inForm Software Release Notes
Software Version: 3.0.0

This file provides information about inForm software, version 3.0.0. Please read this information carefully as it supersedes all printed material or online help.

Overview:
inForm software allows image analysis of proprietary Akoya Biosciences images taken with Mantra, Vectra 3, PhenoImager HT (Vectra Polaris), PhenoImager Fusion , along with standard image formats such as .tif, .jpg and .png images. If you are an existing user, installing version 3.0.0 will not require the uninstallation of previous versions. We suggest that you leave previous versions on the system to complete current studies.

System Requirements:
- U.S. English Version of Microsoft© Windows 10, 64 bit
- .NET 4.8
- Minimum monitor resolution: 1280x768
- Minimum RAM: 8 GB (16 GB strongly recommended)

inForm has been tested and validated on Windows 10. Installation is permitted on Windows 7 but performance is not guaranteed.

Software Installation:
To install inForm on Windows 10:
1. Log in as an administrator
2. Close all open software programs
3. If you have not installed R, please download it from the Akoya Biosciences software downloads page and follow the installation instructions.
4. Double click on inForm's Setup.exe
5. Follow the installer's instructions

Note that Adobe Acrobat Reader is required for context-sensitive help.

Software Activation:
inForm 3.0.0 is licensed software that must be activated for use of anything other than its viewer features.
If you are an existing user of inForm 2.1 or higher, please install inForm 3.0.0 on the same machine as your previous installations; no further action is necessary.
If you have an earlier version of inForm, please install inForm 3.0.0 on the same machine as your previous installations. Contact Akoya Technical Support for assistance with upgrading your license.
If this is a new install, please use the inForm License application to activate your software, found in Start->Akoya Biosciences->inForm License App

inForm Version 3.0.0
New Features and Enhancements:
- Support for the Extended range and unmixed format HT scans
- Creation of unmixing libraries for HT to use in automated unmixing scans

Bug Fixes:
- inForm command-line batch now writes the files necessary for the review/merge step

Known Issues:
- Exceptions may occur when clicking on x or y in a threshold project
- Application error may occur when adding components to a threshold
- Support for TRIO, Nuance, and Lamina imagery has been removed, please use inForm 2.3 for legacy data.
- Counterstain-based segmentation has been deprecated; please use inForm 2.3 for any counterstain-based segmentation projects.
- A long-standing low-level bug fix has changed cell segmentation cytoplasm results. Older algorithms run in this version may yield slightly different results.
- Cell segmentation tables are not calculated when the live preview is present for performance reasons.
- Legacy projects from inForm versions prior to 2.0 are no longer supported
- .im3 files with CJK characters in the directory path may fail to load
- Algorithms must be developed with an image present to run in batch
- The Prepare Image button can be active with no image present
- Double-clicking on a large digital slide in the gallery view doesn't always switch to single view
- The "Image Too Large" dialog is repeatedly shown when converting projects
- Scale Across Layers does not work correctly if the images are not all preprocessed before export
- Stale score settings can cause a failure to segment cells
- The manual tissue segmentation fails to update correctly when deleting a category
- Image not removed from the training set when the last region is removed individually
- Canceling the spectral variability dialog during stain extraction shows a second variable stain dialog
- Phenotyping does not ignore images not in the processing set
- Edit->Delete functionality is not working in editable text fields.
- In batch analysis, trying to access an external drive that has been removed may cause an error.
- Leaving batch analysis for manual analysis with slides loaded in batch will force selection of the algorithm again before loading more slides.
- The tissue segmentation step doesn't not show the Prepare images warning when viewing the color image.
- MOTiF fields that have been ignored cannot be processed in inForm.
- Normalized counts/second displayed in inForm 3.0.0 / Phenochart 2.0.0 for FL imagery acquired by HT 2.0.0 using 2x2 binned protocols are incorrectly reported 4X higher than the proper values.

Notes:
- Nuance library support is deprecated - create an inForm project or algorithm using them, and load that into inForm 3.0
- CODEX algorithms from 2.8 need to be run on 2.8.
- Image pairs that have similar counts may look different in the RGB preview.

