

Lecture “Online Image Analysis Course (OIAC), Institute of Microbiology, Faculty of Biological Sciences” (FSU, SoSe 2021)

Homework assignment, 14.04.2021-15.04.2021, submission deadline 17:00, 15.04.2021.  
Maximum: 36 points (>=18 points required to pass)

In this exercise you will build workflows. Please send us them via E-mail (see instructions below). Please ensure that your name and student ID is present on your submission.  
***Please do not forget to also to fill out the mandatory survey!***

Name: \_\_\_\_\_

Student ID: \_\_\_\_\_

You will analyze image slice of a murine kidney (LSFM image). Download the image slice ([12-39-10\\_Kontrolle\\_1a\\_zoom063\\_z5\\_647\\_Ultrall\\_C00\\_xyz-Table\\_Z0311.ome.tif](#)), the JIPipe project file, the Icy project file, and the KNIME project file from our website<sup>1</sup>. Use the image analysis tools **KNIME**, **Icy**, and **JIPipe** to analyze it. Afterward ***fill out the survey*** at <http://tiny.cc/csfmtsz>. ***You will need to fill out the survey to earn the credits from this class! Please do not forget to add your name, E-mail, and student ID (if available) into the survey!***

You can pre-packaged Windows versions of the image analysis tools on our website. If you use an Apple or Linux computer, please follow the instructions for a manual install. ***If you still have issues, please contact us. We will gladly help you!***

#### **TASKS**

Please create a workflow in each application that extracts the following measurements into a table:

1. The **tissue area** in pixels
2. The **centroid (X, Y)** of each glomerulus

Please ensure that the glomeruli satisfy the following constraints:

- Minimum radius = 15  $\mu\text{m}$
- Maximum radius = 65  $\mu\text{m}$

Use the pixel size of 5.1590  $\mu\text{m}$  x 5.1590  $\mu\text{m}$  to calculate the correct filtering step parameters.

You are provided with workflows (project files) for each tool; these workflows already come with all the blocks/steps inserted that you need to solve the tasks. However, the blocks/steps are NOT connected; your task is to arrange them and connect them in a logical order to carry out the segmentation task for both the kidney tissue and the glomeruli. Please connect the blocks in a way that the resulting workflow generates the results as tables. ***We recommend that you solve the tasks in the following order: 1) read the image into the application, 2) carry out the tissue segmentation, and 3) assemble the glomeruli segmentation workflow.*** It is easier to segment the tissue, thus with the order of execution recommended above you will get familiar with the three programs whilst doing the easier task first. For KNIME and JIPipe it is sufficient to have the final results table as an output of a block. For Icy, please add Display elements that show the content of the final results tables.

---

<sup>1</sup> <https://asb-conference.hki-jena.de/event/16/page/22-exercise>

Please send us the final protocols before the submission deadline (15.04.2021, 17:00) via e-mail to [thilo.figge@leibniz-hki.de](mailto:thilo.figge@leibniz-hki.de), [zoltan.cseresnyes@leibniz-hki.de](mailto:zoltan.cseresnyes@leibniz-hki.de) and [ruman.gerst@leibniz-hki.de](mailto:ruman.gerst@leibniz-hki.de). Earlier submissions are very welcome! Please do **not** package the workflows into a \*.zip file, as they will not come through the HKI e-mail server to us.

**Comment [r1]:** Submission deadline

### Tasks and their point values:

- JIPipe
  - Tissue segmentation (4 points)
  - Glomeruli segmentation (6 points)
- Icy
  - Tissue segmentation (4 points)
  - Glomeruli segmentation (6 points)
- KNIME
  - Tissue segmentation (4 points)
  - Glomeruli segmentation (6 points)
- Survey (**Mandatory!**) (6 points)

### Additional info: KNIME

**KNIME requires downscaling the image before applying the morphological operations with large images and large kernels. We added two nodes for this purpose: one for down- and one for up-scaling. Use the downscaling node right before the morphological operations; use the upscaling node right after the morphological operations.**

1. Open KNIME and set up the workspace (follow the Assistant, choose a new workspace if the program complains and remember its location)
2. Go to File > Import KNIME Workflow ...
3. Click "Browse ..." and select Glomeruli\_exercise.knwf
4. Continue by clicking Next/Finish until the file is imported
5. You will find the exercise in the left top panel
6. Double-click the "Image reader" node
7. Select "12-39-10\_Kontrolle 1a zoom063 z5 647\_UltraII\_C00\_xyz-Table z0311.ome.tif"

When you are finished with the exercise, right-click the "Glomeruli\_exercise" workflow at the left panel and click "Export KNIME workflow".

When you are finished, provide us with the exported workflow file (".knwf" extension).

### Additional info: Icy

**Icy does not provide a normalization ("divide by maximum") block. Continue the analysis without it.**

Open Icy

1. Click "Tools" at the top bar
2. Click "Protocols"
3. Click "Load" and open "Glomeruli\_exercise.protocol"

4. Click the button next to "input file" of the left-most node ("Files to sequence")
5. Select "12-39-10\_Kontrolle 1a zoom063 z5 647\_UltraII\_C00\_xyz-Table Z0311.ome.tif"

**When you are finished, save and send us the protocol file (".protocol" extension)**

**Additional info: JIPipe**

1. Open ImageJ (with JIPipe preinstalled - you can find the download in our Google drive)
2. Click "Click here to search" and type into the field: JIPipe
3. Select "JIPipe GUI" in the left panel
4. Click "Run" in the right panel
5. Go to Project > Open and select "Glomeruli\_exercise.jip"
6. Click "Preprocessing"
7. Select the node called "File"
8. Click the folder icon next to "Filename" in the right panel and select "12-39-10\_Kontrolle 1a zoom063 z5 647\_UltraII\_C00\_xyz-Table Z0311.ome.tif"

**When you are finished, provide us with the .jip file**