

# Distributed & GPU-accelerated Image Processing

## Robert Haase

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und Forschung

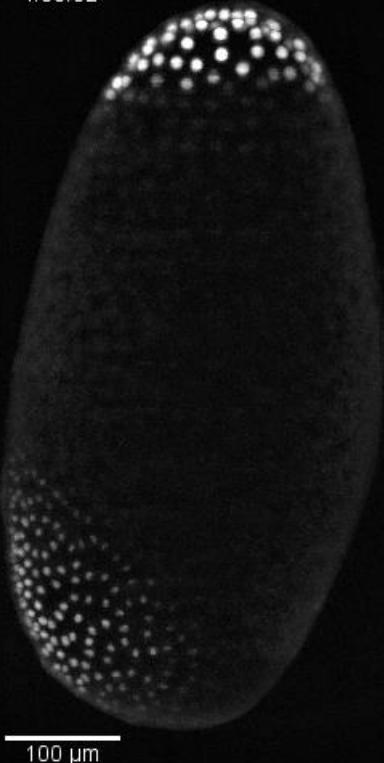


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Landtags beschlossenen Haushaltes.

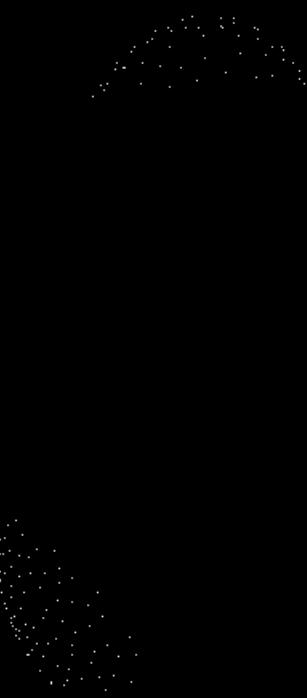
# GPU accelerated image processing in life sciences

... to study embryo development

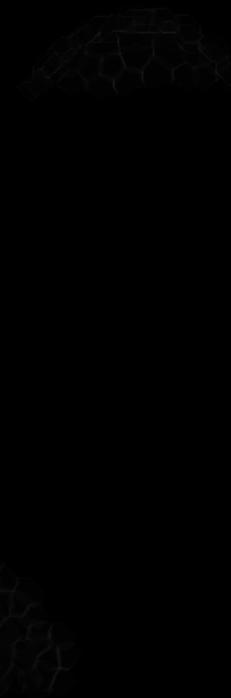
Tribolium castaneum  
nuclei-GFP,  
Background subtracted  
4:00:02



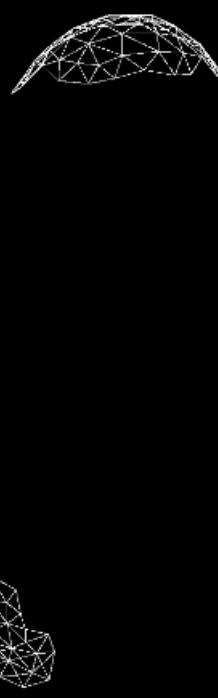
Spot detection (3D)



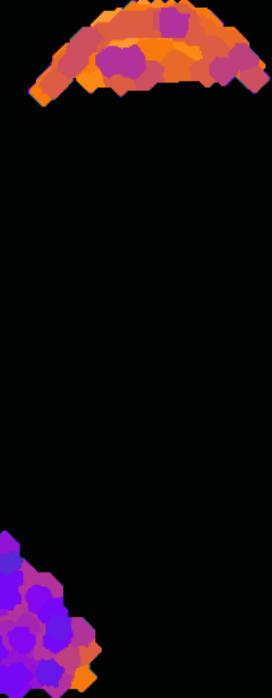
Theoretical membranes  
(pseudo Voronoi map)



Neighbor mesh



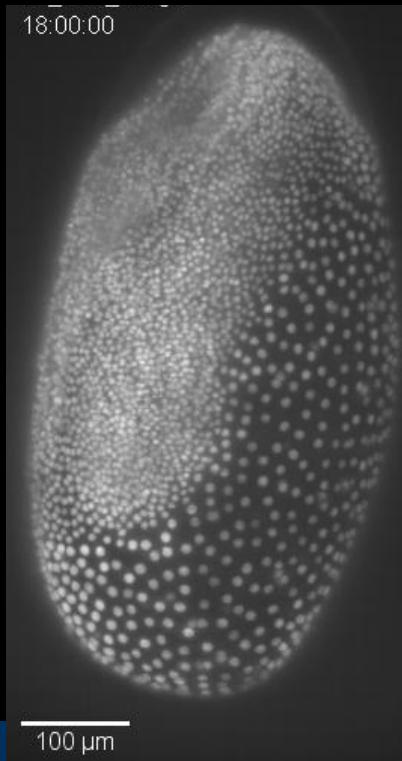
Average centroid distance  
of neighbors



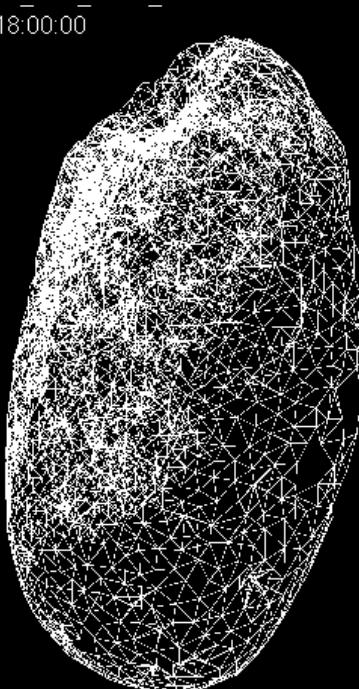
# GPU accelerated image processing in life sciences

Raytracing enables differentiating surface and sub-surface mesh nodes

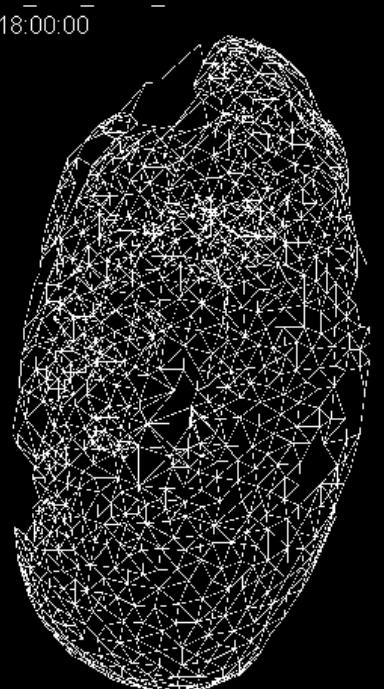
3D stack input



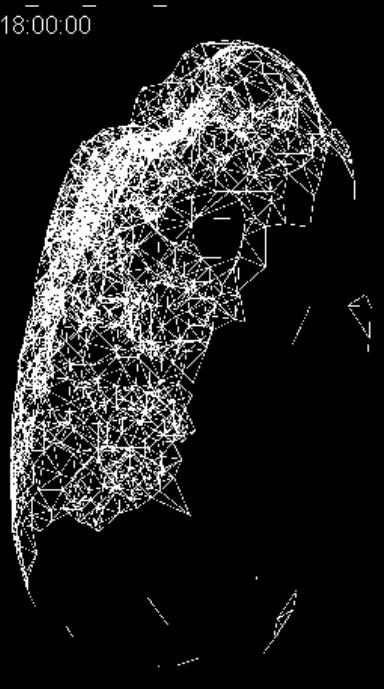
Neighbor mesh



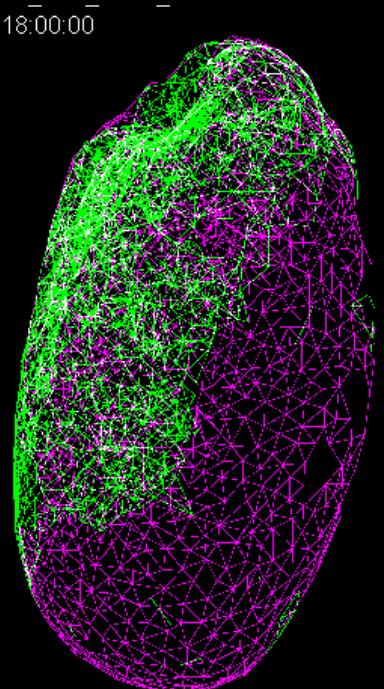
Surface neighbor  
mesh



Sub-surface  
neighbor mesh

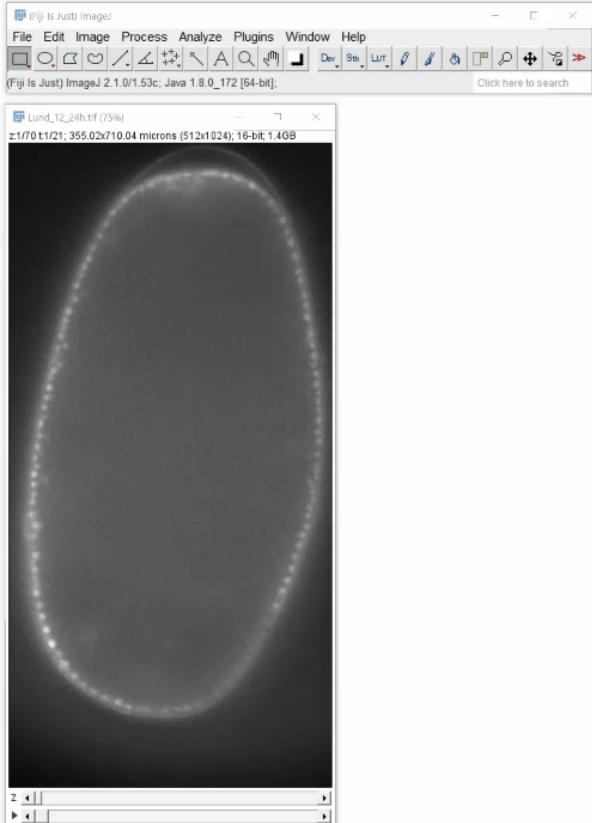


Merge



# Image processing in life-sciences

- State-of-the-art software for more than 20 years: ImageJ / Fiji



2x

# **OpenCL-based GPU-acceleration**

# GPU-acceleration? Learn the Open Computing Language (OpenCL)!

The screenshot shows the PyCharm IDE interface. The top navigation bar includes File, Edit, View, Navigate, Code, Refactor, Run, Tools, Git, Window, Help, and pyclesperanto\_prototype - maximum\_z\_projection\_x.cl. The left sidebar has tabs for Project, Commit, Pull Requests, Structure, and Favorites, with 'Project' currently selected. The main editor window displays the CL code for 'maximum\_z\_projection\_x.cl'. The code implements a kernel to calculate the maximum value along the z-axis for a given source image. The bottom navigation bar includes Git, TODO, Problems, Terminal, Python Console, and Event Log. The bottom status bar shows 'Cannot Run Git: Git is not installed // Download and Install (2 minutes ago)', '23:1 CRLF UTF-8 4 spaces Python 3.8 (pyclesperanto\_prototype)', and 'master'.

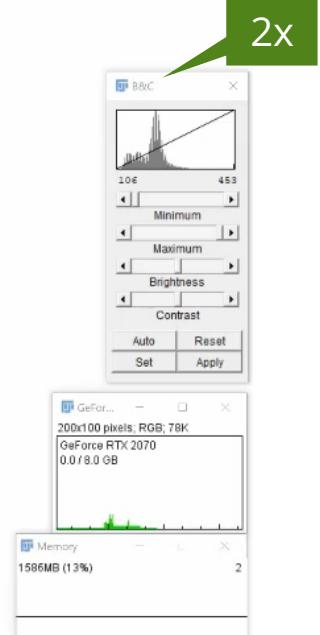
```
1  __kernel void maximum_z_projection(
2      IMAGE_dst_max_TYPE dst_max,
3      IMAGE_src_TYPE src
4  ) {
5      const sampler_t sampler = CLK_NORMALIZED_COORDS_FALSE | CLK_ADDRESS_CLAMP_TO_EDGE | CLK_FILTER_NEAREST;
6
7      const int x = get_global_id(0);
8      const int y = get_global_id(1);
9      float max = 0;
10     for(int z = 0; z < GET_IMAGE_DEPTH(src); z++)
11     {
12         POS_src_TYPE pos = POS_src_INSTANCE(x,y,z,0);
13         float value = READ_src_IMAGE(src,sampler,pos).x;
14         if (value > max || z == 0) {
15             max = value;
16         }
17     }
18     POS_dst_max_TYPE pos = POS_dst_max_INSTANCE(x,y,0,0);
19     WRITE_dst_max_IMAGE(dst_max, pos, CONVERT_dst_max_PIXEL_TYPE(max));
20 }
```

# Maximum intensity projection along Z

# User-friendly GPU-acceleration

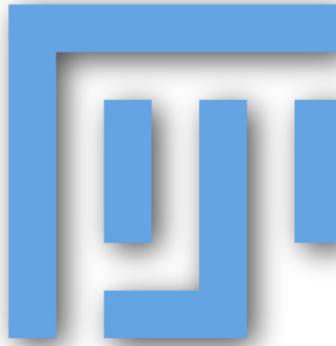


2x



# GPU-accelerated image processing

Performance depends on operation, image size, parameters, hardware, ....

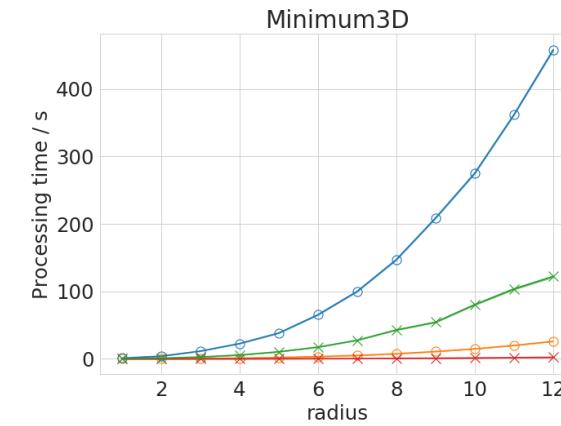
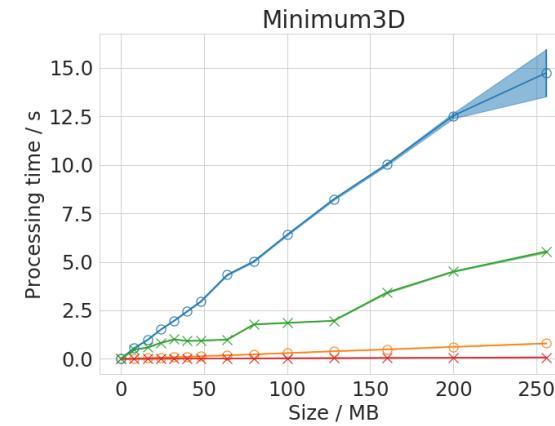
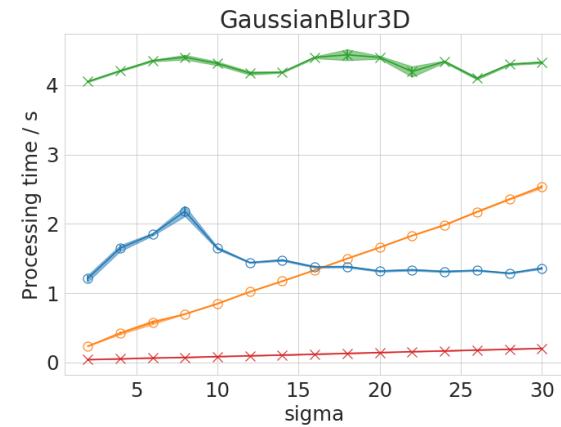
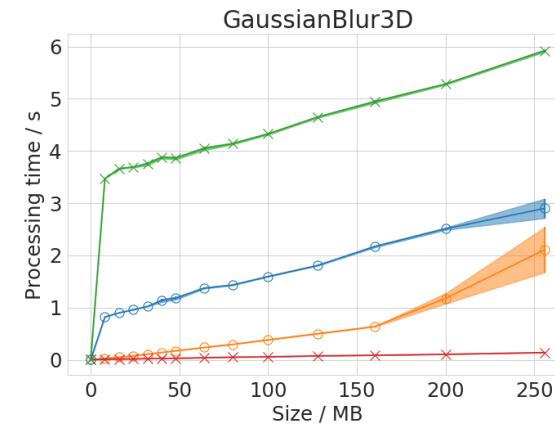


vs.



