

Dr. Armando
Romani

Computational neuroscience: biophysics - Lecture 3

Morphologies

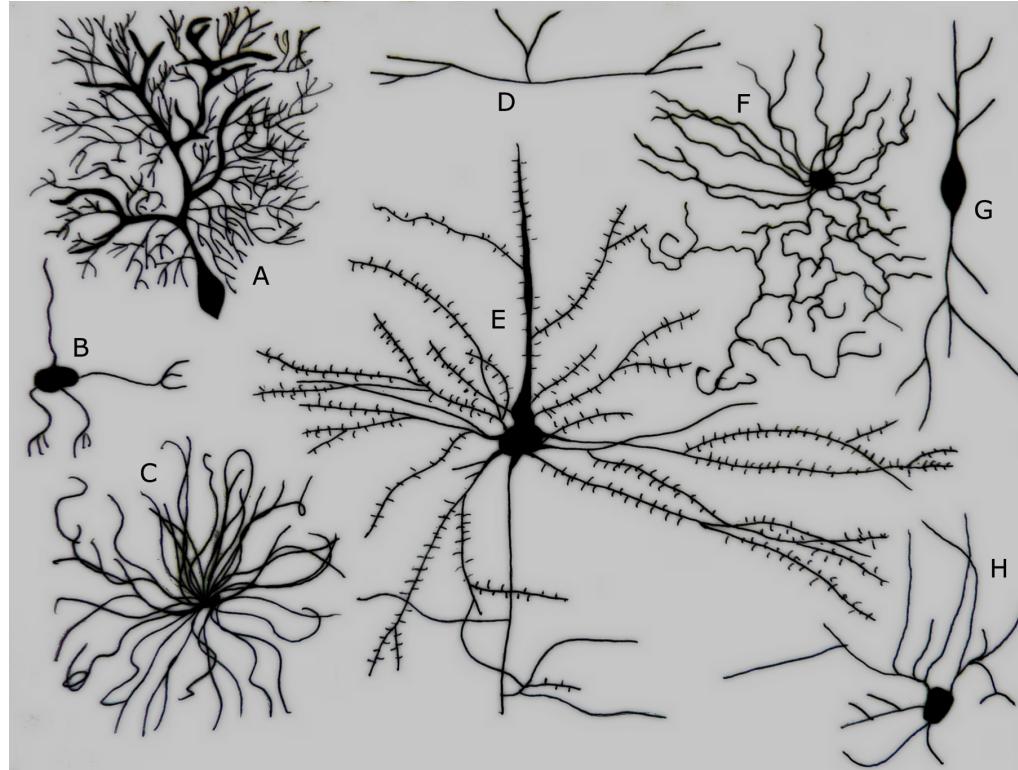
Lecture Overview

- Scope
- Approaches
- Applications

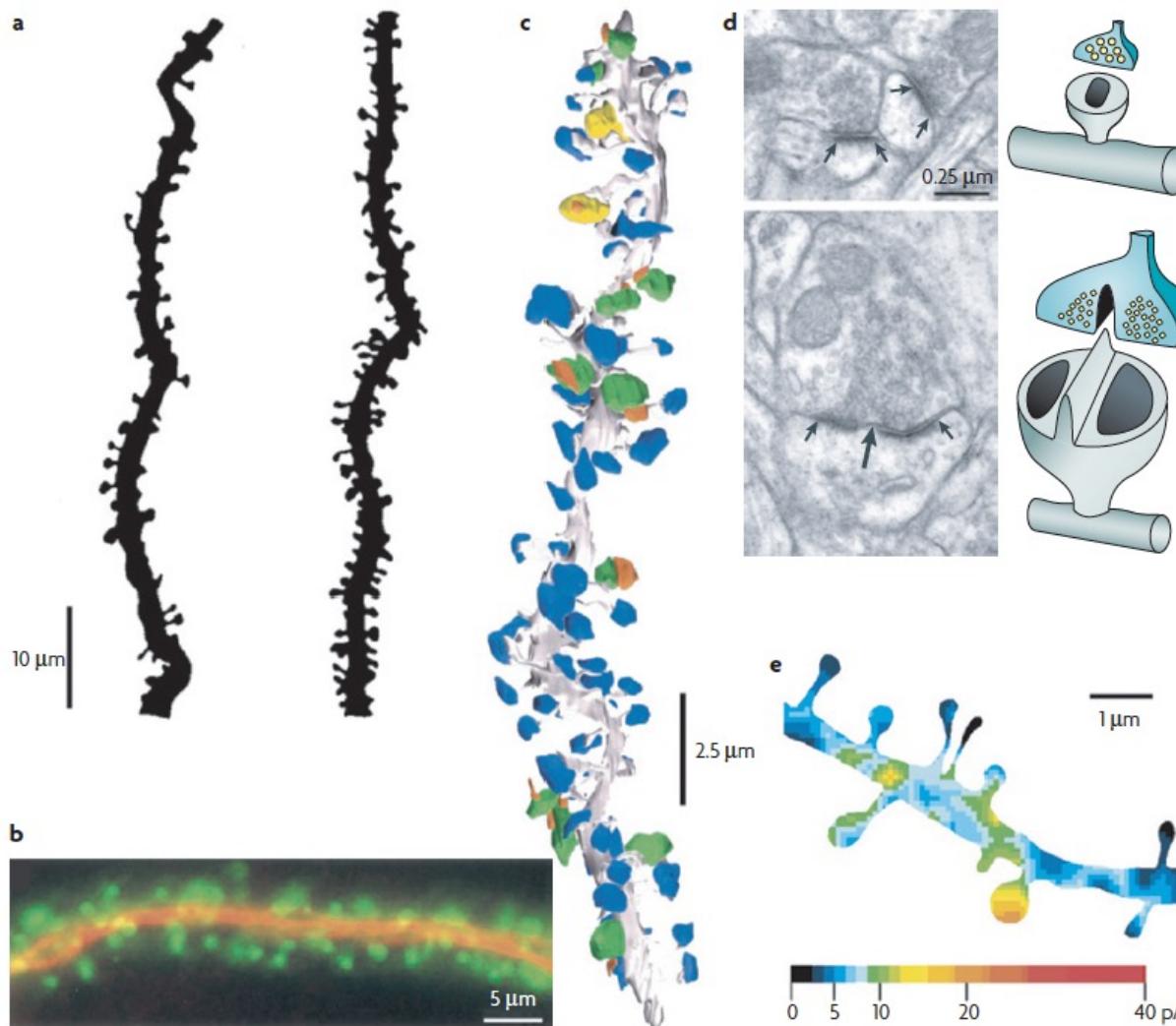
Lecture Overview

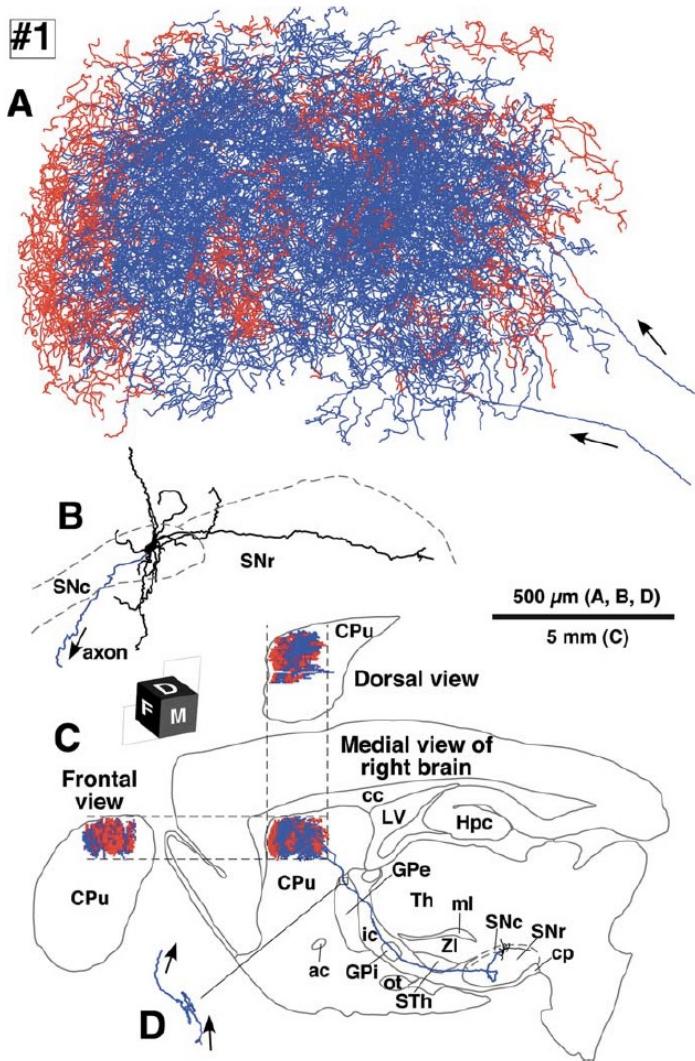
- Scope
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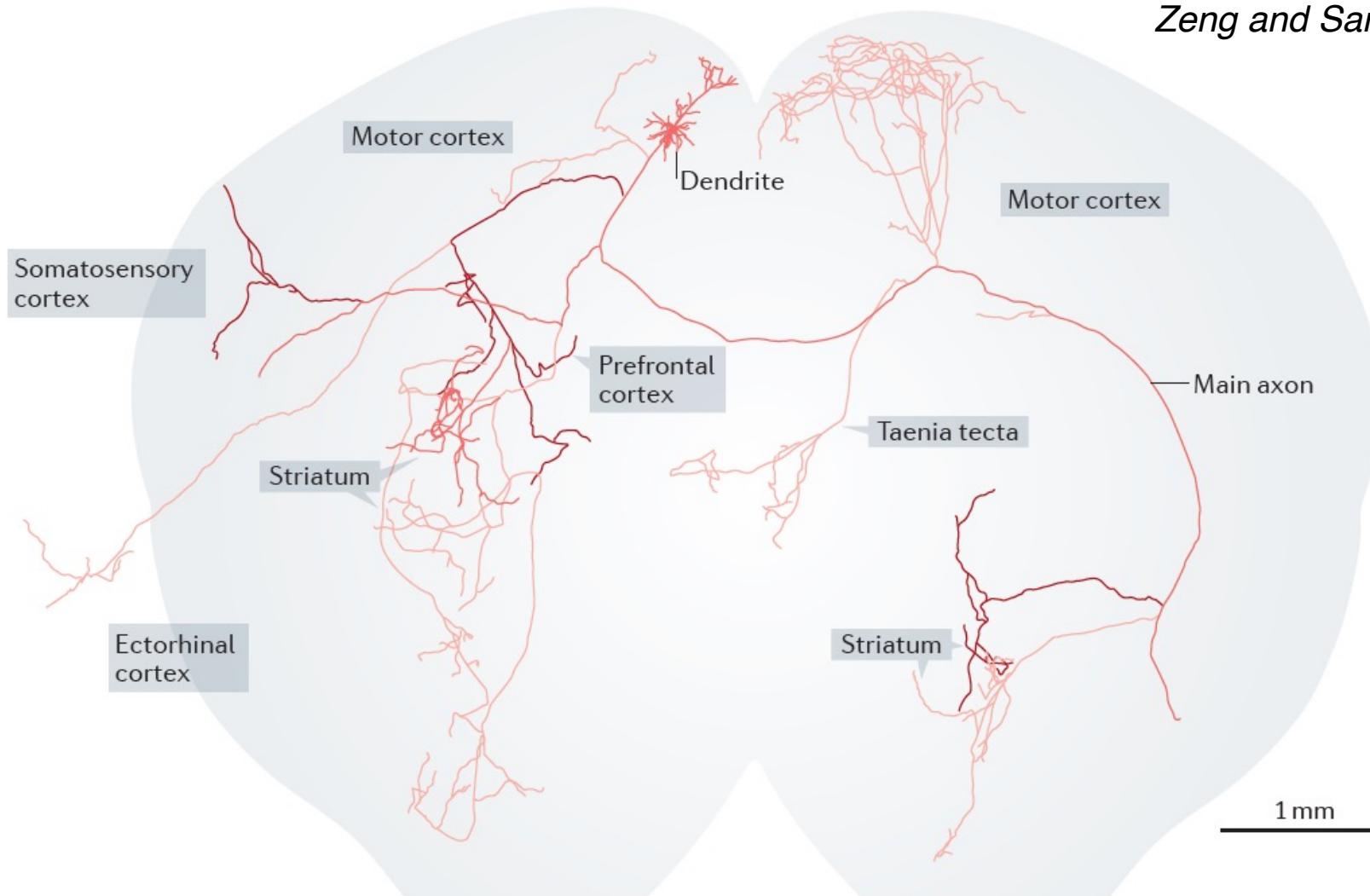
Neuron types by Santiago Ramón y Cajal (1887)



