the population distribution statistics include a

variety of calculations such as the mean, standard deviation, and coefficient of variation (CV).

Interface of the IDEAS Application

The IDEAS Application allows the opening of multiple data files within one instance of the program. Each file is divided into three sections: the Image Gallery, the Statistics Area, and the Analysis Area. The placement and size of these areas are adjustable.



- The **Image Gallery** displays the images of populations of cells, segmentation masks and composite images . For more information, refer to "Overview of the Image Gallery" on page 59.
- The **Statistics Area** displays feature values for objects and populations in tabular form. For more information, refer to "Overview of the Statistics Area" on page 87.
- The **Analysis Area** displays plots and distributions of cellular feature values. Individual images and text panels. For more information, refer to "Overview of the Analysis Area" on page 71.

Overview of the Data File Types

Data from the ImageStream cell analysis system are collected and managed using three types of data files: raw image file (.rif), compensated image file (.cif), and data analysis file (.daf).

This section describes each file type and the table summarizes the features of each file.

Raw Image File (.rif)

The INSPIRE application saves the image data that were acquired by the ImageStream cell analysis system to a .rif file. A .rif file contains:

- Pixel intensity data (counts and location) that the camera collected for each object that the instrument detected
- Instrument settings that were used for data collection

Compensated Image File (.cif)

The IDEAS application creates a .cif file when the user opens a .rif file and applies a compensation matrix. The segmentation algorithm automatically defines the boundaries of each object, creating a mask that is used for calculating feature values. The applied compensation matrix performs pixel-by-pixel fluorescence compensation prior to segmentation.

During the creation of the .cif file, the application makes corrections to the imagery. These corrections include:

- Removal of artifacts from variability in the flow speed, camera background, and brightfield gains.
- Alignment of the objects to subpixel accuracy, which allows the viewing of multi, composite imagery and the calculation of multi feature values, such as the Similarity value.
- Coincident objects are cut apart to place into individual image frames. Note that this will increase the number of objects in the file.

Multiple .cif files can be created from a single .rif file by applying a different fluorescence compensation matrix or correction each time a .rif file is opened and choosing a unique name for the .cif file. Similarly, you can create a new .daf file from a single .cif file by creating a new name and applying a different analysis template.

Data Analysis File (.daf)

The IDEAS application creates a .daf file while it is loading a .cif file into a template file (.ast). The .daf file is the interface to visualize and analyze the imagery that the .cif file contains. The .daf file contains:

- Feature definitions
- Population definitions
- Calculated feature values
- Image display settings
- Definitions for graphs and statistics

Loading a .daf file restores the application to the same state it was in when the file was saved, i.e., with the same views, graphs, and populations. In IDEAS versions 3.0 or later, a .daf file may be used as a template.

Note: When a .daf file is opened, the .cif file must be located in the same directory as the .daf file since the .daf file points to images used for analysis that are stored in the associated .cif file.

Template (.ast)

The IDEAS application saves the set of instructions for an analysis session in a .daf file to a template (.ast file). Note that a template contains no data; it simply contains the structure for the analysis. This structure includes definitions for:

- Features
- Graphs
- Regions
- Populations

The .ast also contains settings for:

- Image viewing
- Image names
- Statistics

The `\templates` subdirectory (under the directory where the IDEAS application was installed) contains the default template, named defaulttemplate.ast. Because a template is required for loading a .cif file, you must use the default template to create the first .daf file. After you save a custom template, you can use it for any subsequent loads of .cif files.

Note: The default template may change between releases of the IDEAS application software. In IDEAS versions 3.0 or later, a .daf file may be used as a template. The default template contains over 200 calculated features per object. An expanded template is also available that includes over 600 calculated features per object.

Compensation Matrix File (.ctm)

The IDEAS application saves the compensation values that are created and saved during the spectral compensation of control files to a compensation matrix file (.ctm file). This file has no associated object data; it is created and saved to be applied to experimental files.

Review of Data File Types

Table 1: Review of Data File Types

File Acronym and Name	File Creation	Description
.rif Raw Image File	Created in INSPIRE	Contains instrument setup data, pixel intensity data, and uncorrected image data from the INSPIRE application. The IDEAS application uses the .rif file to create a compensated image file (.cif file).
.cif Compensated Image File	User creates a .cif from the .rif and .ctm	Contains imagery that has been corrected for variations in the camera background, camera gains, flow speed, and vertical and horizontal positioning between channels. Serves as a database of images used for feature-value calculations and imagery display. The IDEAS application also performs fluorescence compensation, if necessary, when creating a .cif file. The IDEAS application loads the .cif file into a template to create a data analysis file (.daf file)
.daf Data Analysis File	References the .cif	The main working data file that contains the calculated feature values, the graphs, and the statistics used for analysis. The .daf file references the .cif.
.ast Template File	Created from the .daf	This file contains no data; it contains the structure for the analysis, such as, definitions for features, graphs, regions, and populations; image viewing settings; image names; and statistics settings.
.ctm Compensation Matrix File	User creates new .ctm when opening a .rif	Contains compensation values that are created and saved during the spectral compensation of control .rif files. This file has no associated object data; it is created and saved to be applied to experimental .rif files.

Note about Case Sensitivity: Even though Windows does not treat file names as case sensitive, the IDEAS application depends on the case-sensitive .rif, .cif, and .daf file name extensions to identify the file types. Avoid the use of illegal characters for file names such as: "\/:*?<>!".

CHAPTER 4

Getting Started with the IDEAS Application

Guided analysis makes it easy to start analyzing your data. Once you are familiar with the basic analysis available you may want to perform more advanced analysis.

This chapter is divided into two sections. First, guided analysis is described using the analysis wizards and second, advanced analysis with more detailed instructions that describe how to open, compensate, merge, save, and create data files without using the wizards. Building blocks are also discussed which provide a short cut method to building commonly used graphs.

Guided Analysis

Guided analysis consists of Application Wizards that help you to analyze your data for specific applications and "Building Blocks:" on page 27 to define specific parameters for common graphs.

Application Wizards

Application wizards are available to guide you through an analysis. The wizard window is organized so that the instructions for each step are written at the top of the window, the progress through the wizard is shown in the list on the right side and there may be tips provided at the bottom of the window. Follow the instructions in the wizard to complete an analysis.

The following wizards are available:

General:

- "Open File:" on page 19
  - — Guides you through the process of opening a data file
- "Display Properties:" on page 20 (available only after a file is open)
  - — Automatically optimizes the display of the pixel intensities

Application specific:

- "Apoptosis:" on page 21
  - — Guides you through the process of creating the features and graphs for analyzing apoptosis.
- "Cell Cycle - Mitosis" on page 22
  - — Guides you through the process of creating the features and graphs for analyzing the cell cycle and enumerating mitotic events.
- "Co-localization" on page 23
  - — Guides you through the process of creating the features and graphs for analyzing the co-localization of 2 probes.
- "Internalization" on page 24
  - — Guides you through the process of creating the features and graphs for analyzing the internalization of a probe.
- "Nuclear Localization" on page 25
  - — Guides you through the process of creating the features and graphs for analyzing the nuclear localization of a probe.
- "Shape Change" on page 26
  - — Guides you through the process of creating the features and graphs for analyzing the circular shape of a cell using a surface stain or brightfield image.

Open File:

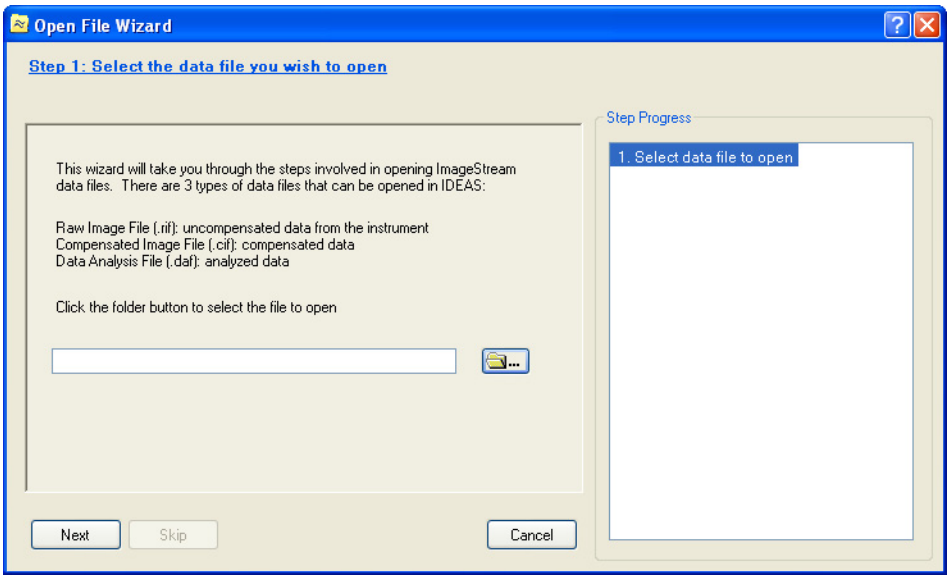
This wizard will guide you through the opening of a data file. Use this wizard to open a file if you are not using one of the application specific wizards. The application specific wizards incorporate opening a file.

To begin, double-click on Open File

Follow the instructions to open your file.

Tip: You can limit the view to specific file types (.daf, .cif or .rif) by using the drop-down menu 'Files of type:' in the Select Data File window.

A .daf file will open directly without further input, a .cif file will require a template and a .rif file will require a template and a compensation matrix. If the template or compensation matrix boxes are left blank, the default template and/or matrix will be applied. For more information on opening data files see "The File Menu" on page 29 .



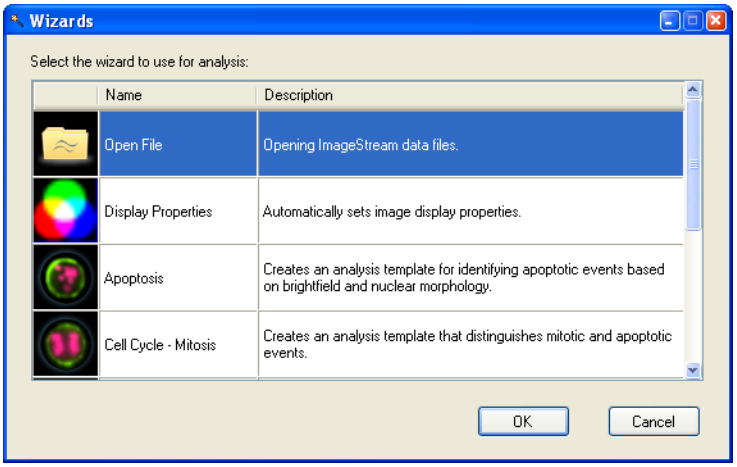
Once a data file is open you may begin analysis.

Display Properties:

Once you have an open data file, this wizard is available from the Guided Analysis menu or from the wizard icon. This wizard will set the image display mapping for the channel images you select. Brightfield and scatter images will be automatically adjusted. This wizard is also incorporated into the first steps of the application specific wizards.

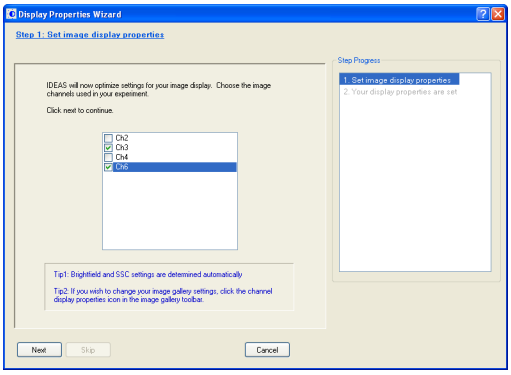
To begin, select Wizards from the Guided Analysis menu or click the wizard icon to the left of the analysis area.

The Wizards window opens.



Double-click on the Display Properties option and follow the instructions.

The Display Properties adjusts the mapping of the pixel intensities to the display range for optimizing the display. This is for display only and does not effect the pixel values. For more information on image display see "Setting the Image Gallery Properties" on page 62.



Apoptosis:

The apoptosis wizard will guide you through the process of creating the features and graphs to measure apoptosis using the images of the nuclear dye and brightfield.

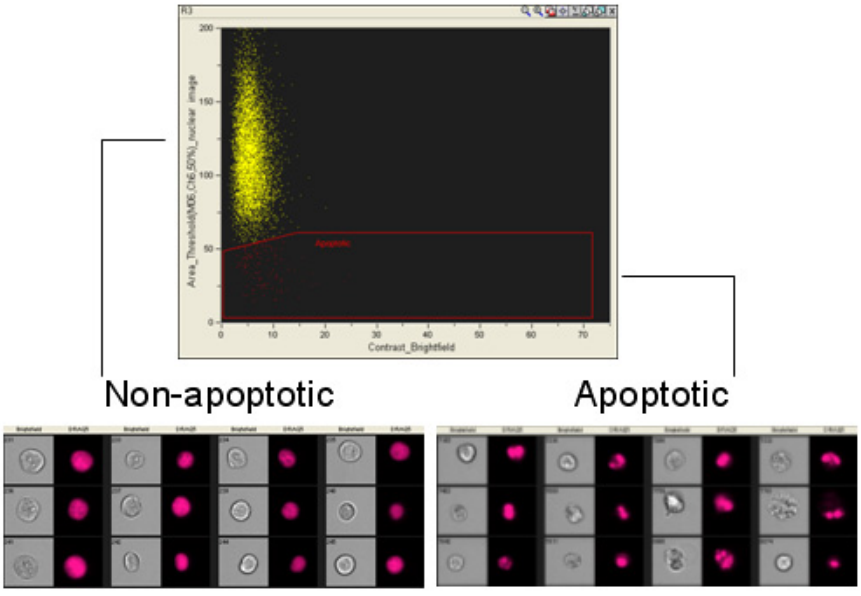
To begin, double-click on Apoptosis

Follow the instructions to open and analyze your file.

The analysis includes:

- Opening the data file
- Setting the display properties
- Gating on single cells
- Gating on focused cells
- Gating on fluorescent positive cells
- Creating and graphing the features that measure apoptosis
- Creating a statistics report

Apoptotic cells are identified in the final graph presented by the wizard. An example is shown below. Apoptotic cells have low nuclear area and high brightfield contrast.



Cell Cycle - Mitosis

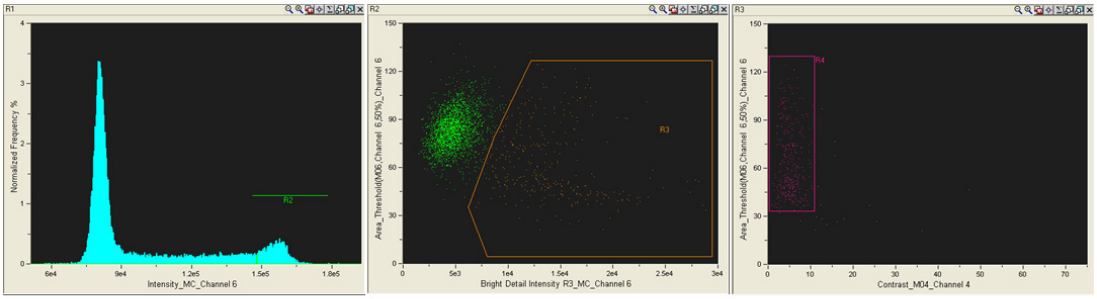
The cell cycle – mitosis wizard will guide you through the process of creating the features and graphs to analyze the cell cycle and identify mitotic events using the images of a nuclear dye.

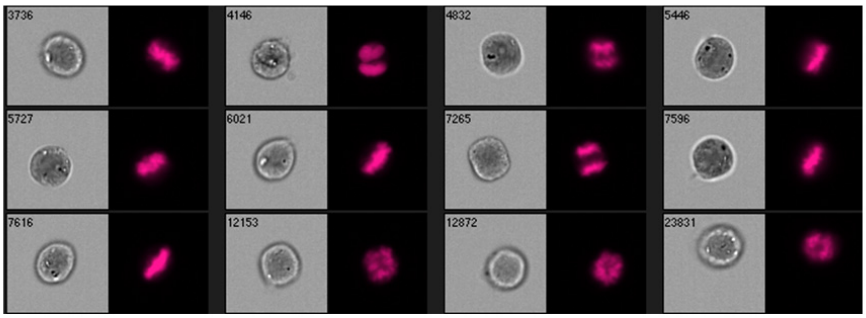
To begin, double-click on Cell Cycle - Mitosis

Follow the instructions to open and analyze your file.

The analysis includes:

- Opening the data file
- Setting the display properties
- Gating on single cells
- Gating on focused cells
- Gating on fluorescent positive cells
- Creating and graphing the features that measure cell cycle and mitosis
- Creating a statistics report





Co-localization

The co-localization wizard will guide you through the process of creating the features and graphs to measure the co-localization of two probes in any population of cells you identify.

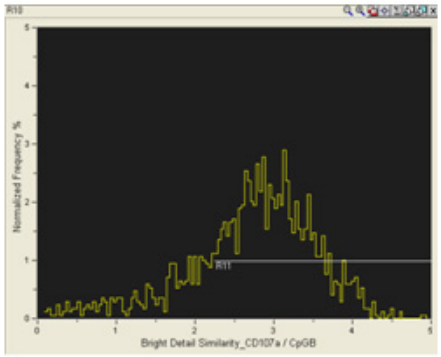
To begin, double-click on Co-Localization

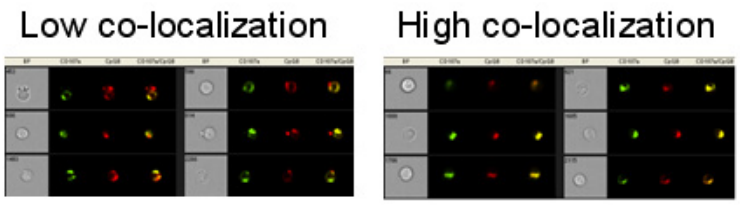
Follow the instructions to open and analyze your file.

The analysis includes:

- Opening the data file
- Setting the display properties
- Gating on single cells
- Gating on focused cells
- Gating on fluorescent positive cells
- Creating and graphing the feature 'Bright Detail Similarity' for measuring co-localization
- Creating a statistics report

Cells with colocalized probes are identified in the final graph presented in the wizard. In this example, cells with high Bright Detail Similarity values have co-localization of the two probes, CD107a (green) and CpG (red).





For a more thorough explanation of the **Bright Detail Similarity** feature see "Bright Detail Similarity R3 Feature" on page 182 .

Internalization

This wizard will create an analysis template for measuring the internalization of a probe in any population of cells you identify.

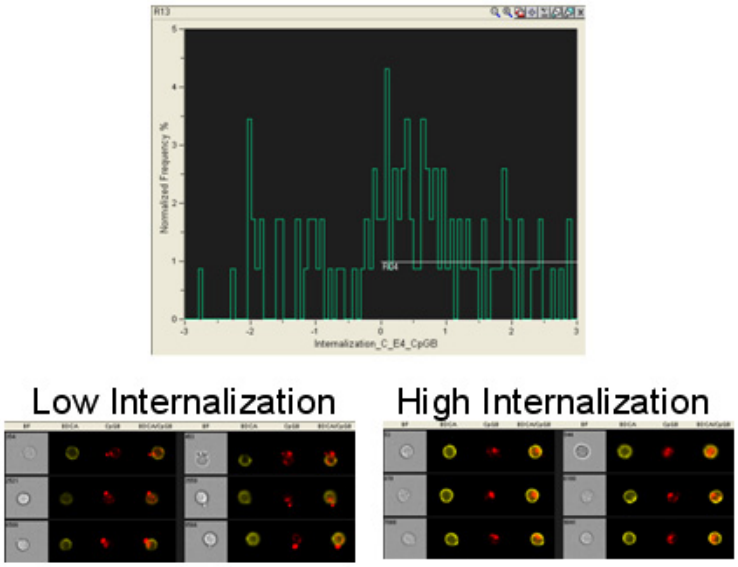
To begin, double-click on Internalization

Follow the instructions to open and analyze your file.

The analysis includes:

- Opening the data file
- Setting the display properties
- Gating on single cells
- Gating on focused cells
- Gating on fluorescent positive cells
- Creating and graphing the feature
- Creating a statistics report

cells with internalized probe are identified in the final graph presented in the wizard. The example below shows the internalization of labeled CpG (red).



For a more thorough explanation of the **Internalization** feature see "Internalization Feature" on page 185

Nuclear Localization

This wizard will create an analysis template for measuring the nuclear localization of a probe in any population of cells you identify.

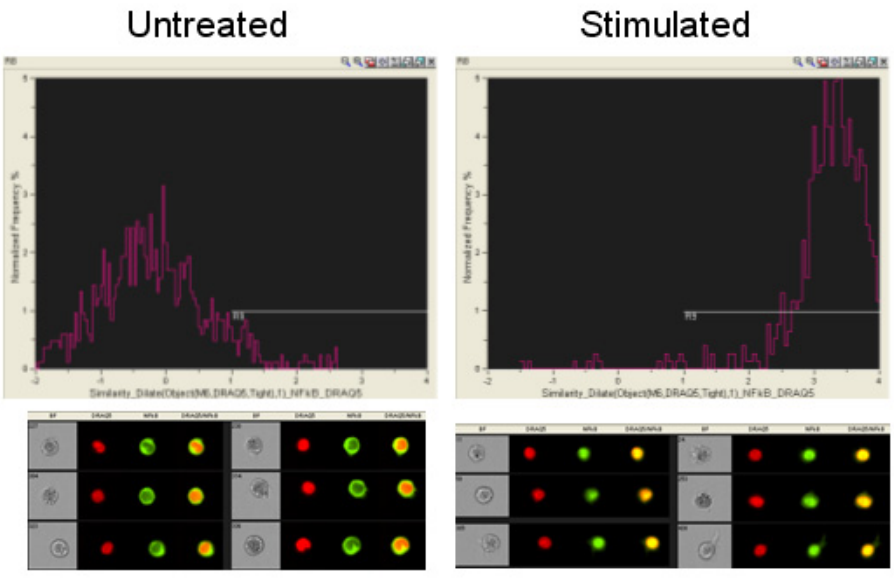
To begin, double-click on Nuclear Localization

Follow the instructions to open and analyze your file.

The analysis includes:

- Opening the data file
- Setting the display properties
- Gating on single cells
- Gating on focused cells
- Gating on fluorescent positive cells
- Creating and graphing the feature
- Creating a statistics report

Nuclear localization of a probe is measured using the Similarity feature in the final graph presented in the wizard. The example shown here is of THP1 cells stimulated with 1 ug LPS for 90 minutes and stained with DRAQ5 (red) and NFkB (green) to measure the nuclear localization of the NFkB.



For a more thorough explanation of the **Similarity** feature see "Similarity Feature" on page 186 .

Shape Change

This wizard will create an analysis template for measuring the shape (circularity) of any population of cells you identify.

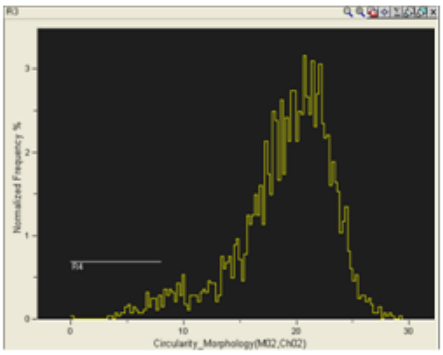
To begin, double-click on Shape Change

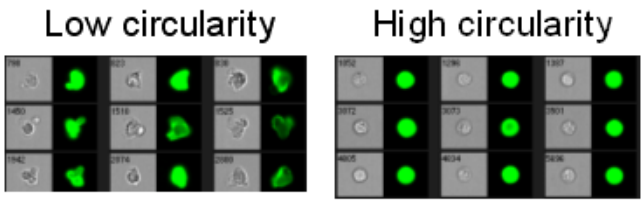
Follow the instructions to open and analyze your file.

The analysis includes:

- Opening the data file
- Setting the display properties
- Gating on single cells
- Gating on focused cells
- Gating on fluorescent positive cells
- Creating and graphing the feature Circularity of a surface stain or brightfield image
- Creating a statistics report

Shape change is measured in the final graph presented in the wizard. Cells with low circularity scores have a highly variable radius. In this example monocytes in whole blood were stained with CD14 (green).





For a more thorough explanation of the **Circularity** feature see "Circularity Feature" on page 154 .

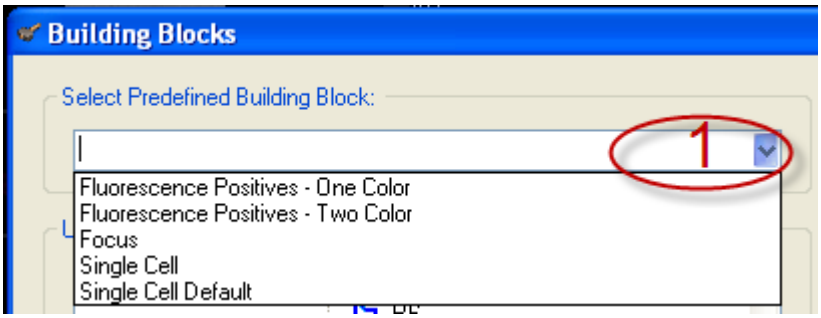
Building Blocks:

Building blocks may be used to create a graph for finding single cells, focused cells or positive cells based on Intensity. The building blocks are shortcuts to creating a graph that provide a limited list of relevant features with set X and Y axis scales set for the graph. For more information on creating graphs see "Creating Graphs" on page 73.

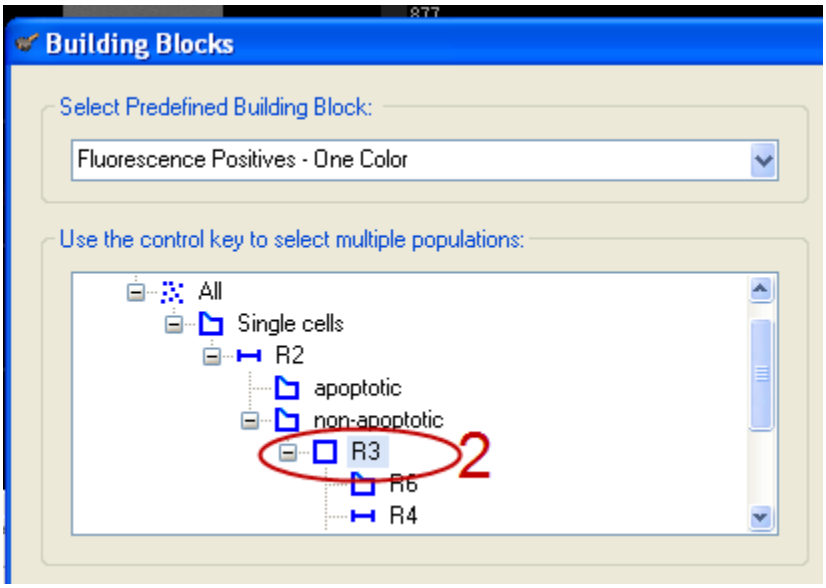
To begin, choose Building Blocks from the Guided Analysis Menu or click on the Building Blocks icon to the left of the analysis area.

The Building Blocks window opens. This window is used to define a graph with a specified set of features available depending on the purpose of the graph.

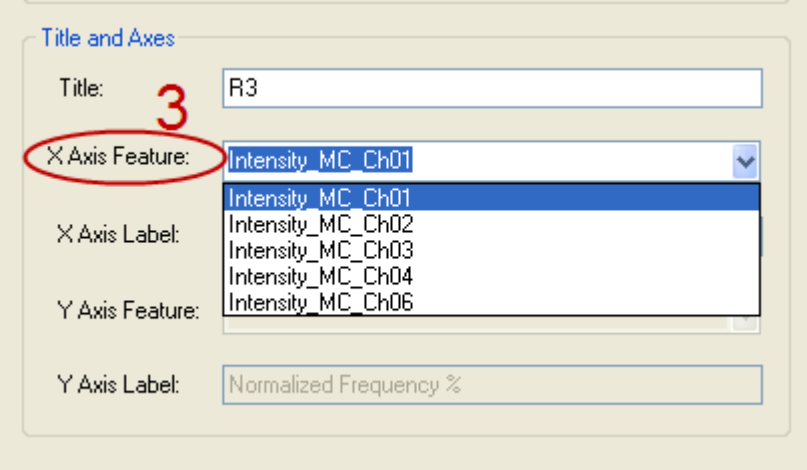
1 Choose the specific Building Block from the drop-down menu.



2 Choose the population(s) to graph.



3 Choose the X Axis Feature and the Y Axis feature, if applicable.



4 Click OK.

5 The graph is added to the analysis area.

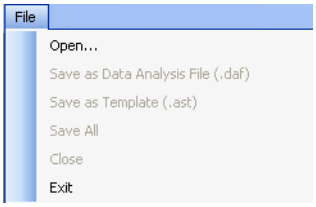
Table 1: Building blocks overview

Building Block	X axisFeatures	Y axis Features
Flourescence Positives - one color	Intensity_MC_ChX (for all channels)	
Flourescence Positives - two color	Intensity_MC_ChX (for all channels)	Intensity_MC_ChX (for all channels)
Focus	Gradient RMS_MX_ChX (for all channels) Note: Gradient RMS of brightfield is default	
Single Cell	Area_brightfield (default) Area_scatter Intensity_MC_ChX (for all channels)	Aspect Ratio_brightfield (default) Aspect Ratio Intensity_MX_ChX (for all fluorescence channels) Intensity_scatter
Single Cell Default	Area_brightfield	Aspect Ratio_brightfield

Advanced Analysis

The File Menu

Use the **File** menu, which is shown in the following figure, to open, save, and close image and analysis files and to quit the IDEAS application. Alternatively, you may open a data file by drag and drop into an open IDEAS window. Muliple data files can be open in one instance of the IDEAS application.



Opening a .rif file

A .rif file is opened when there is new data and the IDEAS application needs to apply corrections. When opening a .rif file, the IDEAS application corrects each image for the spatial alignment between channels, camera background normalization, flow speed, and brightfield gain normalization. If you want fluorescence compensation to correct for spectral overlap, you must create or choose a compensation matrix at this time by using the control files that were collected for a particular experiment. For more information, refer to "Creating a New Compensation Matrix File" on page 39. The application performs the corrections by using calibration information that was saved to the .rif file during acquisition.

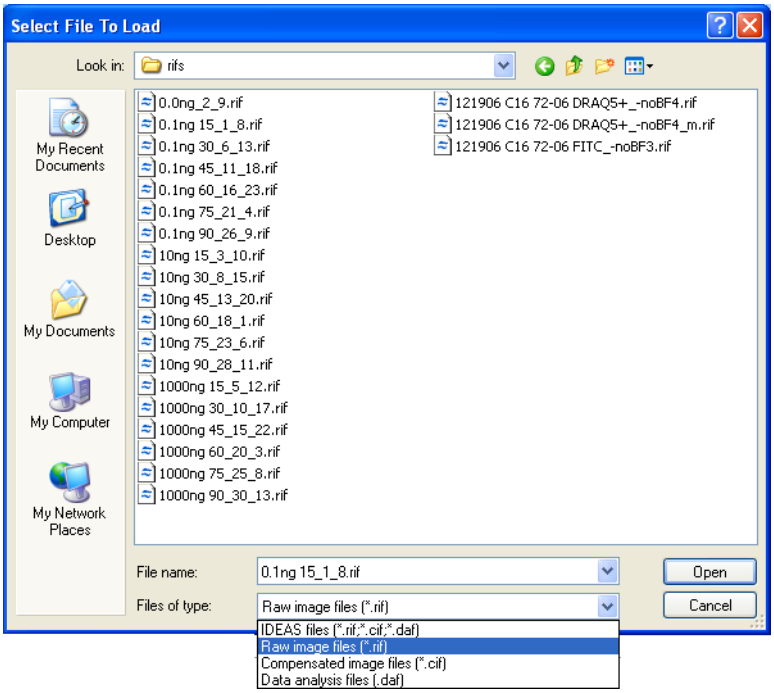
To open a .rif file

To use a wizard to do this see "Open File:" on page 19, otherwise:

1 From the File menu, choose **Open** or drag the file into the IDEAS window**.**

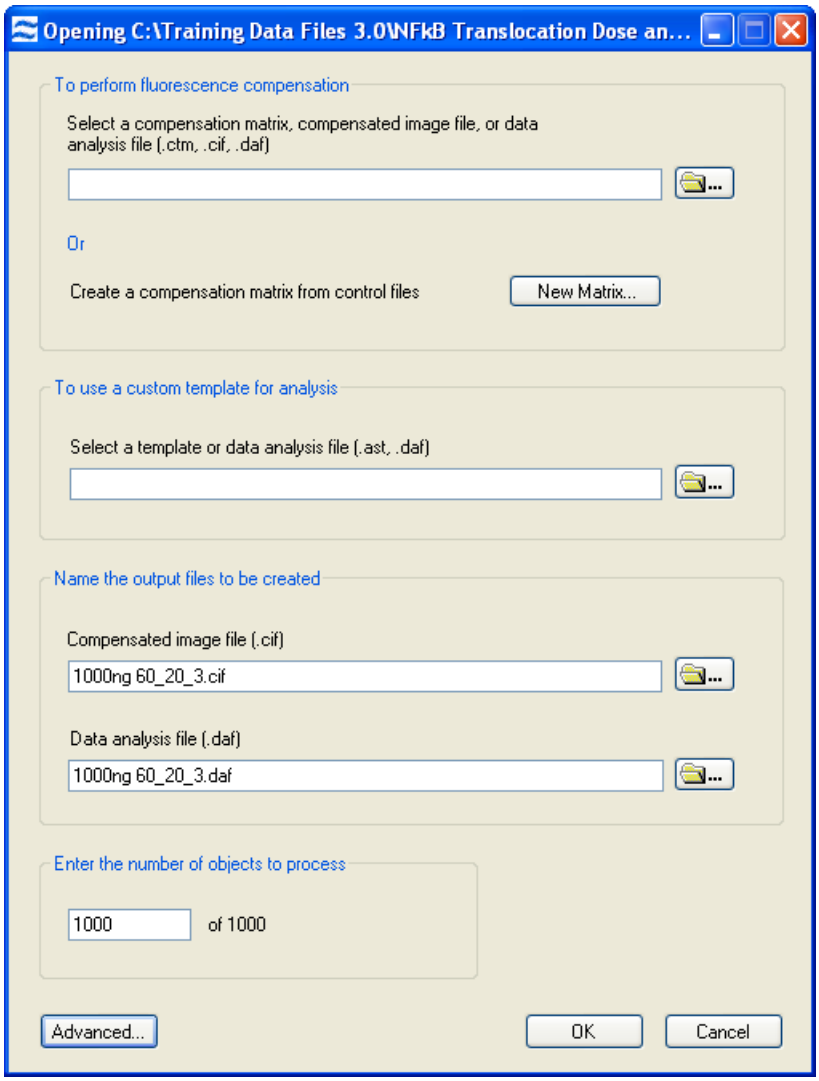
2 Select the .rif file that you want in the **Select File To Load** window.

Tip: while browsing for the file to open you can limit the type of file shown in the window to .rif files.



In the next window you will:

- Choose a compensation matrix
- Choose a template
- Name the output files
- Choose the number of events to process



3 Click the folder next to **Select a compensation matrix, compensated image file, or data analysis file (.ctm, .cif, .daf)** field to choose the matrix that was generated from the controls used for the experiment. If you leave it blank, the default compensation matrix will be used, but this is not recommended unless you do not want to compensate your data.

- If a compensation matrix for the experiment has not been made, click **New Matrix**. For more information on creating a compensation matrix see "Creating a New Compensation Matrix File" on page 39.

4 In the **Select a template or data analysis file (.ast, .daf)** field, select a template file to load by clicking the folder and browsing for the file. If left blank, the Default template with the basic features, masks, and settings will be used.

5 Name the output files with a new name, if necessary.

6 You may change the number of objects to load in the box under **Enter the number of objects to process**. The default value is the number of objects in the file.

Tip: you can select a smaller number than the maximum if you have a large number of objects to load. This helps save time for creating a template file. The IDEAS application randomly loads the specified number of objects within the file.

7 Click **OK**.

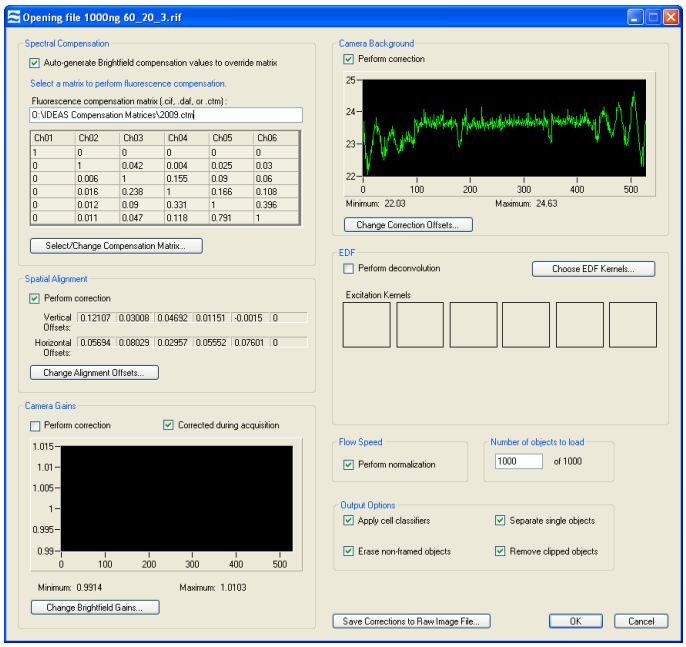
The application then creates the .cif and .daf files and the .daf file is loaded into the Image Analysis area.

.Rif File Option: Setting Advanced Corrections

Most often, the defaults will be adequate. For some older data files, you may need to provide control files for certain settings.

- To view the corrections that will be applied to the .rif file, click **Advanced** within the Opening a .rif file window.

  The **Opening file** window appears.



- Make any changes to the corrections that you need, and then click **OK**. Refer to the Troubleshooting chapter "Troubleshooting" on page 205 for more information about these options.

Opening a .cif file

A .cif file is generated when corrections are applied to a .rif file, as described in "Compensated Image File (.cif)" on page 14. When opening a .cif file, the IDEAS application calculates feature values and creates a .daf file to display images and graphs.

When opening a .cif file, an analysis template is selected. The template provides the initial characteristics of the analysis. Opening the .cif file causes the IDEAS application to calculate feature values and to use populations, graphs, and image viewing settings to display the cells as defined by the template.

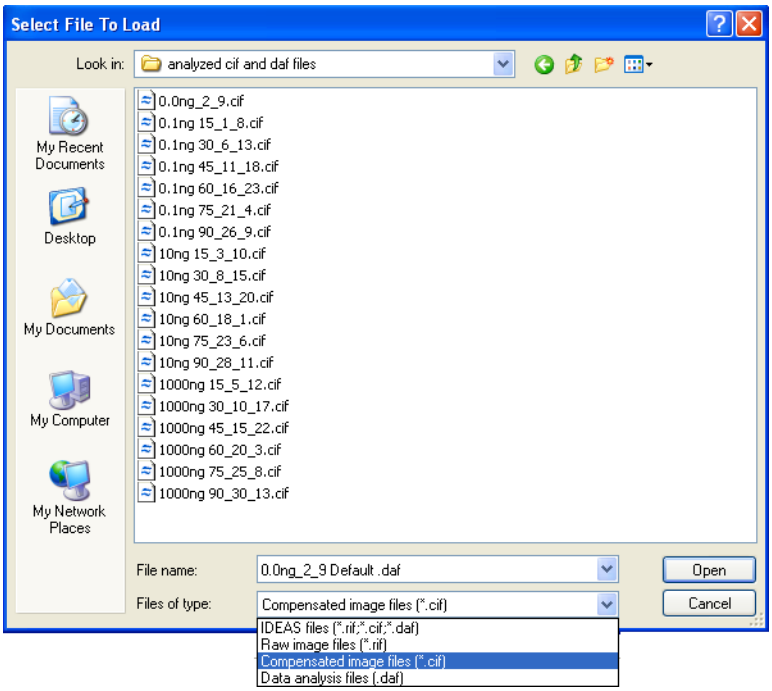
To open a .cif file

To use a wizard to do this see "Open File:" on page 19, otherwise:

1 From the File menu, choose **Open** or drag the file into the IDEAS window**.**

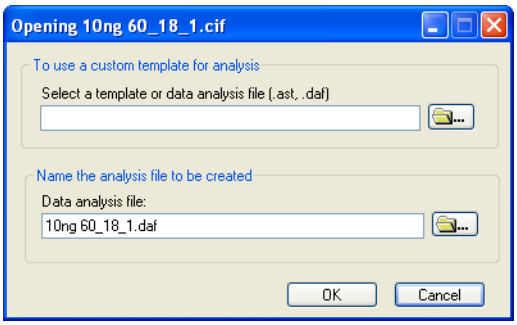
2 Select the .cif file that you want in the Select File To Load window.

Tip: while browsing for the file to open you can limit the type of file shown in the window to .cif.



In the next window you will:

- Choose a template
- Name the output file



3 Click the folder next to **Select a template or data analysis file (.ast, .daf)** and choose the template to use for analysis. If left blank, the IDEAS application will use a default template. However, it is useful to create and save your own templates for specific experimental procedures.

4 Change the **Data analysis file** name, if necessary. The default name matches the name of the .cif.

5 Click **OK**.

During the opening of a .cif file, the IDEAS application calculates the values of the features that are defined in the template you selected. The progress is shown by a progress bar. After the application has successfully opened the .cif file, the .daf file is saved.

See also: "Saving a Compensated Image File (.cif)" on page 50.

Opening a .daf file

A .daf file contains the calculated feature values so that they will not need to be recalculated, as described in "Data Analysis File (.daf)" on page 14. To open a .daf file, the IDEAS application requires the .cif file to reside in the same directory. The .daf file does not contain any image data, so you can think of the .cif file as the database that contains the imagery. Because all of the feature values have been saved in it, the .daf file should open quickly.

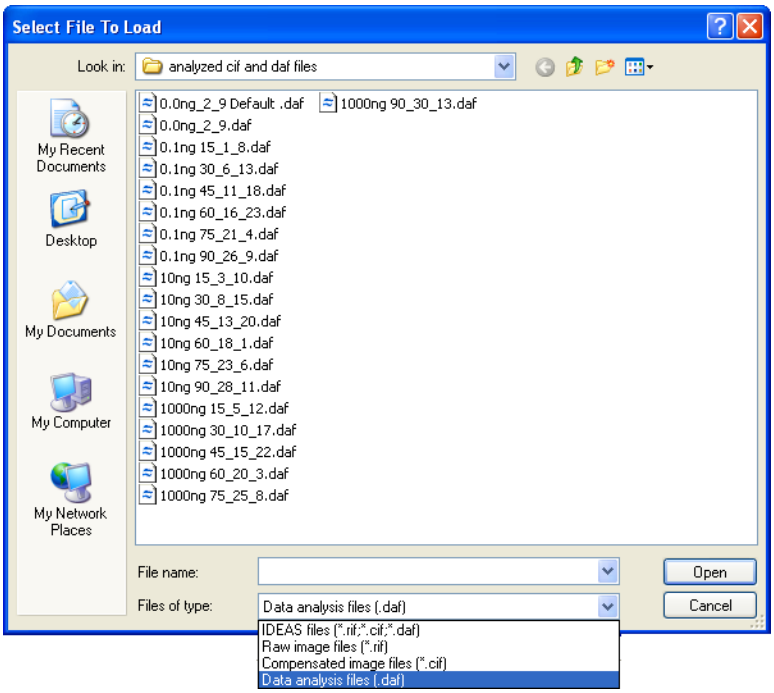
To open a .daf file

To use a wizard to do this see "Open File:" on page 19, otherwise:

1 From the File menu, choose **Open** or drag the file into the IDEAS window**.**

2 Select the .daf file that you want in the Select File To Load window.

Tip: while browsing for the file to open you can limit the type of file shown in the window to .daf.



The progress is shown by a progress bar. The state of the IDEAS application is restored to what it was when the .daf file was saved.

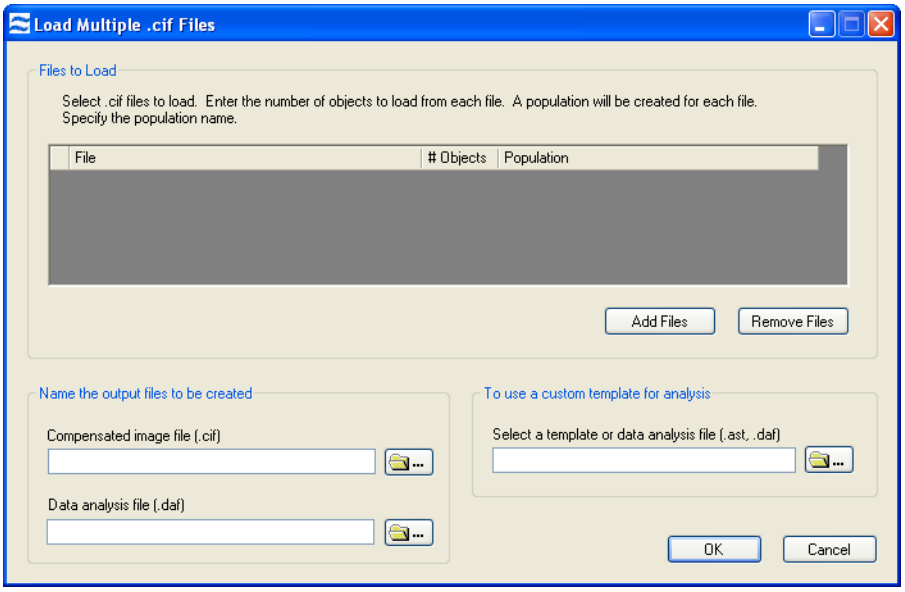
Merging .cif files

You can open multiple .cif files to combine their data and create a single .daf file. This is useful when you would like to create one graph with multiple data files.

To open multiple .cif files, combine their data, and create a single .daf file

1 From the Tools menu, select **Merge .cif Files**.

The Load Multiple .cif Files window appears.



2 Click Add Files, and select the .cif files that you want. Click Remove Files to remove a file from the list.

The file names appear in the Files to Load list.

3 For each file, type the number of objects to load. By default, all objects will load unless specified.

For each file, the IDEAS application creates a population using the file name as the population name.

4 Type or select the resulting .cif and .daf file names.

If you type or select an existing file name, a warning appears that asks you to verify the overwriting of the file.

5 Browse to select a template.

6 Click OK.

The IDEAS application loads the .cif files and creates a single .cif and .daf file.

Viewing Sample Information

All of the information associated with an IDEAS file, such as the collection information, camera settings and corrections, is saved within IDEAS and can be viewed in the Sample Information window.

