How to reconstruct 3D neurons in accuracy and efficiency using Vaa3D_TeraVR platform

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SEU-ALLEN Joint Center

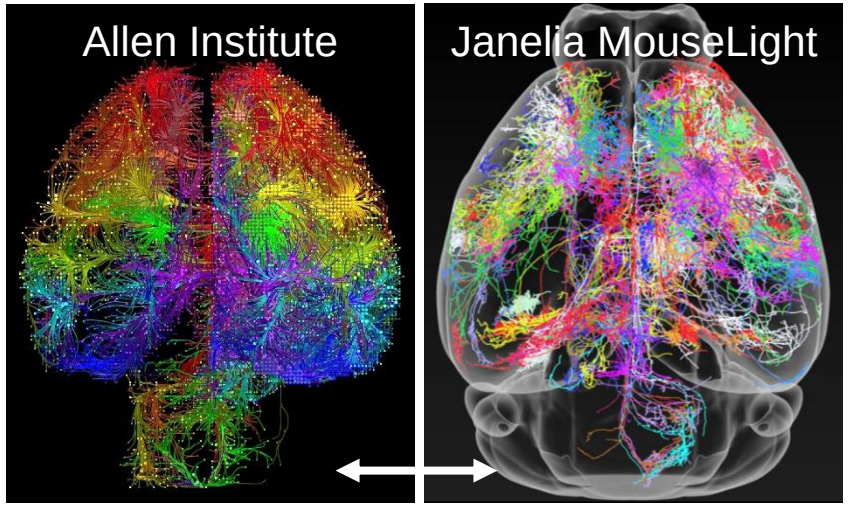
“Full” Morphological Reconstruction – Why?

Classify and identify novel cell types using brain-wide morphological descriptions of single projection neurons

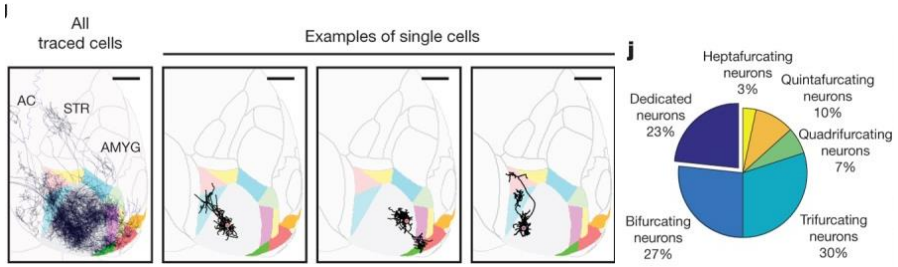
What is the specificity and diversity of projection targets at the single cell level?

How does local morphology relate to long-distance projection patterns?

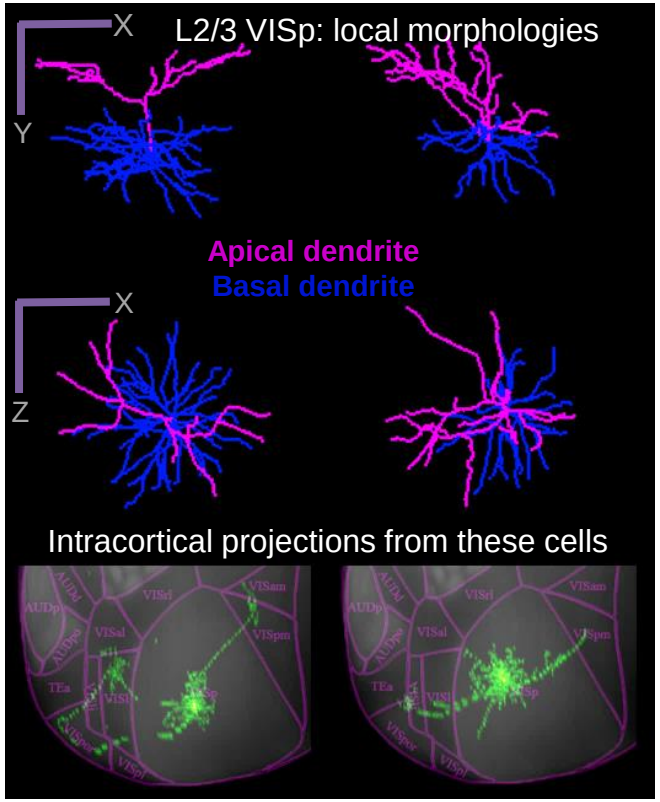
How does full morphology/target specificity relate to cell type classification?

