




NOV 14, 2023

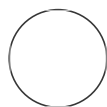
Nutil Data Integration

 In 1 collection

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ABSTRACT

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

ATTACHMENTS

[812-2118.pdf](#)

OPEN  ACCESS



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protocols.io

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Protocol status: Working
We use this protocol and it's working

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Funders

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Nutil Data Quantification

1 Open Nutil and find operation tab.



- 2 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.



3 Navigate to advanced settings In the row labeled Global Pixel Scale/Unit, set it to 36.44778384 um^2 . (6.0 is new value for van andel scans) The NEW images that are scanned here at Van Andel are resolved at 0.5031 microns per pixel, so if we downsized by 12 we get 6.0372 then this number is squared to account for um^2 . the final value is 36.44778384.

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_Olfactory/QVN/Mask
Custom mask colour	Help	