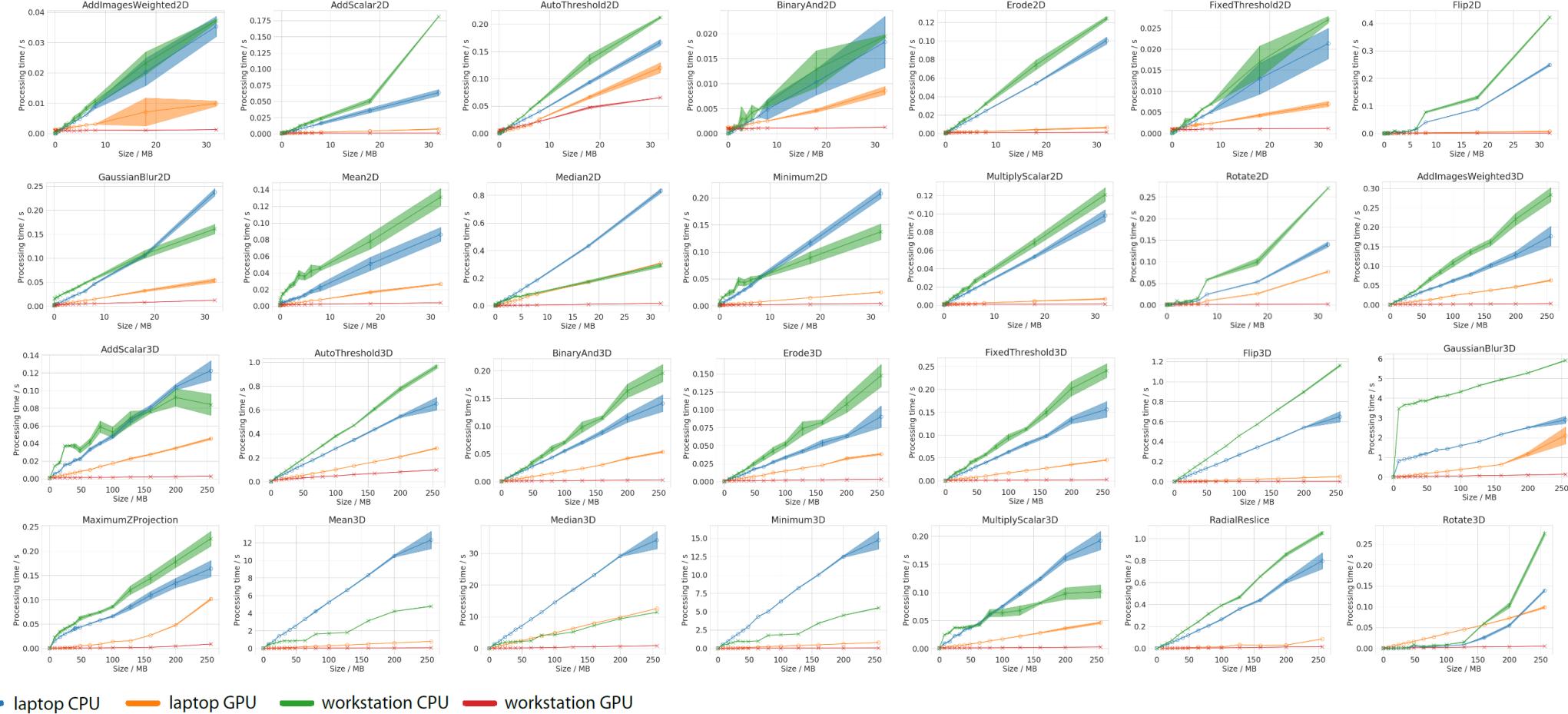
- Workstation CPU  
2x Intel Xeon Silver 4110
- Laptop CPU  
Intel Core i7-8650U

- Workstation GPU  
Nvidia Quadro P6000
- Laptop GPU  
Intel UHD 620 GPU



# GPU-accelerated image processing

Performance depends on operation, image size, parameters, hardware, ....



# GPU-accelerated image processing

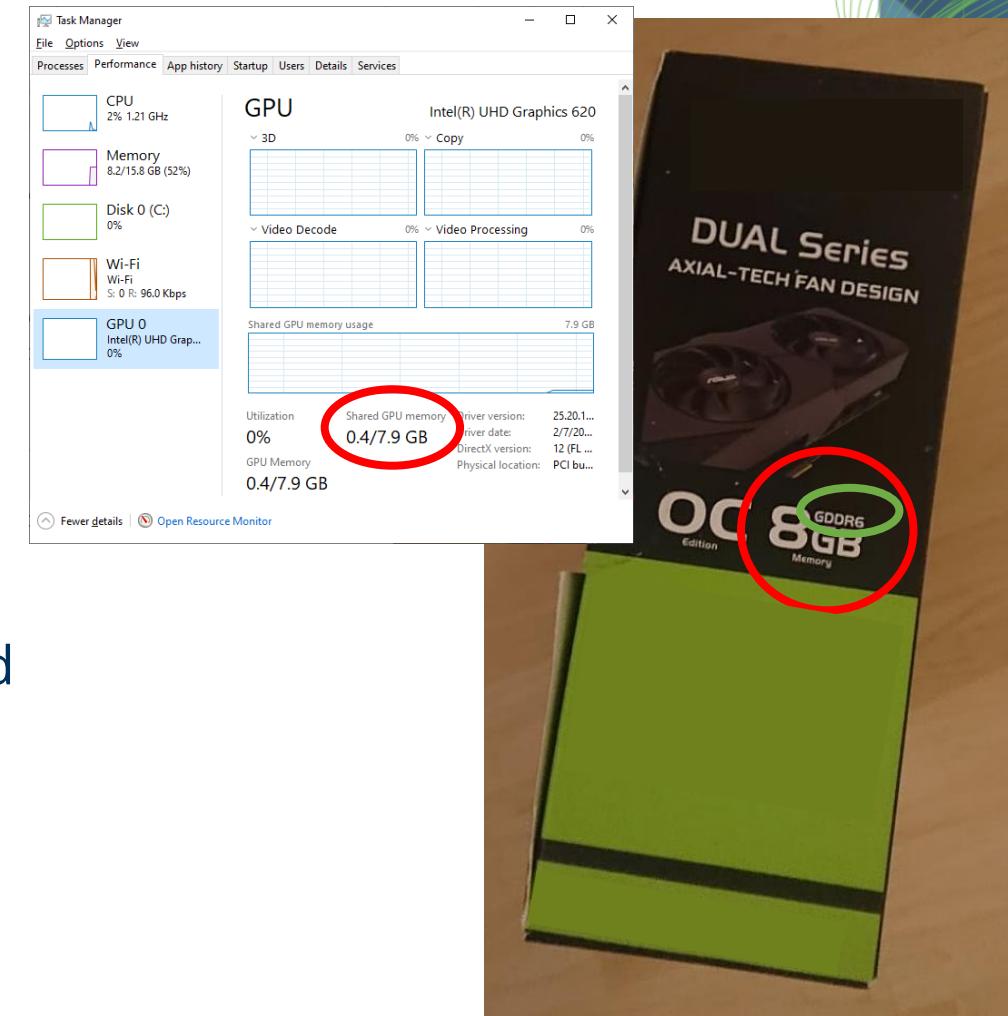
- 8 MB (2D)
- 64 MB (3D)

	Speedup compared to Laptop CPU	
	Laptop GPU	Workstation GPU
AddImagesWeighted2D	3	8
AddScalar2D	7	14
AutoThreshold2D	2	2
BinaryAnd2D	2	4
Erode2D	11	20
FixedThreshold2D	2	5
Flip2D	16	37
GaussianBlur2D	3	9
Mean2D	3	10
Median2D	2	35
Minimum2D	7	22
MultiplyScalar2D	10	21
Rotate2D	3	22
AddImagesWeighted3D	3	26
AddScalar3D	3	23
AutoThreshold3D	3	5
BinaryAnd3D	3	24
Erode3D	2	13
FixedThreshold3D	4	30
Flip3D	15	119
GaussianBlur3D	6	35
MaximumZProjection	7	46
Mean3D	18	150
Median3D	3	43
Minimum3D	23	188
MultiplyScalar3D	4	28
RadialReslice	14	42
Rotate3D	0.1	2

# Checklist: When does GPU-accelerated image processing make sense?

In order to accelerate your image analysis workflow

- The pre-existing workflow should be slow; ideally:  
(processing time / loading time) > 10,
- a single processing step  
(rule of thumb: image size in GB x4)  
should **fit in your graphics card memory**,

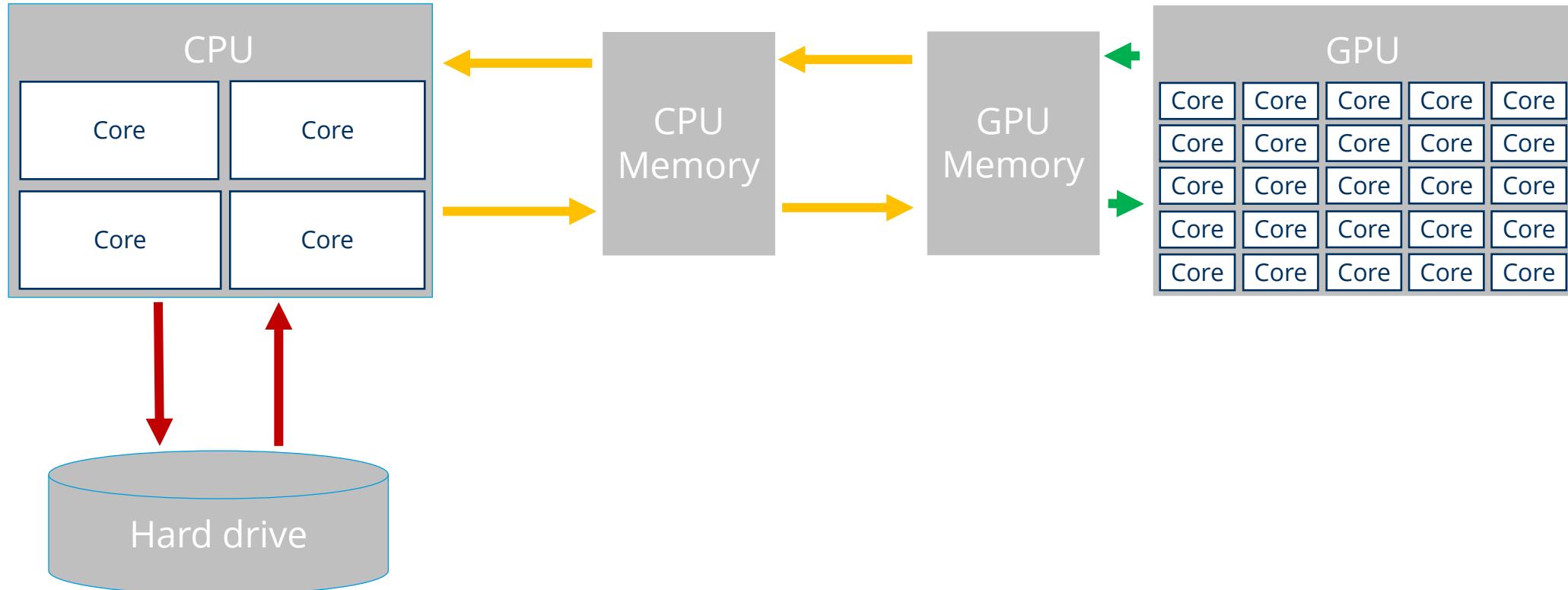


If you really want to get the most out of it, you should own a graphics card with **GDDR6** memory (memory bandwidth > 400 Gb/s).

Comparison: common DDR4 memory has a bandwidth of about 40 GB/s

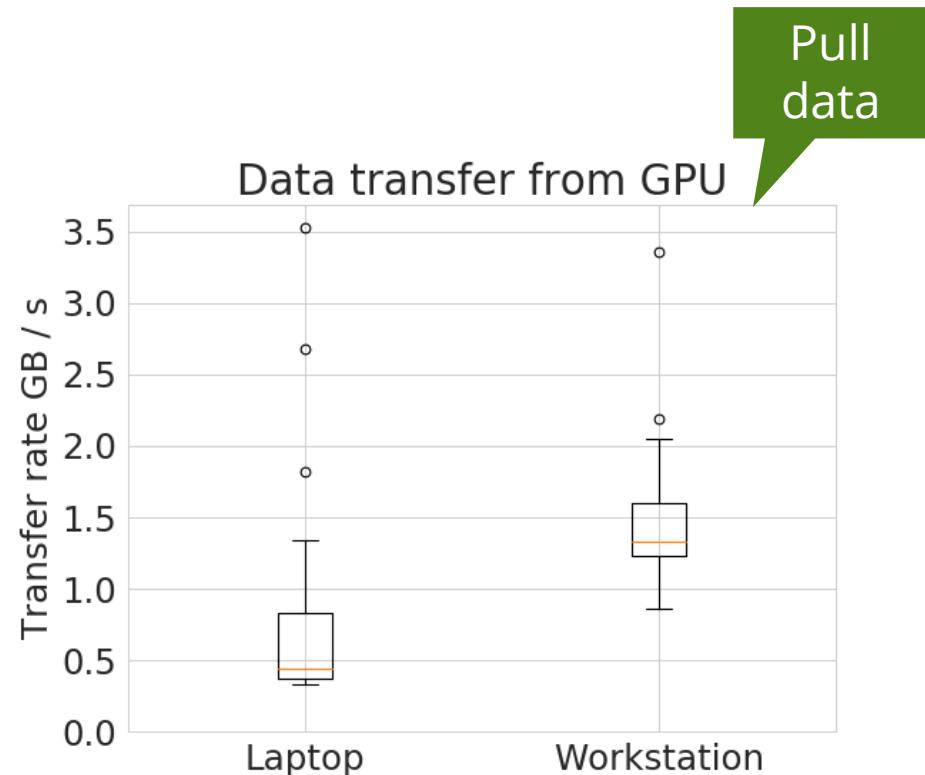
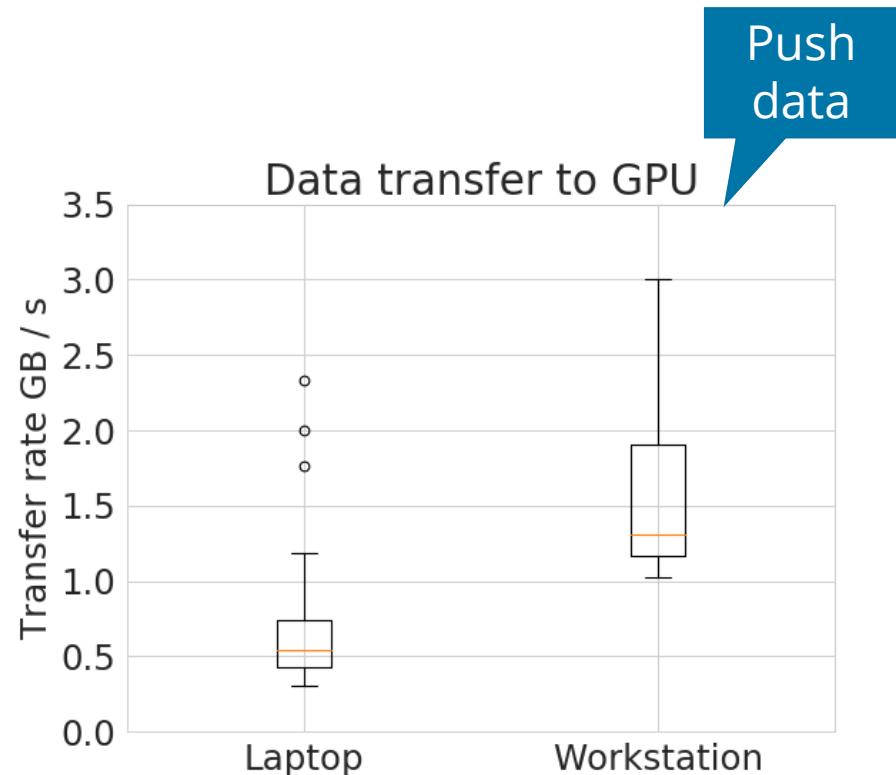
# GPUs allow real-time image processing

GPUs are specialised in processing, very fast thanks to many cores and fast memory access



# Data transfer takes time

Data transfer is the bottle neck



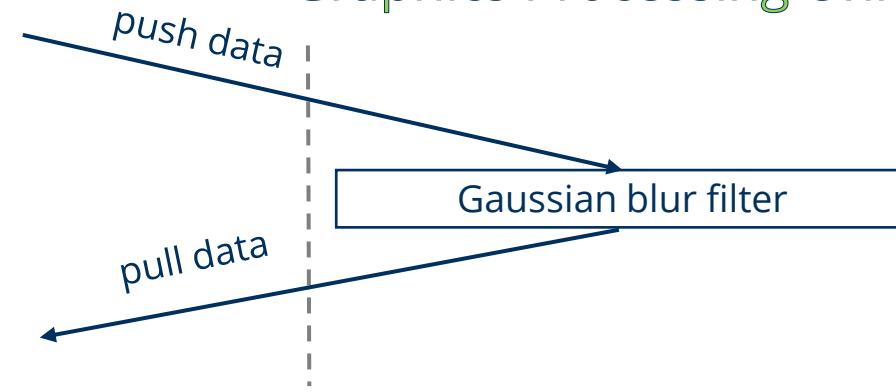
# Build workflows consisting of many operations

GPU acceleration may suffer from data transfer between CPU and GPU

Central Processing Unit (CPU)



Graphics Processing Unit (GPU)



# Optimal performance through smart memory management

Example workflow processing a *Drosophila melanogaster* embryo, histone-  
H2B-GFP