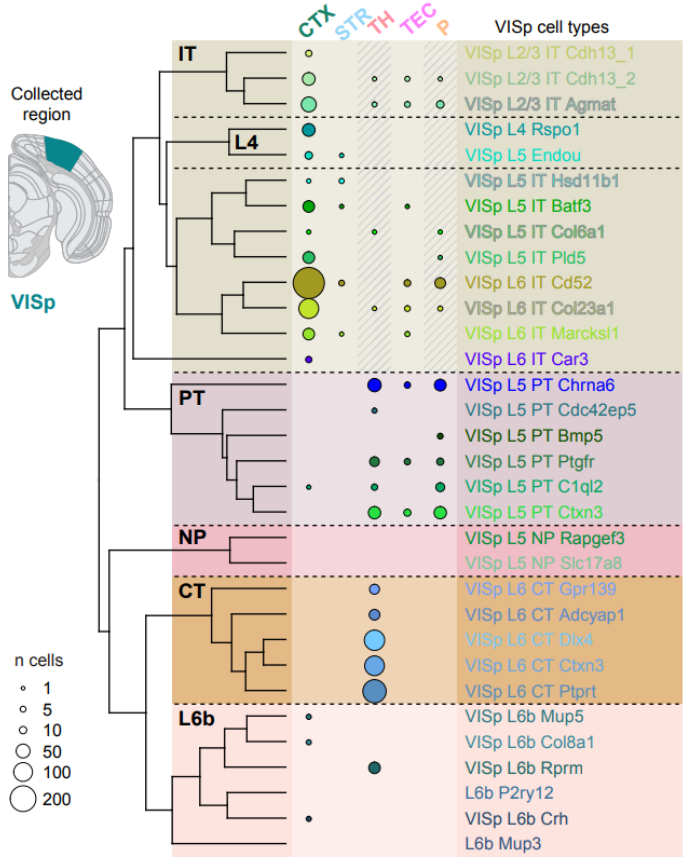


Mesoscale connectome Single cell projectome



Han et al. 2018

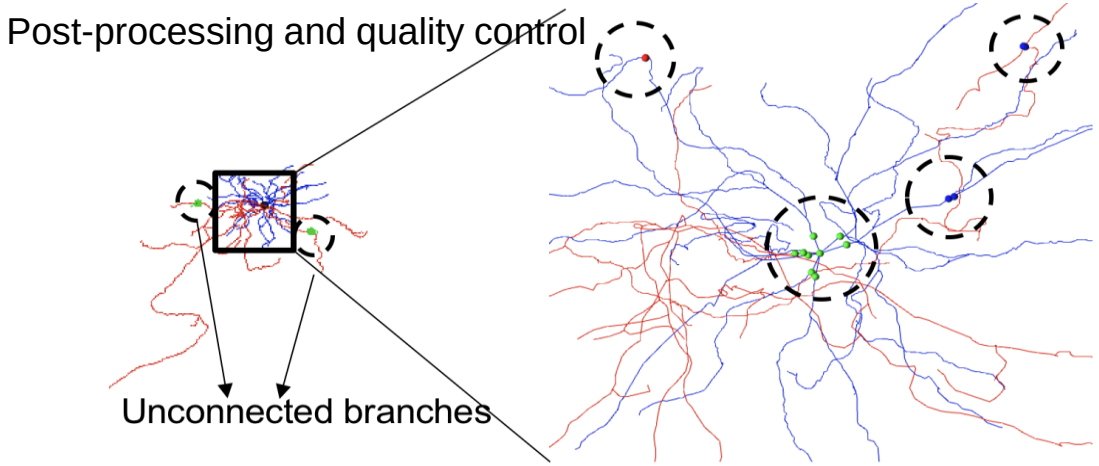




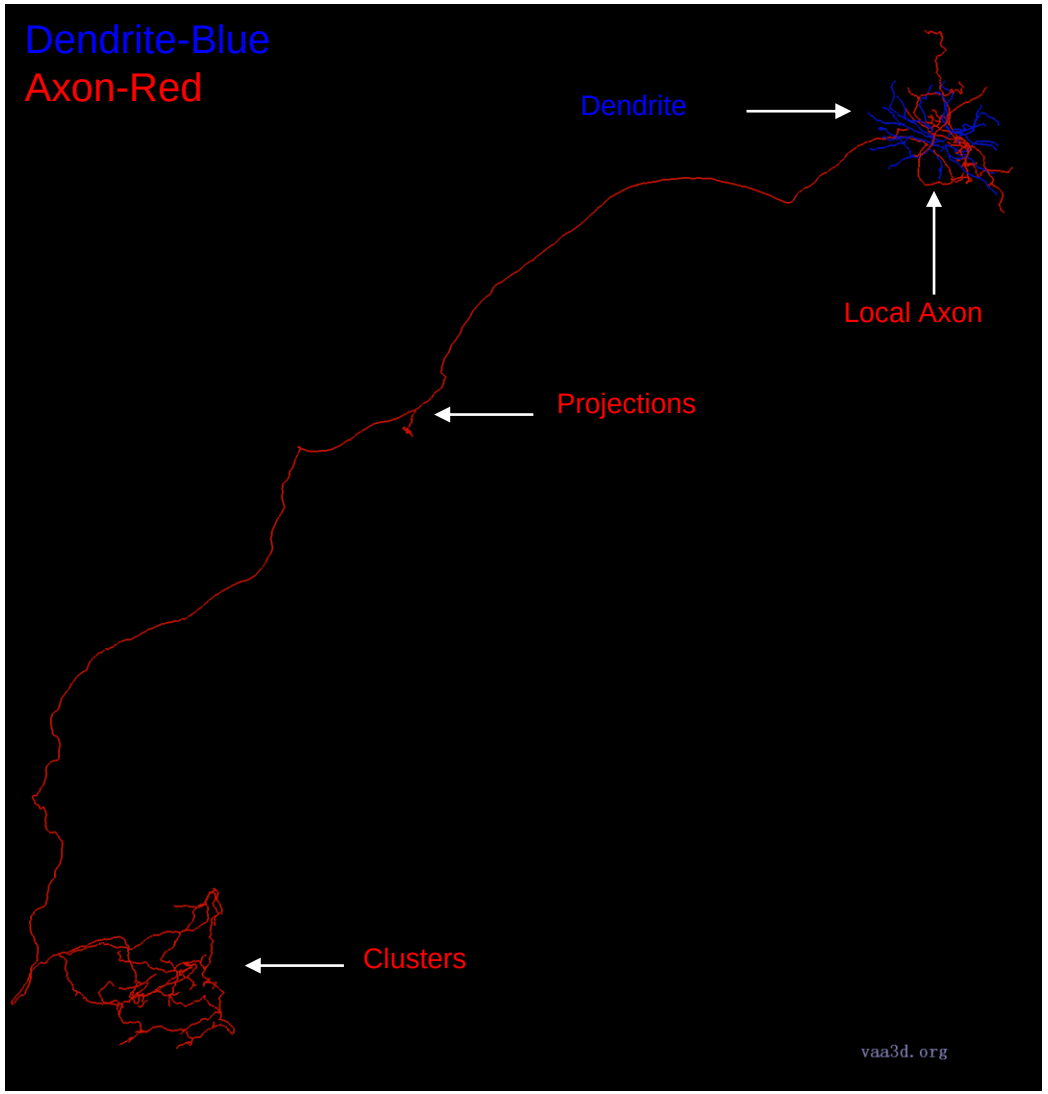
Tasic et al. 2017 bioRxiv