To open the Sample Information window

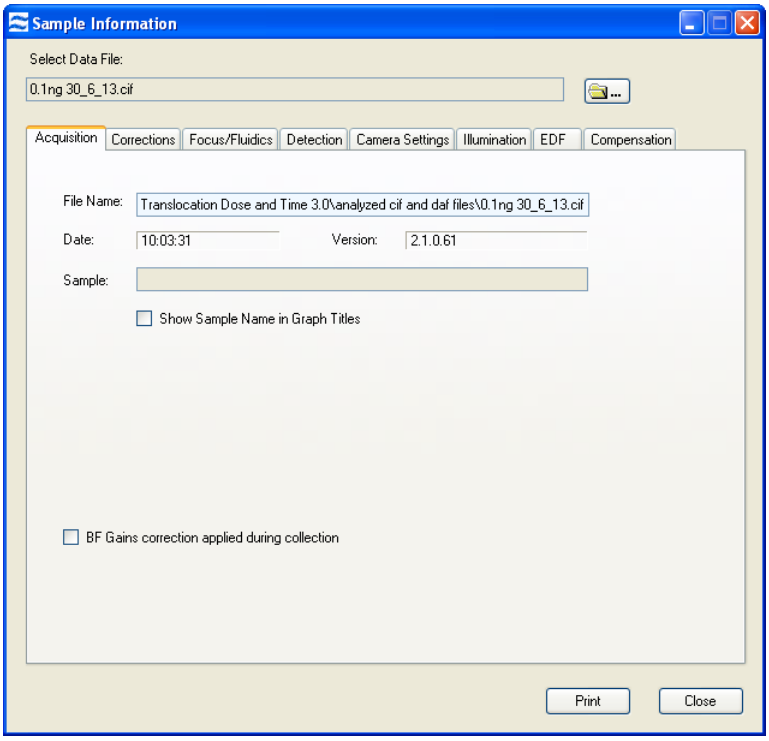
1 Go to **Tools** > **Sample Information** to open the window.

Information for the open data file will be loaded otherwise you can browse for a data file by clicking on the folder. You can open the Sample Information Window for any of three file types: .rif, .cif, or .daf.

2 Select a Tab to see the information for each heading.

3 Click Print to print a report of all of the sample information.

Tip: You may click on the folder and browse for a file to view the sample information for any file without loading the file.

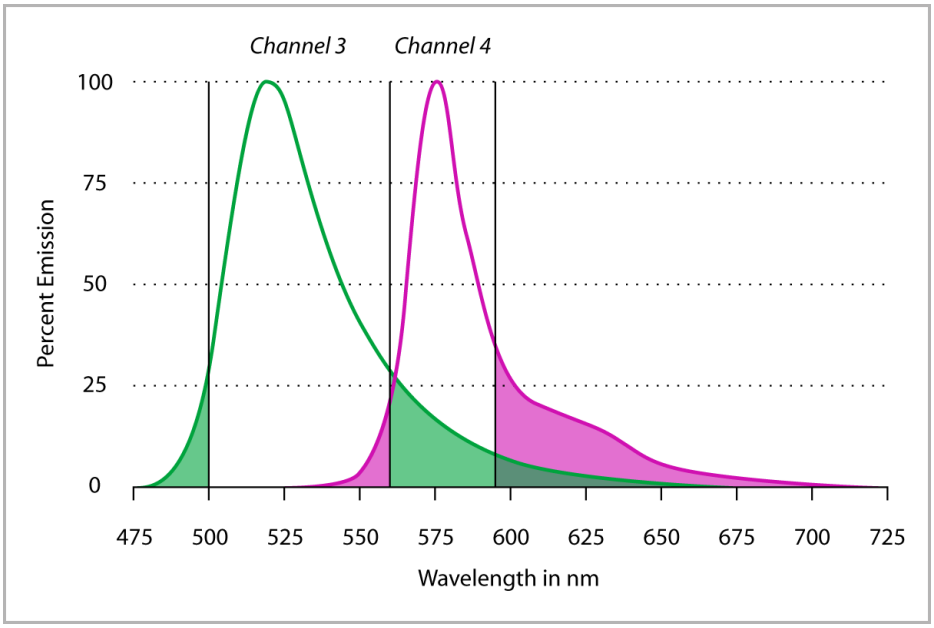


Overview of Compensation

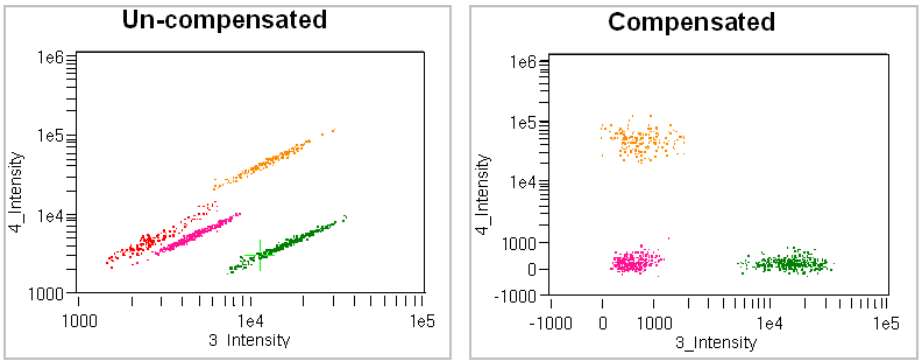
Spectral compensation corrects imagery for fluorescence that leaks into nearby channels so that you may accurately depict the correct amount of fluorescence in each cell image.

For example, the light from one fluorochrome may appear primarily in channel 3, but some of the light from this fluorochrome may appear in channel 4 as well, because the emission spectrum of the probe extends beyond the channel 3 spectral bandwidth. The light from a second fluorochrome may appear primarily in channel 4 but, unless you subtract the light emitted by the first fluorochrome into channel 4, you cannot generate images that accurately represent the distribution of the second fluorochrome.

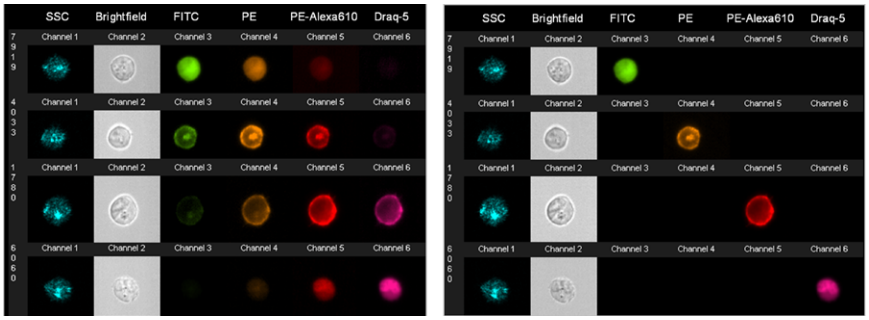
Emmission Spectra for two fluorochromes:



Below is an example of cells stained with two fluorochromes independently and run together as one sample. Intensity scatter plots and images are shown uncompensated and compensated.



Uncompensated **Compensated**

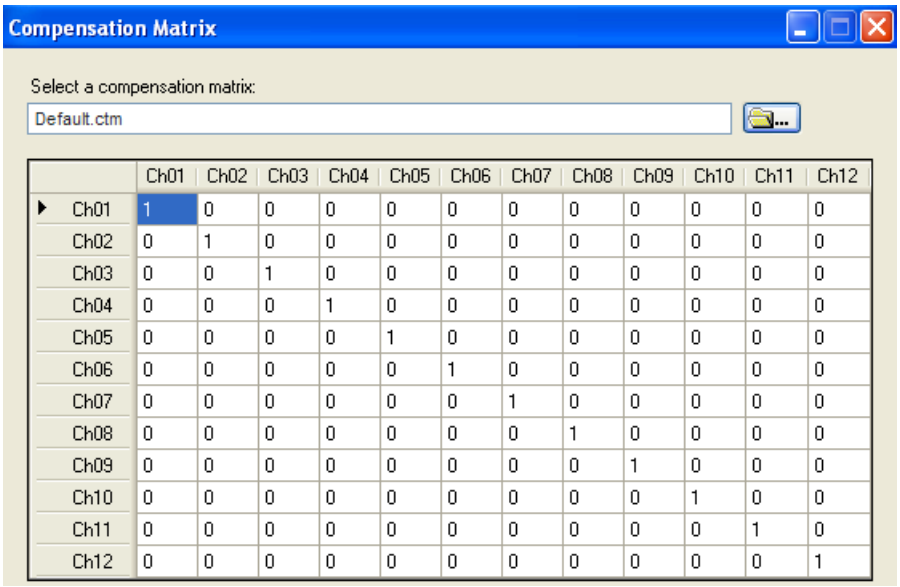


The IDEAS application builds a matrix of compensation values by using one or more control files. A control file contains cells stained with one fluorochrome. You can mix singly stained cells and run them together, but you must be careful that the fluorochromes do not bleed onto other singly stained cells. Because it is critical that matrix values be calculated from intensities derived from a sole source of light, control files are collected without brightfield illumination. The IDEAS application performs brightfield compensation when it loads a .rif file. The process of creating the compensation matrix is described in the next section.

Creating a New Compensation Matrix File

The compensation matrix is a table of coefficients. The IDEAS application uses this table to place the detected light that is displayed in each image into the proper channels, on a pixel-by-pixel basis. The coefficients are normalized to 1. Each coefficient represents the normalized amount of the leakage of the fluorochrome into the other channels.

The default matrix, which is used if no compensation matrix is chosen, is the identity matrix.



	Ch01	Ch02	Ch03	Ch04	Ch05	Ch06	Ch07	Ch08	Ch09	Ch10	Ch11	Ch12
Ch01	1	0	0	0	0	0	0	0	0	0	0	0
Ch02	0	1	0	0	0	0	0	0	0	0	0	0
Ch03	0	0	1	0	0	0	0	0	0	0	0	0
Ch04	0	0	0	1	0	0	0	0	0	0	0	0
Ch05	0	0	0	0	1	0	0	0	0	0	0	0
Ch06	0	0	0	0	0	1	0	0	0	0	0	0
Ch07	0	0	0	0	0	0	1	0	0	0	0	0
Ch08	0	0	0	0	0	0	0	1	0	0	0	0
Ch09	0	0	0	0	0	0	0	0	1	0	0	0
Ch10	0	0	0	0	0	0	0	0	0	1	0	0
Ch11	0	0	0	0	0	0	0	0	0	0	1	0
Ch12	0	0	0	0	0	0	0	0	0	0	0	1

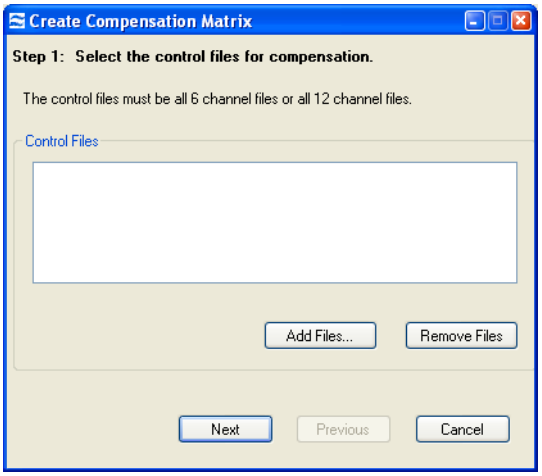
To generate a new compensation Matrix file

1 Start the Compensation Wizard in one of two ways:

— Click the **New Matrix** button when opening a .rif file

— **OR** select **Compensation>Create New Matrix** .

The compensation wizard opens to **Step 1**:



2 Add compensation control files by clicking Add Files and browsing for the no brightfield control files for the experiment. Hold down the control key to select multiple files at once.

3 When all of the control files for the experiment have been added to the list, click **Next**.

The control file(s) are merged and loaded. Background and spatial offset corrections are performed, the imagery is displayed, bivariate plots of adjacent channels Intensity are added to the analysis area and the compensation matrix values are computed and displayed in a table.

The following tables are provided as a guide for each instrument configuration.

Table 2: First generation ImageStream

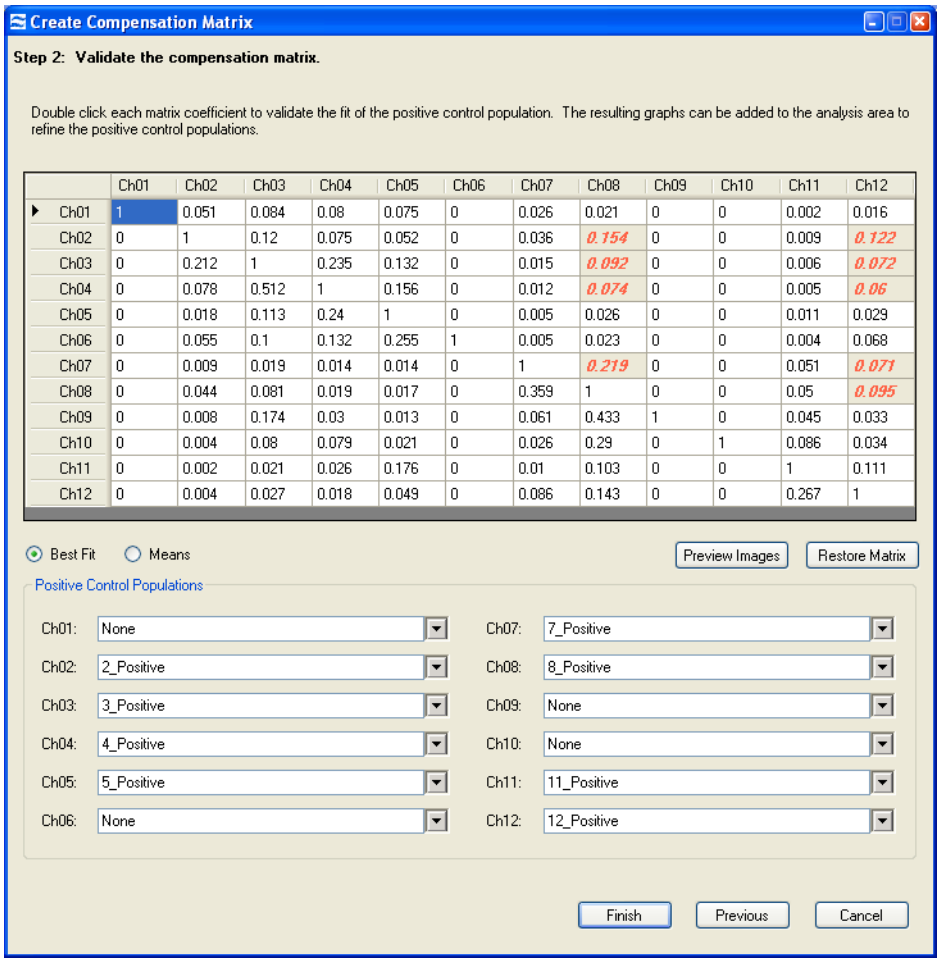
Ch 1	Ch 2	Ch3	Ch 4	Ch 5	Ch 6
470-500nm	**400-470nm**	**500-560nm**	**560-595nm**	**595-660nm**	**660-735nm**
Scatter	DAPI	Fluorescein	PE	7-AAD	PE-Cy5

Table 3: ImageStream^X- 1 camera

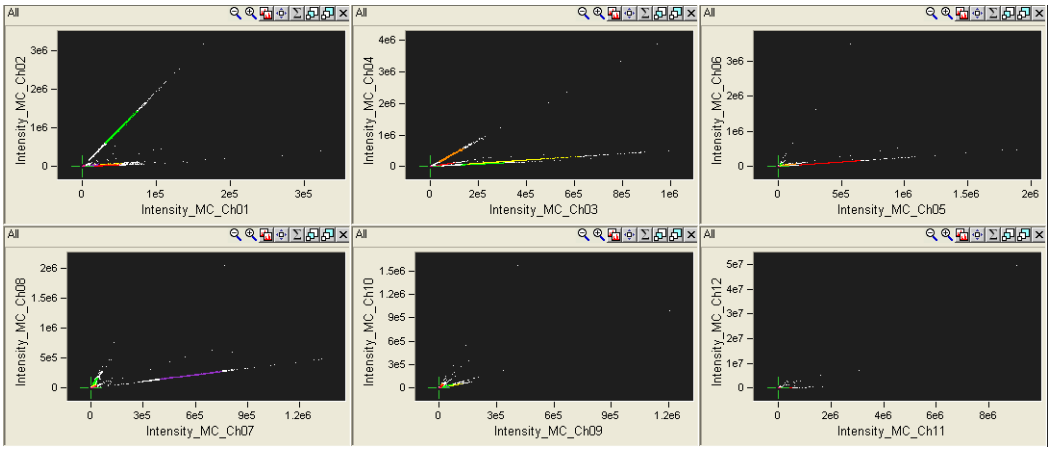
Ch 1	Ch 2	Ch 3	Ch 4	Ch 5	Ch 6
430-505nm	**505-560nm**	**560-595nm**	**595-660nm**	**660-745nm**	**745-800nm**
DAPI	Fluorescein	PE	PE-Texas-Red	AF647	APC-Cy7

Table 4: ImageStream^X- 2 camera

Ch 1	Ch 2	Ch 3	Ch 4	Ch 5	Ch 6
430-480nm	**480-560nm**	**560-595nm**	**595-660nm**	**660-745nm**	**745-800nm**
BF	Fluorescein	PE	PE-Texas-Red	PE-Cy5	PE-Cy7
Ch 7	**Ch 8**	**Ch 9**	**Ch 10**	**Ch 11**	**Ch 12**
430-505nm	**505-570nm**	**570-595nm**	**595-660nm**	**660-745nm**	**745-800nm**
DAPI	Pacific Orange	BF	Texas Red	AF647	APC-Cy7



	Ch01	Ch02	Ch03	Ch04	Ch05	Ch06	Ch07	Ch08	Ch09	Ch10	Ch11	Ch12
Ch01	1	0.051	0.084	0.08	0.075	0	0.026	0.021	0	0	0.002	0.016
Ch02	0	1	0.12	0.075	0.052	0	0.036	*0.154*	0	0	0.009	*0.122*
Ch03	0	0.212	1	0.235	0.132	0	0.015	*0.092*	0	0	0.006	*0.072*
Ch04	0	0.078	0.512	1	0.156	0	0.012	*0.074*	0	0	0.005	*0.06*
Ch05	0	0.018	0.113	0.24	1	0	0.005	0.026	0	0	0.011	0.029
Ch06	0	0.055	0.1	0.132	0.255	1	0.005	0.023	0	0	0.004	0.068
Ch07	0	0.009	0.019	0.014	0.014	0	1	*0.219*	0	0	0.051	*0.071*
Ch08	0	0.044	0.081	0.019	0.017	0	0.359	1	0	0	0.05	*0.095*
Ch09	0	0.008	0.174	0.03	0.013	0	0.061	0.433	1	0	0.045	0.033
Ch10	0	0.004	0.08	0.079	0.021	0	0.026	0.29	0	1	0.086	0.034
Ch11	0	0.002	0.021	0.026	0.176	0	0.01	0.103	0	0	1	0.111
Ch12	0	0.004	0.027	0.018	0.049	0	0.086	0.143	0	0	0.267	1



Note: The IDEAS application automatically finds the singly stained populations. The automatically-generated control populations appear on the graphs. This example contains control files for channels 3,4 and 6.

4 In **Step 2**, choose one of two methods for calculating the coefficients.

- The **Best Fit** method is used for objects such as cells where intensities vary.

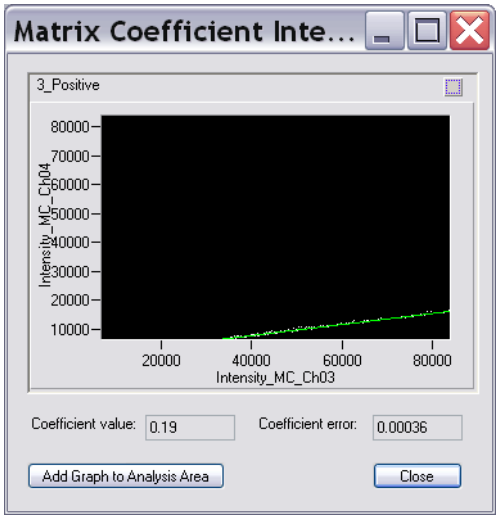
- The **Means** method is used for objects such as beads that have only slight variations in intensity.
- To show/hide the legend, right-click inside the graph and then choose **Show/Hide Legend**.
- For each fluorochrome, the application automatically identifies a positive control population, excluding outliers, the brightest and dimmest objects, and assigns it to the proper channel.

5 Inspect the matrix values in the table of coefficients.

Coefficients should always be less than 1, and decrease from the assigned channel. In other words, leakage should be greater in the channel nearest to the assigned channel. Fluorescence always extends in the long-wavelength direction from the exciting light.

- Verify that no coefficients are larger than 1.
- Verify that, in a column corresponding to a fluorochrome, the coefficients decrease from the assigned channel.
- Verify that the coefficient is greater in the channel below the 1 in the table than the value above the 1 in the table. Verify that these coefficients also decrease in subsequent channels below the 1.
- Verify that there are no changes from the identity matrix in the columns where there are no fluorochromes, including the scatter and brightfield channels.
- Inspect the coefficients in the matrix by double-clicking on the coefficient. Coefficients highlighted by red have errors greater than 1%.

  A graph representing the coefficient appears. The population potted in the graph is the positive control population of the column of the coefficient. The X Axis represents the intensity in the assigned channel of the fluorochrome. The Y Axis represents the intensity in the channel of leakage. The coefficent value and error are also displayed.



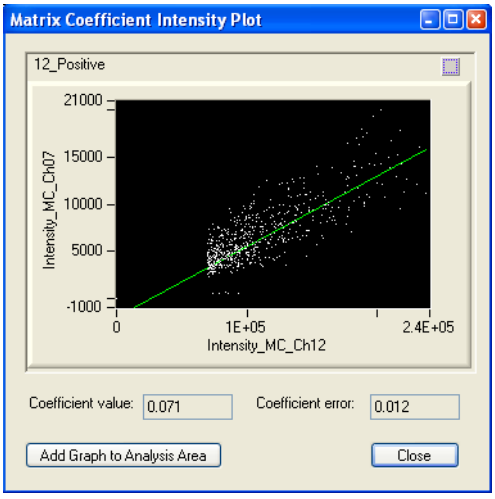
- You can use the automatically generated control populations as they are, or you can refine them and create different populations by using the region tools. See the option below to remove objects from the population. By default, the populations are named 3_Positive, 5_Positive, and so on. You can view the populations in the Image Gallery. Some populations may be empty.
- To choose a different population, use the arrow and select the population from the list. The hierarchical relationship is shown in the population list. Assign populations only to the channels that correspond to the fluorochromes used in the experiment.
- If you want to clear a column, double click on the channel heading.
- If needed, you can create new scatter plots by using the Analysis Area toolbar. For example, a 4_Intensity versus 5_Intensity plot may be useful. See "Creating Graphs" on page 73 for more information.

The slope of the line on the plot is the coefficient in the matrix.

If objects in the population exist that are outliers, they should most likely be removed from the positive population within the compensation matrix by the following optional steps.

Option: Remove Objects from the Population

1 Within Step 2 of the compensation wizard, double-click the coefficient to display the intensity plot.



2 If you notice outliers, click **Add Graph to Analysis Area**.

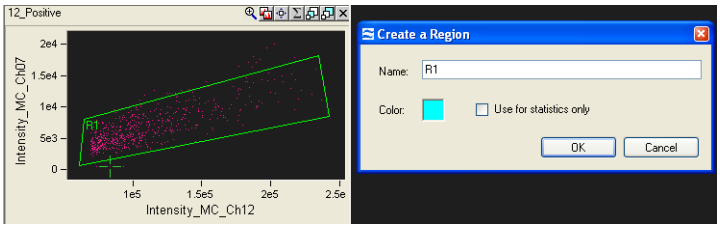
The plot populates in the Analysis Area.

3 Return to the Analysis Area and use the region tools to draw a new region on the plot that defines a new positive control population, excluding the outliers. Refer to "Creating Regions on Graphs" on page 77 for more information.

- Create a new region to exclude outliers.

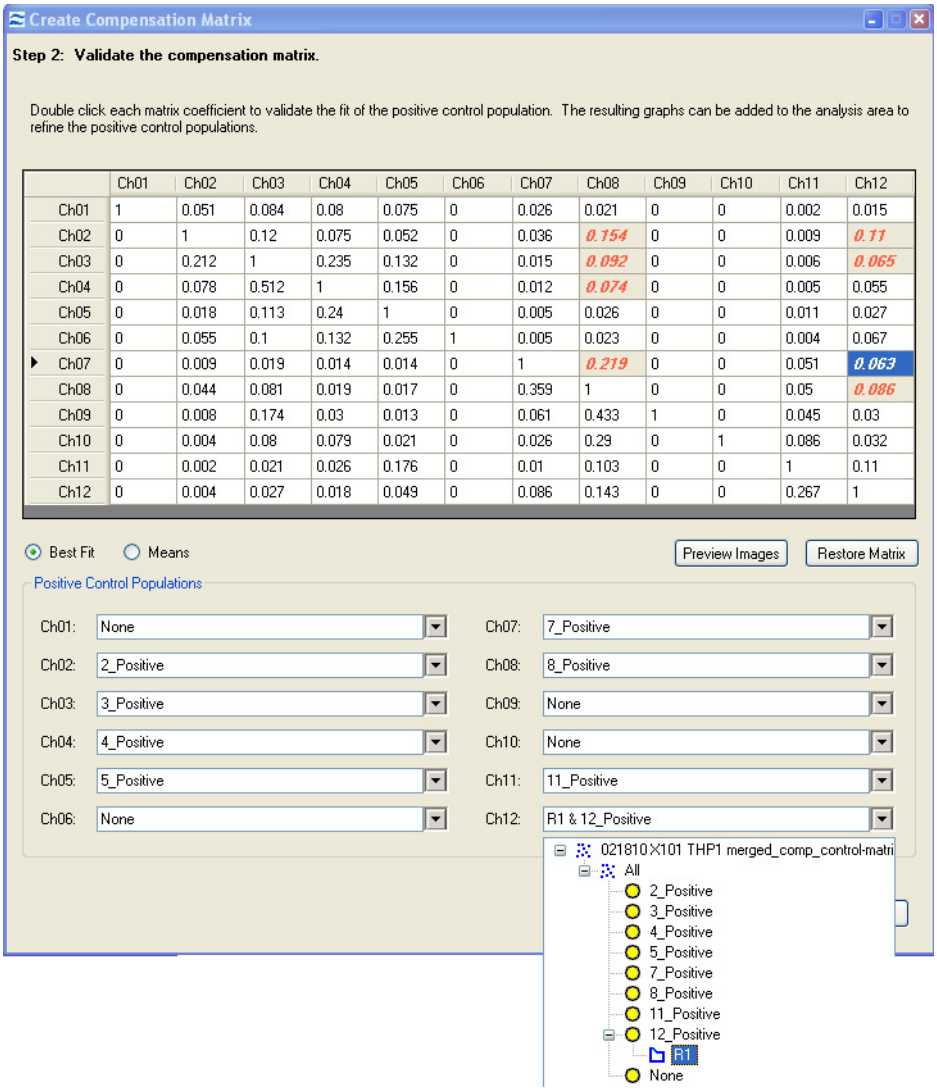
Click the Resize  and Zoom  buttons on the graph toolbar to more clearly see the population of interest. Using one of the region buttons on the toolbar, draw a region that contains only the cells you want to use for determining compensation. You can click a point on the graph and view the image to help you decide where the region boundaries should be.

In the example below, the Polygon Region tool was selected to draw a border around a selection of cells. Clicking within the graph anchors the line and double-clicking completes the region.



For more information, refer to "Creating Regions on Graphs" on page 77.

4 Assign the new population to the appropriate channel by using the **Positive Control Populations** list for that channel.



	Ch01	Ch02	Ch03	Ch04	Ch05	Ch06	Ch07	Ch08	Ch09	Ch10	Ch11	Ch12
Ch01	1	0.051	0.084	0.08	0.075	0	0.026	0.021	0	0	0.002	0.015
Ch02	0	1	0.12	0.075	0.052	0	0.036	*0.154*	0	0	0.009	*0.11*
Ch03	0	0.212	1	0.235	0.132	0	0.015	*0.092*	0	0	0.006	*0.065*
Ch04	0	0.078	0.512	1	0.156	0	0.012	*0.074*	0	0	0.005	0.055
Ch05	0	0.018	0.113	0.24	1	0	0.005	0.026	0	0	0.011	0.027
Ch06	0	0.055	0.1	0.132	0.255	1	0.005	0.023	0	0	0.004	0.067
Ch07	0	0.009	0.019	0.014	0.014	0	1	*0.219*	0	0	0.051	*0.063*
Ch08	0	0.044	0.081	0.019	0.017	0	0.359	1	0	0	0.05	*0.086*
Ch09	0	0.008	0.174	0.03	0.013	0	0.061	0.433	1	0	0.045	0.03
Ch10	0	0.004	0.08	0.079	0.021	0	0.026	0.29	0	1	0.086	0.032
Ch11	0	0.002	0.021	0.026	0.176	0	0.01	0.103	0	0	1	0.11
Ch12	0	0.004	0.027	0.018	0.049	0	0.086	0.143	0	0	0.267	1

5 The coefficient value is automatically recalculated when a new population is selelcted.

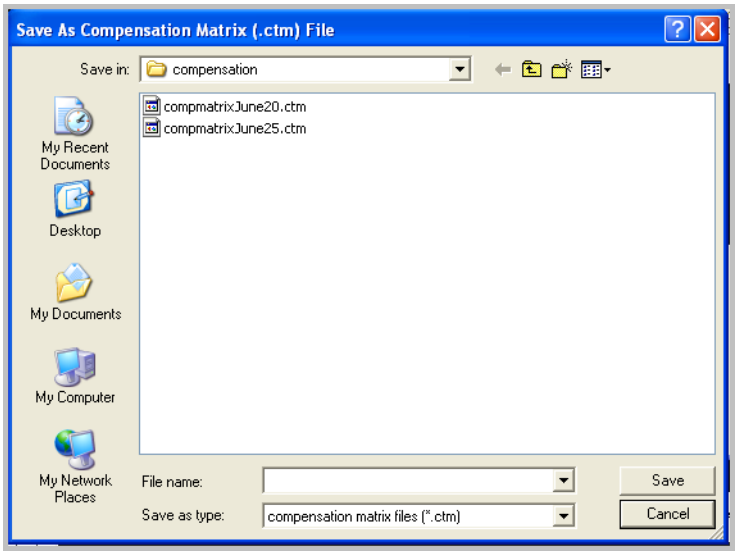
6 Repeat these steps as required to redefine the coefficients.

7 Click Preview Images to view individual objects with corrections applied. Double click on an image to add it to the preview window. Note: the corrections are only applied to on-camera channels. For example, if the object is brightest in channel 3 on the first camera, only channels 1-6 are shown corrected for that object.

8 When the matrix appears satisfactory, click **Finish**.

9 Enter a name for the compensation matrix file (.ctm) and click **Save**

.



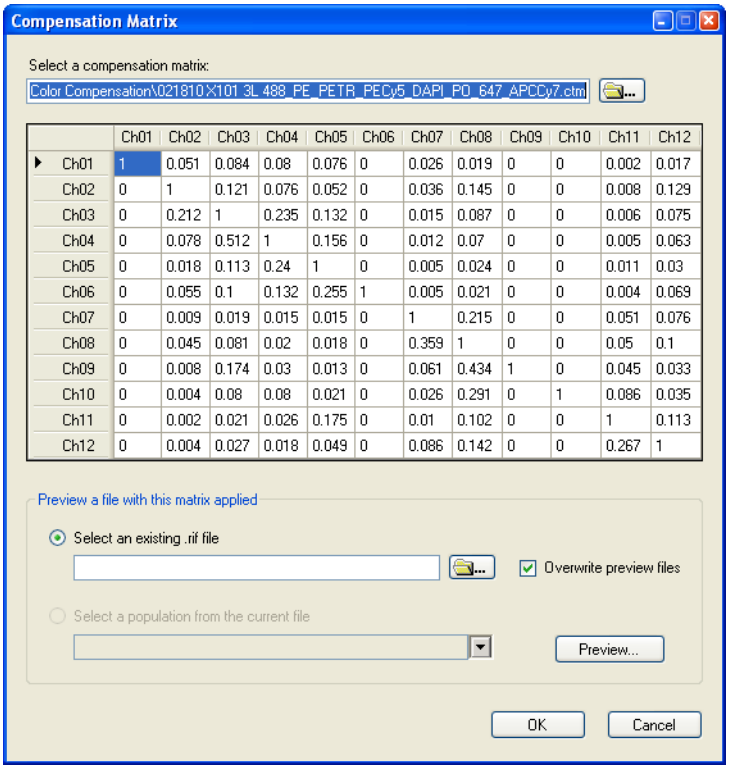
Note: The matrix is saved as a compensation matrix file (.ctm file). This file contains the compensation values and can be opened later for editing. To provide the values for fluorescence compensation, you select a .ctm file when opening a .rif file. See "Opening a .rif file" on page 29 for more information.

Preview a compensation matrix

A compensation matrix can be applied to a population or .rif file in a preview mode for editing a matrix.

To open a compensation Matrix

1 Select Open>Compensation Matrix from the File menu or Select View/Edit compensation matrix from the Compensation menu to view, edit or preview the matrix on image data.The matrix values are displayed in a table and may be edited.



2 To preview the matrix on image data, browse for a file or select a population from the current file to preview and click Preview.

3 You may repeat editing the matrix and previewing until satisified.

4 When done, click OK and save the matrix.

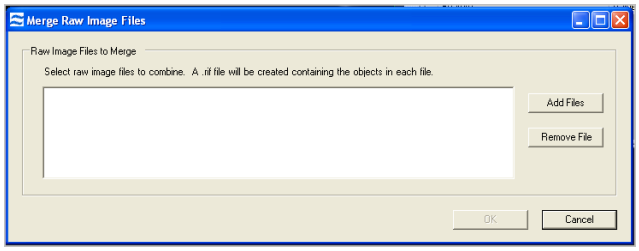
Merging Raw Image Files

You can merge .rif files together for analysis.

To merge .rif files

1 On the **Tools** menu, click **Merge .rif Files**.

The **Merge Raw Image Files** window appears.



2 To select the .rif files to merge, click **Add Files**.

The .rif file names appear in the list.

3 If you want to remove a file from the list, select it and then click **Remove File**.

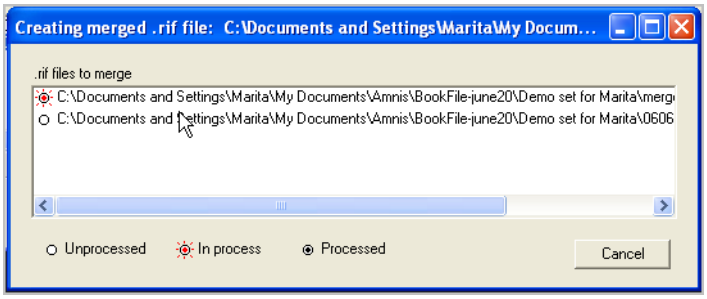
4 When the merge list is complete, click **OK**.

The **Save Merged Raw Image (.rif) File** dialog box appears.

5 Type a unique file name.

6 Click **Save**.

The Creating merged .rif file window appears.



When the merge is complete, the **Merged .rif Created** message appears.

7 Click **OK**.

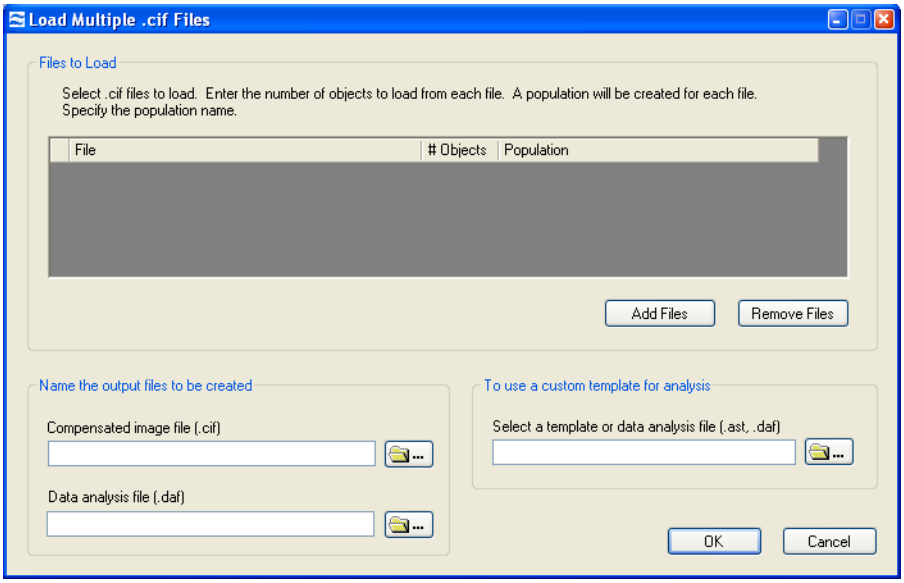
Merging Compensated Image Files

You can merge .cif files together for analysis.

To merge .cif files

1 On the **Tools** menu, click **Merge .rif Files**.

The **Merge Raw Image Files** window appears.



2 To select the .cif files to merge, click **Add Files**.

The .cif file names appear in the list.

3 If you want to remove a file from the list, select it and then click **Remove File**.

4 Type a unique name for the output files.

5 Select a template..

6 Click **OK**.

7 The merged files are created and the new .daf file is loaded with a population created from each file.

Saving Data Files

Data files are saved at several stages of analysis. Raw image files are saved during data acquisition, by merging multiple .rif files or by creating new files from populations. Compensated image files and Data analysis files are saved when opening .rif files, opening multiple .cif files, using the file menu or when running a batch analysis. The IDEAS application also saves other types of files that are used for data correction and presentation. Template files (.ast) save the structure of an analysis and compensation matrix files (.ctm) save the compensation matrices.

Application Defaults are set that direct the files into specific folders and can be viewed or changed by the user. See "Viewing and Changing the Application Defaults" on page 8 for more information.

Saving a Data Analysis File (.daf)

A .daf file contains a snapshot of an analysis as described in "Data Analysis File (.daf)" on page 14. Saving the analysis as a .daf file allows you to recall that analysis simply by opening the file. When you quit the IDEAS application, you are always prompted to save changes to a .daf file. You can also save changes from the File menu. Remember that the .daf file does not contain image information, so opening the .daf file requires the related .cif file to reside in the same directory.

To save a .daf file

1 On the **File** menu, click **Save as Data Analysis File (.daf)**.

2 Enter a file name. Note that the default directory is the one where the .cif file was saved.

If you select an existing file name, a warning appears that asks you to verify the overwriting of the existing file.

3 Click **Save**.

The data is now ready for analysis. You can create graphs, view imagery, and display feature values and statistics. After you have defined an analytical procedure in the .daf file, you can save the file as a template, which allows you to use the procedure for analyzing other files. Refer to "Using the Data Analysis Tools" on page 57 for more information.

Saving a Compensated Image File (.cif)

The IDEAS application creates and saves a .cif file when a .rif file is opened. By default, the application names the .cif file with the same name that the .rif file has, replacing the .rif extension with .cif. The application also places the .cif file in the same

directory as the .rif file. The .cif file will be larger than the .rif file because the .cif file contains masking information as well as corrected and/or compensated images.

Saving a Template (.ast)

Saving an analysis as a template allows you to apply the structure of the analysis to other .cif files. Save a template file after saving a .daf file. A template includes all graph definitions, Image Gallery settings, feature definitions, and statistics settings. No data are saved in a template. Therefore, selected images and populations that are dependent on specific objects, such as tagged populations, are not saved.

To save a template

1 On the **File** menu, click **Save As Template File (.ast)**.

A **Save File** dialog box appears.

2 Enter the name of the file to save.

3 Click **Save**.

If you select an existing file name, a warning appears that asks you to verify the overwriting of the existing file.

Tip: You can change the default template directory in the menu **Analysis** > **Application Defaults**.

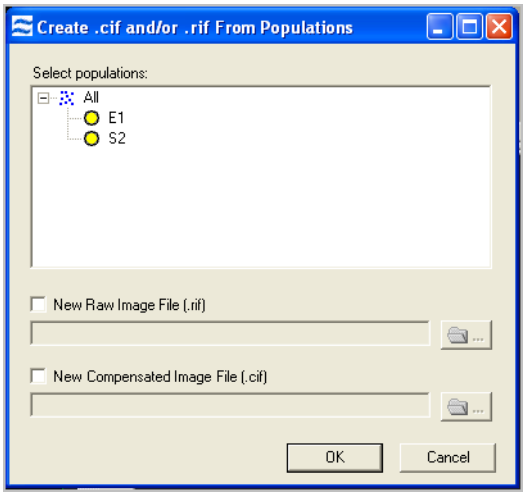
Creating Data Files from Populations

To further analyze a population or merge it with other data when working in a .daf, you can save it to a new data file. This course of action is useful if your data file contains a large number of objects that are not pertinent to your experiment. Decreasing the data file size results in better performance by the IDEAS application, as described in "Creating Regions on Graphs" on page 77. Note that you cannot create a new .cif or .rif when multiple data files are open.

To create data files from populations

1 On the **Tools** menu, click **Create Data File from Populations**.

The **Create .cif and/or .rif From Populations** window appears.



2 In the **Select populations** list, select the populations that you want to include in the new data file(s). Ctrl click to select multiple populations.

3 To create a .rif file, select the **New Raw Image File (.rif)** check box, the population name is used as a default. You may enter a new name.

4 To create a .cif file, select the **New Compensated Image File (.cif)** check box, the population name is used as a default. You may enter a new name.

5 Click **OK**.

If you created a new .cif file, you can choose to load it. When loading the .cif file, the application will prompt you for the template.

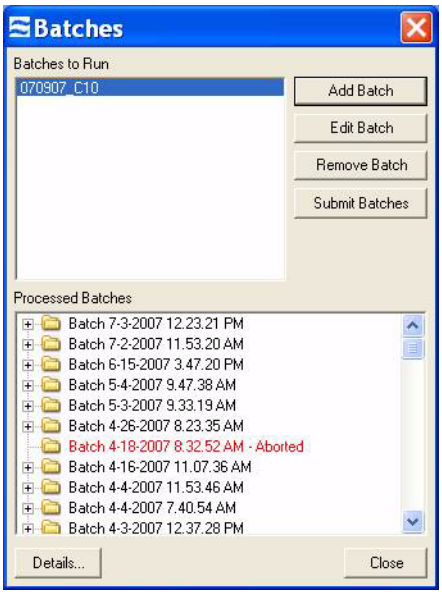
Batch Processing

Batch processing allows you to automatically analyze a group of files with one template when a compensation matrix has already been generated for the experiment.

To perform batch processing

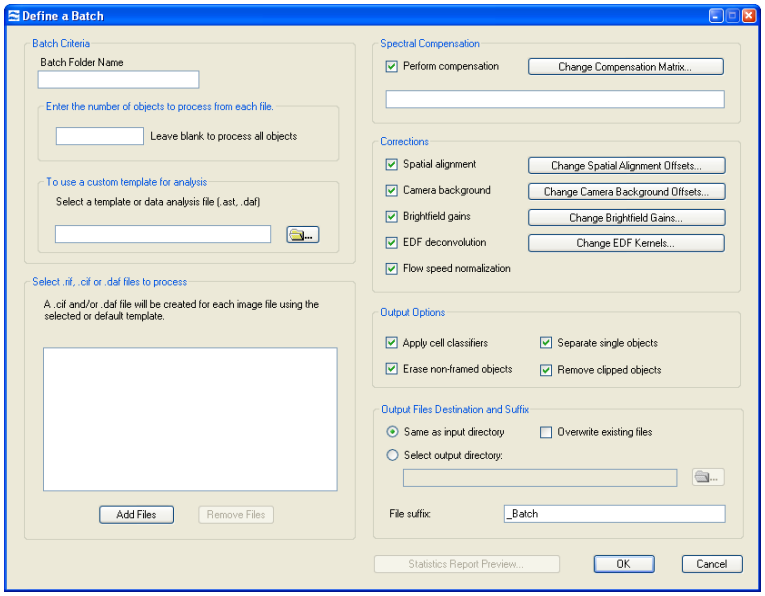
1 On the **Tools** menu, select **Batch Data Files**.

The **Batches** window appears. It lists a record of all batches you have processed.



2 Click **Add Batch**.

The **Define a Batch** window appears.



3 In the **Batch Folder Name** box, type a new batch name.

4 In the next box, type the number of objects to process from each file, or leave it blank to process all objects.

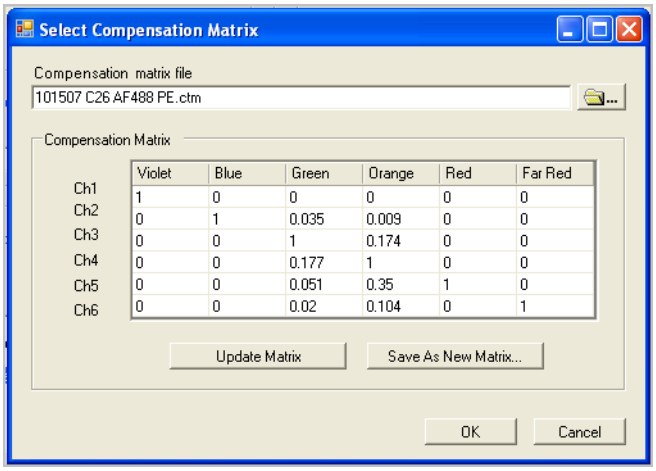
5 Select a **Template file**, which the IDEAS application will use to analyze all the data files in the batch. Otherwise, the default template will be used.

6 To select the files for the batch, click **Add Files**. Navigate to the files and select by clicking on the file. Select multiple files to add by holding down the Ctrl key while selecting the files.

- To remove files from the **Files to Process** list, click **Remove Files**.

7 If the files require spectral compensation, select the **Perform compensation** check box. The default matrix will be used if the box is left blank. Click **Change Compensation Matrix** and click the folder to browse for your .ctm file.

Option: To change the compensation values in the matrix



- Click on the coefficient to change and type in the number
- Click **Update Matrix**
- Click Save As A **New Matrix**
- Name the file and click **OK**

8 In the **Corrections** area, all corrections are checked by default. EDF deconvolution is performed on EDF files as required.

9 In the Output Options area, all options are checked by default.

- Apply cell classifiers: processes the objects in the file using the cell classifiers that were set during acquisition in INSPIRE.
- Separate single objects: separates objects that were collected as coincident events in INSPIRE. As objects are separated their object number will increment up and therefore the number of objects in the file will increase.
- Erase non-framed objects: replaces areas around the object that were occupied by the other objects in the frame as they are separated with background values.
- Remove clipped objects: removes objects that cross the edge of the channels.

10 Select the **Output Files Destination** option that you want:

Same as input file directory: writes files to the existing input file.

Select output directory: allows you to specify the folder.

Overwrite existing files: writes over existing files with the same name.