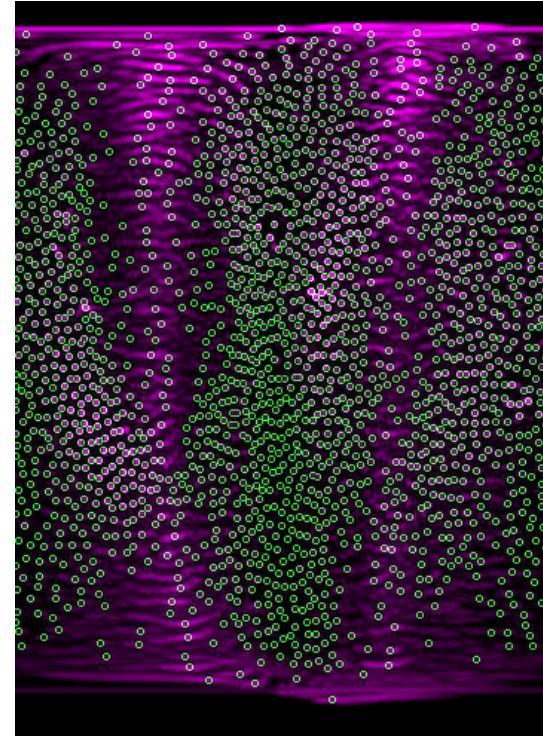
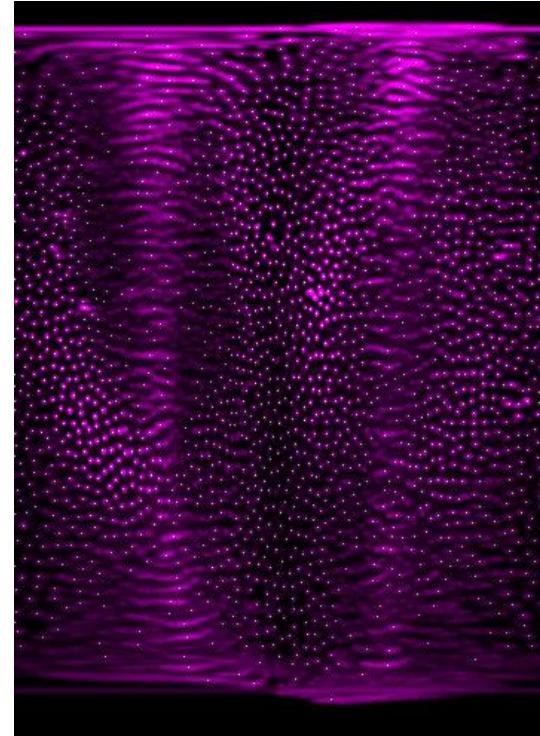
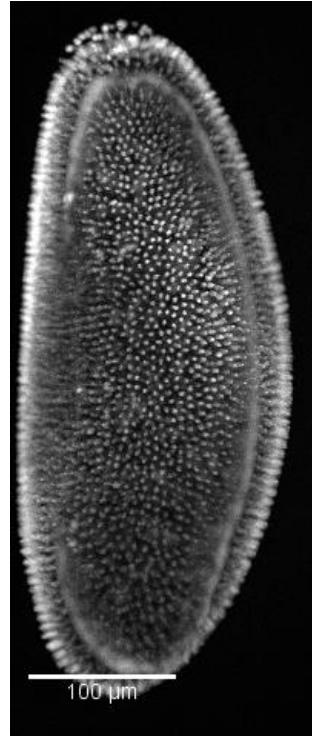
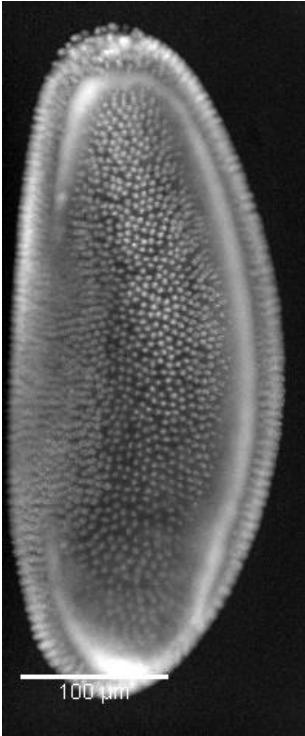
Load data

Preprocessing

Transformation

Segmentation

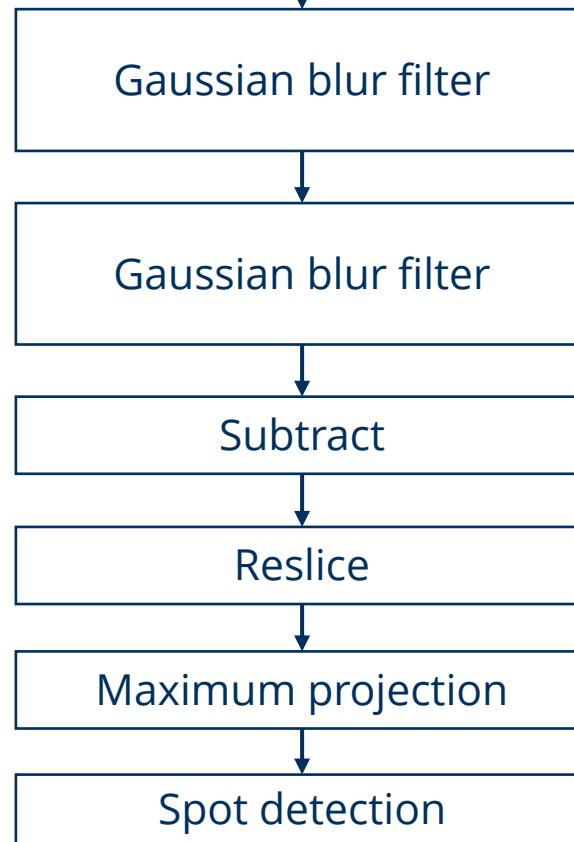
Save data



# Build workflows consisting of many operations

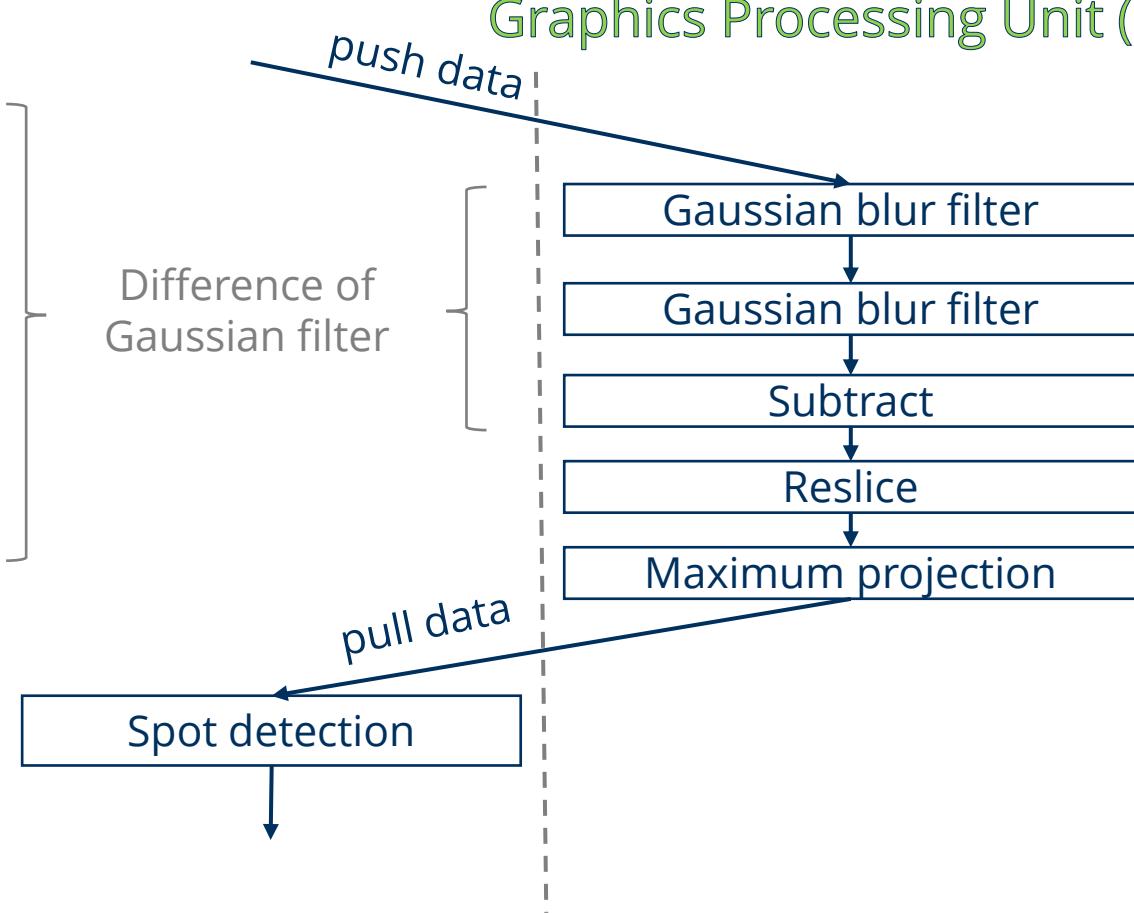
GPU acceleration may suffer from data transfer between CPU and GPU

## Central Processing Unit (CPU)



Time ↓

## Graphics Processing Unit (GPU)



# GPU-accelerated Image Processing in Python: OpenCL / clesperanto

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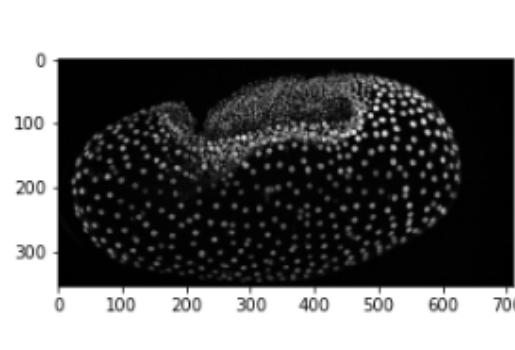
# Python Jupyter Notebooks

- Image processing using pyclesperanto

```
[1]: import stackview  
import pyclesperanto_prototype as cle  
from skimage.io import imread
```

```
[2]: image = imread("c:/structure/data/Lund_18.0_22.0_Hours-11-resampled.tif").swapaxes(1,2)
```

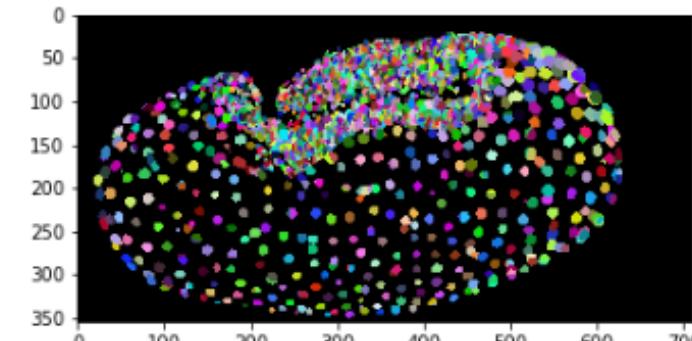
```
[3]: background_subtracted = cle.top_hat_box(image, radius_x=5, radius_y=5)  
background_subtracted
```



```
cle._image  
shape (140, 355, 710)  
dtype float32  
size 134.6 MB  
min 0.0  
max 790.0
```



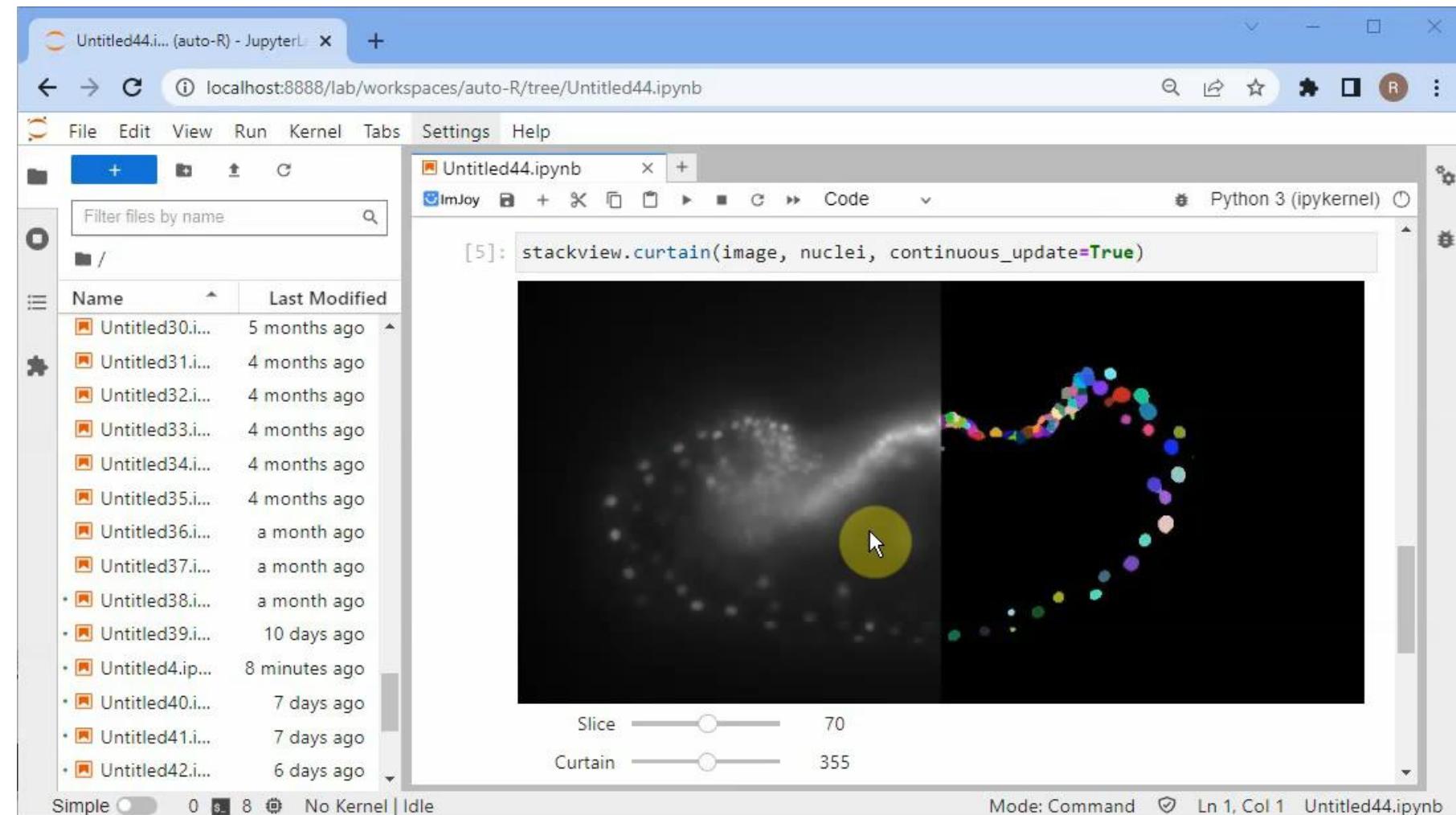
```
[4]: nuclei = cle.voronoi_otsu_labeling(background_subtracted, spot_sigma=  
nuclei
```



```
cle._image  
shape (140, 355, 710)  
dtype uint32  
size 134.6 MB  
min 0.0  
max 1756.0
```

# Python Jupyter Notebooks

- When working on the cluster / Jupyter Hub, consider using stackview instead of napari for inspecting images in 3D.





# GPU-accelerated Image Processing in Python: CUDA / cupy

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# cupy

CUDA-based GPU-accelerated [image] data processing in Python

The image displays two side-by-side browser windows. The left window shows the official CuPy website at [cupy.dev](https://cupy.dev). The page has a dark background featuring a green and white cube logo and the word "CuPy". A purple box highlights the text "NumPy/SciPy-compatible Array Library for GPU-accelerated Computing with Python". Below the logo are three buttons: "GET STARTED" (red), "API REFERENCE" (teal), and "GITHUB" (blue). The right window shows the GitHub repository for CuPy at [github.com/cupy/cupy/](https://github.com/cupy/cupy/). The repository page includes a summary card with statistics: 451 issues, 63 pull requests, 128 watchers, 707 forks, and 7.1k stars. A purple box highlights the "NumPy & SciPy for GPU" tag in the repository's "About" section. The GitHub interface also shows recent activity, including several merge pull requests from the ".github" and ".pfnci" branches.

# drop-in replacement for numpy and scipy

The API of some cupy packages is close to the scipy/numpy API.

This allows *easy* switching from scipy to cupy.

```
import scipy.ndimage as ndi
```

```
ndi.gaussian_filter(image, sigma=5)
```

```
import cupyx.scipy.ndimage as xdi
```

- However, image data still needs to be pushed to GPU memory.

```
xp_image = xp.asarray(image)
```

```
xdi.gaussian_filter(xp_image, sigma=5)
```

# Common patterns

To make code independent from cupy availability, while minimizing if-else blocks, some common design patterns emerged:

```
try:  
    import cupy as xp  
except:  
    import numpy as xp  
  
import numpy as np
```

If this fails because cupy is not installed,

This will execute and xp will be available.

We can still use np anyway.

The same pattern works with scipy.ndimage

```
try:  
    import cupyx.scipy.ndimage as xdi  
except:  
    import scipy.ndimage as xdi  
  
import scipy.ndimage as ndi
```

# Common patterns

You can then call magic code like this, which will do different things depending on cupy-availability.

- If cupy is available:

```
[3]: image = imread("../data/blobs.tif")
```

```
xp_image = xp.asarray(image)
```

```
type(xp_image)
```

```
[3]: cupy.ndarray
```

- If cupy is not available:

```
[3]: image = imread("../data/blobs.tif")
```

```
xp_image = xp.asarray(image)
```

```
type(xp_image)
```

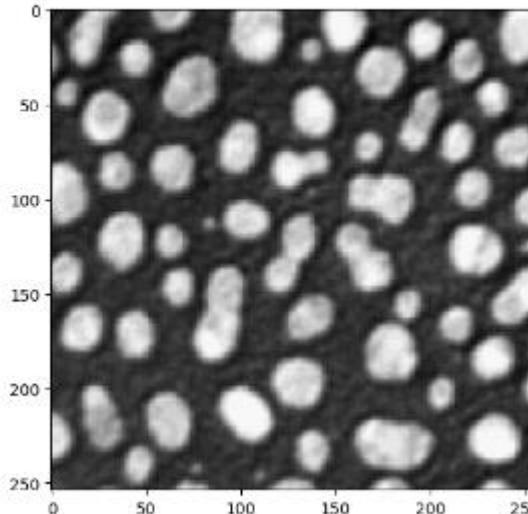
```
[3]: numpy.ndarray
```

# Common patterns

Some if-else blocks are hard to avoid

```
[7]: if np == xp:  
    np_image = xp_image  
else:  
    np_image = xp.asarray(xp_image)  
  
imshow(np_image)
```

```
[7]: <matplotlib.image.AxesImage at  
0x24692ef85e0>
```

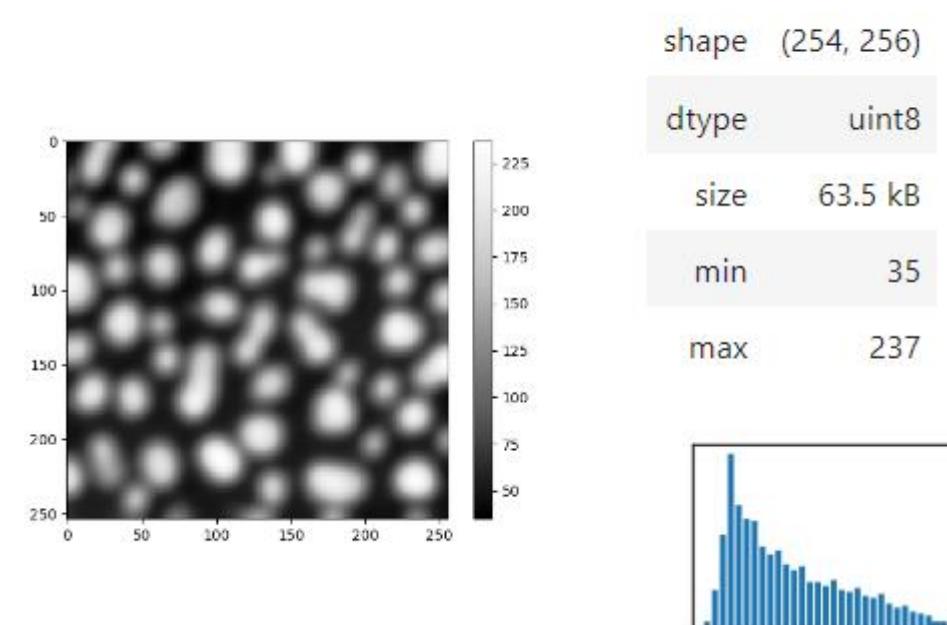


- Stackview aims to be cupy/numpy agnostic

```
[4]: xp_blurred = xdi.gaussian_filter(xp_image, sigma=5)
```

```
[5]: stackview.insight(xp_blurred)
```

```
[5]:
```

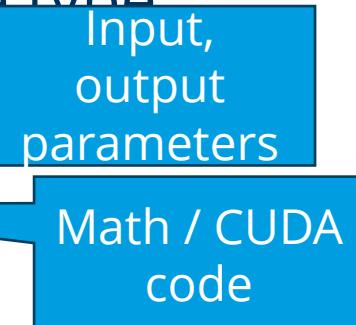


# Custom kernels

CUDA is also just C. You can write custom cupy kernels using simple syntax.