Protocol for full morphology reconstruction

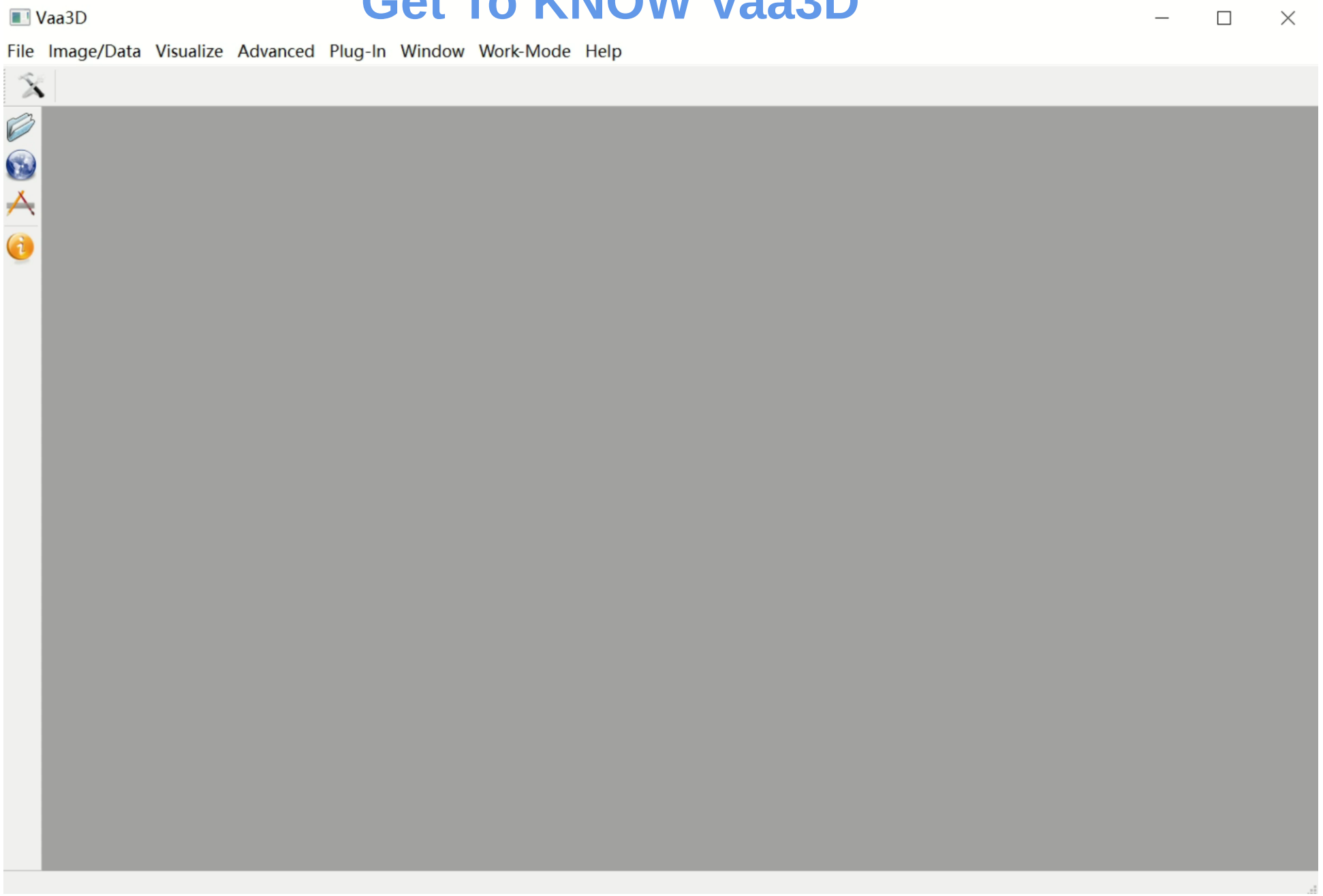
- Level-1: Dendrite, Major branches of Axon and Long projection axon without fully-traced cluster;
- Level-2: Level-1 and clusters of axon in detail

