CytoPacq

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Introduction CytoPacq is a toolbox that consists of three individual modules: 3D-cytogen, 3D-optigen, and 3D-acquigen. Each one is a virtual machine capable of simulating selected real processes:

- 3D-cytogen* ... a module generating the digital cell phantoms (spatial objects imitating cells and their components as well as their structure).
- 3D-optigen ... a module simulating the transmission of the signal through the optical system.
- 3D-acquigen ... a module simulating the phenomenons manifesting themselves during image capture with digital CCD cameras (various types of noise, sampling, digitization, etc.)

Composition of all these toolkits together into a single sequence forms a complex toolbox, which we call "CytoPacq". It covers the most common phenomenons appearing during each real acquisition process.

3D-cytogen
This module is responsible for digital phantom generation. Recently, four types of objects have been implemented: HL-60 cell nuclei, granulocyte nuclei, microspheres, and tissue colons. However, there is no restriction put on the number of objects and the object complexity. As soon as a suitable model is defined, the corresponding digital phantom can be simply generated. The current version of 3d-cytogen supports plugins, i.e. each user can implement his/her own digital phantom.

3D-optigen
The second module (3d-optigen) simulates the optical system. Namely, it involves the blurring process occurring in the optical system. Aside from blur, the devitation of the illumination axis is also taken into account.

3D-acquigen
The last stage (3d-acquigen) imitates the job of the digital CCD camera. Here, the phenomenons like noise, sampling, and quantization are simulated.

(*) ... 3D-cytogen can be optionaly substituted with the alternative modules that are capable of generating the cell types with conceptually different structure from those generated in 3d-cytogen. These modules include:
- TRAGen - Motility of population of living cells (2D+time)

In order to imitate the behaviour of cells in densely populated microscopic slide, we developed a tool that allows for generating 2D image sequences showing simulated living cell populations together with ground-truth images for evaluation of cell tracking tasks. The simulated events include namely cell motion, cell division, cell death, and cell clustering up to tissue-level density. TRAgen features complete cell cycle with shape changes due to rounding and elongation of a cell just before its division. The user can add his own internal structure to simulate, for example, either fluorescently stained cells or cells as observed using phase-contrast microscopy.
- MitoGen - Mitosis of living cells (3D+time)

MitoGen is a complex module capable of generating the fully 3D time-lapse image sequences depicting the population of living cells. The typical events that can be observed include: cells division, cell motility, cell appearance and disappearance near the border of the region of interest. The data generated using the MitoGen is an integral part of training and testing dataset of the 1st a the 2nd edition of Cell Tracking Challenge joined to IEEE International Symposium on Biomedical Imaging.
- Vasculogenesis - Formation of tubular networks (2D+time)

This module allows to generate visually plausible synthetic image sequences of evolving fluorescently labeled vascular networks with ground truth data. Such generated datasets can be subsequently used for testing and validating methods employed for the analysis and measurement of the images of real vascular networks.

{mospagebreak title=Simulated Phenomena} Simulated Phenomena
- various digital phantoms available (HL60 nuclei, granulocyte nuclei, microspheres, colon tissue)
- uneven illumination
- virtual camera
- virtual microscope
- virtual objective

- virtual excitation/emission filters

- dark current signal
- (re)sampling

- fixed pattern noise
- quantification uncertainty (poisson noise)
- amplifier (readout noise)
- A/D conversion (quantization)

{mospagebreak title=Execution and Downloading}
Web Toolkit
Currently, the version 2.0 is available. All the previous versions are listed in the history of changes.
If you meet some failure or if you like to contact developers please write an e-mail to David Svoboda. Source codes
The source codes are freely available and are subject to GNU GPL. If you want to get them all you have to do is to register yourself. After that, you will obtain a free access to the download section. Before you start compiling, building or running this application, please read the documentation carefully. Running CytoPacq with Docker

Compiling the whole CytoPacq from scratch on your own may seem a bit complicated. For this purpose Volker Baecker (BioCampus Montpellier, France) prepared a Dockerfile that simplifies the whole building process. All you have to do is to install Docker into your computer and follow the instructions written in the abovementioned Dockerfile.

{mospagebreak title=Documentation} Documentation

The detailed documention is available in the following languages: Czech
- English (under construction)

{mospagebreak title=Examples} Examples

- See some screenshots which illustrate the advance of simulation process:
Step 1 -> Step 2 -> Step 3 -> Step 4 -> Step 5

- An example of five real images of (a-b) two granulocyte nuclei, (c-d) two HL60 nuclei and (e) one tissue colon section. Each 3D figure consists of three individual images: the top-left image contains selected xy-slice, the top-right image corresponds to selected yz-slice, and the bottom one depicts selected xz-slice. Three mutually orthogonal slice planes are shown with ticks.

(a)

(b)

(c)

(d)

(e)

- An example of five synthetic images of (a-b) two granulocyte nuclei, (c-d) two HL60 nuclei and (e) one tissue colon section. Each 3D figure consists of three individual images: the top-left image contains selected xy-slice, the top-right image corresponds to selected yz-slice, and the bottom one depicts selected xz-slice. Three mutually orthogonal slice planes are shown with ticks.