Different Types of Neurons. A. Purkinje cell B. Granule cell C. Motor neuron D. Tripolar neuron E. Pyramidal Cell F. Chandelier cell G. Spindle neuron H. Stellate cell (Credit: Ferris Jabr; based on reconstructions and drawings by Cajal)





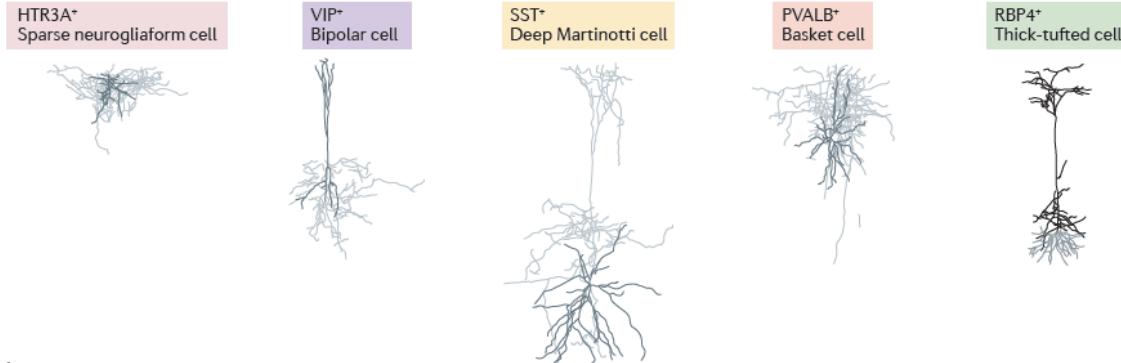
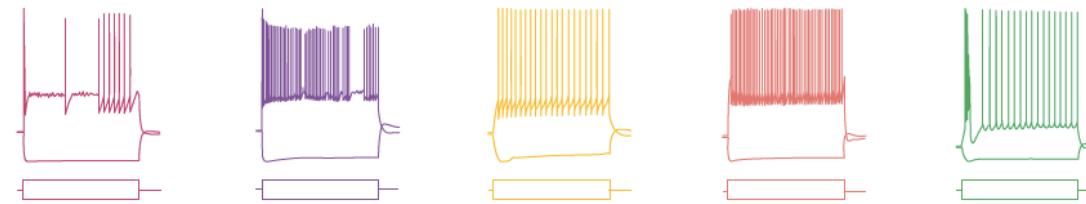
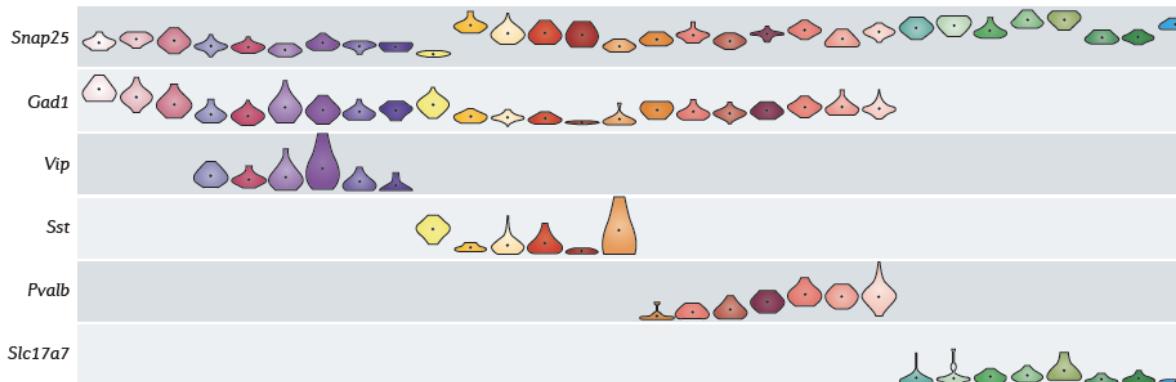


1 mm

Neuron Classification

Why?

- Understand the brain. Dimensionality reduction
- Communication among scientists
- Improve reproducibility
- Study diseases
- Understand evolution. Comparison among species
- Understand development
- Identify new cell types

a Morphology**b Physiology****c Molecular signature**

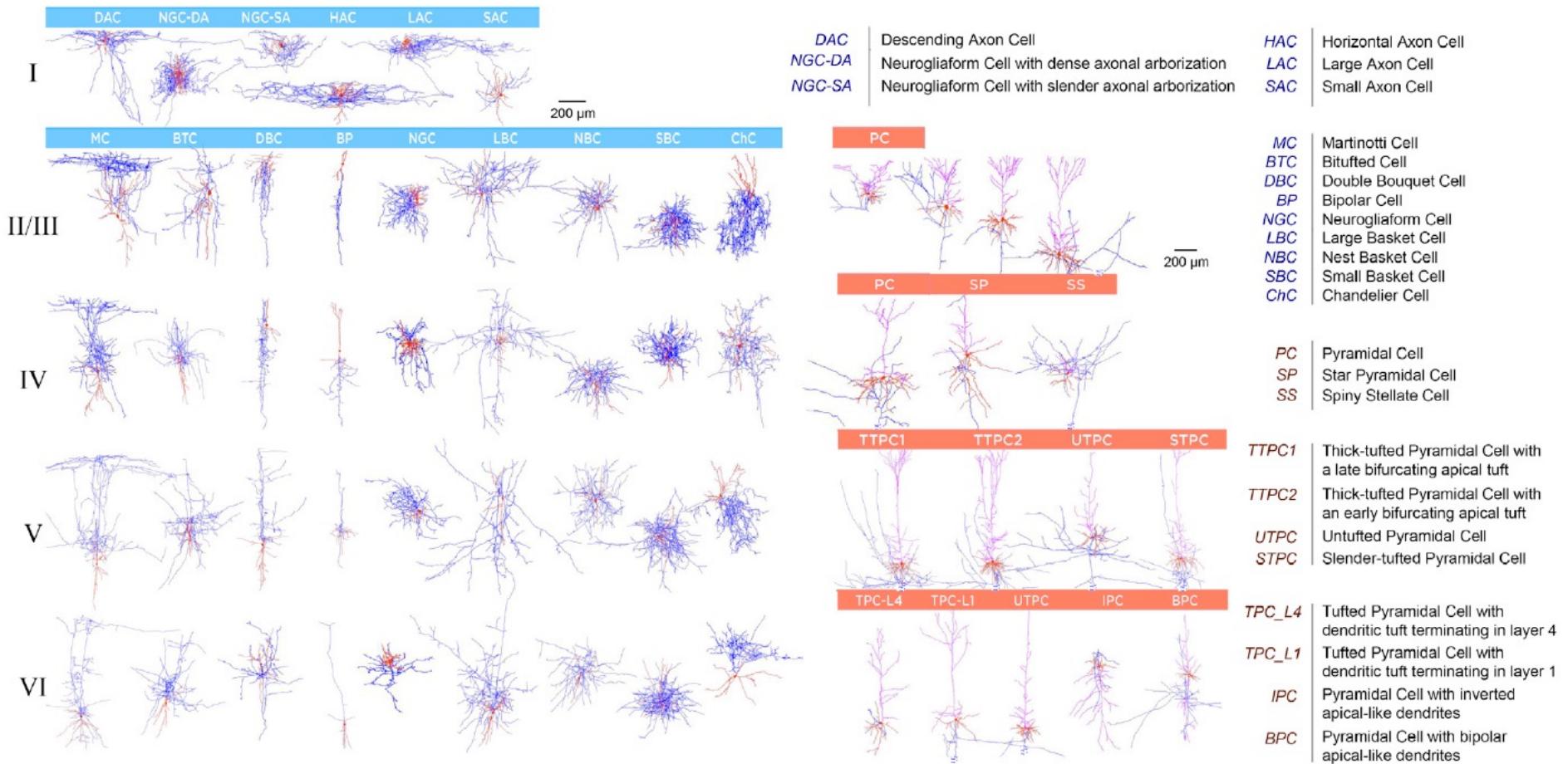


Figure 2. Table of Neocortical Neuronal Morphologies

Exemplar 3D reconstructions of 55 m-types. Morphologies in L2 and L3 are not separated. Axon in blue, dendrites in red. Full morphologies are not always shown.

Markram et al 2015

Challenges

- Definition a ‘cell type’ is still elusive
- Find the correct granularity
- Morphologies change during development
- Some features are continuous
- Morphologies change over time due to activity, hormones, ...
- The three classification methods not always vary together

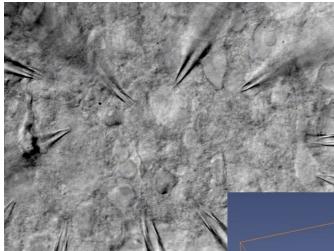
Summary 1

- Research is revealing a wonderful complexity of morphologies
- Morphological diversity correlates with a functional diversity
- We have to bridle this diversity but challenges still exist:
 - Unknown number of morphologies.
 - Define a cell type. Classification.
 - Faithful reconstruction of the morphology.

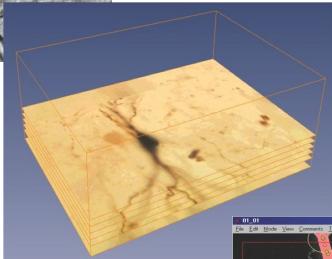
Lecture Overview

- Scope
- **Approaches**
- Applications

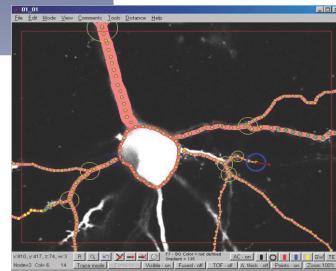
How to reconstruct a morphology



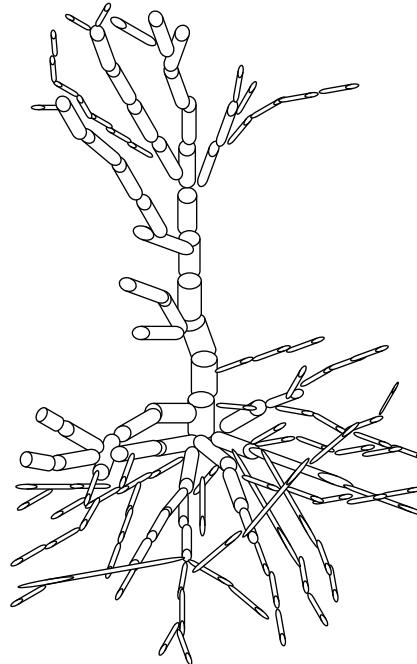
Labeling of cells



Histology



3D reconstruction



Staining techniques

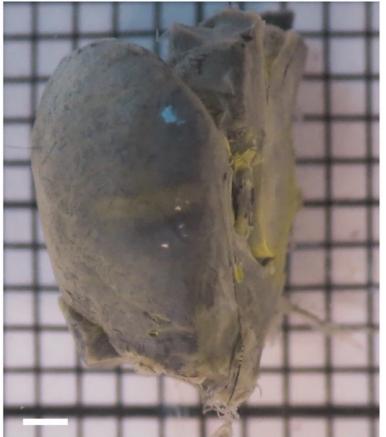
- In-vitro staining
- In-vivo staining

Staining techniques

- Staining with heavy metals (Golgi). Light microscopy (LM)
- Fluorescence proteins (GFP, RFP, YFP) introduced transgenically in selected cells. Fluorescence microscopy
- Immunostaining. Antibody labelled with fluorescent or chromogenic tags. Light, fluorescent, or electron microscopy (EM) depending on the label.
- Direct injection of fluorescent dyes or biotin variants (biocytin or neurobiotin) *in-vivo* or *in-vitro* (during electrophysiology experiments).