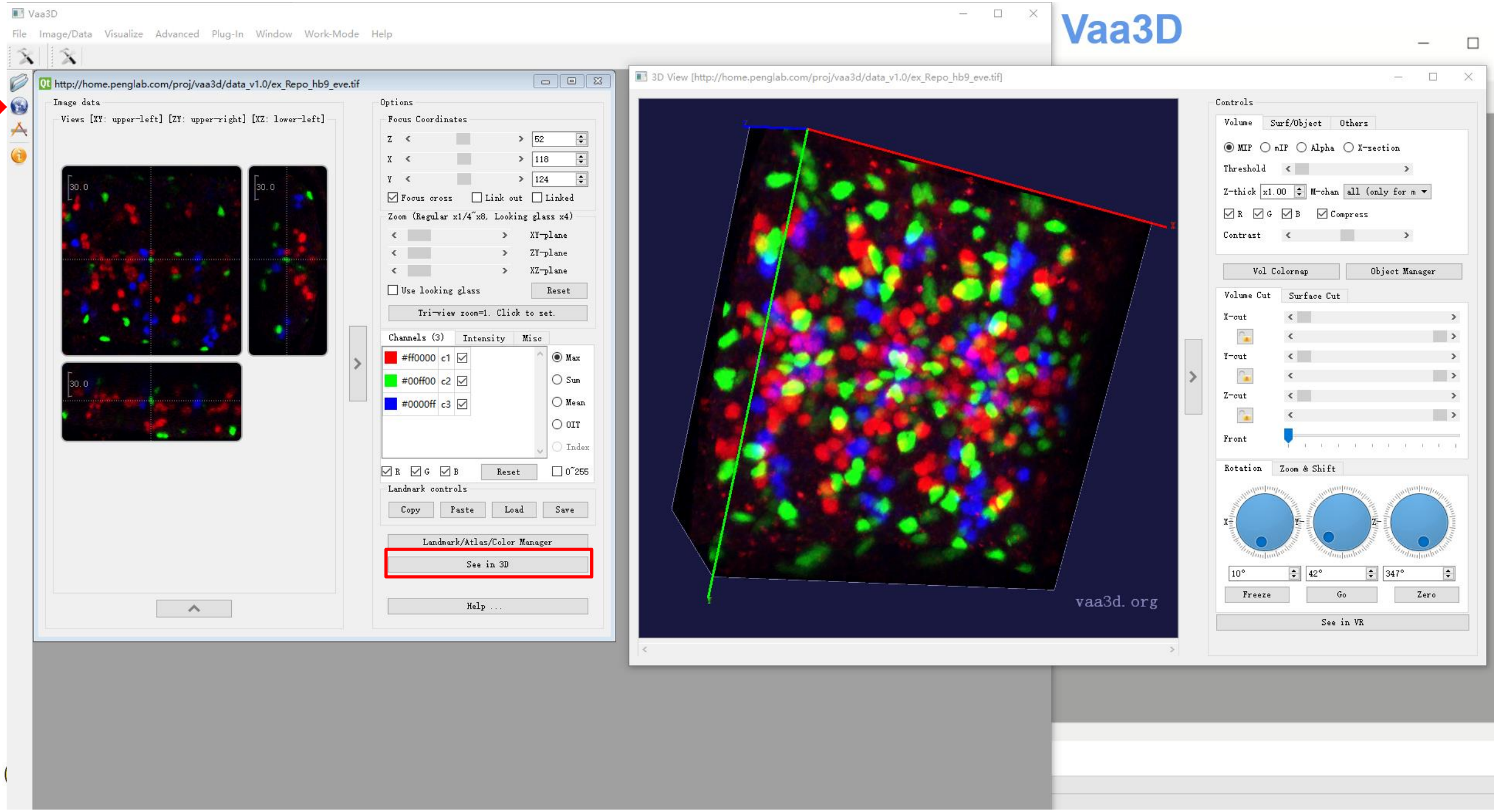


An example of Level-2 reconstruction



Get To KNOW Vaa3D




Vaa3D
File Image/Data Visualize Advanced Plug-In Window Work-Mode Help
http://home.penglab.com/proj/vaa3d/data_v1.0/ex_Repo_hb9_eve.tif
Image data
Views [XY: upper-left] [ZY: upper-right] [XZ: lower-left]
30.0
30.0
30.0
Options
Focus Coordinates
Z 52
X 118
Y 124
Focus cross
Link out
Linked
Zoom (Regular x1/4~x8, Looking glass x4)
XY-plane
ZY-plane
XZ-plane
Use looking glass
Reset
Tri-view zoom=1. Click to set.
Channels (3)
Intensity
Misc
#ff0000 c1
#00ff00 c2
#0000ff c3
Max
Sum
Mean
OIT
Index
R G B
Reset
0~255
Landmark controls
Copy
Paste
Load
Save
Landmark/Atlas/Color Manager
See in 3D
Help ...
