QuPath

Open source software for analysing (awkward) images

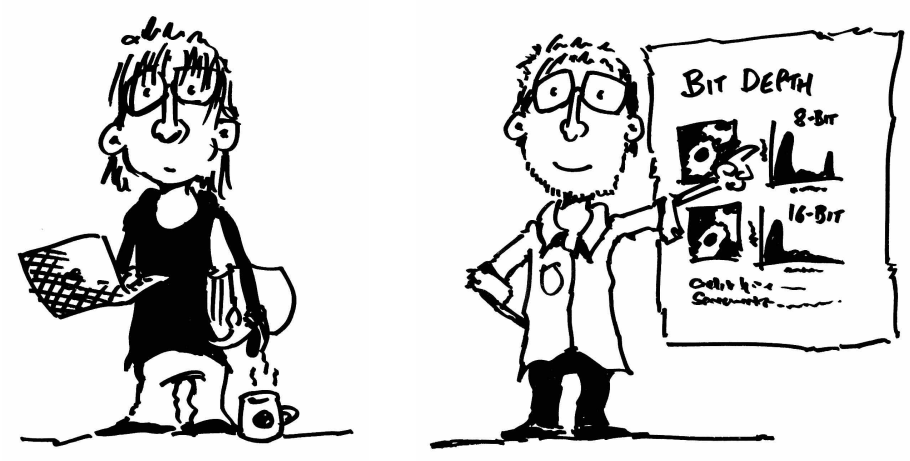
Peter Bankhead

Melvin Gelbard & Mahdi Lamb

University of Edinburgh

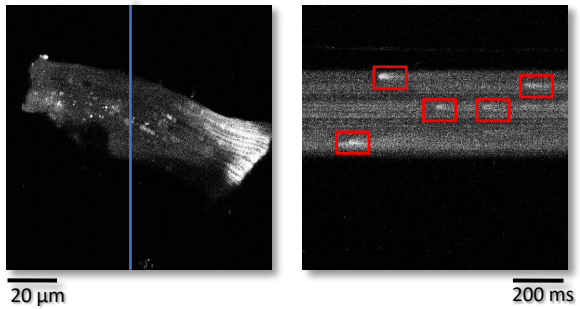
p.bankhead@ed.ac.uk

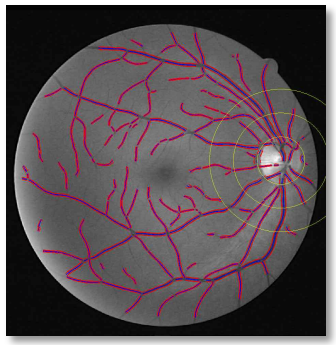
Why *QuPath* exists

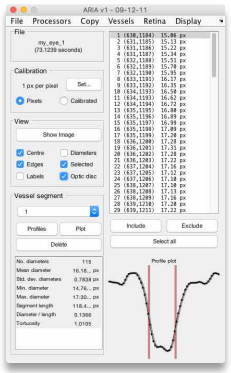


My background is in bioimage analysis

Extracting information from microscopy & biomedical images

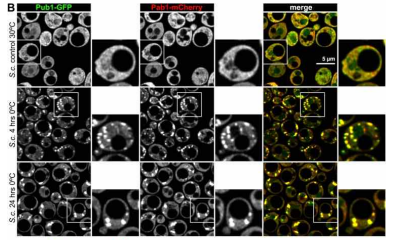




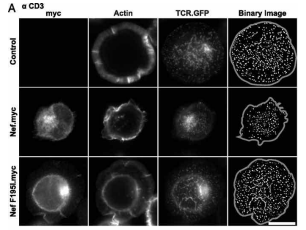


PhD @ Queen's University Belfast (2005 – 2009)

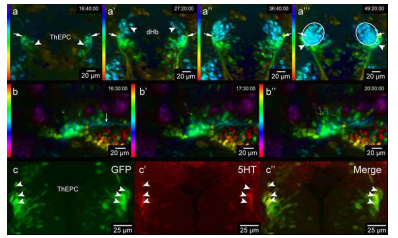
Analyzing Ca^{2+} signals & retinal vessels



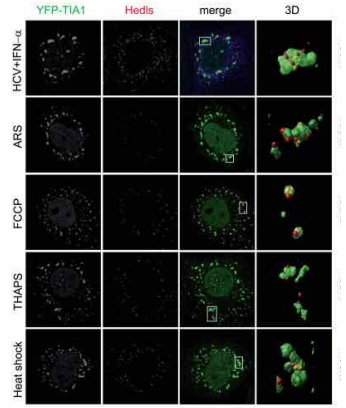
Hoffmann et al. *Mol Biol Cell.* (2012)



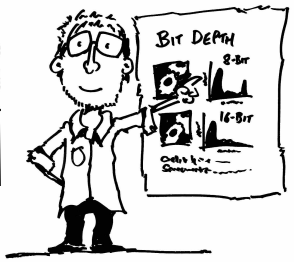
Abraham et al. *J Immunol.* (2012)



Beretta et al. *Neural Dev.* (2013)



Ruggieri et al. *Cell Host Microbe.* (2012)

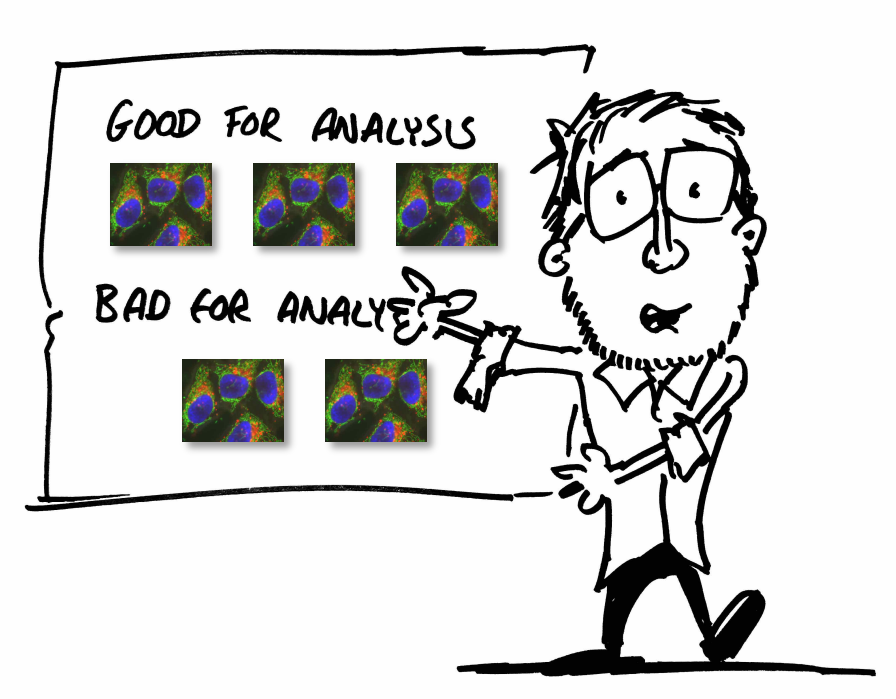


Postdoc @ Heidelberg University (2010 – 2012)

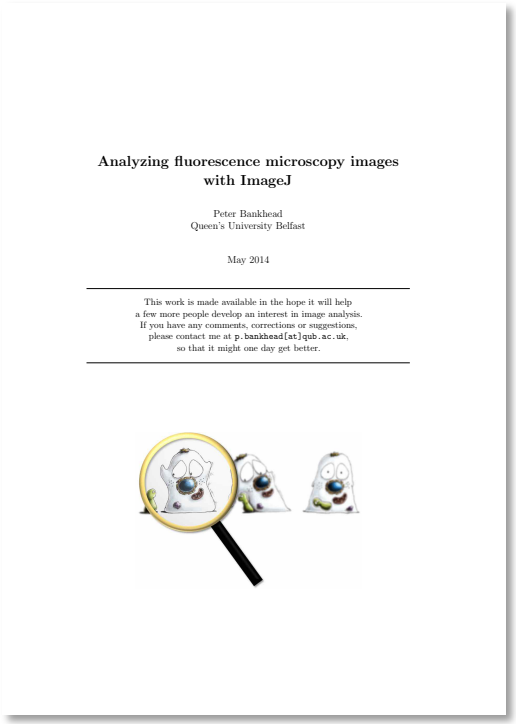
Image analysis specialist at Nikon Imaging Center

Bioimage analysis is hard!

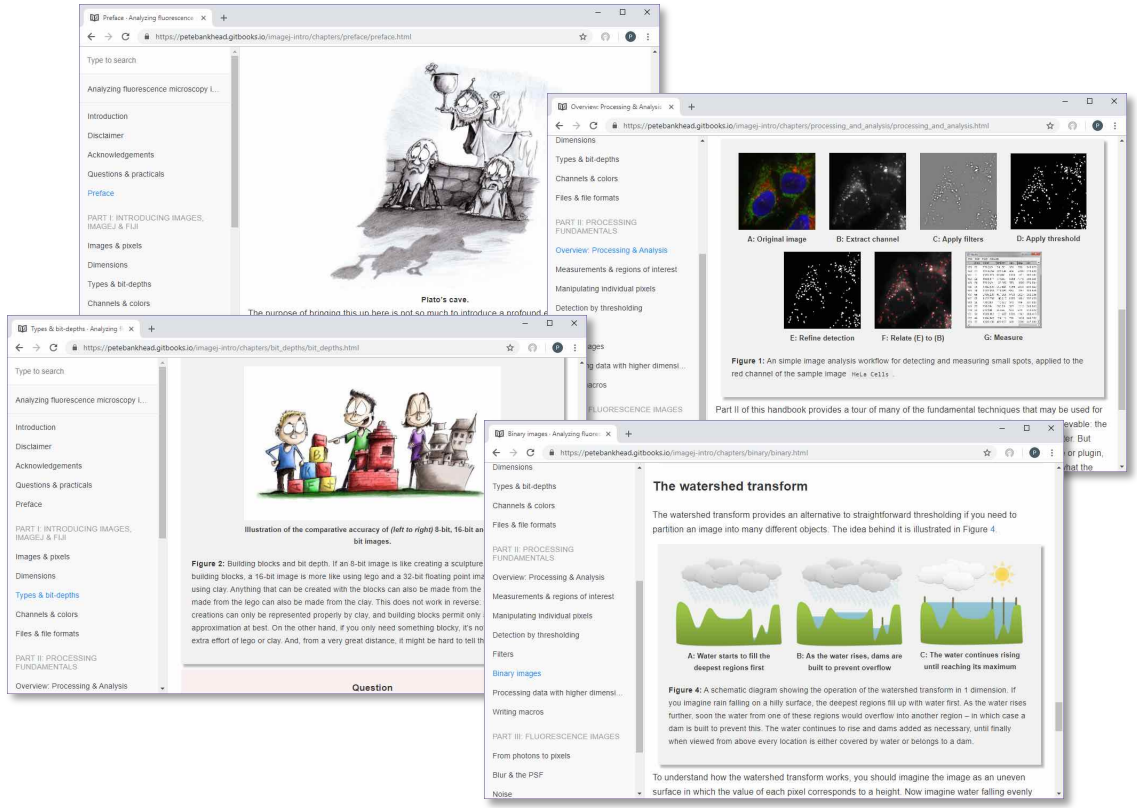
There is no right way to do it, but lots of wrong ways –
Understanding the key concepts is essential!



Analyzing fluorescence microscopy images with ImageJ



PDF version



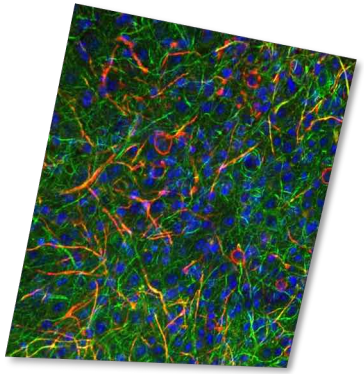
GitBook version

https://petebankhead.gitbooks.io/imagej-intro

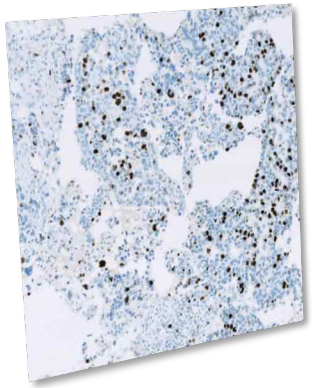
Even if you *do* know the concepts, *bioimage analysis is still hard!*

Almost nothing ‘just works’ –
existing algorithms & software weren’t designed
for the specifics of your case or mine

Image analysis is often seen as a black box



Images go in



Stuff happens

Results come out

Image analysis is often seen as a black box

The people who interpret the data need to understand what happens in the box…

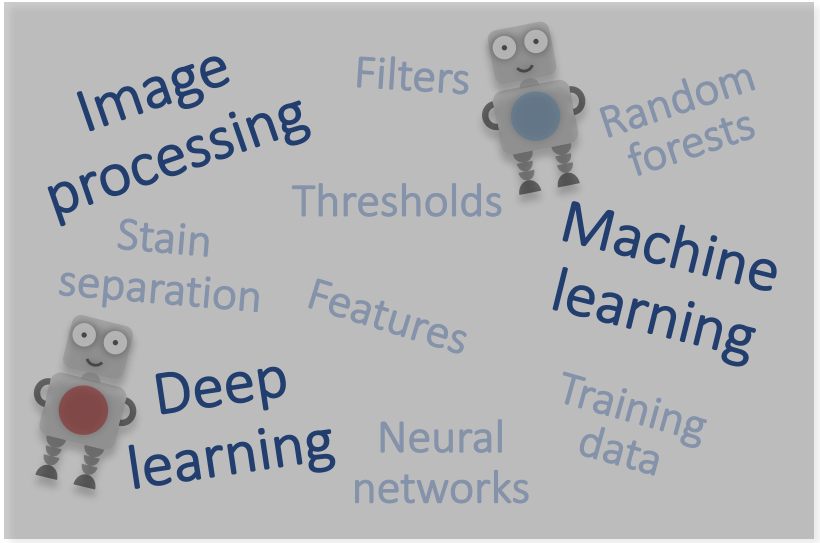
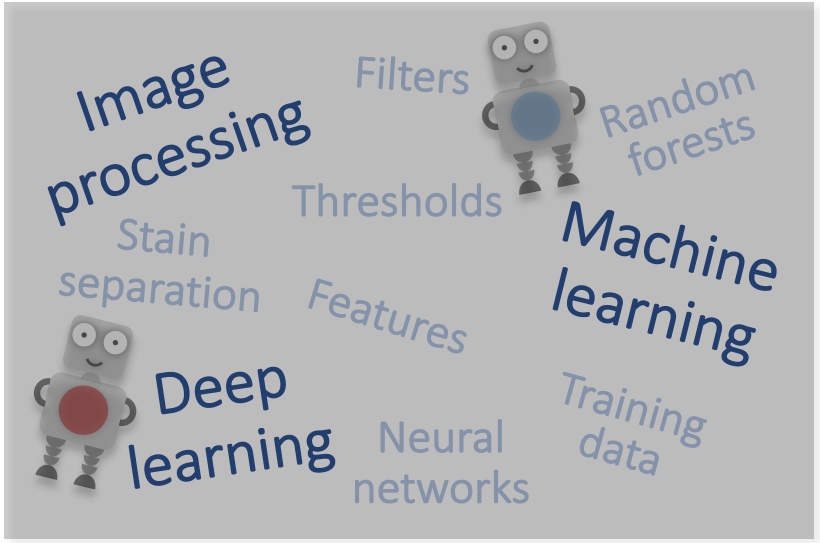


Image analysis is often seen as a black box

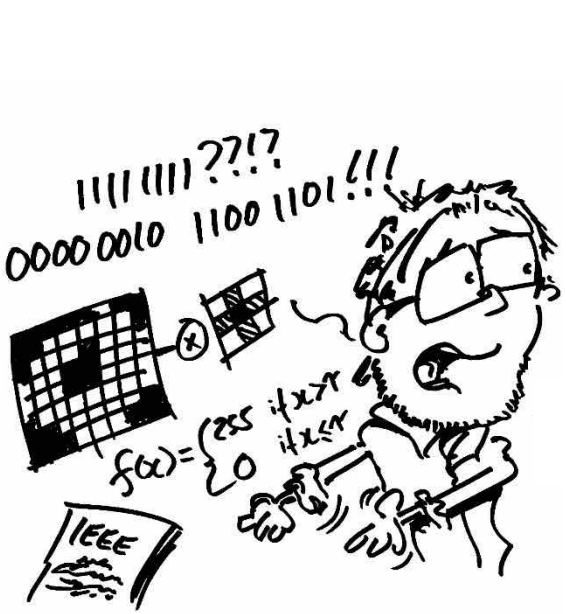
The people who interpret the data need to understand what happens in the box…

