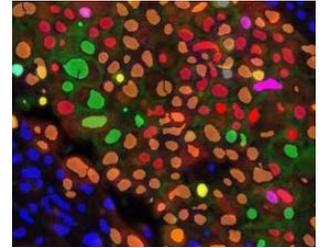
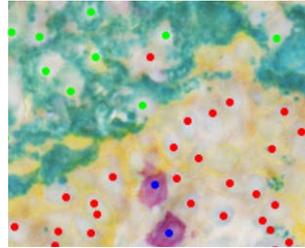
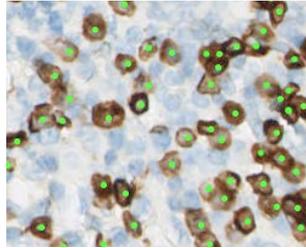
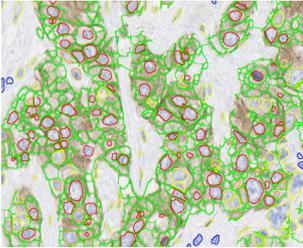


Automatic slide series quantification with preset algorithms

Cell Recognition

Segmentation and phenotyping of cells and objects

Cells and more generally biological objects are detected regardless their staining type (HE, IHC, IF, simple or multiplex) in brightfield and fluorescence using machine learning. The analysis is based on the color, edge, texture, and morphology of the objects and/or their neighborhood.

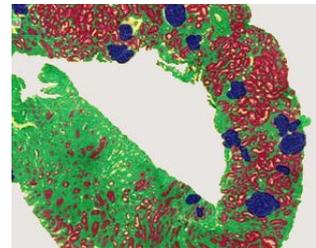
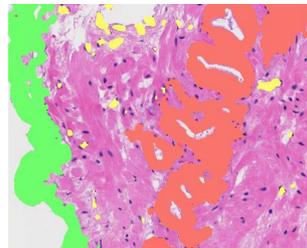
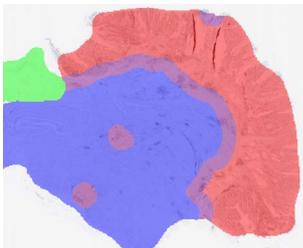


Tissue Recognition

Recognition and segmentation of tissue classes

The algorithm maps tissues by identifying anatomical structures and regions. It allows to define the regions of analysis to be quantified and the invasion margin of the tumor.

Tissue Recognition analyzes tissues (e.g. stroma vs tumor, glands vs tissue) by machine learning from learning images. The analysis is based on criteria of colors, contours, shapes and textures.

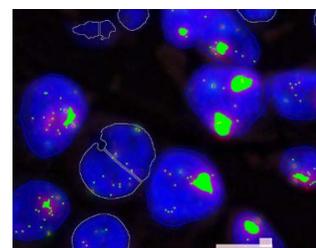
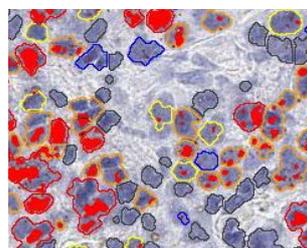
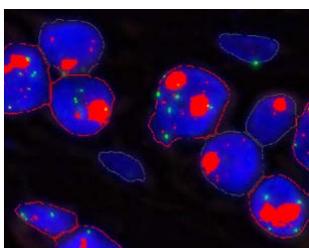


ISH (CISH/FISH/RNA Scope)

Quantification of in situ hybridization slides

For CISH/FISH slides, the algorithm allows to detect and quantify the gene and its control, and to segment the nuclei if necessary. The result thus proposes a number of genes and total control on a region of interest, or a classification of the nuclei based on the amplification of the gene.

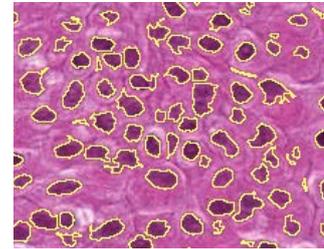
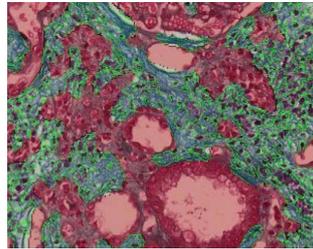
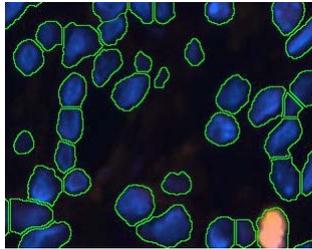
For RNA Scope slides, the algorithm allows to detect and quantify the gene of interest, and to segment the nuclei if needed. The result can be a total gene number over a region of interest, or a nucleus classification based on the gene copy number.



Morphometry

The image is segmented according to luminance, hue and mathematical morphological criteria leading to an exhaustive description of tissues and cells.

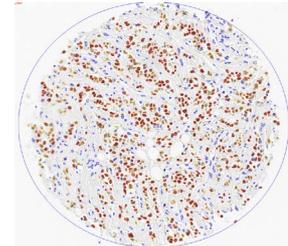
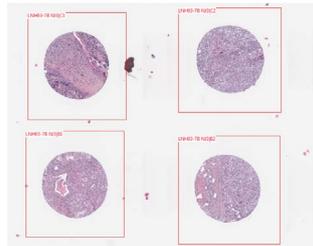
Morphometry allows the creation of various analysis macros. It is commonly used for the quantification of fibrosis, nuclei, histological structures, cellular bodies...



TMA (Crop & Score)

The cores on a slide are identified and individualized for their analysis:

- Location of cores on the slide using the Arrayer production file
- Manual scoring of each core on a reading template
- Exporting of results on an Excel file
- Combined with the other algorithms, TMA Crop & Score allows automatic reading of biomarkers



ImageJ

Module for the integration of image analysis plug-ins developed in ImageJ

It allows the generation of your own image analysis macros and their integration in workstations, in order to benefit from the CaloPix images management system.

TRIBVN
HEALTHCARE