(a)

(b)

(c)
(d)

(e)

{mospagebreak title=MUCIC - Image Datasets} MUCIC - Masaryk University Cell Image Collection
Colon Tissue (fixed cells)

Here, you can find 30 synthetic images of human colon tissue including ground truth (foreground/background) images. The dataset was generated using the virtual microscope imitating the microscope Zeiss S100 (objective Zeiss 63x/1.40 Oil DIC) attached to confocal unit Atto CARV and CCD camera Micromax 1300-YHS. The image data was saved using three different file formats: ICS, HDF5 and 3D-TIFF. Please, feel free to select the format you prefer. All of them contain the same data. The individual image files are aggregated in ZIP archives.

Example images: 3D image 3D foreground

- high SNR: ICS | HDF5 | 3D-TIFF (preview)

- low SNR: ICS | HDF5 | 3D-TIFF (preview)

If you use this dataset in your research papers, please refer the following article:
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Svoboda D., Homola O., Stejskal S. Generation of 3D Digital Phantoms of Colon Tissue, In International Conference on Image Analysis and Recognition - ICIAR 2011, Part II, LNCS 6754, Berlin, Heidelberg: Springer-Verlag, pp 31-39, June 2011, ISBN 978-3-642-21595-7

This research was supported by the Ministry of Education of the Czech Republic (Projects No. LC535 and No. 2B06052).
HL60 Cell Line (fixed cells)

Here, you can find 30 synthetic images of nuclei of HL60 cell line including ground truth (foreground/background) images. Each image set contains 20 cell nuclei with specified probability of clustering (0%, 25%, 50%, and 75%). The dataset was generated using the virtual microscope imitating the microscope Zeiss S100 (objective Zeiss 63x/1.40 Oil DIC) attached to confocal unit Atto CARV and CCD camera Micromax 1300-YHS. The image data was saved using three different file formats: ICS, HDF5 and 3D-TIFF. Please, feel free to select the format you prefer. All of them contain the same data. The individual image files are aggregated in ZIP archives.

Example images: 3D image 3D foreground

- high SNR:
  - probability of clustering 0%: ICS | HDF5 | 3D-TIFF (preview)
  - probability of clustering 25%: ICS | HDF5 | 3D-TIFF (preview)
  - probability of clustering 50%: ICS | HDF5 | 3D-TIFF (preview)
  - probability of clustering 75%: ICS | HDF5 | 3D-TIFF (preview)

- low SNR:
  - probability of clustering 0%: ICS | HDF5 | 3D-TIFF (preview)
  - probability of clustering 25%: ICS | HDF5 | 3D-TIFF (preview)
  - probability of clustering 50%: ICS | HDF5 | 3D-TIFF (preview)
  - probability of clustering 75%: ICS | HDF5 | 3D-TIFF (preview)

If you use this dataset in your research papers, please refer the following article:
- Svoboda D., Kozubek M., Stejskal S. Generation of Digital Phantoms of Cell Nuclei and Simulation of Image Formation in 3D Image Cytometry, Cytometry Part A, Volume 75A, Issue 6, pp 494-509, June 2009, ISSN:1552-4922
This research was supported by the Ministry of Education of the Czech Republic (Projects No. LC535 and No. 2B06052).

Granulocytes (fixed cells)

Here, you can find 30 synthetic images of nuclei of granulocytes including ground truth (foreground/background) images. Each image set contains up to 15 cell nuclei. The dataset was generated using the virtual microscope imitating the microscope Zeiss S100 (objective Zeiss 63x/1.40 Oil DIC) attached to confocal unit Atto CARV and CCD camera Micromax 1300-YHS. The image data was saved using three different file formats: ICS, HDF5 and 3D-TIFF. Please, feel free to select the format you prefer. All of them contain the same data. The individual image files are aggregated in ZIP archives.

Example images: 3D image 3D foreground

- high SNR: ICS | HDF5 | 3D-TIFF (preview)
- low SNR: ICS | HDF5 | 3D-TIFF (preview)

If you use this dataset in your research papers, please refer the following article:
- Svoboda D., Kozubek M., Stejskal S. Generation of Digital Phantoms of Cell Nuclei and Simulation of Image Formation in 3D Image Cytometry, Cytometry Part A, Volume 75A, Issue 6, pp 494-509, June 2009, ISSN:1552-4922

This research was supported by the Ministry of Education of the Czech Republic (Projects No. LC535 and No. 2B06052).
Time-lapse Image Sequences (living cells)

In this section, you can find a reference to collection of computer generated time-lapse image sequences of nuclei of HL60 cells stained with Hoescht (both 2D & 3D). The dataset was generated with the help of our virtual microscope. The dataset was prepared for the 1st a the 2nd edition of Cell Tracking Challenge joined to IEEE International Symposium on Biomedical Imaging.