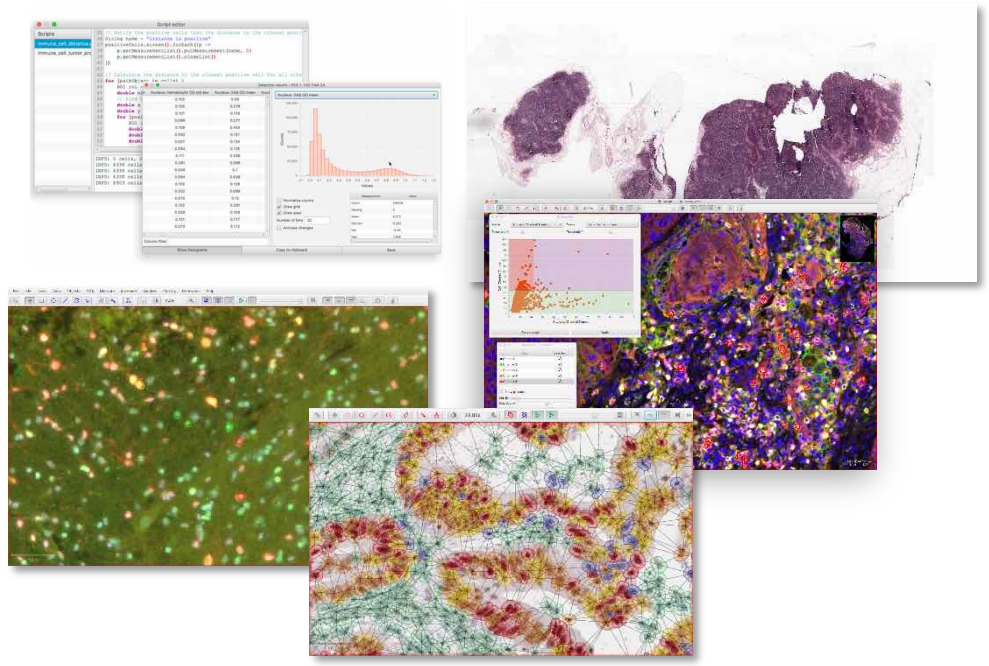


…which means we need transparent algorithms & software

Doing bioimage analysis effectively requires communicating across disciplines

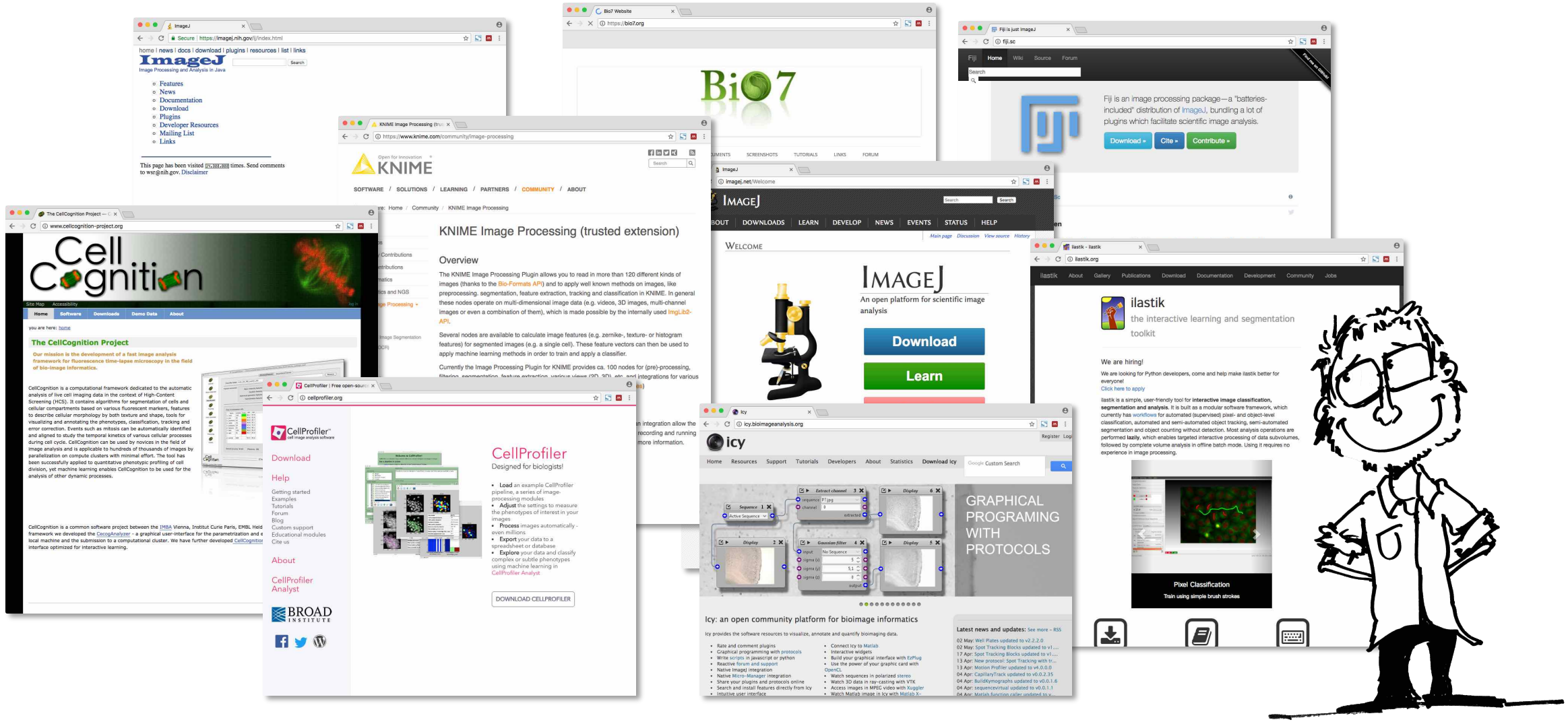
Doing bioimage analysis effectively requires communicating across disciplines





Clever algorithms are sometimes part of this –
but these need software to make them accessible

A fabulous ecosystem of open source bioimage analysis software makes this possible…



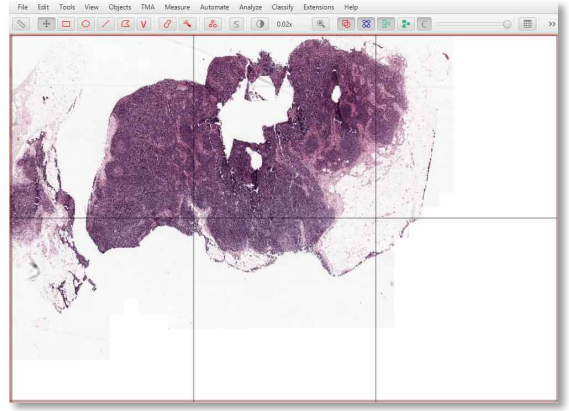
…but there can still be applications that require something new

Digital pathology requires specialised software designed to handle huge, complex images

> 20 billion pixels

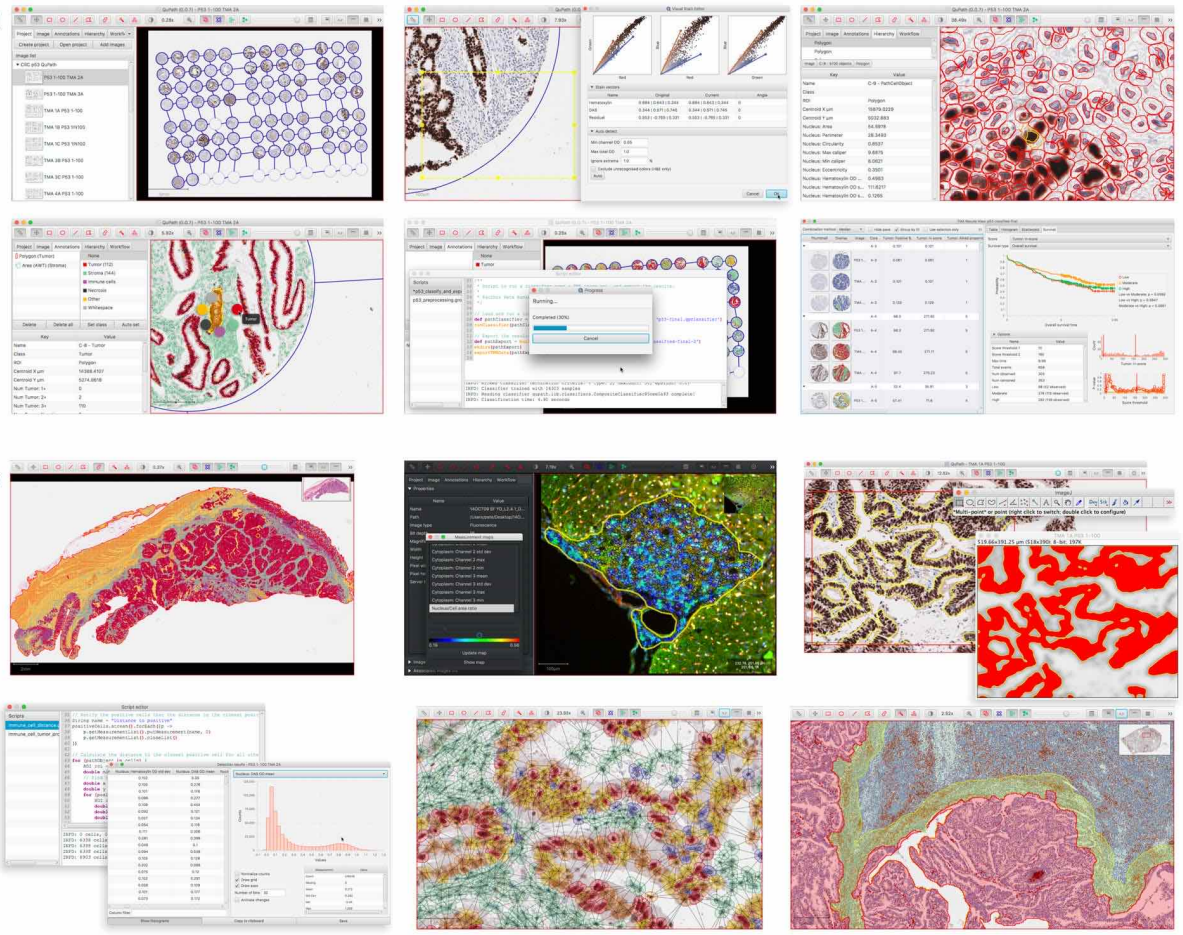
> 60 GB raw data

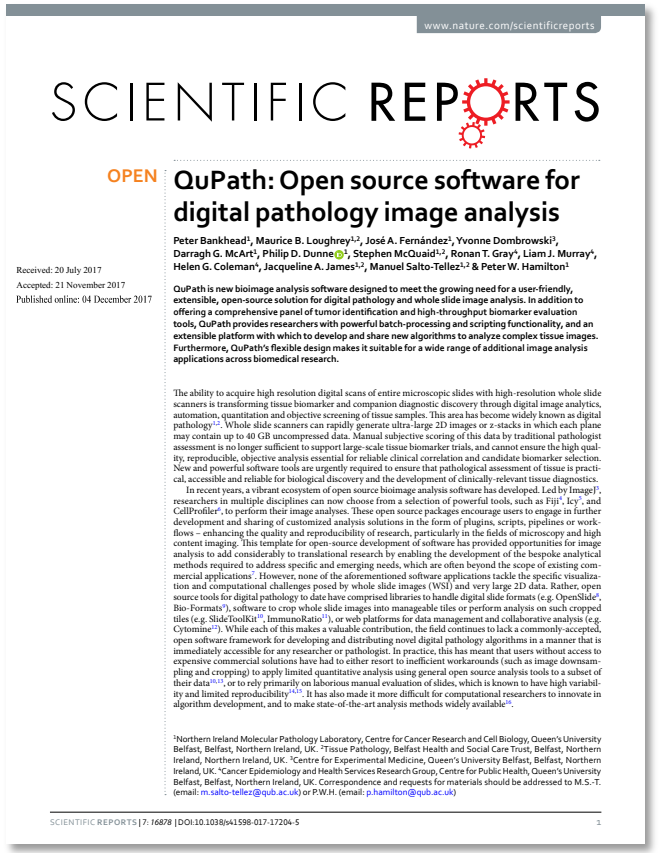
Stored at multiple resolutions



QuPath exists to fill this gap:

Open source software for whole slide analysis (and more)





www.nature.com/scientificreports

SCIENTIFIC REPORTS

OPEN

QuPath: Open source software for digital pathology image analysis

Peter Bankhead[1], Maurice B. Loughrey[1,2], José A. Fernández[1], Yvonne Dombrowski[3], Darragh G. McArt[1], Philip D. Dunne[1], Stephen McQuaid[1,2], Ronan T. Gray[4], Liam J. Murray[4], Helen G. Coleman[4], Jacqueline A. James[1,2], Manuel Salto-Tellez[1,2] & Peter W. Hamilton[1]

Received: 20 July 2017
Accepted: 21 November 2017
Published online: 04 December 2017

QuPath is new bioimage analysis software designed to meet the growing need for a user-friendly, extensible, open-source solution for digital pathology and whole slide image analysis. In addition to offering a comprehensive panel of tumor identification and high-throughput biomarker evaluation tools, QuPath provides researchers with powerful batch-processing and scripting functionality, and an extensible platform with which to develop and share new algorithms to analyze complex tissue images. Furthermore, QuPath's flexible design makes it suitable for a wide range of additional image analysis applications across biomedical research.

The ability to acquire high resolution digital scans of entire microscopic slides with high-resolution whole slide scanners is transforming tissue biomarker and companion diagnostic discovery through digital image analytics, automation, quantitation and objective screening of tissue samples. This area has become widely known as digital pathology[1,2]. Whole slide scanners can rapidly generate ultra-large 2D images or z-stacks in which each plane may contain up to 40 GB uncompressed data. Manual subjective scoring of this data by traditional pathologist assessment is no longer sufficient to support large-scale tissue biomarker trials, and cannot ensure the high quality, reproducible, objective analysis essential for reliable clinical correlation and candidate biomarker selection. New and powerful software tools are urgently required to ensure that pathological assessment of tissue is practical, accessible and reliable for biological discovery and the development of clinically-relevant tissue diagnostics.

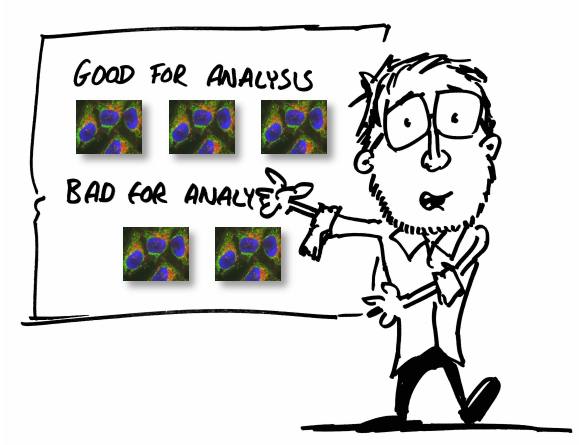
In recent years, a vibrant ecosystem of open source bioimage analysis software has developed. Led by ImageJ[3], researchers in multiple disciplines can now choose from a selection of powerful tools, such as Fiji[4], Icy[5], and CellProfiler[6], to perform their image analyses. These open source packages encourage users to engage in further development and sharing of customized analysis solutions in the form of plugins, scripts, pipelines or workflows – enhancing the quality and reproducibility of research, particularly in the fields of microscopy and high content imaging. This template for open-source development of software has provided opportunities for image analysis to add considerably to translational research by enabling the development of the bespoke analytical methods required to address specific and emerging needs, which are often beyond the scope of existing commercial applications[7]. However, none of the aforementioned software applications tackle the specific visualization and computational challenges posed by whole slide images (WSI) and very large 2D data. Rather, open source tools for digital pathology to date have comprised libraries to handle digital slide formats (e.g. OpenSlide[8], Bio-Formats[9]), software to crop whole slide images into manageable tiles or perform analysis on such cropped tiles (e.g. SlideToolKit[10], ImmunoRatio[11]), or web platforms for data management and collaborative analysis (e.g. Cytomine[12]). While each of this makes a valuable contribution, the field continues to lack a commonly-accepted, open software framework for developing and distributing novel digital pathology algorithms in a manner that is immediately accessible for any researcher or pathologist. In practice, this has meant that users without access to expensive commercial solutions have had to either resort to inefficient workarounds (such as image downsampling and cropping) to apply limited quantitative analysis using general open source analysis tools to a subset of their data[10,13], or to rely primarily on laborious manual evaluation of slides, which is known to have high variability and limited reproducibility[14,15]. It has also made it more difficult for computational researchers to innovate in algorithm development, and to make state-of-the-art analysis methods widely available[16].