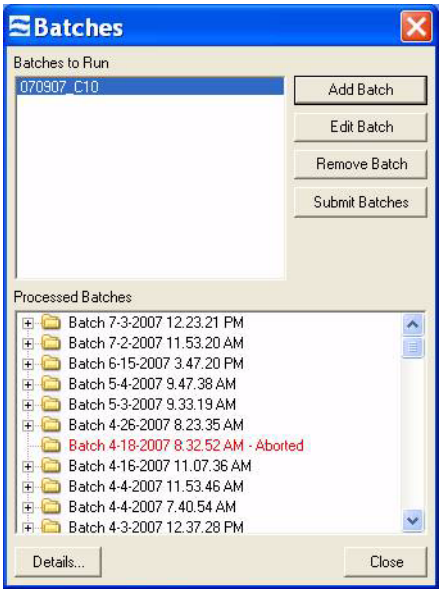
11 File Suffix allows you to specify a **Custom** suffix or the **Default** suffix. If an output file name already exists, but you did not select **Overwrite existing files**, the IDEAS application will include the suffix followed in all the output file names. You

will thus be able to identify all the files that were created by one instance of batch processing.

12 Select **Statistics Report Preview** if you have created a statistics report in your template that you want generated as part of the batch processing. Order the files as you wish them to be reported by selecting a file with a left-click, then right-click the desired position and select 'move here'. See "Creating a Statistics Report Template" on page 113 for more information.

13 Click **OK**.

The **Define a Batch** window closes. The batch appears in the **Batches** window.

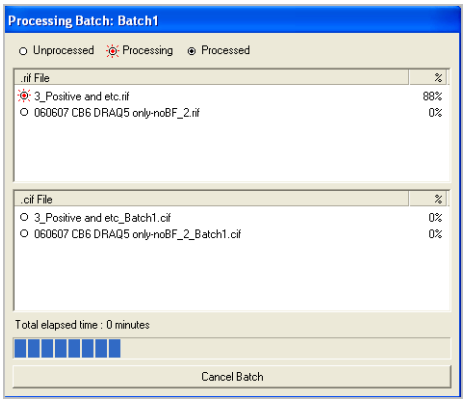


14 The Batches window offers the following options:

- **Add Batch:** If you want to create another batch to add to the list.
- **Remove Batch**: If you want to remove a batch from the Batches to Run list.
- **Edit Batch**: If you want to edit a batch in the Batches to Run list.

15 When you are satisfied with the Batches to Run list, click **Submit Batches**.

The files to process are listed and the progress is displayed in the Processing Batch window. Once you have started processing batches, it may use up a fair amount of your computer's processing power.



Tip: To cancel the batch processing at any time, click **Cancel Batch**. The IDEAS application will confirm cancellation and complete the file it is working on.

When the batch processing is complete, the IDEAS application saves the .rif, .cif, and .daf files in the batch results directory. In the Batches window, a list of processed batches appears in the Processed Batches list. If a batch did not successfully complete, it will appear in red.

Tip: To display the error that occurred during processing, double-click the batch.

16 If you want a batch report, double-click the batch in the Processed Batches list of the Batches window.

The Batch Results window appears.

17 In the Batch Results window, click **Print**.

18 In the Batch Results window, click **Close**.

19 In the Batches window, click **Close**.

Chapter 5

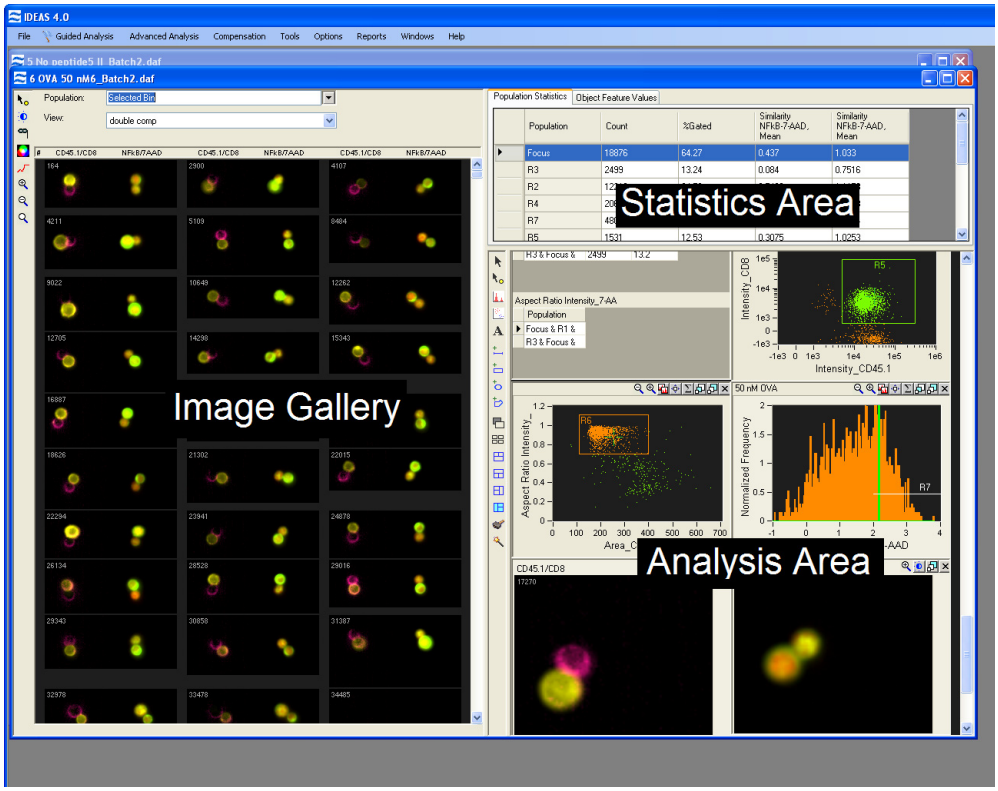
Using the Data Analysis Tools

This section describes how to view imagery; graph data; create populations by drawing regions in graphs, or by tagging objects; perform statistical analysis of data; and create new features.

Overview of the Data Analysis Tools

The IDEAS application provides a powerful tool set that allows you to explore and analyze data. The rich feature set lets you create hundreds of your own features to differentiate objects and statistically quantify your results.

As shown in the following figure, the application window is divided into three panels—Image Gallery, Statistics Area, and Analysis Area—which each provide the corresponding tools that you can use for data analysis. There are muliple window layouts with resizable panels.



You can create populations of objects by tagging hand-selected images, drawing regions on graphs, and using Boolean logic to combine existing populations. Another way to create a population of objects is by basing it on the similarity of a set of feature values to one or more cells in the data set. After you have created a population, you can view it in the Image Gallery or plot it on a graph. You can view the statistics for populations or objects in the Statistics Area.

Graphs show data plotted with one or two feature values, and tools are provided that allow you to draw regions for the purpose of generating new populations. You can show any population on a plot.

Selecting an individual data point in a graph allows you to view it in the Image Gallery or look at its feature values in the Statistics Area. Any object that is selected in the Image Gallery is also shown on the plots in the Analysis Area.

Using the Image Gallery

This section contains the following subsections, which describe how to view populations of objects in various ways, view masks, customize the Image Gallery display, and hand-select objects for a population:

"Overview of the Image Gallery" on page 59

"Setting the Image Gallery Properties" on page 62

"Working with Individual Images" on page 68

"Creating Tagged Populations" on page 69

Overview of the Image Gallery

The Image Gallery displays the imagery and masks of any population of objects.

A toolbar is provided in the upper-left corner of the panel, as shown in the following figure. The Image Gallery also makes different viewing modes available for the imagery. The default template contains the viewing modes which allows you to view all channel images in grayscale or color, or each channel image individually.

Tip: You can build custom viewing modes as shown in this example. For more information, see "Setting the Image Gallery Properties" on page 62.

Table 1: Image Gallery Tools

Tool	Description
Tagging Mode Tool	Allows you to create a population of hand-picked objects. See: "To create a hand-selected population" on page 69.
Image Gallery Properties Tool	Provides custom display features. See: "To customize the Image Gallery display properties" on page 63.
Show Segmentation Mask Tool	Displays masks on the imagery. See: "To show or hide masks" on page 60.
Show Color Tool	Sets the Image Gallery color. See: "To show or hide color" on page 61.

Table 1: Image Gallery Tools

Tool	Description
 Show Saturation Color Tool	Click on the tool and it will show any saturated pixels will turn red. See: "To show saturation" on page 61.
Zoom Tools 	Zoom in or out and reset zoom on the image gallery. See: "To zoom on the image gallery" on page 61

To view the imagery for a population

1 In the **Population** drop down menu of the Image Gallery, click the population that you want. (The list includes all the populations as well as the currently selected bin from a histogram.) To create a population, refer to "Creating Tagged Populations" on page 69.

2 To select an individual image, click it.

A thin, green frame indicates the selected object.

- The Statistics Area displays the object's feature values if an object is selected. See "Overview of the Statistics Area" on page 87.
- The Analysis Area identifies the object in each scatter plot graph with a green cross. See "Overview of the Analysis Area" on page 71.
- The image can be placed in the Analysis area by **right click>Display Single Image**.

  Tip: Conversely in the analysis area, clicking a graphical point causes the Image Gallery to highlight and display the corresponding object.

To change the viewing mode

- In the **View** drop down menu of the Image Gallery, select a specific view. The imagery display changes according to the new view. See "To customize the Image Gallery views images and masks" on page 65 for more information.

To show or hide masks

- Click the **Show Segmentation Masks** toolbar button to toggle between showing and hiding the selected masks for all images in the Image Gallery. See "To change the name or color for each image" on page 63 for more information.

  The mask is shown as a transparent cyan layer over each image.

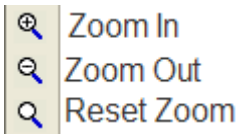
Tip: To hide the mask for a specific channel only, set the individual channel mask to None. For more information, see "Setting the Image Gallery Properties" on page 62.

To show or hide color

- Click the **Show Color** toolbar button to toggle between showing and hiding the colors for all images in the Image Gallery. See "To change the name or color for each image" on page 63 for more information.

To zoom on the image gallery

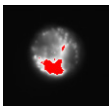
- Click the **Zoom In** toolbar button to view the images in the gallery closer and the **Zoom Out** or **Reset Zoom** to reverse the zoom.



To show saturation

- Click the **Show Saturation Color** toolbar button.

Saturated pixels in images, if any, appear in red.



Setting the Image Gallery Properties

When a new data file opens in the default template, you might find it difficult to clearly see cell morphology because the Image Gallery display properties have not yet been properly adjusted for the data set.

To optimize the display you may use the wizard "Display Properties:" on page 20 to set the pixel intensity mapping to the display range. Manual adjustment is described below.

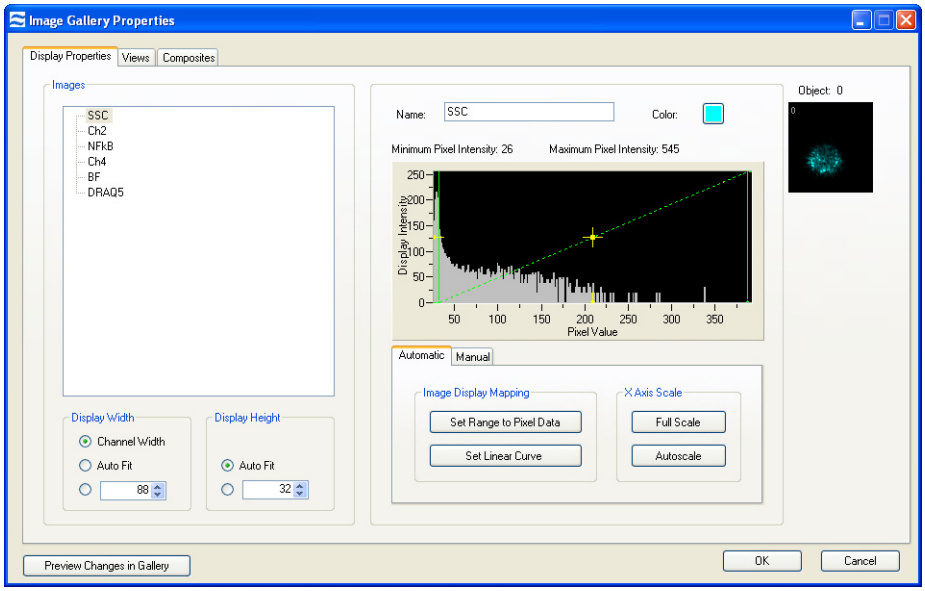
Clicking the **Image Gallery Properties** toolbar button opens the Image Gallery Properties window, which contains the following tabs:

- **Display Properties**—Allows you to define the name, color, and display intensity mapping for each image. Allows adjustment of the image size for the image gallery.
- **Views**—Allows you to customize the views for the Image Gallery.
- **Composites**—Allows you to create composites and adjust the amount of color from a channel that is included in a composite image.

To customize the Image Gallery display properties

1 Click the **Image Gallery Properties** toolbar button to begin.

The **Image Gallery Properties** window appears with the **Display Properties** tab displayed.



To change the size of the panels in the Image Gallery

1 Display Width and Display Height can be specified or changed to Auto Fit in the lower left section of this window.

To change the name or color for each image

1 Select an image in the list of images on the **Display Properties** tab of the **Image Gallery Properties** window.

2 On the right side of the window you can type a new, unique name for the selected image. Note that each image is provided with a default name and the image names appear near the top of the Image Gallery.

3 Click the colored square for the selected image.

4 Click the color that you want in the color palette.

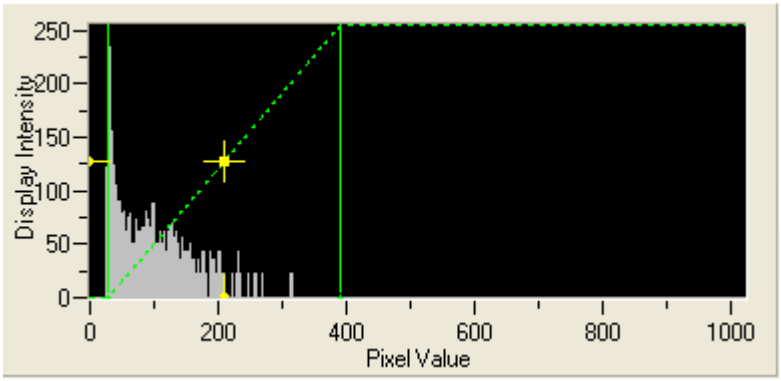
5 Click **OK** to close the palette.

Tip: The grayscale image in each channel is assigned a default color for image display in the gallery. Setting the color to white is equivalent to using the original grayscale image. The colors are also used to build composite images.

To fine-tune the image display intensity for an image

1 On the **Display Properties** tab of the **Image Gallery Properties** window, select an image by clicking the image name in the list. The graph for the currently selected image is shown in the window and updates as the changes are made. Select and image in the image gallery that has intensities for the image channel you are adjusting.

Note: You will adjust the **Display Intensity** settings on the graph (the Y Axis), the value of the display to (the X axis), the range of pixel intensities. The range of pixel intensities will depend on the instrument and the collection mode set during acquisition. The display range is 0–255; the range of intensities from the camera is 0–1023 (10 bits) for the first generation ImageStream or 0-4095 for the ImageStream^{X} or 0-32,767 for EDF mode collection. The limits of the graph enable you to use the full dynamic range of the display to map the pixel intensities of the image.



At each intensity on the X Axis of the graph, the gray histogram shows the number of pixels in the image. This histogram provides you with a general sense of the range of pixel intensities in the image. The dotted green line maps the pixel intensities to the display intensities, which are in the 0–255 range.

Manual setting is done by Click-dragging the vertical green line on the left side (crossing the X Axis at 0) allows you to set the display pixel intensity to 0 for all intensities that appear to the left of that line. Doing so removes background noise from the image.

Click-dragging the vertical green line on the right side allows you to set the display pixel intensity to 255 for all intensities that appear to the right of that line.

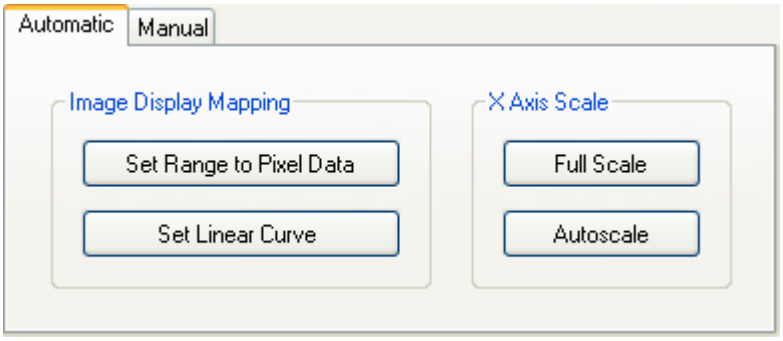
2 From the Image Gallery window, select the object to use for setting the mapping. It appears in the Image Gallery Properties window.

Tip: You might need to select different objects for different channels because an object might not fluoresce in all channels.

3 To adjust the pixel mapping for display, click-drag the vertical green line by clicking near it (but not near the yellow cross).

Tip: For fluorescence channels, set the vertical green line that appears on the left side to the dimmest pixel in the image and set the right vertical green line to the brightest pixel. To get a good mapping range, adjust the same line so that the yellow cross is centered among the pixel intensities on the X Axis. For the brightfield channel, set the vertical lines to about 50 counts to the right and left of the histogram to produce an image with crisp brightfield contrast.

- To change the mapping curve to be logarithmic or exponential, click-drag the yellow cross.
- To restore the mapping to a linear curve, Click **Set Linear Curve**.
- To see the full scale for the X Axis Click **Full Scale**.
- To set the display mapping of the X Axis to the lowest and highest values for a selected object, Click **Set Range to Pixel Data**.
- To set the scale of the X Axis to the range of the vertical green lines or of all the pixel intensities for the selected object—whichever is larger—Click **Autoscale**.
- You may enter values manually by selecting the **Manual** tab.



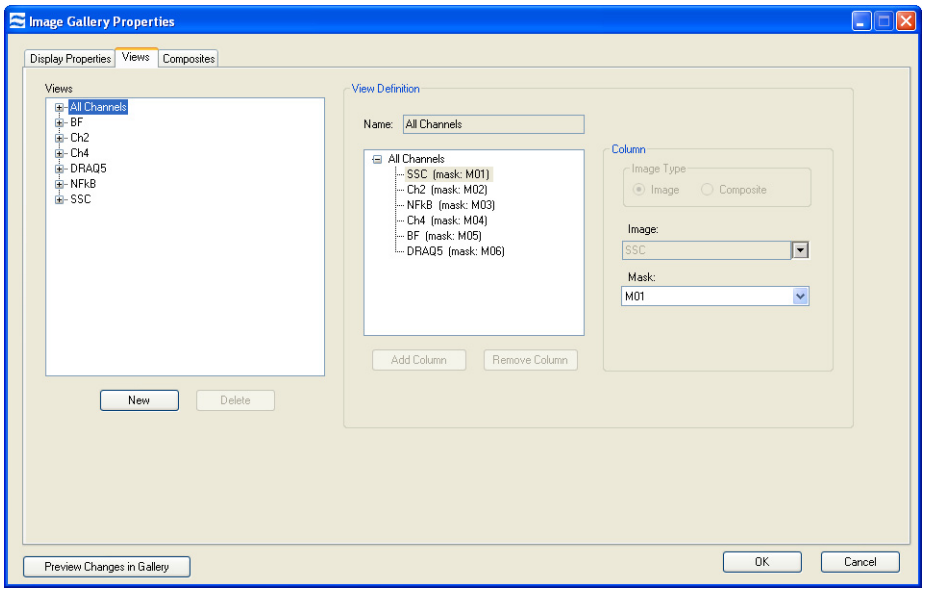
4 If you want to preview the changes in the Image Gallery, click **Preview Changes in Gallery**.

5 Continue customizing the Image Gallery display properties with another procedure in this section, or click **OK** to finish and save changes or **Cancel** to finish and discard changes.

To customize the Image Gallery views images and masks

1 Within the **Image Gallery Properties** window, click the **Views** tab.

Note: The Image Gallery view can be customized to view any combination of channel images or composites. The default view **All Channels** is a view that displays all image channels that were included during acquisition of the file with their associated default masks. This mask may be changed for the default view however, the images in this view cannot be changed.



2 To create a new view, Click **New**.

3 Type in a name for the view.

4 Click **Add Column**.

5 Define the column by selecting an image and a mask or a composite from the dropdown menu.

6 Repeat the previous 2 steps until finished adding columns to the view. A column will be added under the column currently selected. To insert a column click on the image above insertion point.

7 Columns may be removed by clicking on **Remove Column**.

8 A view may be edited at any time by selecting the view and following the same procedures.

9 If you want to delete a view, click the view to select it, and then click **Delete**.

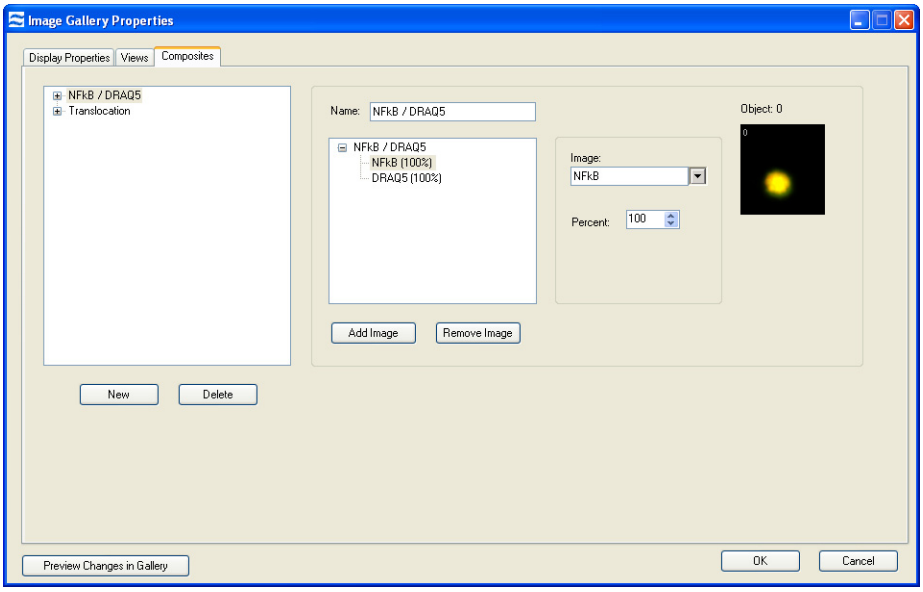
A confirmation window appears.

10 If you want to preview any new changes in the Image Gallery, return to the Image Gallery and choose your new view in the **View** drop down menu. Then return to the **Image Gallery Properties** window and click **Preview Changes in Gallery**.

11 Continue customizing the Image Gallery display properties with another procedure in this section, or click **OK** to finish and save changes or **Cancel** to finish and discard changes.

To create a composite

1 Within the **Image Gallery Properties** window, click the **Composites** tab.



2 Type a name for the composite or leave blank to allow the name to be built automatically from the image names added to the composite.

3 Click **Add Image**. The selected image appears in the **Object** box. Change the **Percent** if desired. The percent specifies the percentage of of the image to include in the composite.

Tip: As you make the changes, the image in the **Object** box updates accordingly. If you want to preview any new changes in the Image Gallery, return to the Image Gallery and select the **View** drop down menu to your new view. Then return to the **Image Gallery Properties** window and click **Preview Changes in Gallery**.

4 Continue to add images as desired.

5 To remove and image from the composite, Click **Remove Image**.

6 The composite is automatically added to the list .

7 A composite can be removed from the list by clicking **Delete**.

8 Continue customizing the Image Gallery display properties with another procedure in this section, or click **OK** to finish and save changes or **Cancel** to finish and discard changes.

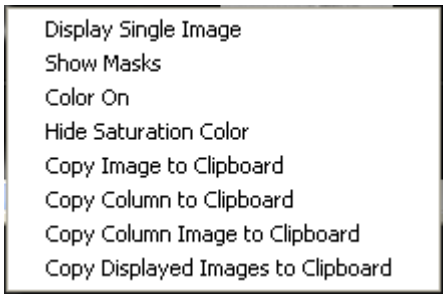
Working with Individual Images

You can work with individual images in the Image Gallery. You can zoom in or out on the images. You can add a larger version of an image to the Analysis Area for further analysis, show or hide masks for a single image in the Image Gallery, and copy one or more images to the Clipboard.

To manipulate individual images

1 In the Image Gallery, right-click an image that you are interested in.

A menu appears.

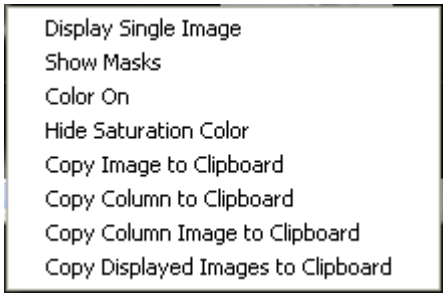


- To place the image in the Analysis Area, click **Display Single Image**. (For more information, see "Analyzing Images" on page 83.)
- To show or hide the masks for the object image, click **Show Masks** or **Hide Masks**, respectively. (One or the other will appear depending on the current state.)
- To turn the colors on or off for the object image, click **Color On** or **Color Off**, respectively.(One or the other will appear depending on the current state.)
- To show or hide the saturation color for the object image, click **Show or Hide Saturation Color** respectively.(One or the other will appear depending on the current state.)

To copy images for use in reports

1 In the Image Gallery, right-click an image that you are interested in.

A menu appears.



- To copy the image to the Clipboard, click **Copy Image to Clipboard**.
- To copy the single channel image to the Clipboard, click **Copy Column Image to Clipboard**.

- To copy the single channel image for all of the displayed images to the Clipboard, click **Copy Column to Clipboard**.
- To copy all the visible images in the Image Gallery to the Clipboard, click **Copy Displayed Images to Clipboard**.

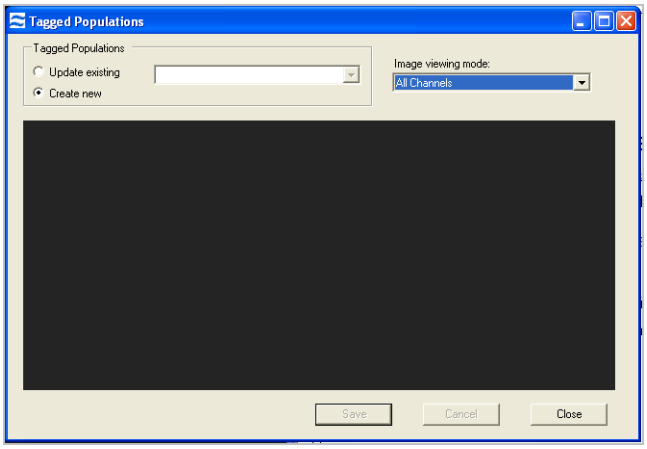
Creating Tagged Populations

You can hand-select objects from either the Image Gallery or a graph and group them into a population.

To create a hand-selected population

1 Within the Image Gallery, click the Tagging Mode toolbar button to begin.

The **Tagged Populations** window appears.



2 Select either **Update existing** or **Create New.**

- To **Create New**, double-click images within the Image Gallery and select **Save**. Create a new population name and display properties in the **Create a New Population** window.

3 If you selected **Update existing**, choose a population to update in the drop down menu.

4 In the **Image viewing mode** list, choose the mode that you want from the drop down menu. See "To customize the Image Gallery views images and masks" on page 65 for more information.

5 To add or remove an image from the tagged population, double-click either the image in the Image Gallery or a dot in a bivariate plot.

The selected channel image for each tagged cell is displayed in the viewing area of the Tagged Populations window. In the Image Gallery, a small smiley-face icon appears on the left side of each tagged image. Each tagged object is also displayed as a yellow star in a graph in the Analysis Area.

6 If you are updating an existing population, click the **Update** button in the Tagged Populations window.

7 When you are finished, click **Close** in the Tagged Populations window.

Note: The tagging mode remains open until you click **Close**, and as long as the Image Gallery is in tagging mode, you cannot create, resize, or move any regions on the graphs.

Using the Analysis Area

This section contains the following subsections, which describe how to create graphs, analyze images, and use text panels in the Analysis Area of the IDEAS application:

"Overview of the Analysis Area" on page 71

"Creating Graphs" on page 73

"Creating Regions on Graphs" on page 77

"Analyzing Images" on page 83

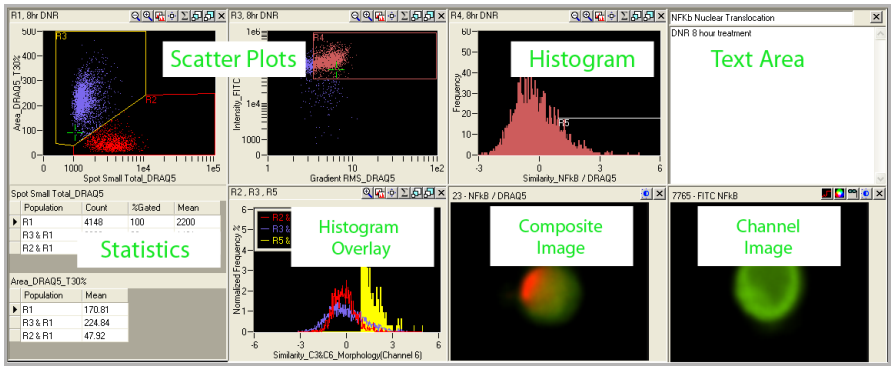
"Adding Text to the Analysis Area" on page 86

Overview of the Analysis Area

The Analysis Area provides display space for individual images, plots of cellular feature values, visualizations of population distributions and statistics, and text annotations. You can select different layouts for the IDEAS window and placement of the analysis area and expand the Analysis Area by dragging it's boundaries.

The Analysis Area is divided into panels of a fixed size. The size of the panels is automatically adjusted to fit in the available display space. A vertical scroll bar appears when the number of panels exceeds the space available on the window.

As illustrated by the following figure, the Analysis Area can contain seven types of panels: histogram, histogram overlay, scatter plot, channel image, composite image, and text. Each panel will contain its own toolbar and context menu. To move a panel click on the bar at the top and drag to another location.



A toolbar is visible on the left side of the Analysis Area. The following table describes the function for each tool..

Table 2: Analysis Area Tools

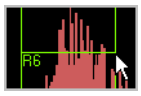
Tool	Description
Pointer Tool	Provides the normal mode of interaction with the graphs. Clicking a point on a scatter-plot graph causes the IDEAS application to display the corresponding image in the Image Gallery (if the population that is currently displayed in the Image Gallery contains that point). Click an image to display the corresponding statistics in the Statistics Area. Click the top of a bin in a histogram to select the bin. In the Image Gallery, you can view images of cells in the bin by clicking the Selected Bin population. Click Pointer Tool while drawing a region on a graph to cancel the creation of a region.
Tagging Tool	Allows you to create a population of hand-picked objects. For more information, see "Creating Tagged Populations" on page 69.
New Histogram Tool	Creates a new histogram. Refer to "To create a graph" on page 73.
New Scatter Plot Tool	Creates a new scatter plot. Refer to "To create a graph" on page 73.
Text Tool	Allows user to add text notes to the Analysis Area. Refer to "Adding Text to the Analysis Area" on page 86.
Line Region Tool	Draws a horizontal line on a histogram to define a region. 
Rectangle Region Tool	Draws a rectangular region on a scatter plot.
Oval Region Tool	Draws an oval region on a scatter plot.
Polygon Region Tool	Draws a polygon region on a scatter plot graph. Each click starts a new segment in the polygon until the entire image is double-clicked to complete the region.

Table 2: Analysis Area Tools

Tool	Description
 Graph Bkgd Tool	Changes the background of the graphs to black or white.
 Tile Graphs Tool	Tiles graphs in the analysis area after changing the size of the analysis area to fit all graphs to the new space.
 Layout Tools	Chooses a layout for the IDEAS window.
 Building Blocks Tool	Short-cut to using Building Blocks for guided analysis.
 Wizards Tool	Short-cut to using Wizards for guided analysis.

Creating Graphs

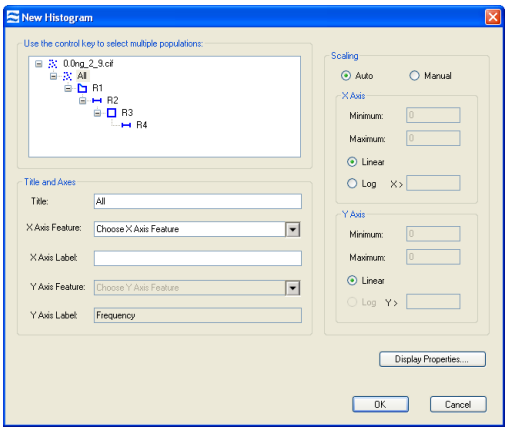
You can add two types of graphs to the Analysis Area:

- Histogram—Graphs a single feature.
- Scatter Plot—Graphs two features.

To create a graph

1 Click the New Histogram or New Scatter Plot toolbar button.

The New Histogram or New Scatterplot window appears, respectively.



2 Select the one or more populations to graph by clicking them. To select more than one population, use the Ctrl key.

The title defaults to the selected population. You can edit the title.

3 In the **X Axis Feature** drop down menu, select the feature that you want to graph on the X Axis.

4 If you want to change the label for the X axis, edit the text in the **X Axis Label** field.

The label defaults to the name of the selected feature.

5 If you are creating a scatter plot, select a feature and a label for the Y Axis.

6 Set the scaling for each axis of the graph. (The default is **Auto**, which allows the application to automatically scale the graph.)

7 To set minimum and maximum values for an axis, select **Manual**.

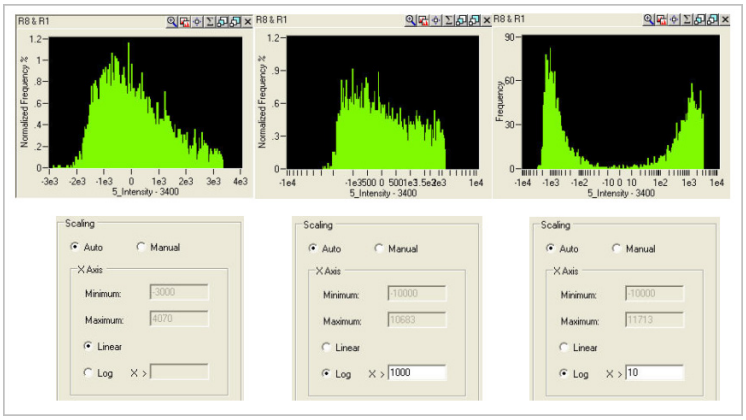
8 Select **Linear** or **Log** and enter **Maximum** and **Minimum** limits.

9 If you selected **Log**, enter the **X >** value.

Note: You can scale the X Axis of a graph or the Y Axis of a scatter plot in one of two modes: **Linear** or **Log**. The Linear mode is the default.

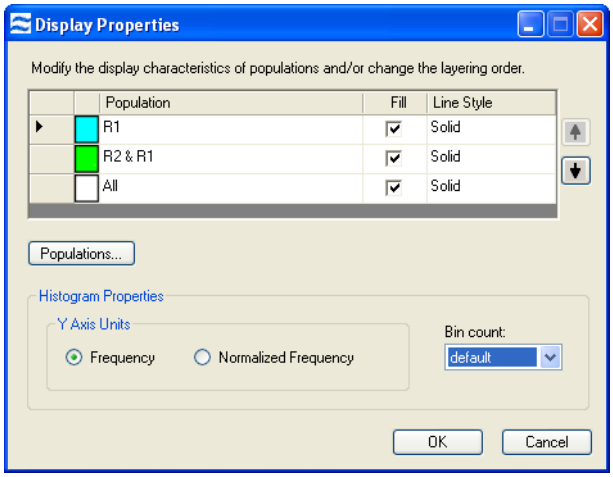
The **Log** mode allows you to logarithmically scale a section of the graph or scatter plot. Selecting this mode causes the IDEAS application to perform bi-exponential plotting. The > X value defines the linear portion of the graph as -X through X. The application plots the values outside of these limits on a logarithmic scale. You can plot negative values as well as positive ones on a logarithmic scale by adjusting the limits.

Take care not to split a population such that it appears to be two separate populations. This splitting is especially likely when negative values exist due to compensation or corrections on the imagery. The graph on the left side was plotted on a linear scale; the ones in the center and on the right side were plotted on logarithmic scales. The graph on the right side split the population because the change from a linear to a logarithmic scale occurred in the middle of the population. The IDEAS application automatically chose 1000 for the scale of the graph that is in the center.



10 To modify the display characteristics of each population or to change the layering order, click **Display Properties**.

The **Display Properties** window opens.



11 Arrange the layering of the populations with the up and down arrows to allow them to be displayed.

12 If you want, click **Populations**... to open the **Population Manager**. (For more information, see "Using the Population Manager" on page 106.)

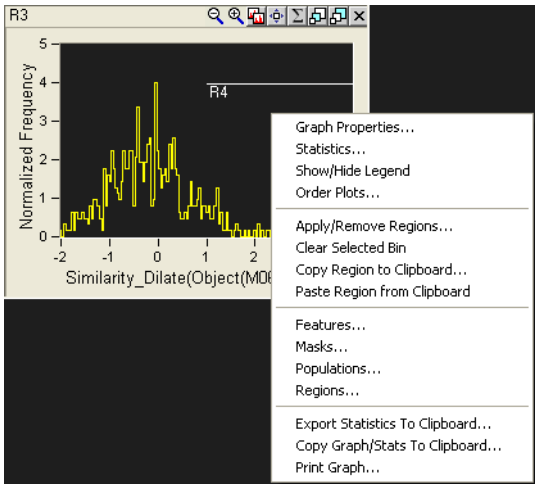
13 If you are creating a histogram overlay, you can customize it by performing the following steps:

- To fill or not fill the line for a population, select or clear the **Fill** checkbox.
- If you want, change the **Bin count**. (The default is determined by the X Axis scale of the plots.)
- Decide whether to plot the **Y Axis Units** as a **Frequency** or a **Normalized frequency** percentage.

14 Click **OK** in each window.

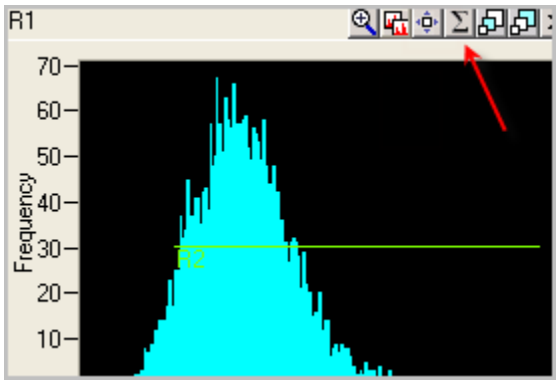
Tip: After you have created a graph, you can change its properties by right-clicking the graph and selecting **Graph Properties**. The same window that you used

to create the graph will reappear, and you can then make any changes that you want.



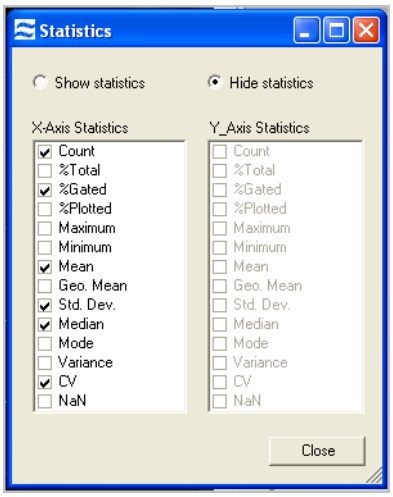
To show selected statistics for a graph

1 You can show and hide statistics is by clicking the Statistics toolbar button in the panel that contains the graph.



2 Or, right-click anywhere on the graph, and, click **Statistics** on the graph context menu that appears.

The **Statistics** window appears.



3 To display the statistics for the graph, select **Show statistics**. To close the Statistics Area for the graph, select **Hide statistics**.

4 Select the statistics that you want to display. The selected statistics will be displayed for each population on the graph. (For a complete definition of all the statistics, see "Using the Statistics Area" on page 87.)

5 When finished, click **Close**.

To show the legend for a graph

1 Right-click anywhere on the graph, and click **Show/Hide Legend** on the graph context menu that appears.

If the legend was hidden, it appears on the graph. If the legend was shown, it disappears from the display.

Note: The legend contains an entry for each population on the graph. If the graph is a scatter plot, the legend shows the population and its associated point style and color. If the graph is a histogram or overlay histogram, the legend shows the population name, associated color, and line type.

- To move the legend, click and drag it. (You cannot drag the legend past the boundary of the graph panel.)

Moving a Graph

- With any graph in the Analysis Area, you can move it to another location by clicking in the upper section of the graph and dragging it.

Creating Regions on Graphs

Regions may be drawn on graphs to create new populations, based on the physical location of objects on a graph, and to compute statistics. Tools for drawing regions are

found on the Analysis Area toolbar. A line region may be drawn only on a histogram. All other types of regions may be drawn only on a scatter plot.

A region can be copied to another graph in the same file or other open files. Regions may also be copied from one instance of the IDEAS application to another.

When you draw a region on a histogram or scatter plot, you create a population of objects defined by the region that may be viewed in the Image Gallery or on other graphs.

To change the attributes of a region or delete a region and the populations dependent on that region see "Using the Region Manager" on page 109 .

To draw a region on a Scatter Plot

On the Analysis Area toolbar, click either the:

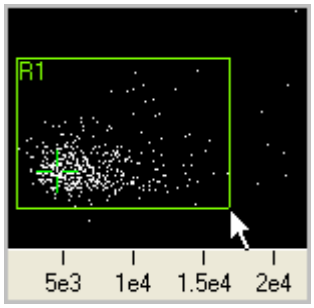
- Rectangle Region, or

- Oval Region, or

- Polygon Region button on the Analysis Area toolbar. Refer to "Polygon Tool Option" on page 79 for more details.

1 The Rectangle and Oval tools work by clicking on the graph at the point where you would like to start the region, and drag to the region endpoint.

The region grows as you drag.



2 Click again to complete the region.

If you are drawing a region on a histogram or scatter plot, the **Create a Region** window appears.

3 Name the region.

4 Click the colored box to select an alternate color.

5 Select **Use for statistics only** if you do not want to create a population from this region.

6 Click **OK**.

The region appears on the graph with the name and color that you selected.

Polygon Tool Option

1 The Polygon tool works by clicking the scatter plot at the point where you would like to start the polygon.

2 Click once for each vertex of the polygon.

3 Double-click to complete the drawing of the region.

A window appears that allows you to name the population created by the polygon region and to assign the region's display properties.

4 Click **OK**.

The region appears on the graph with the name and color that you selected.

Tip: Before you click **OK**, you can click **Cancel** or you can click the Pointer button on the Analysis Area toolbar if you decide not to create the region.

To Draw a region on a Histogram

1 On the Analysis Area toolbar, click the Line Region tool.

2 Drag the line across the histogram.

To move or resize a region on a graph

1 Click the Move/Resize Region toolbar button on the graph panel toolbar.

2 Click the region that you would like to move or resize.

When the region is selected, squares that can be moved appear at the vertices and the label.

3 The first time that you drag the region, the entire region and label move.

4 Dragging a specific vertex or label moves only that vertex or label.

5 To finish moving or resizing the regions on the graph, click the Move/Resize Region toolbar button again.

The populations and statistics are updated, and the Move/Resize Region toolbar button is deactivated.

Note: The recalculation of statistics and populations may take a moment if the data file is large or if many populations are dependent on the regions that are being moved or resized.

To zoom in on the scale of a graph

1 Click the Scaling toolbar button on the graph panel toolbar.

2 Click and drag to define a rectangular region for rescaling.

The Zoom Out Scaling toolbar button appears in the graph panel toolbar, next to the Scaling toolbar button.

3 Click the Zoom Out Scaling toolbar button to automatically scale the graph.

The Zoom Out Scaling toolbar button is removed from the graph panel toolbar.

To resize a graph

- Click the sizing buttons on the graph panel toolbar. (A graph may be resized from small (the default) to medium or large. The two options that are not currently in use are available on the toolbar.)

To copy and paste a region to another graph

1 Right-click anywhere on a graph, and click **Copy Region to Clipboard** on the graph context menu that appears.

   The **Copy a Region to the Clipboard** window appears.

2 Click the region to copy in the list, and click **OK**.

3 Right-click on the graph where you want to paste the region, and click **Paste Region from Clipboard** on the graph context menu that appears.

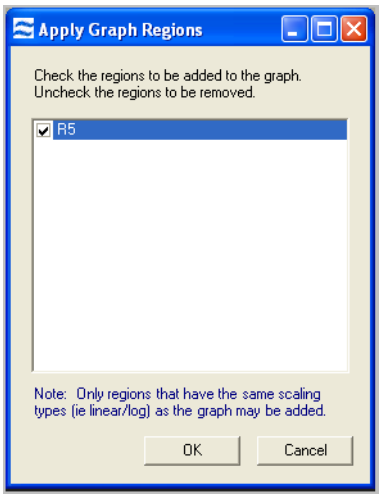
4 If the region already exists (in other words, you are copying it within the same instance of the application), the **Create a Region** window appears.

5 Rename the region and set the display properties for the resulting new population, and click **OK**.

   Note: When you copy a region, the scale is copied and is no longer associated with the feature from which it was originally drawn. Therefore, the region might not fit on the new graph.

To Apply or Remove a region on a graph

1 Right-click anywhere on the graph, and click **Apply/Remove Region** on the graph context menu that appears. The **Apply Graph Regions** window appears.



2 Select the regions that you want to appear on the graph.

3 Clear the regions that you want to remove from the graph.

4 Click **OK**.

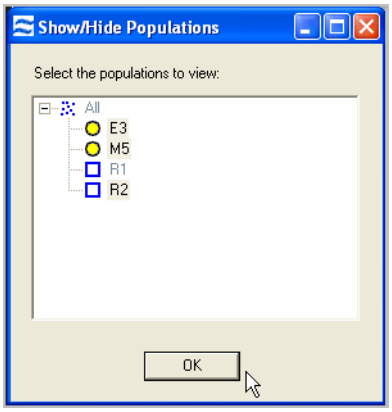
To show or hide a population on a scatter plot

1 Click **Show/Hide Populations** on the graph context menu.

The **Show/Hide Populations** window appears.

2 Select the populations that you want to appear on the graph.

3 Clear the populations that you want to remove from the graph.



4 Click **OK**.

Tip: On a scatter plot, you may show or hide any population on the graph—regardless of the features on the axes. Each scatter plot has an original, or base, pop-

ulation. When you show a population on a scatter plot, only those objects that are also in the base population will be shown.

Analyzing Images

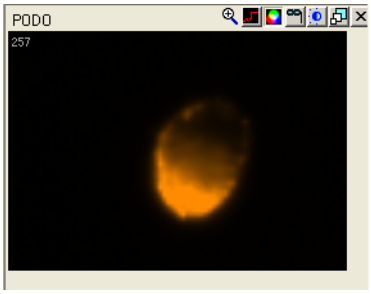
To analyze an image in more detail, place the image in the Analysis Area to view pixel positions and intensities as well as generate statistics for an area of the image. You can also show the Measurement tool for the image.