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inForm Version 2.8.0
New Features and Improvements:
- Phenotyping for PhenoCycler imagery

Bug Fixes:
- Fix for missing imagery when run from the command line
- Fix for tissue segmentation performance when changing marker names

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inForm Version 2.7.1
New Features and Improvements:
- Improved unmixing for Fusion imagery

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inForm Version 2.7.0
New Features and Improvements:
- Support for Fusion imagery

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- Leaving batch analysis for manual analysis with slides loaded in batch will force selection of the algorithm again before loading more slides.
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inForm Version 2.6.0
New Features and Improvements:
- Multiple rounds of phenotyping in a single project.

Bug fixes:
- Bug fix for errant scoring output; in certain circumstances during batch processing, scores calculated from cytoplasm or membrane could be incorrect

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- Phenotyping does not ignore images not in the processing set
- Long Nuance library filenames can cause the Prepare Images UI to be cropped
- Edit->Delete functionality is not working in editable text fields.
- In batch analysis when trying to access an external drive to has been removed may cause an error.

- Leaving batch analysis for manual analysis with slides loaded in batch will force selection of the algorithm again before loading more slides.
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inForm Version 2.5.2
New Features and Improvements:
- Identify which steps are available for CODEX imagery
- Add ability to clear selection in the composite views editor
- Update error messages for clarity
- Update the cursor signal display
- Improve composite view editor performance
- List components in alphabetical order

Bug Fixes:
- Fix for accidental scrolling
- Fix for threshold step error with CODEX imagery

Known Issues:
- Support for TRIO and Lamina imagery has been removed, please use inForm 2.3 for legacy data.
- Counterstain-based segmentation has been deprecated; please use inForm 2.3 for any counterstain-based segmentation projects.
- A long-standing low-level bug fix has changed cell segmentation cytoplasm results. Older algorithms run in this version may yield slightly different results.
- Cell segmentation tables are not calculated when the live preview is present for performance reasons.
- Legacy projects from inForm 0.4.2, 1.0, and 1.0.2 have been deprecated; please load and save those projects in inForm 1.4 before proceeding.
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- The manual tissue segmentation fails to update correctly when deleting a category
- Image not removed from the training set when the last region is removed individually
- Canceling the spectral variability dialog during stain extraction shows a second variable stain dialog
- Phenotyping does not ignore images not in the processing set
- Long Nuance library filenames can cause the Prepare Images UI to be cropped
- Edit->Delete functionality is not working in editable text fields.
- In batch analysis when trying to access an external drive to has been removed may cause an error.
- Leaving batch analysis for manual analysis with slides loaded in batch will force selection of the algorithm again before loading more slides.

- The tissue segmentation step doesn't not show the Prepare images warning when viewing the color image.
- MOTiF fields that have been ignored cannot be processed in inForm.

inForm Version 2.5.1
New Features and Improvements:
- Speed increases for batch processing when writing tables
- Updated tooltips

Bug Fixes:
- Fixes for resolution issues with MOTiF imagery
- Fix for composite editing with MOTiF imagery
- Fix for composite exporting
- Fix for lookup issue when viewing phenotypes

Known Issues:
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inForm Version 2.5.0

New Features and Improvements:
- Customizable composite views
- Composite Legend
- Exporting maps with the composite
- Support for new Polaris camera

Bug Fixes:
- Fix for slide browser error
- Prevent adding imagery in batch until a well-formed algorithm is loaded

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inForm Version 2.4.11
Bug Fixes:
- Fix for odd sized cell segmentation overlay rendering
- Fix for area percentage of all cells
- Update error message when whole slide regions are ignored or deleted.

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inForm Version 2.4.10
New Features and Improvements:
- Support for Opal kit processing

Bug Fixes:
- Fix for merge issues when imagery fails to batch process
- Fix for image selection when the location of whole slide imagery has moved

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inForm Version 2.4.9
Bug Fixes:
- Fix for tissue category capitalization change
- Update the licensing activation email

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inForm Version 2.4.8
Bug Fixes:
- Fix for autofluorescence selection

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inForm Version 2.4.7
New Features and Improvements:
- Support for Vectra 3 LED lamp
- Updated Opal synthetic spectra for whole slide scan imagery

Bug Fixes:
- Cell seg summary table now reports all phenotypes

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inForm Version 2.4.6
New Features and Improvements:
- Support for Mantra Opal 480 filter
- Updated online licensing app server

Bug Fixes:

