CytoSpec
Software for Hyperspectral Imaging

Import Filters
Agilent Resolutions Pro™
Bruker OPUS™
Grams-3D™
Horiba Jobin-Yvon (ASCII)
MATLAB™
PerkinElmer SpectrumSpotlight™
Thermo-Nicolet Atlas™
Thermo/Raman DXR™ xi
Renishaw Wire™ 4.0
WITec (MATLAB), Kaiser-Holospec

Preprocessing
Savitzky-Golay derivatives
Spectral preprocessing: cut, interpolation, smoothing & normalization
Absorbance/transmission conversion
PCA based noise reduction
Non-linear baseline correction
Water vapor correction
Spectral quality tests
Cosmic ray correction
Spatial preprocessing: crop, binning
Spatial filtering, 3D-FSD, edge-preserving denoising

Spectral preprocessing: cut, interpolation, smoothing, normalization, absorbance/transmission conversion, PCA based noise reduction, non-linear baseline correction, water vapor correction, spectral quality tests, cosmic ray correction, spatial preprocessing: crop, binning, spatial filtering, 3D-FSD, edge-preserving denoising.

Imaging Methods
Chemical imaging
Hierarchical cluster imaging
Frequency/FWHM imaging
PCA, n-findr & VCA imaging
Fuzzy C-means cluster imaging
K-means cluster imaging
ANN imaging (SNNS)
Imaging interface to the NeuroDeveloper (artificial neural network analysis)

Download a demo version at http://www.cytospec.com
For more information inquire info at info@cytospec.com

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The Most Powerful Hyperspectral Imaging Software Available

Rel. 2.0
Infrared class mean spectra as obtained by the 'calculate average spectra' option of CytoSpec’s hierarchical cluster imaging routine (6-class classification approach, see Panel A). Class mean spectra were obtained from original absorbance spectra (left) and first derivative spectra (Right). Spectra are color encoded in accordance to the color scheme used in Panel A.

What is new in CytoSpec 2.0?

- A 64-bit stand-alone version of CytoSpec is available. CytoSpec 64-bit requires installation of the free Matlab Compiler Runtime (MCR) R2021a 64-bit. Matlab is not required anymore for using CytoSpec 64-bit
- The graphical user interface has been redesigned and now features a cleaner look that makes it simpler and quicker to use
- New or renamed functions for spatial preprocessing: crop, interpolate/binning, spatial filtering, edge-preserving denoising (EPD), Chambolle algorithm, 3D-Fourier self-deconvolution, a blind deconvolution method and the function replace NaNs have been added
- New function: baseline correction by asymmetric least squares (AsLS)
- New imaging function: create composite images. This function is available from the context menus of the pseudo-color images and allows superimposing up to 6 different images
- Function cosmic spike correction with new functionality and improved performance
- New function replace NaNs (spatial preprocessing menu). The function can be used to replace NaN pixel spectra (e.g., bad spectra from quality tests) by interpolated spectra. These spectra represent averages from the neighboring pixel spectra and are obtained by an iterative procedure
- Import filter for Renishaw *.wof spectral maps. With version 2.00.02 CytoSpec supports importing of WIRE 4.0 *.wof mapping data files
- Updated import filter for WITec Raman data (*.txt, and *.mat [MATLAB format] produced by WITec Project v. 2.1 and WITec Project Four. Note that the Matlab *.mat import filter is supported only by CytoSpec 64-bit
- Many code improvements & bug fixes

EXAMPLE: IR imaging of a tissue specimen from the human colon mucosa. Panels A & B: IR images obtained by agglomerative hierarchical clustering (6 or 15 cluster). Panels C & D: Images reassembling based on k-means clustering (8 or 15 cluster). Panel E: Microphotograph of the tissue area examined (1.34 x 1.39 mm or 232 x 223 spectra). Panel F: Images as obtained by chemical imaging (area of the baseline corrected amide I band 1620-1680 cm⁻¹). Preprocessing and image reassembling was carried out by using the CytoSpec software package.

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What Is CytoSpec?
The multivariate imaging software package CytoSpec™ represents a novel approach for creating pseudo-color displays of spectral imaging data via statistical methods that utilize the entire spectral and imaging information. It is laid out and optimized to work on 3-dimensional spectral data sets from imaging or mapping infrared or Raman experiments. Native data formats from various instrument manufacturers can be analyzed.

Info at Info@CytoSpec.com internet: http://www.CytoSpec.com
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A trial version of CytoSpec can be downloaded from the CytoSpec website: http://www.cytospec.com

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