Image panels, which are shown in the following figure, each contain a toolbar in the upper-right corner and a context menu that appears when you right-click an image. An image in the Analysis Area is three times the size of an image in the Image Gallery.

To add an image panel to the Analysis Area

- Right-click an image in the Image Gallery or Analysis Area, and click **Display Single Image** on the context menu that appears.

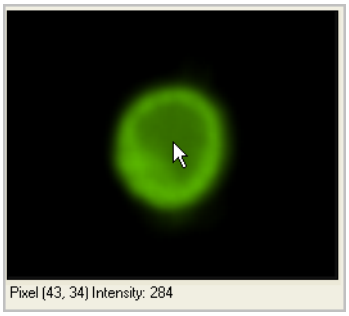
  The image panel appears in the Analysis Area.



To view the individual pixel intensities of a single channel image

- Move the mouse pointer across the image.

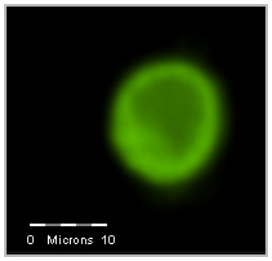
  The pixel positions and intensities appear under the image. (The pixel (0, 0) is positioned at the upper left of the image.)



To display the Measurement tool in an image panel

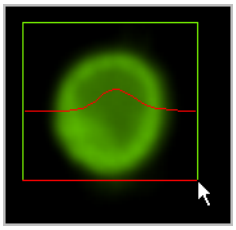
- Right-click the image panel, and click **Show Measurement Tool** on the context menu that appears.

  The 10-micron bar appears.

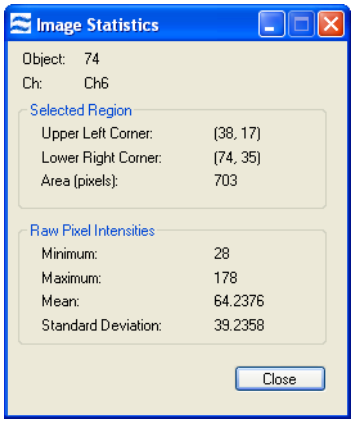


To examine a line profile or the statistics for an area of an image

- Click and drag to create a boxed area on the image.



The **Image Statistics** window appears next to the image panel. The statistics are calculated for the area that is defined by the box. The line profile (the wavy line in the image panel) represents the pixel intensity at each position along the red line of the box.

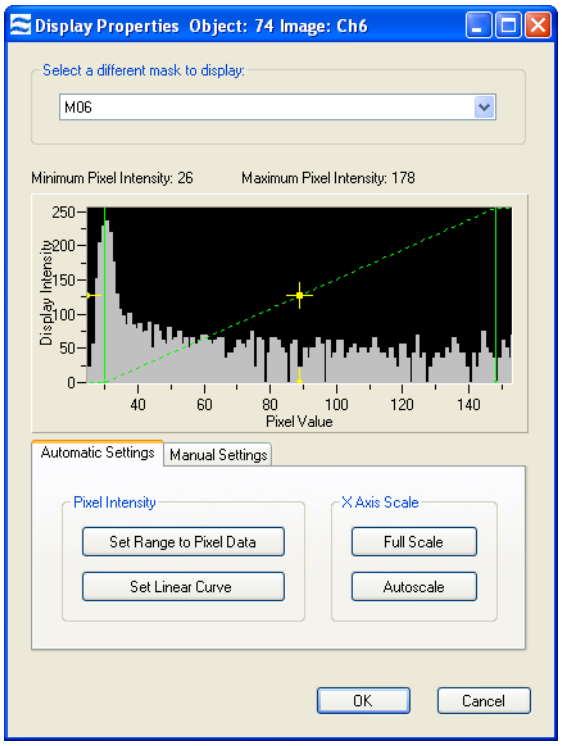


To change the display properties of an image

1 Click the Channel Display Properties button on the image panel toolbar.

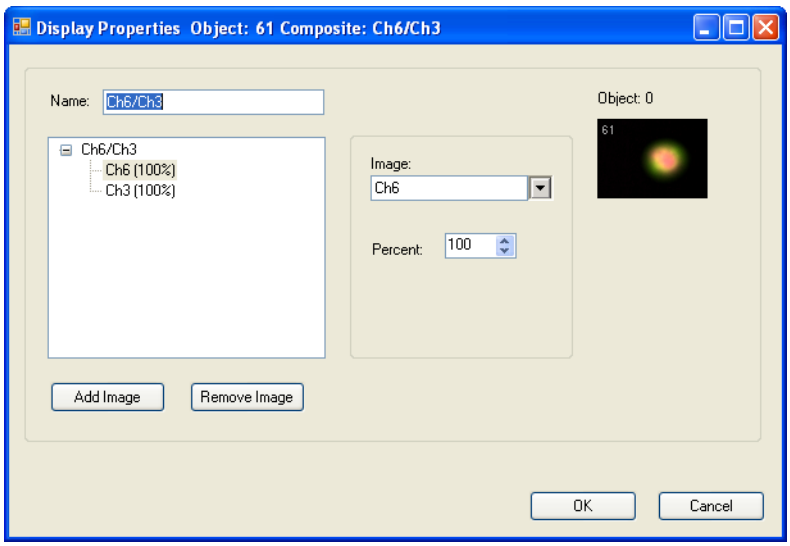
The **Display Properties** window appears.

- For single channel image, you can change the displayed mask and adjust the display intensity mapping. For more information, see "Setting the Image Gallery Properties" on page 62.



- For a composite image, you can change the images in the composite and adjust the percent contribution of each image, see "Setting the Image Gallery Properties" on page 62.

2 Click **OK**.



To show or hide the mask for a single channel image

- Click the Mask button on the image panel toolbar, or right-click the image and then click **Show/Hide Mask** on the image context menu.

The mask appears as a transparent cyan overlay on the image.

To turn the color on or off

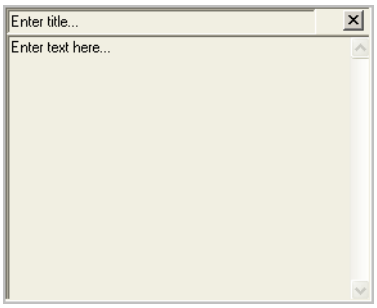
- Click the Color button on the image panel toolbar, or right-click the image and then click **Color Off** or **Color On**.

Adding Text to the Analysis Area

To add text to the Analysis Area

1 Click the Text button on the Analysis Area toolbar.

A text panel appears.



2 Type a title and text.

Using the Statistics Area

This section contains the following subsections, which describe how to view the population statistics, the object feature values, and the compensation matrix:

"Overview of the Statistics Area" on page 87

"Viewing the Population Statistics" on page 87

"Viewing the Object Feature Values" on page 90

Overview of the Statistics Area

The Statistics Area allows you to view both multiple feature values for an object and population statistics. Feature values and population statistics are presented in tabular form, rather than graphical form. You can copy data from the Statistics Area to the Clipboard as well as export the data to applications such as Microsoft Excel® and Microsoft Word®.

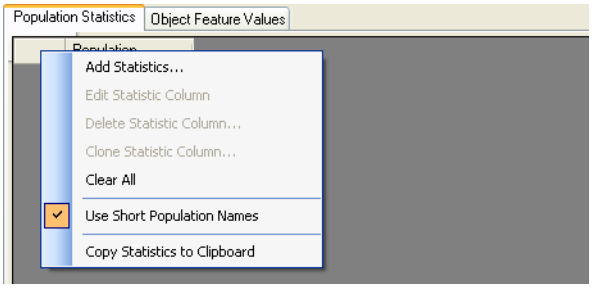
Viewing the Population Statistics

The **Population Statistics** tab displays selected feature values and statistics for chosen populations. The statistics that are supported are the Count, Percent Total, Percent Gated, Percent, Mean, Median, Standard Deviation, MAD (Median Average Deviation) RD -Mean, RD -Median, CV, Minimum, Maximum, Geometiric Mean, Mode, variance, and NaN (not a number).

To view and customize the population statistics

1 Click the **Populations Statistics** tab in the Statistics Area.

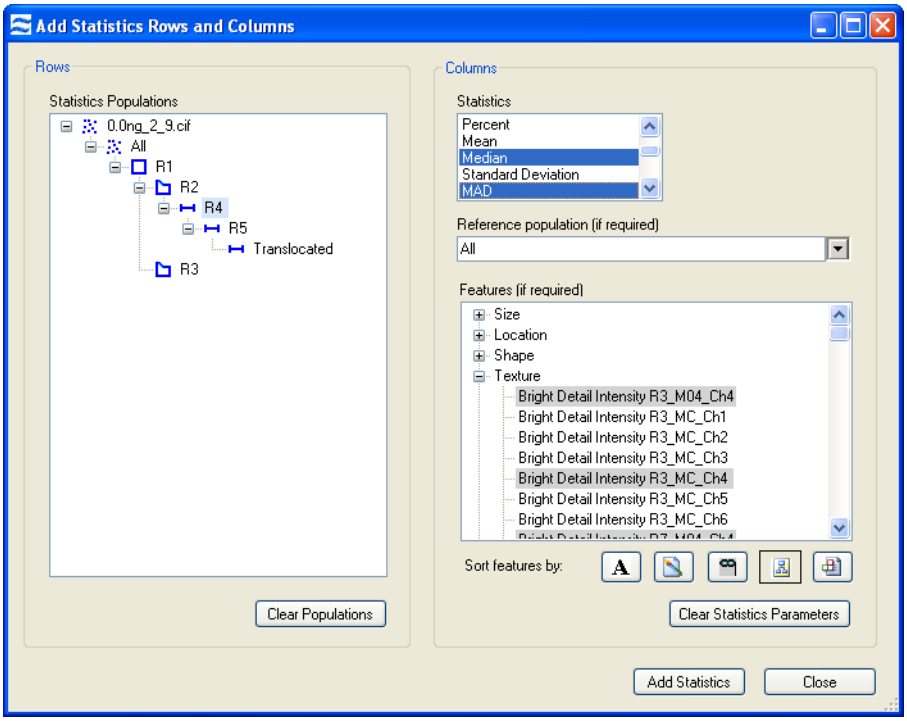
2 Right-click anywhere in the tab and the menu opens.



Use Short Population Names is enabled by default. This will display only the last part of the population name and not the entire tree. For example the short name for Population R1 &R2 &R3 &R4 is R4.

3 Select **Add Statistics**

The **Add Statistics Rows and Columns** window appears.



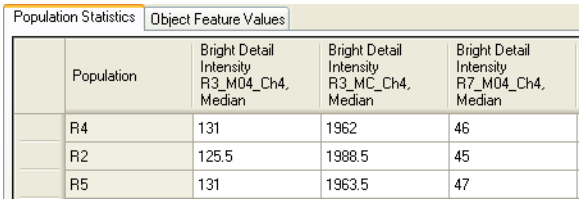
4 Select the populations from the list under Rows.

5 Select the statistics from the list under Columns. If a statistic requires a reference population (percent, RD) choose one.

6 Click **Add Statistics**.

7 The Statistics are added to the statistics table for each population.

8 Click **Close**.

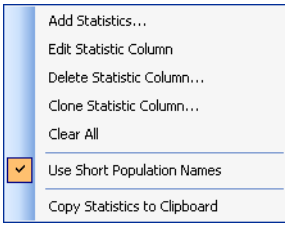


	Population	Bright Detail Intensity R3_M04_Ch4, Median	Bright Detail Intensity R3_MC_Ch4, Median	Bright Detail Intensity R7_M04_Ch4, Median
	R4	131	1962	46
	R2	125.5	1988.5	45
	R5	131	1963.5	47

9 Rows can be deleted by highlighting the row and using the delete key.

10 Rows or columns can be moved by click-dragging.

11 Right-click anywhere in the table to open the menu.



12 Edit Statistic Column opens a Statistics Properties window to enable changes to the statistic.

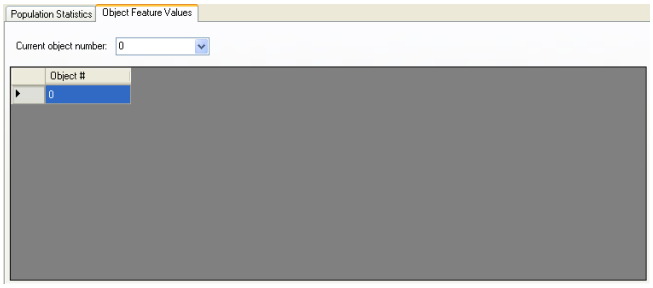
13 Clone Statistic Column opens a Statics Properties window to create a new statistic with the same parameters. This is a quick way to make a statistic that shares some parameters with the original by changing the desired parameters.

14 Clear All removes all of the statistics from the table.

15 Copy Statistics to Clipboard copies the table in a text format that can be pasted into other programs such as Excel.

Viewing the Object Feature Values

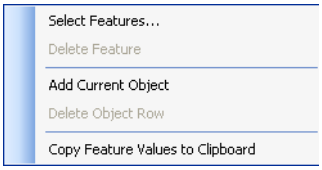
The **Object Feature Values** tab, which is shown in the following figure, displays a selected set of feature values for selected objects. For each feature, the name, value, and description are shown.



To view and customize the features shown on the Object Data tab

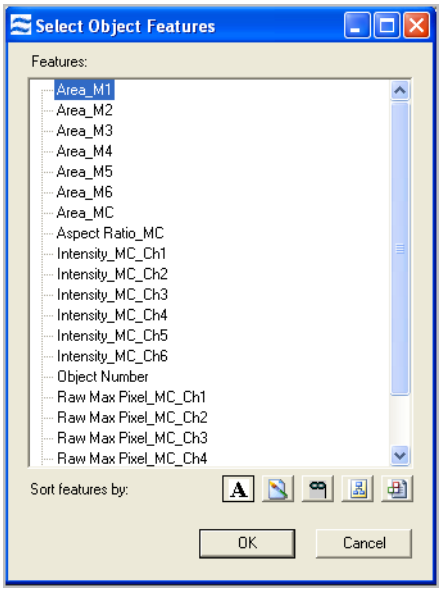
1 Click the **Object Feature Values** tab in the Statistics Area.

2 Right-click anywhere in the tab area to open the menu.



3 Choose **Select Features**.

The **Select Object Features** window appears.



4 Select the features to view.

5 Click **OK**.

The features appear on the Object Data tab.

6 To add selected objects to the table right-click and choose **Add Current Object**.

7 Rows and columns can be moved by click-dragging.

To export or copy statistics

- Right-click the statistics or features shown, and then click **Copy feature values to clipboard**. For more information, see "Exporting Data" on page 116.

Using the Mask Manager

This section contains the following subsections, which describe how to create, edit, and delete a mask:

"Overview of the Mask Manager" on page 92

"Creating New Masks with the Mask Manager" on page 92

Overview of the Mask Manager

A mask defines a specific area of an image to use for displaying feature-value calculations. The IDEAS application contains a Mask Manager for viewing existing masks and creating new ones.

When the IDEAS application loads a .rif file, the application creates a segmentation mask for each channel image and stores the mask along with the image in the .cif file. The masks, labeled M1 through M6, contain pixels that are detected as brighter than the background. In addition, the application generates a Combined Mask, named MC and a Not Combined Mask, Not MC for each object. A combined mask consists of the union of the masks of all the channels of the object. A Not Combined Mask is all of the pixels with no intensities above background.

You might need to adjust the masks or create new ones that include only a specific area of a cell, such as the nucleus. You can combine masks by using Boolean logic, or you can adjust them by applying functions.

Creating New Masks with the Mask Manager

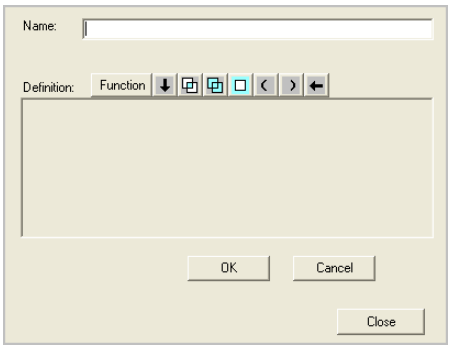
There are two ways to work with new masks in the Mask Manager. First, masks can be created by using functions, which allows you to choose an input mask and, if needed, adjust the channel and scalar input. Alternatively, masks can be created by combining masks through Boolean logic.

To create a new mask using Functions

1 Select **Analysis** > **Masks**.

2 Click **New**.

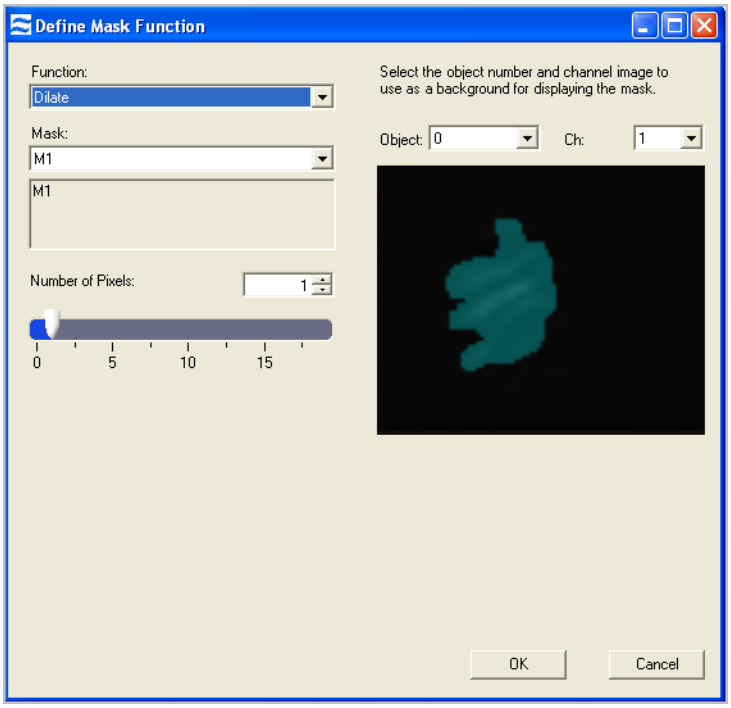
The Name box and Definition toolbar become enabled.



3 Click **Function**.

The Define Mask Function window appears with 13 available masks to use.

- **Dilate**: See "Dilate Mask" on page 193
- **Erode**: See "Erode Mask" on page 193
- **Inspire**: See "Inspire Mask" on page 194
- **Intensity**: See "Intensity Mask" on page 194
- Interface: See "Interface Mask" on page 195
- **Morphology**: See "Morphology Mask" on page 196
- **Object**: See "Object Mask" on page 196
- **Peak**: See "Peak Mask" on page 197
- **Range**: See "Range Mask" on page 197
- **Skeleton**: See "Skeleton Mask" on page 198
- **Spot**: See "Spot Mask" on page 199
- **System**: See "System Mask" on page 201
- **Threshold**: See "Threshold Mask" on page 202
- **Valley**: See "Valley Mask" on page 203



4 Select a mask and change the scalar parameters as needed. The right side of the window adjusts the display and view of the channel image.

- To view a different object in the file, select it in the **Object** list.
- To view a different channel image for the object, select it in the **Ch** list.

5 Click **OK.**

6 The new function is added to the mask definition.

7 Click **OK**.

8 Review your information and click **OK**.

The new mask name will appear in the list of Masks on the left side.

To create a new combined mask

1 Select **Analysis** > **Masks**.

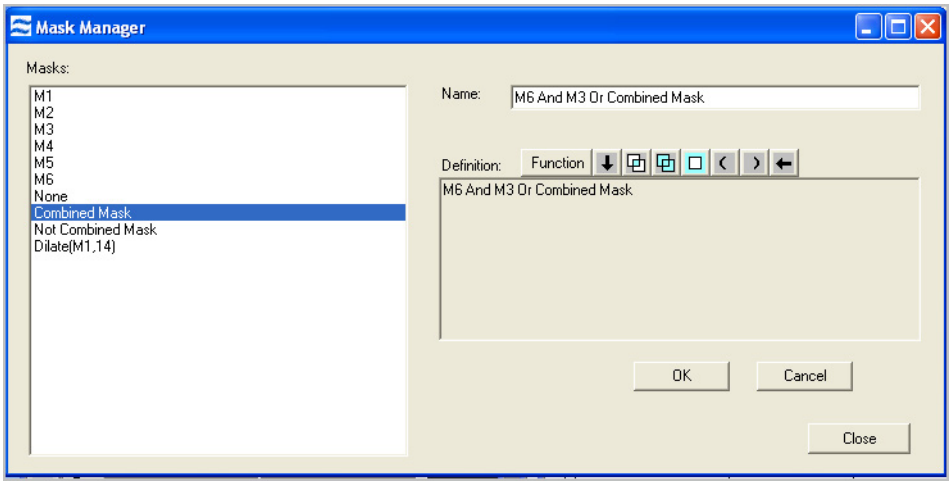
2 Click **New**.

The Name box and Definition toolbar become enabled.

3 Use the **Masks** list on the left and the **Definition** toolbar to build a new mask using the definitions of existing masks with Boolean logic explained in the table below.

Table 3: Mask Tasks and Toolbar

Task	Toolbar
Add a mask to the definition.	Double-click the feature in the **Masks** list. Or, single click the feature in the **Masks** list and click the leftmost down-arrow button on the toolbar. 
Combine two masks.	Use the Boolean AND or OR operator.  Use the AND operator to include only the pixels that are in both of the original masks.  Use the OR operator to include the pixels that are in either one of the original masks.
Select all pixels that are not in the original mask.	Use the Boolean NOT operator.  The NOT operator specifies which mask will not be used.
Affect the order of operations.	Use the parentheses toolbar buttons. 
Remove an item from the end of the definition.	Click the left-arrow button on the toolbar. 



4 Add masks and Boolean logic to the definition as needed.

5 Click **OK** to add the definition to the Masks list.

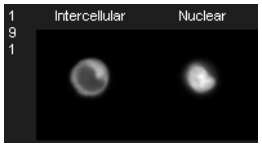
6 Click **Close**.

Example of Creating a Mask

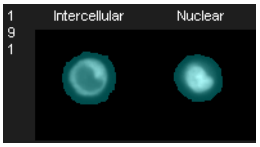
Here is an example of creating a mask of the cytoplasmic membrane.

In this example, cells were stained with a green intracellular marker (in Channel 3) and a red nuclear dye (in Channel 5). You can generate a cytoplasm-specific mask by first refining the intracellular and nuclear masks and then removing the nuclear mask pixels from the intracellular mask.

Grayscale Images
Channel 3 Channel 5



System Masks (Turquoise Overlay)
Mask M3 Mask M5



1 Observe the system masks in the Image Gallery. Since the system masks are designed to capture all the light in an image, they tend to include light that exists beyond the perceived boundaries of the images. In this case, both the intracellular and nuclear masks need to be refined. Start by creating morphology contour masks for both channel images because the Morphology mask is designed to conform to the shape of the image.

2 Select **Analysis** > **Masks**.

3 Click **New**.

4 Click on the Function toolbar button to adjust the mask that will define the whole cell. The **Define Mask Function** window appears.

5 Select Morphology in the Function list.

6 Select a starting Mask.

7 Select Channel 3 (intracellular marker) on the left side of the window.

8 Click **OK**.

9 Click **Set Default Name** or, enter a new mask name.

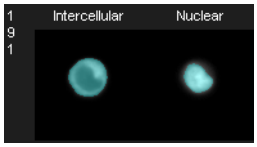
10 Click **OK** to add this mask to the list.

11 To make the Morphology(Nuclear) mask, repeat steps 3–10 using Channel 5.

12 Click **Close**.

13 To view the resulting morphology masks, open the Image Display Properties window and, if necessary, select the new mask for the channel.


(Icon for Image Display Properties)



14 Next, you will subtract the nuclear morphology mask from the intracellular mask. In the Mask Manager window, click **New**.

15 Double-click Morphology(Intracellular) in the Masks list.

16 Click the AND button on the toolbar.

17 Click the NOT button on the toolbar.

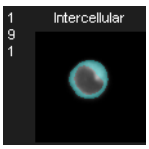
18 Double-click Morphology(Nuclear) in the Masks list.

19 Enter a new mask name.

20 Click **OK** to add this mask to the list.

21 Click **Close**.

22 To view the resulting mask on a Channel 3 image, open the Image Display Properties window and select the new mask for the channel.



23 You can further refine this mask by eroding the Morphology(Nuclear) mask such that it allows the Cytoplasm mask to better capture the cytoplasm close to the nuclear boundary. To do so, open the Mask Manager window.

24 Click Cytoplasm in the Masks list, and click **Edit**.

25 Select the Morphology(Nuclear) mask in the Cytoplasm mask definition.

26 Click the Function toolbar button.

The Define Mask Function window appears.

27 Select Erode in the Function list. The mask will already be selected. Set the number of pixels to 1.

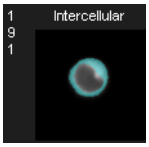
28 Click **OK** to complete the 1-pixel erosion of the Morphology(Nuclear) mask.

The eroded mask appears in the definition.

29 Click **OK** to complete the edit of the Cytoplasm mask.

30 Click **Close** in the Mask Manager window.

31 To view the resulting mask on a Channel 3 image, open the Image Display Properties window and, if necessary, select the new mask for the channel.

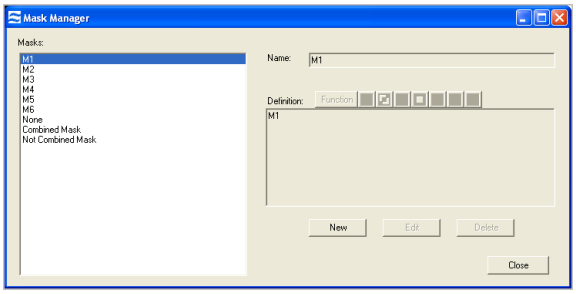


Viewing and Editing a Mask

To view a mask definition

1 Select **Analysis** > **Masks**.

The **Mask Manager** window appears.



2 Click a mask in the **Masks** list to view the definition in the **Definition** area.

3 Click **Close**.

To edit a mask function

1 In the Mask Manager window, select the mask that contains the function you want to edit.

2 Click **Edit**.

3 Remove the definition for the combined mask using the back arrow tool as needed. Refer to "To create a new combined mask" on page 94 for more information on the definition tools.

4 Or click the Function button on the toolbar for a function mask. The **Define Mask Function** window appears. Refer to "To create a new mask using Functions" on page 92 for more information.

5 Click **OK** when finished.

Using the Feature Manager

This section describes how to create and delete features, and it provides a high-level description of the base features that are provided by the IDEAS application. The following subsections cover this information:

Overview of the Feature Manager

The IDEAS application defines a set of base features that you can use to create features for each object. To do so, you use the object's mask or its channel images. After a feature has been created and its value calculated for all cells, you can plot the feature values or view them as statistics for any population. For descriptions of all the base features, see "Overview of the IDEAS® Features and Masks" on page 122.

When the IDEAS application opens a .cif or .rif file, the application calculates the values of features as defined by the selected template. You can refine your template so that it includes only those features of interest for your experiment.

You use the Feature Manager to examine existing features and to define new ones. To gain access to the Feature Manager, select **Analysis** > **Features** or select one of the context menus that are available in the histogram and scatter plot panels. While the Feature Manager is open, all calculations for creating graphs and statistics are disabled. However, you may view images and change the population and channel views. When you close the Feature Manager, any changes to feature names, definitions, and values are reflected in any currently displayed graphs and statistics. The values of newly created features are also calculated at this time.

You can create single features and combined features. You create a single feature by selecting a base feature, such as Area or Intensity, along with a mask and/or an image. You create a combined feature by defining a mathematical expression that includes one or more single features.

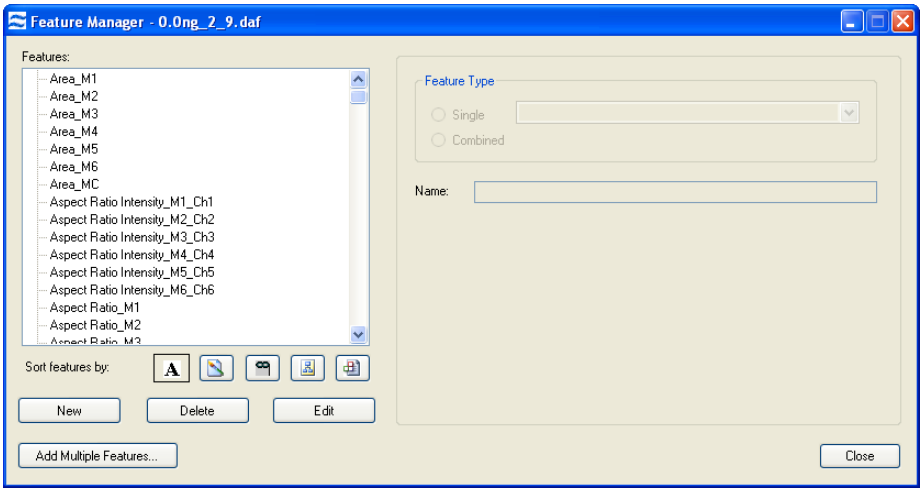
Some features, such as Area, depend on the boundary of a cell. These features require you to select a mask that defines the portion of the image to use for the calculation. Other features, such as Max Pixel, depend on pixel intensity measurements and require you to select an image. Other features require you to select a mask and one or more images.

You can add and remove features from the feature list. The feature definitions are stored in templates, so the definitions are available when you analyze multiple data files. The default template includes most of the base features for each channel image and channel mask that the feature list contains. Certain features, such as Similarity and Spot, require extensive calculations so the default template does not include them. The reason is to save time when you load files. However, you can add these features to the feature list.

To view existing features

1 Click **Analysis** > **Features** or select a graph panel context menu.

The **Feature Manager** window appears.



2 Click a feature in the **Features** list to view its definition.

3 Choose an icon to sort the features:

Table 4: Sorting Features

Feature Icon	Definition
	Sorts features alphabetically.
	Sorts features based on the images used.
	Sorts features based on the masks used.
	Sorts features by category, such as size, location, shape, texture, signal strength, and system.
	Sorts by base features, such as area, aspect ratio, intensity, and object number.

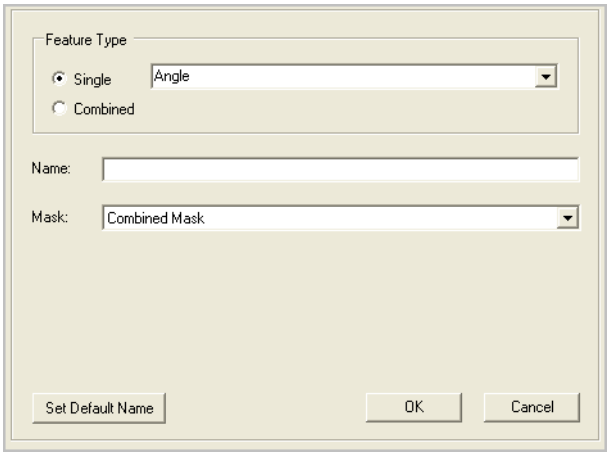
Creating New Features with the Feature Manager

To create a new single feature

A single feature uses the definitions of a base feature along with a mask and/or an image.

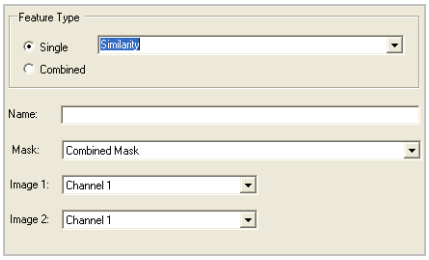
1 Click **New** in the Feature Manager.

The right-hand area of the Feature Manager is enabled.



2 Select **Single** as the **Feature Type**.

The **Mask** and **Image** lists become visible depending on the single feature selected.



3 Select the mask and/or image that you want.

4 Enter a unique feature name or click **Set Default Name**.

The default name is the name of the base feature followed by the name of the mask and name(s) of the image(s).

5 Click **OK** to add the new feature.

It appears in the **Features** list on the left side of the Feature Manager.

6 Click **Close**.

Note: When you close the Feature Manager, the IDEAS application calculates values for the new features. These calculations may take several minutes, depending on the number and complexity of the new features and the size of the image file.

To create multiple features

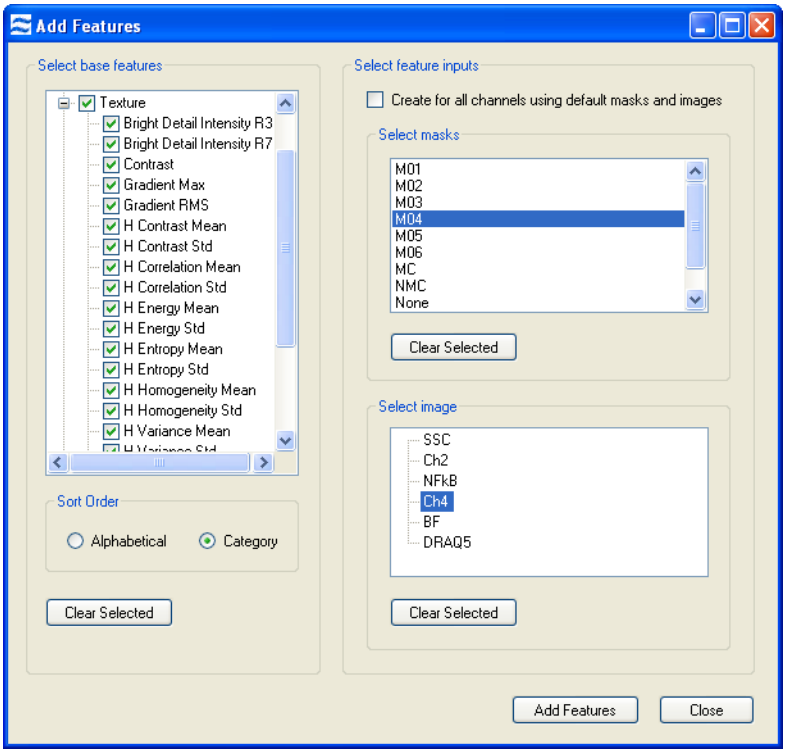
A single feature uses the definitions of a base feature along with a mask and/or an image.

1 Click **Add Multiple Features** in the Feature Manager.

2 Sort the feature list alphabetically or categorically.

3 Select multiple base features and masks

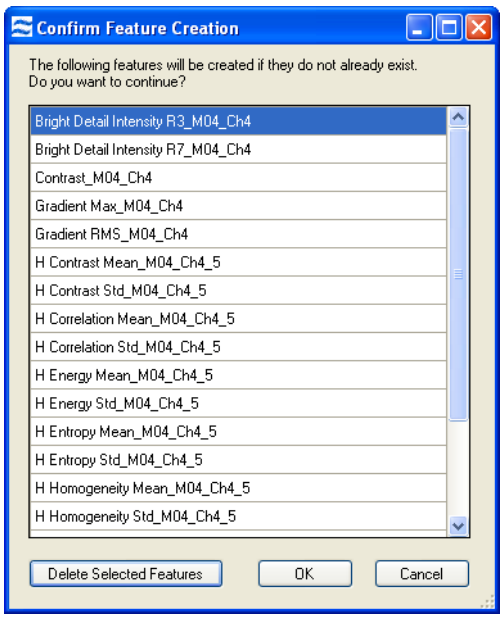
4 Select one image or check the box to create for all channels using default masks and images.



5 Any list can be cleared by clicking the Clear Selected button.

6 When finished click **Add Features** to add the new features to the list.

7 Confirm the features in the next window.



8 Delete any features you do not want to calculate.

9 Click OK when finished. The new features are added to the list in the feature manager.

10 Close the Add Features window.

11 Close the Feature Manager. The new features are calculated when the feature manager closes.

To create a new combined feature

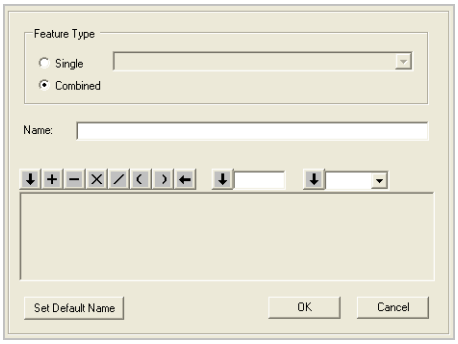
A combined feature uses one or more single features created by a mathematical expression.

1 Click **New** in the Feature Manager.

The right hand area of the Feature Manager is enabled.

2 Select **Combined** as the **Feature Type**:

The editing interface appears.



3 Enter the feature name in the **Name** box or use **Set Default Name** after you have created your expression. The default name is the name of the definition created.

4 Use the toolbar to build a definition (mathematical expression) of features and operators:

Table 5: Combined Feature Tasks and Toolbar

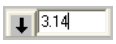
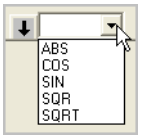
Task	Toolbar
Add a feature to the definition.	Double-click the feature in the **Features** list. Or, single click the feature in the **Features** list and select click the leftmost down-arrow button on the toolbar. 
Add an operator or a parenthesis to the definition.	Click the corresponding button on the toolbar. 
Add a number to the definition.	Enter the number in the box and then click the corresponding down-arrow button.  If the area is greyed-out, an operator must be selected first.

Table 5: Combined Feature Tasks and Toolbar

Task	Toolbar
Add a function to the definition.	Select the function in the list and then click the corresponding down-arrow button.  The available functions are ABS (absolute), COS (cosine), SIN (sine), SQR (square), and SQRT (square root). If the area is greyed-out, an operator must be selected first.
Remove an item from the end of the definition.	Click the left-arrow button on the toolbar. 

5 Click **OK**.

6 Click **Close**.

Note: When you close the Feature Manager, the IDEAS application calculates values for the new features. These calculations may take several minutes, depending on the number and complexity of the new features and the size of the image file.

To delete a feature

1 Select one or more features in the **Features** list by clicking them. To select more than one feature, use the Ctrl key.

2 Click **Delete**.

A warning message will confirm or cancel deletion.

Note: Deleting a feature also deletes any populations that are dependent on that feature. Your feature list may become large and unwieldy. You can narrow down the list without deletions by sorting the list. See "Sorting Features" on page 100 for more information.

Using the Population Manager

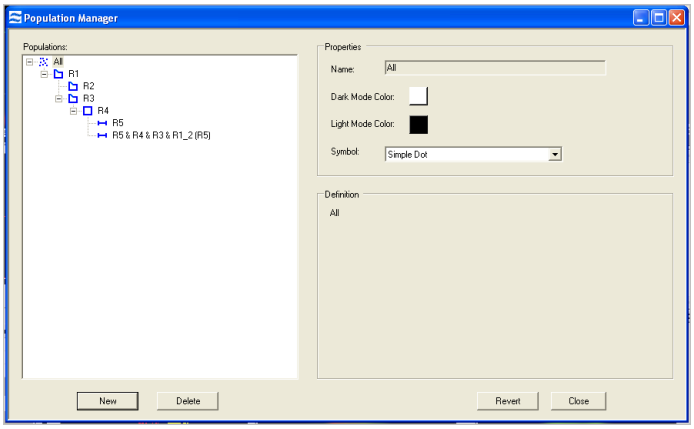
A population is a group of objects. You create populations by drawing regions on graphs, by hand-selecting (tagging) objects in the Image Gallery or on plots, or by combining existing populations. After a population has been defined, you can view it in the Image Gallery or on a plot and you can use it to calculate statistics.

The Population Manager provides a central place for maintaining the display properties of existing populations and for creating new combined populations.

To open the Population Manager and view the population definitions

1 Select **Analysis** > **Populations** or right click a graph and select **Populations**.

The Population Manager window appears.



Note: The list of populations is presented as a hierarchy that shows the dependencies of the populations on each other. The icon associated with a population indicates how the population is defined.

- The tagged icon indicates a tagged population.

- A population defined by a region is indicated by one of the following icons.

  The definition of a selected population is shown in the Definition area.

To edit the display properties of a population

1 Within the **Population Manager**, click a population in the **Populations** list.
2 Change the name in the **Name** box.
3 Click a **Color** square to select a new color on the color palette and click **OK**.
4 Click a display symbol in the **Symbol** drop down menu.
5 Click **Close** to save the population changes.
6 Click **Revert** to reject the changes.

To delete a population

1 Within the **Population Manager**, click a population in the **Populations** list.

2 Click **Delete**.

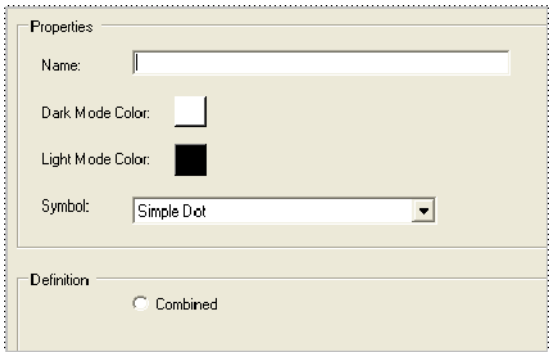
A confirmation warning message appears indicating all the dependent populations that will also be deleted.

3 Click **Yes** to confirm.

To create a new combined population

1 Within the **Population Manager** (**Analysis** > **Populations**), click **New**.

The right side of the Population Manager window changes to allow you to define a new population.



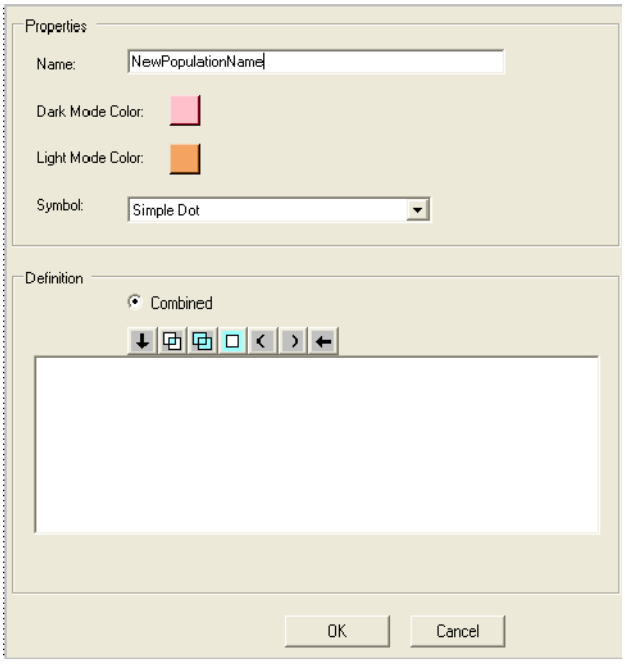
2 Enter a unique population name in the **Name** box.

3 Click a **Color** square to select a new color on the color palette and click **OK**.

4 Click a display symbol in the **Symbol** drop down menu.

5 Select **Combined** for this combined population.

The toolbar for creating a combined population appears.



6 Use the toolbar to build the population definition as described in the table and click OK when done:

TABLE 6: POPULATION TASKS AND TOOLBAR

TASK	TOOLBAR
Add a population to the definition.	Double-click the population. Or, single click the population and select the down-arrow button on the toolbar. 
Combine two populations.	Use the Boolean AND or OR operator.  Use the AND operator to include only the pixels that are in both of the original populations.  Use the OR operator to include the pixels that are in either one of the original populations.
Select all pixels that are not in the original population.	Use the Boolean NOT operator.  The NOT operator specifies which population will not be used.
Affect the order of operations.	Use the parentheses toolbar buttons. 
Remove an item from the end of the definition.	Click the left-arrow button on the toolbar. 

Using the Region Manager

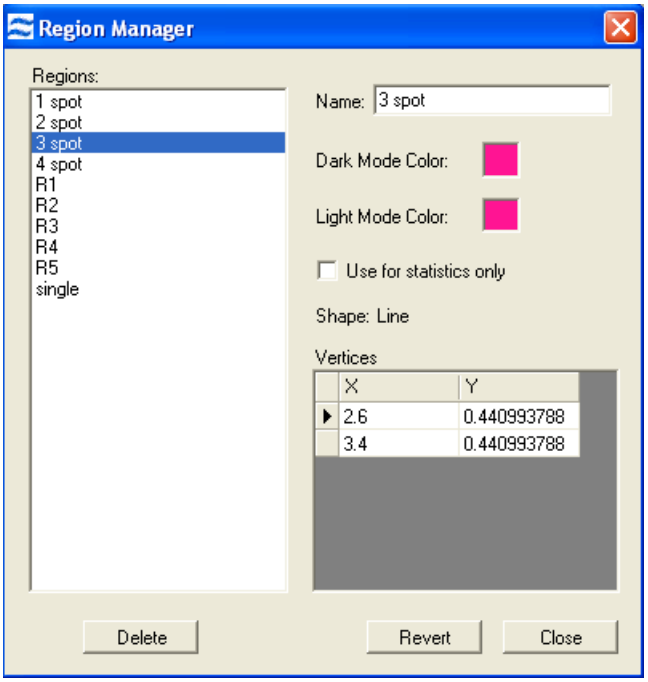
The Region Manager provides a central place for defining the display properties, names, and positions of existing regions. Regions can be deleted in the Region Manager tool.

Regions are drawn on graphs to create new populations, based on the physical location of objects on a graph, and to compute statistics. Tools for drawing regions are found on the Analysis Area toolbar. See "Creating Regions on Graphs" on page 77.

To open the Region Manager and view the region definitions

1 Select **Analysis** > **Regions** or right click a graph and select **Regions**.

The Region Manager window appears.



To edit a region

1 Within the **Region Manager**, click a region in the **Regions** list.

2 Change the name in the **Name** box.

3 Click a **Color** square to select a new color on the color palette and click **OK**.

4 Change the X or Y position of the vertices in the **Vertices** box.

5 Select or de-select the Use for statistics only box.

6 Click **Delete** to delete a region.

7 Click **Revert** to reject the changes.

8 Click **Close** when finished.

Note: When a region is deleted, all populations that are defined by that region will be deleted. A warning dialog box appears listing the populations that will be deleted.

Chapter 6

Creating Reports and Exporting Data

The following subsections describe how you can print data directly from the IDEAS application or export data to other applications, such as those in Microsoft Office.

Printing Reports

The IDEAS application provides color mapping from the dark mode that you see in the Analysis Area to a light mode that has a white background for the printing and exporting of data. Because the population colors might not show on a white background, you can change the colors when using the light mode.

To print the Analysis Area data

- Select **Reports** > **Print Analysis Area**.

  The IDEAS application prints all the graphs, statistics, text panels, and images that are displayed in the Analysis Area.

To print the Image Gallery data

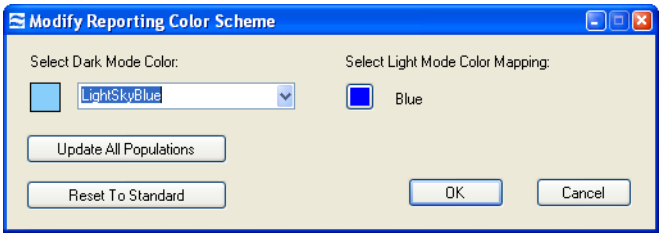
- Select **Reports** > **Print Image Gallery**.