3D View [http://home.penglab.com/proj/vaa3d/data_v1.0/ex_Repo_hb9_eve.tif]
vaa3d.org
Controls
Volume
Surf/Object
Others
MIP
mIP
Alpha
X-section
Threshold
Z-thick x1.00
M-chan all (only for m
R G B
Compress
Contrast
Vol Colormap
Object Manager
Volume Cut
Surface Cut
X-cut
Y-cut
Z-cut
Front
Rotation
Zoom & Shift
10°
42°
347°
Freeze
Go
Zero
See in VR
Vaa3D

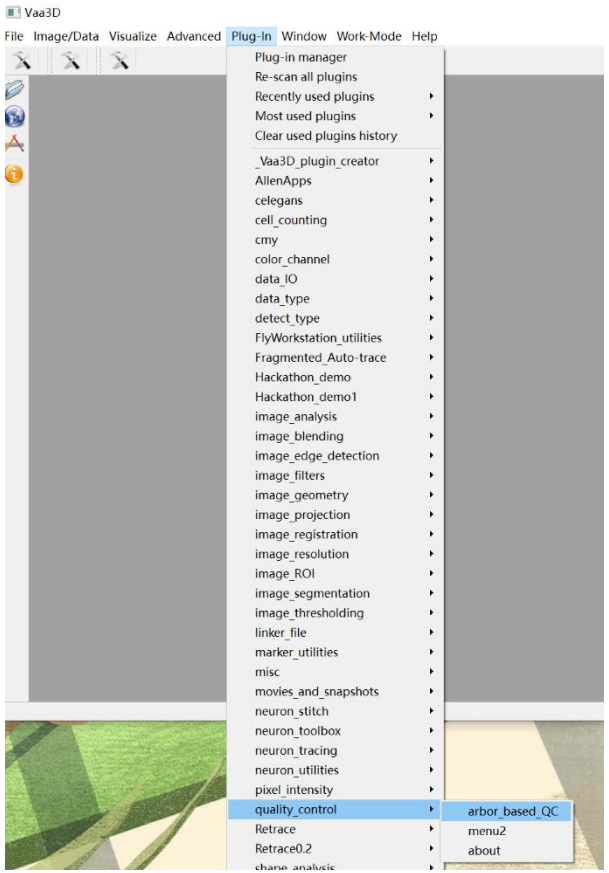
Vaa3D'S demonstration of common functions of reconstruction

Video courtesy from Yuanyuan Song
songyy121@163.com

The bronze, silver and gold standard for quality control of neuron reconstruction

How?

1.Select the "quality control“ plug-in



2.Input data and information

- .swc file（ Registration ）
- .csv excel(Contains information such as ID, region CellType_Rogh.)