- Fix for mislabeled cytoplasm and membrane compartments in rare cases with Adaptive cell segmentation
- Fix silent failures for context sensitive help if help file is not present

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inForm Version 2.4.5
Bug Fixes:
- Fixes for processing whole slide annotations in batch
- Fixes for re-processing whole slide annotations in merge
- Optimize inForm for fewer disk reads of the cube to increase unmixing speed and spectral viewer responsiveness

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- Algorithms must be developed with an image present to run in batch
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- Double-clicking on a large digital slide in the gallery view doesn't always switch to single view
- The "Image Too Large" dialog is repeatedly shown when converting projects
- Scale Across Layers does not work correctly if the images are not all preprocessed before export
- Stale score settings can cause a failure to segment cells
- The manual tissue segmentation fails to update correctly when deleting a category
- Image not removed from the training set when the last region is removed individually
- Canceling the spectral variability dialog during stain extraction shows a second variable stain dialog
- Phenotyping does not ignore images not in the processing set
- Long Nuance library filenames can cause the Prepare Images UI to be cropped
- Edit->Delete functionality is not working in editable text fields.
- In batch analysis when trying to access an external drive to has been removed may cause an error.
- Leaving batch analysis for manual analysis with slides loaded in batch will force selection of the algorithm again before loading more slides.

inForm Version 2.4.4
Bug Fixes:
- Fix for potentially stale data when using threshold, colocalization, or cell segmentation.
- Cell segmentation popup editors close properly when projects are configured.
- Updated minimum size of select stains dialog; labels are no longer cut off.

Known Issues:
- Support for TRIO and Lamina imagery has been removed, please use inForm 2.3 for legacy data.
- Counterstain-based segmentation has been deprecated; please use inForm 2.3 for any counterstain-based segmentation projects.
- A long-standing low-level bug fix has changed cell segmentation cytoplasm results. Older algorithms run in this version may yield slightly different results.
- Cell segmentation tables are not calculated when the live preview is present for performance reasons.
- Legacy projects from inForm 0.4.2, 1.0, and 1.0.2 have been deprecated; please load and save those projects in inForm 1.4 before proceeding.
- .im3 files with CJK characters in the directory path may fail to load
- Algorithms must be developed with an image present to run in batch
- The Prepare Image button can be active with no image present
- Double-clicking on a large digital slide in the gallery view doesn't always switch to single view
- The "Image Too Large" dialog is repeatedly shown when converting projects

- Scale Across Layers does not work correctly if the images are not all preprocessed before export
- Stale score settings can cause a failure to segment cells
- The manual tissue segmentation fails to update correctly when deleting a category
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- Canceling the spectral variability dialog during stain extraction shows a second variable stain dialog
- Phenotyping does not ignore images not in the processing set
- Long Nuance library filenames can cause the Prepare Images UI to be cropped
- Edit->Delete functionality is not working in editable text fields.
- In batch analysis when trying to access an external drive to has been removed may cause an error.
- Leaving batch analysis for manual analysis with slides loaded in batch will force selection of the algorithm again before loading more slides.

inForm Version 2.4.3
New Features and Improvements:
- Support for whole slide region analysis, library development, and batch processing.
- Provide table data in microns or pixels
- Unique Cell IDs per slide in batch processing

Bug Fixes:
- Cell Segmentation is no longer limited to 65K cells per field.
- Memory improvements for large phenotyping training sets
- Speed increase for phenotyping
- Always export slide and field ID information in the data tables

Known Issues:
- Support for TRIO and Lamina imagery has been removed, please use inForm 2.3 for legacy data.
- Counterstain-based segmentation has been deprecated; please use inForm 2.3 for any counterstain-based segmentation projects.
- A long-standing low-level bug fix has changed cell segmentation cytoplasm results. Older algorithms run in this version may yield slightly different results.
- Cell segmentation tables are not calculated when the live preview is present for performance reasons.
- Legacy projects from inForm 0.4.2, 1.0, and 1.0.2 have been deprecated; please load and save those projects in inForm 1.4 before proceeding.
- .im3 files with CJK characters in the directory path may fail to load
- Algorithms must be developed with an image present to run in batch
- The Prepare Image button can be active with no image present
- Double-clicking on a large digital slide in the gallery view doesn't always switch to single view
- The "Image Too Large" dialog is repeatedly shown when converting projects
- Scale Across Layers does not work correctly if the images are not all preprocessed before export
- Stale score settings can cause a failure to segment cells
- The manual tissue segmentation fails to update correctly when deleting a category
- Image not removed from the training set when the last region is removed individually
- Canceling the spectral variability dialog during stain extraction shows a second variable stain dialog

