

Who are you? Identifying cell types in a mixed culture using Knime Analytics Platform

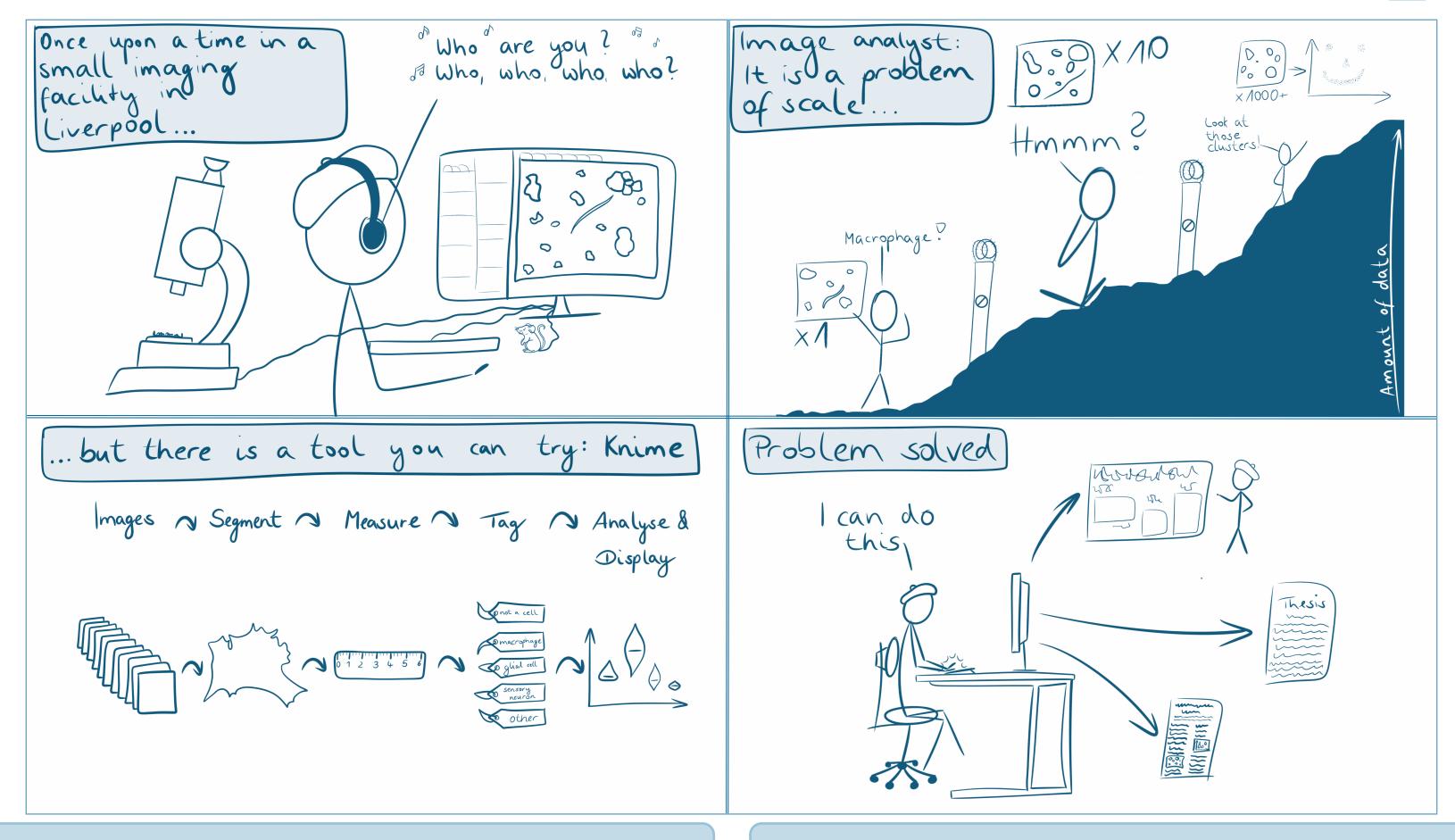


Marie Held¹, Richard Berwick², Tobias Zech¹, Andreas Goebel²

Poster #21

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Background

- Mixed cell populations represent physiological systems better than single populations.
- Identifying cell types in mixed populations is difficult.

Aim

- Identify cells and assign cell types.
- How much IgG does each cell type bind?

Knime nodes used in workflow

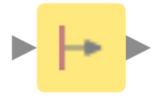


Image reader (Table): Reads images from various file formats supported by the Bio-Formats library and imports them to the KNIME-internal image format.

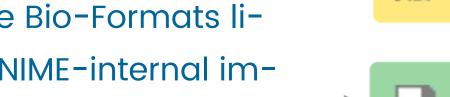




Image Segment Features: Calculate features of an image under consideration of a given labelling.

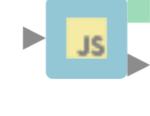




Rule Engine: Matches each row of the input table to a list of user-defined rules.



Cell Segmentation with Cellpose: apply one of the pretrained models ('nuclei' or 'cyto') on the input image.



taneously across various categories or groupmemberships.