T represents the image type

```
squared_difference = cp.ElementwiseKernel(  
    'T x, T y',  
    'T z',  
    'z = (x - y) * (x - y)',  
    'squared_difference')
```

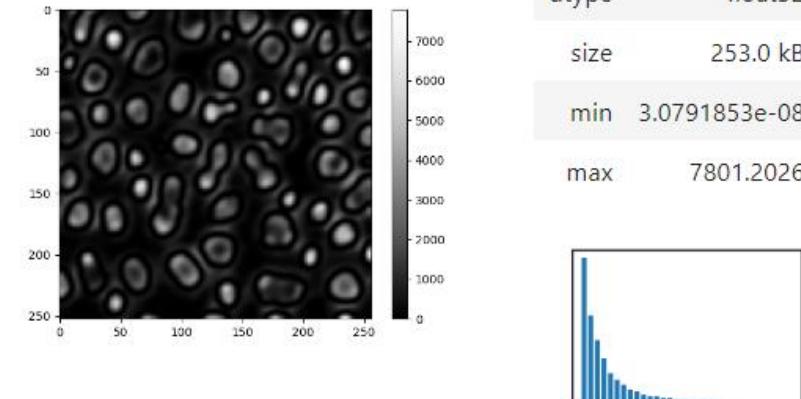


```
[3]: cp_image = cp.asarray(image[1:], dtype=np.float32)  
image1 = gaussian_filter(cp_image, sigma=3)  
image2 = gaussian_filter(cp_image, sigma=7)
```

```
[5]: sqdiff = squared_difference(image1, image2)
```

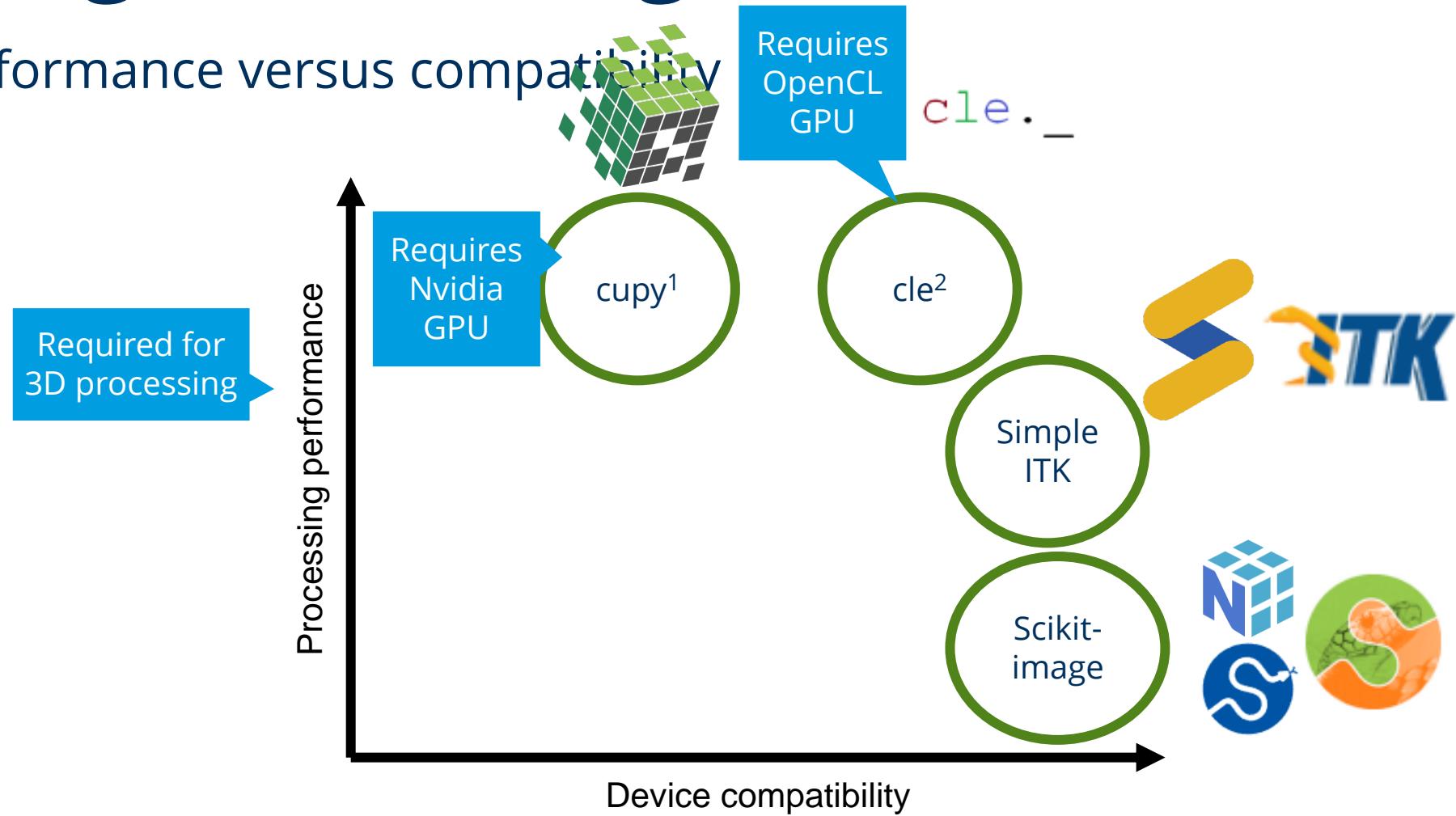
```
[6]: stackview.insight(sqdiff)
```

```
[6]:
```



# Image Processing CPU vs. GPU

Performance versus compatibility



# Tiled image processing

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# Optimal performance through smart memory management

The classical way of dealing with large image stacks...

Load data → Preprocessing

Load data

Load data

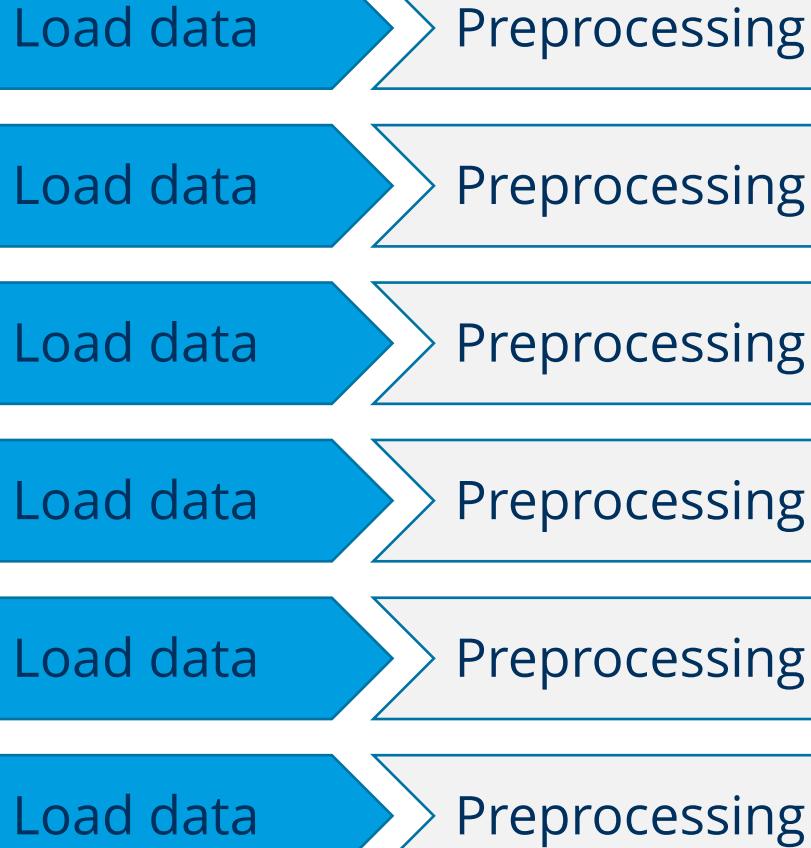
Load data

Load data

Load data

# Optimal performance through smart memory management

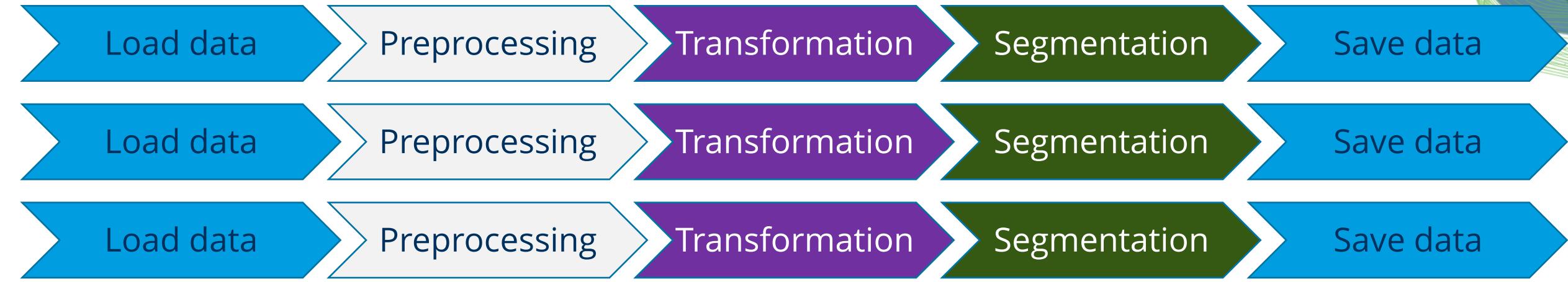
The classical way of dealing with large image stacks... is suboptimal



This strategy does not just take long; it also costs a lot of memory!

# Optimal performance through smart memory management

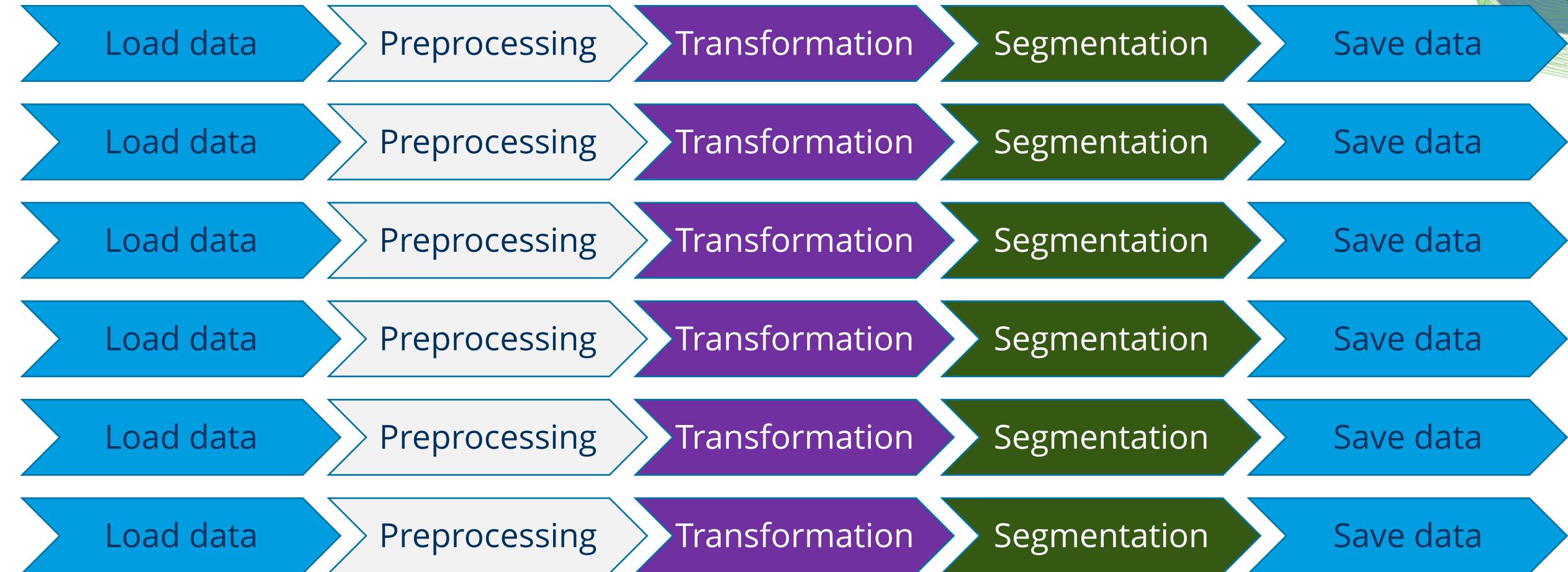
Processing time-point by time-point is more efficient!



This strategy also  
works tile-by-tile on  
large 3D stacks!

# Optimal performance through smart memory management

Even better: Distribute tasks between parallelized computation systems



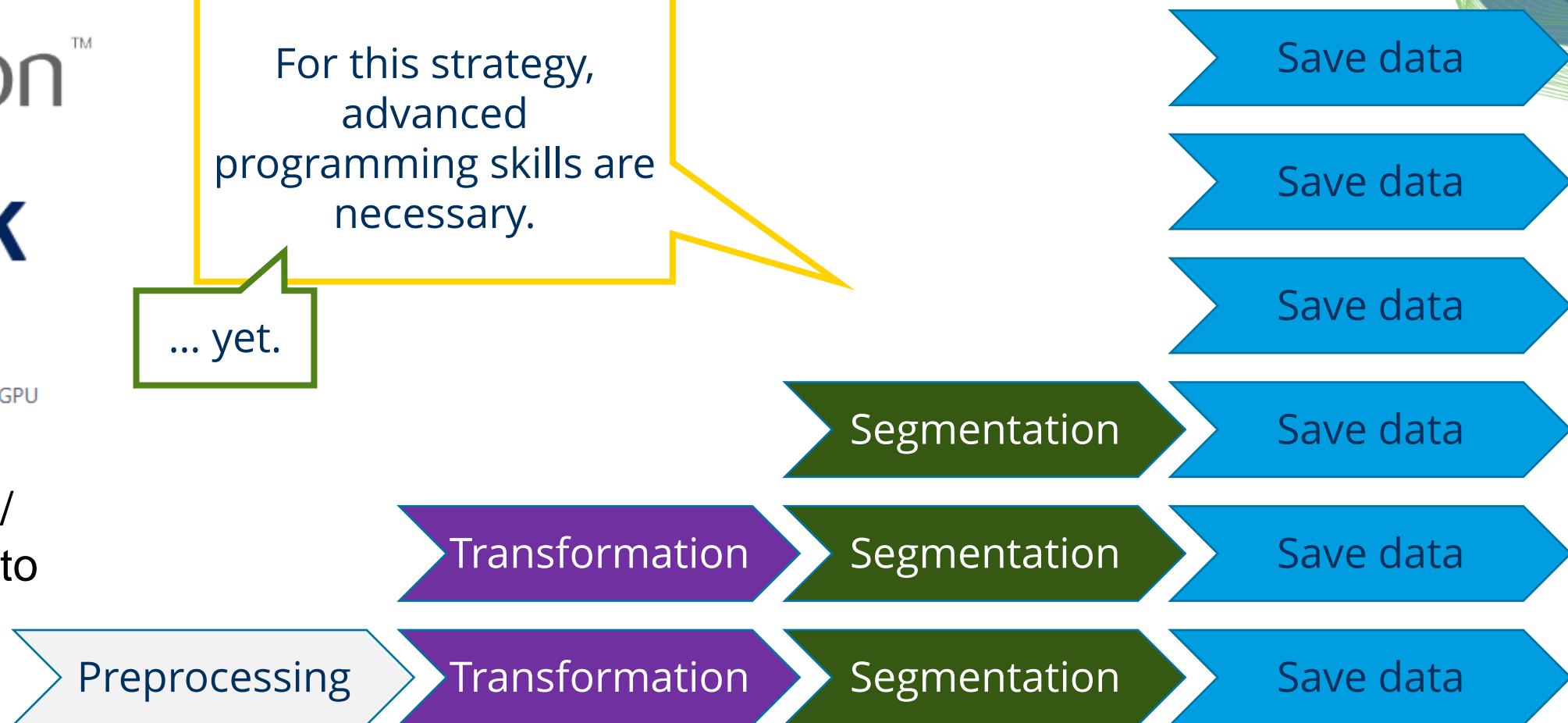
# Optimal performance through smart memory management

