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Run-Length based mathematical morphology for processing of large 3D images of wheat grains

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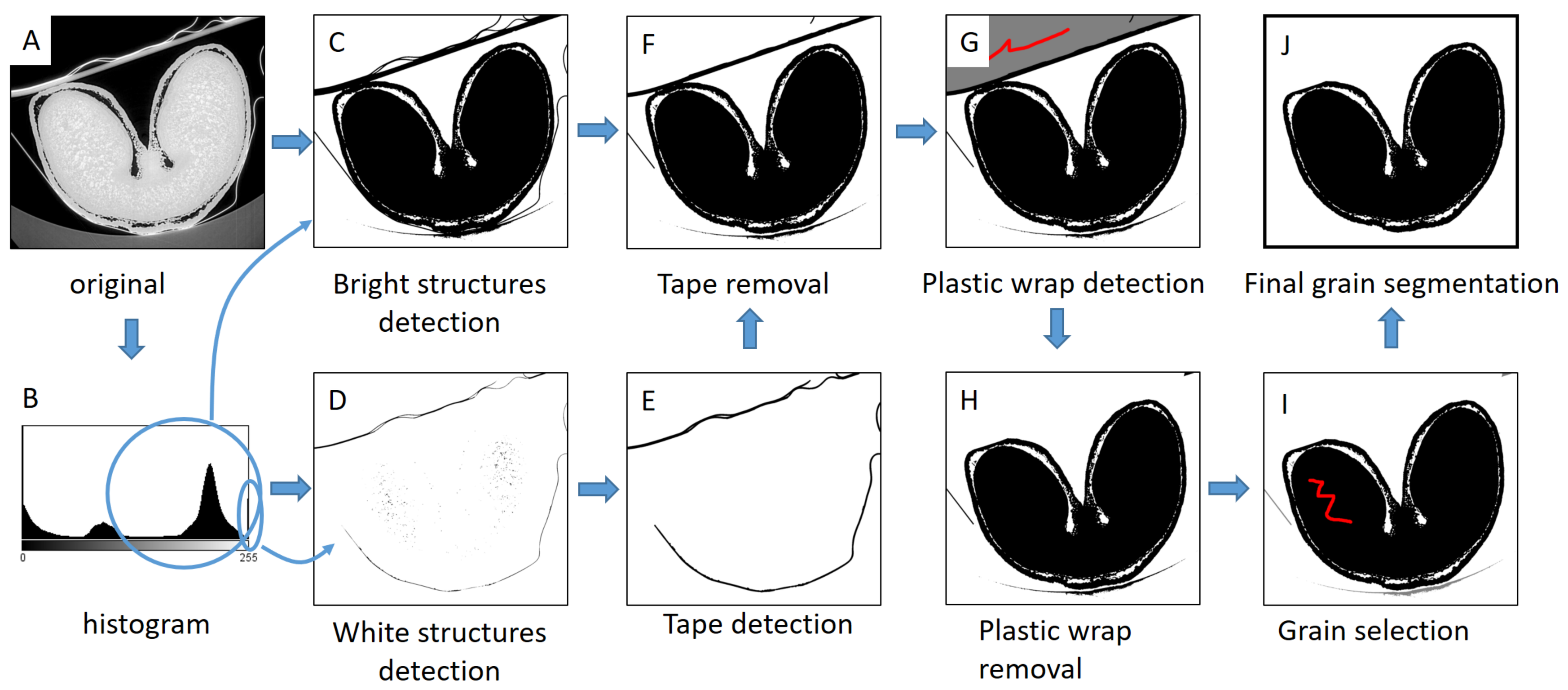
Context

Wheat is an essential agronomic resource for human and animal nutrition. Increasing grain weight and size could improve yields.

In order to understand the phenomena that impact its growth, it is necessary to be able to quantify the changes in size and shape of the grain during its development.

2. Image processing workflow

The segmentation of the grain region within 3D images involved the combination of several operators: thresholds, morphological dilations and erosions with spherical structuring elements, and morphological reconstructions [1]. The size of the images and of the dilation radius resulted in large computation times (several hours per image).