[1]Northern Ireland Molecular Pathology Laboratory, Centre for Cancer Research and Cell Biology, Queen's University Belfast, Belfast, Northern Ireland, UK. [2]Tissue Pathology, Belfast Health and Social Care Trust, Belfast, Northern Ireland, Northern Ireland, UK. [3]Centre for Experimental Medicine, Queen's University Belfast, Belfast, Northern Ireland, UK. [4]Cancer Epidemiology and Health Services Research Group, Centre for Public Health, Queen's University Belfast, Belfast, Northern Ireland, UK. Correspondence and requests for materials should be addressed to M.S.-T. (email: m.salto-tellez@qub.ac.uk) or P.W.H. (email: p.hamilton@qub.ac.uk)

Bankhead et al. *Sci Rep* (2017)

QuPath's goal is to provide…

1. An open source platform for whole slide image analysis
2. New tools to address other bioimage analysis challenges

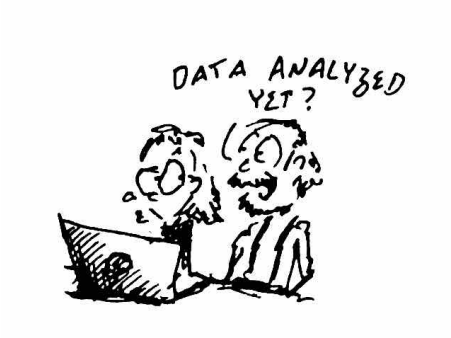


QuPath's goal is to provide…

1. An open source platform for whole slide image analysis
2. New tools to address other bioimage analysis challenges

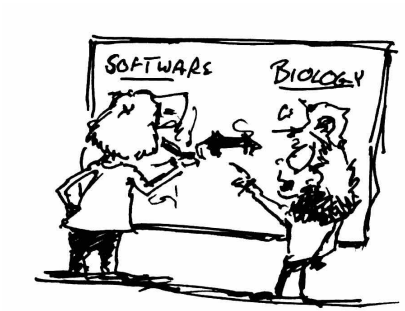
The hard part of analysis should be defining the question

(not wrestling with the software)



Analysis should be verifiable

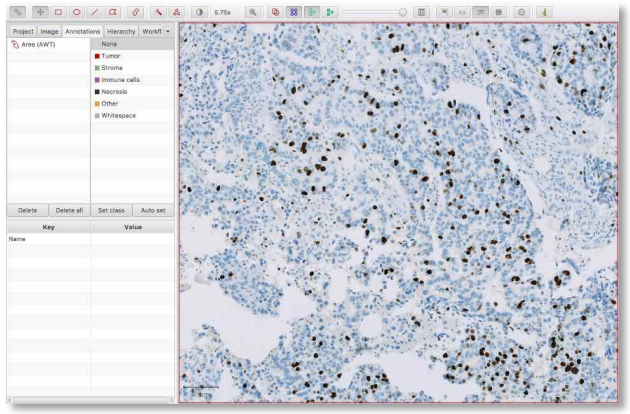
(it's important to be correct)



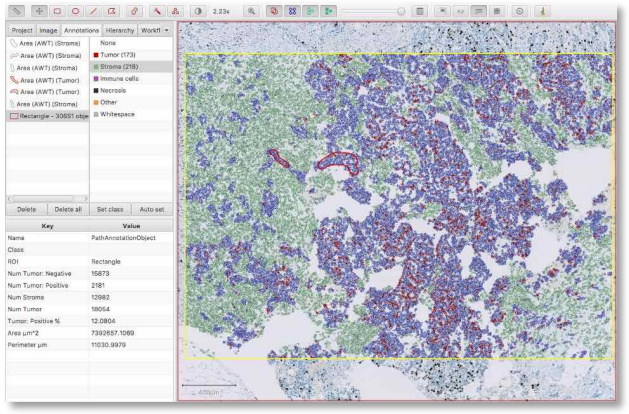
A single solution can solve many problems

(it's worth trying to do it well)

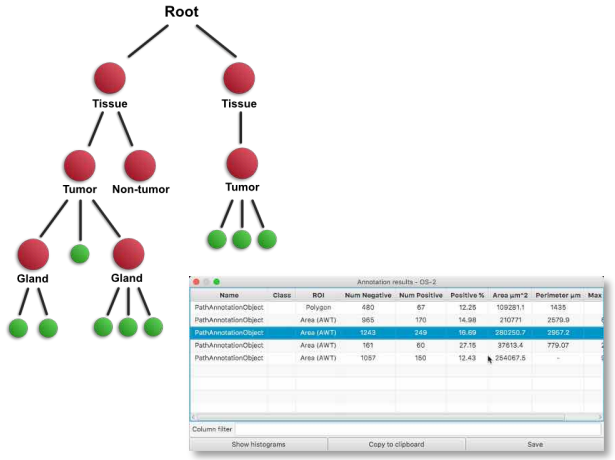
QuPath's approach to image analysis



Start with pixels



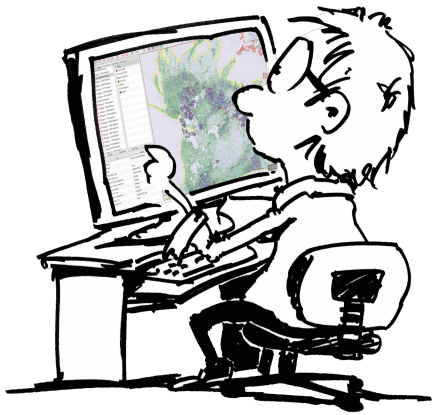
Identify objects



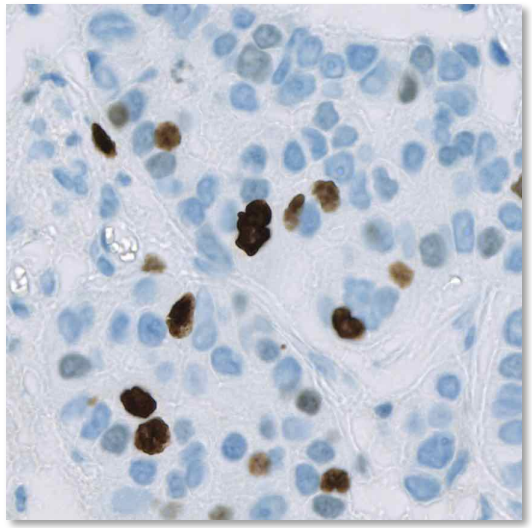
Query the objects

If your application fits with this model,
you might find QuPath a good choice

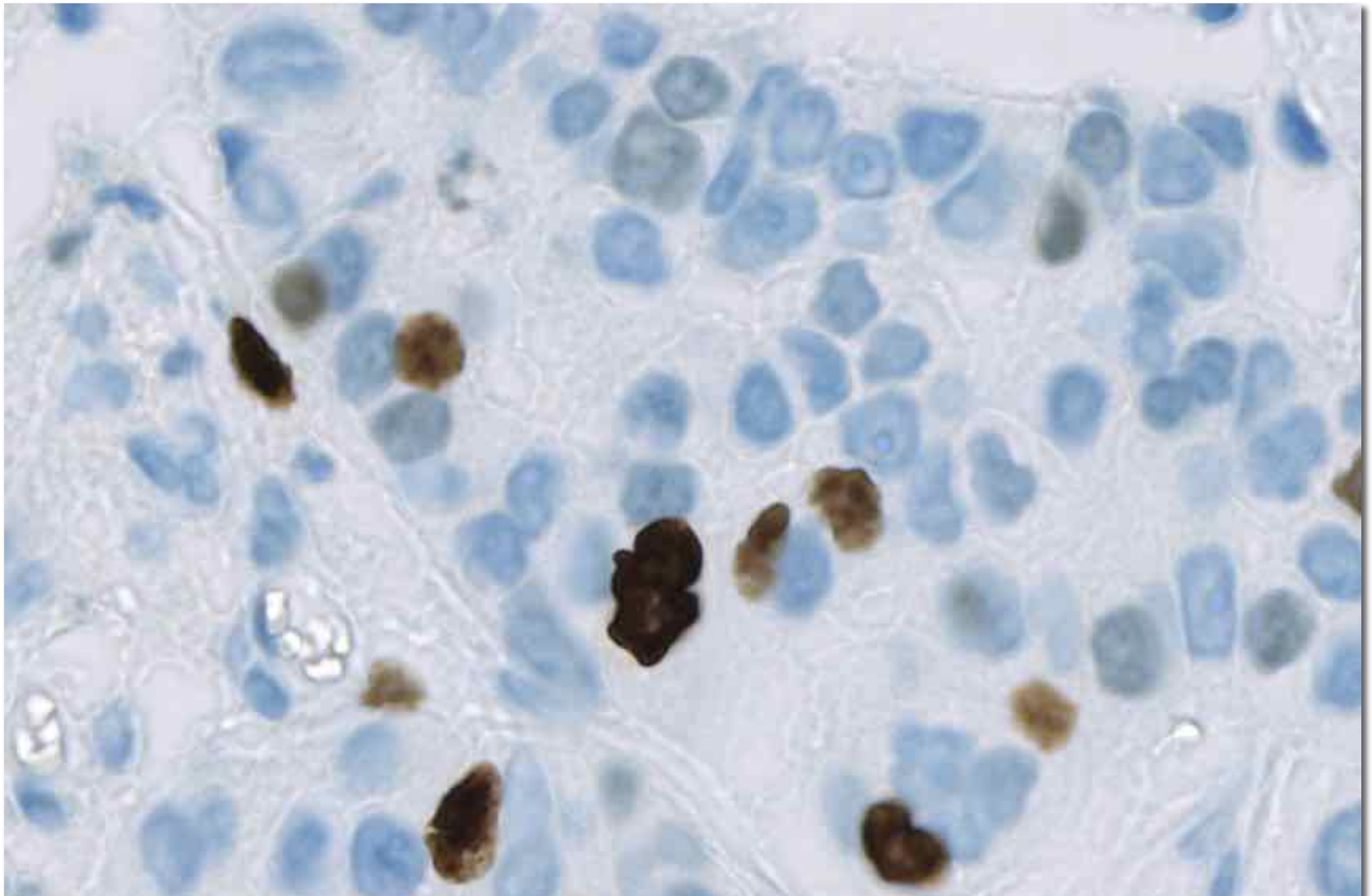
How *QuPath* is used



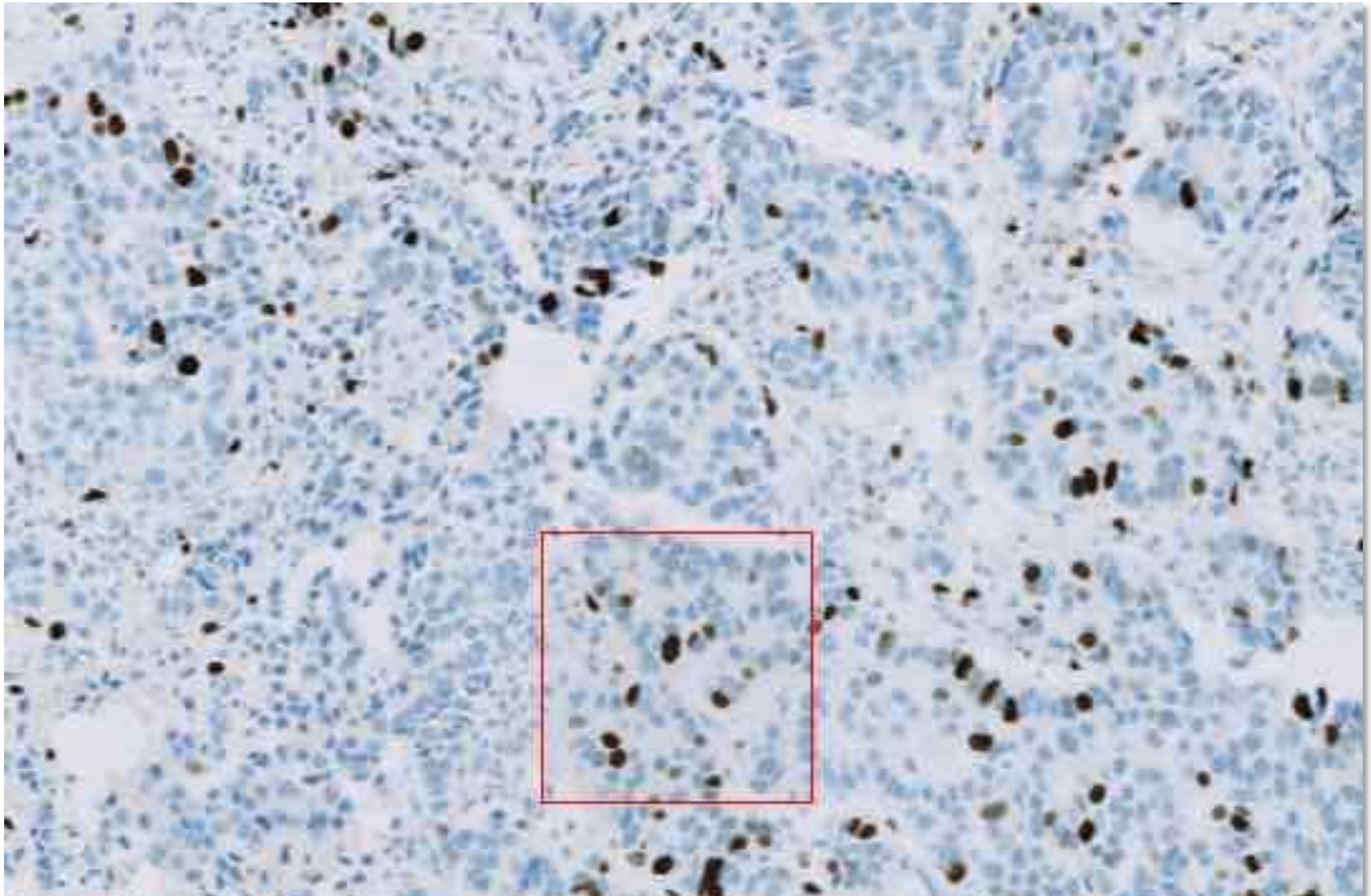
An easy problem in pathology – how many nuclei are brown?



An easy problem in pathology – how many nuclei are brown?



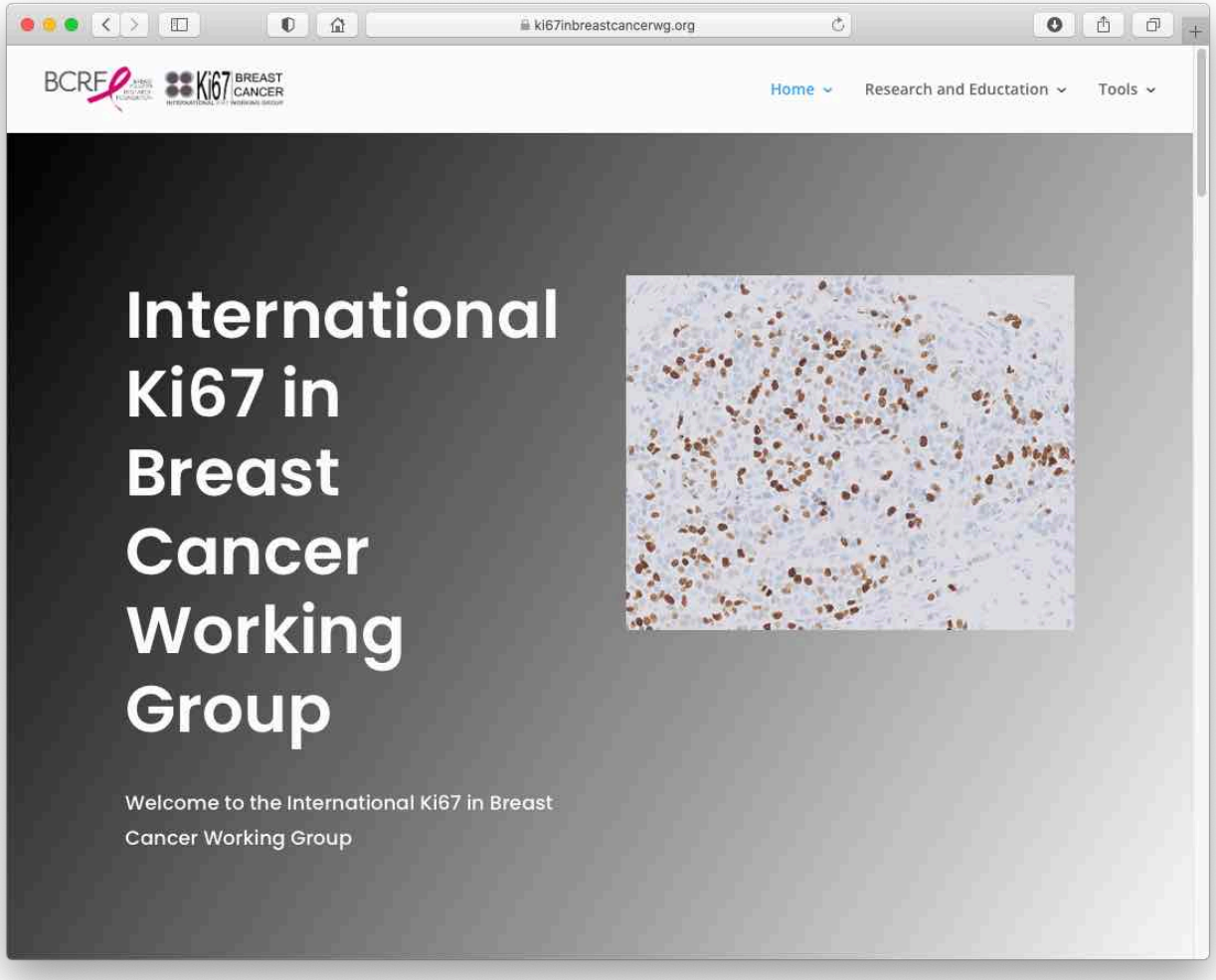
An easy problem in pathology – how many nuclei are brown?