Even better: Distribute tasks between parallelized computation systems



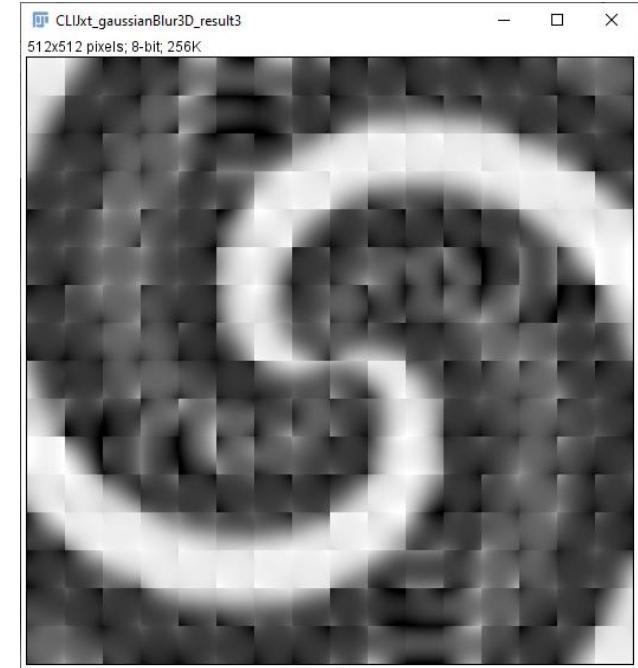
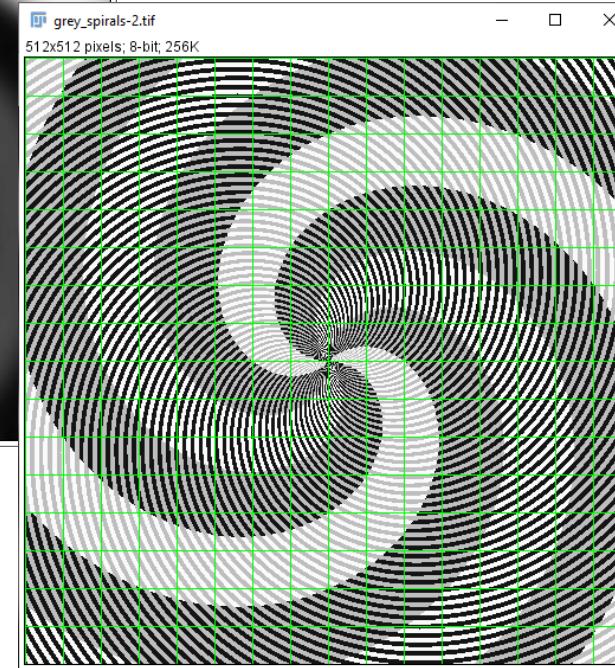
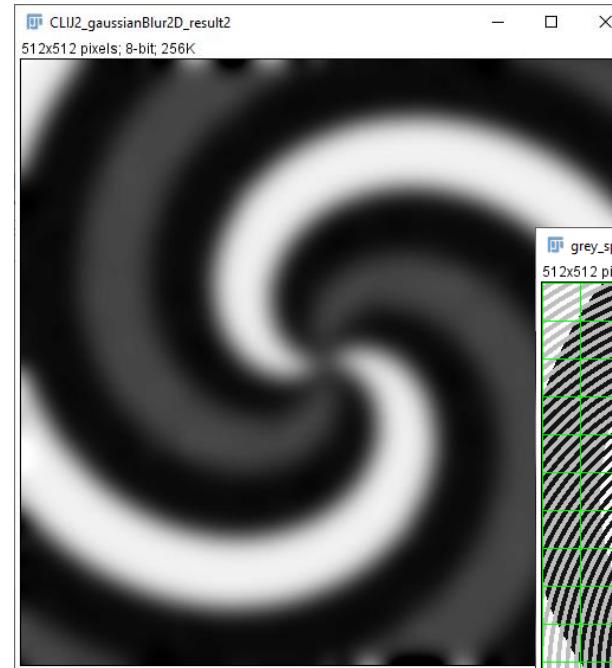
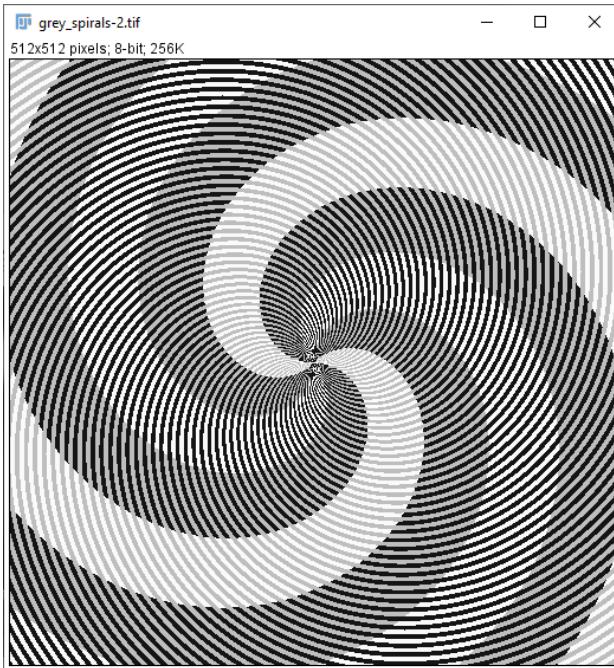
For this strategy,  
advanced  
programming skills are  
necessary.

... yet.



# Tiling

The **last** perimeter against big data



If the image is too large for the computer memory, image processing as a whole is *not* possible.

Processing tile-by-tile poses new challenges

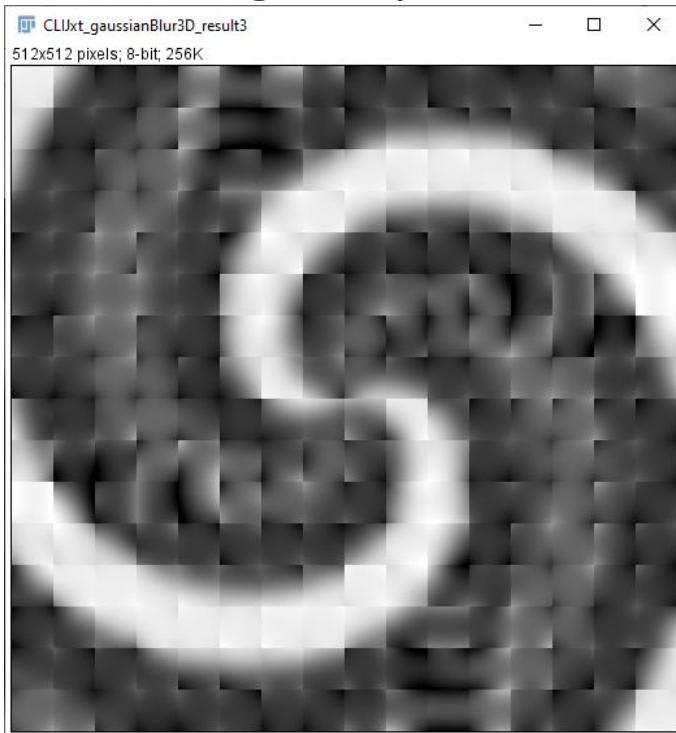
# Tiling

Example: Gaussian blur (sigma = 20)

Solution: Process with overlapping tiles (size + margin)

Optimal margin size  
depends on algorithm  
and its parameters

Margin: 0 pixels



Margin: 10 pixels



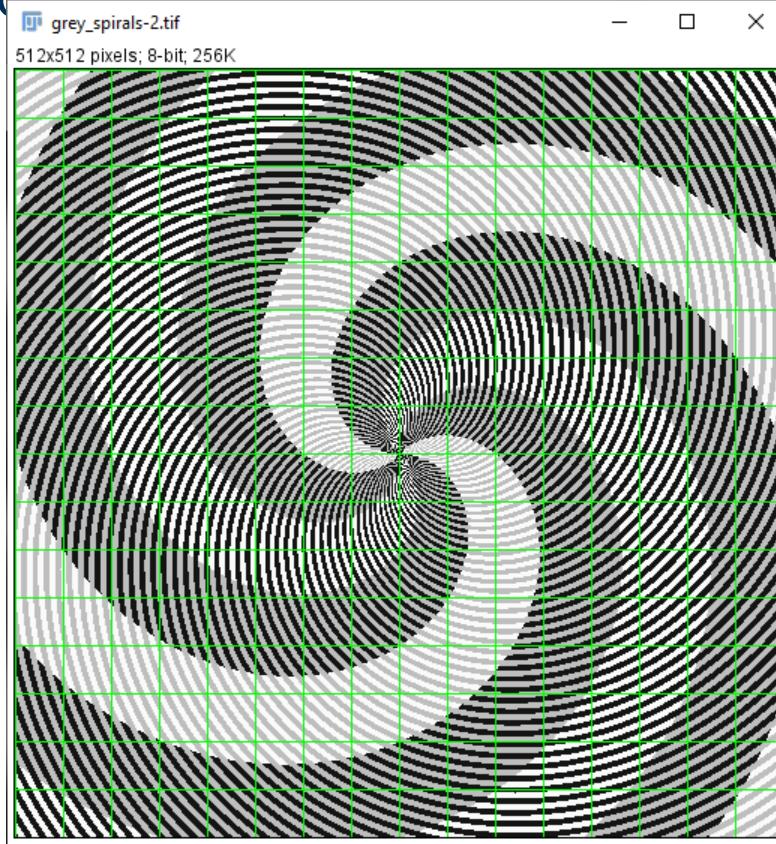
Margin: 20 pixels



# Tiling

Example: Gaussian blur (sigma = 20 pixels)

Solution: Process with overlapping tiles (size + margin)



Computation time depends on tile size and margin width

Margin: 20 pixels  
Size: 5x original

Margin: 10 pixels  
Size: 2.7x original

Tile  
32x32 pixels

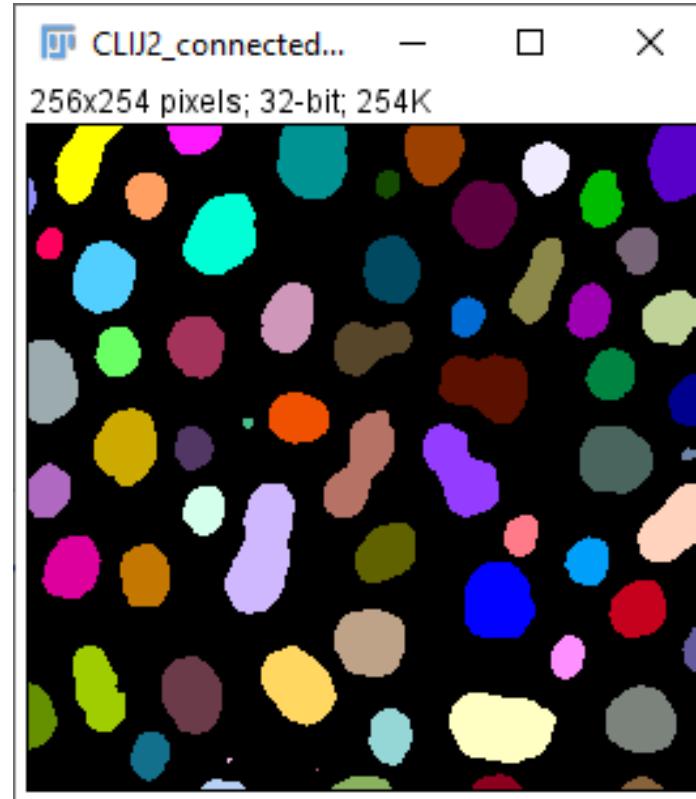
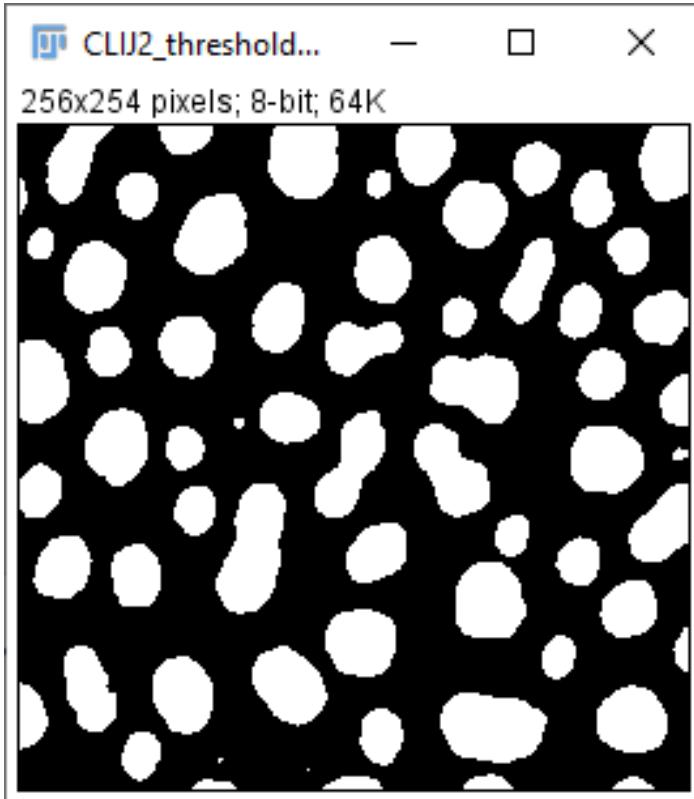
52x52 pixels

72x72 pixels

# Tiling

Some algorithms are hard to solve by processing tiles

Example: Connected component analysis



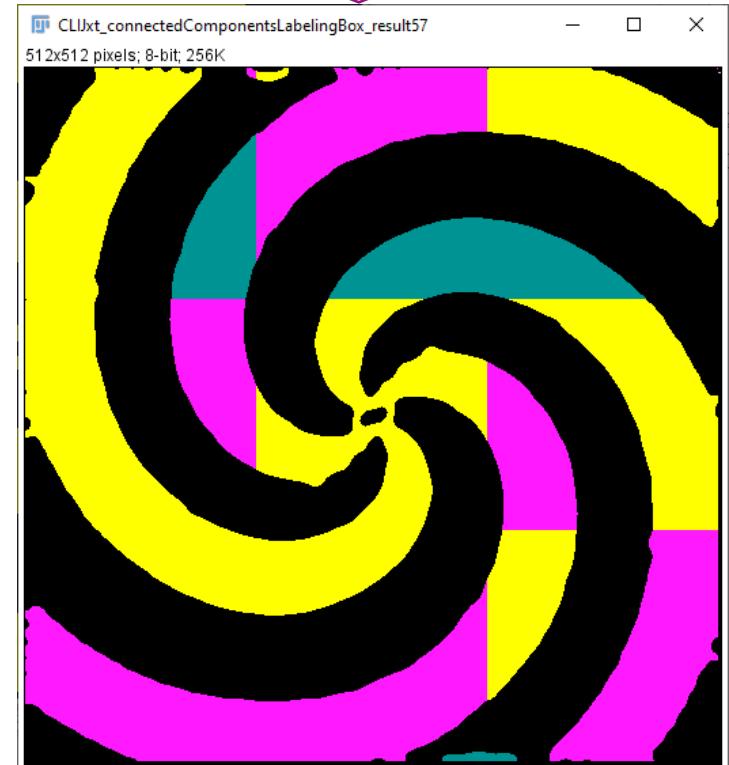
Checking which labels touch and combine them is feasible.

