



FEB 23, 2024

Protocol for "quantification of neurons expressing alpha-synuclein in the non-human primate brain"

jlanciego¹

¹Center for Applied Medical Research (Cima) University of Navarra, Pamplna, Spain.



jlanciego

DISCLAIMER

Nothing to be disclosed

ABSTRACT

Here we describe a method based on an AI deep learning algorithm (Aiforia) for the purpose of accurately quantifying the number and location of neurons expressing alpha-synuclein throughout pre-defined regions of interest (cortical and sub-cortical locations) in the non-human primate brain.

OPEN ACCESS



DOI:

dx.doi.org/10.17504/protocols.io.36wgq3x55lk5/v1

Protocol Citation: jlanciego 2024. Protocol for "quantification of neurons expressing alpha-synuclein in the non-human primate brain". **protocols.io** <https://dx.doi.org/10.17504/protocols.io.36wgq3x55lk5/v1>

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: Feb 23, 2024

Last Modified: Feb 23, 2024

PROTOCOL integer ID: 95666

Funders Acknowledgement:

Aligning Science Across
Parkinson's through the Michael
J. Fox Foundation for Parkinson's
Research
Grant ID: ASAP-020505

Aiforia-based quantification of neurons expressing alpha-synuclein

- 1 Scan sections to be analyzed in the Aperio CS scanner at a magnification of 20x
- 2 Upload digitalized sections to the Aiforia cloud (www.aiforia.com).
- 3 Create a dedicated project for analysis.
- 4 Select up to 3-4 sections for training the model algorithm, these sections showing different morphologies and intensity levels of alpha-synuclein expression.
- 5 Train the model algorithm to analyse potential errors.

- 6 Activate the annotation assistant tool to retrieve additional beneficial inputs that can be added by the platform itself.
- 7 Repeat steps 5 to 7 while increasing the number of annotations and iterations (>1,000) until the model algorithm has learned to properly identify every single phenotype of alpha-synuclein-expressing neurons.
- 8 Release the model algorithm.
- 9 Use the drawing tool to delineate the boundaries of each selected region of interest where positive neurons need to be quantified in every single section of the project.
- 10 Export obtained raw data to an Excel spreadsheet for statistical analysis.