  The IDEAS application prints all the images that are visible in the Image Gallery.

To map the dark mode colors to light mode colors

1 Select **Options** > Manage **Color Schemes**.

The Modify Reporting Color Scheme window appears.



2 In the **Select Dark Mode Color** drop-down menu, select the color that you want to map.

3 To choose a different color, click the **Select Light Mode Color Mapping** color square and click a new color on the color palette.

4 Click **Update All Populations**.

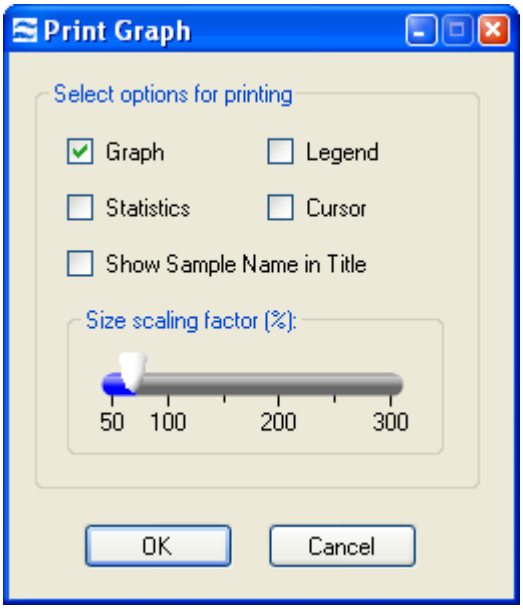
5 If you want to return the settings to the IDEAS defaults, click **Reset to Standard**.

6 Click **OK** to save the changes or **Cancel** to exit.

To print an individual graph

1 Right-click the graph and then select **Print Graph** on the graph context menu.

The Print Graph window appears.



2 Select the checkboxes **Graph**, **Statistics**, **Legend**, **Cursor, Show Sample Name in Title** to include the elements in the report.

3 If necessary, adjust the size scaling factor.

4 Click **OK** to print the graph.

Creating a Statistics Report Template

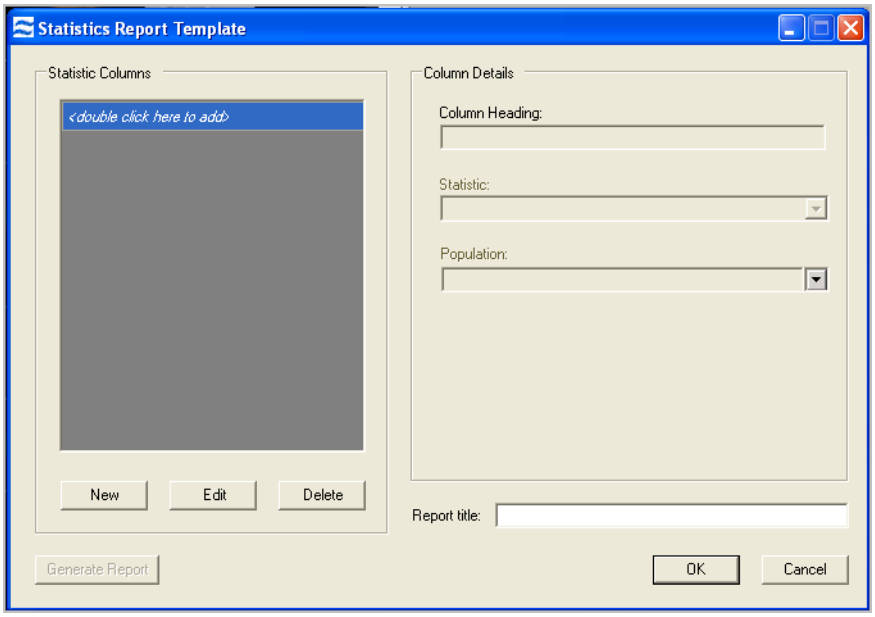
A statistics report template is a separate template in a .daf file or an .ast template file. It allows users to select specific statistics within a .daf file and open the data in Excel.

A statistics report can be applied during batching if it is part of the template used. It may also be applied to preexisting .daf files from the Reporting menu. In this case, the rest of the template is not processed—only the report. The statistics report allows you to specify population percentages and feature statistics and the layout of the report is accessed from the reporting menu.

To create a Statistics Report Template

1 Select **Reports** > **Statistics Report Template**.

The Statistics Report Template appears.



2 Enter a **Report title**.

3 In the **Statistic Columns** area, double click the blue bar or select **New**.

4 Select a statistic in the **Statistic** drop-down menu.

- **%Gated** - the percent of one population as a percentage of another, but not used for tagged populations
- **%Total** - percentage of a population as a percentage of All
- **%** - the percentage of one population as a percentage of another, also is used for tagged populations
- **Count** - the absolute count of the population
- **CV** - the coefficient variable
- **Geometric Mean** - standard statistical definition
- **Maximum** - standard statistical definition
- **Mean** - standard statistical definition

- **Medium** - standard statistical definition
- **Minimum** - standard statistical definition
- **Mode** - standard statistical definition
- **Standard Deviation** - standard statistical definition
- **Variance** - standard statistical definition
- **NaN** - stands for not a number; the number of objects whose values are not valid numbers.

5 Based on the selected statistic, select a population.

6 Select a **Feature**. This is not available for the %-related statistics or the Count.

7 Enter an appropriate name. This will be name of the column in the Excel file.

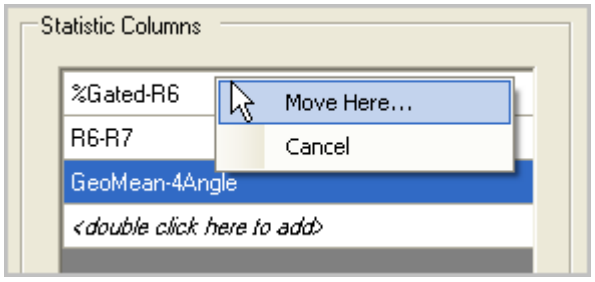
8 Click **Add**.

The information pairs in the Statistic Columns area.

9 Add Statistics Columns as necessary.

10 Adjust the Statistic Columns as necessary.

- **Edit** or double clicking allows changes to a previously created statistic.
- **Delete** removes a selected statistic.
- Right clicking a statistic and drag and dropping it to a new location changes the order of the columns as they will appear in the report table.



- To reorder longer lists, hold the Ctrl key for an individual item or the shift key for multiple items and click each individual statistic in the desired order. Then, right click and select **Move Here**.

11 Click **Generate Report** when complete to generate a report for a current (opened) .daf file.

A prompt appears to save the text file. This text file can be opened from Excel.

12 If you do not want to generate a report, click **OK** to save your changes and exit the window.

13 The saved template can generate statistics for multiple data files during batch processing. See "Batch Processing" on page 52 for more information.

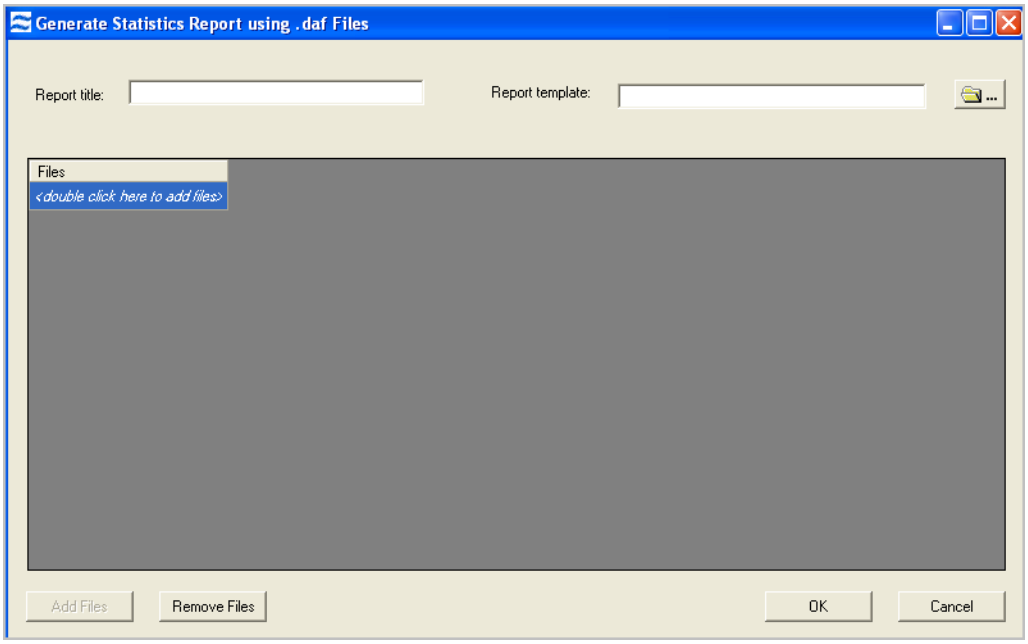
Generating a Statistics Report using .daf Files

Once a Statistics Template has been created, the user can generate a statistics report from multiple .daf files. However, these files must use the same template. The Batch Processing feature can also generate a statistics report where statistics for each required data will be generated either for .rif, .cif, or .daf files. Generating a statistics report under the Reports menu simply adds the statistics template to the specified .daf files.

To Generate a Statistics Report

1 Select **Reports** > **Generate Statistics Report**.

The current .daf file appears in the window with the specified statistics columns.



2 Change the **Report title** or **Report template** if necessary. The template may be obtained from a .daf or .ast file.

3 Additional .daf files can be added or removed with the **Add Files** or **Remove Files** buttons.

4 Click **OK**.

A prompt will confirm that the .daf file will be saved. The report title name will be used as the default file name for the report. In the above example, the file generated will be named "Report 1.txt". If the report title contains illegal characters, such as "\/><" the default filename will change to "Statistics Report.txt". Tab delimited text format is used for the report.

Exporting Data

The IDEAS application allows users to export feature data, pixel data, or TIF files for separate analyses.

You can export graphs, statistics, and images to other applications. See "Setting the Image Gallery Properties" on page 62 to optimize the image display before copying images.

To copy the Image Gallery data to the Clipboard

- Right-click anywhere in the Image Gallery and then click **Copy Displayed Images to Clipboard**.

  The IDEAS application copies all the images that are visible in the Image Gallery to the Clipboard.

To copy a single image to the Clipboard

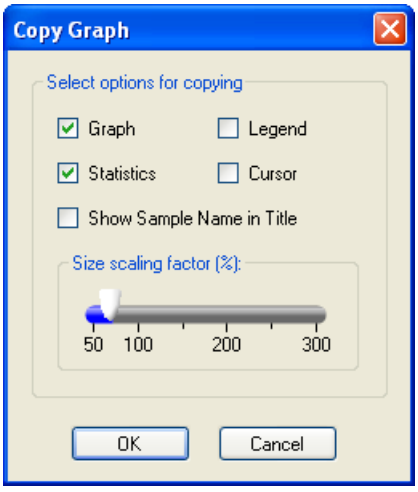
- Right-click an image in the Image Gallery or in the Analysis Area and then click **Copy Image to Clipboard**.

To copy a graph and/or statistics to the Clipboard

1 Select light or dark mode graphs in the analysis area using the tool or selecting **Use Light Mode Graphs** in the Reports menu.

2 Right-click a graph and then click **Copy Graph/Stats To Clipboard**.

The Copy Graph window appears.



3 Select **Graph**, **Statistics**, **Legend**, **Cursor** and/or **Show Sample Name and Title** depending on what you want to copy.

4 Adjust the Size scaling factor as desired.

5 Click **OK**to copy the graph and/or the statistics to the Clipboard.

Note: The IDEAS application copies the statistics as a metafile. If you want to export the data into a table, such as that in Microsoft Excel, you must instead click **Export Statistics to Clipboard** on the context menu.

To export graph statistics to the Clipboard

- Right-click a graph and then click **Export Statistics To Clipboard**.

To export population statistics or object feature values from the Statistics Area

- Right-click the table and then click **Copy data to clipboard**.

To copy the entire screen to the Clipboard

- Press CTRL+PRINT SCREEN.

To copy a window to the Clipboard

- Select the window and then press ALT+PRINT SCREEN.

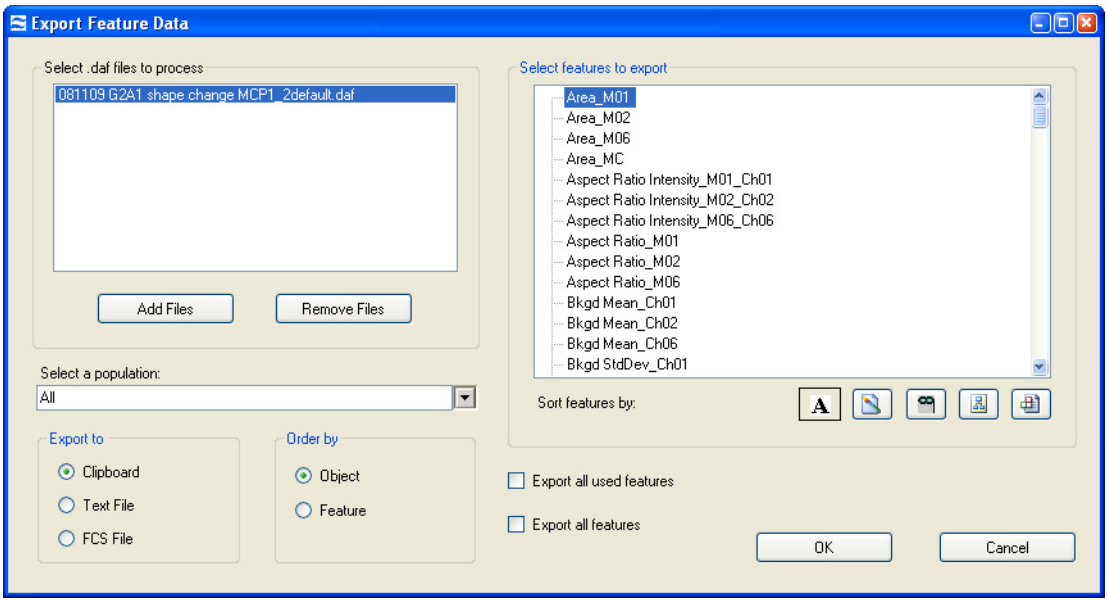
Exporting Feature Data

You can export feature values for a population to the Clipboard, a text file, or a Flow Cytometry Standard (FCS) file. You can export pixel intensity values for an object to the Clipboard or a text file. Later, you can open or paste the FCS file into a spreadsheet or other programs that uses the FCS file format. Keep in mind, however, that limitations might exist on the number of values that these programs can import.

To export feature data

1 On the **Tools** menu, click **Export Feature Value**s.

The **Export Feature Data** window appears.



2 Add files to the list on the left to export values for multiple files.

3 In the **Select a population** drop down menu, select the population that you want.

If you haven't defined any populations, **All** is the default. To make a new population, refer to "Creating Tagged Populations" on page 69.

4 In the **Select feature values to export** area, select features by clicking items in the list or hold down the Ctrl while clicking to select multiple items.

5 Select the **Export to** option that you want. Note that data exported to the Clipboard can be pasted directly into a spreadsheet program.

6 Select the **Order by** option that you want. Note that ordering by object causes the values to be listed in a column, whereas ordering by feature causes the values to be listed in a row.

7 Click **OK**.

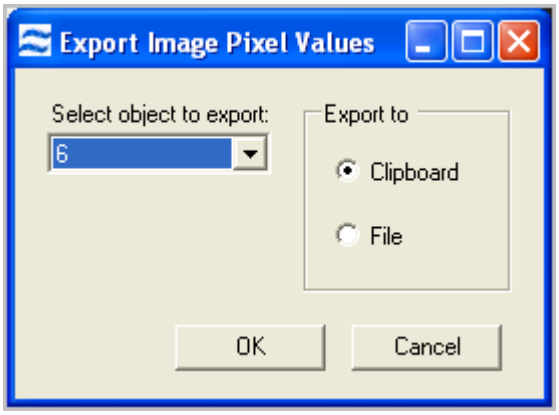
Exporting Pixel Data

Exporting pixel data is useful when importing the data into third-party programs where you would need to graph the individual pixels.

To export pixel data

1 On the **Tools** menu, click **Export Image Pixel Values**.

The **Export Image Pixel Values** window appears.



2 **Select the object to export** in the drop down menu.

3 Select to **Export to** either the **Clipboard** or **File**.

4 Click **OK**.

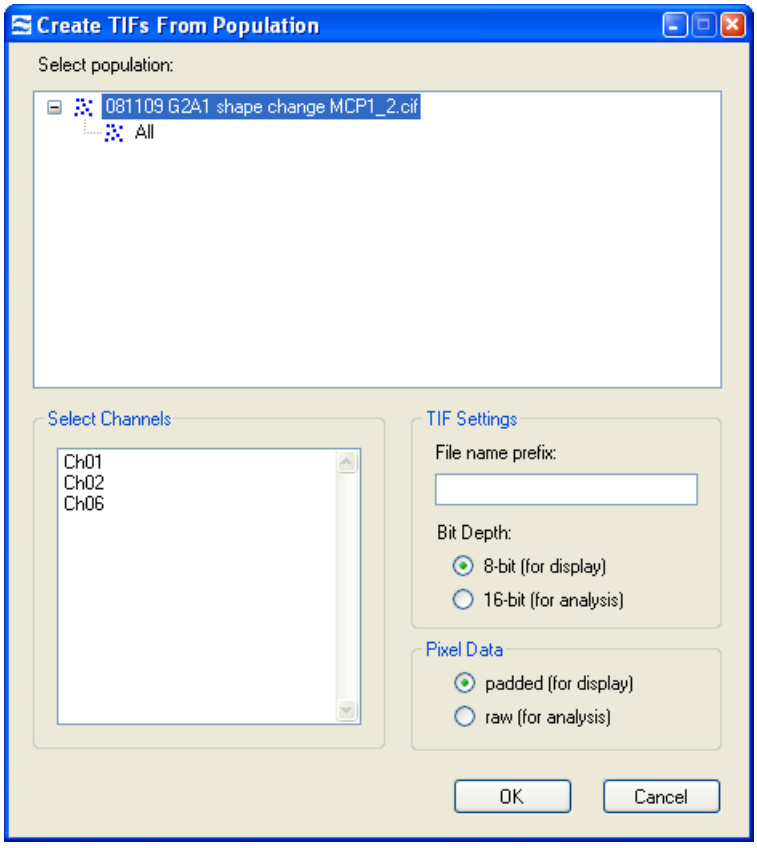
Creating TIFs From Population for Export

The IDEAS application allows users to create separate TIF files for channel images for every event in that population. The exported TIF files can be opened in image viewing applications that support 16 bit Tif format.

to Create TIFs From Population for Export

1 On the **Tools** menu, click **Export .tif Images**.

The Create TIFs From Population window appears.



2 Select the population and channels.

3 Type a prefix for the TIF file name.

4 Select the bit depth.

5 Select padded or raw.

6 Click **OK**.

A TIF file is created for every selected channel within the selected population.

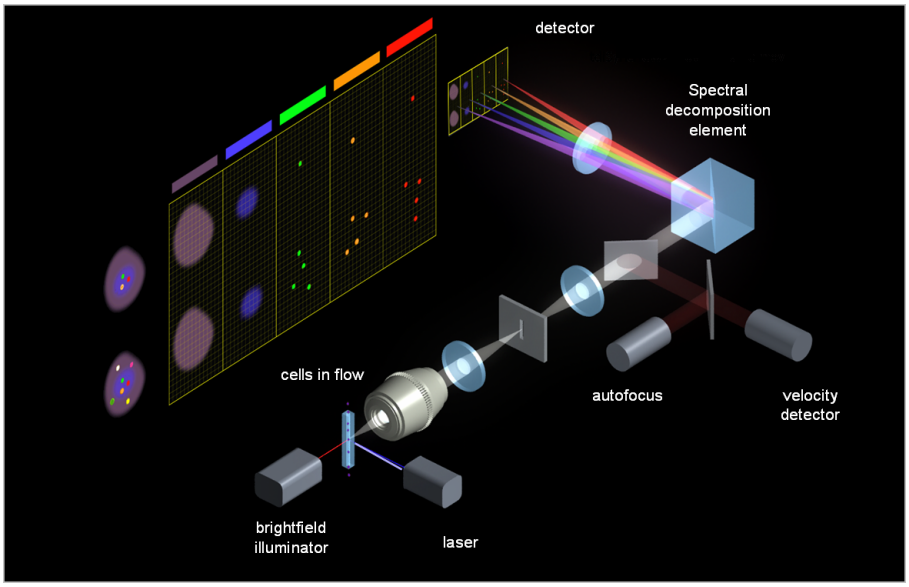
CHAPTER 7

Understanding the IDEAS® Features and Masks

This section contains the following subsections, which describe the features that the IDEAS application uses for data analysis:

Overview of the IDEAS® Features and Masks

Objects passing through the ImageStream cell analysis system are illuminated in different directions by lasers and/or brightfield LEDs. Light emitted from the object is focused through an objective lens and relayed to a spectral decomposition element, which divides the light into six spectral bands located side-by-side across a charge-coupled detector (CCD), as shown in the following diagram. Therefore, each object has six images that can be individually analyzed or, because they are in spatial register with respect to one another, reconstructed. Each of the separate bands is called a channel. Below is an example of collecting 6 images. The ImageStreamx system has a second camera option which enables collection of up to 12 images per object.



The IDEAS application provides a large selection of criteria, or features, for analyzing images. A feature is described by a mathematical expression that contains quantitative and positional information about the image. A feature is applied to specific locations of an image by the use of a mask that identifies pixels within the region of interest of the image. A few system features, such as Object Number, Camera Background and Flow Speed, do not require calculations, masks, or image intensity information.

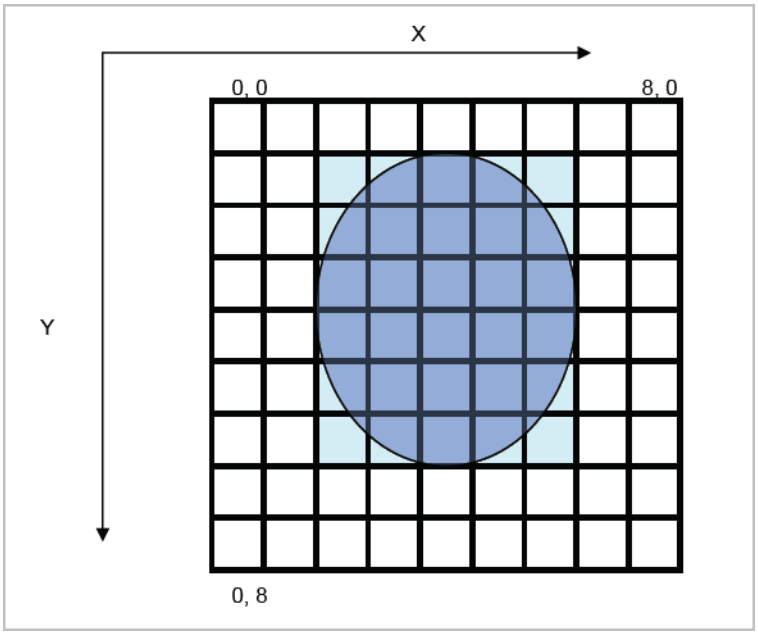
About Features

The IDEAS application provides a large selection of criteria, or features, for analyzing images. A feature is described by a mathematical expression that contains quantitative and positional information about the image. A feature is applied to specific locations of an image by the use of a mask that identifies pixels within the region of interest of the image. A few system features, such as Object Number, Camera Background and Flow Speed, do not require calculations, masks, or image intensity information.

Features are created in IDEAS using base feature algorithms, such as Area or Intensity, along with a mask and/or a channel image. New masks and features can be created by the user using the Mask Manager and Feature Manager tools. New features can be created by combining existing features in mathematical expressions using the Feature Manager.

For more information, see "Using the Mask Manager" on page 92 and "Using the Feature Manager" on page 99.

To calculate the value of a feature, the IDEAS application maps the channel image to X and Y coordinates, as illustrated by the following diagram. Each box in the diagram represents a pixel that equals approximately 0.5 µm × 0.5 µm. Each channel is 88 pixels in the X direction and varies in the Y direction, depending on the size of the imaged object.



IDEAS groups the features into eight categories: size, location, shape, texture, signal strength, comparison, system and combined.

The Base Features at a Glance sorted Alphabetically

Table 1: Features Listed Alphabetically

Feature Name	Category	Feature Name	Category
"Angle Feature" on page 141	Location	"Contrast Feature" on page 163	Texture
"Angle Intensity Feature" on page 141	Location	"Delta Centroid X and Delta Centroid Y Features" on page 144	Location
"Area Feature" on page 132	Size	"Delta Centroid XY Feature" on page 145	Location
"Aspect Ratio Feature" on page 152	Shape	"Diameter Feature" on page 133	Size
"Aspect Ratio Intensity Feature" on page 154	Shape	"Elongatedness Feature" on page 157	Shape
"Bkgd Mean Feature" on page 170	Signal Strength	"Flow Speed Feature" on page 189	System
"Bkgd StdDev Feature" on page 170	Signal Strength	"Gradient Max Feature" on page 164	Texture
"Bright Detail Intensity R3 and Bright detail Intensity R7 Features" on page 161	Signal Strength	"Gradient RMS Feature" on page 165	Texture
"Bright Detail Similarity R3 Feature" on page 182	Comparison	"Height Feature" on page 134	Size
"Camera Line Number Feature" on page 189	System	"H Texture Features" on page 166	Texture
"Camera Timer Feature" on page 189	System	"Intensity Concentration Ratio Feature" on page 184	Comparison
"Centroid X and Centroid Y Features" on page 142	Location	"Intensity Feature" on page 171	Signal Strength
"Centroid X Intensity and Centroid Y Intensity Features" on page 143	Location	"Internalization Feature" on page 185	Comparison
"Circularity Feature" on page 154	Shape	"Length Feature" on page 134	Size
"Compactness Feature" on page 156	Shape	"Lobe Count Feature" on page 158	Shape
"Major Axis and Minor Axis Features" on page 135	Size	"Raw Median Pixel Feature" on page 177	Signal Strength

Table 1: Features Listed Alphabetically

Feature Name	Category	Feature Name	Category
"Major Axis Intensity and Minor Axis Intensity Features" on page 136	Size	"Saturation Count Feature" on page 179	Signal Strength
"Max Contour Position Feature" on page 147	Location	"Saturation Percent Features" on page 180	Signal Strength
"Max Pixel Feature" on page 172	Signal Strength	"Shape Ratio Feature" on page 159	Shape
"Mean Pixel Feature" on page 173	Signal Strength	"Similarity Feature" on page 186	Comparison
"Median Pixel Feature" on page 174	Signal Strength	"Spot Area Min Feature" on page 138	Size
"Min Pixel Feature" on page 174	Signal Strength	"Spot Count Feature" on page 168	Texture
Minor Axis: see "Major Axis Intensity and Minor Axis Intensity Features" on page 136	Size	"Raw Centroid X and Raw Centroid Y Features" on page 148	Location
"Modulation Feature" on page 167	Texture	"Spot Intensity Min and Spot Intensity Max Features" on page 181	Signal Strength
"Object Number Feature" on page 189	System	"Std Dev Feature" on page 169	Texture
"Objects/ml Feature" on page 189	System	"Symmetry 2, 3, 4 Features" on page 160	Texture
"Objects/sec Feature" on page 189	System	"Thickness Max Feature" on page 139	Size
"Perimeter Feature" on page 137	Size	"Thickness Min Feature" on page 139	Size
"Raw Intensity Feature" on page 175	Signal Strength	"Time Feature" on page 190	System
"Raw Max Pixel Feature" on page 175	Signal Strength	"Valley X and Valley Y Features" on page 150	Location
"Raw Mean Pixel Feature" on page 177	Signal Strength	"Width Feature" on page 140	Size
"Raw Min Pixel Feature" on page 178	Signal Strength	"XCorr Feature" on page 188	Comparison

The Base Features at a Glance by Category

Table 2: List of Features by category

Feature category	Feature name	In Default Template?	In Expanded Default Template ?	Mask_Image Used in Default Template
Size	**Size-based Features are in microns.**			
	"Area Feature" on page 132 The size of the mask in square microns.	Yes	Yes	M1-M6,MC
	"Diameter Feature" on page 133 Estimates the diameter of the mask based on Area.	No	Yes	M1-M6
	"Height Feature" on page 134 Based on a bounding rectangle, the Width is the smaller side and the Height is the longer side of the rectangle.	Yes	Yes	M1-M6
	"Length Feature" on page 134 Measures the longest part of the mask.	Yes	Yes	M1-M6
	"Major Axis and Minor Axis Features" on page 135 Describes the widest part of the mask and the narrowest part of the mask, respectively.	No	Yes	M1-M6
	"Major Axis Intensity and Minor Axis Intensity Features" on page 136 Based on a bounding ellipse, the Minor Axis is the narrow part and the Major Axis is the widest part.	No	Yes	M1_Ch1-M6_Ch6
	Minor Axis: "Major Axis and Minor Axis Features" on page 135	No	Yes	M1-M6
	"Perimeter Feature" on page 137 Describes circumference of the mask.	No	Yes	M1-M6
	"Spot Area Min Feature" on page 138 The Area of the smallest spot in the mask. (See also "Raw Centroid X and Raw Centroid Y Features" on page 148, "Spot Intensity Min and Spot Intensity Max Features" on page 181 and "Spot Count Feature" on page 168.	No	No	
	"Thickness Max Feature" on page 139 Describes the longest width of the mask.	No	Yes	M1-M6
	"Thickness Min Feature" on page 139 Describes the shortest width of the mask.	No	Yes	M1-M6

Table 2: List of Features by category

Feature category	Feature name	In Default Template?	In Expanded Default Template ?	Mask_Image Used in Default Template
	"Width Feature" on page 140 Based on a bounding rectangle, the Width is the smaller side and the Height is the longer side of the rectangle.	Yes	Yes	M1-M6
Location	**Location Features are in X,Y pixel coordinates from an origin in the upper left corner, pixels or contour**			
	"Angle Feature" on page 141 The angle of the major axis from a horizontal plane in radians.	No	No	
	"Angle Intensity Feature" on page 141 The angle of the major axis intensity from a horizontal plane in radians.	No	No	
	"Centroid X and Centroid Y Features" on page 142 The central tendency of the pixels along the X Axis and Y Axis, respectively.	No	Yes	M1-M6
	"Centroid X Intensity and Centroid Y Intensity Features" on page 143 The central tendency of the pixels along the X Axis and Y Axis, respectively, with the pixel intensities weighted.	No	Yes	M1_Ch1-M6_Ch6
	"Delta Centroid X and Delta Centroid Y Features" on page 144 The distance between the X or Y Centroids of two images.	No	No	
	"Delta Centroid XY Feature" on page 145 The distance between the Centroids of two images.	No	No	
	"Max Contour Position Feature" on page 147 The location of the contour in the cell that has the highest intensity concentration.	No	No	
	"Raw Centroid X and Raw Centroid Y Features" on page 148 The shortest distance between two components (spots). See also "Spot Area Min Feature" on page 138, "Spot Intensity Min and Spot Intensity Max Features" on page 181 and "Spot Count Feature" on page 168.	No	No	
	"Valley X and Valley Y Features" on page 150 The (X,Y) coordinates of the minimum intensity within the skeletal lines that are used when creating the Valley Mask.	No	No	
Shape	**Shape Features define the mask shape and have units that vary with the feature.**			
	"Aspect Ratio Feature" on page 152 The ratio of the Minor Axis divided by the Major Axis.	Yes	Yes	M1-M6

Table 2: List of Features by category

Feature category	Feature name	In Default Template?	In Expanded Default Template ?	Mask_Image Used in Default Template
	"Aspect Ratio Intensity Feature" on page 154 The ratio of the Minor Axis Intensity divided by the Major Axis Intensity.	Yes	Yes	M1_Ch1-M6_Ch6
	"Circularity Feature" on page 154 The degree of the mask's deviation from a circle.	No	No	
	"Compactness Feature" on page 156 Describes the density of intensities within the object.	No	No	
	"Elongatedness Feature" on page 157 The ratio of the Height/Width which use the bounding box.	No	Yes	M1-M6
	"Lobe Count Feature" on page 158 The number of lobes in a cell. (Also see Symmetry)	No	No	
	"Shape Ratio Feature" on page 159 The ratio of Thickness Min/Length features.	No	Yes	M1-M6
	"Symmetry 2, 3, 4 Features" on page 160 These three features measure the tendency of the object to have a single axis of elongation, a three-fold and a four-fold variation of the shapes. See also "Lobe Count Feature" on page 158.	No	No	
Texture	**Texture features measure pixel or regional variation and indicate the granularity or complexity of the image.**			
	"Bright Detail Intensity R3 and Bright detail Intensity R7 Features" on page 161 The Intensity of the pixels in the bright detail image using a 3 or 7 pixel structuring element. Also, see "Spot Mask" on page 199 for a description of the bright detail image.	Yes (R3) No (R7)	Yes	MC_Ch1-MC_Ch6
	"Contrast Feature" on page 163 Enumerates changes of pixel values in the image to measure the focus quality of an image.	Yes	Yes	M1_Ch1-M6_Ch6
	"Gradient Max Feature" on page 164 The maximum slope of the pixel value changes in the image to measure focus quality of an image.	No	Yes	M1_Ch1-M6_Ch6
	"Gradient RMS Feature" on page 165 Enumerates changes of pixel values in the image to measure the focus quality of an image.	No	Yes	M1_Ch1-M6_Ch6
	"H Texture Features" on page 166 Measures Haralick texture features.	No	Yes	M1_Ch1_5-M6_Ch6_5

Table 2: List of Features by category

Feature category	Feature name	In Default Template?	In Expanded Default Template ?	Mask_Image Used in Default Template
	"Modulation Feature" on page 167 Measures the intensity range of an image, normalized between 0 and 1.	Yes	Yes	M1_Ch1-M6_Ch6
	"Spot Count Feature" on page 168 Enumerates the number of spots. See also "Raw Centroid X and Raw Centroid Y Features" on page 148, "Spot Area Min Feature" on page 138, and "Spot Intensity Min and Spot Intensity Max Features" on page 181.	No	No	
	"Std Dev Feature" on page 169 Describes the overall distribution of pixel intensities.	No	Yes	M1_Ch1-M6_Ch6
Signal Strength	**Signal Strength Features are measured in pixel values.**			
	"Bkgd Mean Feature" on page 170 The average intensity of the camera background.	Yes	Yes	Ch1-Ch6
	"Bkgd StdDev Feature" on page 170 The standard deviation of the background intensities.	No	Yes	Ch1-Ch6
	"Intensity Feature" on page 171 The sum of the pixel intensities in the mask, background subtracted.	Yes	Yes	MC_Ch1-MC_Ch6
	"Max Pixel Feature" on page 172 The largest pixel value within the mask, background subtracted.	Yes	Yes	MC_Ch1-MC_Ch6
	"Mean Pixel Feature" on page 173 The average pixel value within the mask, background subtracted.	Yes	Yes	M1_Ch1-M6_Ch6
	"Median Pixel Feature" on page 174 The median pixel value within the mask, background subtracted.	Yes	Yes	M1_Ch1-M6_Ch6
	"Min Pixel Feature" on page 174 The smallest pixel value within the mask, background subtracted.	No	No	
	"Raw Intensity Feature" on page 175 The sum of the pixel intensities within the mask.	No	No	
	"Raw Max Pixel Feature" on page 175 The smallest pixel intensity.	Yes	Yes	MC_Ch1-MC_Ch6
	"Raw Mean Pixel Feature" on page 177 The average pixel intensity: Raw does not have background subtracted.	No	No	

Table 2: List of Features by category

Feature category	Feature name	In Default Template?	In Expanded Default Template ?	Mask_Image Used in Default Template
	"Raw Median Pixel Feature" on page 177 The median pixel intensity.	No	No	
	"Raw Min Pixel Feature" on page 178 The lowest pixel value within the mask.	Yes	Yes	MC_Ch1-MC_Ch6
	"Saturation Count Feature" on page 179 The number of pixels in the mask that are saturated.	Yes	Yes	M1_Ch1-M6_Ch6
	"Saturation Percent Features" on page 180 The Percentage of pixels in the mask that are saturated.	Yes	Yes	
	"Spot Intensity Min and Spot Intensity Max Features" on page 181 The raw intensity (not background subtracted) of the dimmest component (spot). See also "Spot Count Feature" on page 168, "Raw Centroid X and Raw Centroid Y Features" on page 148, and "Spot Area Min Feature" on page 138.	No	No	
Comparison	**Difference of intensity measurements between masks or pixels.**			
	"Bright Detail Similarity R3 Feature" on page 182 Measures the correlation of the bright details between image pairs.	No	No	
	"Intensity Concentration Ratio Feature" on page 184 Given two masks, the ratio of the intensity in one mask to the total intensity in both masks.	No	No	
	"Internalization Feature" on page 185 The ratio of the intensity inside the cell to the intensity of the entire cell.	No	No	
	"Similarity Feature" on page 186 The Similarity is a measure of the degree to which two images are linearly correlated pixel by pixel within a masked region.	No	No	
	"XCorr Feature" on page 188 The XCorr is a measure of the degree to which two images frequencies are cross correlated.	No	No	
System	**System features do not require a mask and tend to deal with system wide metrics.**			
	"Camera Line Number Feature" on page 189 An incremental count of objects.	No	Yes	

Table 2: List of Features by category

Feature category	Feature name	In Default Template?	In Expanded Default Template ?	Mask_Image Used in Default Template
	"Camera Timer Feature" on page 189 The clock rate in KHz. This is relative time.	No	Yes	
	"Flow Speed Feature" on page 189 The calculated flow speed in mm/sec.	Yes	Yes	
	"Object Number Feature" on page 189 The sequence of objects.	Yes	Yes	
	"Objects/ml Feature" on page 189 The number of objects per ml.	Yes	Yes	
	"Objects/sec Feature" on page 189 The number of objects per second.	Yes	Yes	
	"Time Feature" on page 190 The camera timer feature, converted to seconds.	Yes	Yes	
Combined	**Any combined feature will be listed under Combined**	No	No	

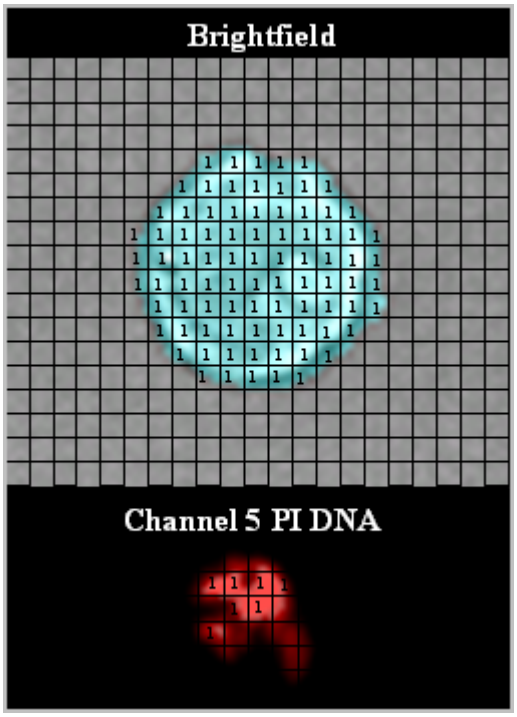
Understanding the Detailed Feature Descriptions

Understanding the Size Features

Size features are in microns and include Area, Diameter, Length, Major Axis, Minor Axis, Major Axis Intensity, Minor Axis Intensity, Perimeter, Thickness Max and Min, Spot Area Min, and Width and Height.

Area Feature

The number of microns squared in a mask is equal to the Area. In the following figure, a 1 symbolizes whether the area is included in the mask. The number of pixels is converted to μm^2. Note that 1 pixel = 0.25 μm^2. As an example, a cell with a mask that includes 2000 pixels is therefore equal to 500 μm^2.



Application Examples:

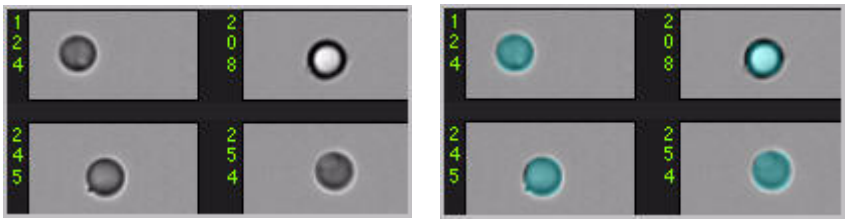
- Quantify and compare cell size.
- Identify single cells.
- Calculate the radius, diameter and volume of the cell.
- Identify apoptosis using the Area of the 30% threshold mask of a nuclear dye.
- Create a pseudo FSC va. SSC plot for comparing with flow cytometry.

Diameter Feature

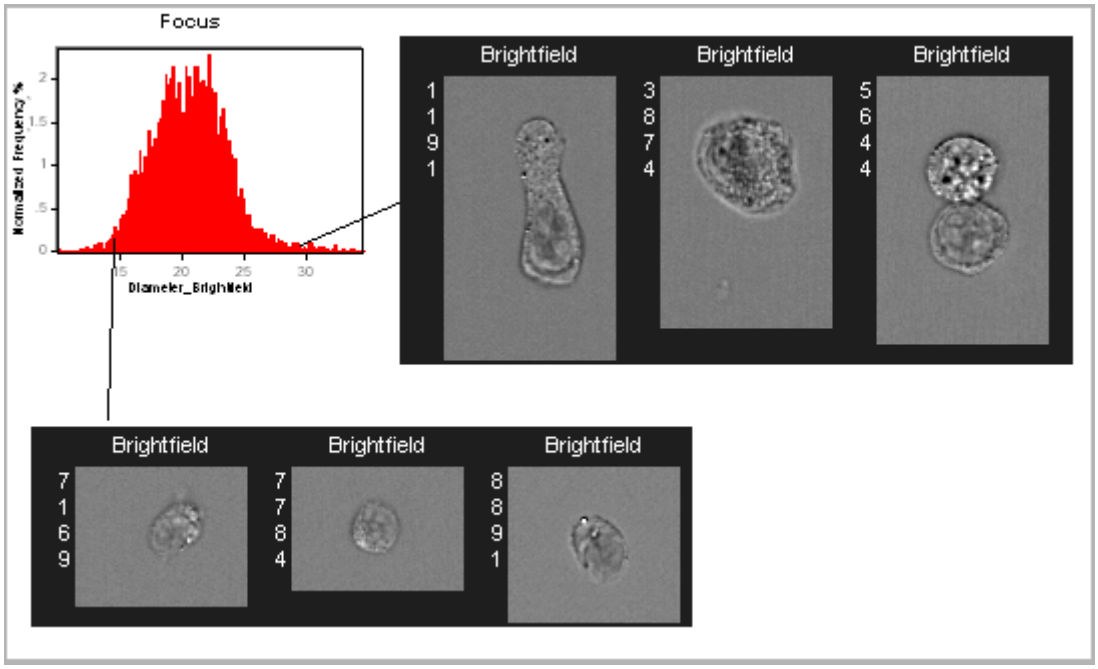
The Diameter feature provides the diameter of the circle that has the same area as the object. The accuracy of the diameter is highly dependent on a close fitting mask and roundness of the cell.

$$Diameter = 2 \times \sqrt{\frac{Area}{\pi}}$$

The images below depicts beads with a uniform diameter of 9 microns.



In the next figure, note that images with longer shapes that have the same area will have the same diameter value.

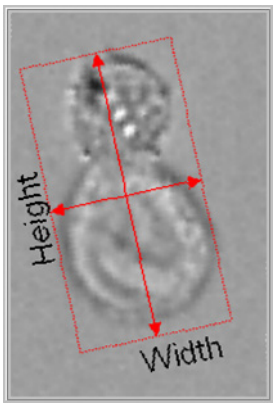


Application Example:

— Used to obtain approximate size of the cell.

Height Feature

Using the bounding rectangle, Height is the number of microns of the longer side and Width the shorter side. See also "Elongatedness Feature" on page 157.



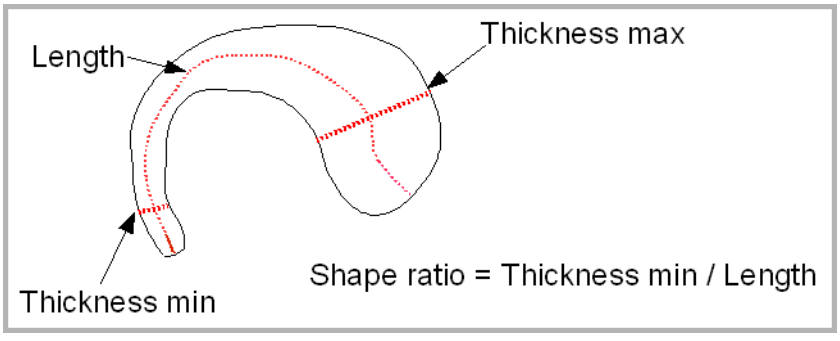
Application Example:

— These features can be used to separate rectangular shaped objects. For curved objects, measurement is more accurately obtained using the thickness features.

Length Feature

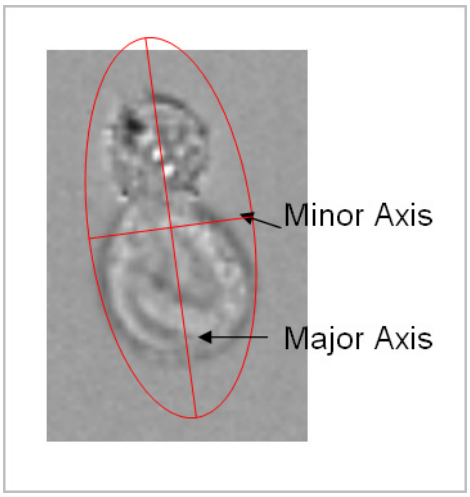
Length measures the longest part of an object. Unlike the Major Axis feature, Length can measure the object's length even if it folds to form a cashew, banana, or doughnut shape, where in many of these cases the major or minor axis features would not be able to differentiate these with true circular shaped objects with no hole.

This feature is based on an input mask and is sensitive to the variation of the input mask shape. Selecting an input mask that can accurately capture the object shape is important. See the "Shape Ratio Feature" on page 159, "Thickness Min Feature" on page 139, and "Thickness Max Feature" on page 139 for more information.



Major Axis and Minor Axis Features

The Major Axis is the longest dimension of an ellipse of best fit. The Minor Axis is the narrowest dimension of the ellipse of best fit. See the "Aspect Ratio Feature" on page 152 for more information.



