AQUAMI

Instruction Manual

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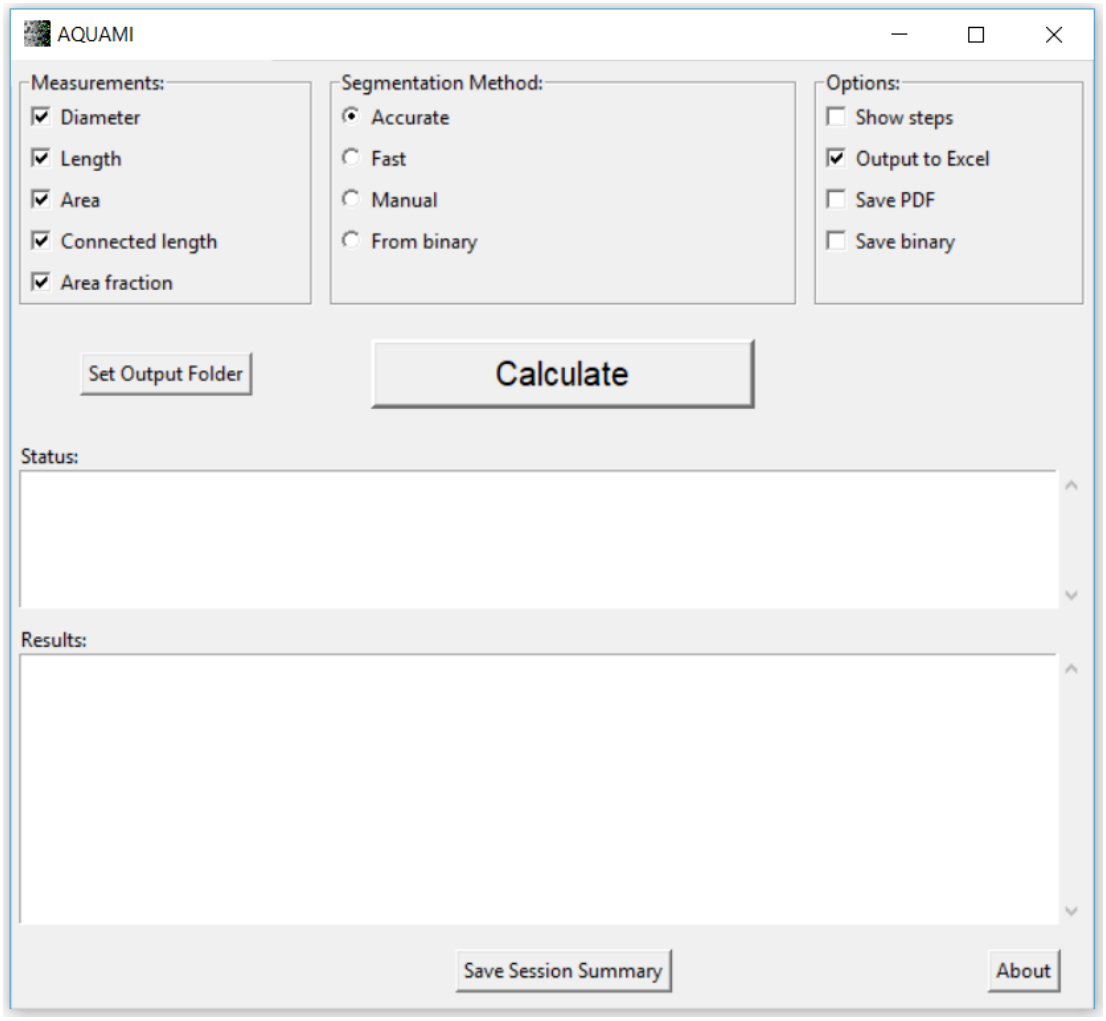
Quick Start Guide

