



CALHippo

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Cell Segmentation for Neuronal Density Inference in the Human Hippocampus

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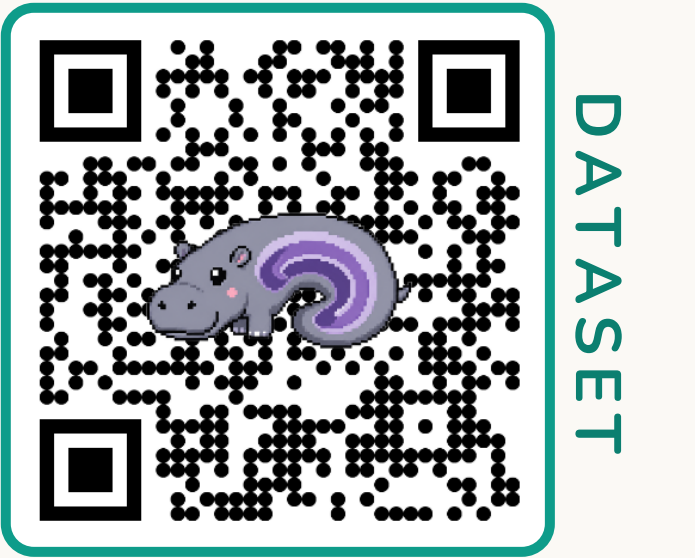
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MICCAI2026

UNIMORE

UNIVERSITÀ DEGLI STUDI DI MODENA E REGGIO EMILIA

AIimageLab



DATASET



CODE

The first complete, cell-type-resolved atlas of the human hippocampus, built from just 24 HR annotated slices.

MOTIVATION

Biologically detailed brain simulation needs **anatomically grounded cellular** scaffolds: models that say how many cells of **which type** sit where. For the human brain, especially for the hippocampus, this knowledge is still missing.

The only BigBrain scaffold to date covers **CA1 alone**, inferring cells positions from 20 $\mu\text{m}/\text{px}$ intensity, with no glial class.

Can a handful of annotated microscopic sections reveal the cell-type organization of the whole hippocampus?

DATA

24

HR sections

1 $\mu\text{m}/\text{px}$ · with cell-level details

2,022

LR sections

20 $\mu\text{m}/\text{px}$ · full CA complex

1,998 LR sections have no high-resolution match — their cell densities must be inferred from the available ones.

RESULTS

SEGMENTATION

0.81

Dice $\uparrow$

0.87

Detect. F1 $\uparrow$

CLASSIFICATION

95.1

Accuracy % $\uparrow$

80.7

Mean F1 % $\uparrow$

Predicted annotations reach an error rate of **0.25** — below the 0.35 inter-annotator disagreement between two experts.