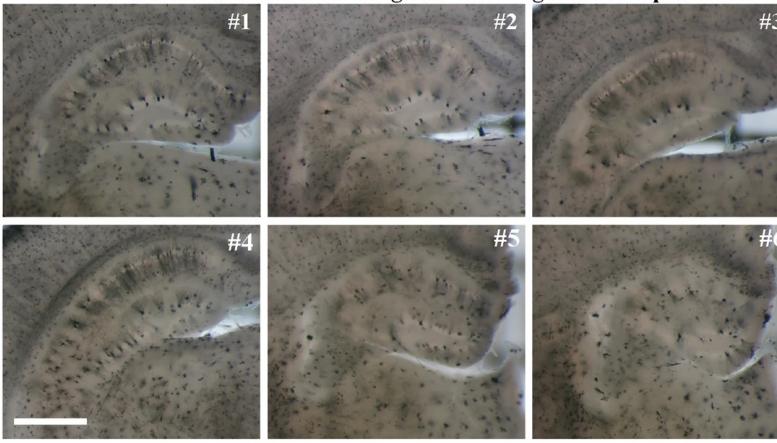
a

Hemisphere after Golgi-Cox staining



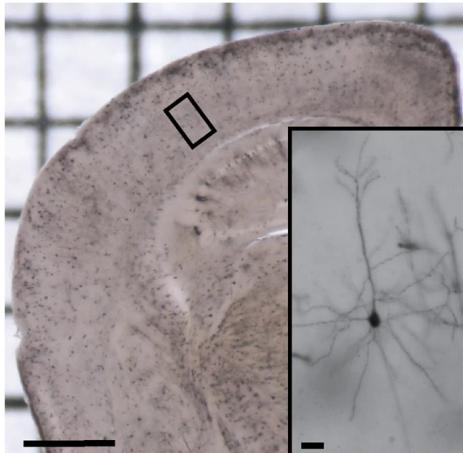
b

Consecutive sections after Golgi-Cox staining of a hemisphere



c

Golgi-Cox staining of a single section



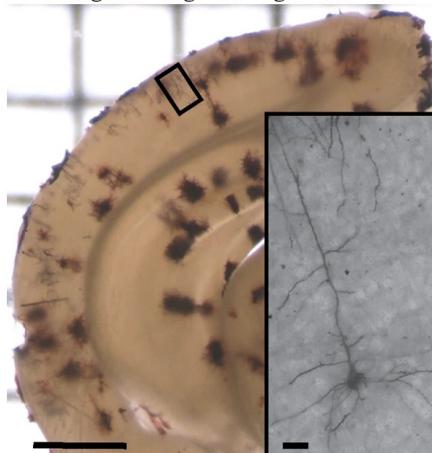
d

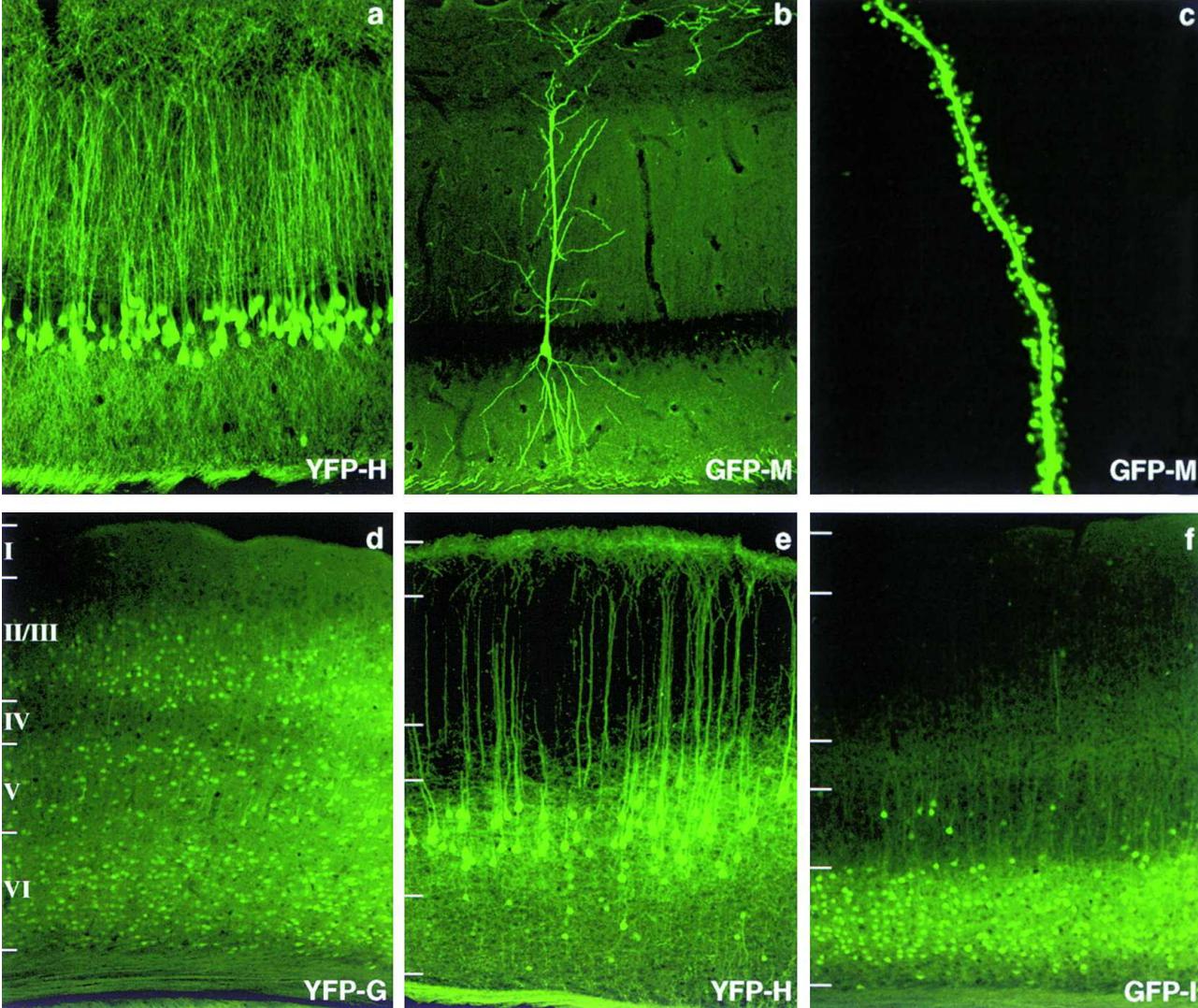
Golgi-Cox on a section



e

Golgi staining of a single section





Immuno-staining

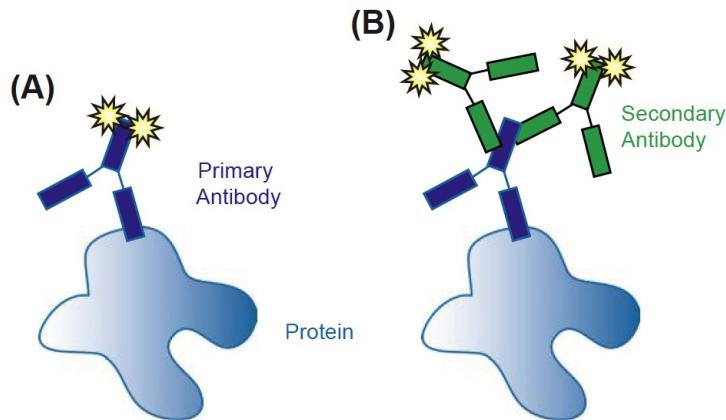


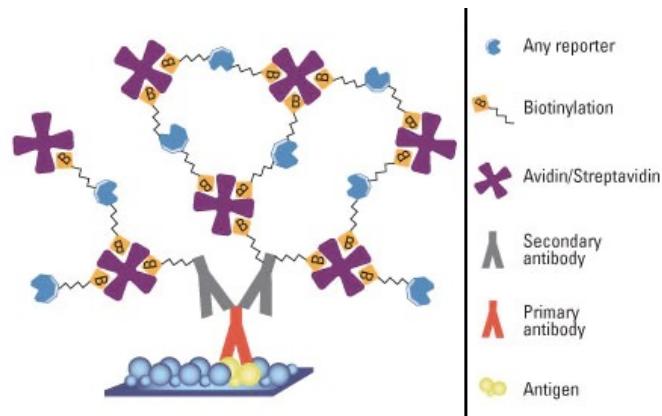
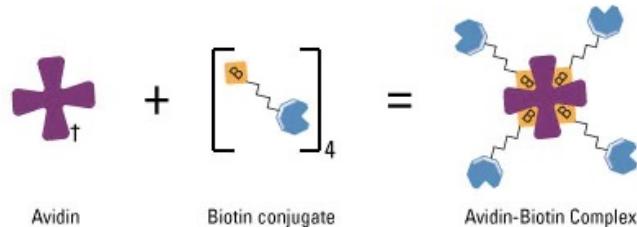
FIGURE 6.6 Immunohistochemistry (IHC). (A) In direct IHC, primary antibodies are conjugated directly to a label that can be visualized. (B) In indirect IHC, primary antibodies attract labeled secondary antibodies, further amplifying the signal.

TABLE 6.3 Commonly Used Antibodies that Label Specific Neural Cell Types

Cell Type	Antibodies
Progenitors/radial glia	Nestin; Pax6; RC2; vimentin; NF (neurofilament)
Young neurons	Doublecortin (DCX); NeuroD
Neurons	Tuj1 (neuron-specific β -tubulin); NeuN
Dendrites	MAP2
Axons	Tau-1, L1, Tag-1
Synapses	PSD95, synapsin
Neuronal subtypes	GAD (GABAergic neurons); vGLUT (glutamatergic); TH (dopaminergic); 5-HT (serotonergic); AChE (cholinergic)
Glia	GFAP (astrocytes); MBP (oligodendrocytes, myelin); PLP
Oligodendrocyte progenitor cells (OPC)	NG2, A2B5, O4 (late progenitor)

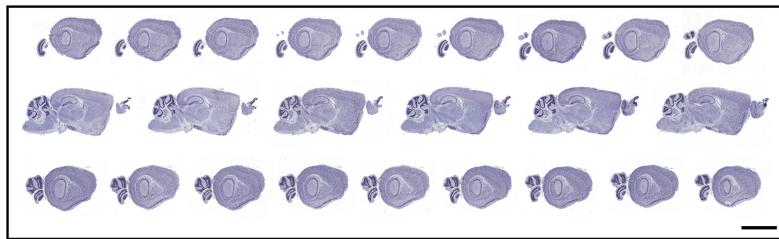
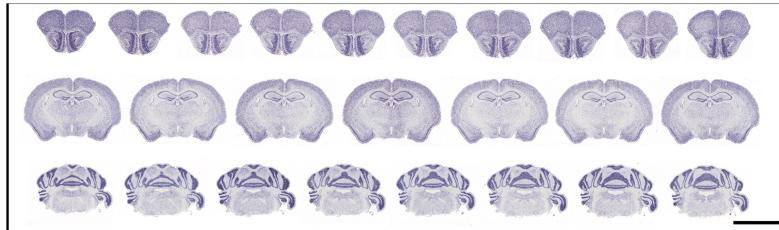
Avidin-Biotin Complex (ABC)