- Phenotyping does not ignore images not in the processing set
- Long Nuance library filenames can cause the Prepare Images UI to be cropped
- Edit->Delete functionality is not working in editable text fields.
- Running Phenotyping projects that have been saved after cell markup without additional training may cause an error.
- In batch analysis when trying to access an external drive to has been removed may cause an error.
- Leaving batch analysis for manual analysis with slides loaded in batch will force selection of the algorithm again before loading more slides.

inForm Version 2.4.2
Bug Fixes:
- Conform to the PerkinElmer tiff spec with regards to barcode and exposure information
- Correct serialization to save double values in a locale-independent format
- When known, display the barcode text in the cube info dialog.
- Handle cells that are removed due to residing in an "unknown" tissue class.

Known Issues:
- Counterstain-based segmentation has been deprecated; please use inForm 2.3 for any counterstain-based segmentation projects.
- A long-standing low-level bug fix has changed cell segmentation cytoplasm results. Older algorithms run in this version may yield slightly different results.
- Cell segmentation tables are not calculated when the live preview is present for performance reasons.
- Legacy projects from inForm 0.4.2, 1.0, and 1.0.2 have been deprecated; please load and save those projects in inForm 1.4 before proceeding.
- .im3 files with CJK characters in the directory path may fail to load
- Algorithms must be developed with an image present to run in batch
- The Prepare Image button can be active with no image present
- Double-clicking on a large digital slide in the gallery view doesn't always switch to single view
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- Phenotyping does not ignore images not in the processing set
- Long Nuance library filenames can cause the Prepare Images UI to be cropped
- Edit->Delete functionality is not working in editable text fields.

inForm Version 2.4.1
Bug Fixes:
- Corrected labels for splitting selections
- Popup editors respond correctly when using the mouse wheel to scroll
- Fixed scenario where nuclei would be removed after membrane segmentation
- Fixed slow membrane segmentation
- Fixed membrane segmentation failures

- Counterstain-based segmentation has been deprecated; please use inForm 2.3 for any counterstain-based segmentation projects.
- A long-standing low-level bug fix has changed cell segmentation cytoplasm results. Older algorithms run in this version may yield slightly different results.
- Cell segmentation tables are not calculated when the live preview is present for performance reasons.
- Legacy projects from inForm 0.4.2, 1.0, and 1.0.2 have been deprecated; please load and save those projects in inForm 1.4 before proceeding.
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inForm Version 2.4

New Features and Improvements:
- New Adaptive Cell Segmentation algorithm
- Live preview window for real time cell segmentation results
- Add the batch algorithm name to the log (if known)
- Add a warning before saving an algorithm with a manual tissue segmentation step

Bug Fixes:
- Add scrolling for group names in the Select Stains dialog
- Handle custom filters for exported slide portions
- Zooming can be unresponsive

Known Issues:
- Counterstain-based segmentation has been deprecated; please use inForm 2.3 for any counterstain-based segmentation projects.
- A long-standing low-level bug fix has changed cell segmentation cytoplasm results. Older algorithms run in this version may yield slightly different results.
- Cell segmentation tables are not calculated when the live preview is present for performance reasons.
- Legacy projects from inForm 0.4.2, 1.0, and 1.0.2 have been deprecated; please load and save those projects in inForm 1.4 before proceeding.
- .im3 files with CJK characters in the directory path may fail to load Algorithms must be developed with an image present to run in batch
- The Prepare Image button can be active with no image present

- Double-clicking on a large digital slide in the gallery view doesn't always switch to single view
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- Edit->Delete functionality is not working in editable text fields.

inForm Version 2.3
New Features and Improvements:
- Support for Vectra Polaris imagery
- Add normalized coefficients to the phenotyper training output
- Add fluorescence response values to the unmixed image metadata

Bug Fixes:
- Loosen the restriction for bands present when using measured stains for unmixing
- Use normalized units when creating the autofluorescence spectrum extraction