3. Output result

- Sorted file: " sort_neuron_swc “ plug-in applied.
- Features information table: " global_neuron_feature “plug-in applied.
- Results information table: “0” means unqualified, “1” means qualified.

Name	Region	Celltype_Rough	Tips	Width	Height	Depth	Length	MaxBranchOrder	QC_result
17300_00056	CP	CNU	20	21.555	15.634	9.788	202.66	10	0
17300_00057	VISpor	CTX	21	10.651	9.543	15.282	126.12	5	0
17300_00058	CP	CNU	9	9.138	6.744	6.182	58.205	6	0
17300_00073	SSs	CTX	30	18.984	10.553	14.456	179.46	7	1
17300_00106	CP	CNU	29	13.658	9.743	10.407	164.08	10	1
17300_00116	TEa	CTX	29	18.111	9.149	16.319	204.96	11	1
17300_00120	CP	CNU	5	21.914	10.225	11.07	68.664	2	0
17300_00149	CA1	CTX	40	18.233	14.95	11.232	285.78	9	1
17300_00205	VISpor	CTX	8	20.075	9.889	18.452	78.8	2	0
17300_00284	CP	CNU	23	18.78	16.567	11.095	206.45	8	0
17300_00315	SSp-n	CTX	32	12.349	12.025	11.194	187.34	12	1
17300_00519	VISli	CTX	6	10.888	8.342	11.375	38.758	2	0
17300_00572	SSp-m	CTX	41	14.427	11.143	11.974	216.03	24	1
17300_00644	SSp-bfd	CTX	48	17.41	13.438	8.149	251.08	20	1
17300_00755	SSp-m	CTX	64	14.534	12.924	14.196	361.02	17	1
17300_00809	VISp	CTX	41	14.691	13.381	12.763	250.79	10	1
17300_00813	VISp	CTX	24	15.557	12.322	7.839	165.86	9	1
17300_00814	SSp-bfd	CTX	36	14.105	14.439	10.097	199.91	14	1
17300_00886	RSPv	CTX	15	10.319	6.705	8.733	74.669	3	0
17300_00898	SSp-ul	CTX	41	16.104	16.855	11.365	282.39	11	1
17300_00941	SSp-ul	CTX	15	10.687	11.255	7.096	84.857	8	0
17300_00974	SSp-tr	CTX	54	13.7	10.728	9.42	243.62	19	1
17300_01015	RSPv	CTX	20	10.507	7.987	8.589	101.51	5	0
17300_01151	COAp	CTX	4	4.048	3.308	2.552	11.234	2	0
17300_01161	PAA	CTX	17	6.557	7.312	9.9	88.62	6	0
17300_01387	SI	CNU	17	19.038	6.968	8.449	197.1	5	1

Done by Lulu Yin
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Checking and Modifying quality of reconstructions using Vaa3D

The whole process of checking

Initial reconstruction completed

1. Check from the soma

2. Start dendritic part

3. Start axon trunk part

4. Start axon terminal part

Check completed

Tips:

1.The branch of the missing dendrite is marked with type 8 (Pink)

2.The branch of the missing axon is marked with type 7 (Green)

3.All wrong branches are marked with type 0(White)

4.Uncertain branches marked with type6(Yellow)

Silver standard and silver standard checking

- **Silver standard:**

1. The 3D space the actual arbor occupied is fully covered;
2. The missing branches of the arbor are less than 1/3;
3. No jumping to neighboring neurons;
4. No over-tracing into background;