Example image sequence:

The data is available for free at this address: http://www.codesolorzano.com/Challenges/CTC/Datasets.htmlIf you use this dataset in your research papers, please refer one of the following articles:
- Svoboda, D. Ulman V. MitoGen: A Framework for Generating 3D Synthetic Time-Lapse Sequences of Cell Populations in Fluorescence Microscopy. IEEE Transactions on Medical Imaging, IEEE Engineering in Medicine and Biology Society, Volume 36, Issue 1, Jan 2017, available on-line: http://dx.doi.org/10.1109/TMI.2016.2606545

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This research was supported by the Czech Science Foundation, Grant No. GA14-22461S. Vaculogenesis (living cells)

Here, you can find the sequence of frames recording the process called vasculogenesis. The endothelial cells, initially spread across the glass slide, tend to attach each other and form the networks with thin and elongated chords. This process forces some cells to be markedly elongated, as can be seen in the figure below. The dataset was generated with the help of our virtual microscope.

Example images: 3D image 3D foreground
- sequence of images with simulated fluorescence: PNG (preview video)
- sequence of corresponding cell labels: PNG (preview video)

If you use this dataset in your research papers, please refer the following article:
- Svoboda D, Ulman V, KováÄ• P, Šalingová B, TesaÅ™ová L, Koutná IK, Matula P. Vascular Network Formation in Silico Using the Extended Cellular Potts Model, In IEEE International Conference on Image Processing, Phoenix, Arizona (USA), 2016, pp. 3180-3183, ISBN 978-1-4673-9961-6.

This research was supported by the Czech Science Foundation, Grant No. GA14-22461S.

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This service is developed and maintained by:
- David Svoboda (software development, web admin)
- Martin Maška (software development)
- Michal Kozubek (optics, signal sensing)
- Stanislav Stejskal (biology)
- Jaromír Coufal (web design)
- Vladimír Ulman (web server and database server maintenance)
- OndÅ™ej Homola (generation of phantom of colon tissues)
- LudÄ›k Matyska jr. (implementation of uneven illumination)

{mospagebreak title=History of Changes} History
- 2015 (March)
Main features (almost bug fixies):
+ cytopacq: removal of memory leaks
+ acquigen: Poisson noise generator fixed
+ iniparser: input format of configuration INI files modified
+ iniparser: new rules imposed by a new version of Bison and Lex

- 2013 (June) - version 2.0
Main features:
+ cytogen: the distribution of objects within the volume of interest can be controlled by the user
+ cytogen: digital phantom (colon tissue) switched into release version
+ optigen: implementation of empiricaly measured quadratic surface defining uneven illumination of the specimen.
+ optigen: implementation of convolution with Neumann boundary condition
+ interface: user notification via e-mail
+ interace: improved logging of errors and warnings
+ interface: simulation process can be iterrupted by a user
+ server: improved stability of the computational kernel
+ already generated datasets are available

- 2010 (October)
Main features:
+ New comprehensive documentation released (currently in Czech only).
+ A bug causing the bad image resolution repaired.

- 2010 (August) - version 1.1
Main features:
+ New type of digital phantom (colon tissue) - development version.
+ Some sample PSFs redistributed with the source codes.

- 2010 (April)

Main features:
+ The user can select the preference of the output image format (ICSv1, ICSv2, 3D-TIFF).
+ The binary mask of the generated digital phantom is available now.

- 2010 (January)
Main feature:
+ The support for the manipulation with large images added (fast tiled convolution).

- 2009 (May)
Main features:
+ Improved input validation.
+ Larger selection of levels of sub-pixel precision.
+ Intermediate results (images) can be downloaded while the consequentical applications are still in progress.

- 2009 (March) - version 1.0
Main features:
+ Enhanced list of available configurations (PSFs).
+ Larger selection of available PSFs (no need for uploading own PSF)
+ Source codes available for free after a registration.
+ All the generated images (digital phantom, ground truth, final synthetic) can be downloaded.
+ Names for all the available components amended.
+ Improved preview of the generated 3D images.

- 2009 (January)
Main features:
+ Error logging - in case of failure, the user is informed what had happened.
+ Flashing effect appearing during page reloading eliminated
+ Configuration used for the simulation process can be downloaded.
+ Stable solution regarding server-to-server and client-to-server communication.
+ Extended information panels for cameras, objectives and microscopes.

- 2008 (October) - version 0.2
Main features:
+ An improved version of web-based interface released.
+ The user can select from a larger list of cameras, objectives, microscopes, excitation and emission filters.
+ The user can watch intermediate results.

- 2008 (May)
Main features:
+ The first version of web-based platform-independent interface.
+ Since all the simulation steps are performed on dedicated server the user is not required to have a powerful PC.
+ A simple web-based interface as compared to the previous console-based version.
+ New digital phantoms available: granulocyte nuclei, microspheres.

- 2007 (December) - version 0.1
Main features:
+ This version supported only the generation of HL-60 cell nuclei.
+ Console application
+ Three individual binaries (each for one part of the simulation process) freely available (licence enclosed) both for Win32 and Linux (kernel 2.6.x) platform.

Add to Anti-Banner