Known Issues:
- Legacy projects from inForm 0.4.2, 1.0, and 1.0.2 have been deprecated; please load and save those projects in inForm 1.4 before proceeding.
- .im3 files with CJK characters in the directory path may fail to load
- Algorithms must be developed with an image present to run in batch
- The Prepare Image button can be active with no image present
- Double-clicking on a large digital slide in the gallery view doesn't always switch to single view
- The "Image Too Large" dialog is repeatedly shown when converting projects
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- Canceling the spectral variability dialog during stain extraction shows a second variable stain dialog
- Phenotyping does not ignore images not in the processing set
- Long Nuance library filenames can cause the Prepare Images UI to be cropped
- Edit->Delete functionality is not working in editable text fields.

inForm Version 2.2.1
New Features and Improvements:
- Windows 10 support
- Phenotyping variables are configurable for hard-to-train projects
- Support for loading Vectra 3 slides in batch
- Support for Pathology views in brightfield imagery
- Exporting Pathology Views

- Menu to show and hide individual phenotype classes
- Add summary counts for phenotype information
- Improve how the phenotype dots draw
- Add Phenotype ID to the debug information
- Add a region of disinterest
- Save the processing mask within the exported segmentation maps
- Add processing regions, regions of disinterest, and in-place reprocessing to merge
- Add mouse wheel zoom and pan behavior to the selection controller
- Support for processing Vectra 3 slides via the command line
- Support batch export with Scale Views Equally
- Show fluorescence imagery rendered as the human eye would see them by default
- Return to the color view after drawing a processing region or region of disinterest

Bug Fixes:
- Phenotyping no longer fails after batch processing
- inForm will no longer load the same image twice
- Fix the autofluorescence picker functionality
- Reduce the need to retrain the phenotype classifier
- Reduce constraints for loading imagery taken on older hardware
- Handle the case where there are two stains of the same type in the library
- Fix the meaning of location in Cube Info
- Rework how features are selected in phenotyping to reduce memory usage
- Explicitly run the 64 bit R installer
- Opening a project should not change the tissue category selection
- Correct the phenotyping documentation
- Close the underlying tiff reader correctly on load failure
- Make decimal places consistent within the score editor
- Fix the component name display in the composite editor
- Make the scoring labels consistent
- Restrict project images and libraries to those with like acquisition parameters
- Make the project dirty on additional image load or deletion
- Correct rendering, unmixing, and library viewer when images have bands in different orders

Known Issues:
- Legacy projects from inForm 0.4.2, 1.0, and 1.0.2 have been deprecated; please load and save those projects in inForm 1.4 before proceeding.
- .im3 files with CJK characters in the directory path may fail to load
- Algorithms must be developed with an image present to run in batch
- The Prepare Image button can be active with no image present
- Double-clicking on a large digital slide in the gallery view doesn't always switch to single view
- The "Image Too Large" dialog is repeatedly shown when converting projects
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- Stale score settings can cause a failure to segment cells
- The manual tissue segmentation fails to update correctly when deleting a category
- Image not removed from the training set when the last region is removed individually
- Canceling the spectral variability dialog during stain extraction shows a second variable stain dialog
- Phenotyping does not ignore images not in the processing set

- Long Nuance library filenames can cause the Prepare Images UI to be cropped
- Edit->Delete functionality is not working in editable text fields.
- Support for TRIO imagery has been removed.
- Windows 10 dropdown menus may have odd drawing effects when inForm windows are on multiple screens

inForm Version 2.2
New Features and Improvements:
- Factory information and synthetic library development for PerkinElmer Opal stains
- Ability to read slide patches from PerkinElmer whole slide .qptiff for non-quantitative processing and classifier training
- Compact export of tissue and segmentation maps
- Compact export of components in PerkinElmer tiff format
- Composite is shown after unmix
- Default library colors can be changed in Prepare Images
- Support for non-factory filters in stain extraction

Bug Fixes:
- Batch processing now works when using a UNC path
- .im3 files can contain non-English characters in their path
- Color, component, and composite toolbar shortcuts are enabled when on a table view
- Clearing the phenotype training will clear all results
- Phenotyping can handle images without cells
- Phenotyping can handle missing tissue segmentation
- Fixed rare cube timestamp reading issue
- Fix for error when deleting a manual tissue category
- Fix for compactness incorrectly reporting as N/A for very large cells
- Installer confirms that the correct version of R is installed