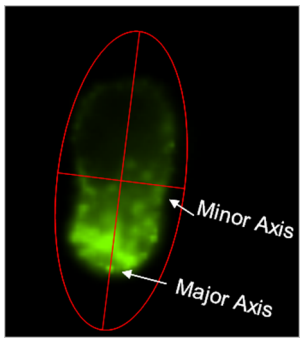
Application Examples:

— Quantify and compare cell shape.

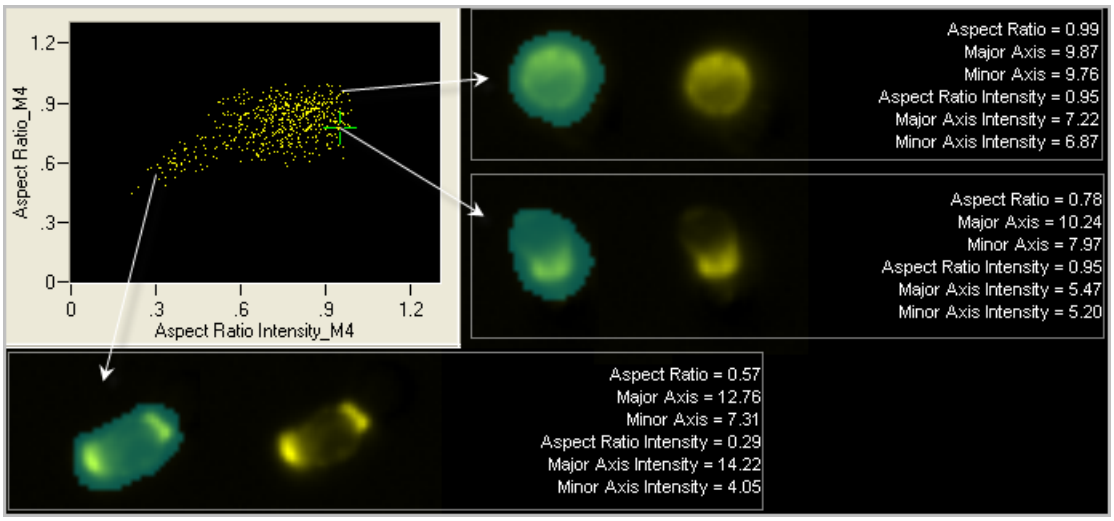
— Identify small, medium, and large cells.

Major Axis Intensity and Minor Axis Intensity Features

The Major Axis Intensity is the longest dimension of an ellipse of best fit and is intensity weighted. The Minor Axis Intensity is the narrowest dimension of the ellipse of best fit and is intensity weighted.



The figure below illustrates the difference between intensity weighted and non-intensity weighted Major or Minor Axis and Aspect Ratio. See the "Aspect Ratio Intensity Feature" on page 154 for more information.



Application Examples:

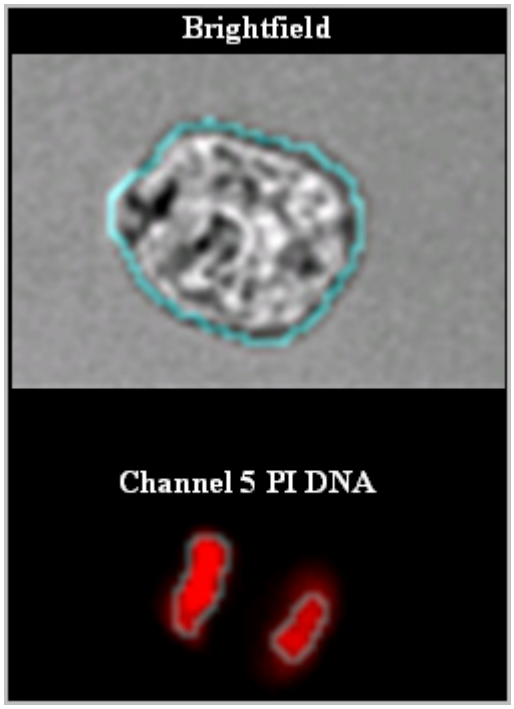
— Quantify and compare the image fluorescence shape.

— Identify single cells.

Perimeter Feature

The perimeter feature measures the boundary length of the mask in the number of microns.

This example uses a 1-pixel wide mask created to illustrate how a perimeter would appear.



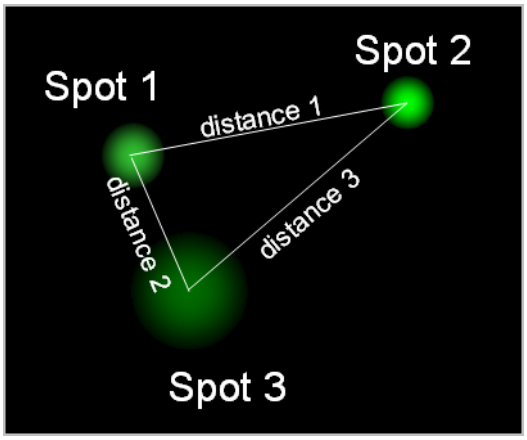
Application Examples:

- Quantify and compare cell circumference.
- Identify cells with highly irregular surfaces from smooth cells.
- Perimeter of the morphology or threshold masks can identify cells with or without dendrites.

Spot Area Min Feature

The Spot Area Min feature provides the area of the smallest spot (connected component) in a spot or peak mask.

This is one of four features that can be used to identify objects with spots that are close together, dim, bright or small when counting spots in an image. To use these features, the spots need to be individually masked, such as using the Spot or Peak Mask. The Spot Area Min, Spot Distance Min, and Spot Intensity Min or Max features measure properties of different spots in an image and are often used with the Spot Count feature (under Texture). For more information see "Raw Centroid X and Raw Centroid Y Features" on page 148"Spot Count Feature" on page 168"Spot Intensity Min and Spot Intensity Max Features" on page 181.



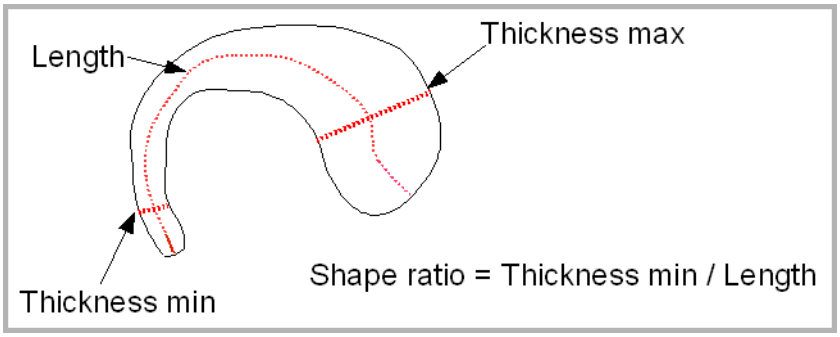
- Spot Area Min is the Area of spot 1
- Spot Distance Min is distance 2 in microns
- Spot Intensity Max is the Raw Mean Pixel of spot 2
- Spot Intensity Min is the Raw Mean Pixel value of spot 3

Application Example:

— In FISH Spot Counting, these features are used to identify objects with ambiguous spots that are located too close together, are too dim to count or are too small in order to remove these objects from the analysis.

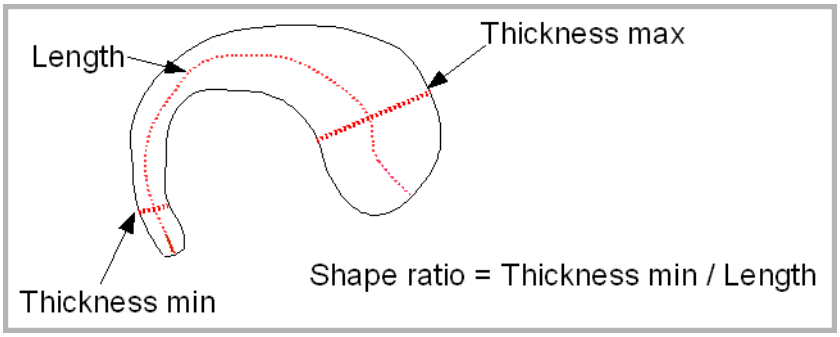
Thickness Max Feature

Thickness Max measures the largest width of an object. This feature is based on an input mask and therefore sensitive to the variation of the input mask shape. Selecting an input mask that can accurately capture the object shape is important. See also "Thickness Min Feature" on page 139, "Length Feature" on page 134 and "Shape Ratio Feature" on page 159 for more information.



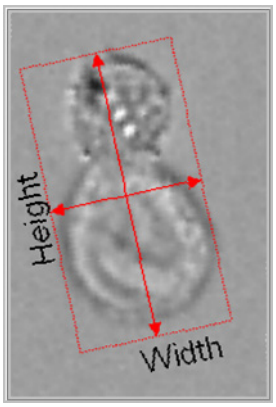
Thickness Min Feature

Thickness Min measures the smallest width of an object. This feature is based on an input mask and therefore sensitive to the variation of the input mask shape. Selecting an input mask that can accurately capture the object shape is important. See also "Thickness Max Feature" on page 139, "Length Feature" on page 134 and "Shape Ratio Feature" on page 159 for more information.



Width Feature

Using the bounding rectangle, Width is the number of microns of the smaller side and Height the longer side. See also "Elongatedness Feature" on page 157.



Application Example:

— These features can be used to separate rectangular shaped objects. For curved objects, measurement is more accurately obtained using the thickness features.

Understanding the Location Features

Location features include Angle, Angle Intensity, Centroid X, Centroid Y, Centroid X Intensity, Centroid Y Intensity, Delta Centroid X, Delta Centroid Y, Delta Centroid XY, Max Contour position, Spot Distance Min, Valley X and Valley Y.

Angle Feature

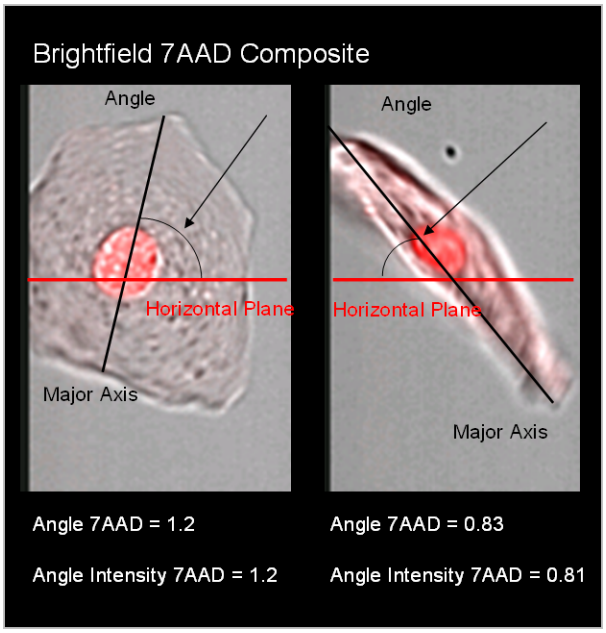
Angle is the angle of the major axis from a horizontal plane in radians.

Application Example:

— Identify the orientation of an image relative to the image frame.

Angle Intensity Feature

Angle Intensity is the angle of the major axis intensity from a horizontal plane in radians.



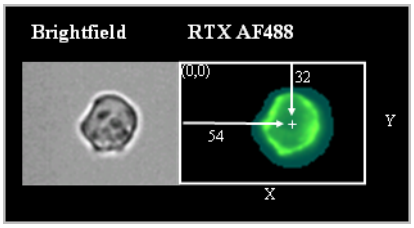
Application Example:

— Identify the orientation of an image relative to the image frame.

Centroid X and Centroid Y Features

Centroid X is the number of pixels in the horizontal axis from the upper, left corner of the image to the center of the mask. Centroid Y is the number of pixels in the vertical axis from the upper, left corner of the image to the center of the mask.

In this example, the Centroid X=54 and the Centroid Y=32.

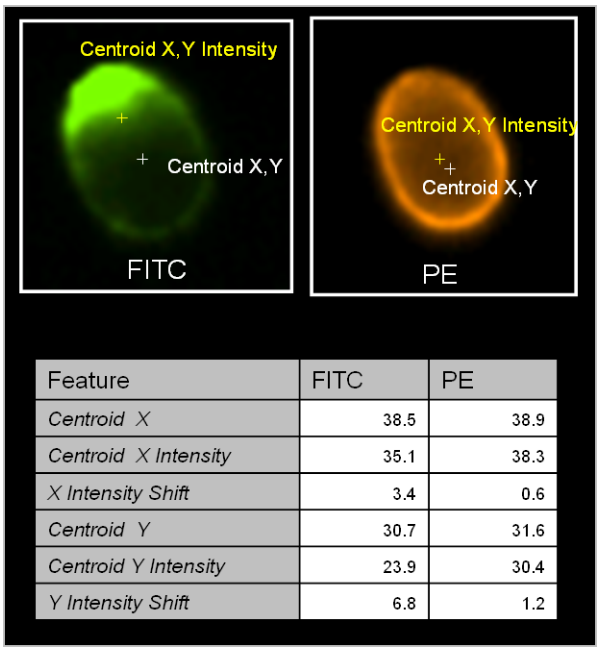


Application Examples:

- Identify the center of the mask.
- Calculate the Delta Centroid or the distance between two fluorescent markers.
- Used by IDEAS to calculate the Delta Centroid X, Y, or XY.

Centroid X Intensity and Centroid Y Intensity Features

Centroid X Intensity is the intensity weighted X centroid and is shifted from the center of the mask toward the center of fluorescence. The Centroid Y Intensity is the intensity weighted Y centroid. X and Y pixel coordinates are calculated from an origin in the upper left corner.



Feature	FITC	PE
Centroid X	38.5	38.9
Centroid X Intensity	35.1	38.3
X Intensity Shift	3.4	0.6
Centroid Y	30.7	31.6
Centroid Y Intensity	23.9	30.4
Y Intensity Shift	6.8	1.2

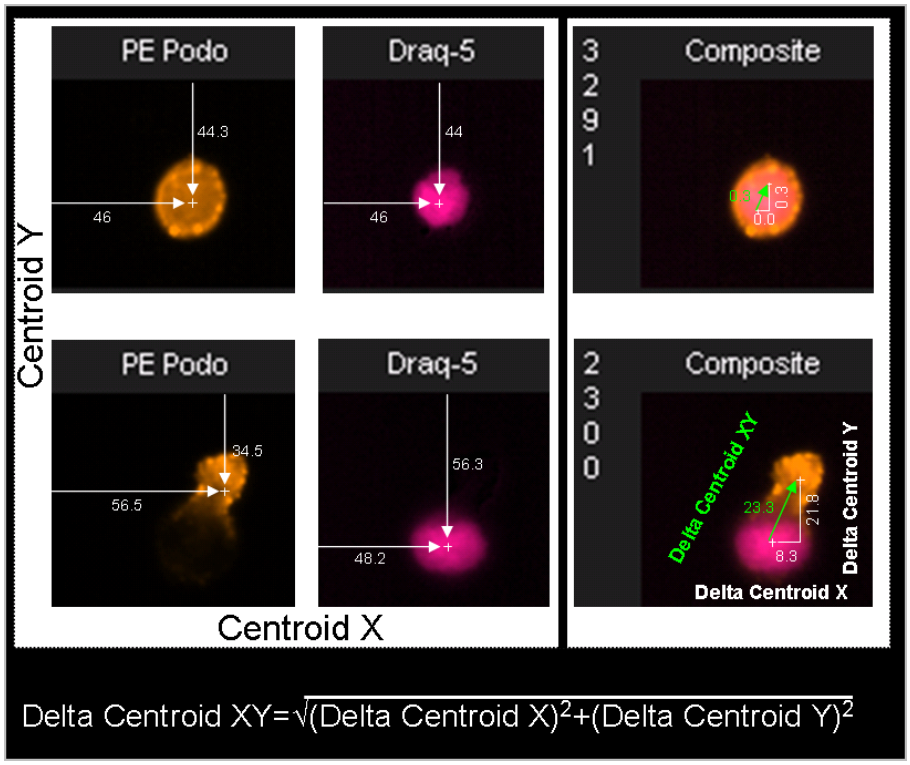
Application Examples:

- Identify the center of peak fluorescence.
- Calculate the distance between two fluorescent markers.
- Used by IDEAS to calculate the intensity weighted Delta Centroid X, Y or XY.

Delta Centroid X and Delta Centroid Y Features

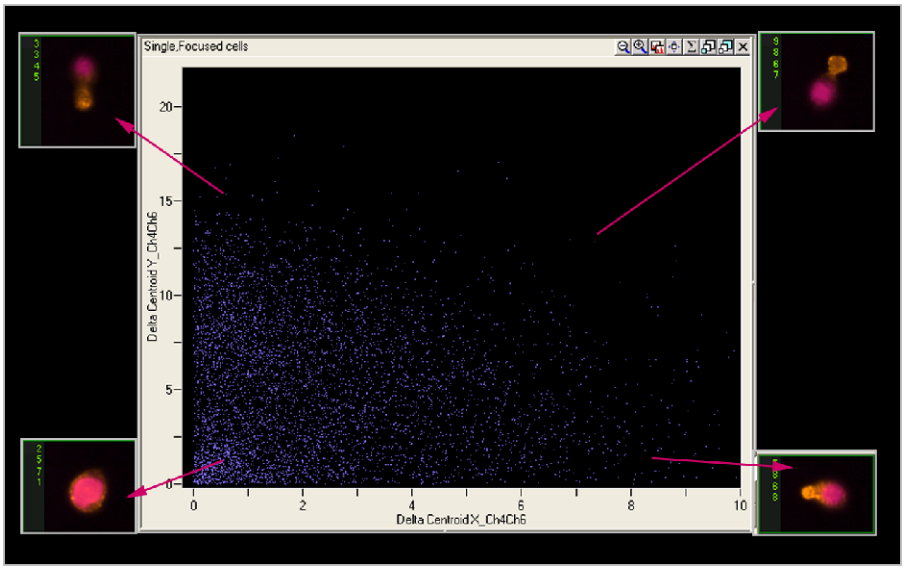
Both the Delta Centroid X and Y features measure the distance between the Centroids X or Centroids Y, respectively, of two images using the user-provided masks for each image. Either one or both the centroids of the images may be intensity-weighted. X and Y pixel coordinates are calculated from an origin in the upper left corner to obtain the centroid positions and the distance between the centroids is converted to microns.

An example is shown below.



The graph below illustrates using the Delta Centroid X versus Delta Centroid Y to identify cells with a variation of location of a protein with respect to the nucleus.

Cells with no spatial shift of signal between the nuclear stain(Ch6) and protein of interest(Ch4) have a low Delta Centroid X and Y and are found in the lower left corner. Cells with a large shift between the images in both the X and Y direction are found in the upper, right section and those with a large shift in X but not Y are found in the lower, right. Similarly a cell with a large shift in the Y direction and not X are found in the upper, left. See "Delta Centroid XY Feature" on page 145 to measure the X and Y shift together.



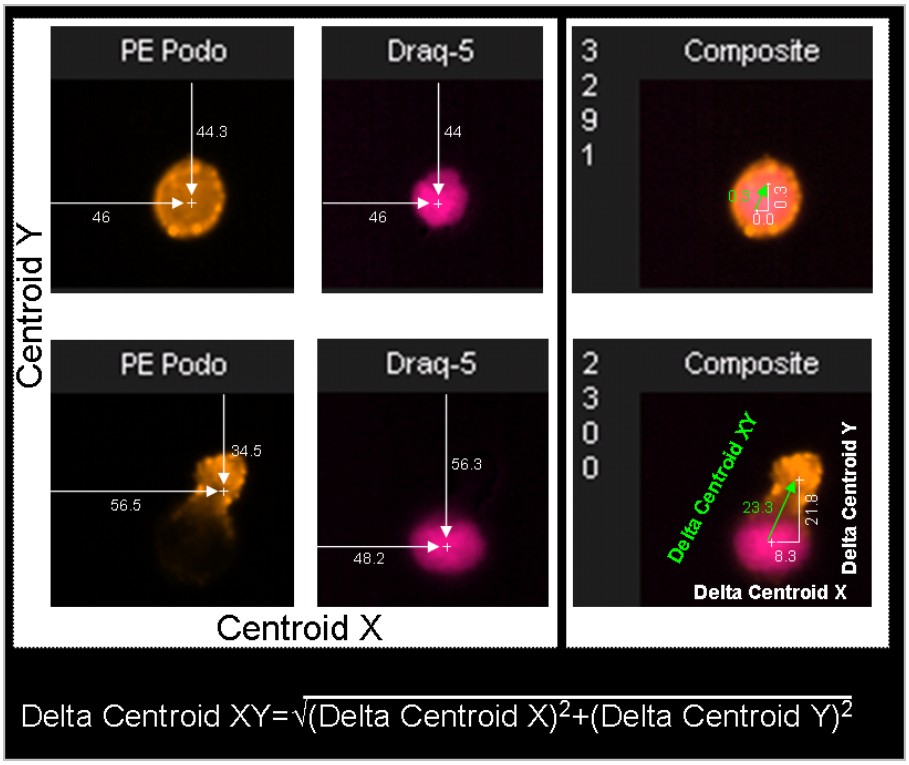
Application Example:

— Used to identify capped versus not capped cells.

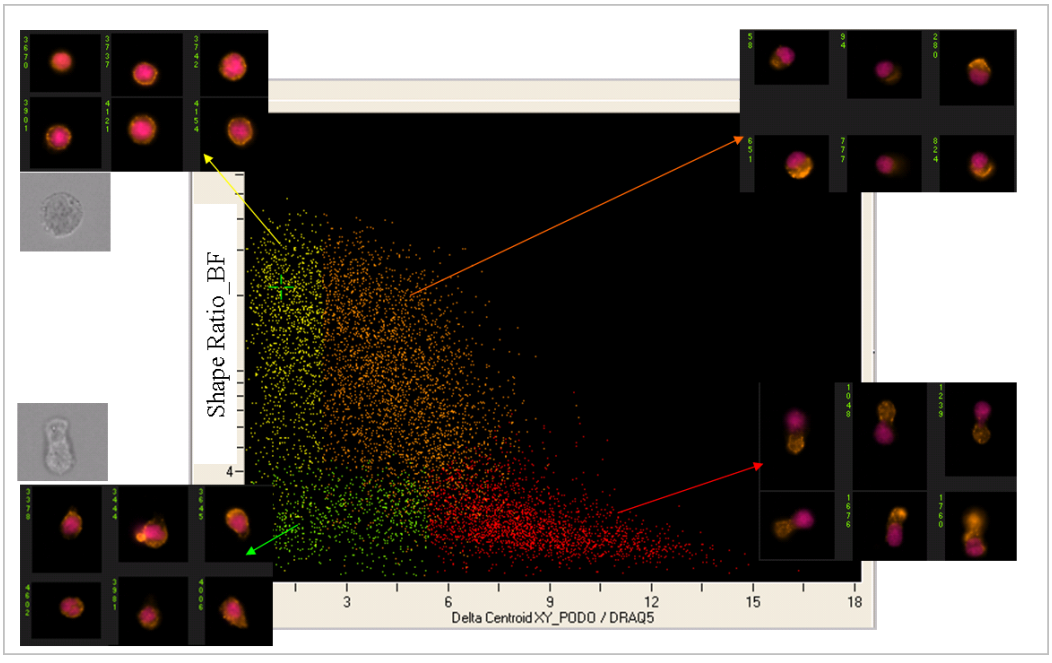
— Used to measure shifts in X or Y direction between two images.

Delta Centroid XY Feature

The Delta Centroid XY feature measures the distance between the Centroid feature of two images using the user-provided masks for each image. Either one or both the centroids of the images may be intensity-weighted. X and Y pixel coordinates are calculated from an origin in the upper left corner to obtain the centroid positions and the distance between the centroids is converted to microns. In the example, below an image pair is shown stained with the nuclear dye Draq 5 and a PE labeled antibody that is differentially expressed two cells, either uniformly or in the pseudopod. The two cells are identified by their different Delta Centroid XY values.



Below is an example of using the Delta Centroid XY. A bivariate graph of a shape ratio versus Delta Centroid XY can identify cells with caps as shown here:



Application Examples:

— Quantify the spatial relationship between two fluorescent probes.

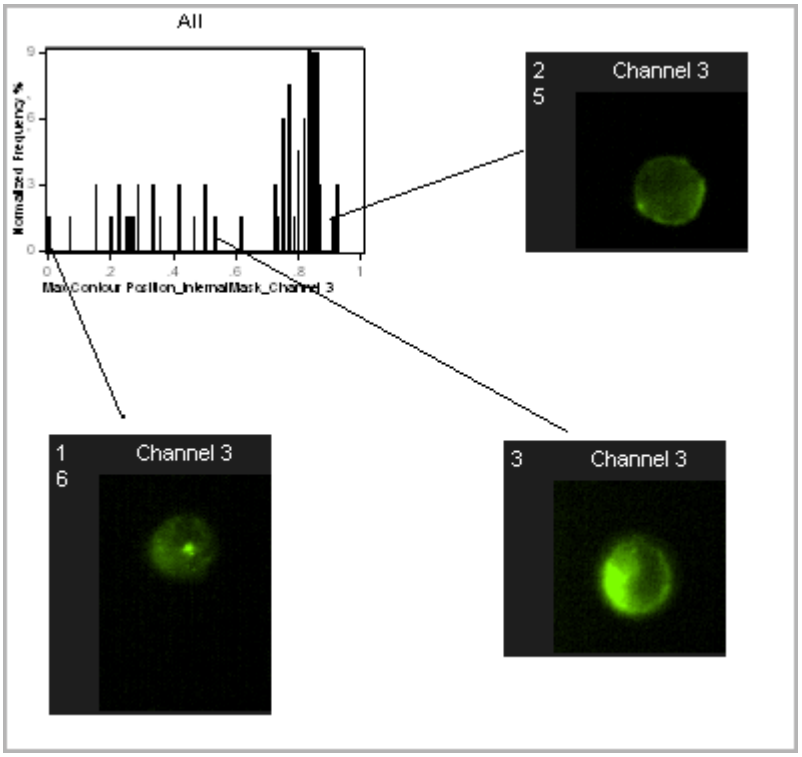
— Identify false apoptotic positive cells in the TUNEL and Annexin V assays.

— Quantify shape change.

— Quantify capping of cell surface antigens.

Max Contour Position Feature

The Max Contour Position is defined as the location of the contour in the cell that has the highest intensity concentration. It is invariant to object size and can accommodate localized intensity concentrations. The actual location in the object is mapped to a number between 0 and 1, with 0 being the object center and 1 being the object perimeter, which allows one to compare the results across cells of different sizes. An example is shown below.



Application Example:

— Used in conjunction with the Internalization feature to determine the distribution of intensity within a cell.

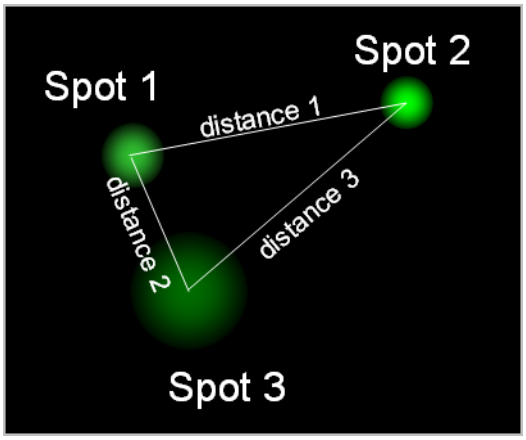
Raw Centroid X and Raw Centroid Y Features

The centroid X and Y of the original position of the image during acquisition before it was centered IDEAS. Data analyzed in IDEAS versions 4.0 or later cut and center objects that were collected as one image in INSPIRE.

Spot Distance Min Feature

The Spot Distance Min feature provides the shortest distance in microns between two spots (connected components) in a spot or peak mask.

This is one of four features that can be used to identify objects with spots that are close together, dim, bright or small when counting spots in an image. To use these features, the spots need to be individually masked, such as using the Spot or Peak Mask. The Spot Area, Distance, and Spopt Intensity Min or Max features measure properties of different spots in an image and are often used with the Spot Count feature (under Texture). For more information see "Spot Area Min Feature" on page 138; "Spot Count Feature" on page 168; "Spot Intensity Min and Spot Intensity Max Features" on page 181.



- Spot Area Min is the Area of spot 1
- Spot Distance Min is distance 2 in microns
- Spot Intensity Max is the Raw Mean Pixel of spot 2
- Spot Intensity Min is the Raw Mean Pixel value of spot 3

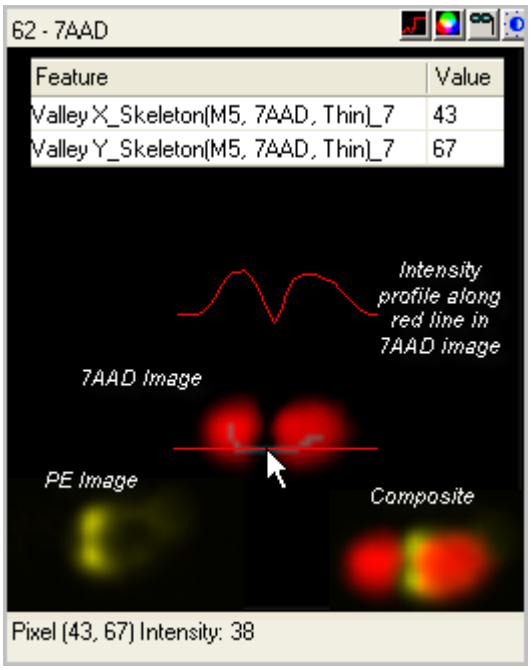
Application Example:

— In FISH Spot Counting, these features are used to identify ambiguous spots that are located too close together, too dim, to bright or too small to count and can be eliminated from the analysis.

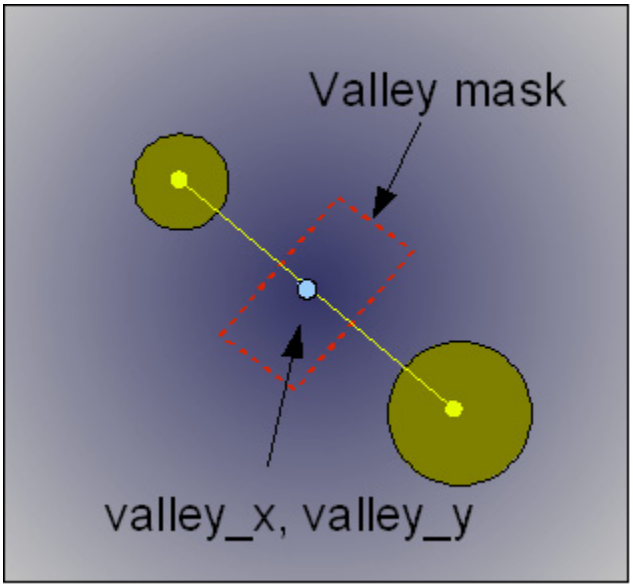
Valley X and Valley Y Features

The Valley X and Y are the exact X,Y coordinates of the minimum intensity within the skeletal lines of the input mask. The objects condensed shape, typically 1-pixel wide skeletal line is determined from the starting mask. This is also the origin of the Valley mask. See "Valley Mask" on page 203 and "Skeleton Mask" on page 198.

In the figure below, the Valley X and Valley Y position of the 7AAD image is shown. In this example a protein of interest in the PE image localizes to the synapse between two cells.



These features define the origin of the Valley mask.



Application Example:

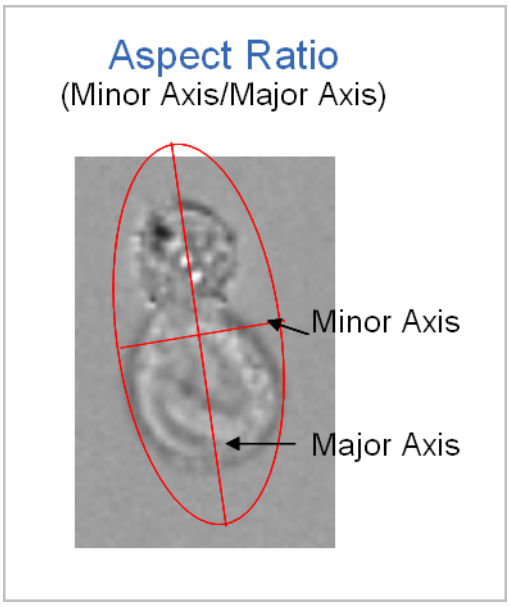
— Measure the exact center of where a synapse between two cells is located.

Understanding the Shape Features

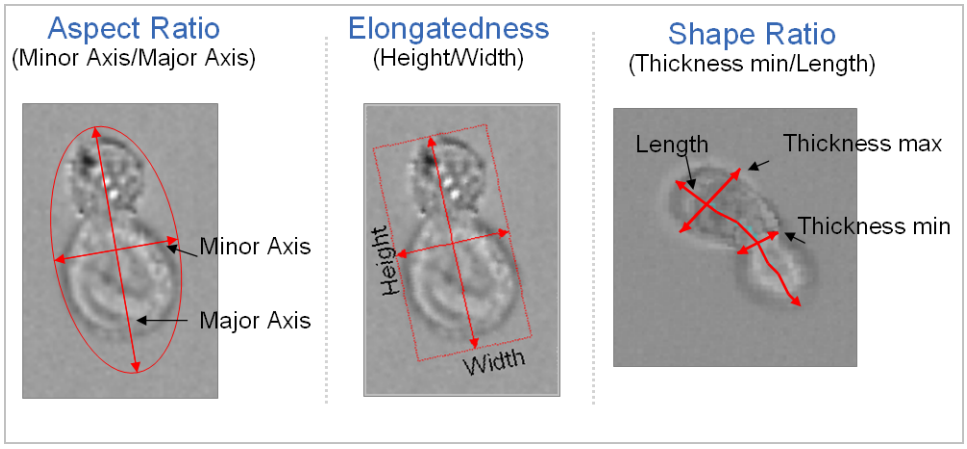
Shape features define the mask shape and have units that vary with the feature. They include the Aspect Ratio, Aspect Ratio Intensity, Compactness, Elongatedness, Lobe Count, and Symmetry 2,3,4.

Aspect Ratio Feature

Aspect Ratio is the Minor Axis divided by the Major Axis and describes how round or oblong an object is. See also: "Major Axis and Minor Axis Features" on page 135.



See also "Elongatedness Feature" on page 157 and "Shape Ratio Feature" on page 159 for other shape ratios.



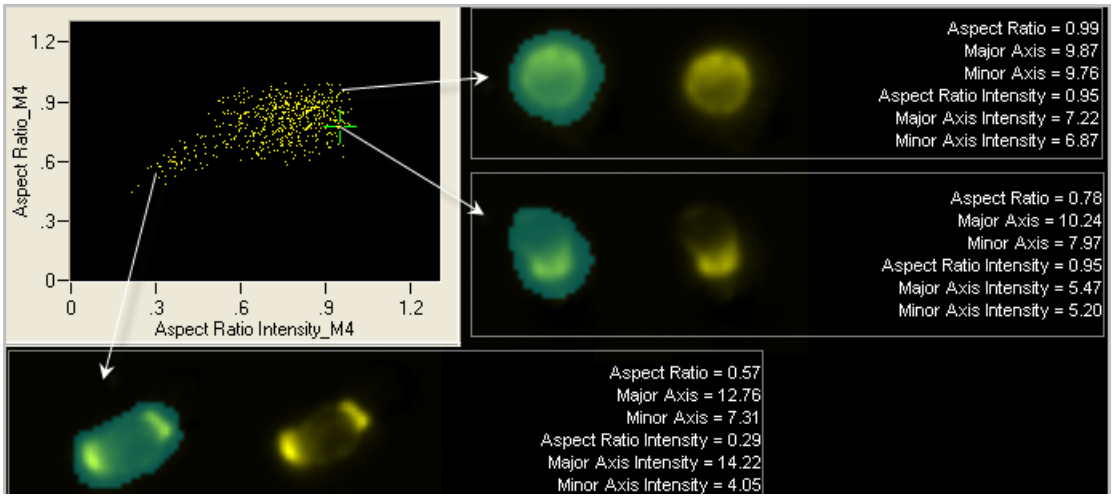
Application Examples:

— Quantify the roundness of the mask.
— Identify single cells vs. doublets.
— Cell classification based on shape change.
— Identify recently divided cells in mitosis.

Aspect Ratio Intensity Feature

Aspect Ratio Intensity is the Minor Axis Intensity divided by the Major Axis Intensity. See also: "Major Axis Intensity and Minor Axis Intensity Features" on page 136.

The figure below illustrates the difference between Aspect Ratio Intensity and Aspect Ratio. See also: "Aspect Ratio Feature" on page 152.

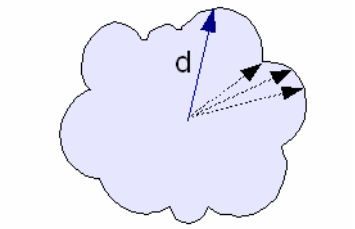


Application Examples:

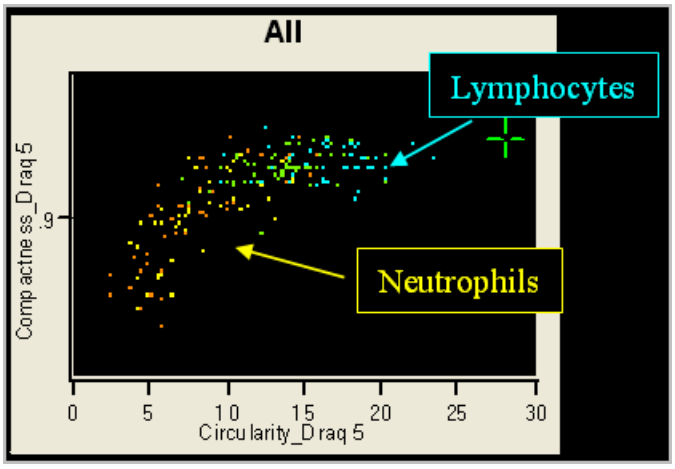
- Quantify the roundness of the fluorescent image.
- Better resolution for identifying single cells vs. doublets in experiments using a DNA dye.
- Cell classification based on fluorescent morphology.

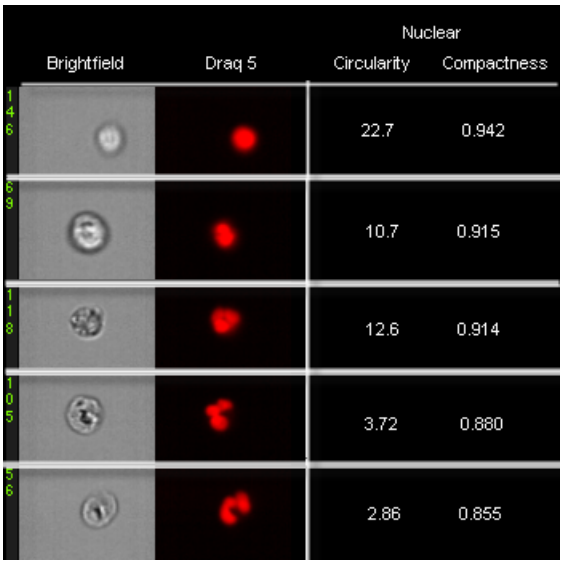
Circularity Feature

This feature measures the degree of the mask's deviation from a circle. Its measurement is based on the average distance of the object boundary from its center divided by the variation of this distance. Thus, the closer the object to a circle, the smaller the variation and therefore the feature value will be high. Vice versa, the more the shape deviates from a circle, the higher the variation and therefore the Circularity value will be low. See also "Compactness Feature" on page 156.



Below is an example using Circularity and Compactness to characterize the shape of peripheral blood mononuclear cells stained with the DNA dye Draq 5.





Application Examples:

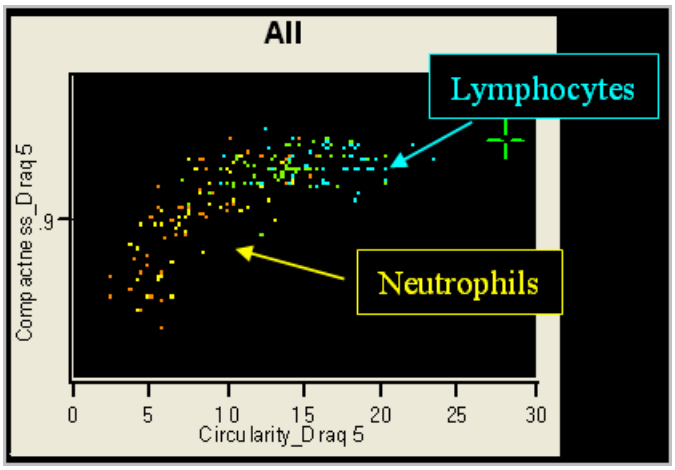
—Distinguish singlets and doublets.

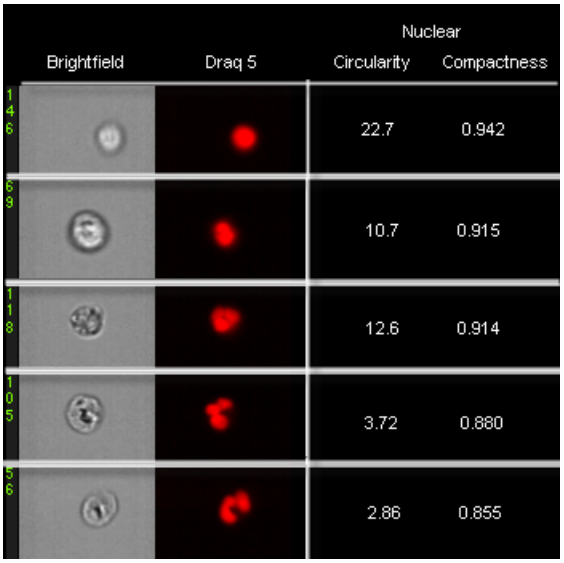
—Separate circular and non circular shapes.

Compactness Feature

Compactness measures the degree of how well the object is packed together. This feature is similar to the Circularity feature but unlike Circularity, this feature includes all of the pixels within the mask and is intensity weighted. The higher the value, the more condensed the object. See also "Circularity Feature" on page 154.

Below is an example using Circularity and Compactness to characterize the shape of peripheral blood mononuclear cells stained with the DNA dye Draq 5.



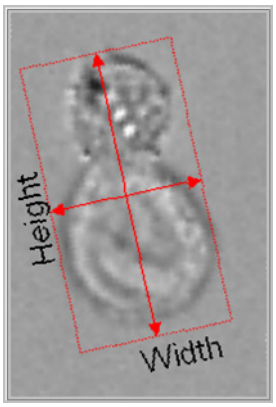


Application Example:

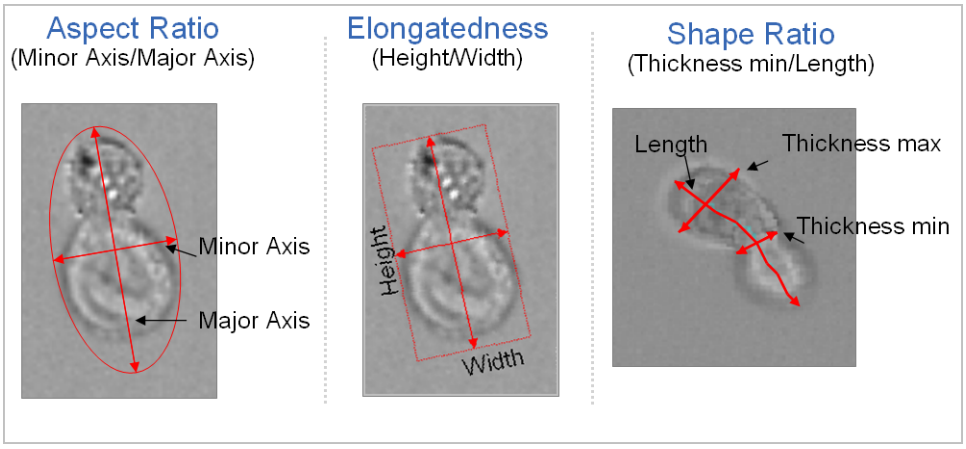
— Differentiate between rounded objects with smooth boundary to less regular objects.

Elongatedness Feature

Elongatedness is the ratio of the Height over Width of the object's bounding box. See also "Width Feature" on page 140.



See also "Aspect Ratio Feature" on page 152 and "Shape Ratio Feature" on page 159 for other shape ratios.



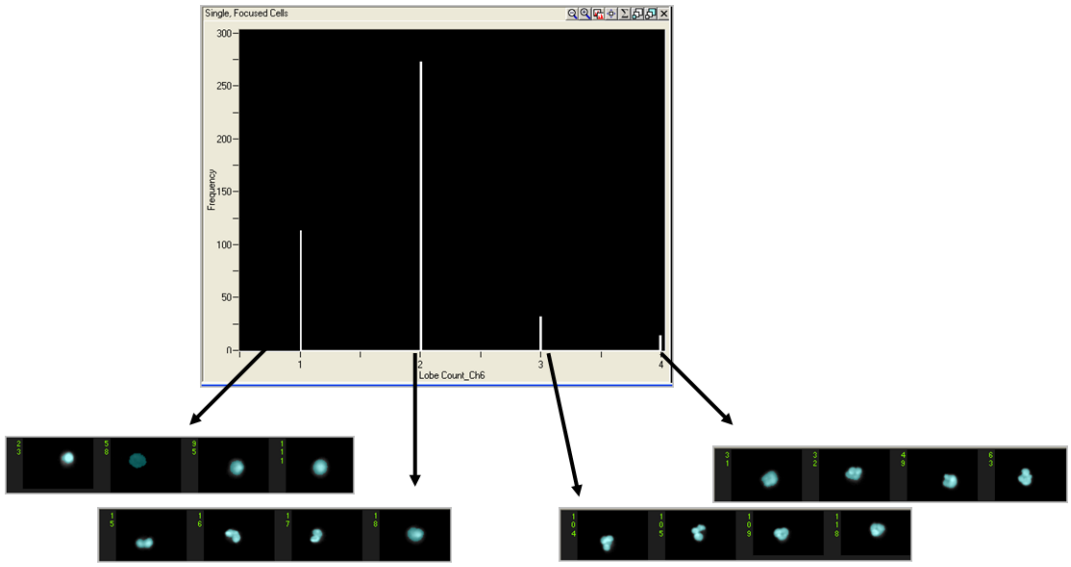
Application Examples:

- Measure object shape properties to differentiate between long and narrow versus short and thick objects.
- Quantify the roundness of the morphology mask.
- Identify single cells and doublets.
- Cell classification based on shape change.
- Identify recently divided cells in mitosis.

Lobe Count Feature

The Lobe Count feature counts the number of lobes in a cell. It is determined based on the maxima of the weighted Symmetry features. The feature reports the values 1,2,3 or 4. If an object does not have a high value for Symmetry 2, Symmetry 3, or Symmetry 4 it is reported as 1 for no lobes. An example is shown below. See also "Symmetry 2, 3, 4 Features" on page 160.