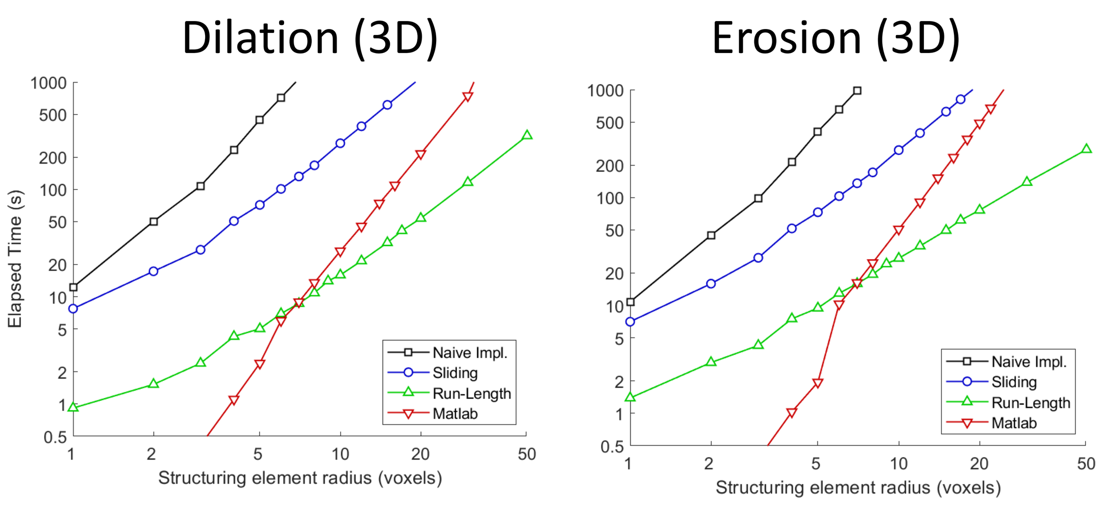


4. Experimental results

Implementations were applied on synthetic and real large 3D binary images, and compared with other approaches (naïve implementation, sliding structuring element [7]). Timing were also compared to that of Matlab implementation.

A large reduction of computation time was obtained for size of the structuring element equal to 10 voxels.

Morphological reconstruction was also noticeably improved.



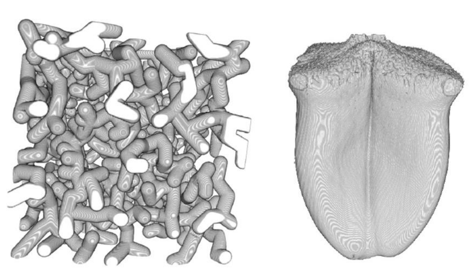


Image		Hybrid		Run-Length		Matlab	
Name	Size (MB)	C=6	C=26	C=6	C=26	C=6	C=26
Spanning_Tree_01	0.95	0.56	0.67	**0.03**	**0.05**	0.21	0.29
Spanning_Tree_02	7.63	0.74	4.11	**0.16**	**0.23**	1.13	1.68
Spanning_Tree_05	120.2	9.78	60.5	**0.90**	**1.10**	17.42	25.9
Spanning_Tree_10	953.6	103.1	470.3	**3.71**	**4.57**	141.8	210.5
L_025_2	1028.1	52.5	166.5	**1.7**	**2.9**	140.3	200.1
L_100_1	2176.2	147.4	396.3	**24.3**	**43.7**	292.3	425.8