- Fluorophore conjugated to biotin
- The complex can amplify the signal



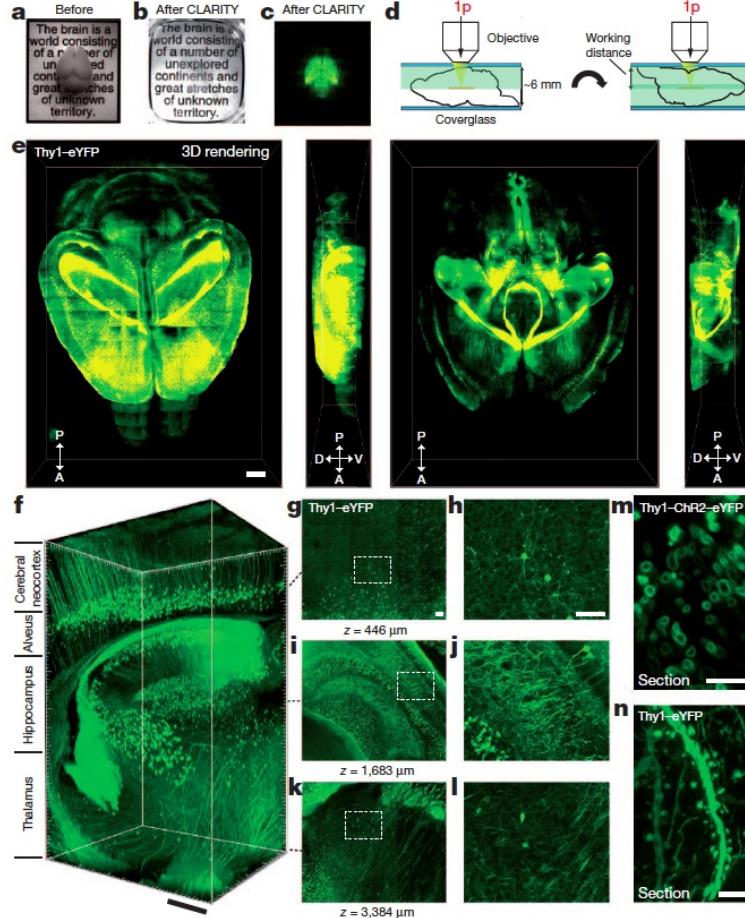
Prepare the tissue for microscope

- Sectioning



Prepare the tissue for microscope

- Sectioning
- CLARITY



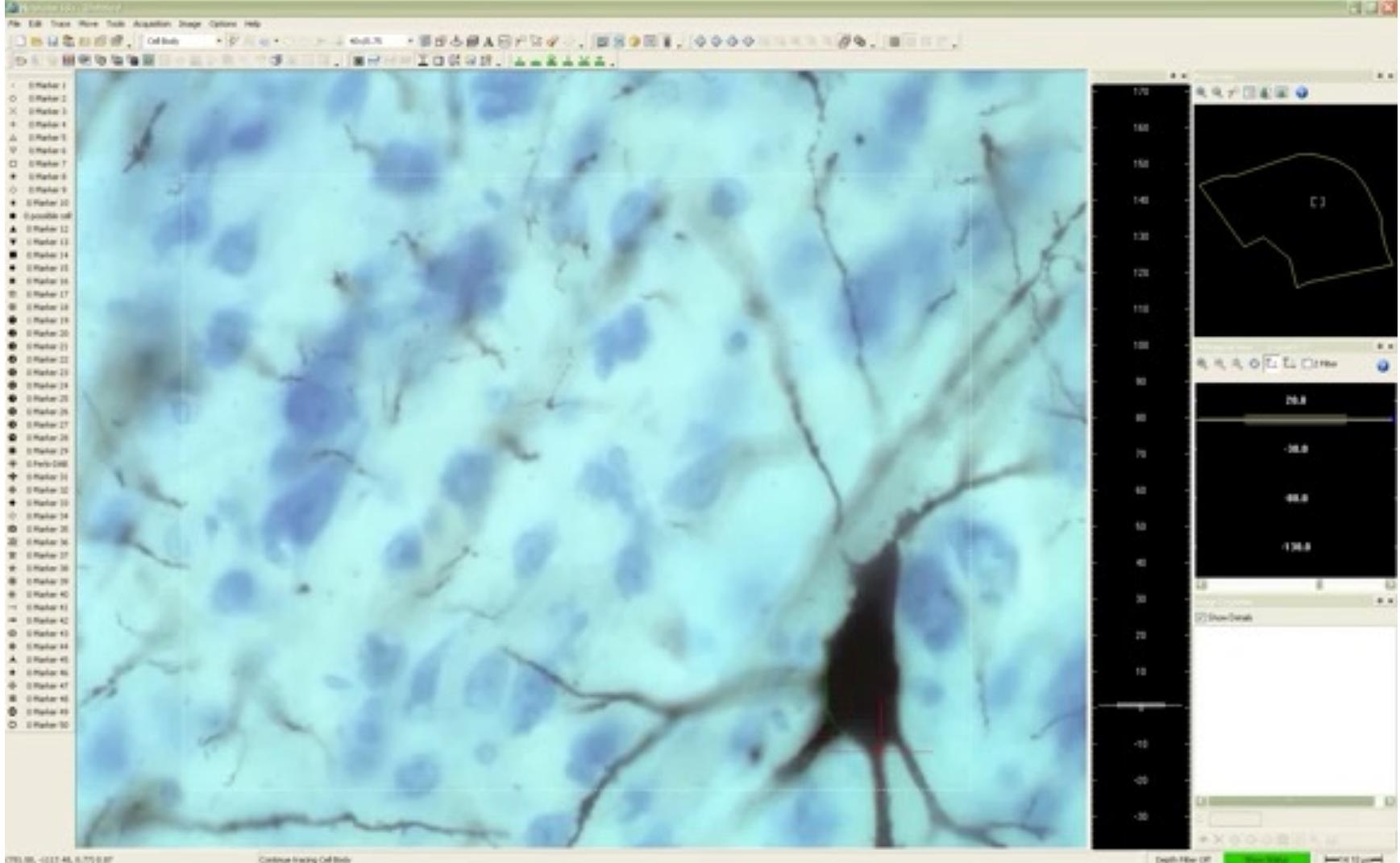
Chung *et al.*, 2013

Microscopy

- Light microscopy
- Fluorescence microscopy
- Electron microscopy (EM)

Neurolucida tracing

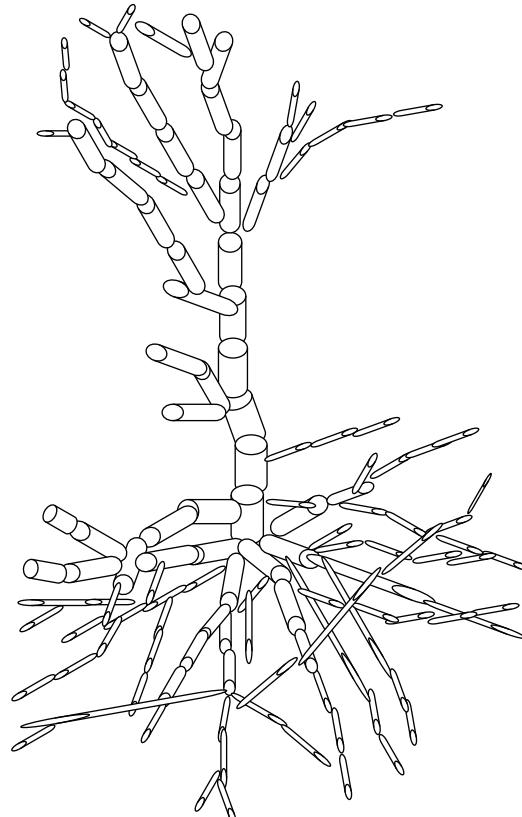




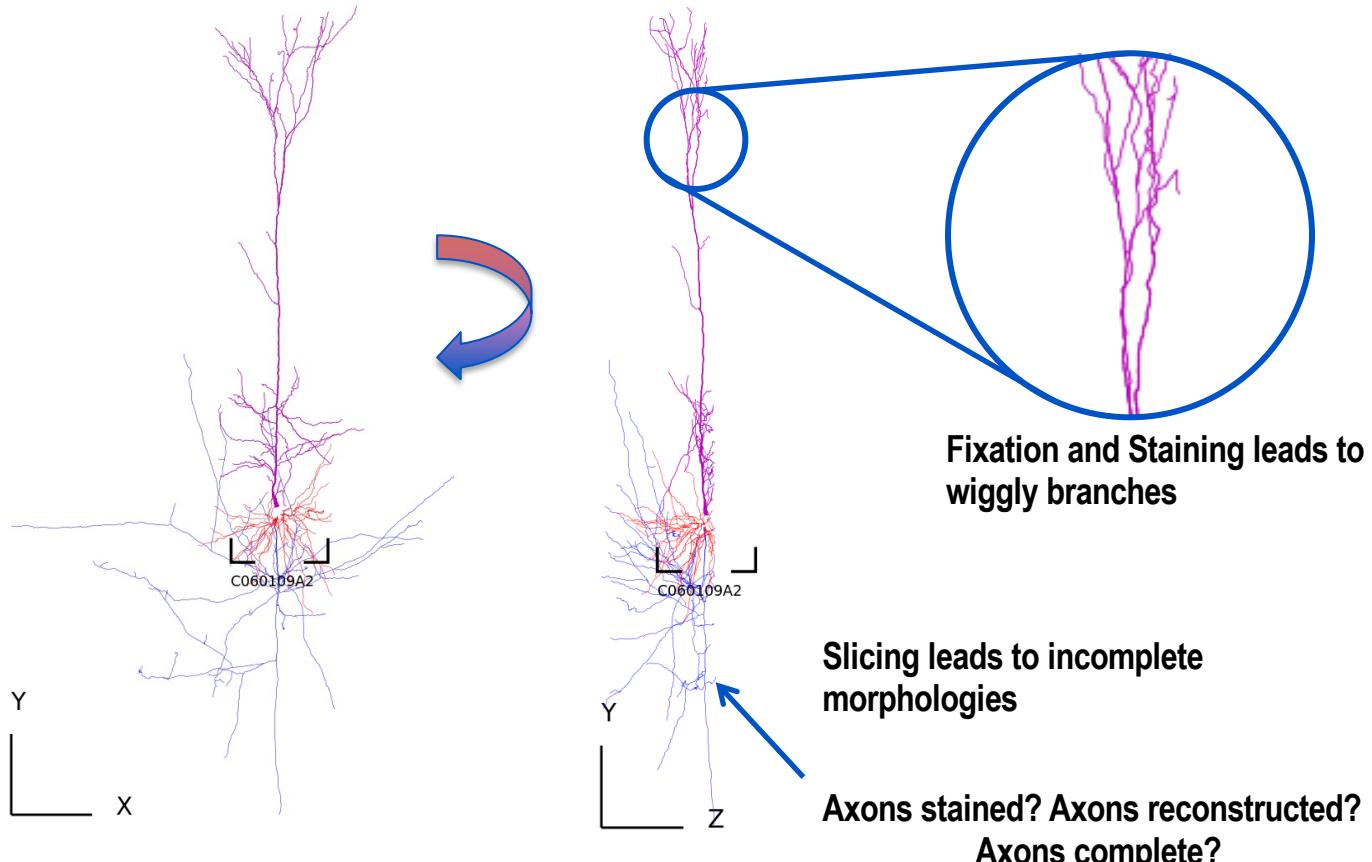


Reconstruction result

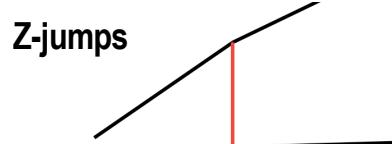
- We assume that the morphology can be faithfully described as a series of truncated cones or frusta
- To increase the precision of our approximation, we can increase the number of segments



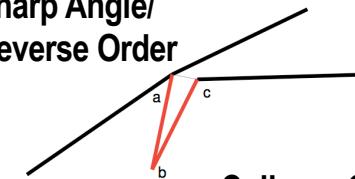
Beware of Systematic Artifacts!



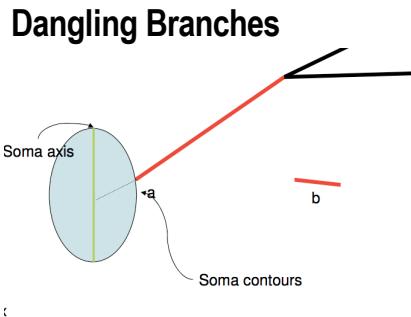
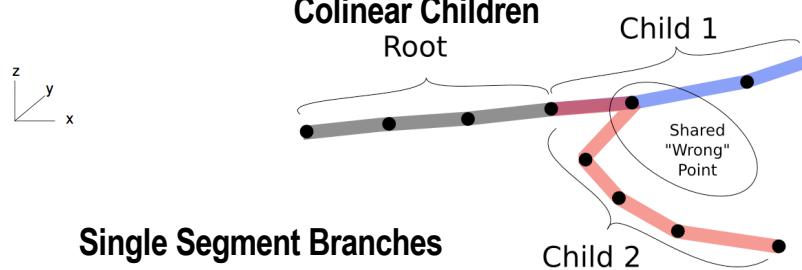
Reconstruction Artifacts



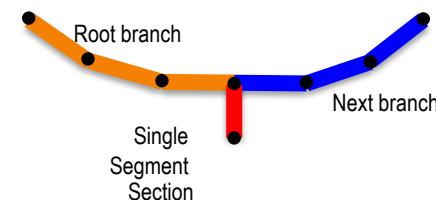
**Sharp Angle/
Reverse Order**



Colinear Children
Root



Single Segment Branches



These artifacts may not matter when publishing a morphology in a paper...
For electrical modeling they matter a lot!

How to deal with artifacts?