Brief Quick Start Guide

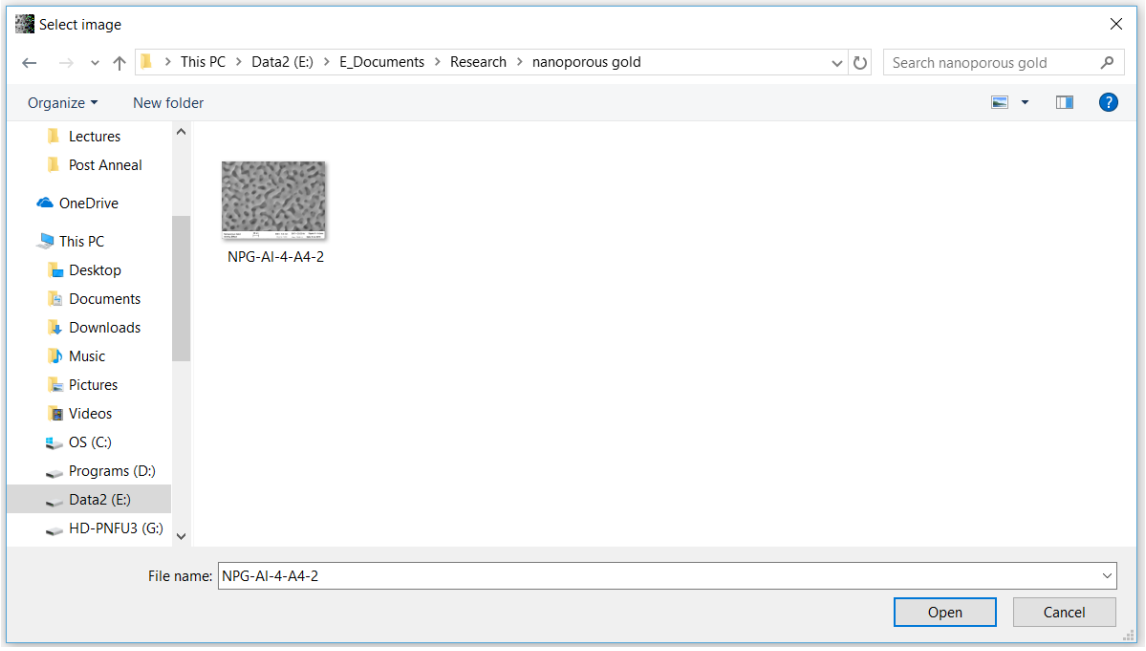
Click calculate and follow the prompts to open a micrograph and measure the scale bar. With this input, AQUAMI will automatically perform measurements and generate a detailed report. Please continue reading for more details and pictures.

Detailed Quick Start Guide

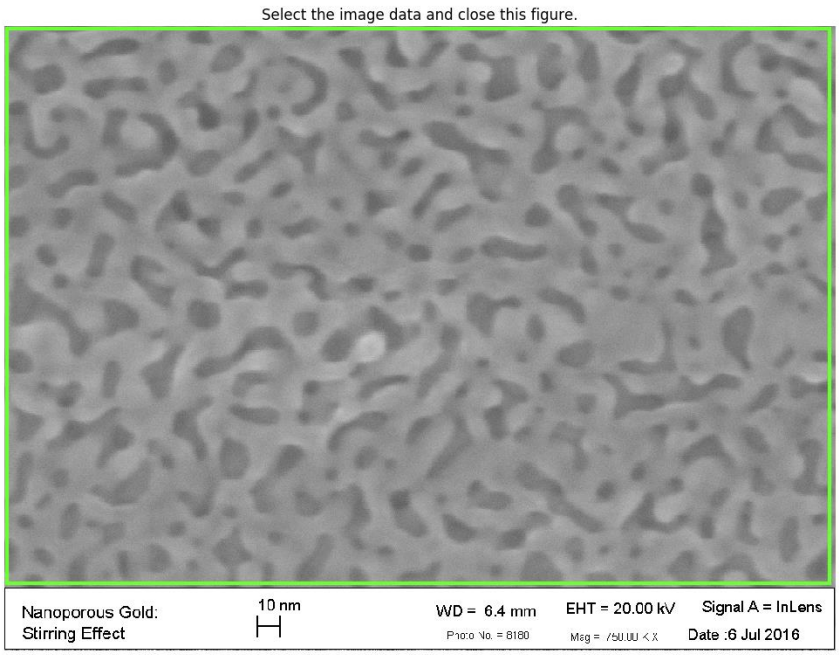
1. Click “Calculate”.