	Symmetry		
Lobe Count	2	3	4
1	Low	Low	Low
2	High	Low	Low
3	Low	High	Low
4	Low	Low	High



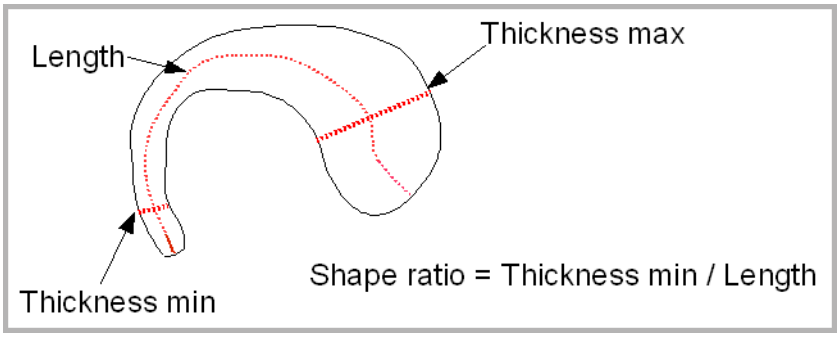
Application Example:

— Used in cell classification studies. Also used to differentiate small round cells from small square cells of similar area.

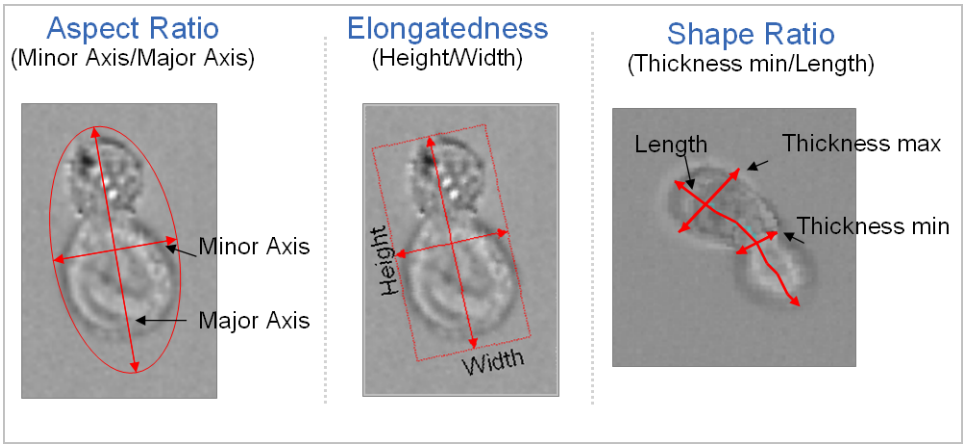
Shape Ratio Feature

The Shape Ratio is Thickness Min divided by Length.

The Shape Ratio feature is based on an input mask and is sensitive to the variation of the input mask shape. Selecting an input mask that can accurately capture the object shape is important.



See also "Aspect Ratio Feature" on page 152 and "Elongatedness Feature" on page 157 for other shape ratios.

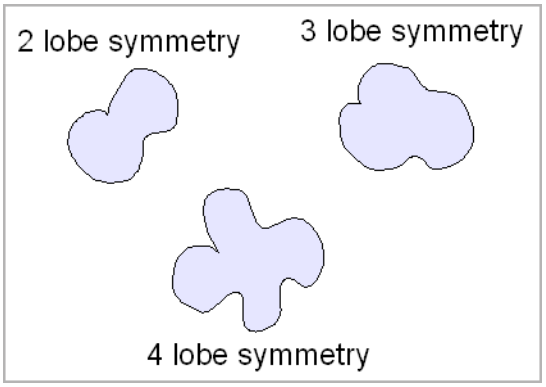


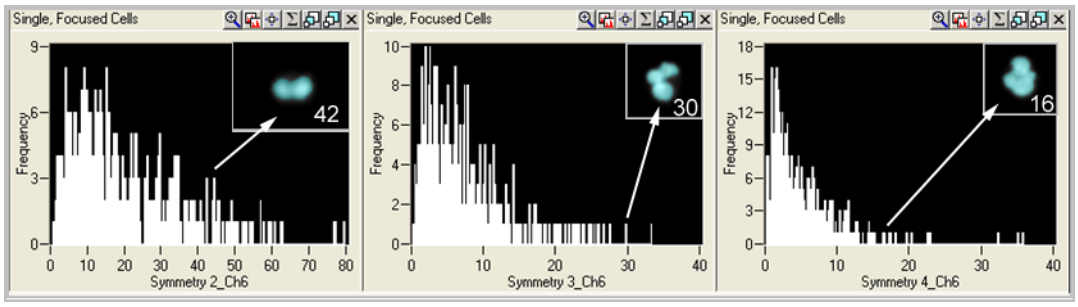
Application Example:

— Measure object's elongatedness to provide shape classification.

Symmetry 2, 3, 4 Features

The Symmetry 2 feature measures the tendency of the object to have a single axis of elongation and therefore 2 lobes. The Symmetry 3 feature measures the tendency of the object to have a three-fold axis of symmetry and likewise, Symmetry 4 a four-fold axis. The absolute value of these features are dependent on the number of lobes. For example an image that has high 4 lobe symmetry will also have high 2 lobe symmetry. See the "Lobe Count Feature" on page 158 for more information.





Application Example:

— Classify different white blood cells based on the morphology of the nuclear image.

Understanding the Texture Features

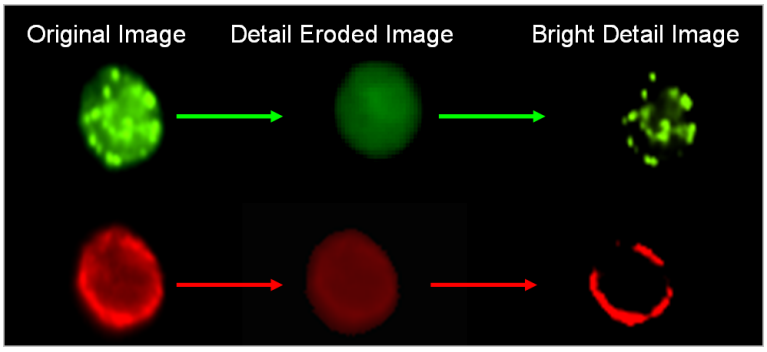
The Texture features determine local intensity variations in images and include Bright Detail Intensity R3 and Bright Detail Intensity R7, Contrast, Gradient Max, Gradient RMS, H Texture (H-Contrast, H-Correlation, H-Energy, H-Entropy, H-Homogeneity, and H-Variance), Modulation, Spot Count, and Std Dev.

Contrast, Gradient Max and Gradient RMS are generally used to determine best focus.

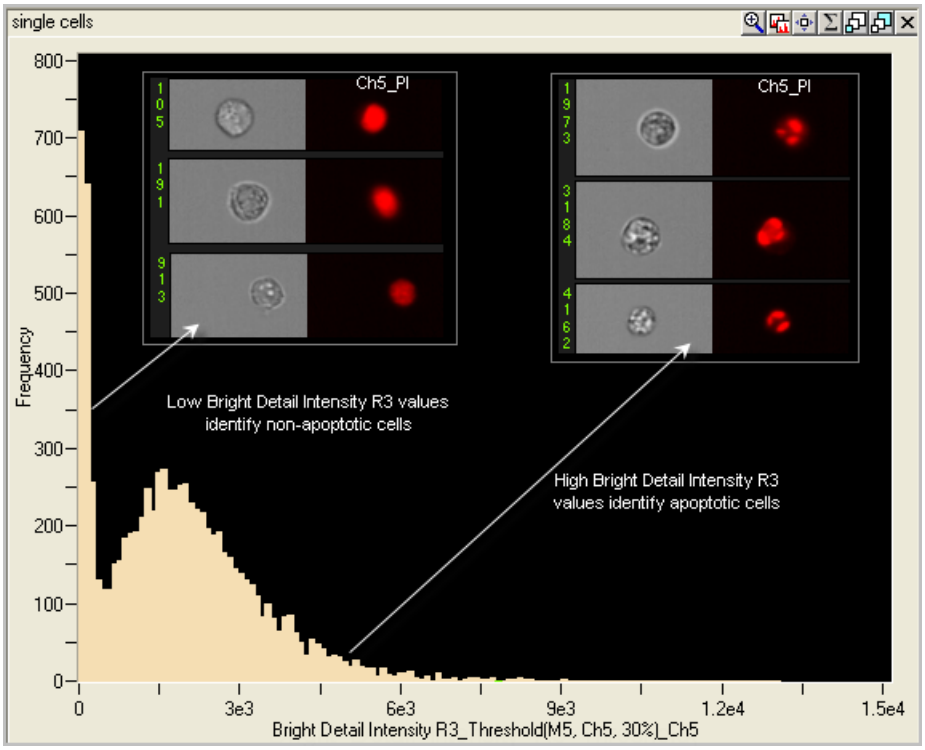
Bright Detail Intensity R3 and Bright detail Intensity R7 Features

The Bright Detail Intensity R3 and Bright Detail Intensity R7 features compute the intensity of localized bright spots within the masked area in the image. Bright Detail Intensity R3 computes the intensity of bright spots that are 3 pixels in radius or less, while Bright Detail Intensity R7 computes the intensity of bright spots in the image that are 7 pixels in radius or less. In each case, the local background around the spots is removed before the intensity computation.

The figure below shows the process of obtaining the localized bright spots in the image.



The graph below illustrates the use of the Bright Detail Intensity R3 feature on a nuclear image to separate apoptotic cells from non-apoptotic cells.

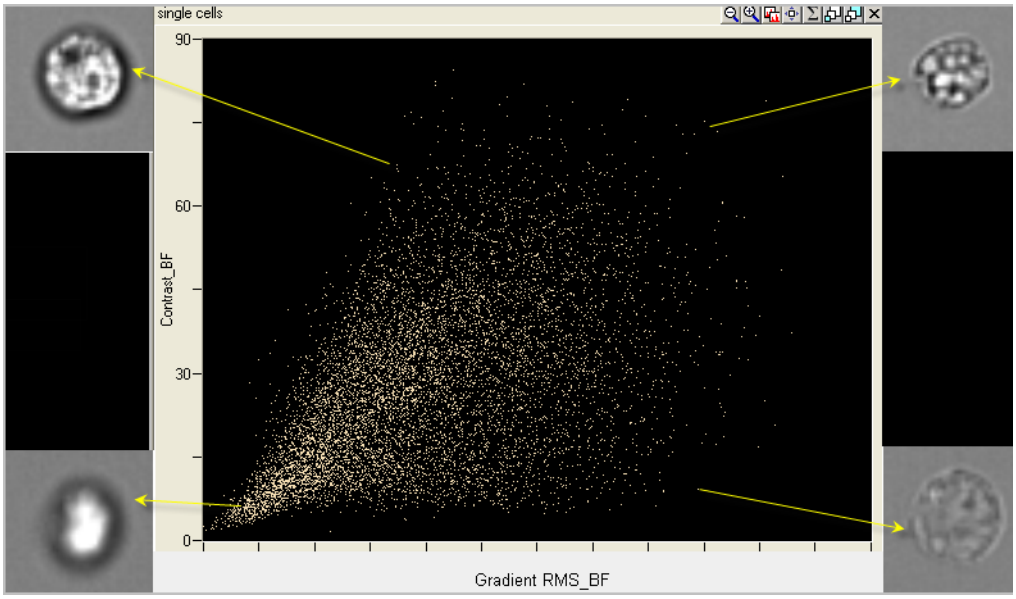


Application Example:

— Identify cells that have bright specks such as Apoptotic cells.

Contrast Feature

The Contrast feature measures the sharpness quality of an image by detecting large changes of pixel values in the image and is useful for the selection of focused objects or apoptotic brightfield images. For every pixel, the slopes of the pixel intensities are computed using the 3x3 block around the pixel. This is similar to the Gradient RMS calculation with different weighted assignments to the pixel arrays with no background subtraction. Example images are shown in the figure below.



Application Examples:

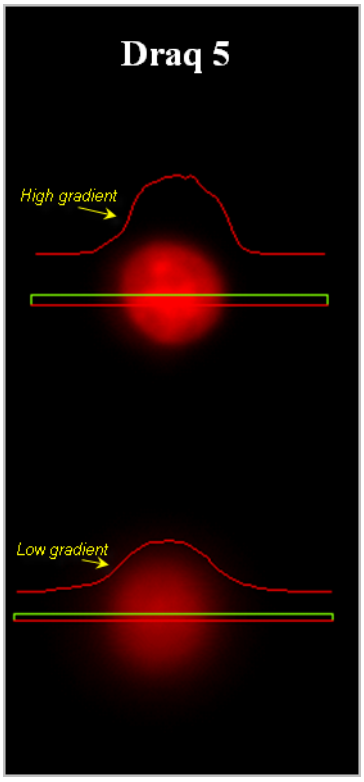
- Find apoptotic images with high contrast in brightfield imagery.
- Determine overall focus quality of images.
- Use with Gradient RMS to determine focus quality.
- Characterize texture.

See also: "Gradient Max Feature" on page 164 and "Gradient RMS Feature" on page 165.

Gradient Max Feature

The Gradient Max feature measures the sharpness quality of an image by detecting largest change of pixel values in the image and is useful for the selection of focused objects.

This figure shows the change in intensity across the red line. The top image has a larger slope change than the lower image.



Application Example:

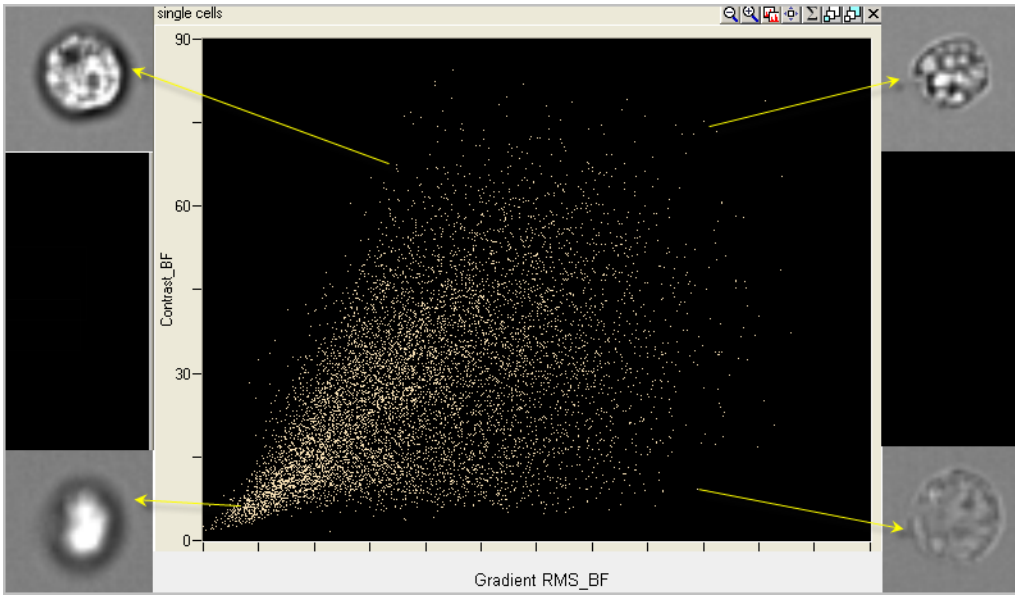
— Determine peak focus quality of images.

— Also used to characterize texture. However, the Gradient RMS and Contrast feature are more robust for these applications.

See also: "Gradient RMS Feature" on page 165 and "Contrast Feature" on page 163.

Gradient RMS Feature

The Gradient RMS feature measures the sharpness quality of an image by detecting large changes of pixel values in the image and is useful for the selection of focused objects. The Gradient RMS feature is computed using the average gradient of a pixel normalized for variations in intensity levels. This is similar to the Contrast calculation with different weighted assignments to the pixel arrays and with background subtracted. Example images are shown in the figure below.



Application Examples:

- Determine overall focus quality of images.
- Used with Contrast to determine focus quality.
- Characterize texture.

See also: "Gradient Max Feature" on page 164 and "Contrast Feature" on page 163.

H Texture Features

H Texture features include the following: H Energy Mean and Std, H Entropy Mean and Std, H Contrast Mean and Std, H Homogeneity Mean and Std, H Correlation Mean and Std, H Variance Mean and Std Features.

R.M. Haralick (H) defined a set of texture features that characterize the spatial relationships amongst the pixel values in an image[1]. IDEAS uses a common normalization method so that images with different intensities can be directly compared. For each H texture feature, the mean reflects the average value and the standard deviation (Std) reflects the presence of texture orientation.

The user defines the texture grain by assigning a granularity value. For very fine textures, this value is small (1-3 pixels), while for very coarse textures, it is large (>10). In the IDEAS default template, the granularity value is 5.

While these features have value for distinguishing cellular texture when used individually, images often contain a mixture of different textures at different grains. Therefore, these features are most powerful when combined.

Application Example:

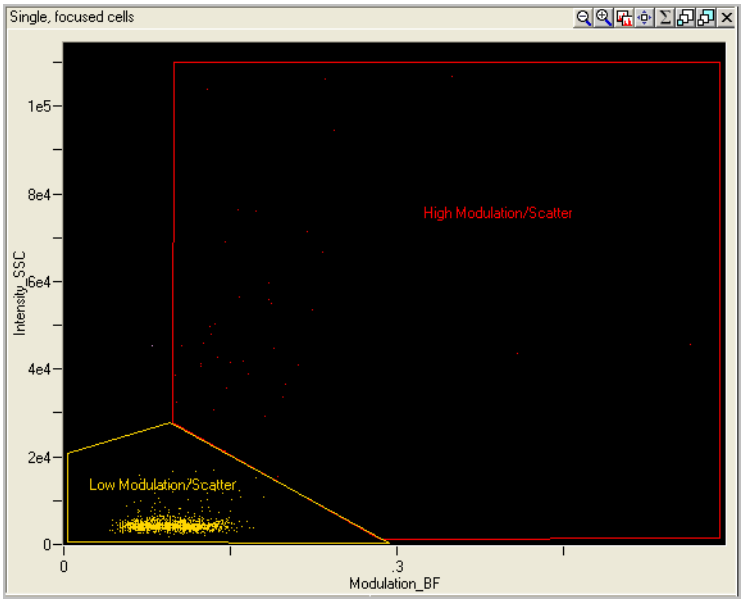
— Quantify texture in cells.

[1]Haralick, R.M., K. Shanmugan, and I. Dinstein, "Textural Features for Image Classification", *IEEE Transactions on Systems, Man, and Cybernetics*, Vol. SMC-3, 1973, pp. 610-621.

Modulation Feature

The Modulation feature measures the intensity range of an image, normalized between 0 and 1.

The following example illustrates Modulation on brightfield images and Intensity of scatter in channel 1.



High Modulation

Low Modulation

Low Modulation

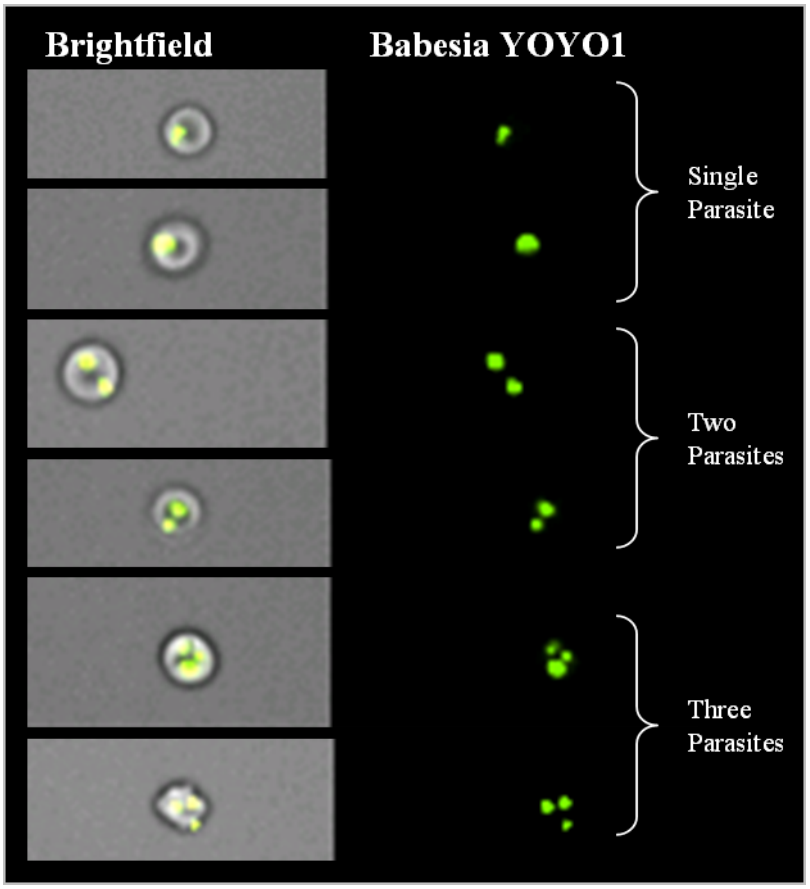
Application Example:

— Quantify image quality and characterize contrast and texture in cells.

Spot Count Feature

The Spot Count feature provides the number of connected components in an image. The connected component algorithm examines the connectivity of each pixel based on whether this pixel is connected to a particular spot or the background. In order to count the number of connected components the mask input is very important. See "Spot Mask" on page 199, "Peak Mask" on page 197, and "Range Mask" on page 197 for information on masking spots. See also "Spot Area Min Feature" on page 138, "Raw Centroid X and Raw Centroid Y Features" on page 148, and"Spot Intensity Min and Spot Intensity Max Features" on page 181 for more information.

The following figure illustrates the application of Spot Counting to quantify parasitic infection of Babesia in erythrocytes by staining nuclei with YOYO (green).



Application Examples:

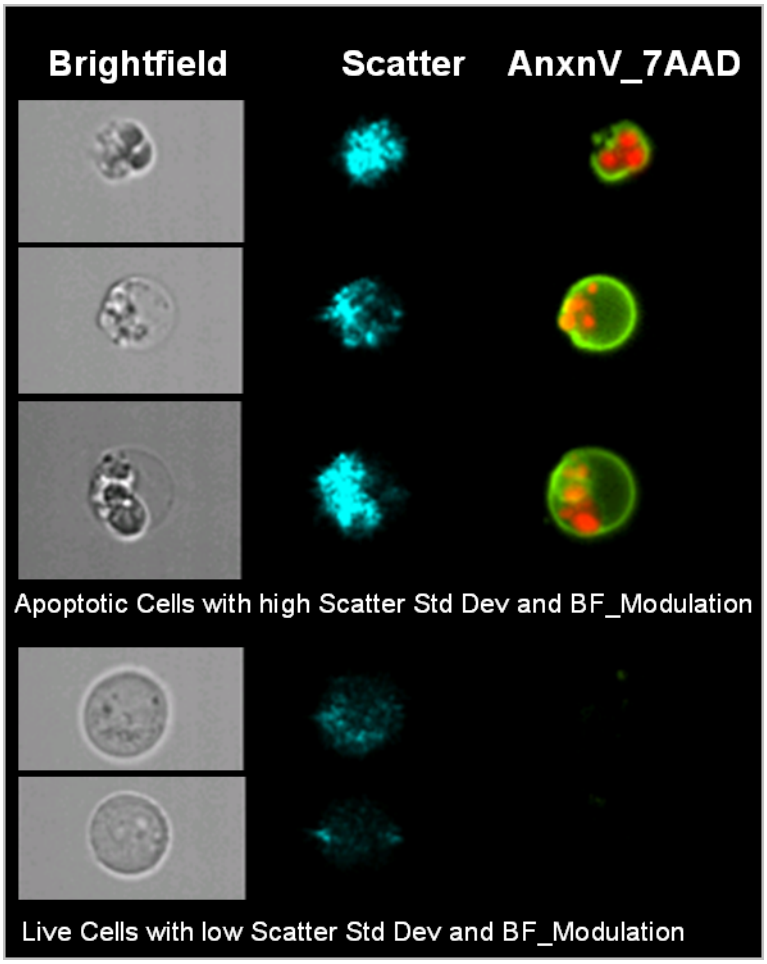
- Counting parasites.
- Counting phagocytosed particles.
- FISH spot counting.
- Counting punctate spots in images.

Std Dev Feature

The Std Dev feature describes the overall distribution of pixel intensities.

The Std Dev is the standard deviation of the pixel intensity values in the mask. The Std Dev value provides an indication of the texture or complexity of an object.

The following illustrates that apoptotic cells (AnxnV positive) exhibit higher Std Dev values in the darkfield channel (scatter) and higher brightfield Modulation values than non-apoptotic cells (AnxnV negative).



Application Example:

— Quantify intensity variation within a mask.
— Distinguish apoptotic and necrotic cells.

Understanding the Signal Strength Features

Signal Strength features include the following:

- Bkgd Mean and Bkgd StdDev features describe the background of the image.
- Intensity and Raw Intensity features quantify the intensities in the region of interest.
- Raw Max, Raw Min, Raw Mean and Raw Median Pixel report single pixel values in an image.
- Max, Min, Mean and Median Pixel report background subtracted single pixel values in an image.
- Saturation Count and Saturation Percent quantify the saturated pixels.
- Spot Intensity Min is used when counting spots.

Bkgd Mean Feature

The Bkgd Mean feature estimates the average camera background level in an image by taking the mean of the background pixels.

Application Examples:

— Obtain estimate of the mean camera background level.

— Compute background-subtracted pixel values in other feature computations.

Bkgd StdDev Feature

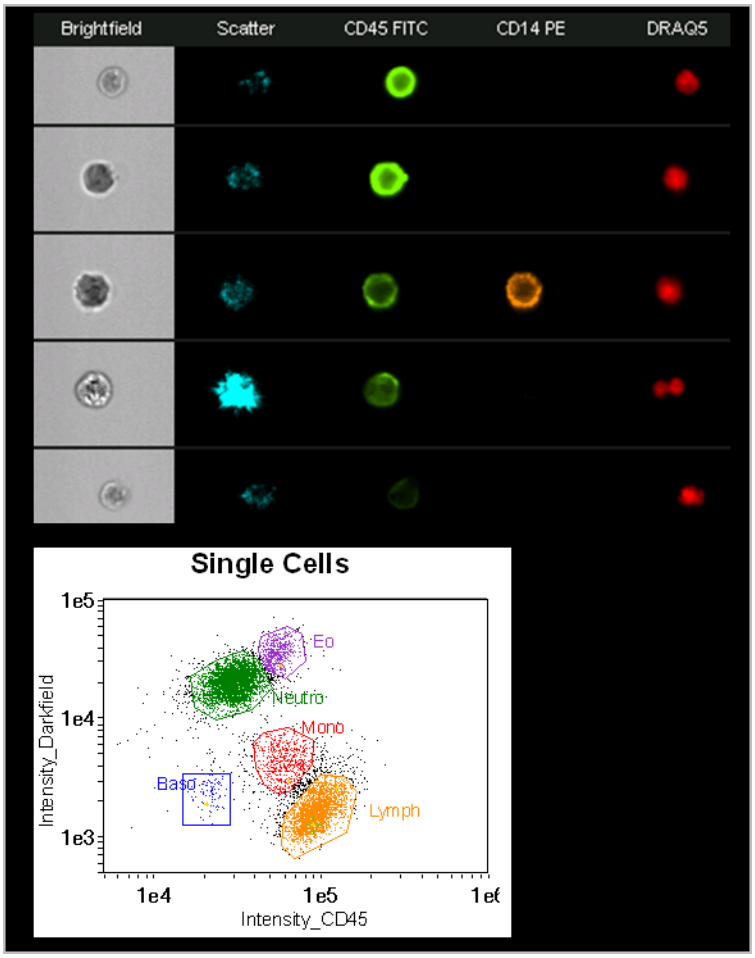
The Bkgd Std Dev feature estimates the standard deviation of the camera background level in an image computed using the background pixels.

Application Example:

— Obtain estimate of the camera background noise.

Intensity Feature

The Intensity feature is the sum of the background subtracted pixel values within the masked area of the image.



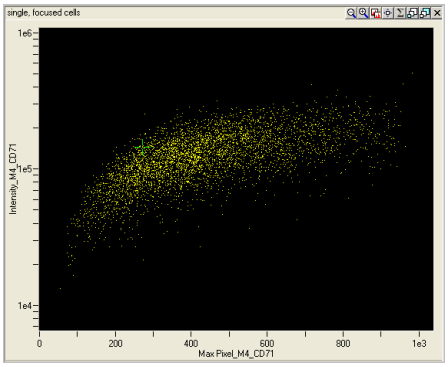
Application Examples:

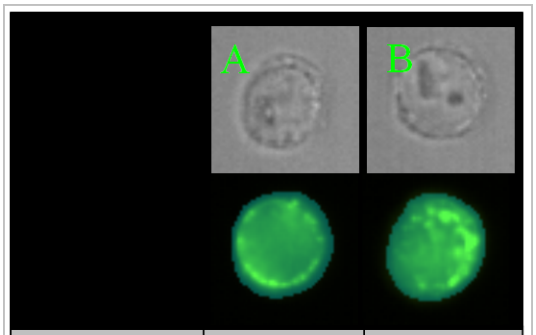
- Quantify relative levels of fluorescence between cells and within different regions of the same cell.
- Immunophenotyping.
- Cell cycle analysis.
- Protein expression.
- Protein activation.

Max Pixel Feature

The Max Pixel feature is the largest value of the background-subtracted pixels contained in the input mask. An example plot is shown below that demonstrates the advantage of using this feature over the Intensity feature for identifying true positive events. For a concentrated signal, Max Pixel is more sensitive than Intensity as shown in the figure below.

The relationship of Max, Mean, Median, and Min Pixel is shown in the figure below:





FITC	Cell A	Cell B
Max Pixel	576	838
Mean Pixel	152	152
Median Pixel	178	130
Min Pixel	-0.05	-0.1
Intensity	230,000	230,000

Application Examples:

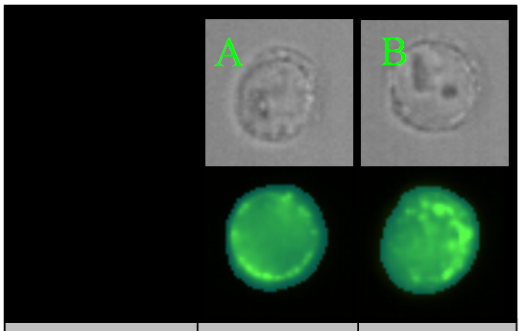
— Used to estimate the true peak fluorescence activity. Is preferred over the Raw Max Pixel for this application.

— Max Pixel to Mean Pixel ratio identifies bright punctate staining vs. uniform staining.

Mean Pixel Feature

The Mean Pixel feature is the mean of the background-subtracted pixels contained in the input mask. This is computed as Intensity/number of pixels.

The relationship of Max, Mean, Median and Min Pixel is shown in the figure below:



FITC	Cell A	Cell B
Max Pixel	576	838
Mean Pixel	152	152
Median Pixel	178	130
Min Pixel	-0.05	-0.1
Intensity	230,000	230,000

Application Examples:

— Estimate the average fluorescence activity. This feature is preferred over the Raw Mean Pixel feature.

— Quantify relative levels of mean fluorescence between cells.

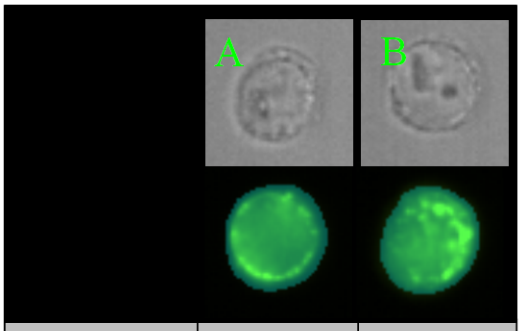
— Identify bright punctate spots by calculating the max to mean pixel ratio.

— Track internalization of surface bound antibodies.

Median Pixel Feature

The Median Pixel feature is the median of the background-subtracted pixels contained in the input mask. It is more robust than the mean as an estimate of the average fluorescence since it is less influenced by outliers.

The relationship of Max, Mean, Median and Min Pixel is shown in the figure below:



FITC	Cell A	Cell B
Max Pixel	576	838
Mean Pixel	152	152
Median Pixel	178	130
Min Pixel	-0.05	-0.1
Intensity	230,000	230,000

Application Example:

— Estimate the average fluorescence activity. This feature is preferred over the Raw Median Pixel feature.

Min Pixel Feature

The Min Pixel feature is the smallest value of the background-subtracted pixels contained in the input mask. There will be some negative numbers due to the background subtraction, therefore the Raw Min Pixel feature is preferred.

Application Examples:

— Obtain the minimum value in an image after background subtraction. Very likely to be negative in brightfield imagery.

— Quantify spectral absorbance using the brightfield image.

— Identify over compensated images.

Raw Intensity Feature

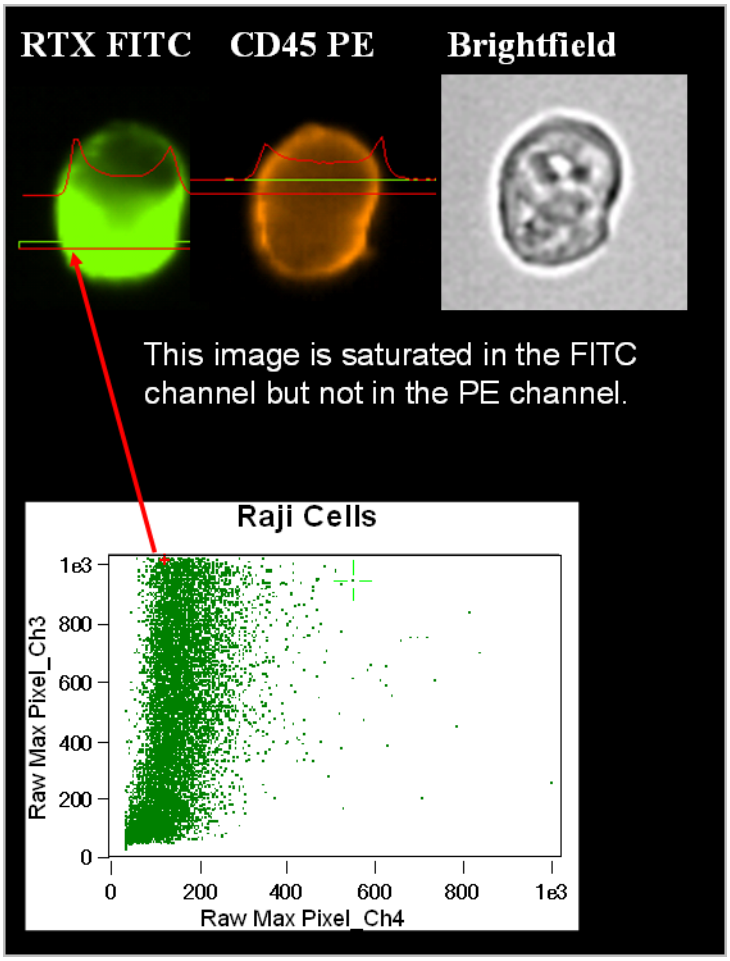
The Raw Intensity feature is the sum of the pixel values within the mask including camera background.

Application Example:

— Estimate raw fluorescence activity. This feature is less relevant than the Intensity feature because it includes camera background intensity.

Raw Max Pixel Feature

The Raw Max Pixel feature is the largest value of the pixels contained in the input mask.



Application Examples:

— Determine the presence of saturated events.

— May also be used to estimate the peak fluorescence activity, though the Max Pixel feature is recommended for this application.

— Measure the maximum pixel value within the mask.

— Identify cells that saturate the CCD, Saturation Count feature can also be used for this application.

Raw Mean Pixel Feature

The Raw Mean Pixel feature is the mean of the pixels contained in the input mask. This is computed as Raw Intensity/number of pixels.

Application Example:

— Estimate the raw average fluorescence activity. This feature is less relevant that the Mean Pixel feature.

Raw Median Pixel Feature

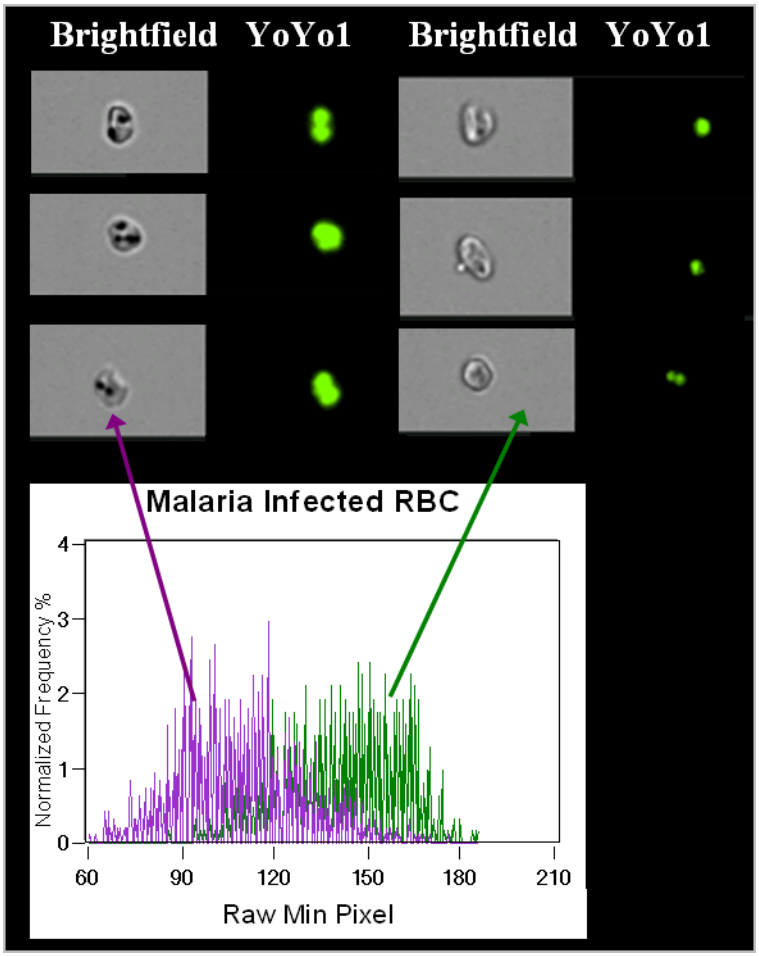
The Raw Median Pixel feature is the median of the pixels contained in the input mask.

Application Example:

— Estimate the raw average fluorescence activity that is robust to outliers. This feature is less relevant than the Median Pixel feature.

Raw Min Pixel Feature

The Raw Min Pixel feature is the smallest value of the pixels contained in the input mask. The example below illustrates quantifying the level of malarial infected cells by using Min Pixel values of brightfield imagery.



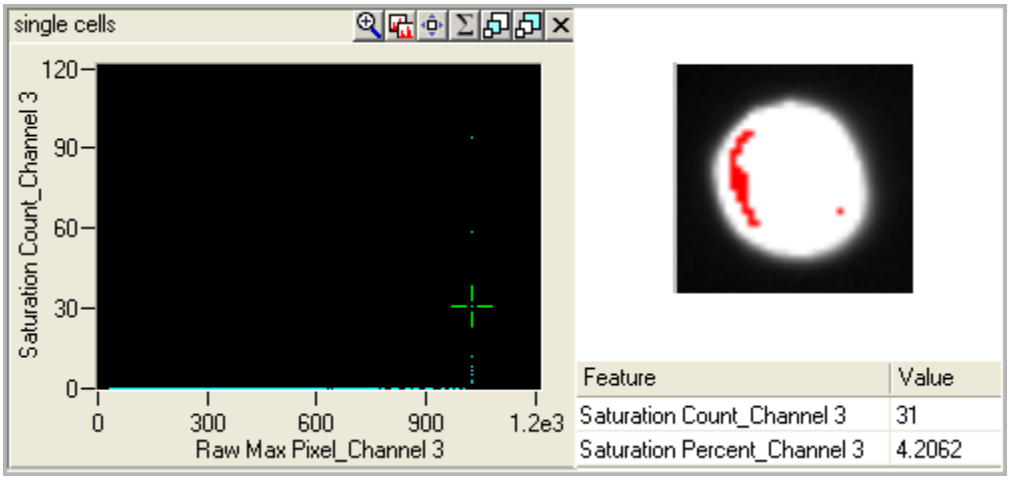
Application Example:

— Quantify spectral absorbance using the brightfield image.
— Identify over compensated images.
— Measure the level of malaria infection in RBCs.

Saturation Count Feature

The Saturation Count feature reports the number of saturated pixels in an object. See also "Saturation Percent Features" on page 180.

In the figure below, objects with saturated pixels are lined up at the Raw Max Pixel value of 1023 and a selected image is shown with saturated pixels in red.



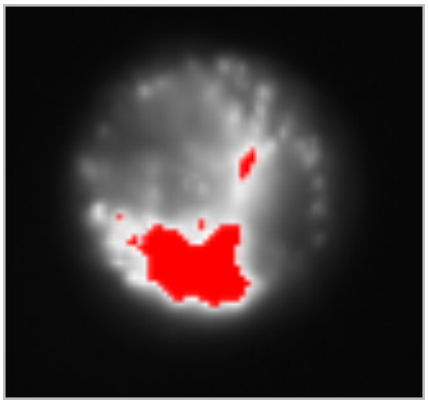
Application Example:

— Measure the validity of the experiment setup. Saturated data may not produce useful information.

Saturation Percent Features

The Saturation Percent feature reports the percentage of saturated pixels in an image. Pixel intensities are measured on the camera pixels from 0 to 1023 (10 bit) and therefore become saturated and cannot be quantified after 1023. See also "Saturation Count Feature" on page 179.

An object with saturated pixels shown in red:



Application Example:

— Measure the validity of the experiment setup. Saturated data may not produce useful information.

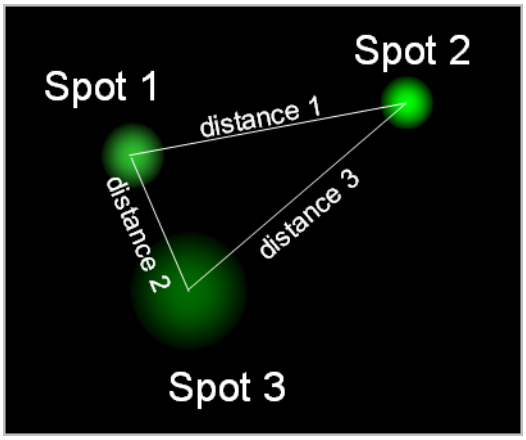
Spot Intensity Min and Spot Intensity Max Features

Spot Intensity Min provides the smallest Raw Mean Pixel value (not background subtracted) of the dimmest spot (connected component). The Raw Mean Pixel values for each spot is computed and the smallest value is reported.

Spot Intensity Max provides the largest Raw Mean Pixel value (not background subtracted) of the brightest spot (connected component). The Raw Mean Pixel values for each spot is computed and the largest value is reported.

These are two of four features that can be used to identify objects with spots that are close together, dim, bright or small when counting spots in an image. To use these features, the spots need to be individually masked, such as using the Spot or Peak Mask. The Spot Area, Distance, and Intensity Min or Max features measure properties of different spots in an image and are often used with the Spot Count feature (under Texture). Spot Area Min (Size) provides the area of the smallest spot. Spot Distance Min (Location) provides the shortest distance between two spots. See also "Spot Area Min Feature" on page 138, "Raw Centroid X and Raw Centroid Y Features" on page 148, and "Spot Count Feature" on page 168.

The following diagram illustrates these features:



- Spot Area Min is the Area of spot 1
- Spot Distance Min is distance 2 in microns
- Spot Intensity Max is the Raw Mean Pixel value of spot 2
- Spot Intensity Min is the Raw Mean Pixel value of spot 3

Application Example:

— In FISH Spot Counting, these features are used to identify ambiguous spots that are located too close together, too dim, to bright or too small to count and can be eliminated from the analysis.

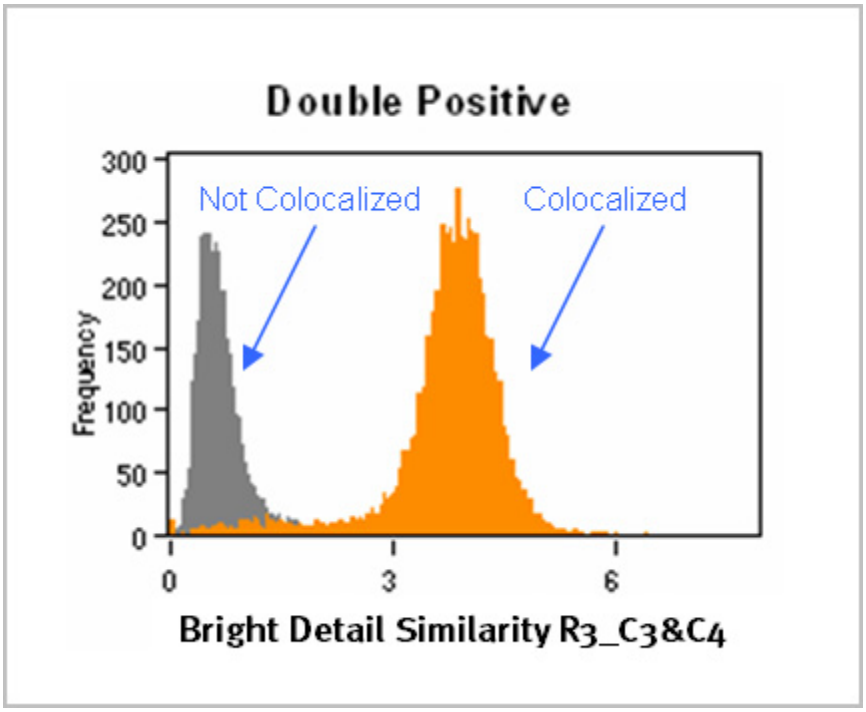
Understanding the Comparison Features

The Comparison features describe the difference of intensity measurements between masks or pixels in different images or the same image with different masks. These include Bright Detail Similarity R3, Intensity Concentration Ratio, Internalization, and Similarity.

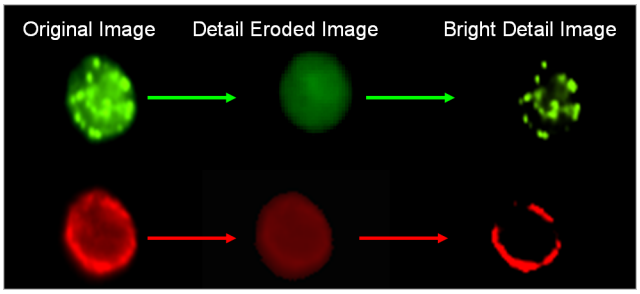
Bright Detail Similarity R3 Feature

The Bright Detail Similarity R3 feature is designed to specifically to compare the small bright image detail of two images and can be used to quantify the co-localization of two probes in a defined region, such as that of endosomes. The Bright Detail Similarity R3 feature is the log transformed Pearson's correlation coefficient of the localized bright spots with a radius of 3 pixels or less within the masked area in the two input images. Since the bright spots in the two images are either correlated (in the same spatial location) or uncorrelated (in different spatial locations), the correlation coefficient varies between 0 (uncorrelated) and 1 (perfect correlation), and does not assume negative values. The coefficient is log transformed to increase the dynamic range between {0, inf}.