- Manual curation
- Automatic correction

Most Common Morphology Formats

Neurolucida ASCII

```

; V3 text file written for MicroBrightField products.
(Sections)

("CellBody"
  (Color Red)
  (CellBody)
  ( 43.94    27.22    -8.51    0.28) ; 1, 1
  ( 46.63    24.62    -8.51    0.28) ; 1, 2
  ( 47.56    19.11    -8.51    0.28) ; 1, 3
  ( 47.23    16.02    -8.99    0.28) ; 1, 4
  ( 46.54    13.75    -8.99    0.28) ; 1, 5
  ( 42.23    11.77    -7.41    0.28) ; 1, 6
  ( 38.09    11.20    -7.46    0.28) ; 1, 7
  ( 36.08    12.18    -7.46    0.28) ; 1, 8
  ( 34.00    13.99    -7.46    0.28) ; 1, 9
  ( 33.43    18.13    -9.39    0.28) ; 1, 10
  ( 34.60    21.28    -9.39    0.28) ; 1, 11
  ( 34.63    24.91    -9.39    0.28) ; 1, 12
  ( 36.10    27.80    -12.04   0.28) ; 1, 13
  ( 39.36    28.86    -12.02   0.28) ; 1, 14
) ; End of contour

( (Color Blue) ; [10,21]
(Axon)
( 37.98    12.22    -6.49    1.39) ; Root
( 38.15    9.73     -6.49    1.39) ; R, 14
( 37.82    6.63     -6.49    1.11) ; R, 2
( 36.33    4.02     -8.67    1.11) ; R, 3
( 35.65    -2.16    -10.28   0.83) ; R, 4
( 36.65    -4.59    -11.55   0.83) ; R, 5
( 39.33    -10.10   -5.05    0.83) ; R, 6
( 41.24    -17.49   -5.05    0.83) ; R, 7
( 42.86    -20.72   -5.05    0.83) ; R, 8

(
( 49.78    -66.77   -9.80    0.56) ; R-1, 1
(
( 50.16    -66.18   -6.76    0.28) ; R-1-1, 1
( 52.61    -65.45   -6.52    0.28) ; R-1-1, 2
( 53.00    -62.92   -6.76    0.28) ; R-1-1, 3

```

SWC (e.g. NeuroMorpho)

Sample	Structure	Type	X	Y	Z	radius	parent
1	1	40.03	19.34	-8.95	8.592	-1	
2	1	40.03	27.93	-8.95	8.592	1	
3	1	40.03	10.75	-8.95	8.592	1	
4	2	99.36	-13.16	-63.91	0.14	1	
5	2	104.33	-12.54	-64	0.14	4	
6	2	111.2	-15.13	-59.85	0.14	5	
7	2	114.84	-15.43	-62.52	0.14	6	
8	2	115.89	-14.52	-62.52	0.14	7	
9	2	118.18	-15.47	-62.52	0.14	8	
10	2	123.96	-18.42	-62.95	0.14	9	
11	2	134.11	-20.21	-62.28	0.14	10	
12	2	138.22	-23.27	-62.28	0.14	11	
13	2	142.22	-24.66	-62.28	0.14	12	
14	2	154.66	-27.42	-62.28	0.14	13	
15	2	160.08	-31.22	-58.66	0.14	14	
16	2	168.86	-33.39	-58.66	0.14	15	
17	4	33.54	16.22	-7.52	1.665	1	
18	4	32.45	15.86	-7.52	1.665	17	

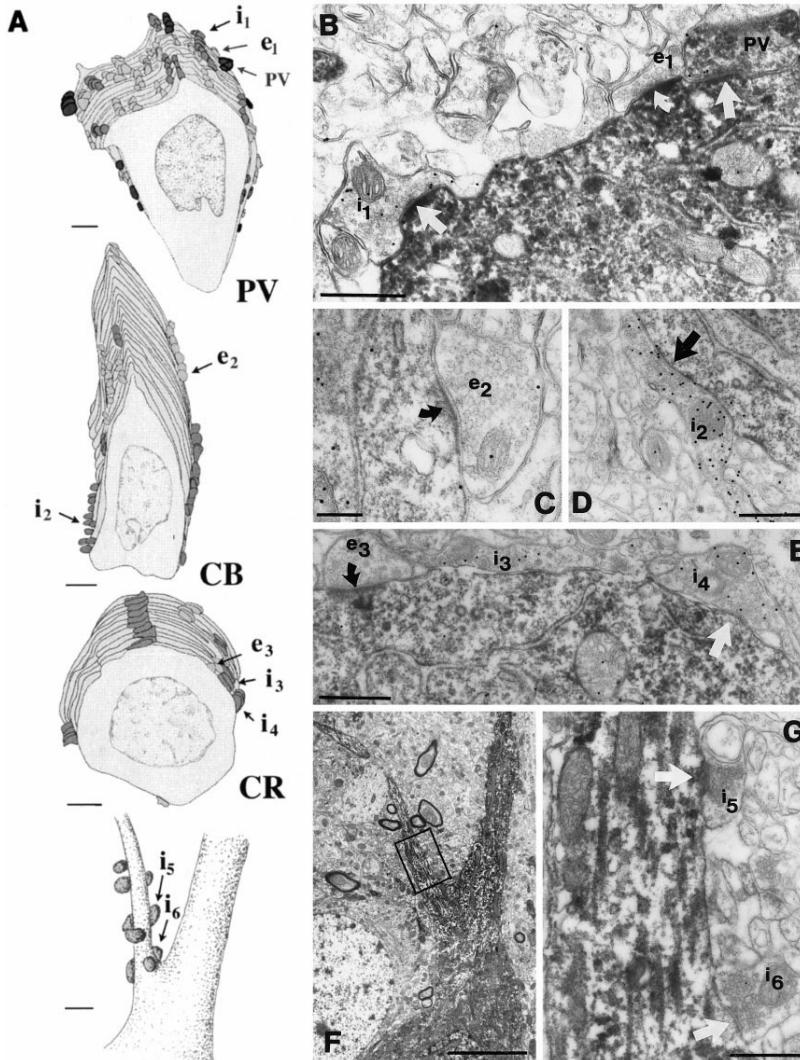
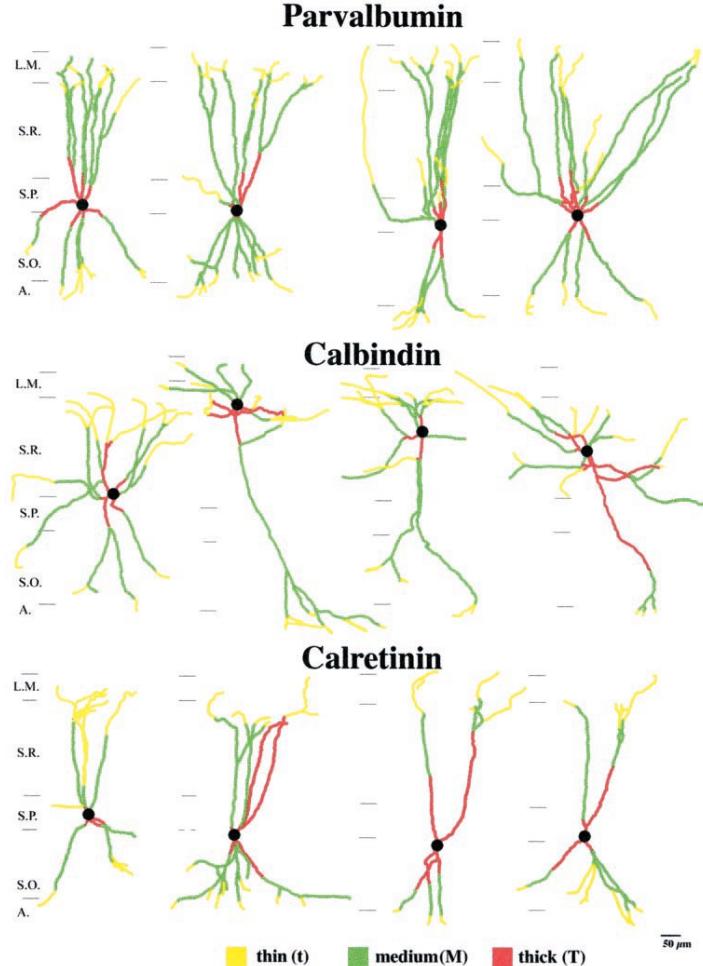
MorphML