Violin Plot (Plotly): Visualise multiple plots simul-



Labeling to image: Converts segmentations in a (set of) column(s) to images.

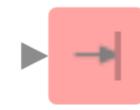


Image Writer: Write image to formats support by scifio library.

Feature Calculator (BETA): Calculate numerical features of an image, segmentations or segment on an image.



CSV Writer: Write string/numerical data to file.

Results -2M large glial/other cell or dim macrophage glial/other cell sensory neuron Cell classification

Acknowledgements

- NEUBIAS Academy @ Home: Introduction to KNIME for Image Processing (4 & 11 March 2021, tinyurl.com/4csm5k3m)
- KNIME self-paced learning courses and community forum
- Development team of the KNIME Image Processing Extension (tinyurl.com/24enj9vt)





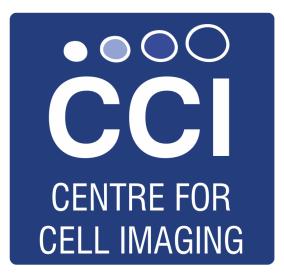












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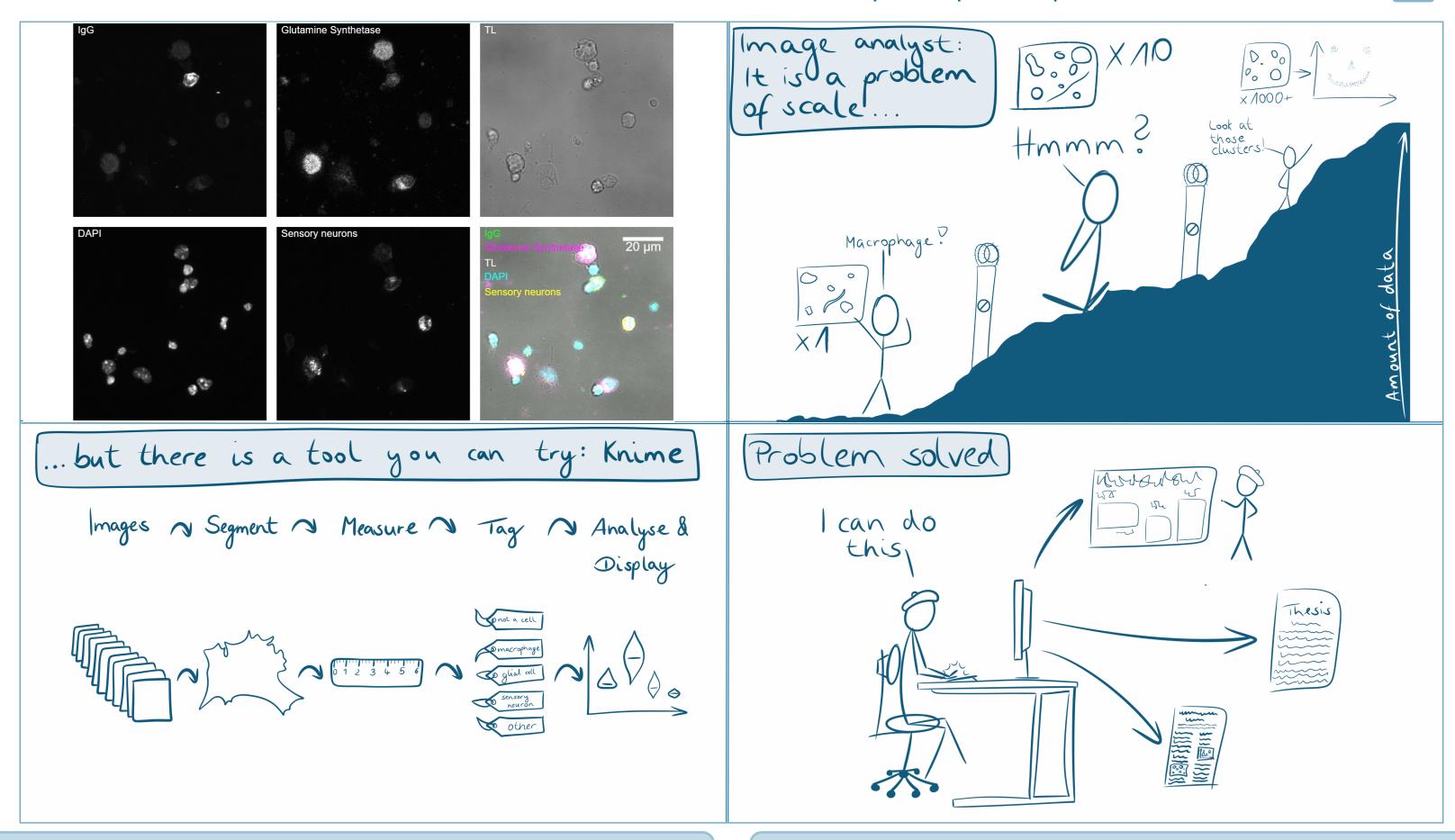


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Knime workflow Workflow on KNIME hub: https://kni.me/w/58kwwNnscEl5ikr Workflow on KNIME hub: https://kni.

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