DENSITY ESTIMATION %

Baseline CA1

CALHippo CA1

CALHippo All CA

Excitatory · NAE $\downarrow$

82.8

22.8

29.5

Excitatory · SSIM $\uparrow$

7.2

49.4

50.7

Inhibitory · NAE $\downarrow$

90.9

79.2

21.6

Inhibitory · SSIM $\uparrow$

58.4

47.7

48.2

Glial · NAE $\downarrow$

—

25.3

20.9

Glial · SSIM $\uparrow$

—

33.0

28.9

RECONSTRUCTION

18 M

Excitatory

15 M

Glial

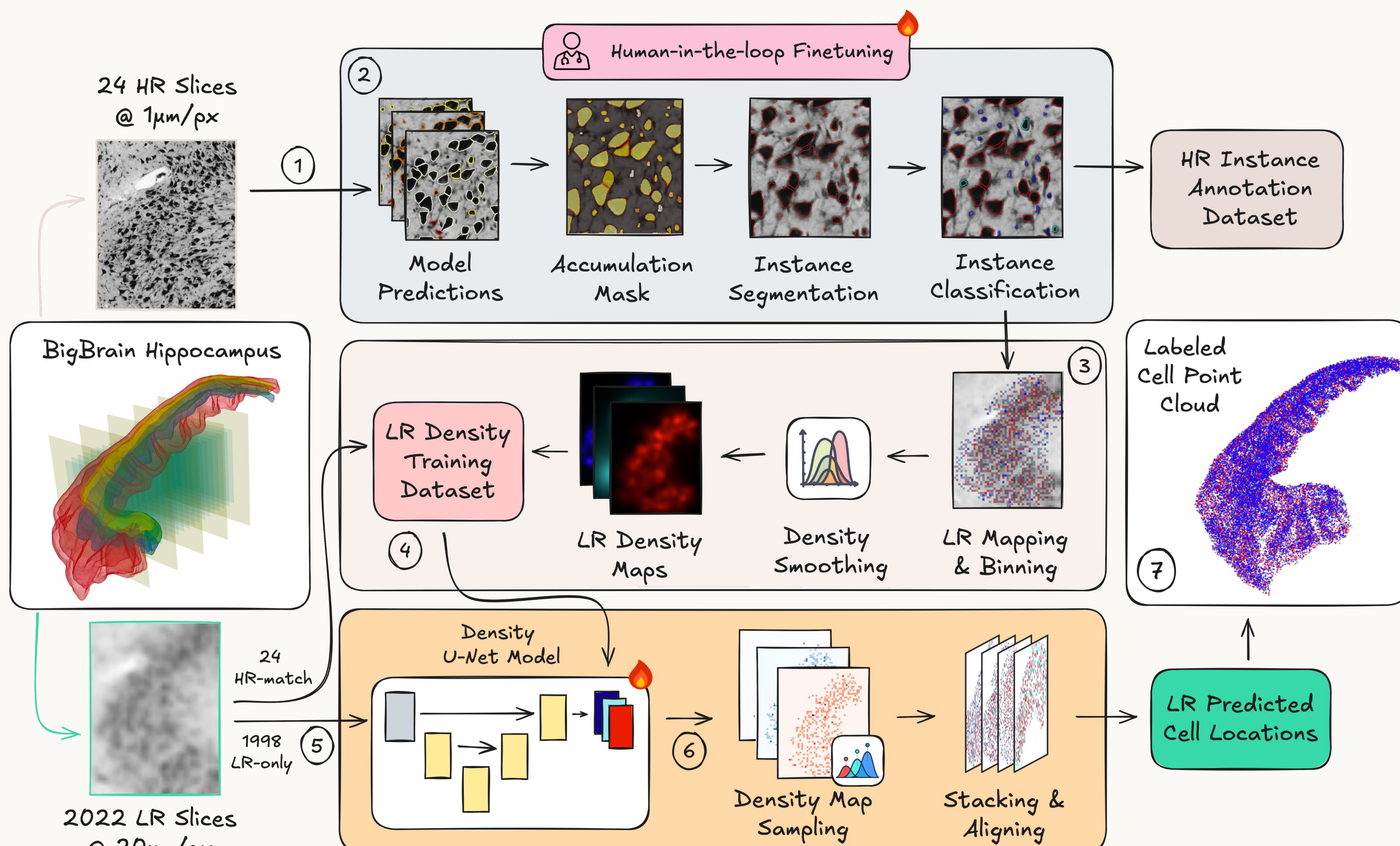
2.2 M

Inhibitory

~12%

I : E ratio

PIPELINE



STEP 1-2

Annotate cells at 1 $\mu\text{m}/\text{px}$

CellPose-SAM proposals are fused with trained StarDist, HoVer-Net, InstanSeg, and a glial-specific detector. A **hybrid classifier**, using morphology, neighborhood, and UNI2-h features, labels each cell **excitatory, inhibitory, or glial**.

STEP 3-4

Density Estimation Training

HR centroids are projected to 20 $\mu\text{m}/\text{px}$ space and smoothed into **continuous density maps** with Gaussian kernels, yielding 505 patches. These train a compact **4-stage UNet** with a hybrid NGAME + asymmetric L1 loss.

STEP 5-6

Infer every slice

The **1,998 unmatched slices** are inferred with a 50%-overlap sliding window over the CA1–CA4 regions. **Multinomial sampling** then converts each continuous density map into discrete, class-labelled cell locations.

STEP 7

Reconstruct in 3D

Per-slice cells are stacked into the **isotropic BigBrain space**, giving a class-resolved point cloud of **>35 M cells** across the CA complex; released as a reusable **cellular scaffold** for multiscale simulation.

MESOSCALE RESULTS

Watch the reconstructed point cloud

Predicted cell positions and classes over the full CA hippocampal complex, obtained by inferred density masks from the single LR slices stacked.