# Tiling

Some algorithms are hard to solve by processing tiles

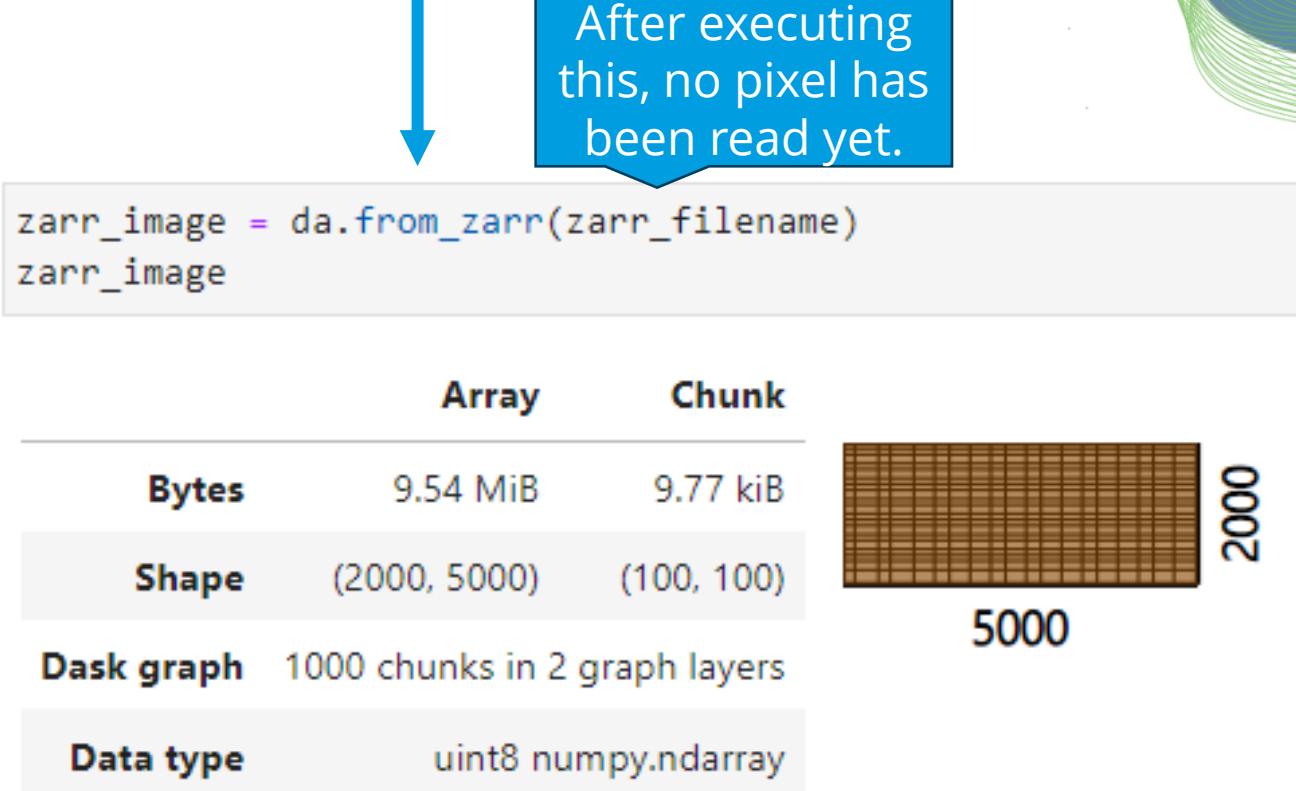
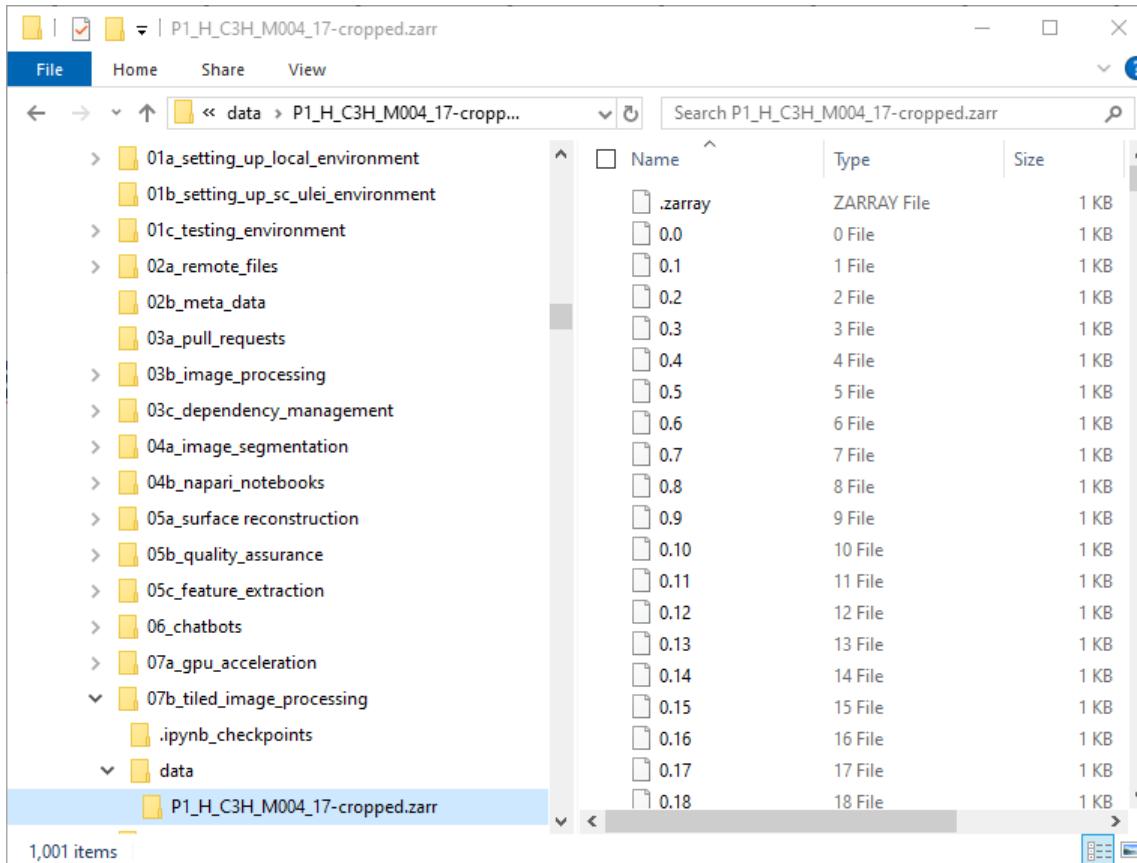
Example: Connected component analysis

There are algorithms for that, but hardly available tools.



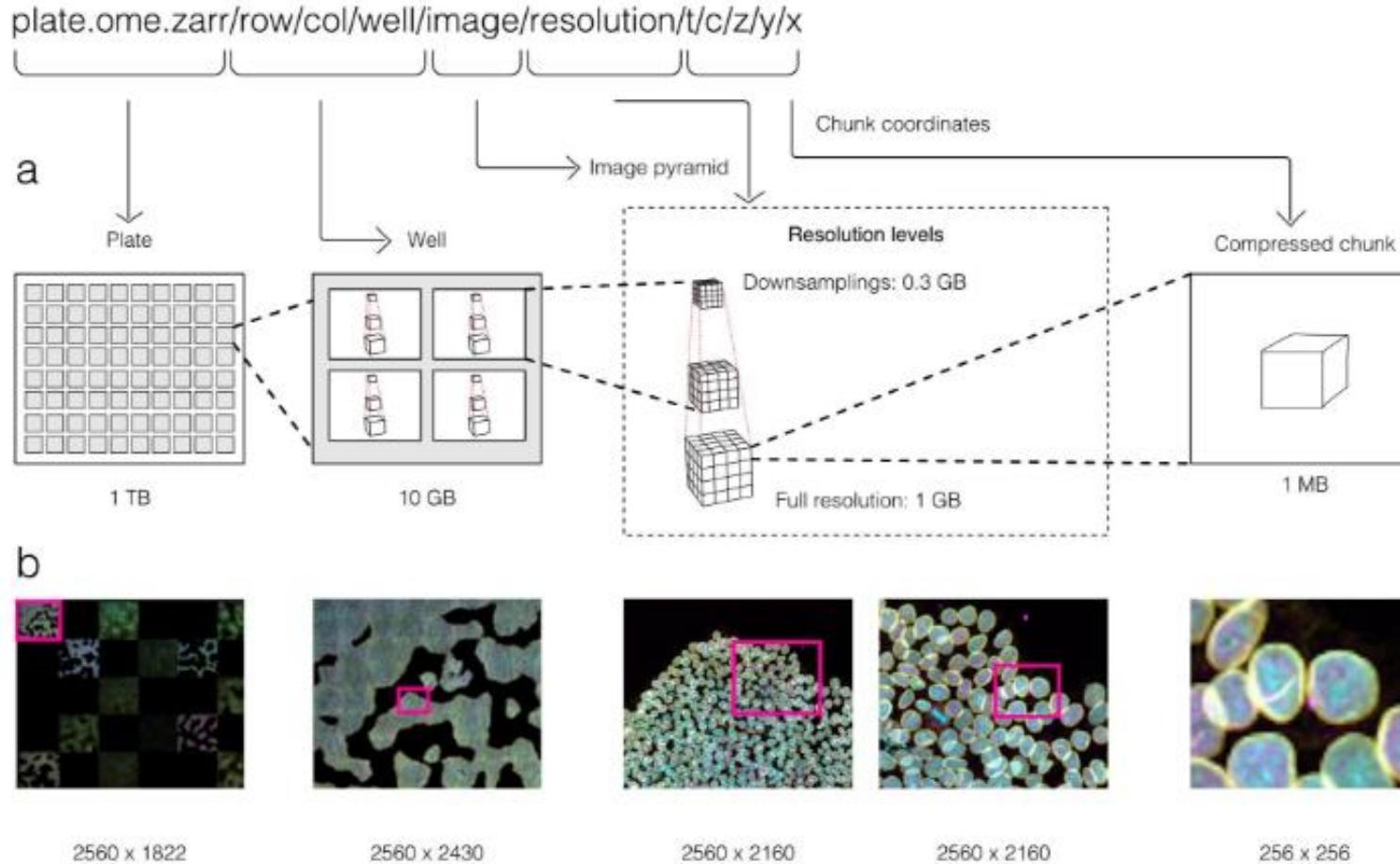
# Tiled image processing in Python

Key: tiled file formats, for parallel, distributed, lazy loading



# Tiled image processing in Python

Key: tiled file formats, for parallel, distributed, lazy loading



# Tiled image processing in Python

## Lazy processing

After executing  
this, no pixel has  
been read yet.

```
[5]: tile_map = da.map_blocks(count_nuclei, zarr_image)

tile_map
```

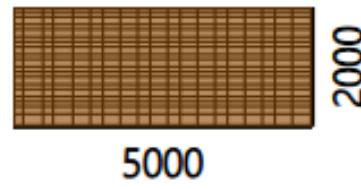
```
Processing image of size (0, 0)
(1, 1)
Processing image of size (1, 1)
(1, 1)
```

```
[5]:
```

	Array	Chunk
Bytes	76.29 MiB	78.12 kB
Shape	(2000, 5000)	(100, 100)

Dask graph 1000 chunks in 3 graph layers

Data type float64 numpy.ndarray



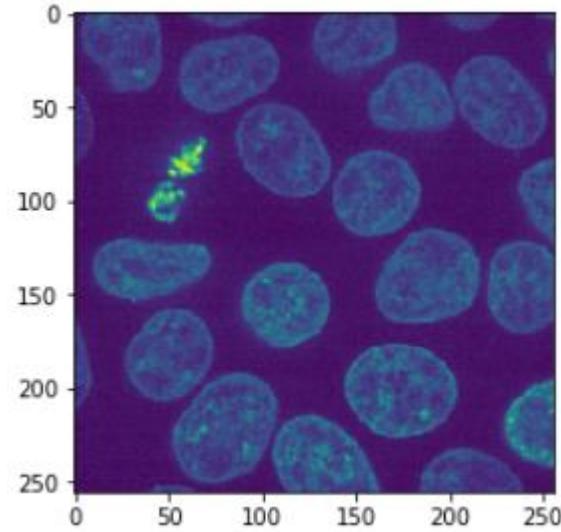
After that,  
results are  
available

```
result = tile_map.compute()
```

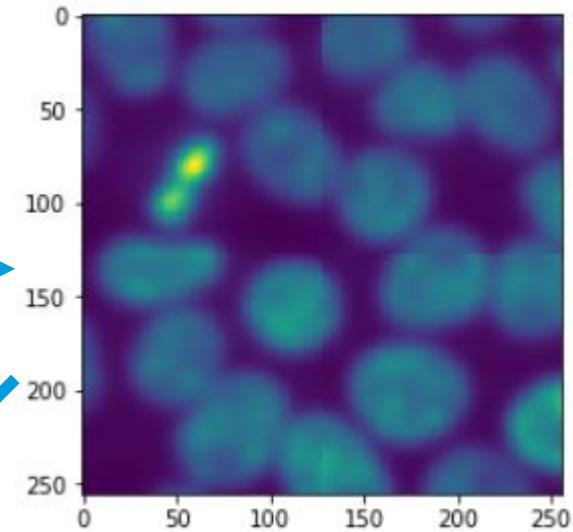
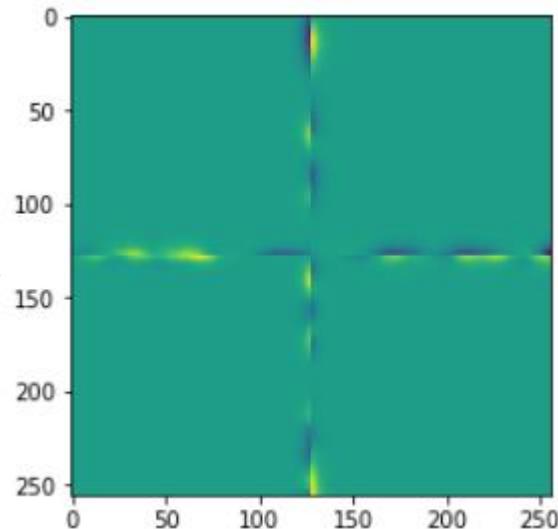
```
Processing image of size (100, 100)
```

# Tiling with/out overlap

Processing of images in tiles: artifacts ad tile borders

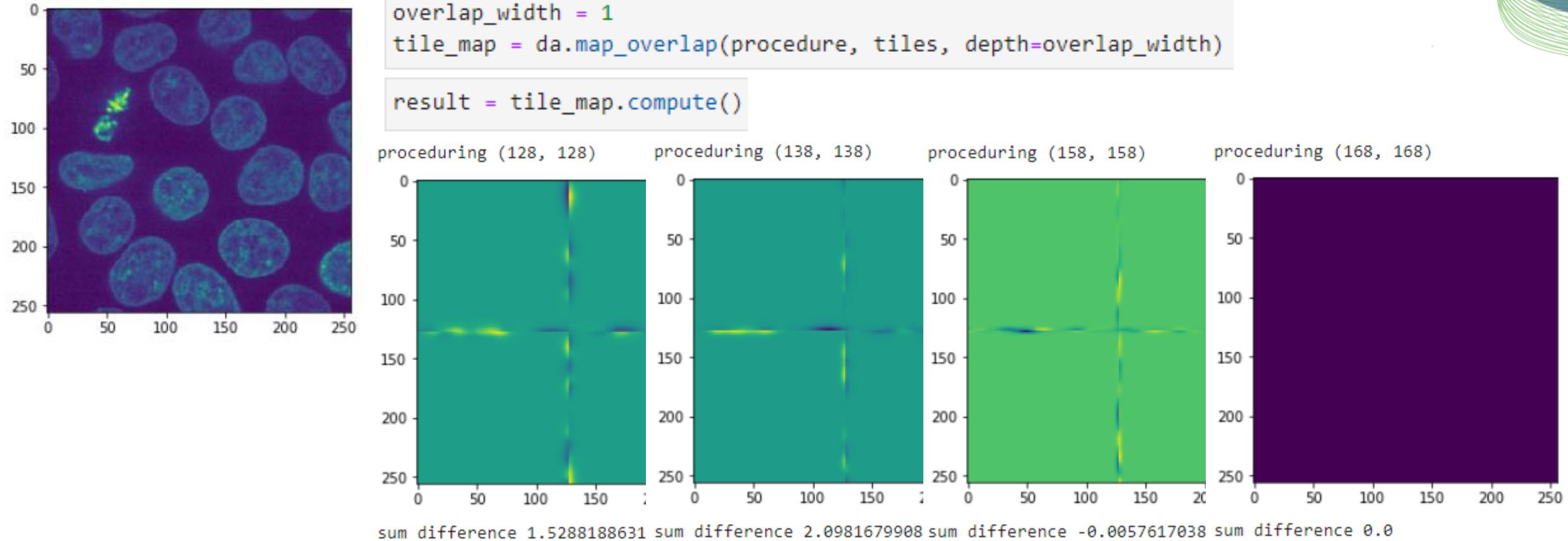


```
tile_map = da.map_blocks(procedure, tiles)  
  
result = tile_map.compute()
```



# Tiling with/out overlap

Processing of images in tiles: artifacts ad tile borders



# Methods for comparing measurement methods

Robert Haase

Using materials Reusing materials from Daniela Vorkel,  
Douglas G. Altman and J. Martin Bland

GEFÖRDERT VOM

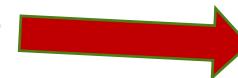


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Diese Maßnahme wird mitfinanziert durch Steuermittel auf der Grundlage des von den Abgeordneten des Sächsischen Landtags beschlossenen Haushaltes.

# Method comparison studies

## Scenario

- You work in a lab and try to improve procedures
- Chemical protocols
- Sample preparation
- Analysis protocols
  - Physical measurements
  - Image analysis



### Unpaired data

- Analyze independent sample sets
- Conclude about their similarity or relationship

### Inferential statistics

### Paired data

- The same dataset analyzed twice with different methods
- The same dataset analyzed twice with the same method

### Direct method comparison –descriptive statistics

# Method comparison studies

Martin Bland and Douglas Altman work on Method Comparison (excerpt)

The Statistician 32 (1983) 307-317  
© 1983 Institute of Statisticians

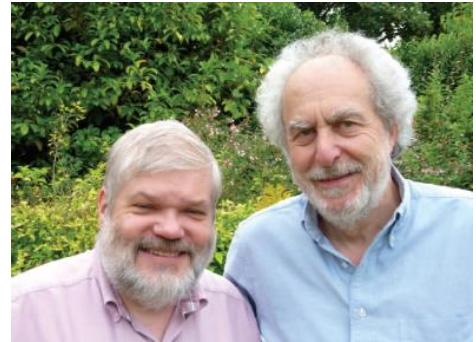
## Measurement in Medicine: the Analysis of Method Comparison Studies†

D. G. ALTMAN and J. M. BLAND‡

Division of Computing  
Research Centre, Wat...  
‡ Department of Clinical  
St George's Hospital L...



Copyright J. Martin Bland and Douglas G. Altman.