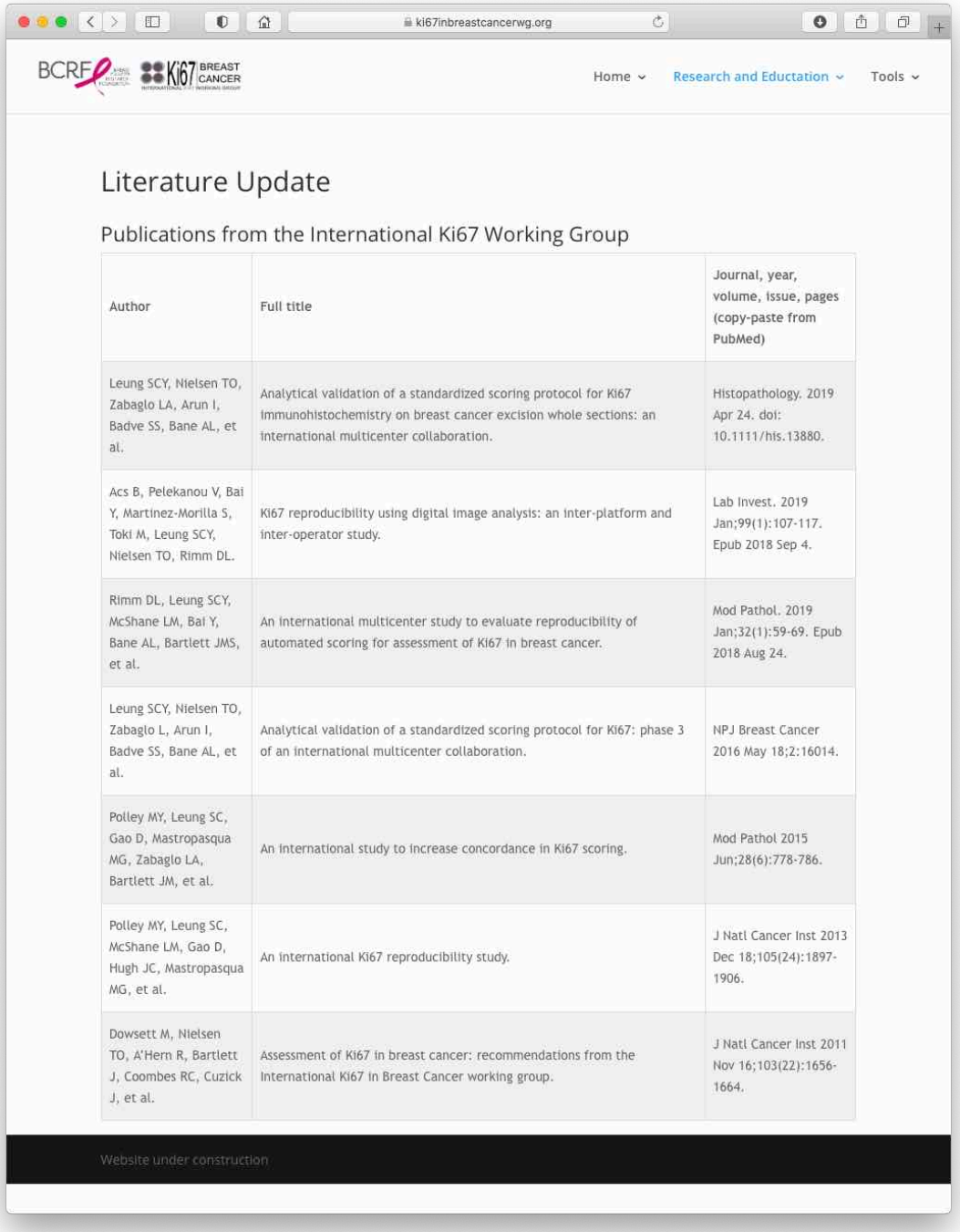


An easy problem in pathology – how many nuclei are brown?

A *not so* easy problem in pathology – how many ***tumour*** nuclei are brown?

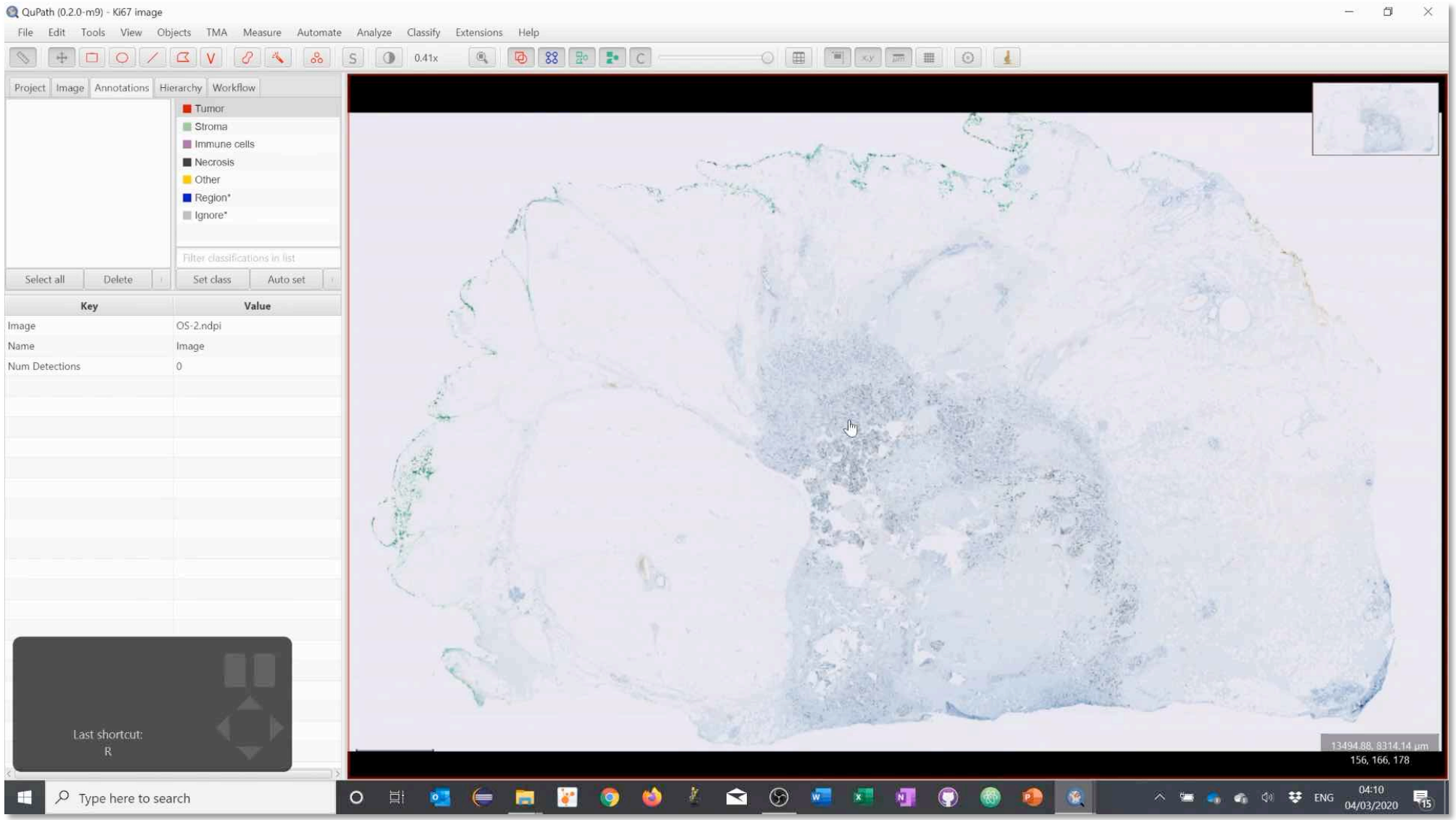
Accurate & reproducible Ki67 scoring is hard!



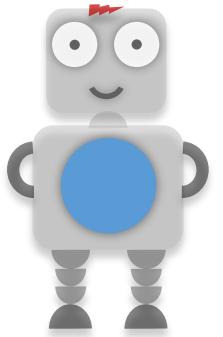


Author	Full title	Journal, year, volume, issue, pages (copy-paste from PubMed)
Leung SCY, Nielsen TO, Zabaglo LA, Arun I, Badve SS, Bane AL, et al.	Analytical validation of a standardized scoring protocol for Ki67 immunohistochemistry on breast cancer excision whole sections: an international multicenter collaboration.	Histopathology. 2019 Apr 24. doi: 10.1111/his.13880.
Acs B, Pelekanou V, Bai Y, Martinez-Morilla S, Toki M, Leung SCY, Nielsen TO, Rimm DL.	Ki67 reproducibility using digital image analysis: an inter-platform and inter-operator study.	Lab Invest. 2019 Jan;99(1):107-117. Epub 2018 Sep 4.
Rimm DL, Leung SCY, McShane LM, Bai Y, Bane AL, Bartlett JMS, et al.	An international multicenter study to evaluate reproducibility of automated scoring for assessment of Ki67 in breast cancer.	Mod Pathol. 2019 Jan;32(1):59-69. Epub 2018 Aug 24.
Leung SCY, Nielsen TO, Zabaglo L, Arun I, Badve SS, Bane AL, et al.	Analytical validation of a standardized scoring protocol for Ki67: phase 3 of an international multicenter collaboration.	NPJ Breast Cancer 2016 May 18;2:16014.
Polley MY, Leung SC, Gao D, Mastropasqua MG, Zabaglo LA, Bartlett JM, et al.	An international study to increase concordance in Ki67 scoring.	Mod Pathol 2015 Jun;28(6):778-786.
Polley MY, Leung SC, McShane LM, Gao D, Hugh JC, Mastropasqua MG, et al.	An international Ki67 reproducibility study.	J Natl Cancer Inst 2013 Dec 18;105(24):1897-1906.
Dowsett M, Nielsen TO, A'Hern R, Bartlett J, Coombes RC, Cuzick J, et al.	Assessment of Ki67 in breast cancer: recommendations from the International Ki67 in Breast Cancer working group.	J Natl Cancer Inst 2011 Nov 16;103(22):1656-1664.

Early *QuPath* applications focussed on brightfield IHC analysis



Calculate
Ki67 positive %
in tumour cells

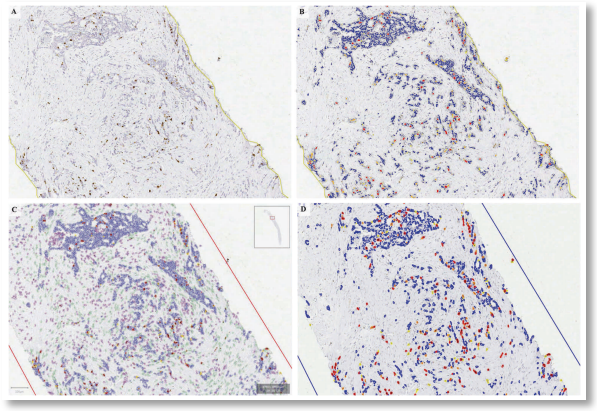


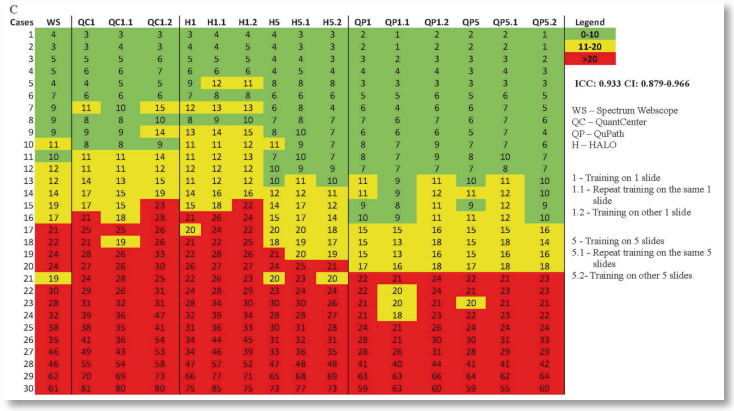
Combines image processing + AI

Sample image: OpenSlide

Independent comparison of digital pathology software

Ki67 scoring in breast cancer biopsies using HALO, QuPath, QuantPath





Cases	WS	QC1	QC1.1	QC1.2	H1	H1.1	H1.2	H5	H5.1	H5.2	QP1	QP1.1	QP1.2	QP5	QP5.1	QP5.2
1	4	3	3	3	3	4	4	4	3	3	2	1	2	2	2	1
2	3	3	4	3	4	4	5	4	3	3	2	1	2	2	2	1
3	5	5	5	6	5	5	5	4	4	3	3	2	3	3	3	2
4	5	6	6	7	6	6	6	4	5	4	4	4	4	3	4	3
5	4	4	5	5	9	12	11	8	8	8	3	3	3	3	3	3
6	7	6	6	6	7	8	8	6	6	6	5	5	6	5	6	5
7	9	11	10	15	12	13	13	6	8	4	6	4	6	6	7	5
8	9	8	8	10	8	9	10	7	8	7	7	6	7	6	7	6
9	9	9	9	14	13	14	15	8	10	7	6	6	6	5	7	4
10	11	8	8	9	11	11	12	11	9	7	8	7	9	7	7	6
11	10	11	11	14	11	12	13	7	10	7	8	7	9	8	10	7
12	12	11	11	12	12	12	12	10	9	9	7	7	7	7	8	7
13	12	14	13	15	11	12	12	10	11	10	11	9	11	10	11	10
14	14	17	15	19	14	16	16	12	12	11	11	9	12	11	12	10
15	19	17	15	23	15	18	22	14	17	12	9	8	11	9	12	9
16	17	21	18	28	20	26	24	15	17	14	10	9	11	11	12	10
17	21	25	25	26	20	24	22	20	20	18	15	15	16	15	15	16
18	22	21	19	26	21	22	25	18	19	17	15	13	18	15	18	14
19	24	28	26	33	22	28	26	21	20	19	15	13	16	15	16	16
20	24	27	26	30	26	27	27	24	25	21	17	16	18	17	18	18
21	19	24	28	25	22	26	23	20	23	20	22	21	24	22	21	23
22	30	29	26	31	24	28	29	23	24	24	22	20	24	21	23	23
23	28	31	32	31	28	34	30	30	30	26	21	20	21	20	21	21
24	32	39	36	47	32	39	34	28	28	27	21	18	23	22	23	22
25	38	38	35	41	31	36	33	30	31	28	24	21	26	24	24	24
26	35	41	36	54	34	44	45	31	32	31	28	21	30	30	31	33
27	46	49	43	53	34	46	39	33	36	35	28	26	31	28	29	29
28	46	55	54	58	47	57	52	47	48	48	41	40	44	41	41	42
29	62	70	69	73	66	77	71	65	68	69	63	63	66	64	62	64
30	61	81	80	80	75	85	75	73	77	73	59	63	60	59	55	60

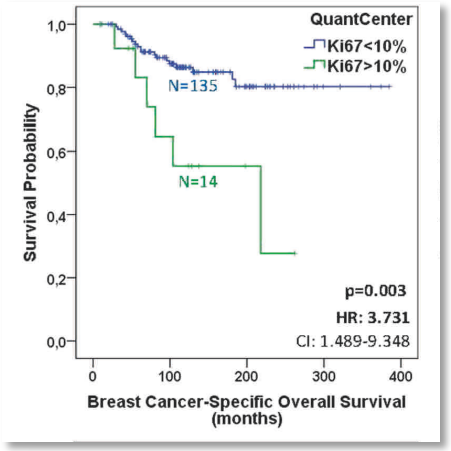
Legend
0-10
11-20
>20

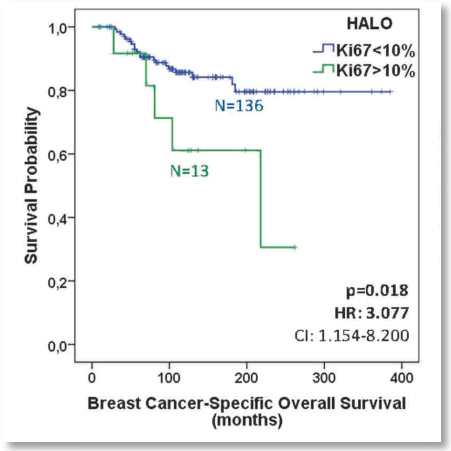
ICC: 0.933 CI: 0.879-0.966

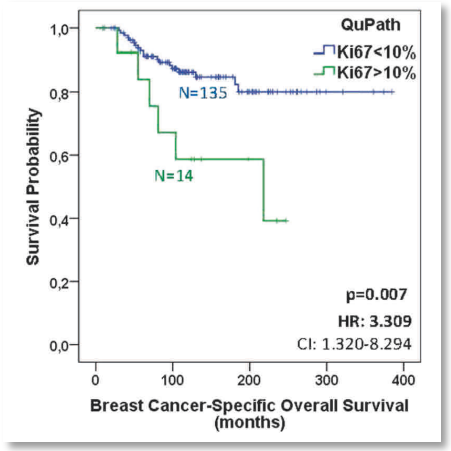
WS – Spectrum Webscope
QC – QuantCenter
QP – QuPath
H – HALO