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"http://www.w3.org/2001/XMLSchema-instance" xsi: Schema Location =
"http://morphml.org/morphml/schema
http://morphml.org:8080/NeuroMLValidator/NeuroMLFiles/
Schemata/v1.5/Level1/MorphML_v1.5.xsd" lengthUnits = "micron">
<cells>
<cell name = "SampleCell">
<meta:notes>A Simple cell</meta:notes> <segments>
<segment id = "0" name = "SomaSegment" cable = "0">
<proximal x="0.0" y="0.0" z="0.0" diameter = "16.0"/>
<distal x = "0.0" y = "0.0" z = "0.0" diameter = "16.0"/>
</segment>
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<proximal x = "8.0" y = "0.0" z = "0.0" diameter = "5.0"/>
<distal x = "28.0" y = "2.0" z = "0.0" diameter = "6.0"/>
</segment>
```

For a good description: <http://www.neuroconstruct.org/docs/import.html>

Challenge: find the correct granularity

- Incorporate the salient features given our scope
- Do no incorporate noise (staining artefacts)



Summary 2

- Reconstruction is still a quite manual process.
- There is no perfect method. Each method has pros and cons.
- Data format is still an open problem.

Lecture Overview

- Scope
- Approaches
- **Applications**

Table 1.1 List of frequently used morphometric measures to quantify neuronal morphologies

Property	Brief description
Number of stems ^a	Total number of segments leaving from the dendritic root
Number of branch points ^a	Total number of branch points in the tree
Branch order	Topological distance from the dendritic root. The root has order 0, and the order of a segment in the tree equals the number of branch points along the path to the root + 1
Maximum branch order ^a	Maximum branch order in a neuron
Degree	Number of termination points downstream of the node under investigation
Maximum degree ^a	Maximum degree in a tree. By definition the degree at the dendritic root
Total length ^a	Summed segment lengths of all segments in a tree (see next)
Segment length	Path length of the incoming segment toward a node
Stem length	Path length between a branch point with order=1 and the dendritic root
Interbranch length	Path length between branch points
Terminal segment length	Path length between the termination point and the last branch point length
Euclidean distance	Can be applied in a similar fashion as the path length. Often used to measure the distance between the soma and the termination points
Dimension ^a	Width, height, and depth of the bounding box
Taper rate ^a	The uniform decrease in diameter across a dendritic branch
Somatofugal tropism ^a	Quantification of the preference of a neurite to grow away from the soma. Defined as the ratio of a segment's path length and the Euclidean distance between its starting and end point
Fractal dimension ^a	Fractal dimension used as a measure of space-filling
Contraction	Quick proxy of the fractal dimension: the Euclidean length of a branch divided by the path length
Partition asymmetry ^a	Topological complexity of a tree. A completely asymmetric tree has PA=1, symmetric has PA=0
Lacunarity ^a	A measure of “holes” in a volume spanned by a tree. See Sect. 1.4.2
Horton–Strahler index	Measure of topological complexity of a tree relating the order and asymmetry in that tree. Computed for each branch point. See Sect. 1.4.1
Strahler number ^a	The Horton–Strahler index associated with the root of the tree

Light shading—topological measures

Medium shading—geometrical measures

Dark shading—compound measures

^aGlobal measure as opposed to distribution of local measures. However, often derived features are used as global feature. For instance, to describe the branch order in a tree, a distribution of all orders can be given, or the distribution can be characterized by considering the maximum branch order, the average branch order, etc. This holds for all local measures



NeuroMorpho.Org



Version 7.9 - Released: 12/13/2019 - Content: 121544 neurons

Total number of downloads: 13894 177

Total site hits since August 1, 2006: 49 191

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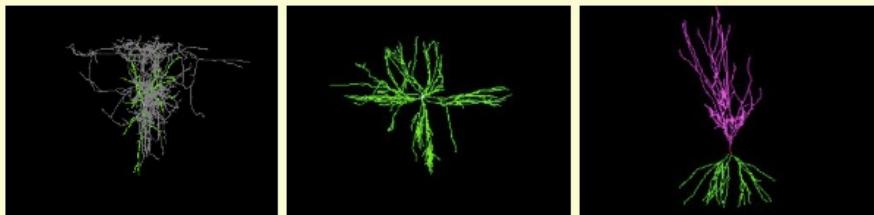
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Contributors from 194 countries

121544 digital reconstructions

Contributors



NeuroMorpho.Org is a centrally curated inventory of **digitally reconstructed neurons** associated with peer-reviewed publications. It contains contributions from over 500 laboratories worldwide and is continuously updated as new morphological reconstructions are collected, published, and shared. To date, NeuroMorpho.Org is the largest collection of publicly accessible 3D neuronal reconstructions and associated metadata.

The goal of NeuroMorpho.Org is to provide dense coverage of available reconstruction data for the neuroscience community. Data sharing through NeuroMorpho.Org enables the full and continuing research potential of existing digital reconstruction data.



Animal	Experiment
Species	Protocol
Gender	Experimental Condition
Minimum Weight	Stain
Maximum Weight	Slicing Thickness
Development	Slicing Direction
Minimum Age	Tissue Shrinkage
Maximum Age	Reconstruction Method
	Objective Type
	Objective Magnification
Anatomy	Source
Brain Region	Archive
Cell Type	PMID
Completeness	
Structural Domain	Original Format
Physical Integrity	Date of Deposition
Morphological Attributes	Date of Upload

[Hits from current criteria](#)

Your search results can be arranged:

[By animal species](#) [By brain region](#) [By cell type](#) [By archive](#)



73 Neurons found

Esclapez

rat

hippocampus

Trilaminar

[DEV104T1](#)

[DEV119T4](#)

[DEV166T1](#)

Perforant pathway-associated

[DEV119T3](#)

[DEV122T3](#)

[DEV131T3](#)

[DEV133T2](#)

[DEV157T2](#)

perisomatic targeting

[DEV125T1](#)

[DEV128T2](#)

[DEV133T3](#)

[DEV174T1](#)

[R155T1](#)

[R61](#)

[R75C1](#)

oriens-lacunosum moleculare

[DEV127T1](#)

[DEV159T2](#)

[DEV169T1](#)

[DEV95T7](#)

[DEV82T1m](#)

Schaffer-collateral associated

[DEV127T3](#)

[DEV160T3](#)

[DEV172T1](#)

[DEV52T1](#)

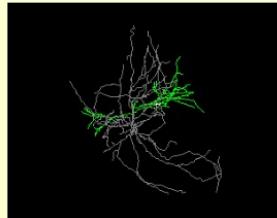
[Dev97T1](#)

[R161T1m](#)

bistratified

[DEV174T4](#)

[DEV50T2](#)