Known Issues:
- Legacy projects from inForm 0.4.2, 1.0, and 1.0.2 have been deprecated; please load and save those projects in inForm 1.4 before proceeding.
- .im3 files with CJK characters in the directory path may fail to load
- Algorithms must be developed with an image present to run in batch
- The Prepare Image button can be active with no image present
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- Canceling the spectral variability dialog during stain extraction shows a second variable stain dialog
- Phenotyping does not ignore images not in the processing set
- Long Nuance library filenames can cause the Prepare Images UI to be cropped
- Edit->Delete functionality is not working in editable text fields.

inForm Version 2.1.1
Bug Fixes:

- Fix for license upgrade issue. All other features are unchanged.

inForm Version 2.1.0
New Features and Improvements:
- Spectral library development for brightfield and fluorescent samples
- Synthetic library development for fluorescent samples
- Stain management
- Counterstain-based cell segmentation with DAB compensation
- Enable up to 4 membrane stains
- Cell Phenotyping
- Pathology Views
- Markers can be added to spectra
- Save spectral charts as Windows meta file
- Added batch logs for successful batch runs
- Better window resizing
- Make TRIO libraries viewable

Bug Fixes:
- Composite view editor would show the previous components
- Out of bounds exception on export
- Membrane segmentation had holes
- Leaking cytoplasm in cell segmentation
- Changed maroon to brown in the color dropdown list
- Fixed conversion problems for colocalization algorithms
- Fixed extraneous data export after conversion
- Draw error with differing images sizes
- Update stale editor icon
- Provide more space to view editor widgets
- Editing the export directory directly failed

Known Issues:
- Legacy projects from inForm 0.4.2, 1.0, and 1.0.2 have been deprecated; please load and save those projects in inForm 1.4 before proceeding.
- .im3 files with CJK characters in the directory path may fail to load
- Algorithms must be developed with an image present to run in batch
- The Prepare Image button can be active with no image present
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- Stale score settings can cause a failure to segment cells
- The manual tissue segmentation fails to update correctly when deleting a category
- Image not removed from the training set when the last region is removed individually
- Canceling the spectral variability dialog during stain extraction shows a second variable stain dialog

inForm Version 2.0.2
New Features and Improvements:
- Spectral Library viewing
- New units for brightfield and fluorescence unmixing

- Composite/Component view scaling based on selected images
- The batch tab supports opening of projects along with algorithms
- View editor stays on top of the inform application
- Cell number is now displayed in the information tooltip
- What's new menu item that displays new features for the release
- Updated about box with PerkinElmer support phone number and link
- Read full spectral segment basis information if present in .im3 image file
- Tables are now sortable by column
- Remember the file type for right clicking on an image and saving
- Only allow scoring in categories where cell segmentation has happened

Bug Fixes:
- Save algorithm dialog shows full path after cancelling overwrite
- Update error message for the training failed dialog
- Show the component data info tooltip even when there are no components
- Aligned the group boxes on the view editor
- Disconnected mapped drive no longer causes a long delay in the slide browser dialog
- Image name not updated when data table is displayed
- Improved application performance in manual segmentation with many images
- Fixed the "Discard If Touching an Edge" check box to reflect state accurately
- Exporting RGB with score map now works
- Double clicking on an inForm project now launches inForm without errors
- Sample format was locked for im4 images
- Can now convert to optical density with brightfield RGB image
- Converting a project caused a null reference exception
- Batch table choices were not exporting
- Restrict use of deficient spectra with .im3 images
- Always open a project with the color image view
- Improved performance of the cell segmentation table
- Cell segmentation table was throwing a null reference exception
- Inconsistent colors in component view fixed
- Problem unmixing RGB image using "Raw" reported units
- The "Discard If Touching an Edge" check box now has a consistent location
- Toolbar no longer disabled after loading a project

Known Issues:
- Legacy projects from inForm 0.4.2, 1.0, and 1.0.2 have been deprecated; please load and save those projects in inForm 1.4 before proceeding.
- More than 65,536 objects will fail to write a cell or object map
- 32 bit systems will throw an out of memory exception when loading projects created on a 64 bit system that contain more than 20 images.
- Training regions sporadically do not fill in and vanish
- .im3 files with CJK characters in the directory path may fail to load
- A strange series of actions can cause conversion problems for colocalization algorithms
- Under certain conditions after converting a project, the export step exports items from the original project before the conversion

inForm Version 2.0.1
New Features and Improvements:
- Updated table headings and axes precision
- Update the gallery right-click menu