1 - Training on 1 slide
1.1 - Repeat training on the same 1 slide
1.2 - Training on other 1 slide

5 - Training on 5 slides
5.1 - Repeat training on the same 5 slides
5.2- Training on other 5 slides







Acs et al. *Lab Invest* (2018)

Laboratory Investigation
https://doi.org/10.1038/s41374-018-0123-7

USCAP

ARTICLE

Ki67 reproducibility using digital image analysis: an inter-platform and inter-operator study

Balazs Acs[1] · Vasiliki Pelekanou[1,2] · Yalai Bai[1] · Sandra Martinez-Morilla[1] · Maria Toki[1] · Samuel C. Y. Leung[3] · Torsten O. Nielsen[3] · David L. Rimm[1]

Received: 21 June 2018 / Revised: 16 August 2018 / Accepted: 16 August 2018

Abstract

Ki67 expression has been a valuable prognostic variable in breast cancer, but has not seen broad adoption due to lack of standardization between institutions. Automation could represent a solution. Here we investigate the reproducibility of Ki67 measurement between three image analysis platforms with supervised classifiers performed by the same operator, by multiple operators, and finally we compare their accuracy in prognostic potential. Two breast cancer patient cohorts were used for this study. The standardization was done with the 30 cases of ER+ breast cancer that were used in phase 3 of International Ki67 in Breast Cancer Working Group initiatives where blocks were centrally cut and stained for Ki67. The outcome cohort was from 149 breast cancer cases from the Yale Pathology archives. A tissue microarray was built from representative tissue blocks with median follow-up of 120 months. The Mib-1 antibody (Dako) was used to detect Ki67 (dilution 1:100). HALO (IndicaLab), QuantCenter (3DHistech), and QuPath (open source software) digital image analysis (DIA) platforms were used to evaluate Ki67 expression. Intraclass correlation coefficient (ICC) was used to measure reproducibility. Between-DIA platform reproducibility was excellent (ICC: 0.933, CI: 0.879–0.966). Excellent reproducibility was found between all DIA platforms and the reference standard Ki67 values of Spectrum Webscope (QuPath-Spectrum Webscope ICC: 0.970, CI: 0.936–0.986; HALO-Spectrum Webscope ICC: 0.968, CI: 0.933–0.985; QuantCenter-Spectrum Webscope ICC: 0.964, CI: 0.919–0.983). All platforms showed excellent intra-DIA reproducibility (QuPath ICC: 0.992, CI: 0.986–0.996; HALO ICC: 0.972, CI: 0.924–0.988; QuantCenter ICC: 0.978, CI: 0.932–0.991). Comparing each DIA against outcome, the hazard ratios were similar. The inter-operator reproducibility was particularly high (ICC: 0.962–0.995). Our results showed outstanding reproducibility both within and between-DIA platforms, including one freely available DIA platform (QuPath). We also found the platforms essentially indistinguishable with respect to prediction of breast cancer patient outcome. Results justify multi-institutional DIA studies to assess clinical utility.

Introduction

Ki67 labeling index (Ki67 LI) is currently one of the most promising yet controversial biomarkers in breast cancer [1]. The European Society for Medical Oncology (ESMO) Clinical Practice Guidelines suggests that Ki67 LI may provide useful information, if the assay can be standardized [2]. The St. Gallen Consensus Conference in 2017 also agreed that Ki67 LI could be used to distinguish between HER2-negative luminal A-like and luminal B-like breast cancer subtypes [3]. However, the panel also emphasized the reproducibility issue of Ki67 LI, suggesting calibration of Ki67 scoring [3]. The American Society of Clinical Oncology recommended against the use of Ki67 LI for prognosis in newly diagnosed breast cancer patients because of lack of reproducibility across laboratories [4]. The International Ki67 in Breast Cancer Working Group (IKWG) has nevertheless published consensus recommendations for the application of Ki67 IHC in daily practice [5]. According to this group, parameters that predominantly influence the Ki67 IHC results include pre-analytical

✉ David L. Rimm
david.rimm@yale.edu

[1] Department of Pathology, Yale School of Medicine, New Haven, CT, USA

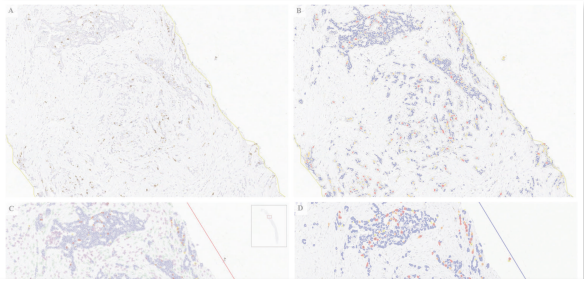
[2] Precision Oncology, Sanofi US Services Inc, Cambridge, MA, USA

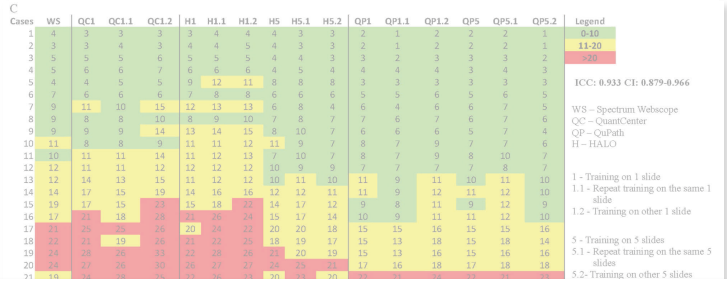
[3] Department of Pathology and Laboratory Medicine, University of British Columbia, Vancouver, BC, Canada

Independent comparison of digital pathology software

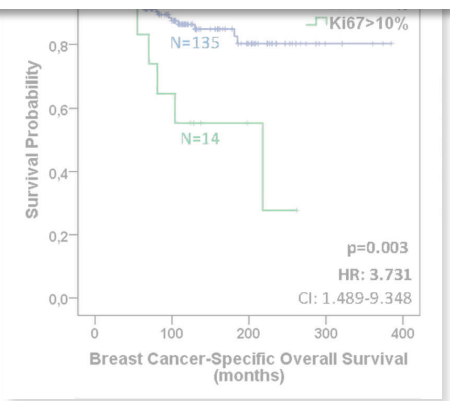
Ki67 scoring in breast cancer biopsies using HALO, QuPath, QuantPath

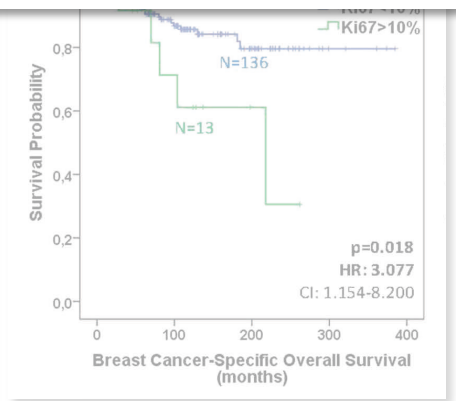
Acs et al. *Lab Invest* (2018)

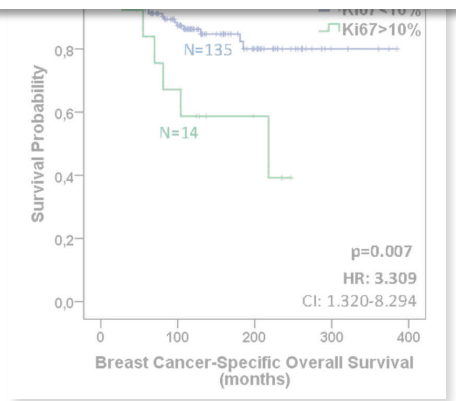


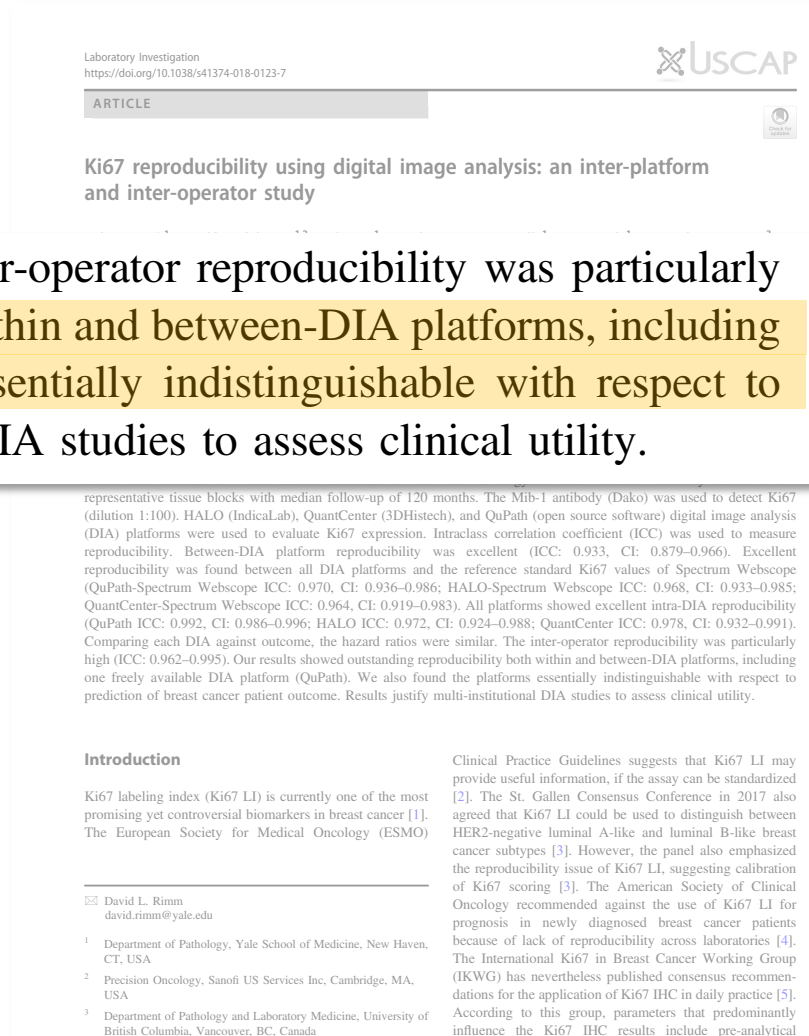


Comparing each DIA against outcome, the hazard ratios were similar. The inter-operator reproducibility was particularly high (ICC: 0.962–0.995). Our results showed outstanding reproducibility both within and between-DIA platforms, including one freely available DIA platform (QuPath). We also found the platforms essentially indistinguishable with respect to prediction of breast cancer patient outcome. Results justify multi-institutional DIA studies to assess clinical utility.









Laboratory Investigation
https://doi.org/10.1038/s41374-018-0123-7

USCAP

ARTICLE

Ki67 reproducibility using digital image analysis: an inter-platform and inter-operator study

representative tissue blocks with median follow-up of 120 months. The Mib-1 antibody (Dako) was used to detect Ki67 (dilution 1:100). HALO (IndicaLab), QuantCenter (3DHistech), and QuPath (open source software) digital image analysis (DIA) platforms were used to evaluate Ki67 expression. Intraclass correlation coefficient (ICC) was used to measure reproducibility. Between-DIA platform reproducibility was excellent (ICC: 0.933, CI: 0.879–0.966). Excellent reproducibility was found between all DIA platforms and the reference standard Ki67 values of Spectrum Webscope (QuPath-Spectrum Webscope ICC: 0.970, CI: 0.936–0.986; HALO-Spectrum Webscope ICC: 0.968, CI: 0.933–0.985; QuantCenter-Spectrum Webscope ICC: 0.964, CI: 0.919–0.983). All platforms showed excellent intra-DIA reproducibility (QuPath ICC: 0.992, CI: 0.986–0.996; HALO ICC: 0.972, CI: 0.924–0.988; QuantCenter ICC: 0.978, CI: 0.932–0.991). Comparing each DIA against outcome, the hazard ratios were similar. The inter-operator reproducibility was particularly high (ICC: 0.962–0.995). Our results showed outstanding reproducibility both within and between-DIA platforms, including one freely available DIA platform (QuPath). We also found the platforms essentially indistinguishable with respect to prediction of breast cancer patient outcome. Results justify multi-institutional DIA studies to assess clinical utility.

Introduction

Ki67 labeling index (Ki67 LI) is currently one of the most promising yet controversial biomarkers in breast cancer [1]. The European Society for Medical Oncology (ESMO) Clinical Practice Guidelines suggests that Ki67 LI may provide useful information, if the assay can be standardized [2]. The St. Gallen Consensus Conference in 2017 also agreed that Ki67 LI could be used to distinguish between HER2-negative luminal A-like and luminal B-like breast cancer subtypes [3]. However, the panel also emphasized the reproducibility issue of Ki67 LI, suggesting calibration of Ki67 scoring [3]. The American Society of Clinical Oncology recommended against the use of Ki67 LI for prognosis in newly diagnosed breast cancer patients because of lack of reproducibility across laboratories [4]. The International Ki67 in Breast Cancer Working Group (IKWG) has nevertheless published consensus recommendations for the application of Ki67 IHC in daily practice [5]. According to this group, parameters that predominantly influence the Ki67 IHC results include pre-analytical

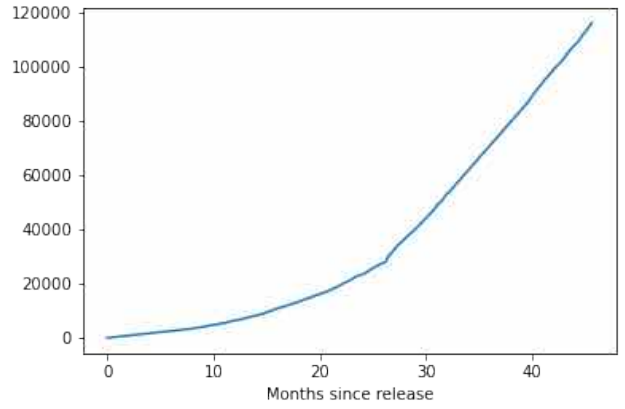
David L. Rimm
david.rimm@yale.edu

1 Department of Pathology, Yale School of Medicine, New Haven, CT, USA

2 Precision Oncology, Sanofi US Services Inc, Cambridge, MA, USA

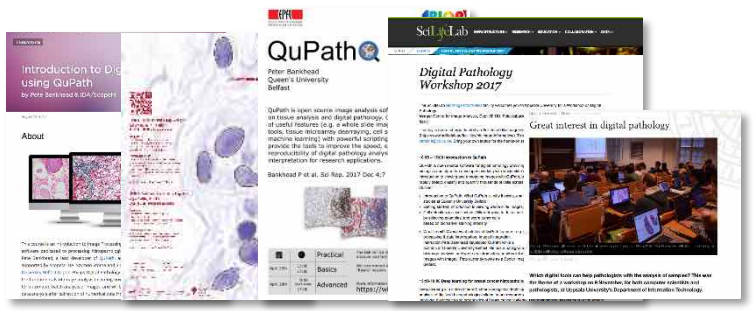
3 Department of Pathology and Laboratory Medicine, University of British Columbia, Vancouver, BC, Canada