[Morphology File \(Standardized\)](#)

[Morphology File \(Original\)](#)

[Log File \(Standardized\)](#)

[Log File \(Original\)](#)

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[3D Neuron Viewer - Java, legacy](#)

[3D Neuron Viewer - WebGL, novel](#)

[Animation](#)

Details about selected neuron

NeuroMorpho.Org ID : NMO_02325

Neuron Name : DEV104T1

Archive Name : Escalpez,Cossart_Bernard

Species Name : rat

Strain : Wistar

Structural Domains : Dendrites, Soma, Axon

Physical Integrity : Dendrites Complete, Axon Moderate

Morphological Attributes : Diameter, 3D, Angles

Min Age : 14.0 days

Max Age : 21.0 days

Gender : Not reported

Min Weight : Not reported

Max Weight : Not reported

Development : young

Primary Brain Region : hippocampus

Secondary Brain Region : CA1

Tertiary Brain Region : stratum radiatum

Primary Cell Class : interneuron

Secondary Cell Class : Trilaminar

Tertiary Cell Class : Not reported

Original Format : Neurolucida.dat

Experiment Protocol : in vitro

Experimental Condition : Control

Staining Method : biocytin

Slicing Direction : horizontal

Slice Thickness : 400 μ m

Tissue Shrinkage : Not reported

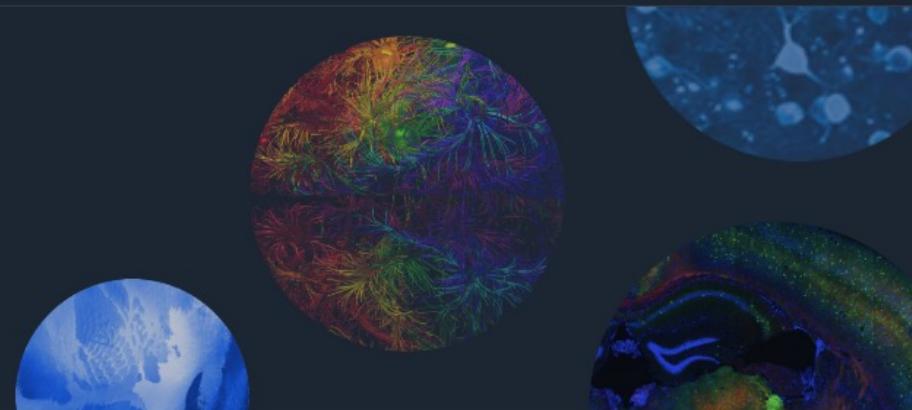
Objective Type : Not reported

Magnification : Not reported



	With axon	Layer info	Orientation hints	Soma	Complete axon
BC	33	8	8	2d	33
OLM	2	2	2	3d , 2d	0
SCA	6	6	6	3d (1), 2d (5)	6
IS3	1	1	1	2d	1

Accelerating progress
toward understanding
the brain.



New Data and Tools



MOUSE TRANSCRIPTOMIC CELL TYPES

Explore the latest dataset and



HUMAN TRANSCRIPTOMIC CELL TYPES

Explore the latest dataset and



VISUAL CODING WITH NEUROPIXELS

The latest from Allen Brain



SYNAPTIC PHYSIOLOGY

Dive into the first Synaptic Physiology dataset, which brings together

Cell Types: Overview of the Data

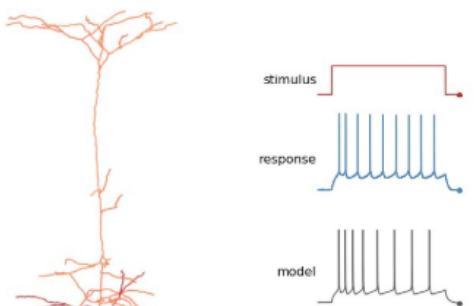
This brain cell database contains a survey of biological features derived from single cell data, from both human and mouse. It is part of a multi-year project to create a census of cells in the mammalian brain.

The database contains [electrophysiological](#), [morphological](#), and [transcriptomic](#) data measured from individual cells, as well as models simulating cell activity. Thus far, data generation has focused on select areas of cerebral cortex, and thalamic neurons.

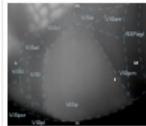
Browse electrophysiological response data and reconstructed neuronal morphologies using the [Cell Feature Search](#) tool. Single cell gene expression data is described on the [RNA-Seq Data](#) page.

Use the [Allen Software Development Kit](#) (SDK) to programmatically access and analyze raw data, and to run models.

Data can be downloaded by selecting individual experiments in the Cell Feature Search tool, by accessing transcriptomic [RNA-Seq files](#), or through the Allen SDK or API.

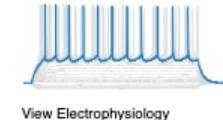
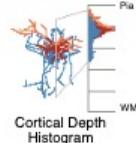


Morphology Summary



Mouse Line	Oxtr-T2A-Cre
ID	584254833
Area	Primary visual area
Layer	2/3
Cell Reporter	
Dendrite Type	spiny
Apical Dendrite	intact
Hemisphere	left

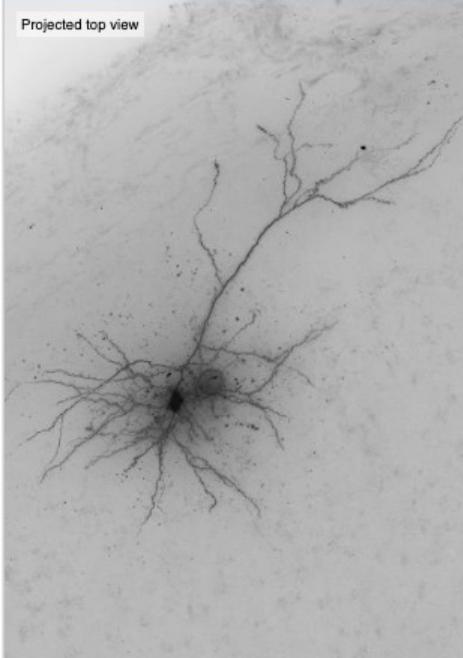
Max Euclidean Distance 329.6
Number of Stems 7
Number of Bifurcations 41
Average Contraction 0.876
Parent:Daughter 0.990



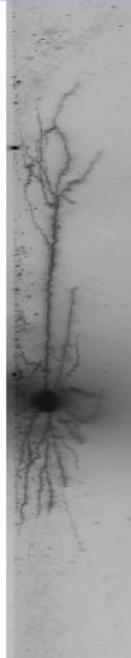
View Electrophysiology

Browse Morphology Data

Projected top view



Projected side view



3D neuron reconstruction



- Truncated
- Not Reconstructed
- Soma
- Axon
- Dendrite
- Apical Dendrite

View image stack



Contrast

Reset

-45 +45



Download Morphology

Download Morphological Measurements

MouseLight / NeuronBrowser

This is an interactive web platform to explore, search, filter and visualize single neuron reconstructions generated by the Janelia MouseLight project.



Reconstructions are presented registered to the Allen Reference Atlas. Queries for neuronal morphology can be made based on soma position or location of projection targets within the brain. Filtered results can be visualized in 3-D along with the Allen brain compartments. We will periodically add to this collection of reconstructed neurons in future releases. Query results can also be downloaded for offline analysis (see [Terms of Use](#)).

A quick overview of currently available features and how to use the NeuronBrowser can be found in a Tutorial Video [here](#).

For additional information on how the data was generated please refer to the documentation in the [Resources](#) section. A description of the core MouseLight technology can also be found [here](#).



Connect With Us

For data feedback, questions, and comments please contact us.

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Join in on the conversation and follow us on Twitter.

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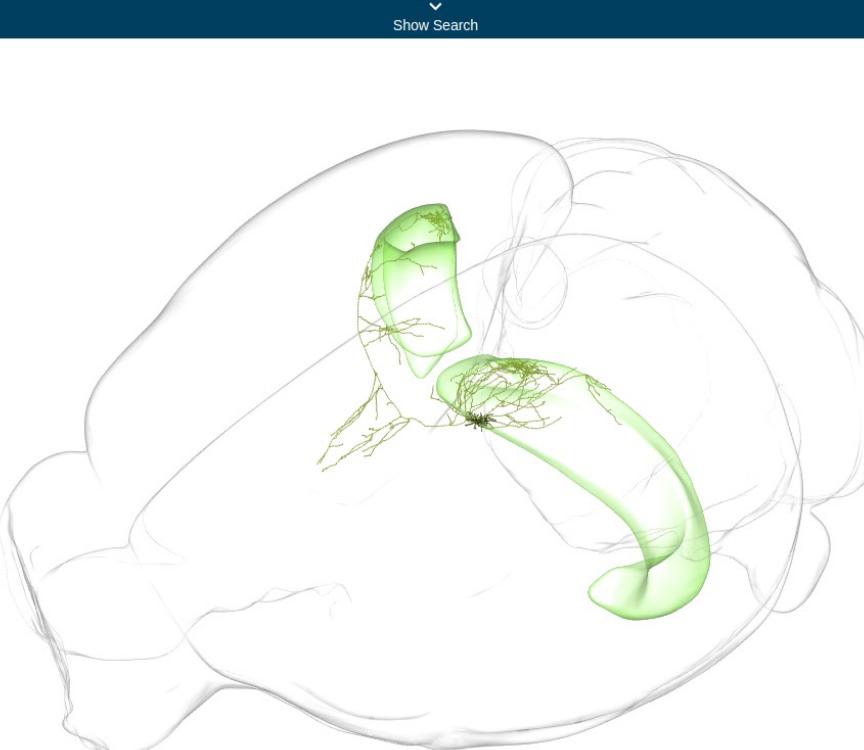
Reset

Matched 155 of 1094 neurons in 6.007 seconds

+ Add Filter

Search

Neurons					
<input type="checkbox"/>	All	<input type="checkbox"/>	AA0960	CA2	<input type="checkbox"/>
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<input type="checkbox"/>	All	<input type="checkbox"/>	AA0890	SUB	<input type="checkbox"/>
<input type="checkbox"/>	All	<input type="checkbox"/>	AA0881	PRE	<input type="checkbox"/>
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<input type="checkbox"/>	All	<input type="checkbox"/>	AA0848	SUB	<input type="checkbox"/>



Compartments	
	History
<input checked="" type="checkbox"/>	Whole Brain
<input checked="" type="checkbox"/>	Field CA1
	All Compartments
	Filter compartments...
<input checked="" type="checkbox"/>	Whole Brain
	Basic cell groups and regions
	Brain stem
	Cerebellum
	Cerebrum
	Cerebral cortex
	Cortical plate
	Hippocampal formation
	Hippocampal region
	Ammon's horn
	Field CA1
	Field CA2
	Field CA3
	Dentate gyrus
	Fasciola cinerea
	Induseum griseum
	Retrohippocampal region
	Isocortex
	Olfactory areas
	Cortical subplate
	Basolateral amygdalar nucleus
	Basomedial amygdalar nucleus
	Clastrum
	Endopiriform nucleus
	Lateral amygdalar nucleus
	Posterior amygdalar nucleus