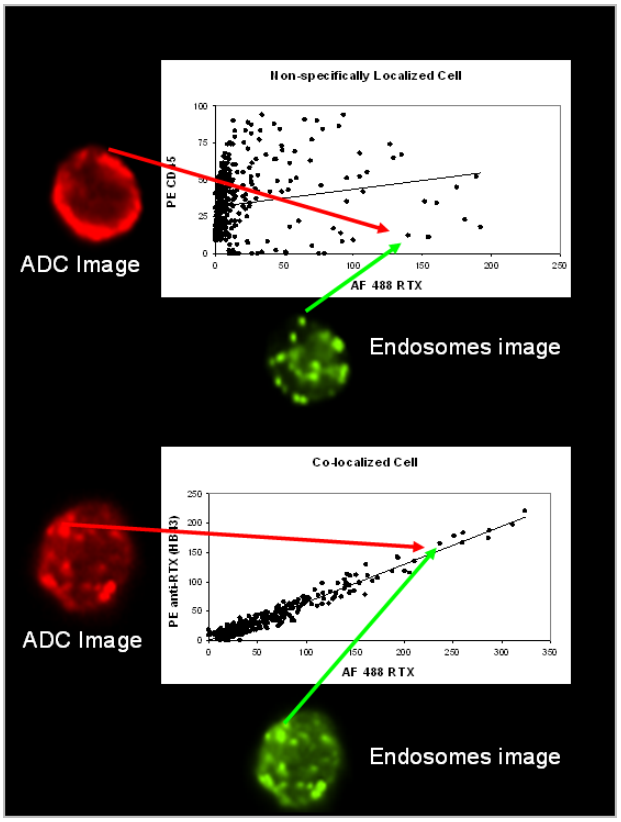
The following figure shows the Bright Detail Similarity R3 graph of two populations, one that has colocalization and one that has no colocalization.



The figure below illustrates the process of obtaining the localized bright spots. The bright areas are eroded from the original image and the detail eroded image is subtracted from the original image resulting in the bright detail image.



The figure below shows the correlation analysis between an image pair.



Application Examples:

- Quantify the degree of colocalization between two probes.
- Track internalization and intracellular trafficking of antibody drug conjugates to either the endosomes or the lysosomes.
- Colocalization of Rituxan and compliment C3b.

Intensity Concentration Ratio Feature

The intensity concentration ratio is defined as the ratio of the intensity inside the first input mask to the intensity of the union of the two masks - the higher the score, the greater the concentration of intensity inside the first mask. All pixels are background-subtracted. The ratio is invariant to cell size and can accommodate concentrated bright regions and small dim spots. The ratio is mapped to a log scale to increase the dynamic range to values between {-inf, inf}. This feature is a generalization of the Internalization feature. See "Internalization Feature" on page 185 for more information.

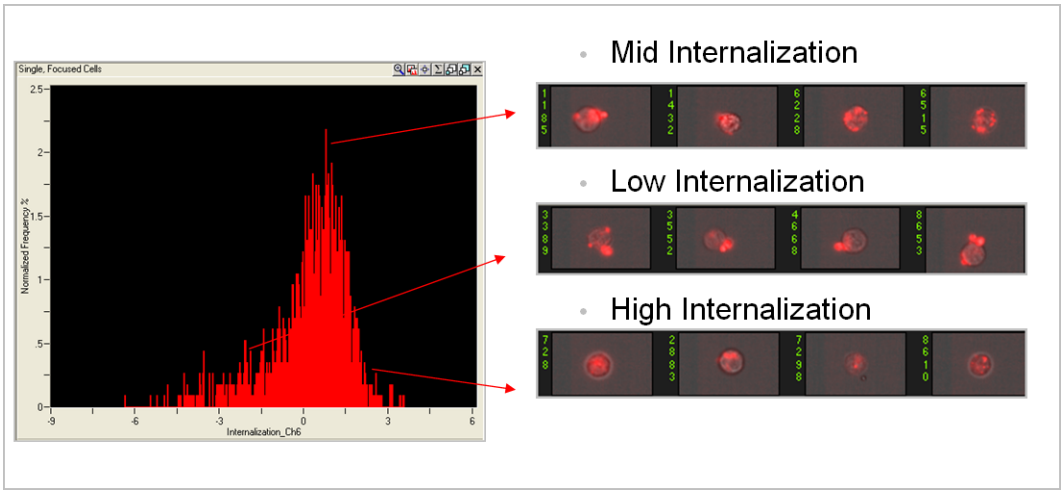
Application Example:

— Quantify relative intensity concentrations between different cellular compartments. Internalization is a special case of this where the first mask is the internal compartment and the second is the membrane region.

Internalization Feature

The Internalization feature is defined as the ratio of the intensity inside the cell to the intensity of the entire cell. The higher the score, the greater the concentration of intensity inside the cell. All pixels are background-subtracted. The user must create a mask to define the inside of the cell for this feature (see "About Masks" on page 191 and "Overview of the Mask Manager" on page 92). The feature is invariant to cell size and can accommodate concentrated bright regions and small dim spots. The ratio is mapped to a log scale to increase the dynamic range to values between {-inf, inf}. Internalized cells typically have positive scores while cells with little internalization have negative scores. Cells with scores around 0 have a mix of internalization and membrane intensity.

Composite Images of brightfield and channel 6 are shown for High, Medium, and Low Internalization values.



Application Examples:

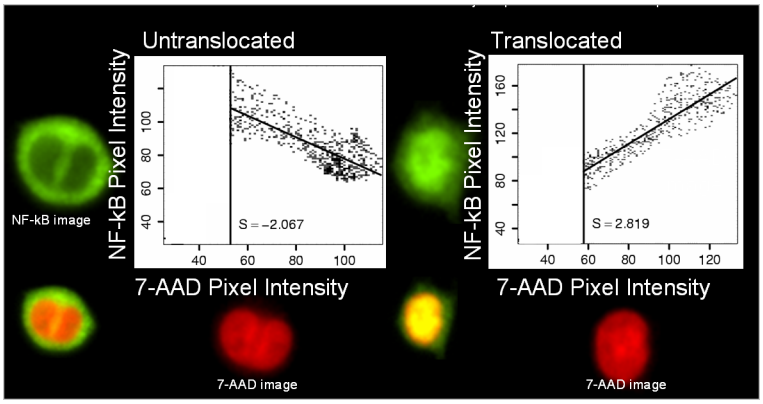
— Quantify internalization when supplied with the internal mask.

— Quantify the intensity ratio of a region of interest to the whole cell.

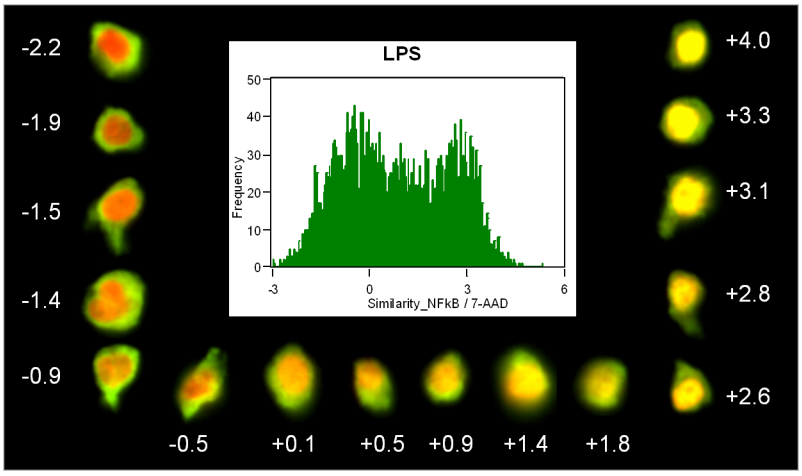
Similarity Feature

The Similarity feature is the log transformed Pearson's Correlation Coefficient and is a measure of the degree to which two images are linearly correlated within a masked region.

The following figure shows two image pairs that are in spatial registry to one another. On the left the NF-*k*B (green) is predominantly located in the cytoplasm of the cell and has a dissimilar distribution compared to the 7-AAD image (red). When the intensity of the green is high, the intensity of the red is low and vice versa. The Similarity value for this cell is -2.067 indicating that the image pair has a high degree of dissimilarity. Analysis of the image pair on the right shows that when the intensity of the green is high, the intensity of the red is high and the Similarity value is a high positive number.



Below are examples of cells with varying amounts of similarity between the NF*k*B image in green and 7-AAD image in red shown here as a composite image. The most dissimilar image pairs in the upper left to the most similar image pairs in the upper right.



Application Examples:

— Quantify translocation.

— Identify copolarization of two probes.

XCorr Feature

The XCorr feature is a measure of similarity or 'sameness' between two images - the higher the value, the more similar the images. It is robust to intensity variations and relative shifts between the images and is typically used with the combined mask MC. It is computed using the normalized cross correlation between the two input images.

Application Examples:

— Used as a mask-independent measure of similarity between two images.

Understanding the System Features

The system features do not require a mask.

Camera Line Number Feature

The Camera Line Number feature returns the camera line number values. This feature is obtained from INSPIRE.

Application Example:

— Used in Cells per mL feature.

Camera Timer Feature

The Camera Timer feature returns the camera timer values that are in ticks. This feature is obtained from INSPIRE.

Application Example:

— Used in Time feature.

Flow Speed Feature

The Flow Speed is the calculated flow speed, in mm/sec, of the object.

The Flow Speed feature is the speed of flow of the cells. It is obtained from INSPIRE. It should be very consistent across all cells in a file.

Application Example:

— Determine consistency of flow.

Object Number Feature

The Object Number feature denotes the serial number of a cell in a file.

Application Example:

— Reference an object in a file.

Objects/ml Feature

The Objects per mL feature returns the object concentration with respect to volume.

Application Example:

— Determine cell concentration.

Objects/sec Feature

The Objects per sec feature returns the object concentration with respect to time.

Application Example:

— Obtain the throughput.

Time Feature

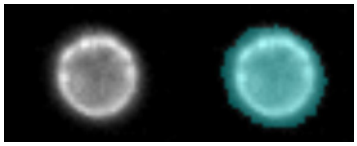
The Time feature returns the camera timer values that are in ticks, converted to secs with a formula.

Application Example:

— Obtain the time taken to collect a sample

About Masks

The set of pixels that contains the region of interest is called the mask. In the following picture, the mask consists of the set of pixels in the right image that are colored cyan. The cell is represented in the greyscale image on the left. Calculating some feature values, such as the Area value, requires only a mask. Calculating others, such as Intensity value, requires a mask and intensity values.

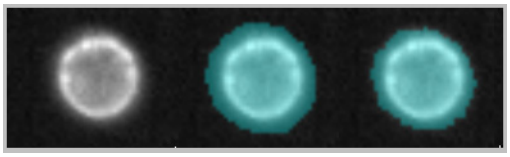


There are three types of masks: Default masks, Combined Masks and Function Masks:

1 Default masks named M01 through M12 are created when a .rif file is opened. The default masks obtain a region of interest corresponding to objects in the imagery using the Object function, default option described below. These masks are stored in the .cif file and cannot be changed by the user.

Conversion note: Versions of IDEAS prior to 3.0 were using the System function mask with a weight of 5 for the default masks which was more permissive and resulted in larger masks. Below is an example of the difference between the old and new default masks.

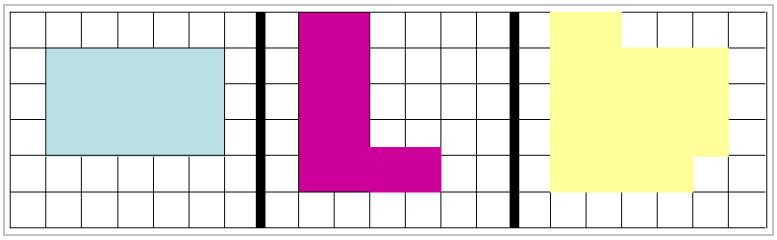
Image System(5) Object(default)



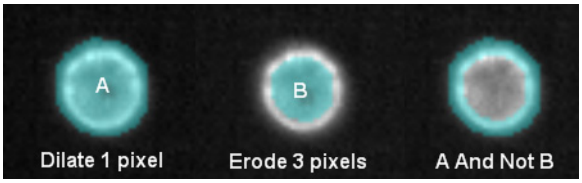
2 Combined masks are created using Boolean logic to combine and subtract masks. For example, the cytoplasmic mask is created by taking the brightfield mask and not the morphology mask of the nuclear image.

You can use the Mask Manager to combine masks of different regions or images. The IDEAS application default template provides a combined mask named MC that is the union of the pixels from all six channel masks and a NMC mask that is everything outside of MC. The following illustration shows two channel masks

that are combined into one mask, which is shown in the right-most panel.



Below is an example of making a membrane mask using Boolean Logic.



3 Function masks are created with user input. There are fourteen types of function masks, Dilate; Erode; Fill; Inspire; Intensity; Interface; Morphology; Threshold; Spot; System; Object; Peak; Range; Skeleton; and Valley. Each of the functions masks are defined here.

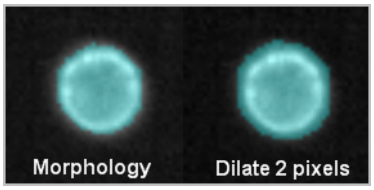
Refer to "Using the Mask Manager" on page 92 for more details about how to create new masks.

List of Function Masks

The IDEAS application provides thirteen functions that can be used to create new masks:

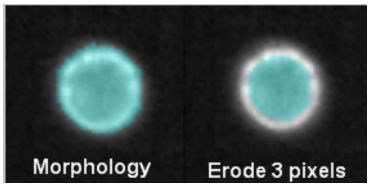
Dilate Mask

The Dilate mask adds the selected number of pixels to all edges of the starting mask.



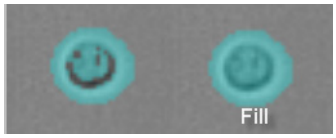
Erode Mask

The Erode mask removes the selected number of pixels from all edges of the starting mask.



Fill Mask

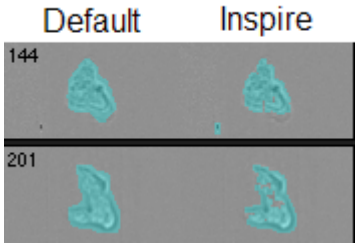
The Fill mask fills in any holes in the starting mask.



Inspire Mask

The Inspire mask masks pixels above background and is the mask used during data acquisition in INSPIRE. This mask is available to understand what is being masked during collection and is not generally used for feature calculations.

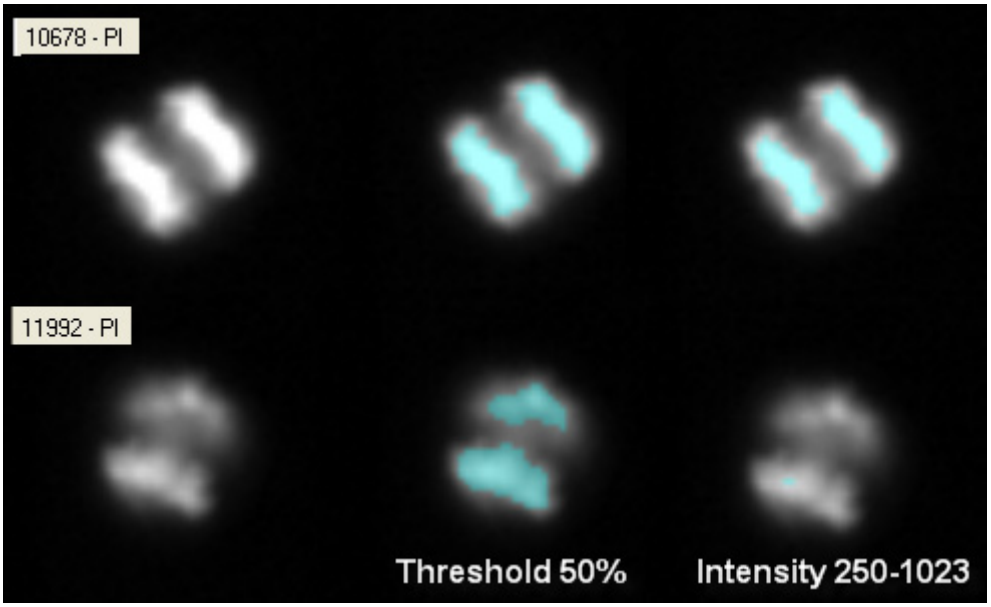
Note: this mask is new in IDEAS versions 4.0 or later.



Intensity Mask

The Intensity mask masks pixels between the lower and upper raw intensity thresholds not background subtracted. See also "Threshold Mask" on page 202.

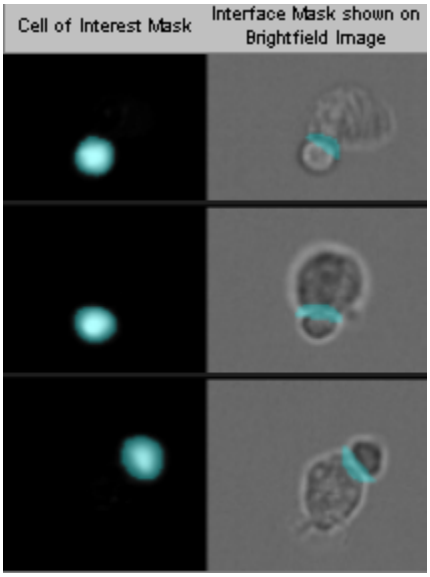
In the example below, cell #10678 is bright and cell #11992 is dim. The 50% Threshold mask is similar for both images whereas the Intensity mask 250+ is quite different, since only a few pixels in the dim image are greater than 250 counts, while most of the metaphase plates in the bright image are masked.

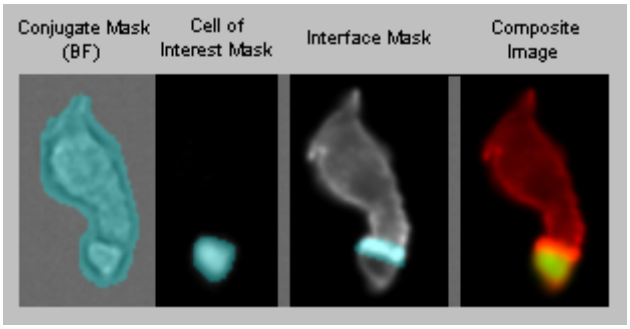


Interface Mask

The interface mask identifies pixels in an object where the object is in contact with a second object. Three input parameters are defined. First, the mask of one of the objects (cell of interest). Next, the mask that covers both objects (conjugate). A close fitting mask using another function mask such as Object (tight) can be used for the cell of interest mask. A brightfield mask can be used for the conjugate. Finally, the width of the interface mask from the contact point towards the cell of interest is entered.

Examples are shown below:





Application Examples:

— Used to quantify synapses in T cell APC (antigen presenting cell) conjugates.

Morphology Mask

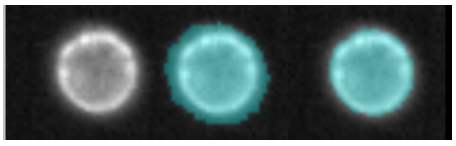
The Morphology mask includes all pixels within the outermost image contour. This mask, which is used in fluorescence images, is best used for calculating the values of overall shape-based features.

Object Mask

The Object mask segments images to closely identify the area corresponding to the cell. It is based on the assumption that background pixels exhibit high uniformity to each other. This helps distinguish the background from the cell pixels. The mask characterizes the background pixels using a set of features and then segments the image by determining all the pixels that deviate from the background feature set. The default option is used for the default segmentation masks. The tight option uses a different set of features to characterize the background which results in a tighter fit around the cell.

Examples are shown below:

Image	Object (default)	Object (tight)



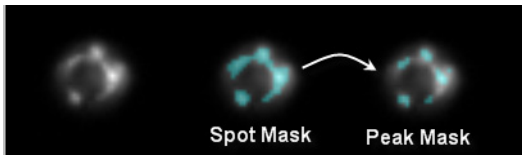
Application Examples:

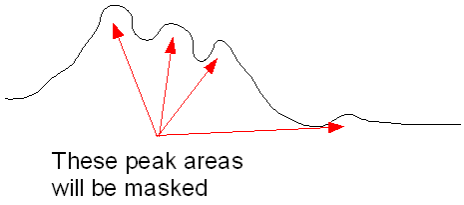
- Used to get a close fit around the cellular area (tight option).
- Can be used in lieu of the morph mask for applications where the morph is so tight that it provides incomplete masking, sometimes splitting cells into two regions, such as a nuclear dye image of cells in anaphase or telophase.
- Can be used in lieu of the morphology mask with the Similarity feature when measuring nuclear translocation for better separation between untranslocated and translocated cells (tight option).
- Used as the default segmentation masks (default option).

Peak Mask

The Peak mask identifies intensity areas from an image that have local maxima (bright) or minima (dark). Initially, the peak mask will identify all peaks in the image. To select peaks which have certain brightness, the spot to cell background ratio is used. This is the ratio between the spot pixel value to the mean camera background value in the original image.

Below is an example of the Peak, bright option.





Application Examples:

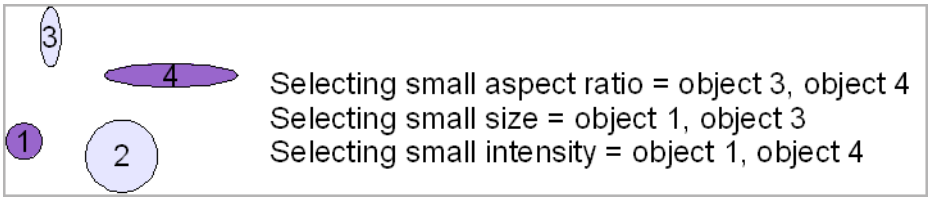
— Used with the Spot Count feature to quantify the speckleness of cells.

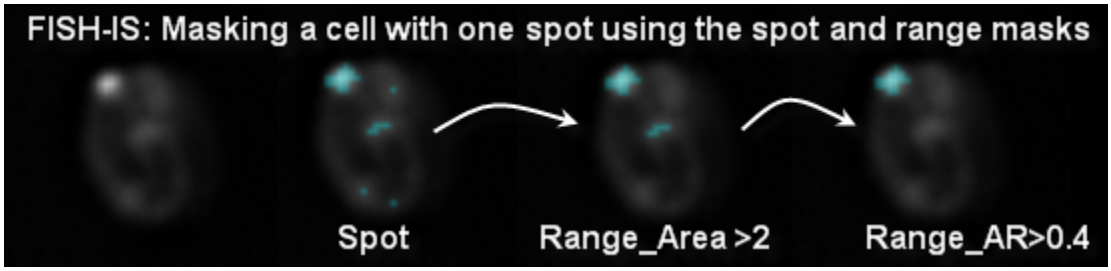
— Separate connected spots in a Spot Mask into individual components.

Range Mask

The Range mask provides a capability to select components in an image within a selected size and/or aspect ratio by setting a minimum and maximum area and minimum and maximum aspect ratio.

To select pixels within a range of intensity values, see "Intensity Mask" on page 194.





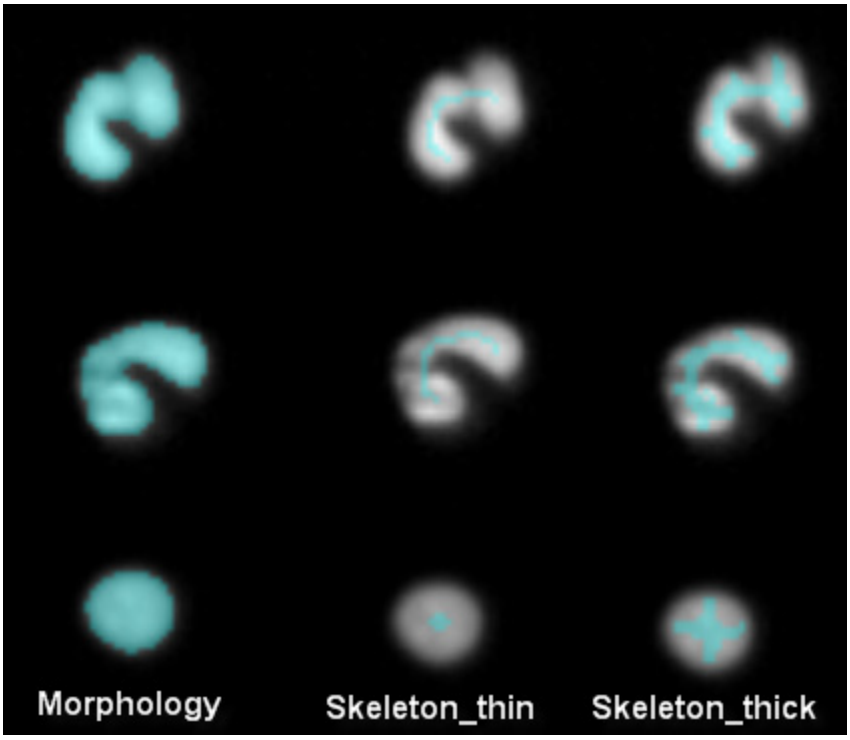
Application Examples:

— Use with a Spot Mask to constrain the Spot Count feature to round spots.

— Use on any other mask that has multiple components to define unwanted objects such as debris, objects that are too small or whose shapes are not circular.

Skeleton Mask

The skeleton mask provides the barebone structure of the object from the starting mask. Two options are available: thin or thick skeletons. The thin option produces the condensed shape of the object and typically takes a form of 1-pixel wide skeletal line. The thick option is intensity weighted. The thin option is dependent on the shape of starting mask; thick uses the pixel intensities and is less sensitive to the shape of the starting mask. The user will need to pay careful attention to the starting mask. In the example below the Morphology mask of the image was used as the starting mask for creating the skeleton.



Application Examples:

— Thick skeletons can be used with shape-based features such as symmetry to accentuate the shape of an object, and provide greater separations.

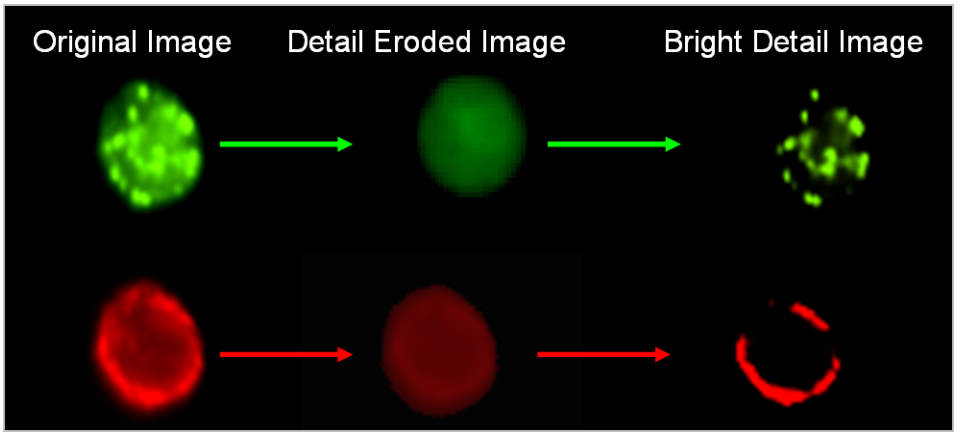
— Separate singlets and doublets by computing the area of the thin skeleton mask. We have used the object(tight) for this case.

— Nuclear morphology measurements with lobe count feature for cell classification cells.

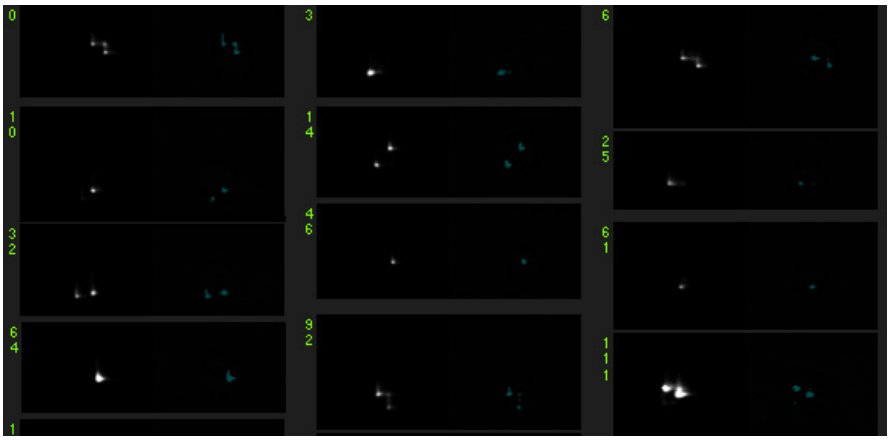
Spot Mask

The Spot Mask has two options: bright or dark. The bright option obtains bright regions from an image regardless of the intensity differences from one spot to another. The ability to extract bright objects is achieved using the an image processing step that erodes the image and leaves only the bright areas. The dark option obtains dark regions. The spot to cell background ratio and radius are specified by the user. The spot to cell background ratio is the spot pixel value divided by the background in the bright detail image. A radius value of x implies that the image contains spots with thickness of $2x+1$ pixels.

The figure below illustrates the open residue process. The bright areas are eroded from the original image and the detail eroded image is subtracted from the original image resulting in the bright detail image.



The image pairs below show objects in grayscale next to their corresponding Spot Masks in cyan. Spot masks can be further refined using the Peak and/or Range masks. See "Peak Mask" on page 197"Range Mask" on page 197.



Application Examples:

— Used with the Spot Count feature to enumerate spots in images such as for FISHIS®.

— Used with Intensity features to quantify intensity in spots.

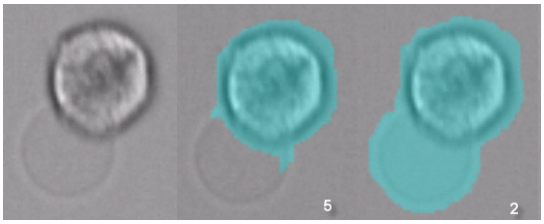
— Dark spot finds valleys in images such as the low intensity between 2 stained nuclei and is useful for finding immune synapses.

— Identifies the dark areas in red blood cells or parasitic infections in bright-field imagery.

System Mask

The System mask segments objects in an image based on a probability model of how pixels should be grouped together. The user sets a weight value that defines a loose or tight grouping. A low weight value groups in a more permissive manner.

Shown is an example of a cell with a apoptotic bleb that is not masked with the System mask weight set at 5 but is masked with the System mask weight set at 2.



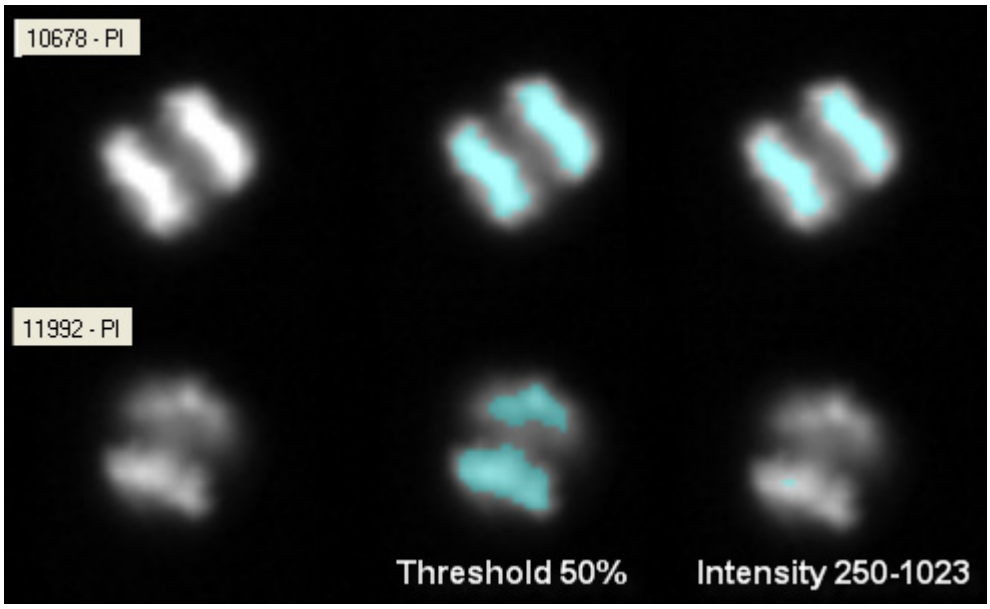
Application Example:

— Used on brightfield images to capture a low contrast areas such as cells that undergo a blebbing process, tails of sperm or other low contrast type of structures.

Threshold Mask

The Threshold mask is used to exclude pixels, based on a percentage of the range of intensity values as defined by the starting mask. The user chooses the starting mask when creating the Threshold mask. See also "Intensity Mask" on page 194.

In the example below, cell #10678 is bright and cell #11992 is dim. The 50% Threshold mask is similar for both images whereas the Intensity mask 250+ is quite different, since only a few pixels in the dim image are greater than 250 counts, while most of the metaphase plates in the bright image are masked.

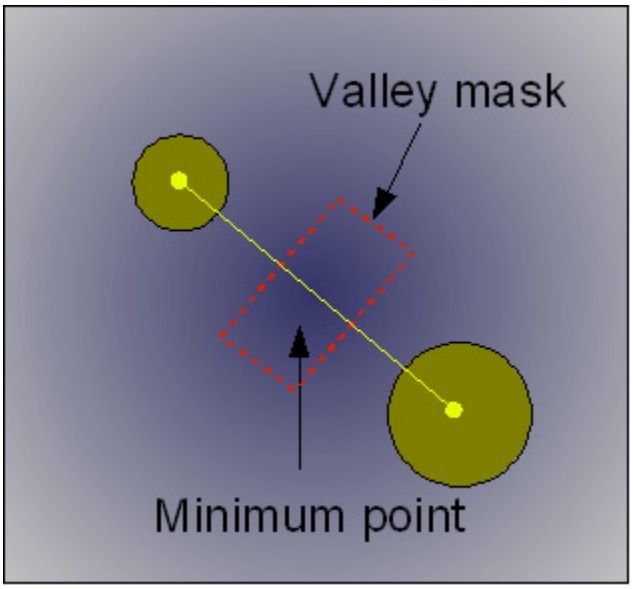


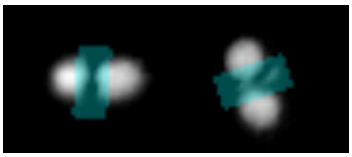
Application Example:

— Used with the Area feature to define apoptotic cells.

Valley Mask

The Valley mask is a rectangular mask that sits between two bright regions in a starting mask, such as between two nuclei. It is constructed by finding the minimum intensity along the skeletal line between these two bright regions. The skeletal line is obtained internally using the skeleton (thin) masking as described in "Skeleton Mask" on page 198. This minimum intensity identifies the intersection between the two objects. The mask is drawn perpendicular to this skeletal like. The length of the valley mask rectangle is equal to the minor axis of the object and the width of the mask is defined by the user in pixels.





Application example:

— Quantify the intensity of a probe in an immune synapse.

—

Chapter 8

Troubleshooting

This chapter covers common issues and provides solutions.

Application Hanging

If the IDEAS application is hanging, there may be a memory issues, especially with large file processing. You must use the Task Manager to force quit the application.

1 Press and hold Ctrl + Alt + Delete.
2 The Window Task Manager appears.
3 Under the **Applications** tab, select IDEAS Application.
4 If the status is Not Responding, select **End Task**.
5 The manager will force quit the application after a confirmation.

Compensation

Sometimes an applied matrix produces poorly compensated data. This can happen for a number of reasons: 1) miscalculation of the compensation matrix by inclusion of inappropriate events (such as doublets, saturated pixel events, or artifacts), 2) controls used for matrix calculation differ significantly from the experimental samples (different cell type, different probe), or 3) cells exhibit substantial autofluorescence. This protocol describes a method for manually adjusting and validating a compensation matrix for difficult samples.

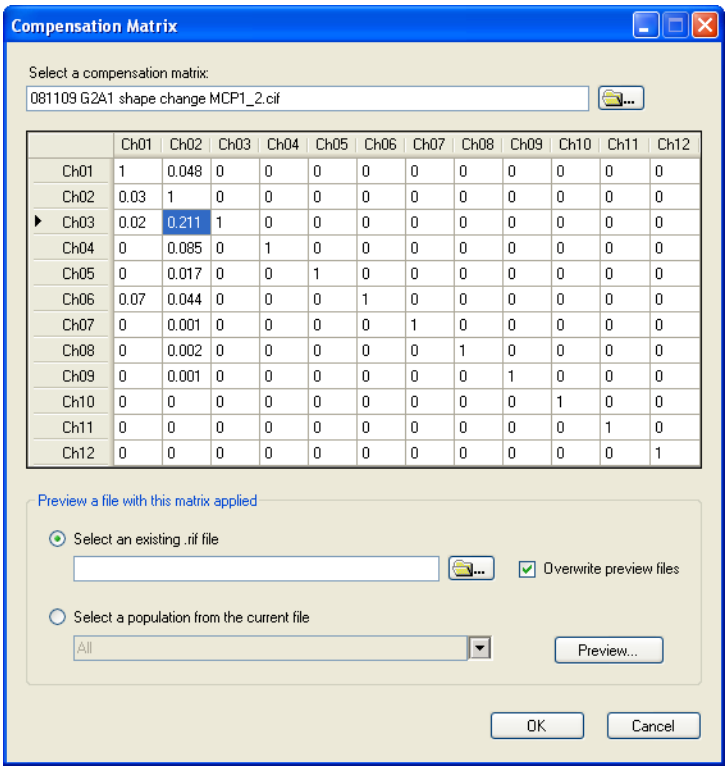
To troubleshoot and repair a compensation matrix:

1Create a population of cells that are miscompensated using the tagging tool. See "Creating Tagged Populations" on page 69. Choose single cells that are exhibiting crosstalk. Choose a range of intensities from negative to bright but not saturated,

preferably single color. If single color cells are not available, choose cells with a distinct staining pattern in the peak channel.

2 Create Intensity scatter plots of adjacent channels in order to observe the over- or under-compensation.

3 Identify the matrix values that need adjusting by inspecting the scatter plots and images. Each column contains the coefficients for the peak channel into the corresponding crosstalk channels (rows). For example the crosstalk of channel 2 (green) into channel 3 is highlighted in the matrix below.



	Ch01	Ch02	Ch03	Ch04	Ch05	Ch06	Ch07	Ch08	Ch09	Ch10	Ch11	Ch12
Ch01	1	0.048	0	0	0	0	0	0	0	0	0	0
Ch02	0.03	1	0	0	0	0	0	0	0	0	0	0
Ch03	0.02	0.211	1	0	0	0	0	0	0	0	0	0
Ch04	0	0.085	0	1	0	0	0	0	0	0	0	0
Ch05	0	0.017	0	0	1	0	0	0	0	0	0	0
Ch06	0.07	0.044	0	0	0	1	0	0	0	0	0	0
Ch07	0	0.001	0	0	0	0	1	0	0	0	0	0
Ch08	0	0.002	0	0	0	0	0	1	0	0	0	0
Ch09	0	0.001	0	0	0	0	0	0	1	0	0	0
Ch10	0	0	0	0	0	0	0	0	0	1	0	0
Ch11	0	0	0	0	0	0	0	0	0	0	1	0
Ch12	0	0	0	0	0	0	0	0	0	0	0	1

- Undercompensation (crosstalk coefficient is too low):

  Plots: Intensity mean for the single color positive population is higher than the unlabeled population in the crosstalk channel or the intensity in the crosstalk channel trends diagonally upwards.

  Images: the crosstalk channel contains an apparent fluorescent mirror-image.

- Overcompensation (crosstalk coefficient is too high):

  Plots: Intensity mean for the single color positive population is lower than the unlabeled population in the crosstalk channel or the intensity in the crosstalk channel trends diagonally downwards.

  Images: the crosstalk channel contains dark spots corresponding to the bright spots in the fluorescent channel of interest.

4 In the Compensation menu choose **View/Edit Matrix** and manually change the incorrect crosstalk matrix values identified above. Start with changes of ~.1 or ~.05 and use smaller and smaller increments as you refine the matrix.

5 Click **Preview** and choose the tagged population to view the results of the changed coefficient.

6 Repeat steps 4 and 5 until the matrix is corrected.

7 Click **Save**, append manual to the matrix name, then click OK.

8 Open the .cif file and use the new matrix to create a new .daf file.

Creating a TIFF

If you cannot see the TIFF image that you created, trying changing the resolution to 8-bit.

Deleting a Population and Region

Often, a user deletes a population but forgets to delete the region. Deleting a population does not delete the region. You must delete the region itself.

Delay in Copy/Paste

When copying and pasting histogram information to a clipboard, you may experience a delay. In this case, there may be too many bins displaying. Adjust the number of bins through the following steps.

1 Right click on the histogram and select **Graph Properties**.

2 In the Graph Properties window, click **Display Properties**.

3 In the **Bin count** drop-down menu, decrease the bin count as needed.

4 Click **OK** in both windows to return to the histogram.

Object Number set to Zero

When opening a .daf file, there may be an error if the object number is set to zero. This can happen if the data was collected during a crash within INSPIRE. This error can be corrected with the following procedure.

1 Select **Tools** > **Merge .rif Files**.

2 Click **Add Files** to select the single .rif file.

3 Click **OK**. Enter a new name if desired. The single .rif file will merge with itself and rewrite the file with the proper object count.

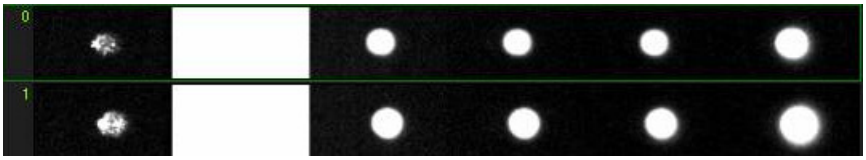
Buttons or options in windows are not appearing

When the font size setting is set to large some windows will not size properly causing buttons or text boxes to not appear. To change the font size in Windows go to the Control Panel>Display>Appearance and select Font size Normal.

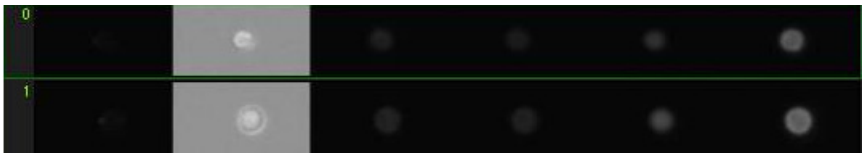
Images and brightfield channel appear uniformly bright

Image files collected on early ImageStream instruments may have incorrect flowspeed information. IDEAS versions 2.2 and later automatically perform flow speed normalization and will attempt to use the incorrect information, causing the imagery to appear uniformly bright.

Here is an example of imagery taken from IDEAS for a file with this problem:



Here is what the imagery should look like:



The user must disable flow speed normalization when loading these older, problematic files. If this problem occurs on recently acquired files call Amnis customer support for help.

To load a file with incorrect flow speed values

When loading a .rif file:

1 Click Advanced in the opening a .rif window.
2 Uncheck the Perform Normalizaation checkbox in the Flow Speed section and proceed loading the file.

When batching files

1 Uncheck the Flow speed normalization checkbox in the Corrections section.

Chapter 9

Glossary

Table 1: Glossary of Terms

Term	Definition
acquisition	The process of collecting data from the ImageStream cell analysis system.
brightfield	A type of illumination that uses transmitted light. On the ImageStream cell analysis system, this light is provided by a halogen lamp.
brightfield image	An image that is produced by transmitted light. On the ImageStream cell analysis system, this light is provided by a halogen lamp.
brightfield	The camera channel that the brightfield image appears in.
calibration	The precise adjustment of instrument components based on test results for the purpose of optimizing functionality.
CCD	See charge-coupled detector (CCD).
channel	One of the six physical partitions on the camera. Each camera channel collects a different spectral band of imagery, which allows for the collection of brightfield, darkfield, and up to four fluorescence images per object.
charge-coupled detector (CCD)	A sensor for recording images that consists of a particular type of integrated circuit—one that contains an array of linked, or coupled, capacitors. Under the control of an external circuit, each capacitor can transfer its electric charge to either of its neighbors.
coefficient of variation (CV)	The mean-normalized standard deviation, expressed as a percentage. The CV measures the variation of a feature value independent of the population mean value. The formula is: CV = 100 × standard deviation / mean
CV	See coefficient of variation (CV).

Table 1: Glossary of Terms

Term	Definition
compensation	The process of removing intensity—specifically, intensity that was derived from fluorescence crosstalk that originated from dyes centered in other channels. The IDEAS application performs compensation on a pixel-by-pixel basis.
compensation matrix	The set of values that report the relative amount of fluorescence of each probe in each channel. The compensation matrix is used to subtract intensity originating from dyes centered in other channels.
crosstalk	Leakage of fluorescence signal from a fluorochrome into adjacent channels.
darkfield	A type of illumination in which the sample is illuminated at angles that do not directly enter the objective. On the ImageStream cell analysis system, 90-degree angle side scatter from the 488-nm laser provides the darkfield imagery.
FISH	See fluorescent in situ hybridization (FISH).
fluorochrome	A fluorescent dye used to label cellular constituents or specific probes of cellular constituents.
fluorescence	Light emitted by a fluorescent dye following excitation.
fluorescence compensation	The adjustments made to remove the fluorescence emissions of a fluorochrome into adjacent channels.
fluorescent in situ hybridization (FISH)	A physical mapping approach that uses fluorescent tags to detect the hybridization of probes with metaphase chromosomes or the less-condensed somatic interphase chromatin.
gain	The amplification of a detector signal.
grayscale	The brightness level, ranging from black to white, of a pixel or group of pixels.
pixel	A pixel is equal to a half micron in length with the 40X objective, 1 micron with the 20X objective and 0.33 microns with the 60X objective. Note that 1 pixel = x μm^2.
saturation	The state of a pixel that has a value at or above 1023 for the IS100 or 4095 for the ImageStream^X.

Table 1: Glossary of Terms

Term	Definition
segmentation	The process of discriminating an object from its background.
spectral decomposition element	A custom set of longpass dichroic filters arranged in an angular array. The spectral decomposition element directs different spectral bands to laterally distinct channels on the detector. With this technique, an image is optically decomposed into a set of six sub-images, each corresponding to a different color component and spatially isolated from the remaining sub-images.
spatial offset	The registration error of the six channel images for a single cell. The spatial offset is measured during calibration and the values are saved to the image database.
Table of Coefficients	The table used by the compensation matrix to place the detected light that is displayed in each image into the proper channels, on a pixel-by-pixel basis.
template	A file that saves the set of instructions for an analysis session. Note that a template contains no data; it simply contains the structure for the analysis. This structure includes definitions of features, graphs, regions, and populations; image viewing settings; channel names; and statistics settings.

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