



Development of an Automated Annotation Pipeline for Mouse Brain Cell Clusters

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ABSTRACT

How can we use data effectively without proper curation? We can't, or at least not efficiently.

The developing mouse brain is a highly dynamic system, comprising a vast repertoire of temporary and specialized cell types.

This project aims to advance the annotation and interpretation of single-cell transcriptomic clusters in the mouse brain across developmental stages.

METHODOLOGY

OLD NAME

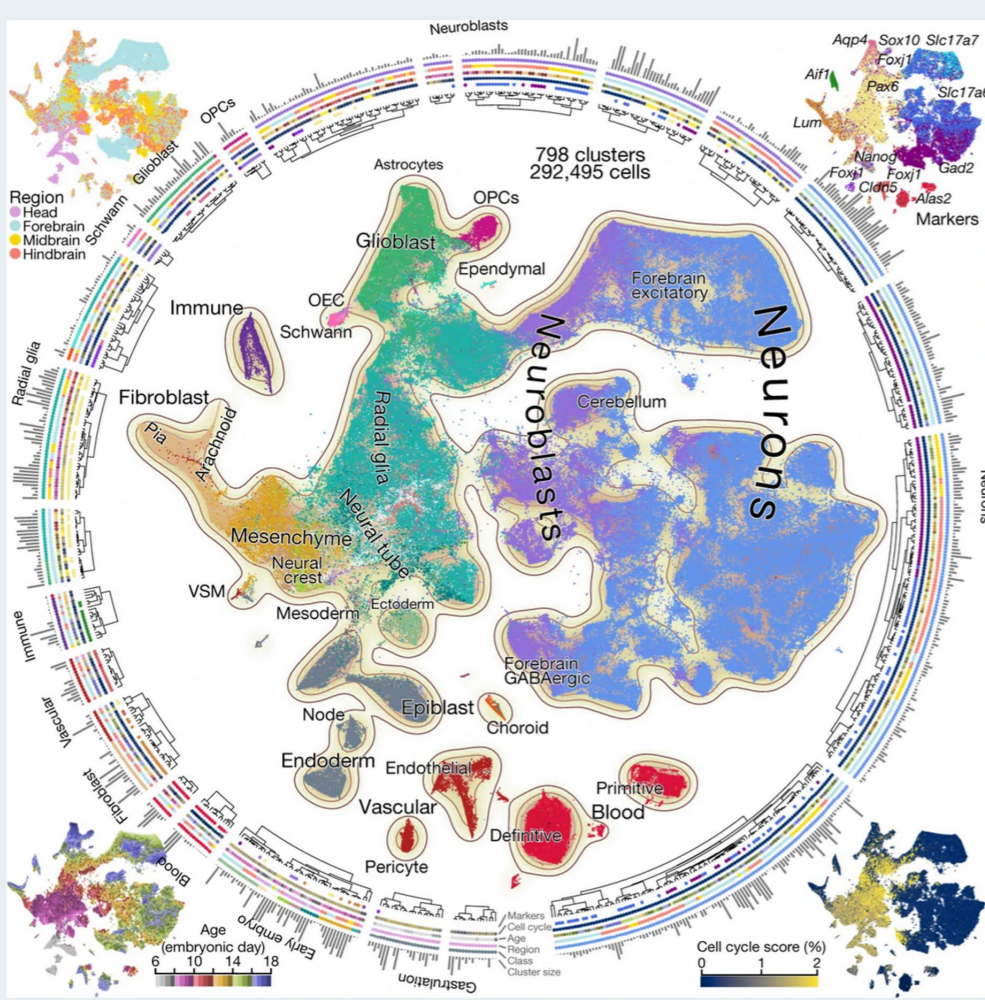
Neur633

Run the program

Acronym :