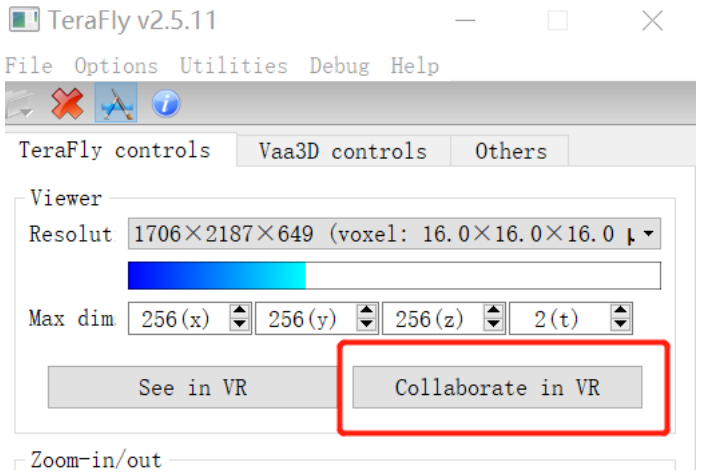
- **Silver standard checking:**

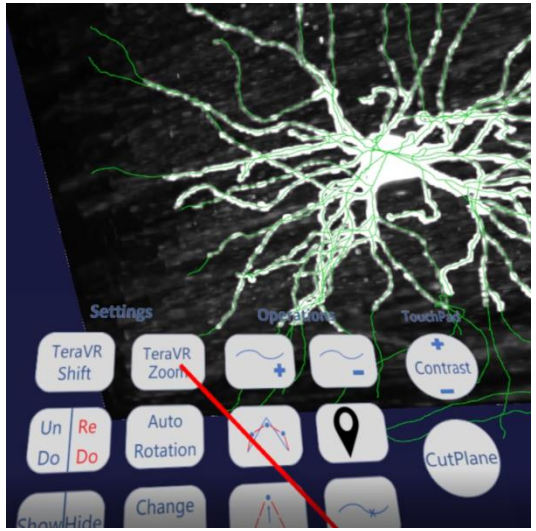
we developed functions check mode under the Hi5 mobile application. Check mode supports efficient browsing and annotating operations, saving the time for data loading and recording.

Gold standard and gold standard checking and revising

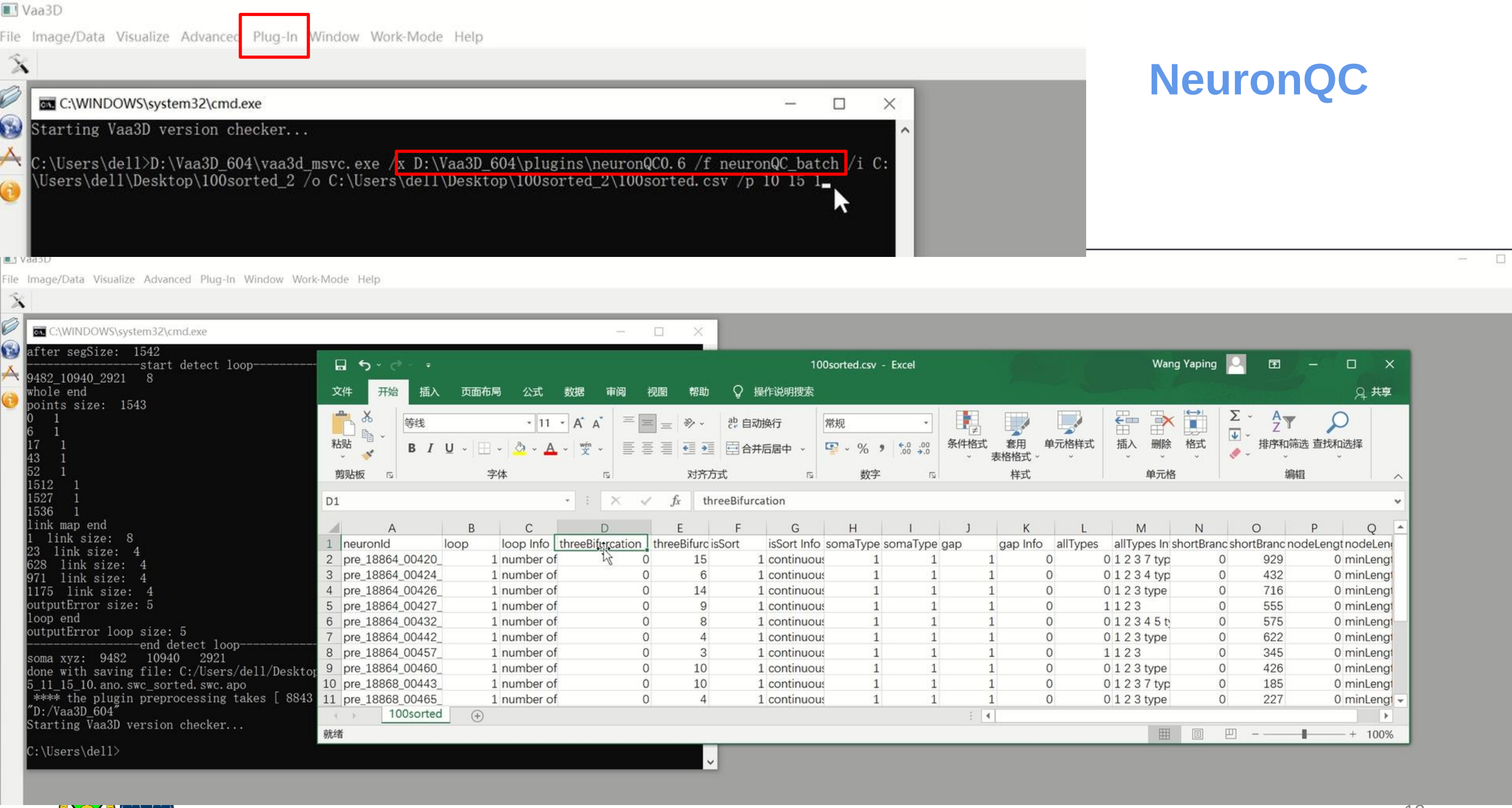
- **Gold standard:**
  1. Soma node is defined and labeled as type ‘1’;
  2. The primary branches start at soma node;
  3. No missing branches;
  4. No crossing between branches;
  5. No background traced;
  6. No gaps in branches;
  7. No circle or multifurcation.