THE LANCET

Volume 327, Issue 8476, 8 February 1986, Pages 307-310

Measurement

## STATISTICAL METHODS FOR ASSESSING AGREEMENT BETWEEN TWO METHODS OF CLINICAL MEASUREMENT

J. Martin Bland <sup>a b</sup>, Douglas G. Altman <sup>a b</sup>

Show more ▾

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[https://doi.org/10.1016/S0140-6736\(86\)90837-8](https://doi.org/10.1016/S0140-6736(86)90837-8)

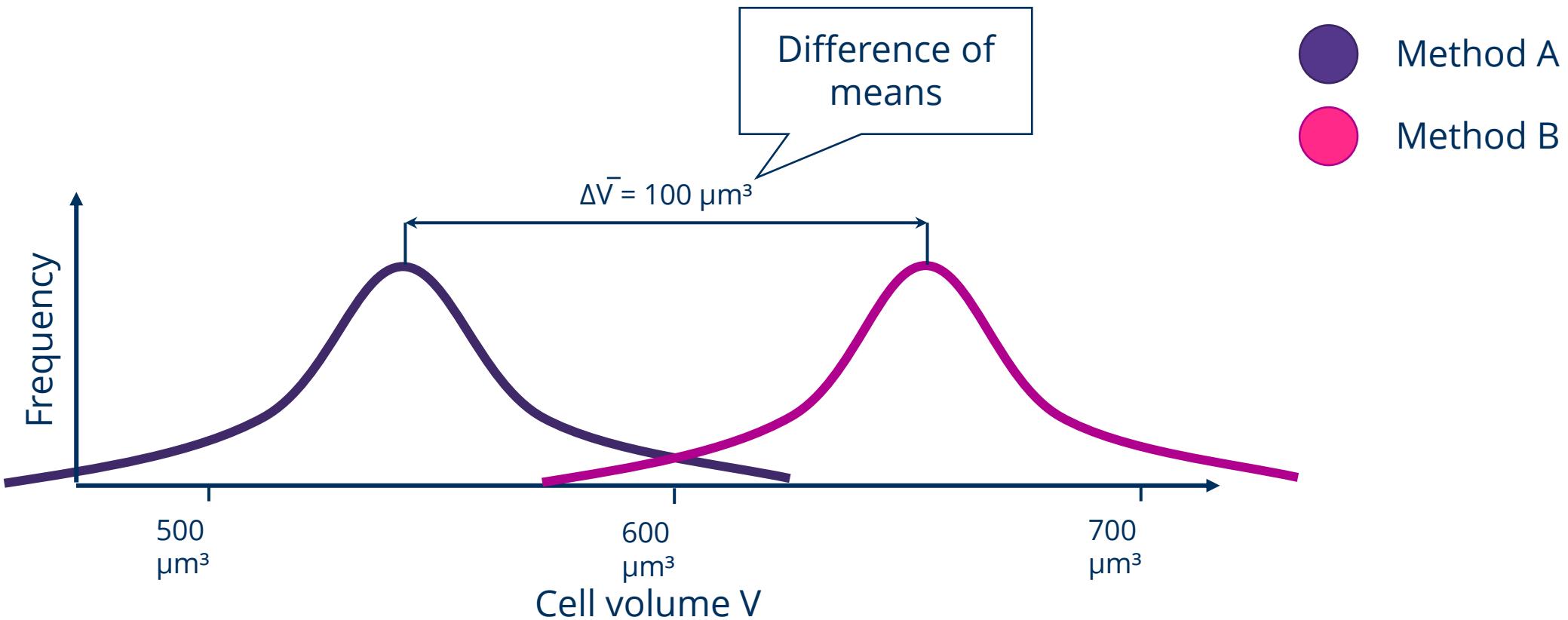


Cited by (40162)

Cited by (40162)

# Comparison of means

Comparing mean measurements appears reasonable on the first view.



# Comparison of means

Are two methods doing the same if their mean measurement is similar?

A	B
1	4
9	5

$$\begin{aligned}\text{Mean}(A) &= 5.0 \\ \text{Mean}(B) &= 5.0\end{aligned}$$

What if mean values were  
“very” different?

7	5
---	---

1	7
---	---

2	4
---	---

8	5
---	---

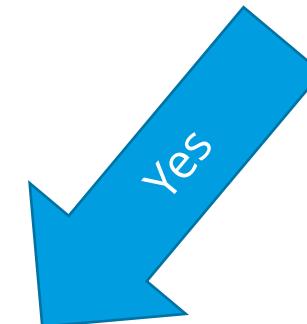
9	4
---	---

2	6
---	---

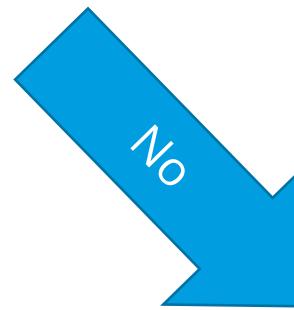
1	6
---	---

7	5
---	---

8	4
---	---



Method B cannot  
replace method A



Similar means is a  
necessary condition,  
but is it sufficient?

# Comparison of means

Are two methods doing the same if their mean measurement is similar?

A	B
1	4
9	5

7	5
1	7

2	4
8	5

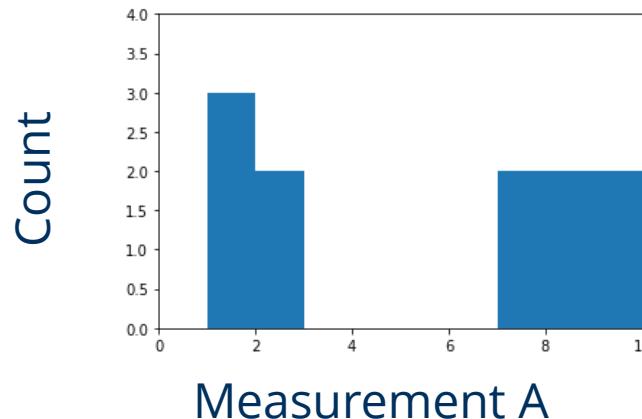
9	4
2	6

1	6
7	5

8	4
7	5

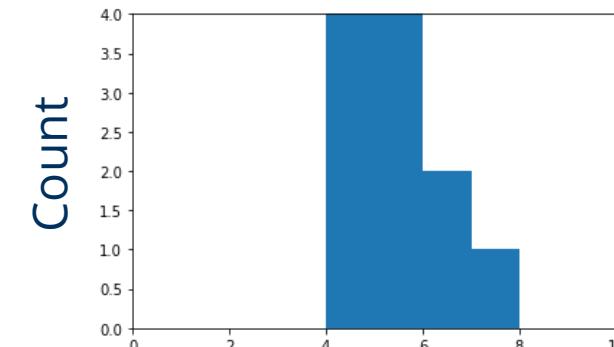
$$\begin{aligned}\text{Mean}(A) &= 5.0 \\ \text{Mean}(B) &= 5.0\end{aligned}$$

- Draw histograms! How can two methods do the same if histograms from their measurements are different?



Measurement A

Similar means is a necessary condition, but it is NOT sufficient!



Measurement B

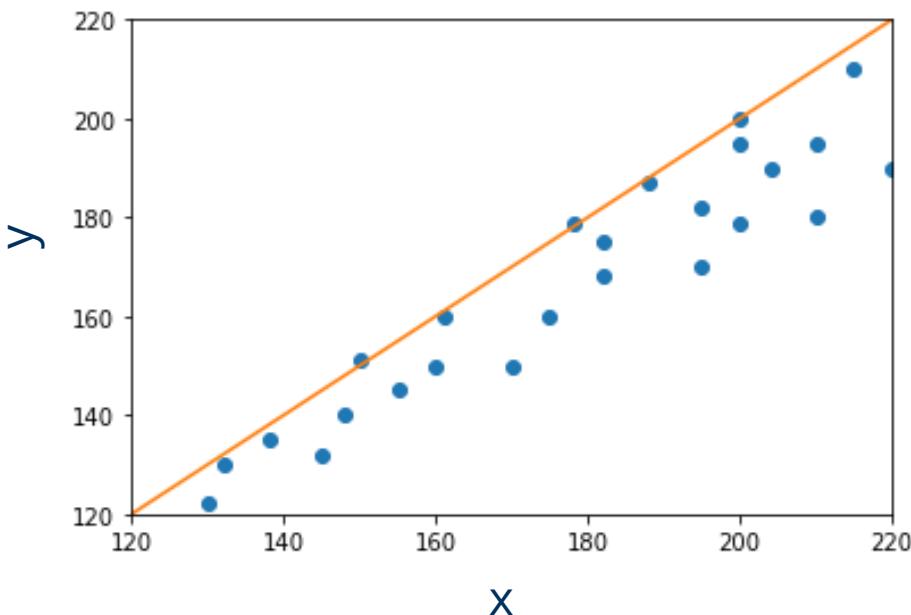
The scientific method: Show that a method doesn't work with *just one* example. And you have *proven* that the method doesn't work in general.

# Correlation

Are two methods doing the same if they correlate?

- Correlation: Any kind of relationship.
- Measurable; e.g. using Pearson's Correlation Coefficient  $r$  enumerated linear correlation.

Comparison of two methods of measuring systolic blood pressure (Data taken from <sup>1</sup>)



Expectation E

Mean average  $\mu$

$$r(X, Y) = \frac{E(X - \mu_X)(Y - \mu_Y)}{\sigma_X \sigma_Y}$$

Standard deviation  $\sigma$

In practice  $E$  is the weighted sum:

$$r(X, Y) = \frac{\sum_{x \in X, y \in Y} \frac{(x - \mu_X)(y - \mu_Y)}{n}}{\sigma_X \sigma_Y}$$

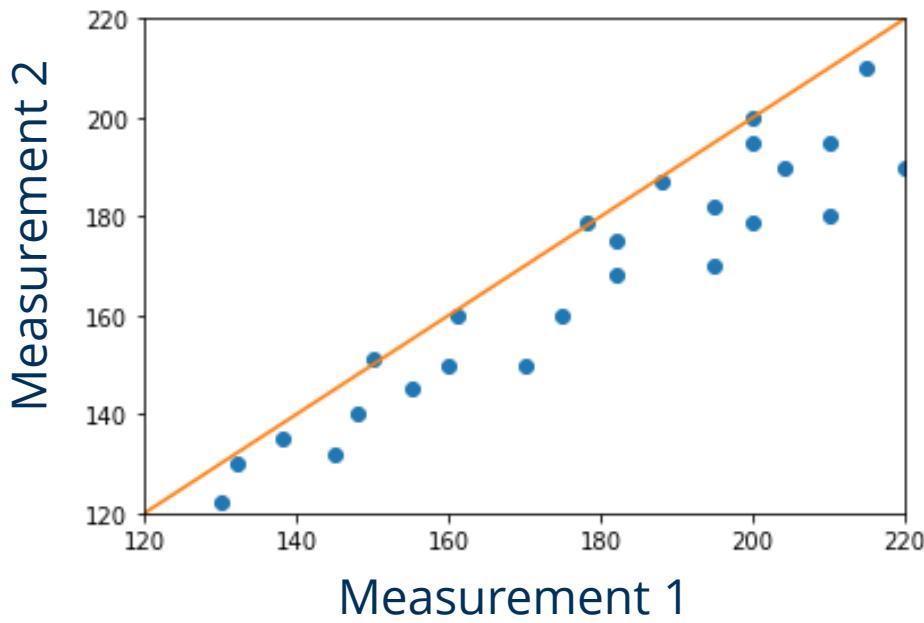
Number of measurements  $n$

# Correlation

Are two methods doing the same if they correlate?

- Correlation: Any kind of relationship.
- Measurable; e.g. using Pearson's Correlation Coefficient  $r$  enumerated linear correlation.

Comparison of two methods of measuring systolic blood pressure (Data taken from <sup>1</sup>)

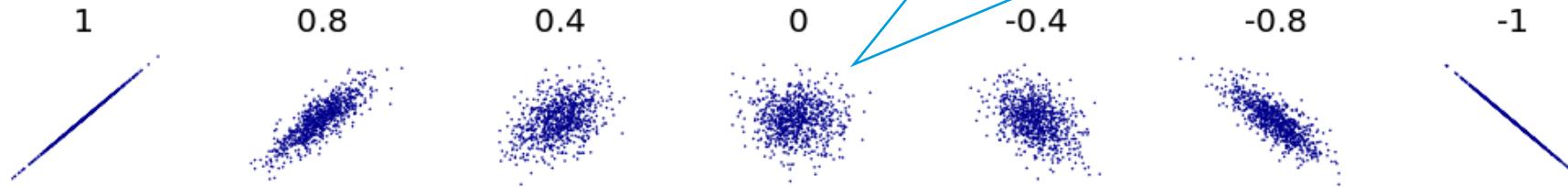


$$r(X, Y) = \frac{\sum_{x \in X, y \in Y} \frac{(x - \mu_x)(y - \mu_y)}{n}}{\sigma_x \sigma_y} = 0.94$$

# Correlation: Pearson's $r$

Pearson's  $r$  lies between -1 and 1

- 1: Positive linear correlation
- 0: No linear correlation
- -1: Negative linear correlation

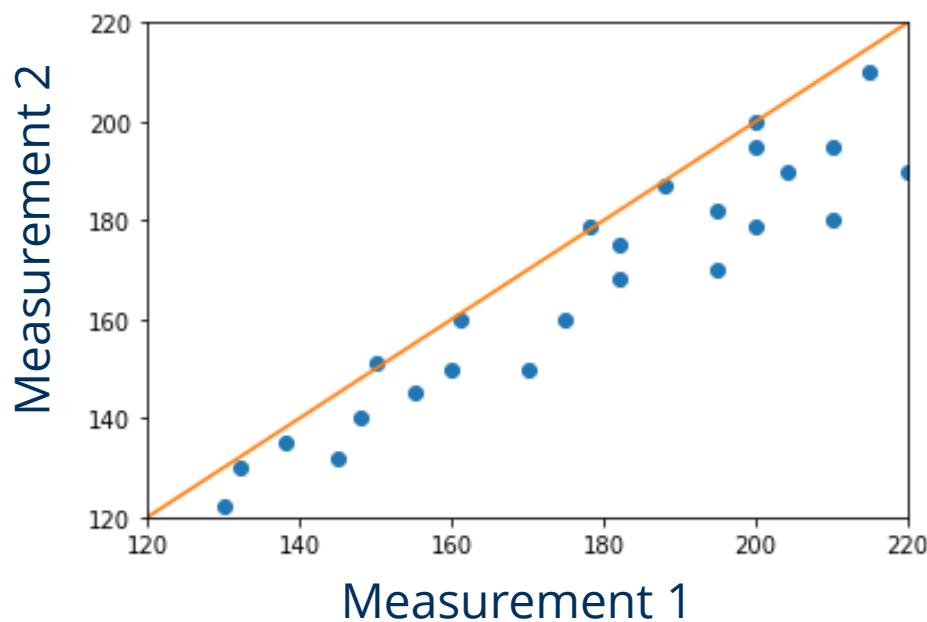


# Correlation

Are two methods doing the same if they correlate?

- Correlation: Any kind of relationship.
- Measurable; e.g. using Pearson's Correlation Coefficient  $r$  enumerated linear correlation.

Comparison of two methods of measuring systolic blood pressure (Data taken from <sup>1</sup>)



Measurement 1 is almost always larger than measurement 2

The scientific method: Show that a method doesn't work with *just one* example. And you have *proven* that the method doesn't work in general.

"Positive linear correlation"

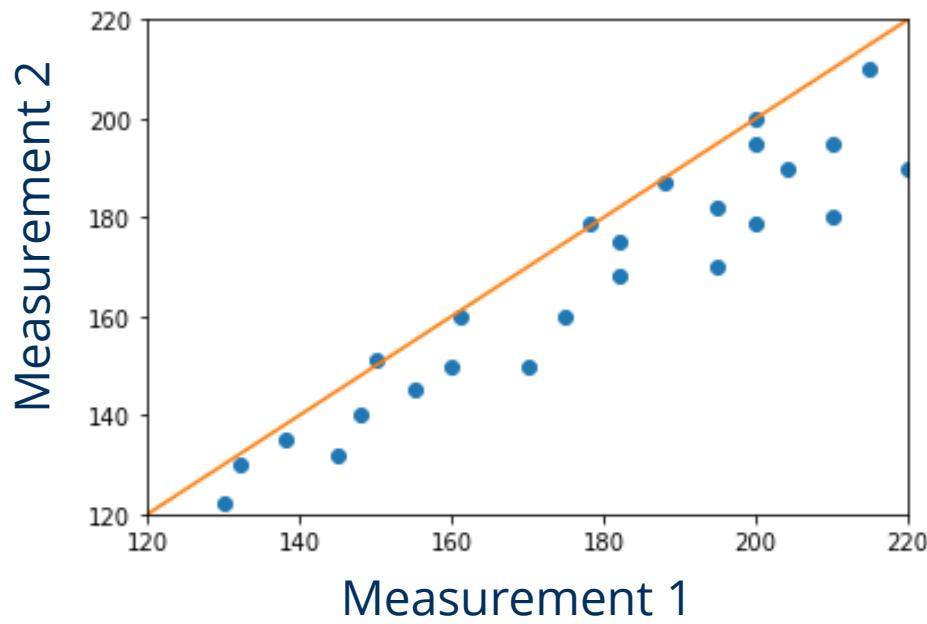
$$r(X, Y) = \frac{\sum_{x \in X, y \in Y} \frac{(x - \mu_x)(y - \mu_y)}{n}}{\sigma_x \sigma_y} = 0.94$$

# Correlation

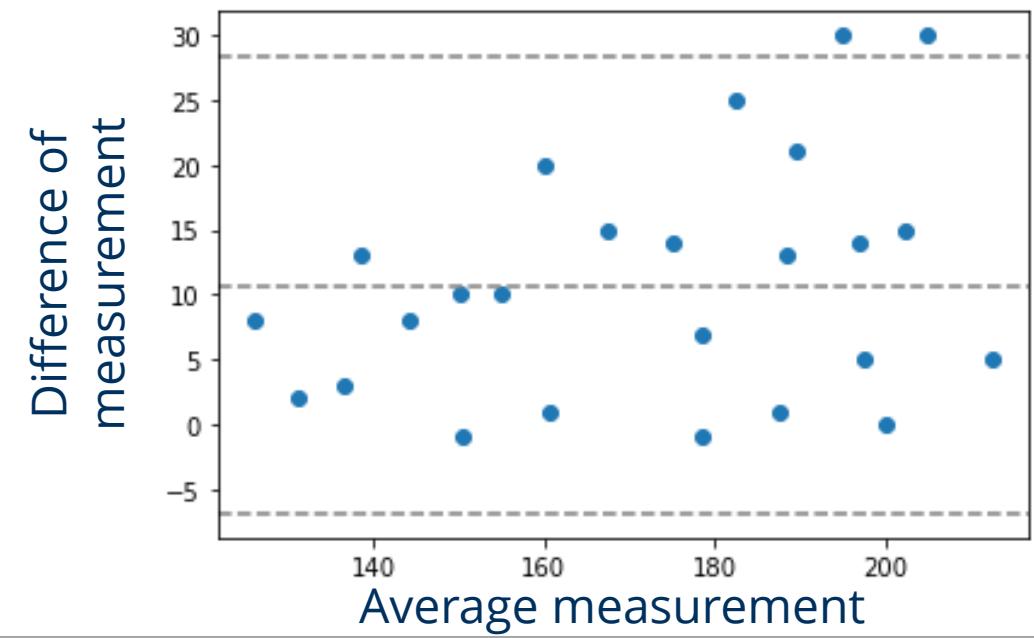
In order to evaluate the difference between two methods, you should visualize them first.