Since 2017, *QuPath* has become used worldwide

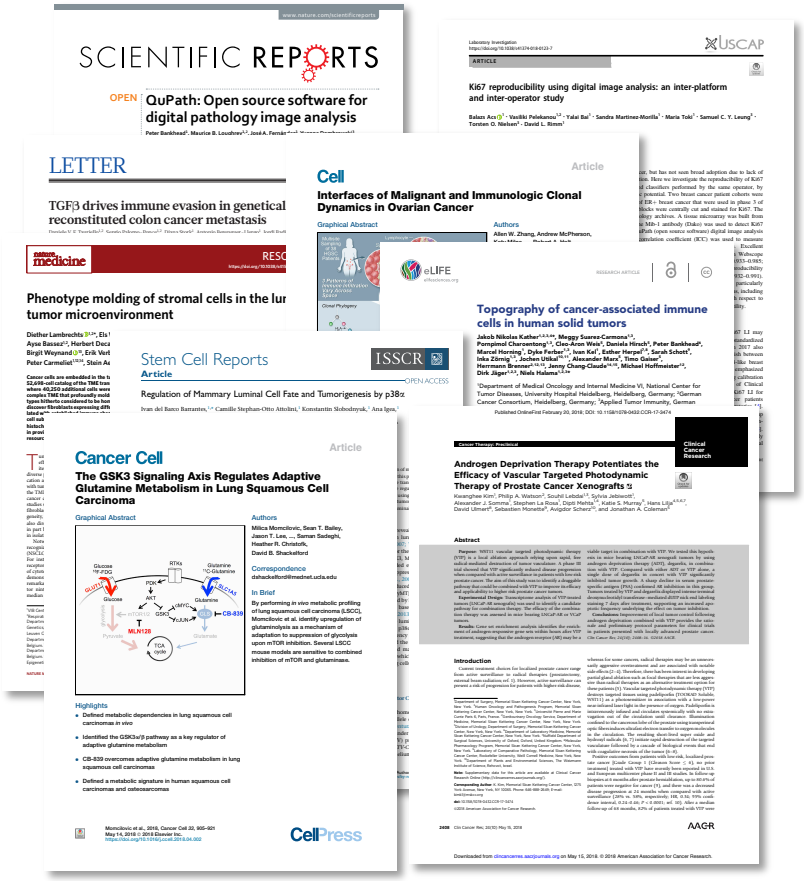


More than 120,000 downloads

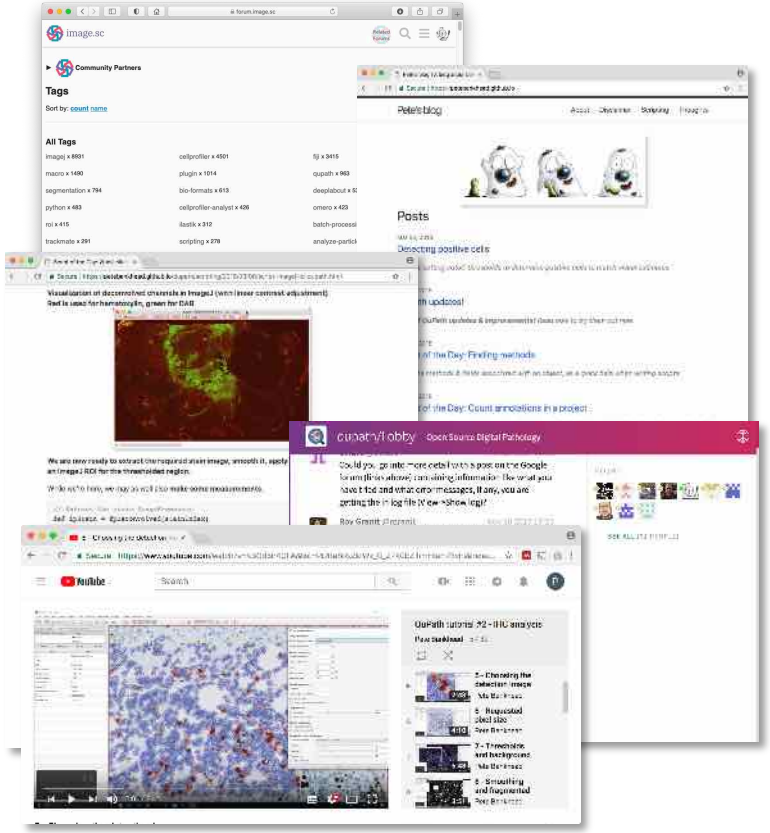
(> 60,000 for a single version)



Workshops across
Europe & North America



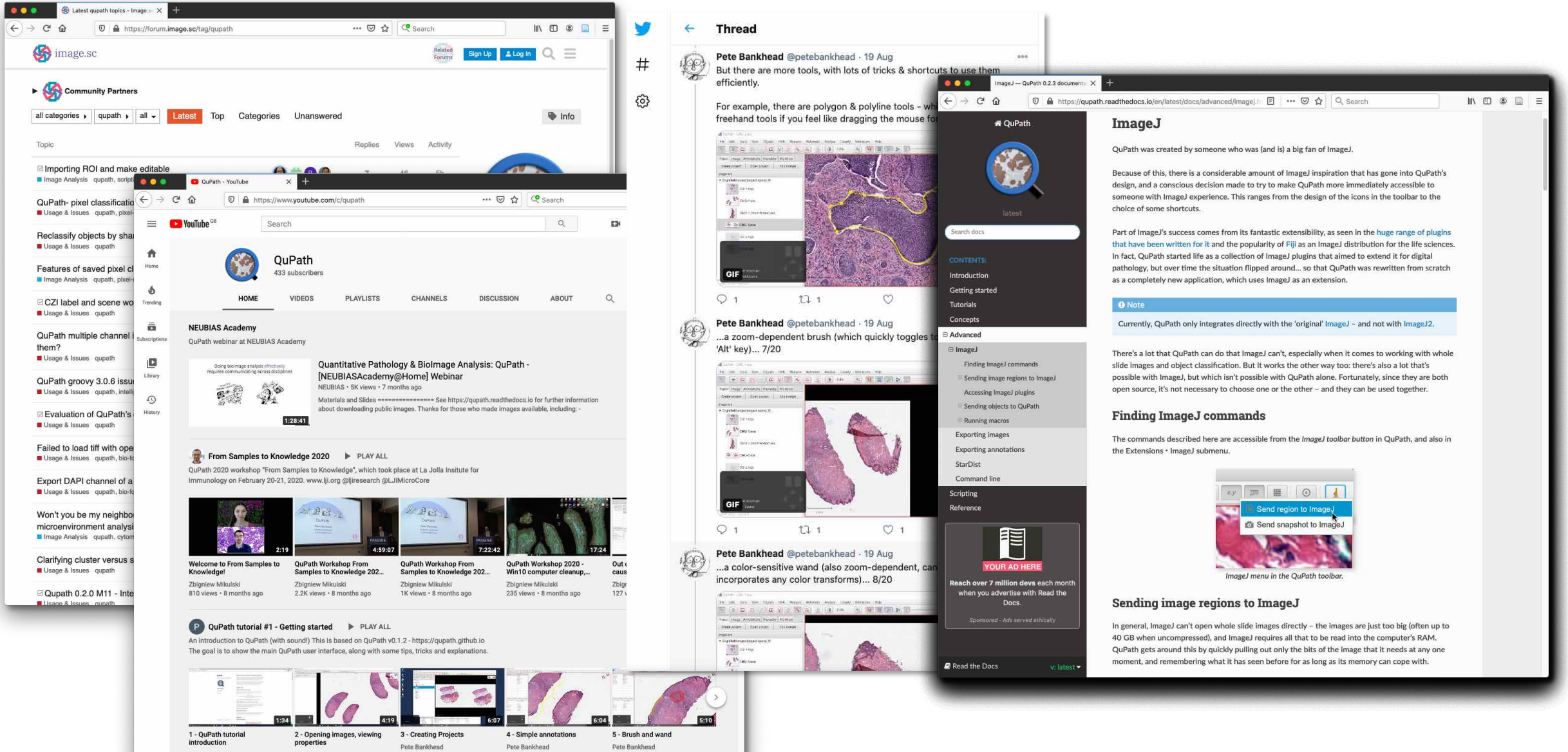
Used in over 400 publications



Not just software:

User community, documentation, YouTube, Twitter, blog…

Training, support & documentation are essential!



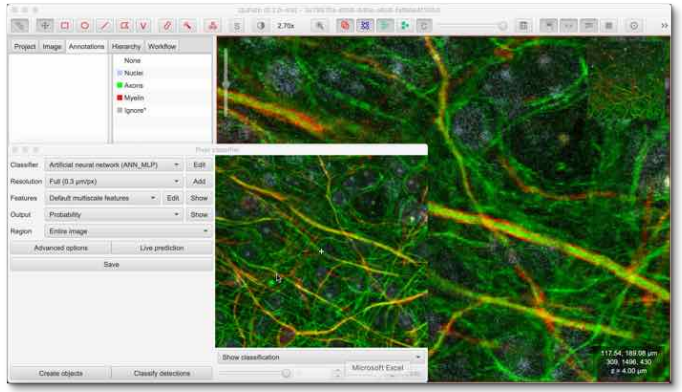
QuPath is still mostly used for pathology applications