Gold standard manual checking: Mainly use MR-Farm



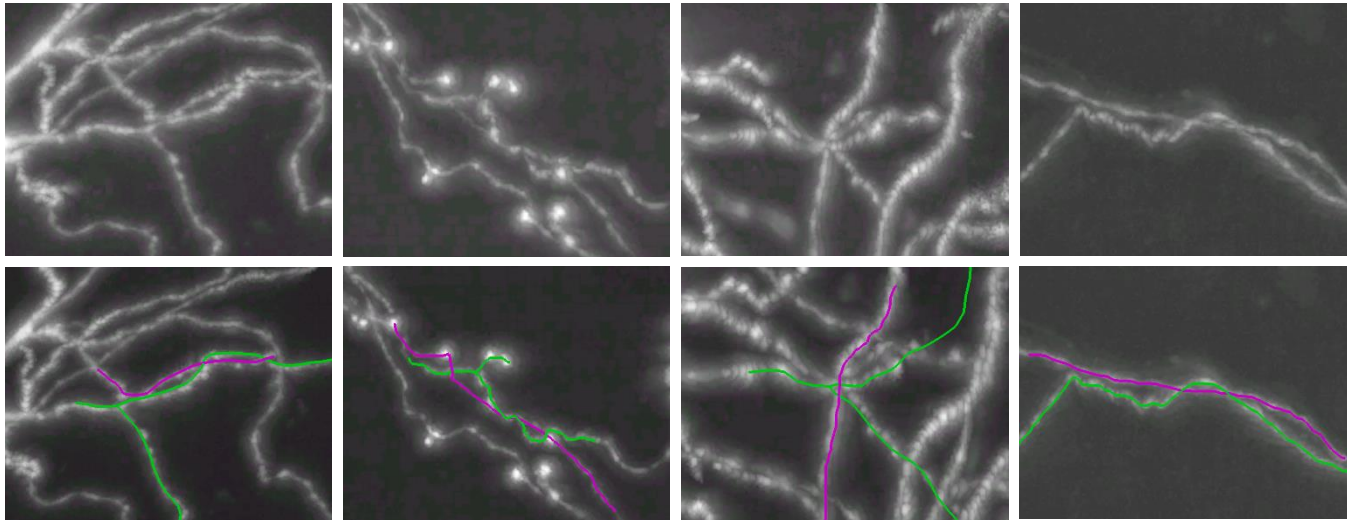


NeuronQC



	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q
1	neuronId	loop	loop Info	threeBifurcation	threeBifurc	isSort	isSort Info	somaType	somaType	gap	gap Info	allTypes	allTypes In	shortBranc	shortBranc	nodeLengt	nodeLen
2	pre_18864_00420_	1	number of	0	15	1	continuous	1	1	1	0	0	1 2 3 7 typ	0	929	0	minLengt
3	pre_18864_00424_	1	number of	0	6	1	continuous	1	1	1	0	0	1 2 3 4 typ	0	432	0	minLengt
4	pre_18864_00426_	1	number of	0	14	1	continuous	1	1	1	0	0	1 2 3 type	0	716	0	minLengt
5	pre_18864_00427_	1	number of	0	9	1	continuous	1	1	1	0	1	1 2 3	0	555	0	minLengt
6	pre_18864_00432_	1	number of	0	8	1	continuous	1	1	1	0	0	1 2 3 4 5 t	0	575	0	minLengt
7	pre_18864_00442_	1	number of	0	4	1	continuous	1	1	1	0	0	1 2 3 type	0	622	0	minLengt
8	pre_18864_00457_	1	number of	0	3	1	continuous	1	1	1	0	1	1 2 3	0	345	0	minLengt
9	pre_18864_00460_	1	number of	0	10	1	continuous	1	1	1	0	0	1 2 3 type	0	426	0	minLengt
10	pre_18868_00443_	1	number of	0	10	1	continuous	1	1	1	0	0	1 2 3 7 typ	0	185	0	minLengt
11	pre_18868_00465_	1	number of	0	4	1	continuous	1	1	1	0	0	1 2 3 type	0	227	0	minLengt

Signals that are difficult to judge：



Use MR-Farm

Collaborative discussion

Thank you!

To download Vaa3D, and for the latest information & help visit the Vaa3D website at http://vaa3d.org

Visit us: http://braintell.org