

Sep 25, 2024 Version 2

## Nutil Data Integration V.2

DOI

[dx.doi.org/10.17504/protocols.io.3byl4qrz8vo5/v2](https://dx.doi.org/10.17504/protocols.io.3byl4qrz8vo5/v2)

Michael X. Henderson<sup>1</sup>

<sup>1</sup>Van Andel Institute

Michael X. Henderson: ORCHID: 0000-0001-9710-0726

ASAP Collaborative Rese...

Team Biederer

1 more workspace



Michael Henderson

Van Andel Research Institute

OPEN  ACCESS



DOI: [dx.doi.org/10.17504/protocols.io.3byl4qrz8vo5/v2](https://dx.doi.org/10.17504/protocols.io.3byl4qrz8vo5/v2)

**Protocol Citation:** Michael X. Henderson 2024. Nutil Data Integration. **protocols.io**

<https://dx.doi.org/10.17504/protocols.io.3byl4qrz8vo5/v2> Version created by [Lindsay Meyerdirk](#)

**License:** This is an open access protocol distributed under the terms of the [Creative Commons Attribution License](#), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited

**Protocol status:** Working

**We use this protocol and it's working**

**Created:** August 17, 2023

**Last Modified:** September 25, 2024

**Protocol Integer ID:** 108116

**Keywords:** ASAPCRN



**Funders Acknowledgement:**

**Aligning Science Across**

**Parkinson's**

**Grant ID: ASAP-020616**

**National Institute on Aging**

**Grant ID: R01-AG077573**

## Abstract

This protocol describes Nutil data integration from segmentation and registration of mouse brain data.

## Attachments



**812-2118.pdf**

4.6MB

## Nutil Data Quantification

- 1 Open Nutil and find operation tab.

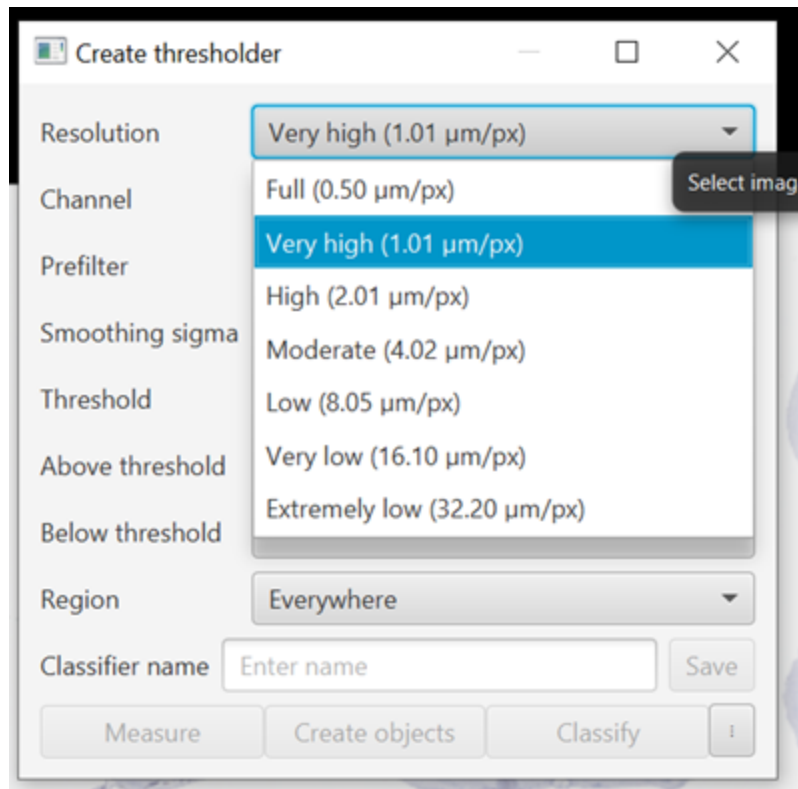


1. Find the 3 folders you created at the beginning of this workflow and populated during the workflow and populate them into their corresponding list above. (segmentation is your input folder, brain atlas map folder is your atlas folder, output folder is output and should be empty still XML or JSON anchoring file is the QuickN JSON file that you created earlier – you can also use visualign json file it doesn't matter the anchor is set in quickNII and nonlinear adjustments are made in reference to it. Object color is black because that's what the staining of our segmentations look like if it were a different color we would need to look for another object color code it corresponds to during the segmentation step.



3

Navigate to advanced settings in the row labeled Global Pixel Scale/Unit, set it to the resolution of your classifier, converted to area per pixel ( $\mu\text{m}^2/\text{px}$ ). This can be calculated by squaring the resolution value in the QuPath thresholder (given in  $\mu\text{m}/\text{px}$ -length). For example, if using brightfield images scanned at Van Andel (usually scanned at  $.503 \mu\text{m}/\text{px}$ ) and using the “Very High” resolution in QuPath (scaled by factor of 2), the resolution you would put into Nutil would be  $1.02 \mu\text{m}^2/\text{px}$  ( or  $(1.01\mu\text{m})^2/\text{px}$ ). Set Pixel Scale Unit to  $\mu\text{m}^2$



It is mainly important to have this completely accurate if your analysis contains variables that take area into account (e.g. +ve objects/ $\mu\text{m}^2$ ). It is not as crucial if only looking at percent area occupied as ratios will not be affected by scale conversions. More info on this can be found in the Nutil docs FAQs, item 9.6: <https://nutil.readthedocs.io/en/latest/FAQ.html>

4 Also, under advance settings change custom masking to yes and select the color of the hemisphere of interest i.e. white to view hemisphere masked in white mask. Also select the folder location of the mask. Repeat the color selection with black to view the other hemisphere masked by black.



|                         |      |  |
|-------------------------|------|--|
| Custom masks (optional) | Help | Yes  |
| Custom mask folder      | Help | //ph.val.org/projects_secondary/henderson/NOAH/QUINT/Quint_Oilfactory/QVN/Mask |
| Custom mask colour      | Help |  |