- Use N/A values in table output for improved import into Spotfire and R
- Use different region IDs for each tissue category
- New ability to read in 3DH compressed images

Bug Fixes:
- Allow simple threshold with process regions
- Provide the Equal RGB checkbox only when appropriate
- Update active buttons, highlighting, and tab order
- Report when the maximum generated regions has been reached
- Fix the creation/erasing of threshold regions with MCP
- Remove an extraneous dialog
- Update the scores when changing from single to double pos
- Close the popup editor when a new project is created
- Correct the white picker cursor in 120 DPI
- Update error message, tool tips
- Select radio buttons by default in the new project editor
- Update too-strict image loading rules
- Fix the off-by-1 region number in the interrogator controller
- Corrected image edges when zoomed in
- Fixed 120 DPI GUI issues
- Link the view editor help to the correct section
- Remove the configure button in the viewer
- Correct the batch log time (Local, not UTC)
- Loaded coloc projects should only have sliders for the user components
- Correctly load the false color setting for composite
- Make the project dirty when deleting a process region
- Do not show tissue columns when there is no tissue seg
- Make the export directory does not exist dialog dismissable
- Update the tables after project configuration
- Export all columns from the coloc quantitation table
- Gracefully shut down when access to a project is terminated
- Correctly calculate process region membership and count data values when processing regions or tissue regions are used
- Clip cell compartments correctly
- Fail gracefully when images cannot be found
- Fix 1:2 upsampling thumbnails
- Correct right click delete region in single view
- Show the data export table in batch

Known Issues:
- Legacy projects from inForm 0.4.2, 1.0, and 1.0.2 have been deprecated; please load and save those projects in inForm 1.4 before proceeding.
- More than 65,536 objects will fail to write a cell or object map
- 32 bit systems will throw an out of memory exception when loading projects created on a 64 bit system that contain more than 20 images.
- Training regions sporadically do not fill in and vanish

inForm Version 2.0.0
New Features and Improvements:
- New Custom Project Configuration

- New levels of functionality: inForm Viewer, inForm Basic Analysis, inForm Cell Analysis, and inForm Tissue Finder with upgrading capability
- New Processing Steps: Threshold, Colocalization, Manual Tissue Segmentation
- New Cube and Component Visualization Tools
- New Composite View and Visualization Tools
- New H-Score and Visualization within Scoring
- New Table Export Format and Additional Statistics
- Improved Cell Rendering
- Improved Component Rendering
- Improved mandatory field notification
- Improved thumbnail rendering
- Improved Gallery selection and ability to save images
- Improved size requirements allow inForm to run on smaller monitors
- Improved tooltips within the application
- New Region Numbers for Processing Regions
- Updated Graphic design
- Enabled loading of Vectra slides for batch processing
- Enabled zoom to full functionality

Bug Fixes:
- Corrected the mouse offset when zooming in/out at long distances
- Corrected drawing errors at the edge of zoomed in images
- Changed Brightfield signal scaling default to autoscale
- Corrected default values for scoring
- Corrected the white picker selection region
- Corrected filenames and training image folder issues when names had '.' in them
- Corrected view editor GUI problems
- Editor selection no longer causes projects to need saving
- Minimized calculation differences between 32 and 64 bit
- Merge now handles drive letter changes gracefully
- Improved error messages to pinpoint processing failure
- Corrected the Prepare Images editor's locking of the TRIO dropdown
- Corrected text overrun in the licensing dialog
- Corrected default browse location when inForm was launched from a project or algorithm, using an RGB library
- Corrected the inForm RGB export to use the view settings
- Corrected Data reading error with a multi-filter acquisition with only one filter segment

Known Issues:
- Legacy projects from inForm 0.4.2, 1.0, and 1.0.2 have been deprecated; please load and save those projects in inForm 1.4 before proceeding.
- When changing from one scoring type to another, the scoring image will be stale until processed again
- 32 bit systems will throw an out of memory exception when loading projects created on a 64 bit system that contain more than 20 images.
- Training regions sporadically do not fill in and vanish
- The region ID in the pixel value controller is off by 1
- Commandline help starts the application

Support:
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