DEFINIENS®
Understanding Images

Definiens TissueMap 3.1

Release Notes

DEEPER INSIGHTS
FASTER RESULTS
BETTER DECISIONS

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Imprint and Version

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Dear User,

Thank you for using **Definiens** software. We appreciate being of service to you with image intelligence solutions.

At Definiens we constantly strive to improve our products. We therefore appreciate all comments and suggestions for improvements concerning our software, training, and documentation.

Feel free to contact us via web form on the Definiens support website **http://www.definiens.com/support/index.htm**.

Thank you.

Legal Notes

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Overview

Definiens TissueMap™ is an image analysis software component that provides functionality to support the pathologist in analyzing standard assays in histopathology. It enables non-technical users to configure, calibrate and execute versatile image analysis workflows. The software supports all major acquisition devices and users can analyze all kinds of tissue slides, tissue microarrays and microscope images.

A library of pre-defined image analysis solutions for typical every-day problems is provided that can be calibrated for the particular image data set, using simple graphic sliders. These calibrated applications can be saved and submitted for batch execution.

Definiens TissueMap™ allows the user to quantify IHC, fluorescence and other histological assays on a cell-by-cell basis.

Definiens TissueMap runs on top of the Definiens XD 1.2 platform.

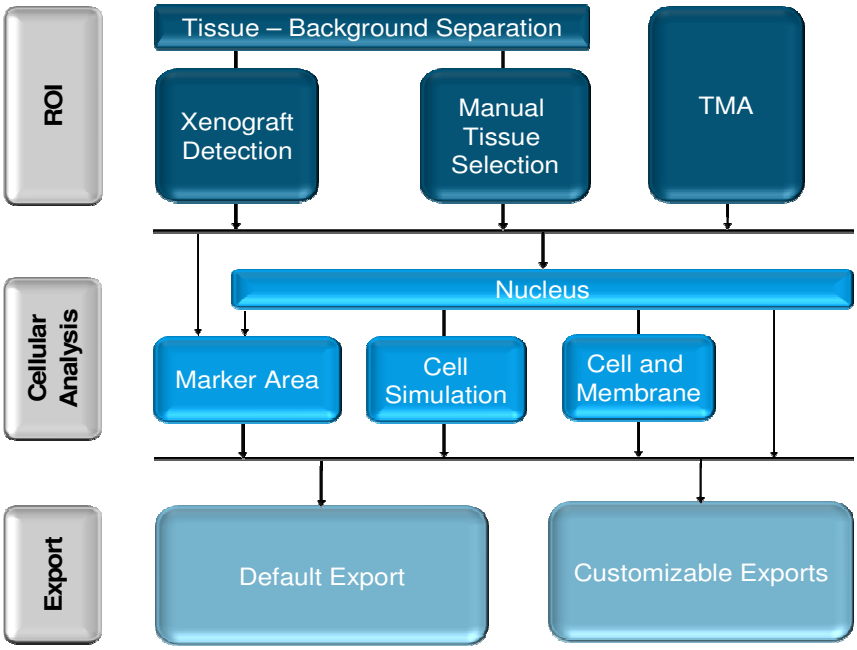

Figure 1: Definiens TissueMap image analysis capabilities

About Definiens TissueMap 3.1

Definiens TissueMap 3.1 is a minor release for all customers running with Definiens TissueMap 3.0 or earlier versions. It contains many fixes which improve the overall stability, the workflow and image analysis routines.

A summary of the most important improvements are detailed below.

Key Benefits

- Improved automatic image analysis routines
  - nucleus detection
  - membrane detection
  - tissue detection
  - xenograft detection

- Works on red chromogenes in addition to brown chromogenes

- Improved workflow
  - Automatic import of metadata, all configurations and exports in real world units (not pixels)
  - Manual selection of a subset for calibration
  - Improved workflow for manual ROI selection

- Actions with new functionality
  - Cell Simulation
  - Customizable Export
  - Cell Classification

- TMA
  - Improved export functionality
  - Import of patient metadata per core

Bug Fixes

Category	Reference	Description
Action	Bug-14225	Nucleus: Bad detection for black or dense nuclei
Action	Bug-14338	Out of memory while running segmentation
Export	Bug-14360	Wrong Export of features in Standard_ROI Stats and Tile Stats
Export	Bug-14209	Export: Nucleus Negative is reset for Nucleus Class export and never set again
Export	Bug-14340	round-off differences in Export Tile Statistics vs Slide Statistics
Export	Bug-14174	Hematoxylin Marker Area not reported in Subset statistics
Processing	Bug-14383	Server processing: Can't create small map error message
Workflow	Bug-14362	Wrong path if solution is loaded and simply run without any configuration

Enhancements

Category	Reference	Description
Action	Enh-13098	New Features for Export
Action	Enh-12822	Xenograft: Switches for Host and Necrotic
Action	Enh-13032	Detect Tissue: switch for artefact classification
Action	Enh-12918	NucleusDetection: Use performance updates
Export	Enh-13598	Export: Checkboxes for type of image view
Export	Enh-12819	Export: Customized Export with use of Feature variable
Export	Enh-13533	Make actions cust. Export
New Feature	Enh-13315	IHC blue/red: check if also works similar to blue/brown
TMA	Enh-14128	DetectCores: revisit and use homogenity
TMA	Enh-13364	Change TMA grid item naming to ensure correct sorting order
TMA	Enh-13852	Automatically export annotations to project statistics if present
TMA	Enh-12828	Added annotation support for cores and import from .csv file. Annotations are added as thematic layer "CoreROI" attributes for

		access in the ruleset
Workflow	Enh-13199	Allow subset selection on slide
Workflow	Enh-12818	Manual: change segmentation from manual to automatic
Workflow	Enh-14176	switch back to ROI detection map after ROI subset has been selected for analysis

Known Issues and Limitations

Category	Reference	Description
Known Issue	Iss-14430	If the resolution metadata of small images (e.g. TIFF) is incorrect and the import template “Generic – one file per scene – with resolution” is used, this incorrect metadata is read and cannot be modified. Use the template “Generic – one file per scene” (without resolution) for import in these cases.
Limitation	Lim-14388	Action: Xenograft ROI Detection Option “Inside ROI” does not work in some cases

Documentation Errata

None

Additional Information

For additional information please contact support@definiens.com