	Cerebral nuclei
	fiber tracts
	ventricular systems

FEATURE ARTICLE

Differential Structure of Hippocampal CA1 Pyramidal Neurons in the Human and Mouse

Ruth Benavides-Piccione^{1,2,*}, Mamen Regalado-Reyes²,
Isabel Fernaud-Espinosa², Asta Kastanauskaite², Silvia Tapia-González²,
Gonzalo León-Espinosa^{2,3}, Concepcion Rojo⁴, Ricardo Insausti⁵,
Idan Segev^{6,7} and Javier DeFelipe^{1,2}

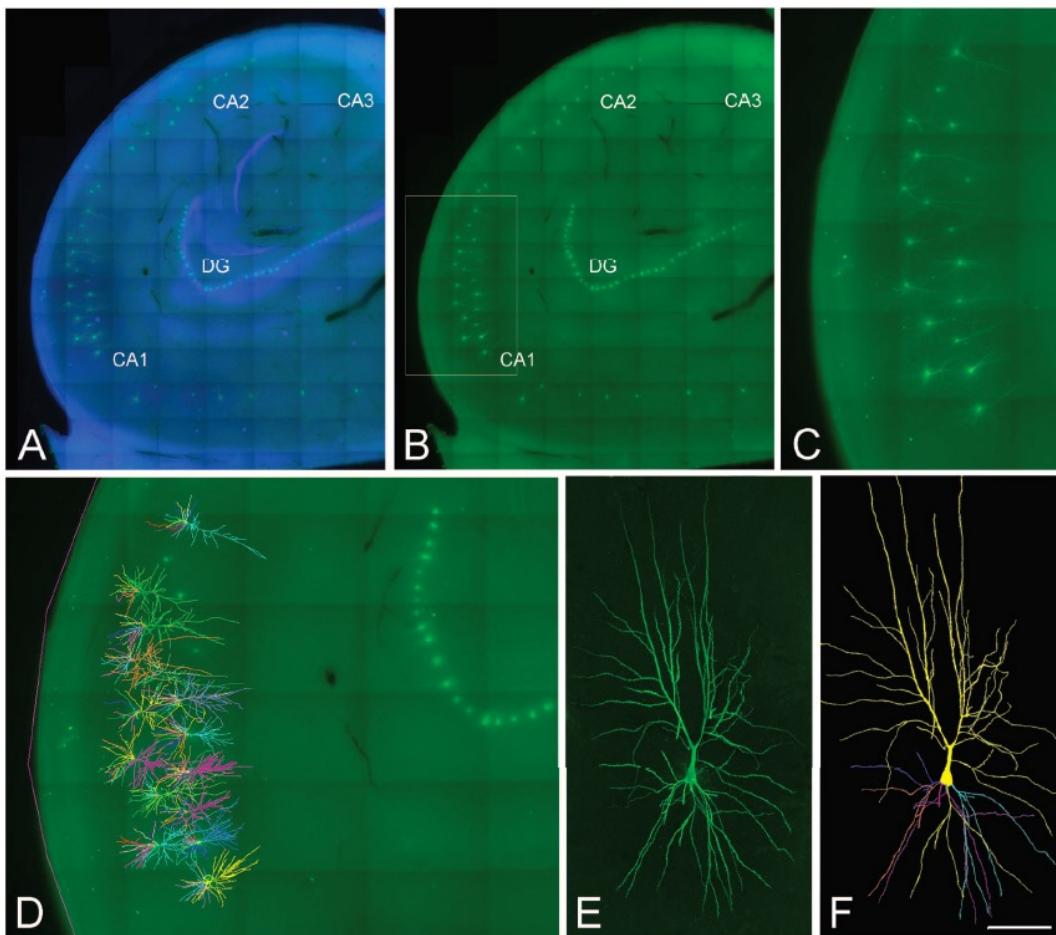
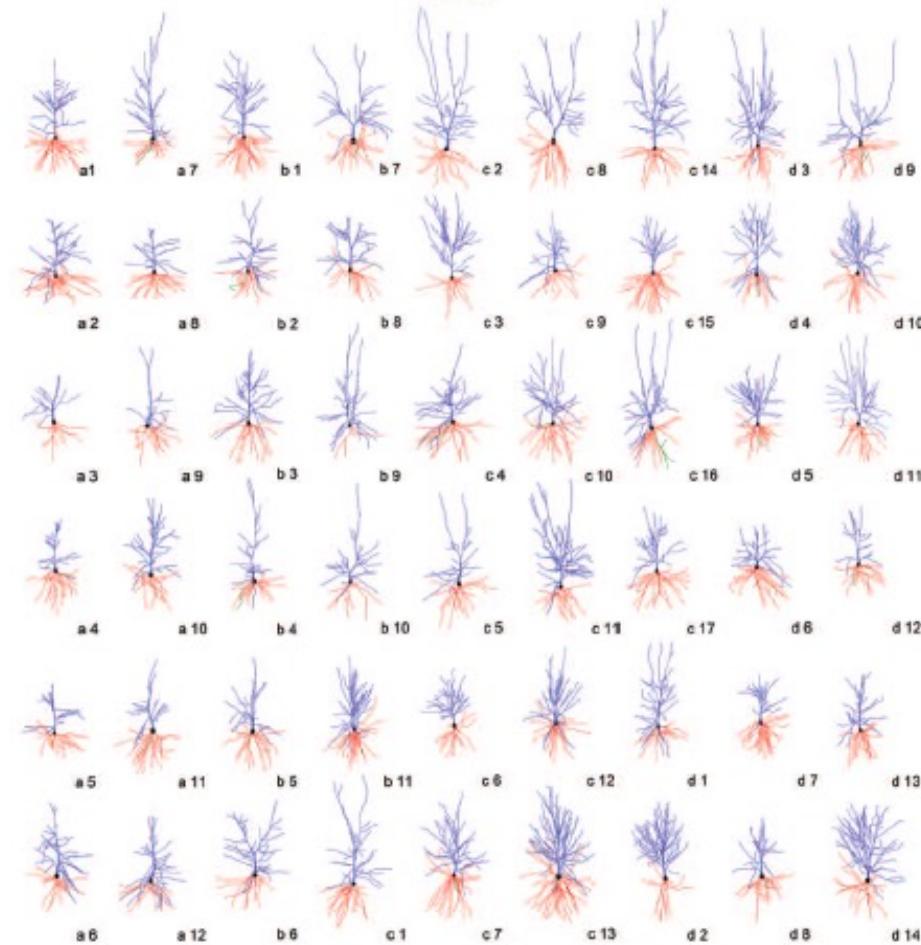
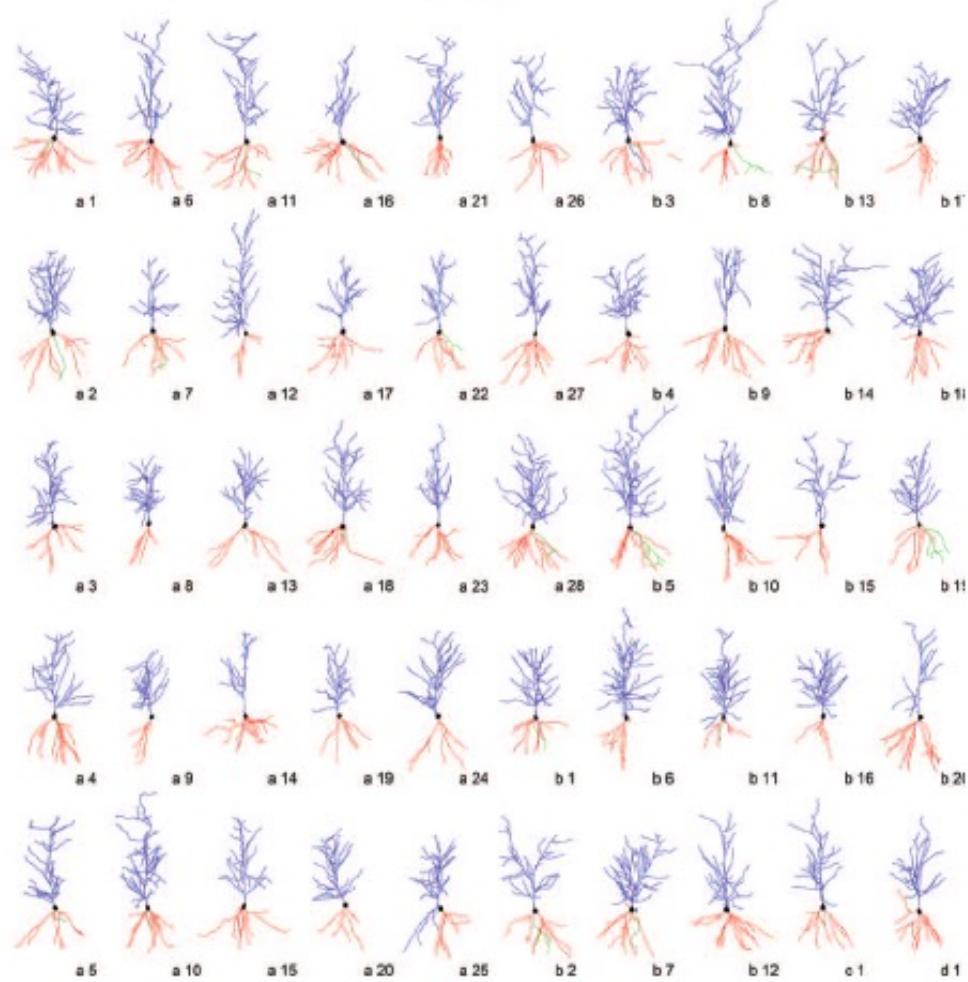


Figure 2. Confocal microscopy images of human neurons injected with LY in the hippocampus. (A and B) Labeled pyramidal cells (green) and DAPI staining (blue) in different regions of the human hippocampus, including CA1, CA2, CA3, and the dentate gyrus (DG) region. (C) Higher magnification image of the boxed region shown in (B). (D) 3D-reconstructed cells superimposed on the confocal image shown in (C). (E and F) High-magnification z projection showing an injected CA1 pyramidal cell (E) and the 3D reconstruction of the same cell (F). Scale bar (in panel F) is equal to 1100 μ m in (A) and (B); 460 μ m in (C) and (D); 100 μ m in (E) and (F).

Human



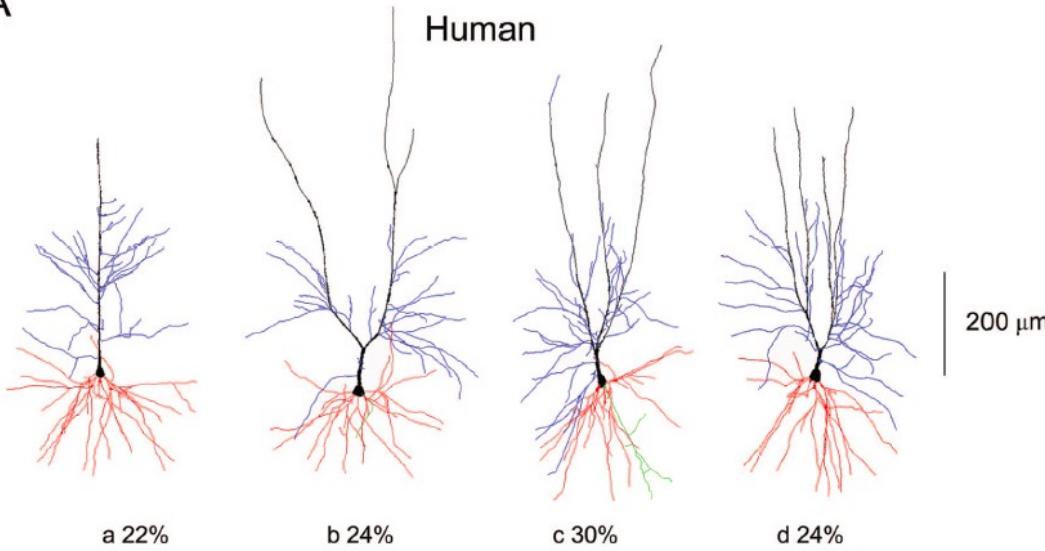
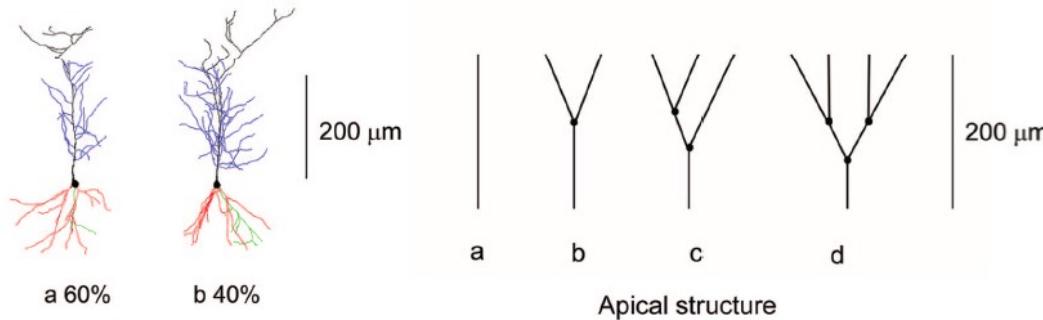
Mouse



200 μ m

50 μ m

	Human	Mouse	% Difference
Area of the maximum perimeter of the soma (μm^2)	350 ± 9.7	137 ± 3.0	255
Number of primary basal dendrites	6.37 ± 0.25	3.04 ± 0.15	209
Basal extent (μm)	300	190	158
Distance peak basal nodes (μm)	40	30	133
Segment diameter first-order main apical (μm)	5.74 ± 0.18	1.82 ± 0.05	302
Segment diameter second-order main apical (μm)	3.31 ± 0.15	1.19 ± 0.04	278
Segment diameter first-order apical collateral (μm)	1.33 ± 0.02	0.71 ± 0.01	187
Segment diameter second-order apical collateral (μm)	1.07 ± 0.01	0.65 ± 0.005	165
Segment diameter first-order basal (μm)	1.98 ± 0.04	1.19 ± 0.04	166
Segment diameter second-order basal (μm)	1.50 ± 0.02	0.88 ± 0.02	170
Segment length first-order main apical (μm)	84.77 ± 10.75	157.6 ± 13.54	54
Segment length second-order main apical (μm)	130.9 ± 21.08	124 ± 14.60	105
Segment length first-order apical collateral (μm)	60.99 ± 2.36	60.48 ± 1.33	101
Segment length second-order apical collateral (μm)	99.4 ± 2.94	64.54 ± 1.45	154
Segment length first-order basal (μm)	16.63 ± 0.80	11.48 ± 0.98	145
Segment length second-order basal (μm)	48.32 ± 3.28	33.64 ± 3.30	144
Segment branching diameter apical collateral (μm)	1.41 ± 0.02	0.81 ± 0.01	175
Segment terminal diameter apical collateral (μm)	0.96 ± 0.004	0.65 ± 0.002	148
Segment branching diameter basal (μm)	1.63 ± 0.01	0.90 ± 0.01	181
Segment terminal diameter basal (μm)	1.01 ± 0.005	0.64 ± 0.005	159
Segment branching length apical collateral (μm)	25.32 ± 0.80	14.57 ± 0.64	174
Segment terminal length apical collateral (μm)	147.1 ± 1.64	77.9 ± 0.78	188
Segment branching length basal (μm)	20.55 ± 0.66	16.43 ± 0.73	125
Segment terminal length basal (μm)	169.2 ± 1.78	93.51 ± 1.76	180
Average diameter at 10 μm Sholl main apical distance (μm)	7.19 ± 0.21	3.12 ± 0.15	230
Average diameter at 10 μm Sholl collateral distance (μm)	1.87 ± 0.33	0.80 ± 0.07	234
Average diameter at 10 μm Sholl basal distance (μm)	2.36 ± 0.20	1.36 ± 0.07	173
Average diameter at 10 μm Sholl axon distance emerging from soma (μm)	3.92 ± 0.42	1.18 ± 0.05	332
Average diameter at 10 μm Sholl axon distance emerging from dendrite (μm)	1.88 ± 0.25	0.85 ± 0.23	221
Average diameter of basal dendrites containing an emerging axon (μm)	4.97 ± 0.27	2.4 ± 0.18	207

A**B****Mouse**

Key points

- On average human cells are 2 times bigger than mouse cells
- Human brain is 2800 times bigger. There is a biophysical limit for the size of a neuron.
- Human cells are not just a larger version of the mouse cells
- There is no linear scaling for all the characteristics
- The morphologies appear larger and more complex
- This may correspond to more complex information processing. Multiple semi-independent dendritic subunits

Reconstruction of 1,000 Projection Neurons Reveals New Cell Types and Organization of Long-Range Connectivity in the Mouse Brain

Johan Winnubst,¹ Erhan Bas,^{1,5} Tiago A. Ferreira,¹ Zhuhao Wu,² Michael N. Economo,¹ Patrick Edson,³ Ben J. Arthur,¹ Christopher Bruns,^{1,6} Konrad Rokicki,¹ David Schauder,¹ Donald J. Olbris,¹ Sean D. Murphy,¹ David G. Ackerman,¹ Cameron Arshadi,¹ Perry Baldwin,¹ Regina Blake,¹ Ahmad Elsayed,¹ Mashtura Hasan,¹ Daniel Ramirez,¹ Bruno Dos Santos,¹ Monet Weldon,¹ Amina Zafar,¹ Joshua T. Dudman,¹ Charles R. Gerfen,⁴ Adam W. Hantman,¹ Wyatt Korff,¹ Scott M. Sternson,¹ Nelson Spruston,¹ Karel Svoboda,¹ and Jayaram Chandrashekhar^{1,7,*}

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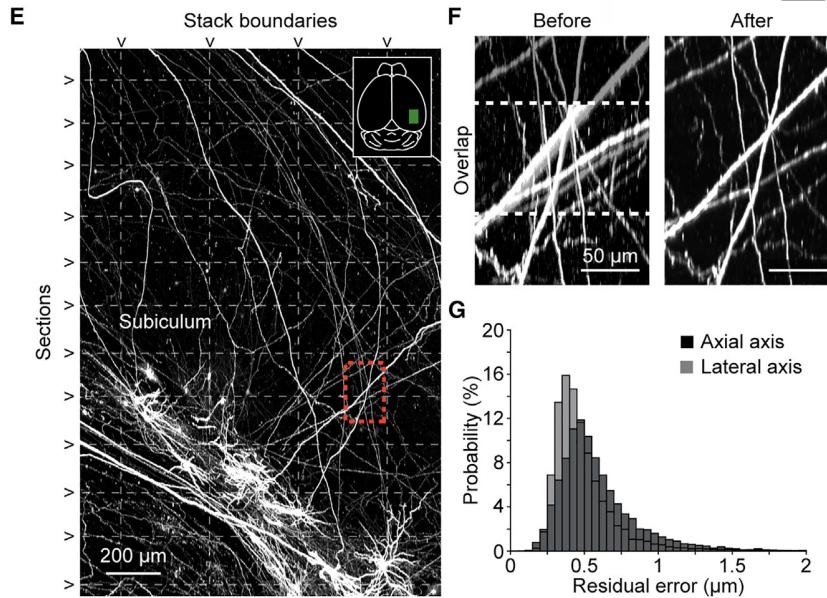
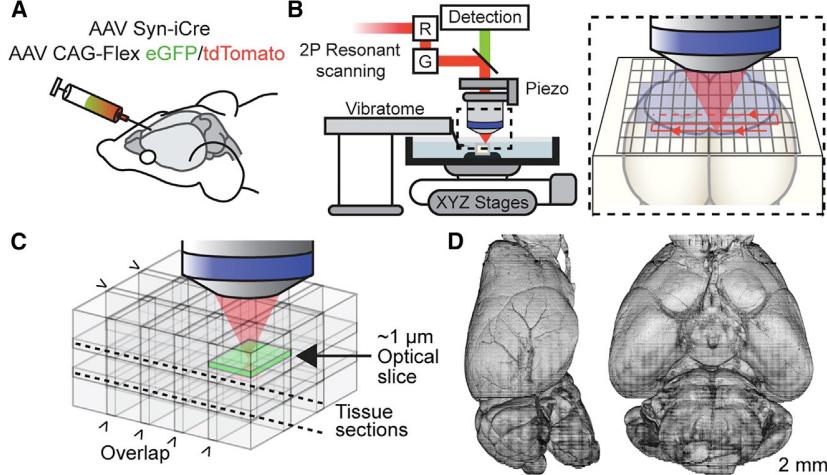
⁶Present address: Environmental Systems Research Institute, Redlands, CA 92373, USA

⁷Lead Contact

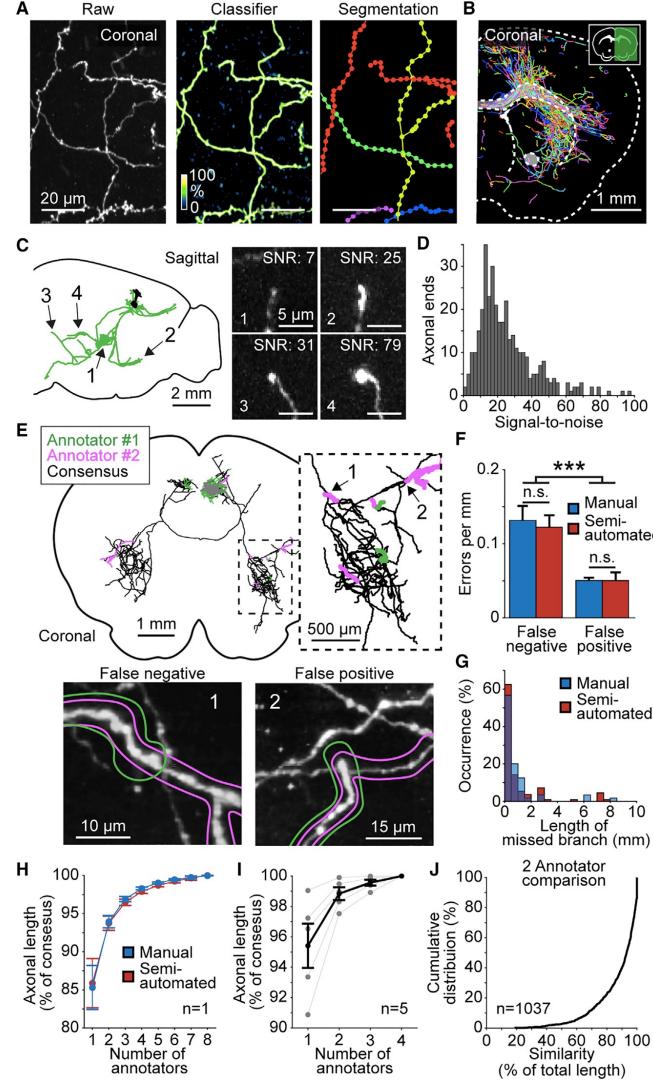
*Correspondence: chandrashekharj@janelia.hhmi.org

<https://doi.org/10.1016/j.cell.2019.07.042>

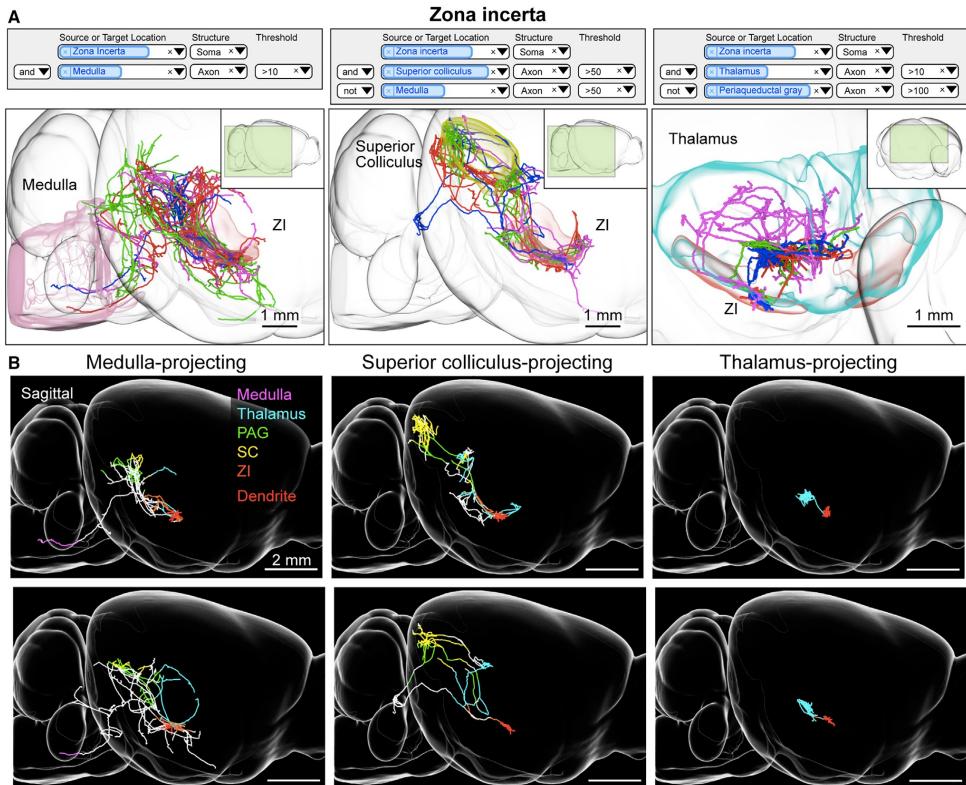
- Fluorescence labelling
- > 100 labelled neurons / brain
- Brain optically cleared
- Re-assemble of 40,000 stack images



- Semi-automatic reconstruction
- Automatic segmentation
- Segments were broken at each branchpoints and close cross points
- Manual linking and proofreading
- Multiple annotators
- +5-fold increase in speed compare to pure manual reconstruction without loose in precision



- Register the morphologies in Allen Mouse Common Coordinate Framework
- Collect and organize data highlights patters
- New projecting classes



Summary 3

- More systematic analysis of the morphologies
- High throughput technologies are emerging
- Databases allow users to access better data and
- organized in a better way
 - Metadata
 - Quality, completeness
 - Registered in atlas

What you have learnt

- Cell type.
- Cell classification.
- Reconstruction process.
- Reconstruction artefacts.
- File formats.
- Morphometrics.
- Familiarize with database of morphological reconstructions (e.g., neuromorpho.org)