NT : Neurotransmitter

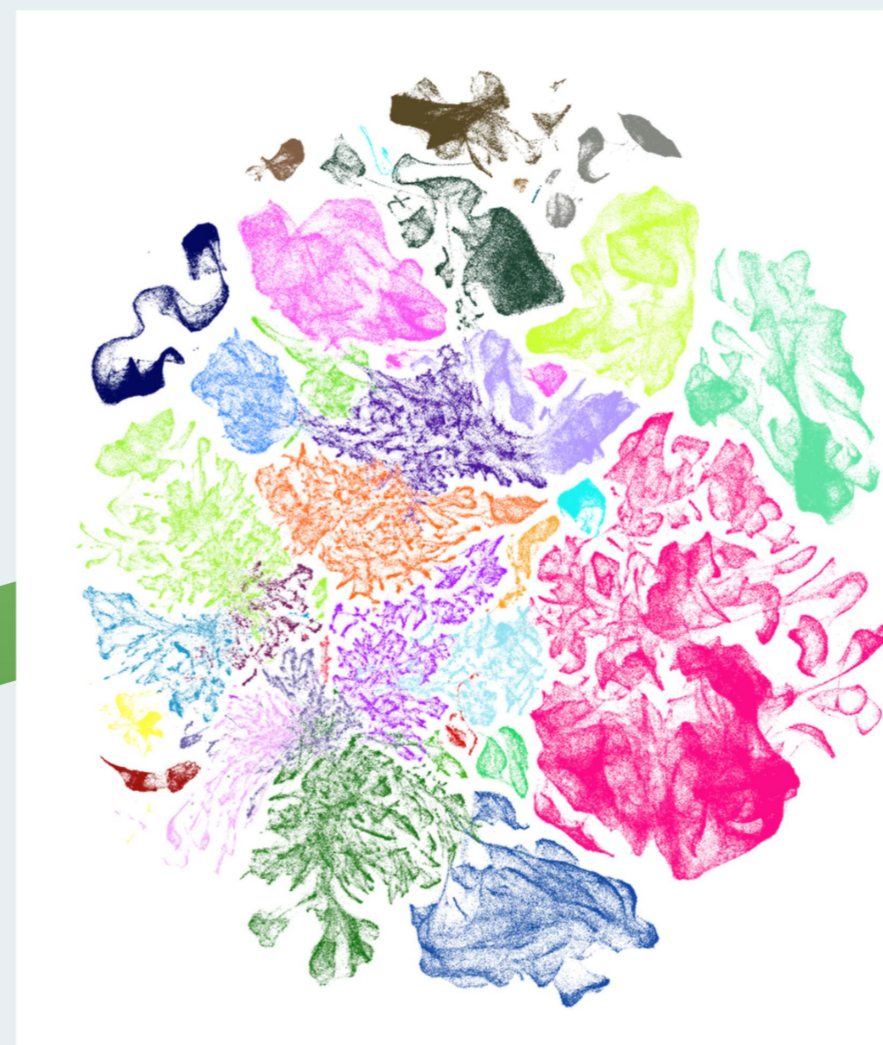
NP : Neuropeptide



Reference for cell class and subclass

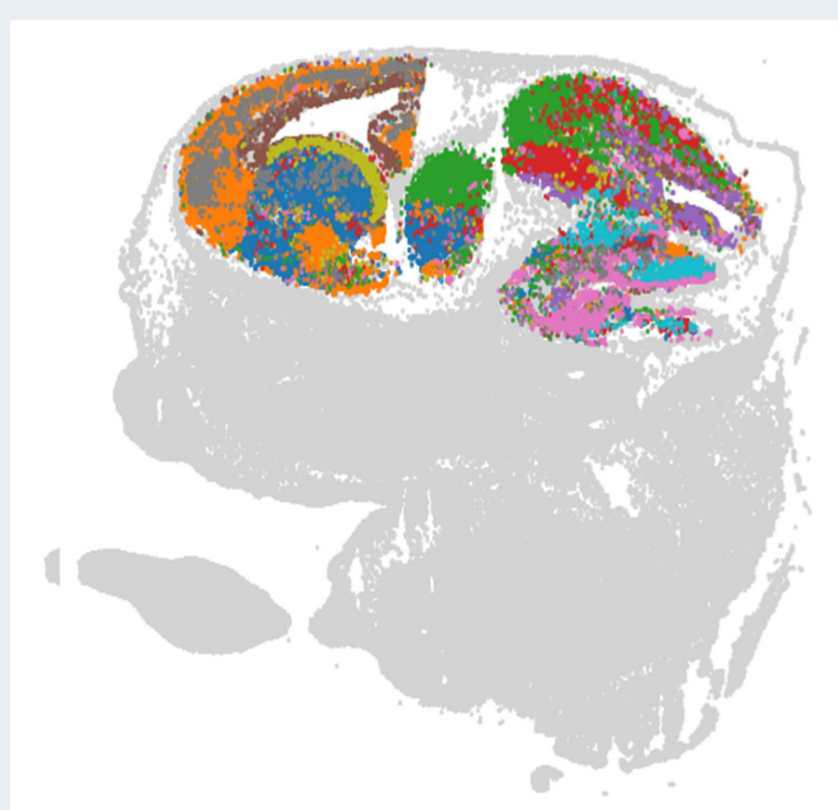
(A) scRNAseq data from the Atlas of the developing mouse brain (La Manno 2021)

Class	Subclass
Neuron	Hindbrain glutamergic



Reference for neurotransmitter (NT) and neuropeptide (NP) markers

(B) scRNAseq data from the Adult Brain Atlas (ABA) (Yao Z. 2023)



Top Cell subclasses

- Forebrain GABAergic
- Forebrain glutamergic
- Midbrain glutamergic
- Midbrain GABAergic
- Midbrain
- Dorsal forebrain
- Hindbrain glutamergic
- Cortical or hippocampal glutamergic
- Forebrain
- Hindbrain GABAergic

Reference for the precise anatomical region

(C) Spatial transcriptomic of the mouse developing brain.

Location

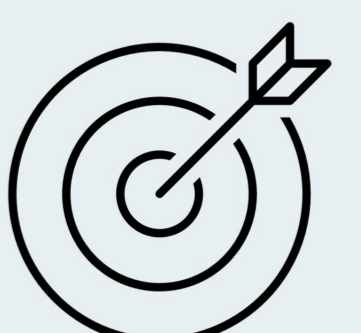
Medullary hindbrain (MH)

NT from subclass	NT from Auto-Annotation
Glu	Glu

NT from expression	NP from expression
Glu	Sst

NEW NAME

Neur_Glu_Sst_MH_2



(A) La Manno G. et al., Nature, 2021. doi:10.1038/s41586-021-03775-x

(B) Yao Z. et al., Nature 624, 317–332 (2023). doi:10.1038/s41586-023-06812-z

(C) Unpublished data, provided by A. Herrera (La Manno Lab, EPFL).