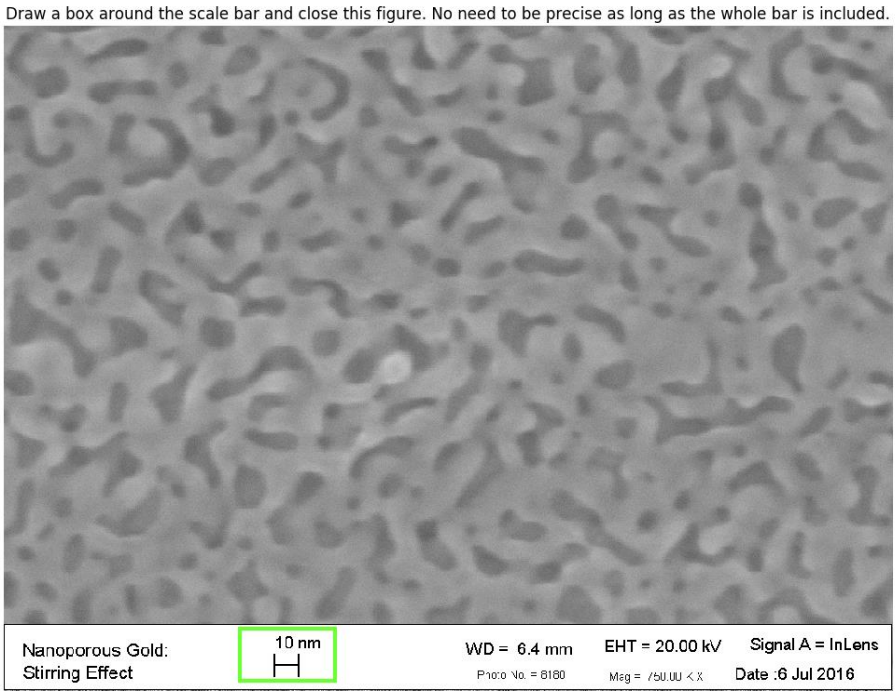
2. In the dialog that opens, select the micrograph to measure. An example micrograph is bundled with the software.



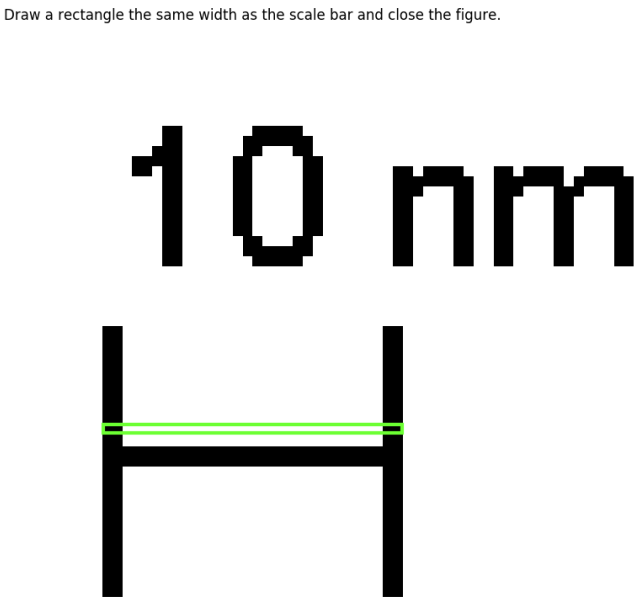
3. A new window showing the micrograph will open. Press and hold the left mouse button to draw a green rectangle around the part of the micrograph you wish to measure. Close the window.



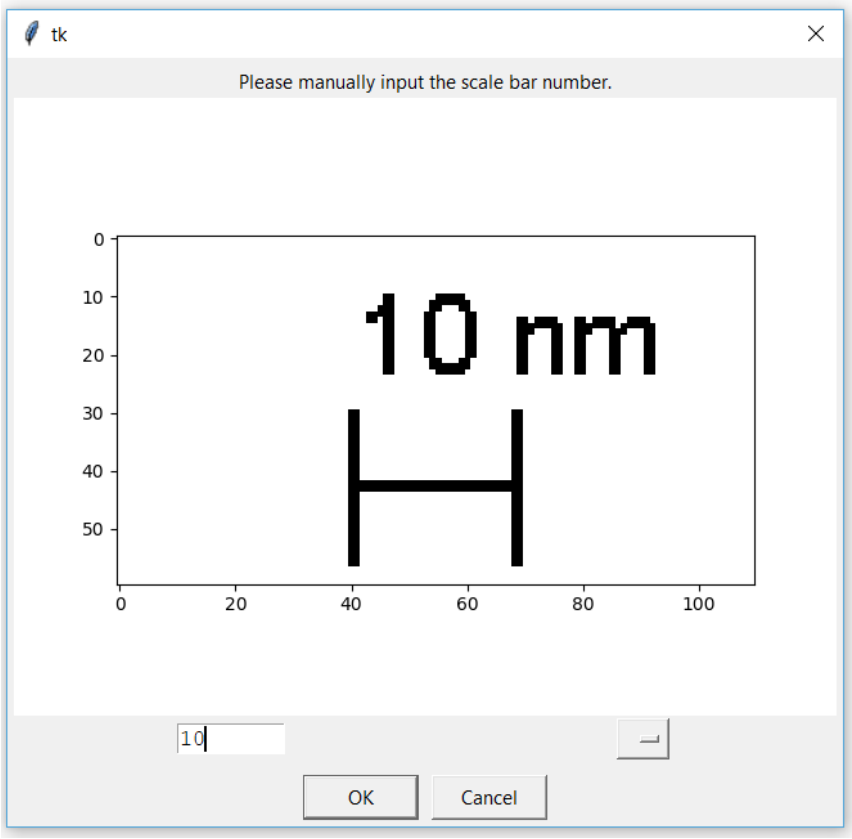
4. A second window showing the micrograph will open. Draw a rectangle around the scale bar. Close the window.