*"The purpose of computing is insight, not numbers." , Richard Hamming*

Scatter plot

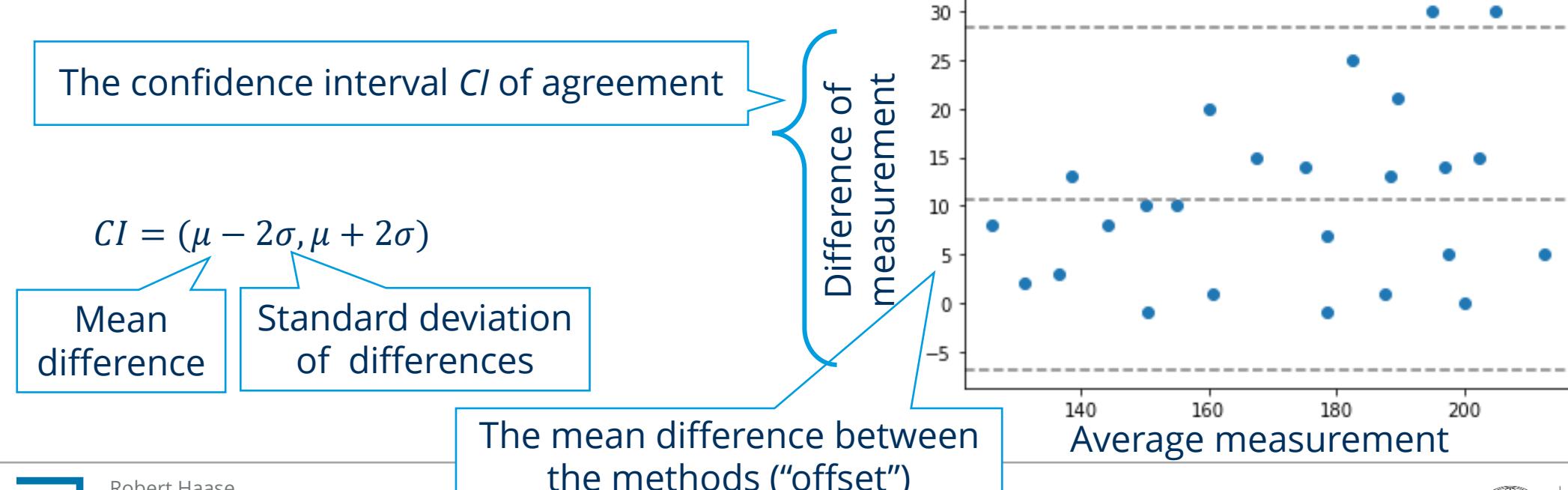


Bland-Altman plot



# The confidence interval

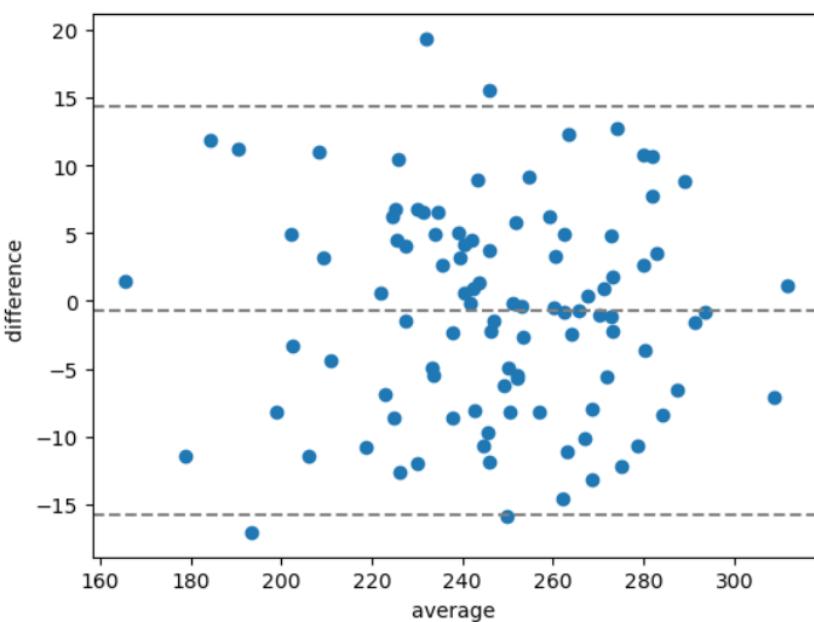
"The British Standards Institution (1979) define a coefficient of repeatability as 'the value below which the difference between two single test results ... may be expected to lie with a specified probability; in the absence of other indications, the probability is 95 per cent.'"<sup>1</sup>



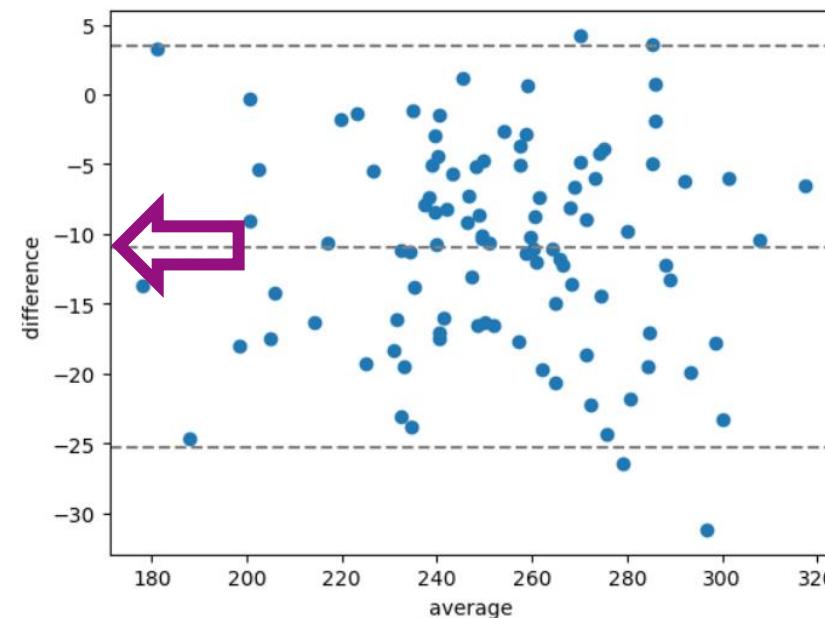
# Bland-Altman plots in practice

Depending on the shape of the point-cloud, different systematic bias might be present.

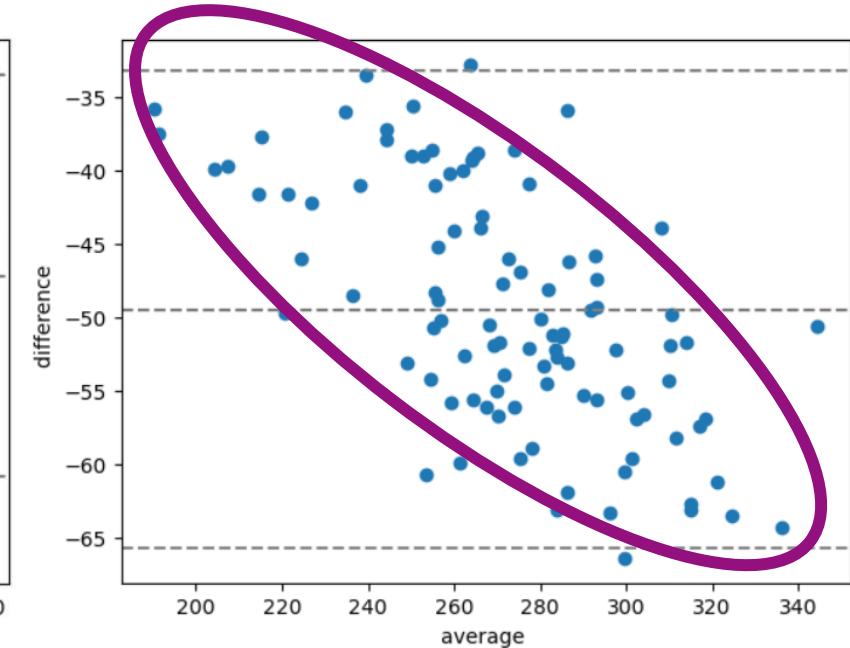
Agreement with a given random error



Absolute error or “offset”

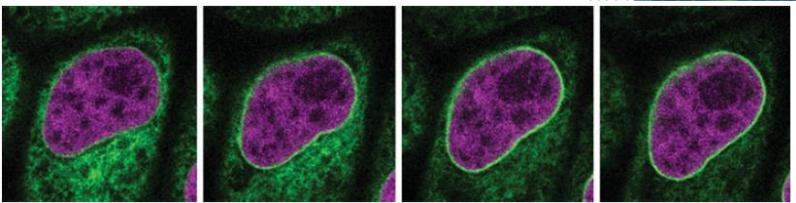


Relative error



# Bland-Altman plots in practice

Comparison: ImageJ versus GPU-accelerated script to measure intensity in the nuclear envelope of a nucleus

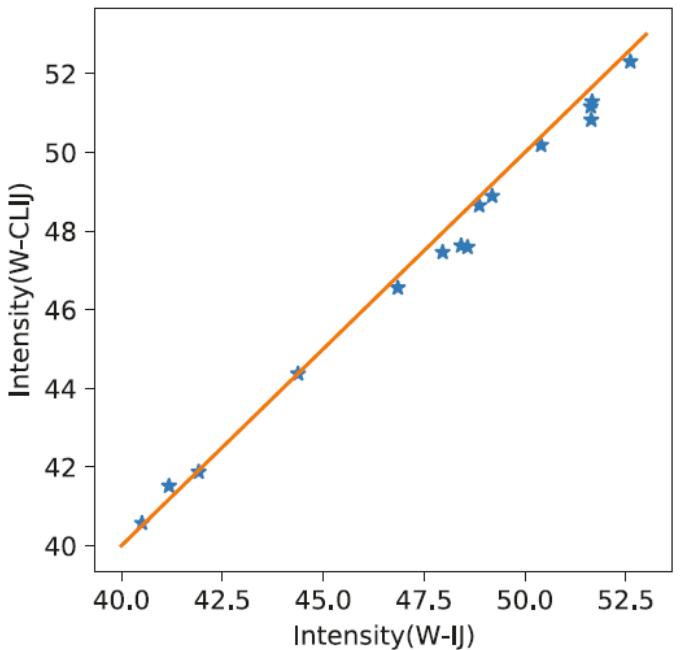


A screenshot of a chapter page from the book "Bioimage Data Analysis Workflows – Advanced Components and Methods". The page title is "GPU-Accelerating ImageJ Macro Image Processing Workflows Using CLIJ". It includes author information (Daniela Vorkel & Robert Haase), access details (Open Access, First Online: 29 September 2022), and citation information (2338 Accesses, 19 Altmetric). The page is part of the "Learning Materials in Biosciences" book series (LMB).

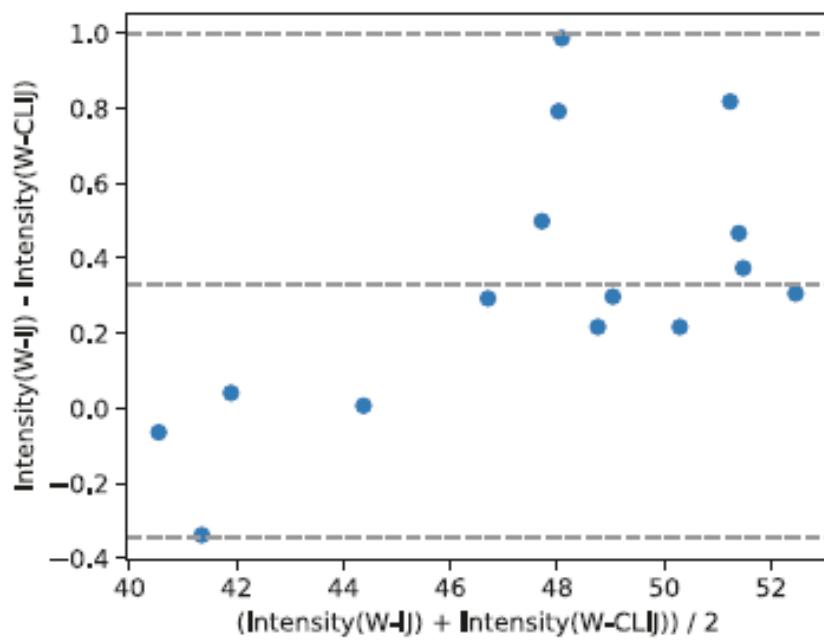


Dani Vorkel  
(Myers lab)  
@happifocus

## Scatter plot



## Bland-Altman plot



# Exercises

## Robert Haase

Funded by



Bundesministerium  
für Bildung  
und Forschung



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der Grundlage des von den Abgeordneten des Sächsischen  
Landtags beschlossenen Haushaltes.

# Exercise: GPU-accelerated image processing

Compare CPU processing speed with a GPU

The image shows two side-by-side screenshots of a Jupyter Notebook environment.

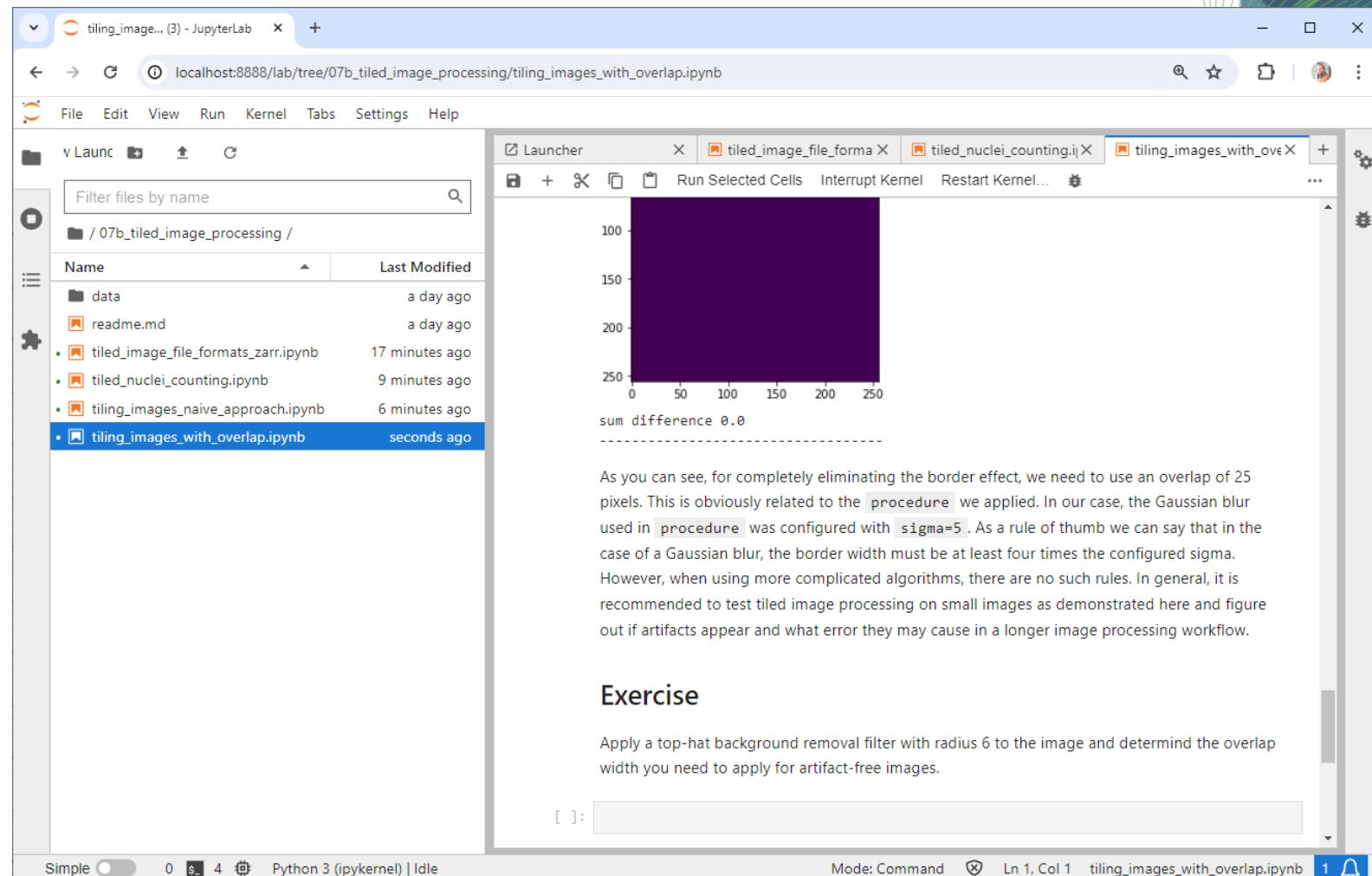
**Left Screenshot:** A Jupyter Notebook interface with a sidebar showing a file tree under the path `/07a_gpu_acceleration/`. The files listed include `10_cupy_basics.ipynb`, `11_cle_basics.ipynb`, `20_cupy_dropout_replacement.ipynb`, `30_cupy_filtering.ipynb`, `40_cupy_custom_kernels.ipynb`, `41_cle_custom_kernel_execution.ipynb`, `60_benchmark_affine_transforms.ipynb` (which is currently selected), `maximum_z_projection.cl`, and `readme.md`. The main notebook area displays an "Exercise" section with the following text:

Run the benchmark using different input sizes. Make the input image much smaller e.g. by skipping to every 2,3,4th voxel in X,Y and Z (reducing the image size by factor 8, 27, 64). In which case does it make sense to use a GPU and in which not?

**Right Screenshot:** A "Resource selection" dialog box. It includes fields for "Memory" (8 GB), "Number of CPUs" (4), "Partition" (clara), and a "GPU" dropdown menu. The "GPU" dropdown is currently set to "No GPU" and contains options: "No GPU", "No GPU", "RTX 2080Ti", and "Tesla V100". A red border highlights the "No GPU" option. At the bottom right of the dialog is a "Start" button.

# Exercise: Tiled image processing

Apply background-removal to an image in tiles. Determine the overlap width that's necessary to have artifact-free results.



# Exercise: Bland-Altman plots

Compare two measurement libraries: scikit-image versus SimpleITK