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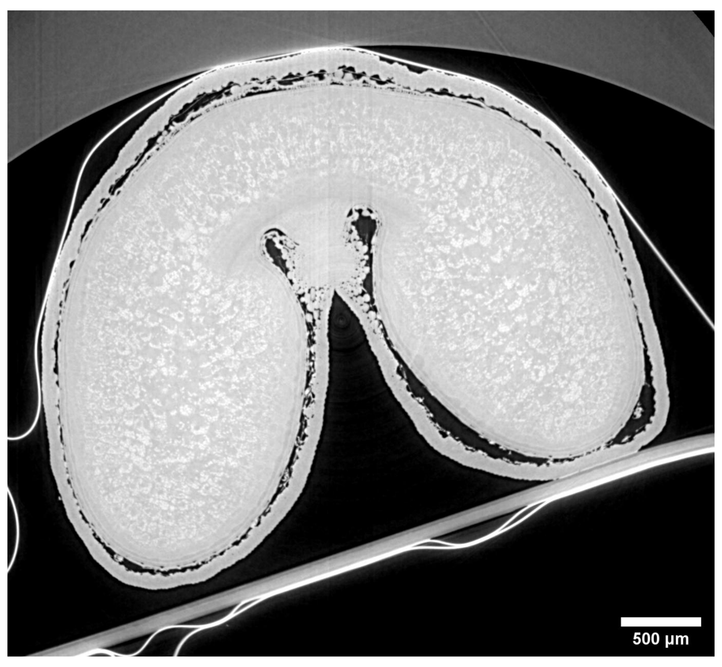
1. Imaging



Phase-contrast X-ray tomography imaging obtained on the Psiché beamline of SOLEIL synchrotron facility provided 3D images with increased resolution and contrast compared to that obtained with laboratory µ-CT devices.

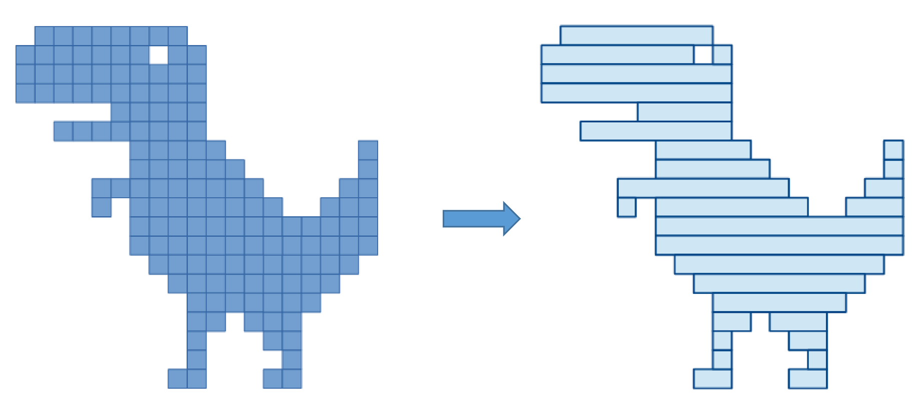
3D images of whole grains at various development stages could be obtained. The overall shape of the grain was clearly visible. Different regions (endosperm, embryo, external regions) could be distinguished in the grain. The size of the resulting files was often several GB, complicating the processing and visualization of images [1].

3. Run length encoding of morphological operators

Run length encoding is a representation of binary image data that is very efficient for accelerating and reducing the memory footprint of morphological operations on binary images.

Three-dimensional images can be defined as a union of disjoint (3d) runs. Runs are defined as $R=<l_x,r_x,y,z>$ where l_x and r_x are the x-coordinates of the leftmost and rightmost voxel within the run, and y and z are coordinates of the run.

Dilation, erosion and morphological reconstructions can be efficiently computed using run-length representation [2,3,4,5].



$$X = \bigcup_x R_x$$

$$B = \bigcup_b R_b$$

$$\delta_B(X) = \bigcup_x \bigcup_b (\delta_{R_b} R_x)$$

$$\varepsilon_B(X) = \bigcap_b \bigcup_x (\varepsilon_{R_b} R_x)$$

Algorithms were implemented with the java language and incorporated into in-house developed library to facilitate future integration within existing software (ImageJ/Fiji [6]). Sources were made freely available (https://github.com/SciCompJ/cs4j).

Conclusions and perspectives

3D segmentations and visualization of whole grains could be obtained, making it possible to investigate changes in its morphology during development.

Current work concern the enhancement of the implementation (in particular parallelization), comparison with more recent ones, and integration with other algorithms (e.g. connected components labelling).

In the longer term, it would be interesting to manage label images, as well as to inter-operate with in-file representation for large image data (BigTiff, HDF5, zarr…).

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