5. A magnified view of the scale bar will appear. Measure the scale bar by drawing a rectangle the same width as the scale bar. Close the window.



6. In the window that appears, type in the scale bar number and select the appropriate units. Please note that the software converts final values to nanometers or nm^2



7. The software will perform the measurements. Afterwards, an excel file containing all the measurements will be created in the folder of the input micrograph. Depending on the image size and resolution, tens of thousands of measurements may be made.

8. Repeat steps 1-7 for as many micrographs as desired.

9. Click the "Save Session Summary" icon at the bottom to create an excel file that summarizes the results of all micrographs measured since the software was opened.

Software Installation

Windows

1. Download the application from: https://goo.gl/9FUwfX
2. Extract the .rar folder to a location of your choice.
3. To run, open the extracted folder and double click the aquami shortcut.
    - May take 20 seconds to launch the first time.

Python Open Source Version

1. Install Python
    a. Download Anaconda from https://www.anaconda.com/download/
    b. Install Anaconda
2. Install AQUAMI
    a. Open a command prompt.
    b. Type “pip install aquami” without quotation marks.
        - Requires pip to be installed and added to the system path.
    c. Run the program with either of the following methods:
        i. Navigate to PATH/TO/ANACONDA/Lib/site-packages/aquami and run the gui.py file using your favorite Python editor.
        ii. In the command prompt type:

```
python
from aquami import gui
gui.run()
```