But it *can* do more…

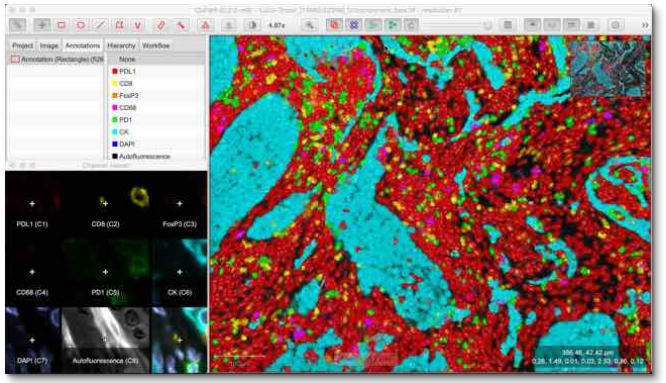
What *QuPath* can do

The first new stable release since 2016
was made in **June 2020**

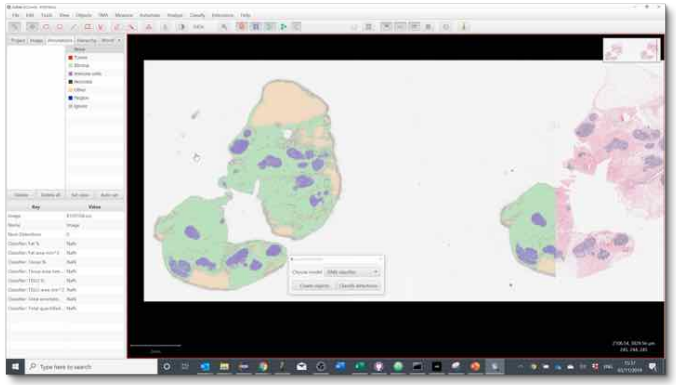
What *QuPath* can do



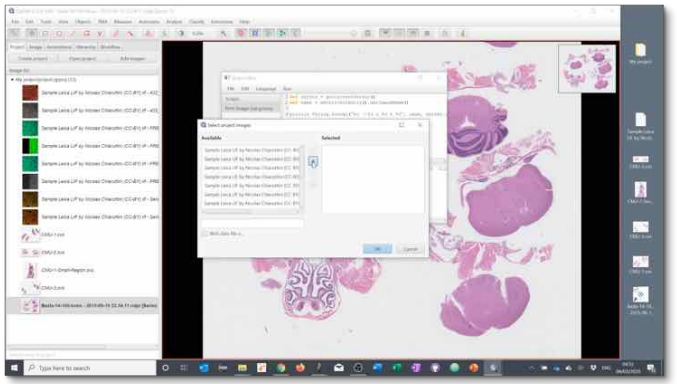
Pixel classification



Multiplexed analysis

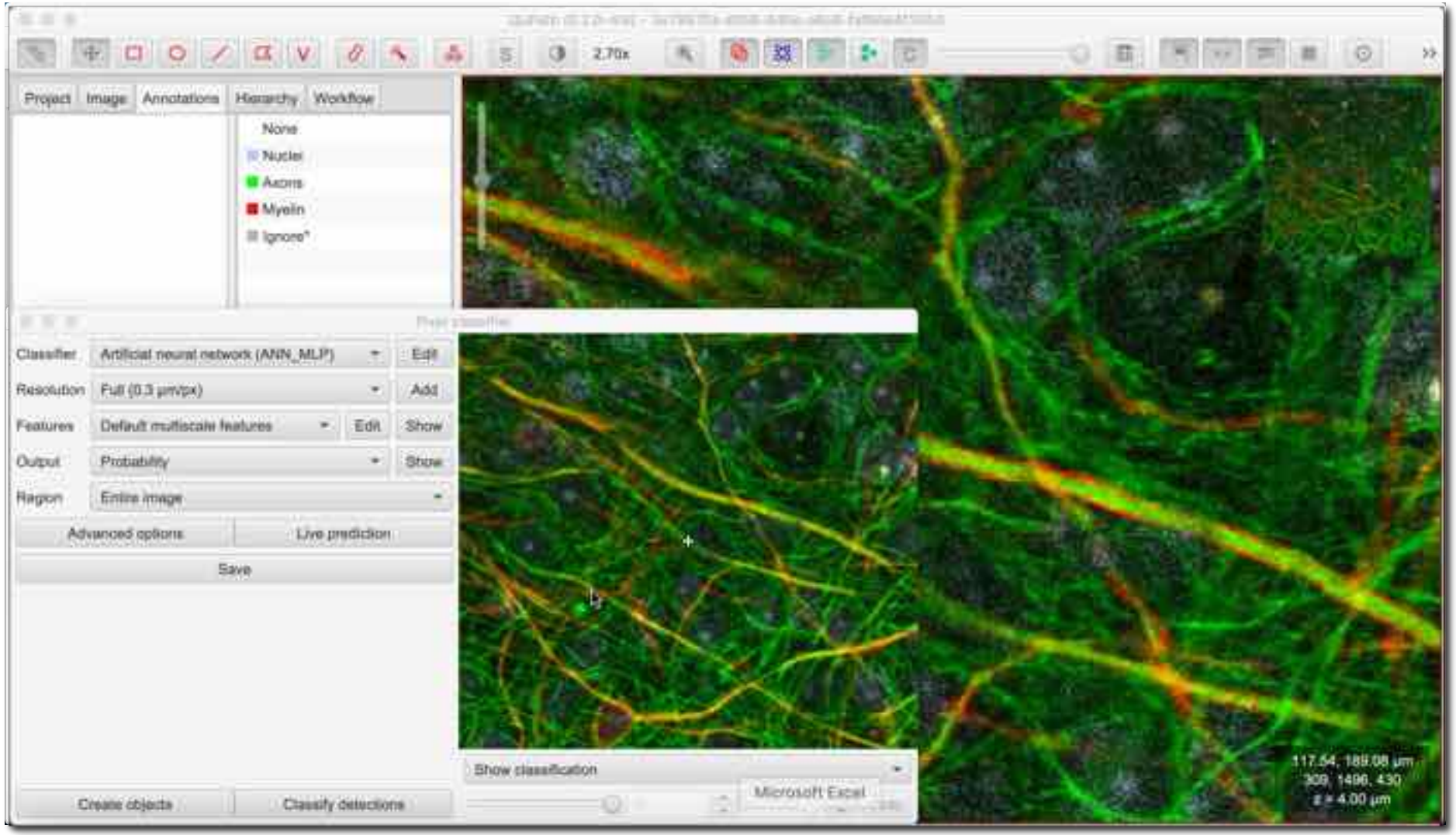


Deep learning



Workflow integration

Pixel classification

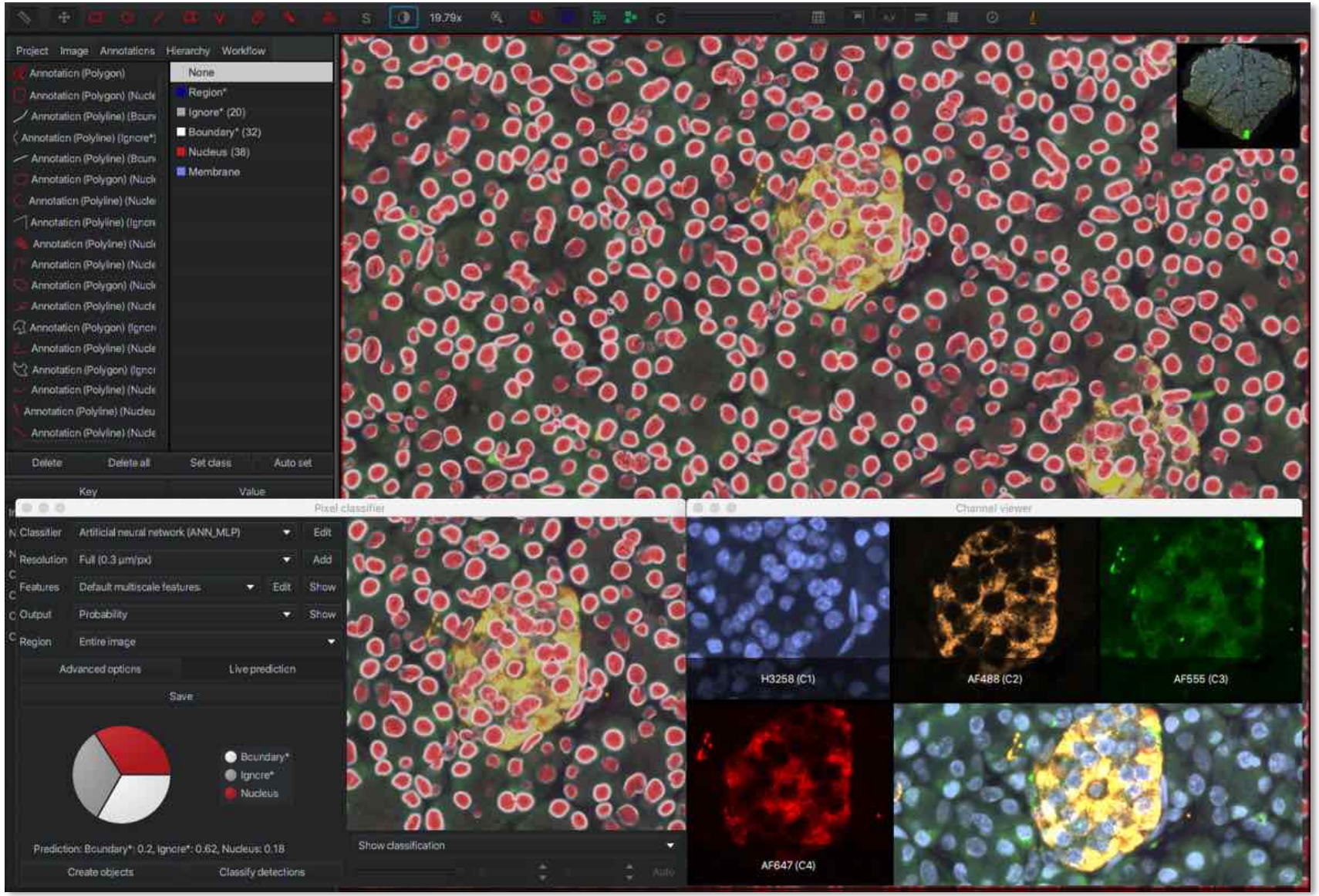


Train interactively
Support z-stacks

Identify
myelinated axons

Collaboration with
Dr Yvonne Dombrowski
Queen's University Belfast

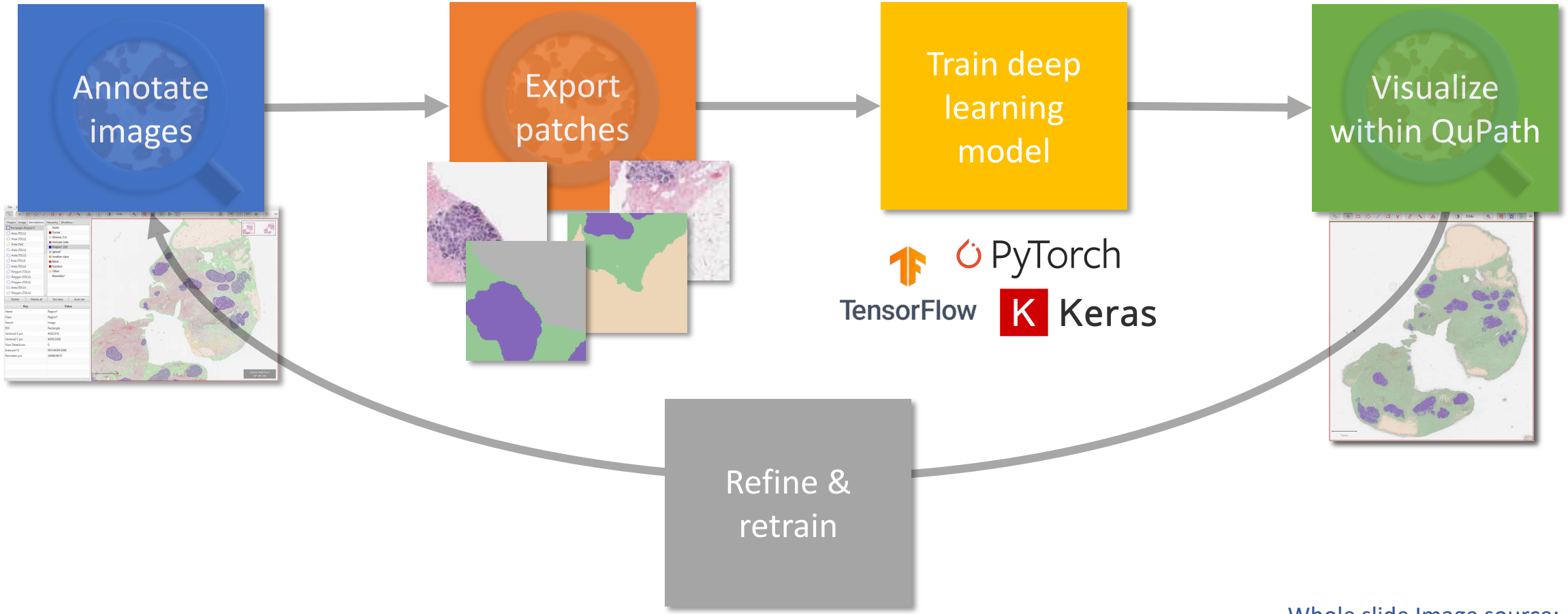
Pixel classification



Train to aid
object separation

Assign boundary class,
Specify line thickness,

A deep learning workflow in *QuPath (in progress!)*



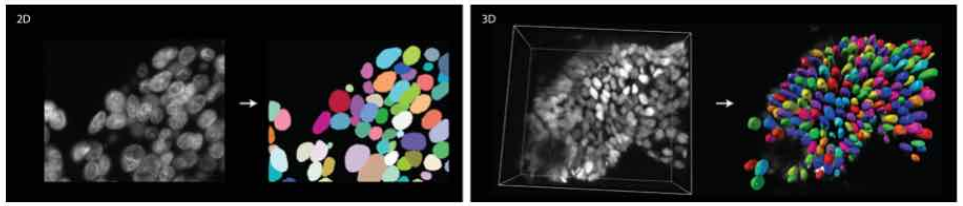
Whole slide Image source:
Virtual Tissue Bank of the
Susan G. Komen for the Cure® Tissue Bank
at the IU Simon Cancer Center

QuPath + StarDist can help resolve tricky nucleus-identification problems

README.md

pypi package 0.5.0 | build passing | build passing

StarDist - Object Detection with Star-convex Shapes



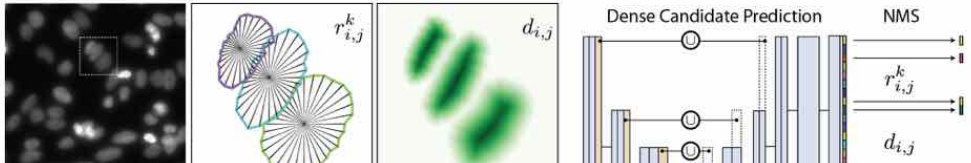
This repository contains the implementation of star-convex object detection for 2D and 3D images, as described in the papers:

- Uwe Schmidt, Martin Weigert, Coleman Broaddus, and Gene Myers.
  Cell Detection with Star-convex Polygons.
  International Conference on Medical Image Computing and Computer-Assisted Intervention (MICCAI), Granada, Spain, September 2018.
- Martin Weigert, Uwe Schmidt, Robert Haase, Ko Sugawara, and Gene Myers.
  Star-convex Polyhedra for 3D Object Detection and Segmentation in Microscopy.
  The IEEE Winter Conference on Applications of Computer Vision (WACV), Snowmass Village, Colorado, March 2020

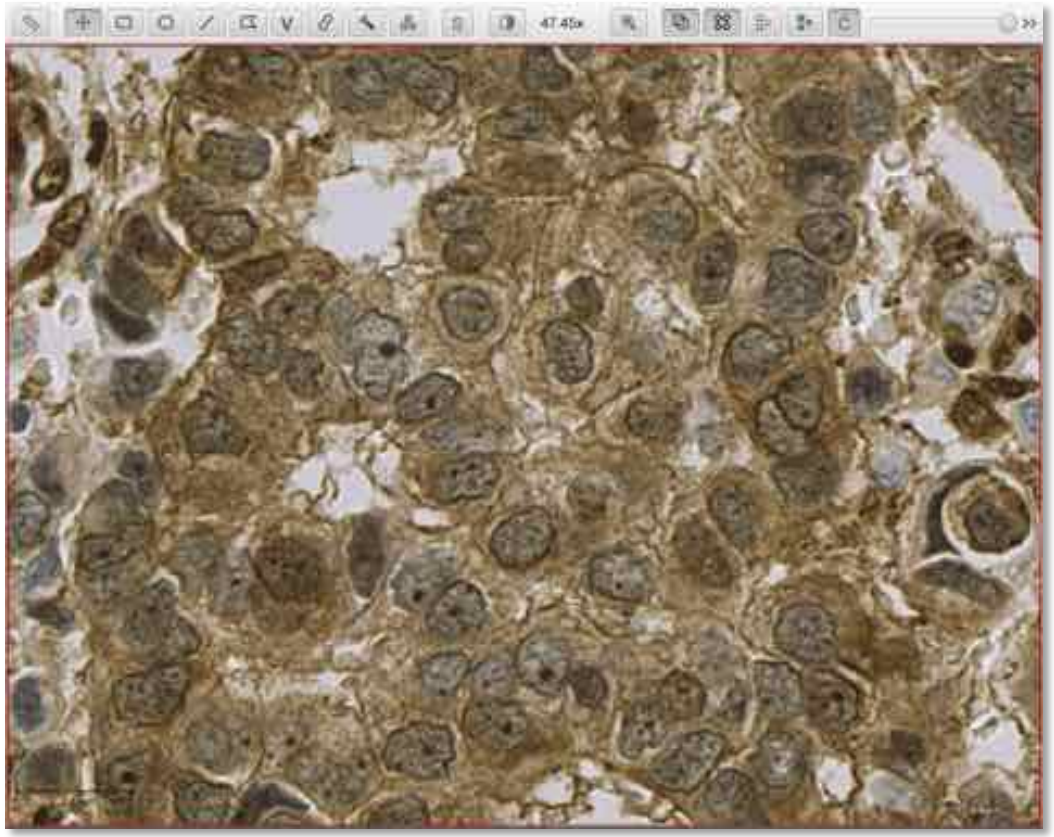
Please cite the paper(s) if you are using this code in your research.

Overview

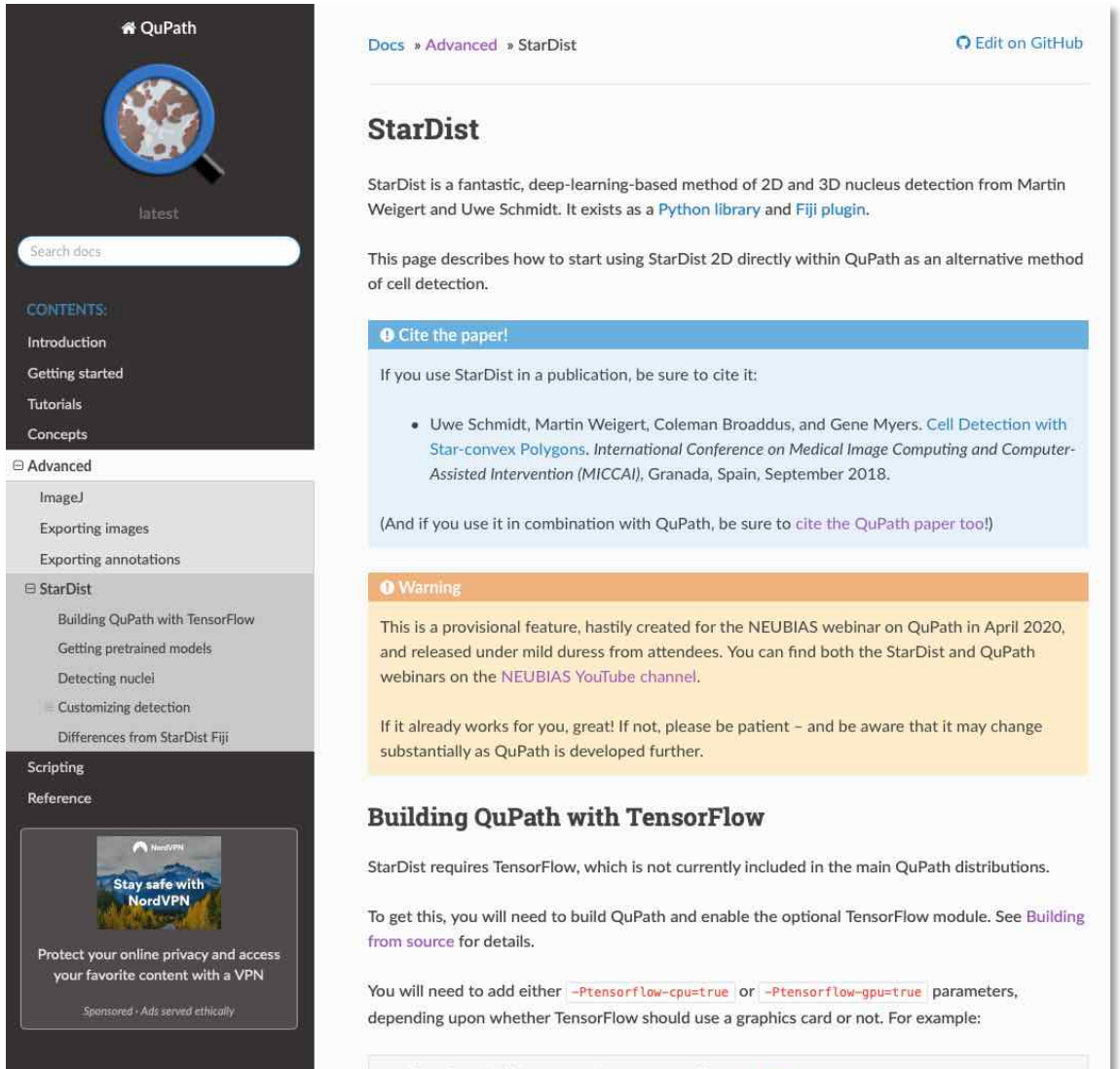
The following figure illustrates the general approach for 2D images. The training data consists of corresponding pairs of input (i.e. raw) images and fully annotated label images (i.e. every pixel is labeled with a unique object id or 0 for background). A model is trained to densely predict the distances (r) to the object boundary along a fixed set of rays and object probabilities (d), which together produce an overcomplete set of candidate polygons for a given input image. The final result is obtained via non-maximum supression (NMS) of these candidates.



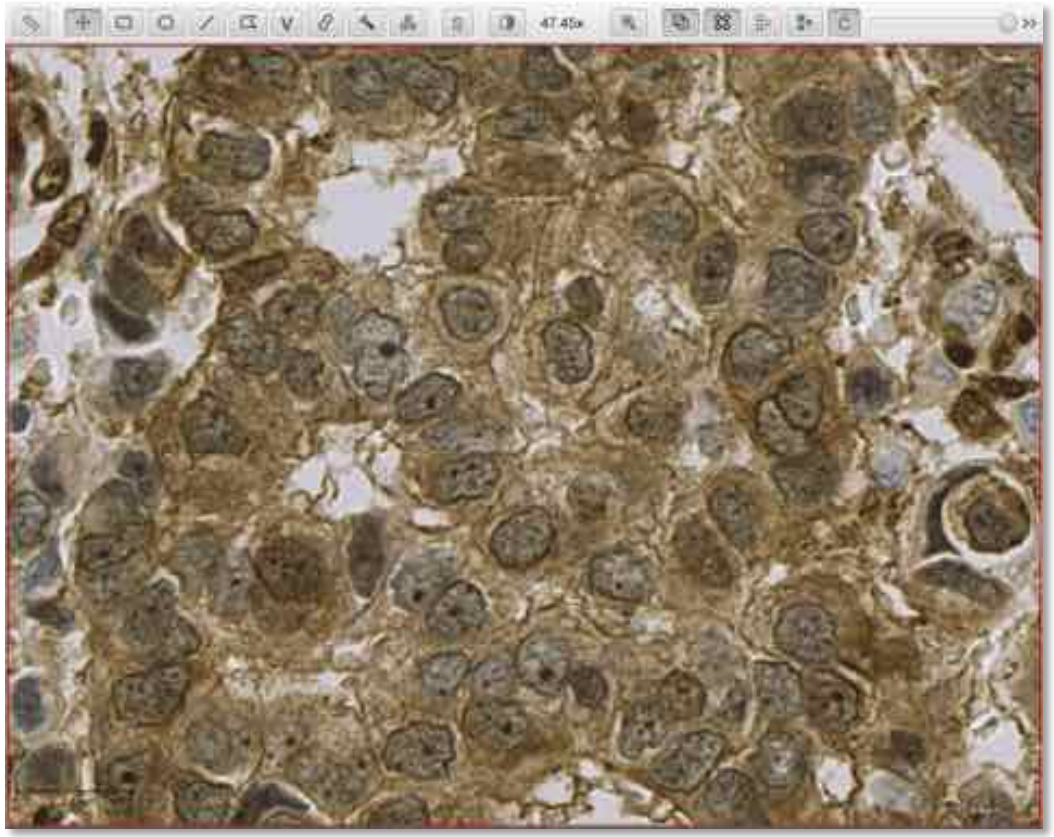
StarDist by Uwe Schmidt & Martin Weigert



