

MetaSystems White Paper Tissue Microarray (TMA) Analysis with Metafer

Introduction

The major limitations in molecular clinical analysis of tissues include the laborious nature of procedures, limited sample material, and limitations in the availability of reagents for diagnostics. With the tissue microarray (TMA) technique these issues are addressed by obtaining tissue cores from regions of interest in paraffin embedded tissues, assembling them in array fashion, and mounting them to a standard glass slide for microscopy. Each of these cores is then subject to an independent analysis.

Due to the special layout of samples automation of TMA has to be done based on the following considerations:

1. Analysis should take the general layout of the TMA into account,
2. It should be possible to correct contortions, rotations, or other spatial aberrations generated during slide preparation,
3. Each TMA core should be clearly identifiable by a label,
4. Analysis results should be separable so that data can be assigned to the single core.

With the unique combination of **Metafer MetaCyte**, the integrated tool for TMA analysis, and the **VSlide** digital slide imaging software, MetaSystems offers a complete package for precise and effortless, automated TMA analyses.

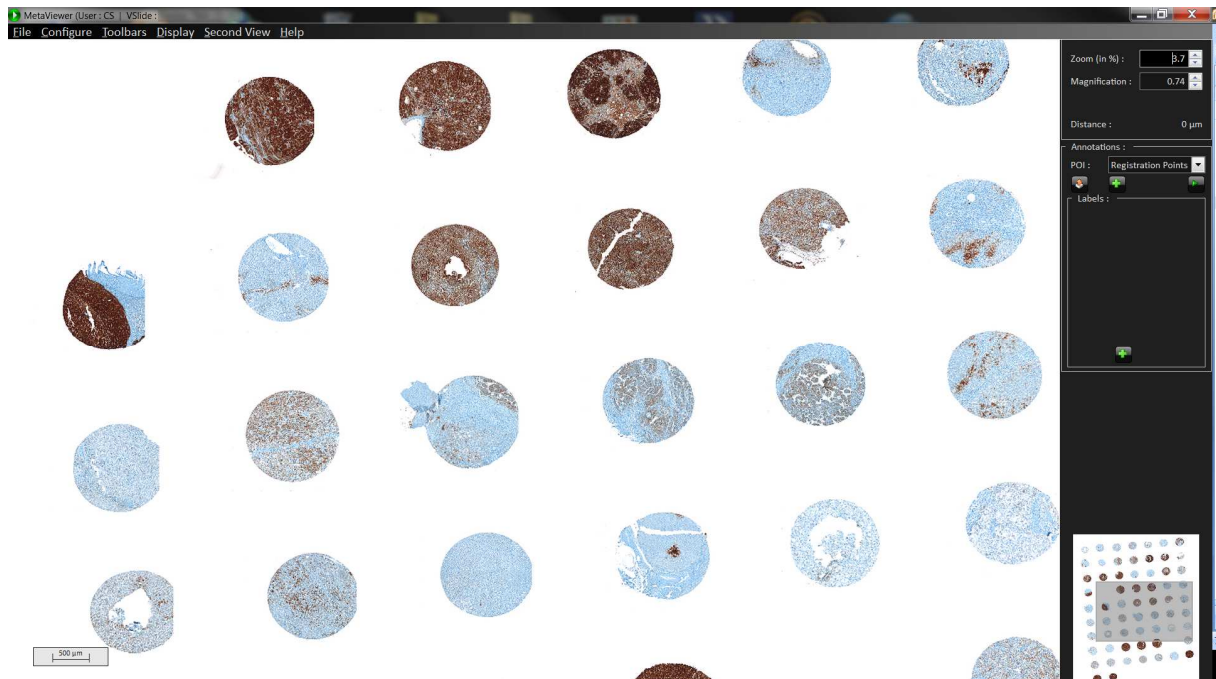


Fig. 1: A tissue microarray image acquired with Metafer VSlide and shown in MetaViewer. In addition to the overview image also single images of each core can be stored automatically.

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Functionality

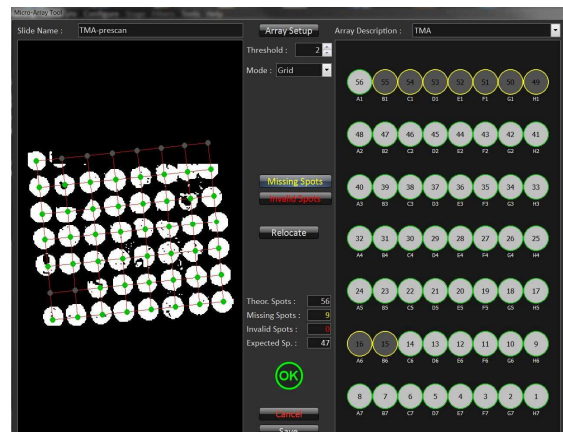
Once a tissue microarray (TMA) is created, its layout can be expressed with the number of cores per row, the number of rows in the array, the diameter of the cores, and the distance of cores. In the integrated Metafer TMA tool these values can be used to generate a TMA map file that is used as basis for the analysis. Additionally each core can receive a unique identifier.

A fast pre-scan at low magnification is used to generate a map of the current slide. The result of the pre-scan is displayed side by side with the TMA map, and with a flexible grid the actual image can be matched to the map in order to correct any spatial aberrations. Also missing or invalid cores can be marked in this interface.

On confirmation the TMA tool converts the data into a position list, which contains the exact positions of each core, and also the core identifiers. MetaCyte is now capable to re-locate each core and acquire and analyze the core images. If the VSlide image stitching software is available, core images are automatically stitched in the background, and also an overview image of the whole TMA can be generated.

1. **Easy Creation of TMA Layout Files**
TMA layouts are stored in the system as basis for the TMA tool.
2. **TMA Tool with Innovative Grid Matching Functionality**
A pre-scan image of the TMA can be matched to the TMA layout file with a flexible, adaptable grid. Missing or invalid cores can be marked in the grid.
3. **Automated Generation of Core Position List for High Magnification Scan**
The analysis is done at the target magnification (e.g., 40x). Images of each core are acquired and analyzed automatically.
4. **Overview Images**
Overview images of the whole TMA can be automatically generated during the scan, e.g. for documentation purposes.
5. **Slide Digitization with VSlide**
If Metafer VSlide is installed, high magnification images are automatically stitched during scan for later analyses. Single core images and high-resolution image of the whole TMA can be generated simultaneously.

The TMA tool with the innovative flexible grid matching functionality facilitates the matching of the pre-scan to the TMA layout.



Contact MetaSystems Worldwide

Headquarters:	MetaSystems Germany	tel +49 6205 39610	info@metasystems.de
Asia and Australia:	MetaSystems Asia	tel +852 2587 8333	info@metasystems-asia.com
USA and Canada:	MetaSystems Group	tel +1 617 924 9950	info@metasystems.org
Web:	www.metasystems-international.com		