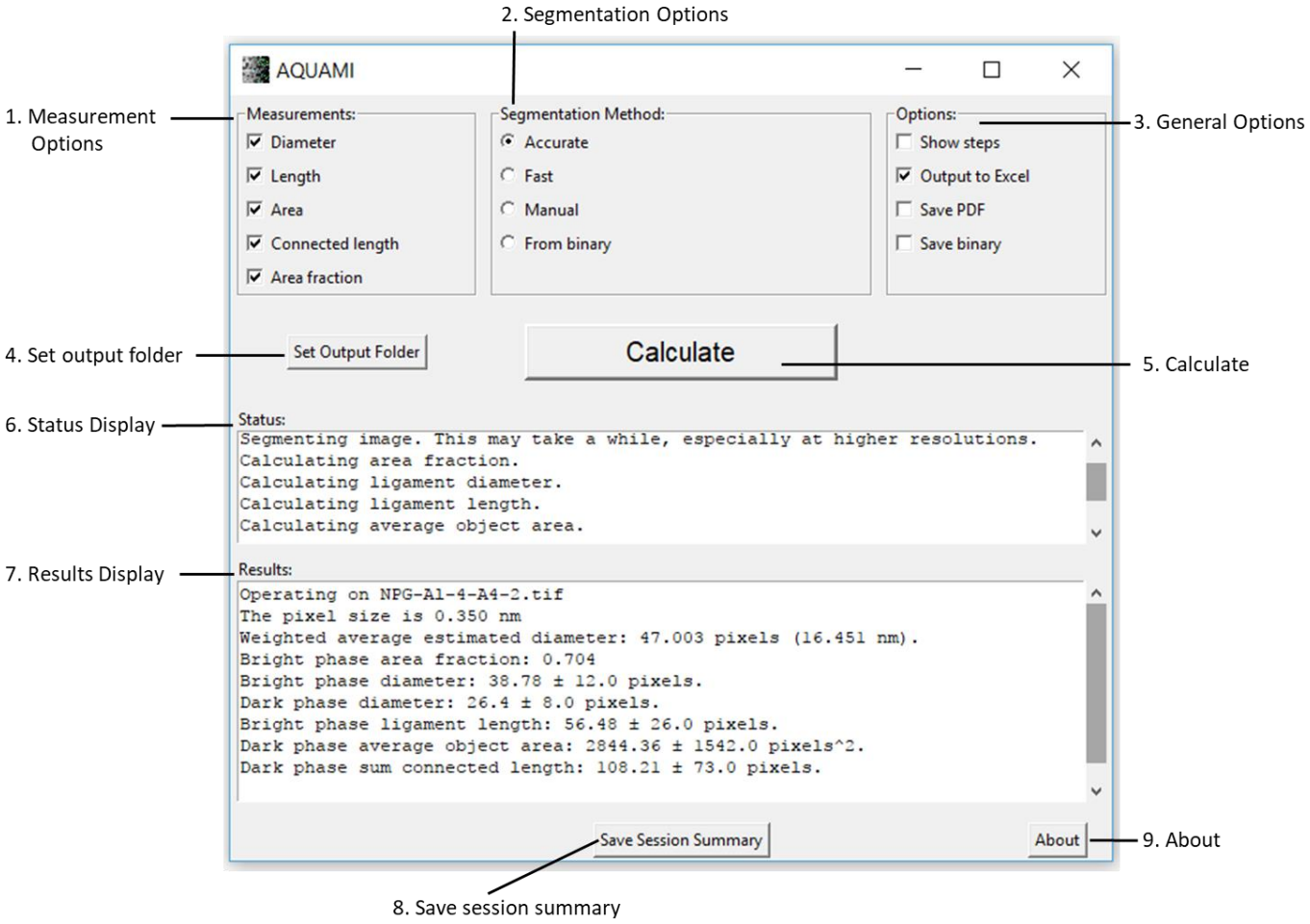
Citing AQUAMI

If this software is useful to your research, please consider citing:

J. A. Stuckner *et al.* “AQUAMI: An Open Source Python Package and GUI for the Automatic Quantitative Analysis of Morphologically Complex Multiphase Materials,” *Computational Materials Science,* vol. 139, pp.320-329, Nov. 2017

DOI: 10.1016/j.commatsci.2017.08.012

Detailed Feature Information



1. **Measurement Options** – Available measurement calculations can be turned on or off by toggling the appropriate checkbox. The available measurements are as follows:
    a. **Diameter** – Performs diameter measurements of ligaments, chords, or pores in both phases. A measurement is made on each pixel along the skeletal backbone.
    b. **Length** – Measures the length of ligaments and/or pores in each phase between branching. I.e. the node-to-node length.
    c. **Measures** the area of each enclosed feature. This measurement is only performed on the phase that does not have in-plane connectivity.
    d. **Connected length** – The sum of the ligaments or pore lengths in each enclosed feature. This measurement is only performed on the phase that does not have in-plane connectivity.
    e. The fraction of pixels belonging to the bright phase.

2. **Segmentation Methods** – The desired segmentation method can be chosen by selecting the appropriate radio button. The methods are described below:
    a. **Accurate** – Uses Local Otsu's method which automatically determines a proper threshold value at each pixel. This method is much slower than the other methods but is the most accurate. It is effective even when there are illumination changes throughout the micrograph.
    b. **Fast** – Uses global Otsu's method which automatically determines a global threshold value. Much faster than Local Otsu's method, but should be avoided if there are illumination changes in the micrograph which may occur during acquisition from sample height differences or contamination.
    c. **Manual** – Allows the user to manually select a threshold value using a built in interface.
    d. **From binary** – Allows the user to import a dark and bright phase binary mask which has been segmented using an outside tool. When "Calculate" is clicked, the user will be prompted to open the dark and bright phase mask images.

3. **General Options**
    a. **Show steps** – Figures will be displayed while the software is performing segmentation and measurements to allow visualizion of each step. This is useful to monitor the software's performance and accuracy.
    b. **Output to Excel** – An Excel file will be generated for each micrograph that is measured. This file will list every measurement that is made and can be used to create custom figures, fit a probability distribution function to the data, or perform advanced statistical analysis. By default, this file will be saved in the same folder as the input micrograph.
    c. **Save PDF** – Saves a PDF summary of each measured micrograph. The summary includes average and standard distributions of each measurement performed as well as visualizations of each step in performing those measurements. By default, this file will be saved in the same folder as the input micrograph.
    d. **Save binary** – Saves the bright and dark segmentation masks as image files. These can then be loaded using the "From binary" segmentation option. By default, these files will be saved in the same folder as the input micrograph.

4. **Set Output Folder** – Allows the user to select a folder to save the result files such as the PDF summary and the Excel measurement list file. By default, these files are saved in the same folder as the input micrograph.

5. **Calculate** – Directs the software to begin performing segmentation and measurements based on the selected options. The user will be directed to select a micrograph and measure the scale bar before calculations begin. After performing calculations, result files will be generated.

6. **Status Display** – Displays what the software is doing.

7. **Results Display** – Displays measurement results as they are determined.

8. **Save session summary** – Creates an Excel file which contains a summary of average measurements performed on each micrograph since the software was opened.

9. **About** – Shows author contact information, information about the software, and a link to the article on this software.