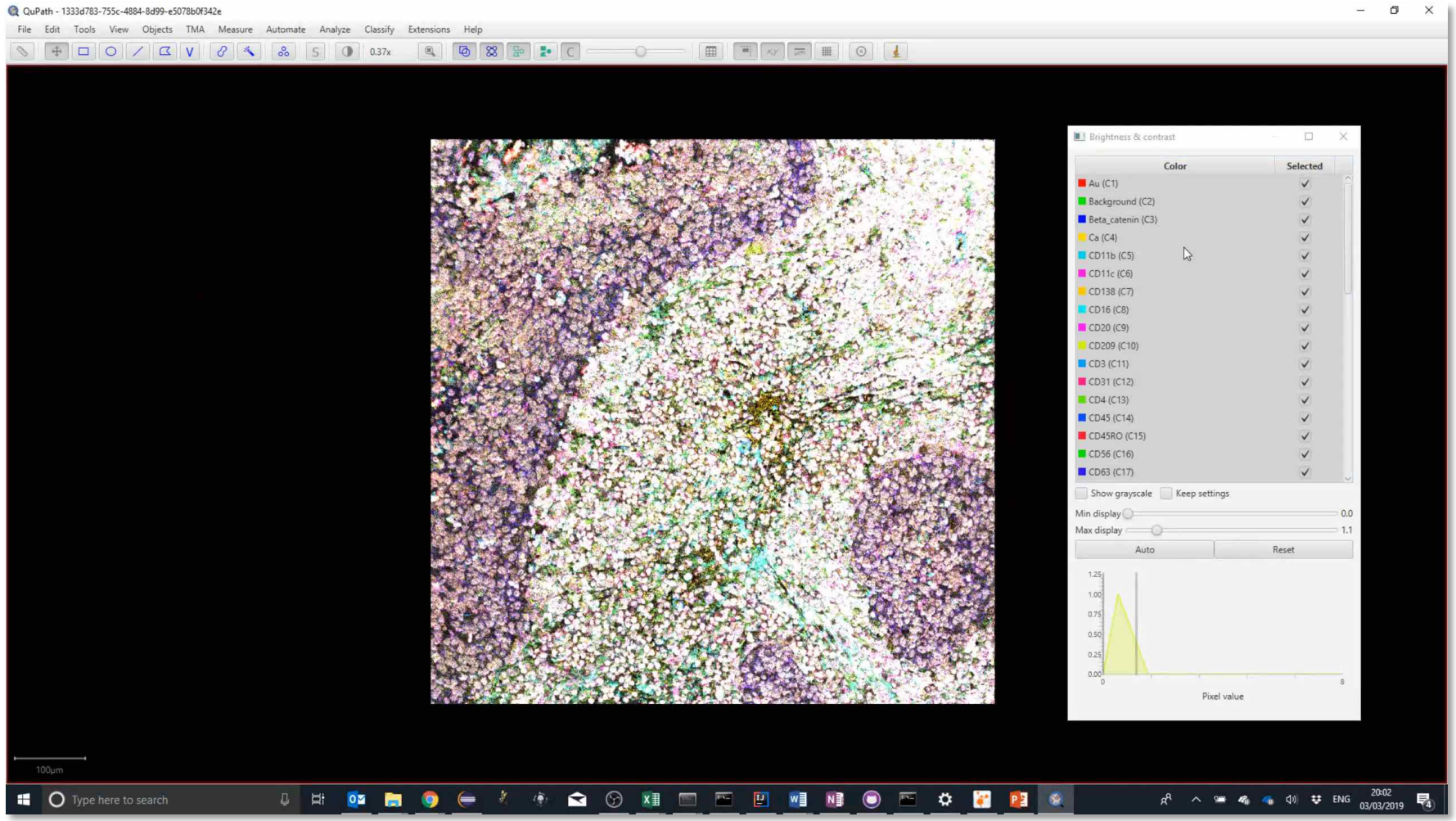
QuPath + StarDist can help resolve tricky nucleus-identification problems



StarDist by Uwe Schmidt & Martin Weigert



Multiplexed analysis



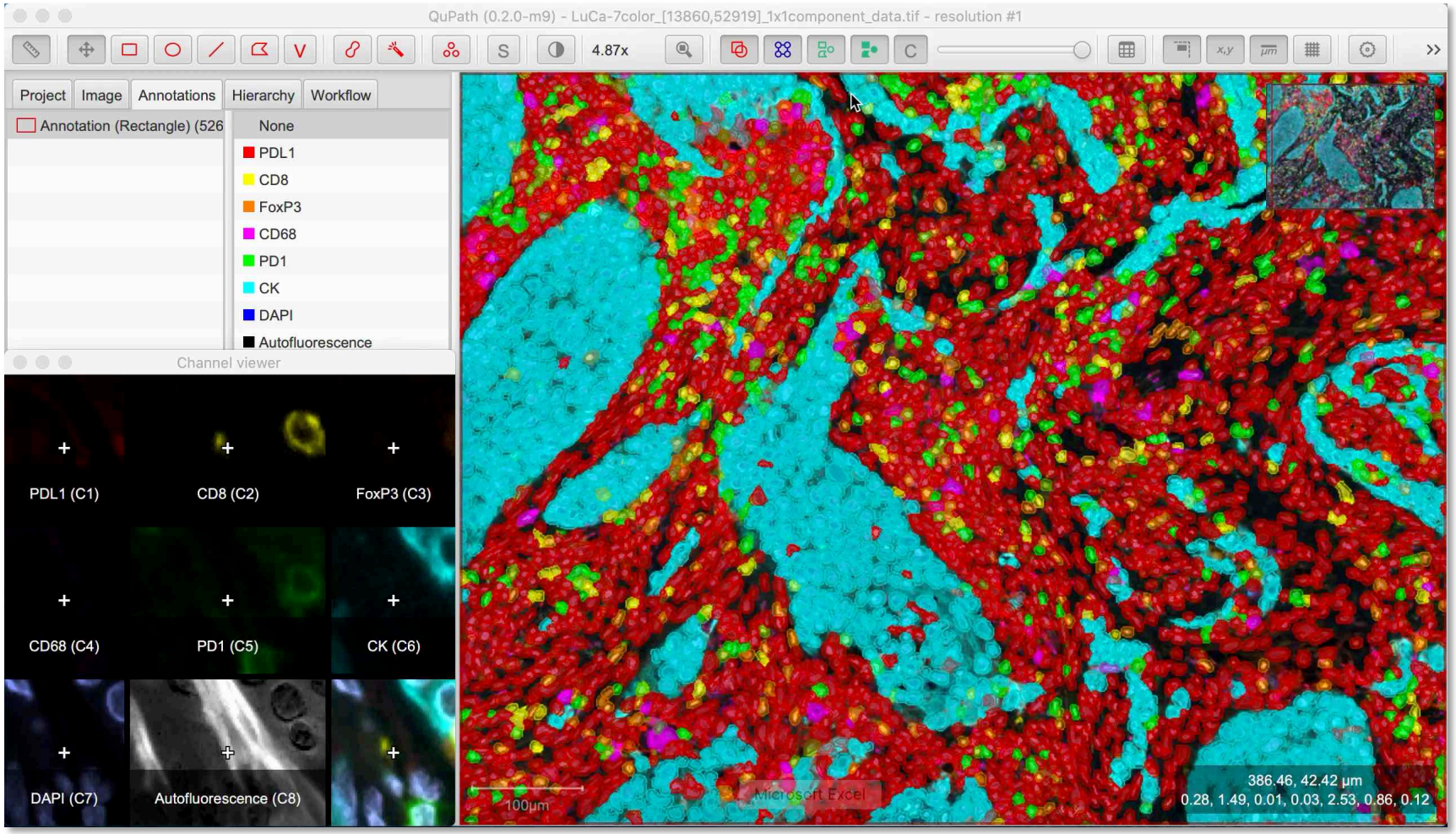
Support for multiplexed images

Channel viewer to visualize
> 40 channels
simultaneously

Multiplexed Ion Beam Image source:
Keren et al. *Cell* (2018)
https://mibi-share.ionpath.com

BIO-FORMATS

Multiplexed analysis



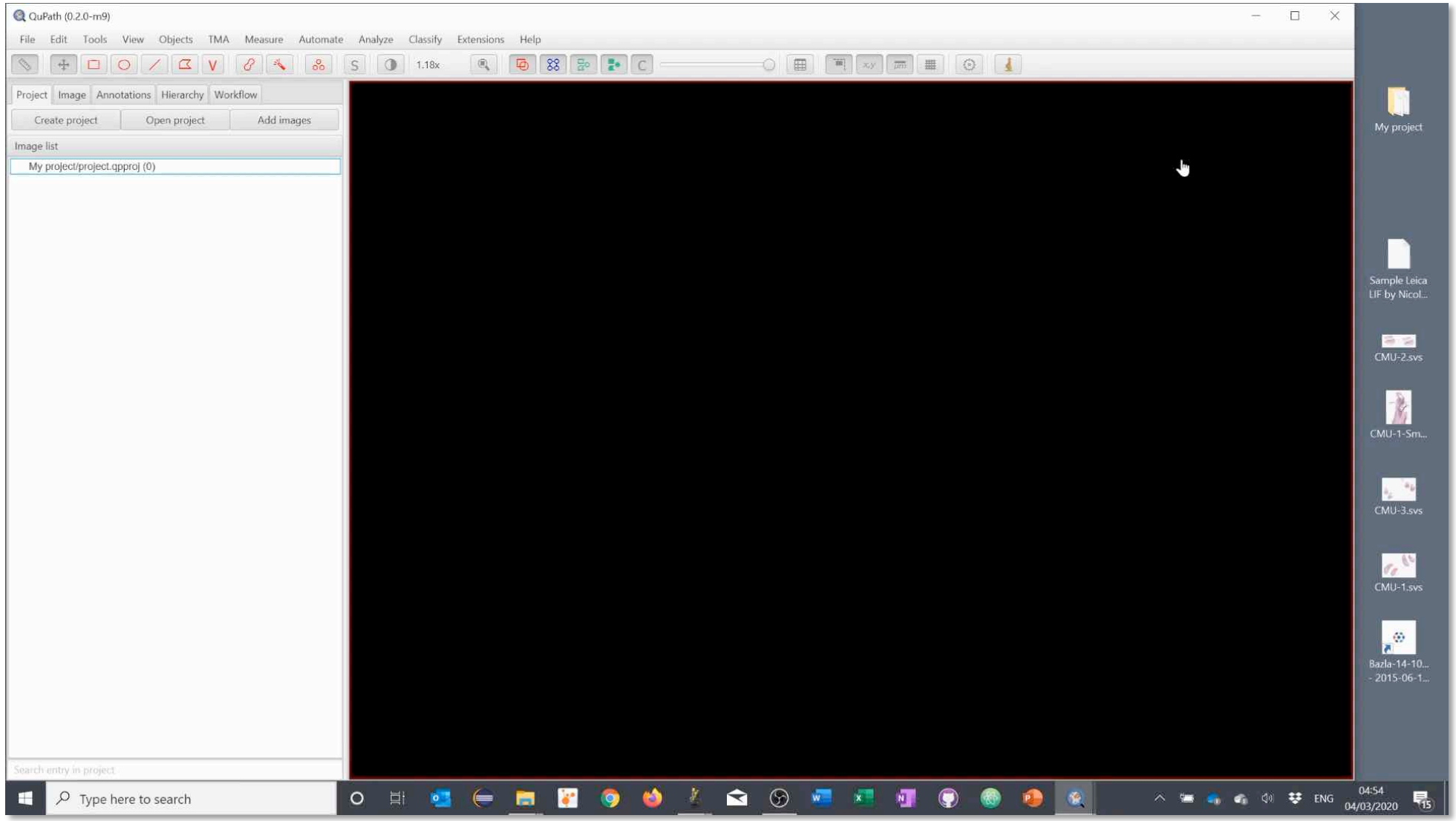
Single-class & composite classifiers

Cell phenotyping, Toggle visibility, Query locations & distances

Original image source:
LuCa-7color_[13860,52919]_1x1component_data.tif

BIO-FORMATS

Workflow integration

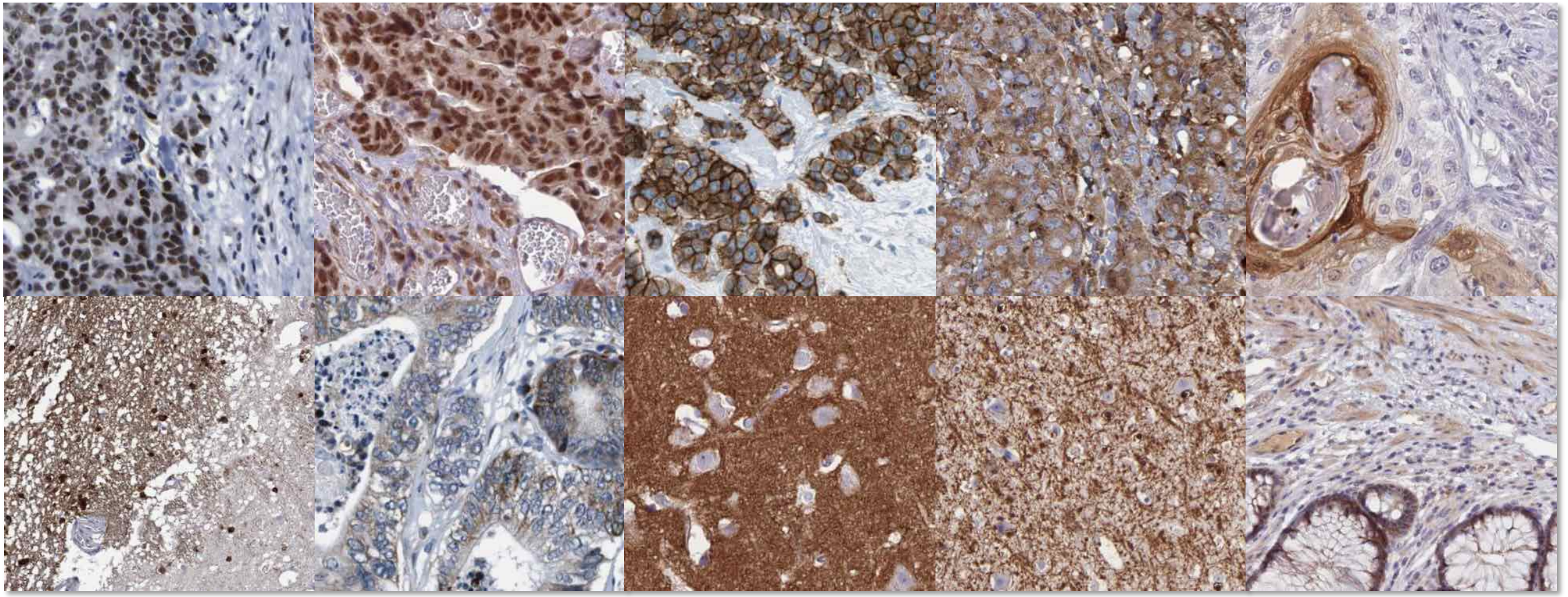


Projects to manage data

Add images (local & remote), Mask file names, Run batch scripts

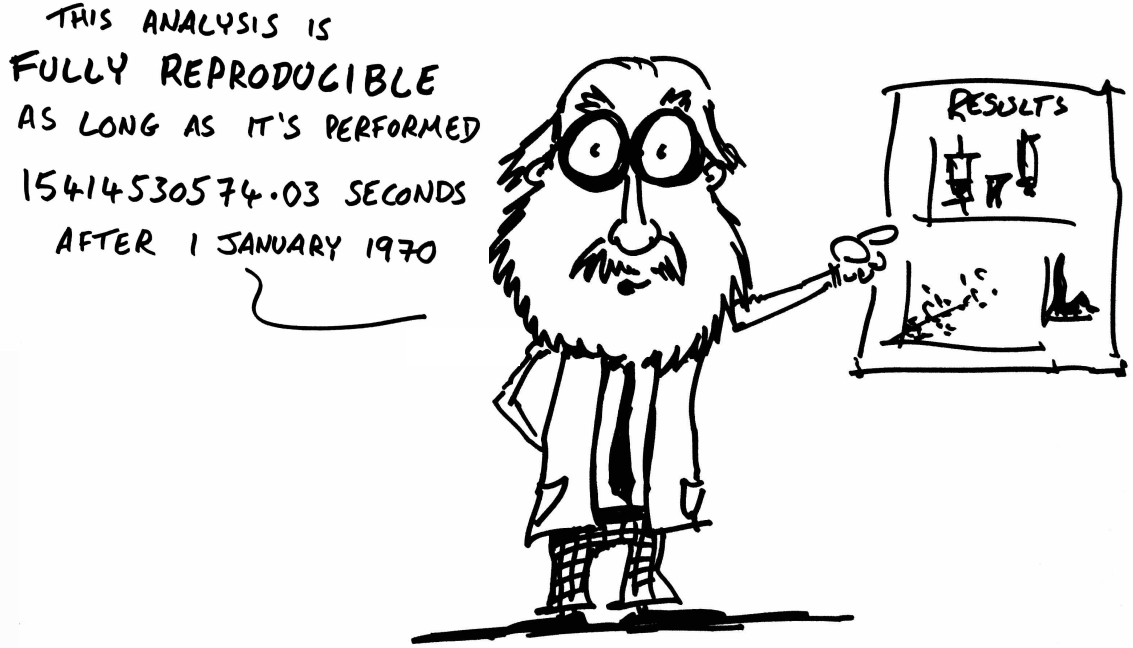
A plea to users of bioimage analysis software…

Similar-sounding problems often pose *very* different computational challenges!



Haematoxylin & DAB images from the Human Protein Atlas

Automated does not equal unbiased!



Replicability is hard to achieve!

Even with all the software tools available

bioimage analysis is still hard!

Creating & supporting user-friendly software for researchers is important!

Thanks!

Chan Zuckerberg Initiative

wellcome

CANCER RESEARCH UK

THE UNIVERSITY OF EDINBURGH

The creators & maintainers of many other open source projects

OpenJDK

BIO-FORMATS

JavaFx

OpenSlide

Groovy

OpenCV

CONTROLS FX

JTS

AdoptOpenJDK

Everyone who participates on the community forum

Everyone who makes datasets available

What is QuPath?

QuPath is software for **whole slide image analysis**...

...that is **freely available & pathologist-friendly** ...

...but is **open source, extensible & scriptable** for developers...

...and **isn't locked down** with fixed algorithms...

...and has a **wide user base** sharing ideas & insights...

https://qupath.github.io