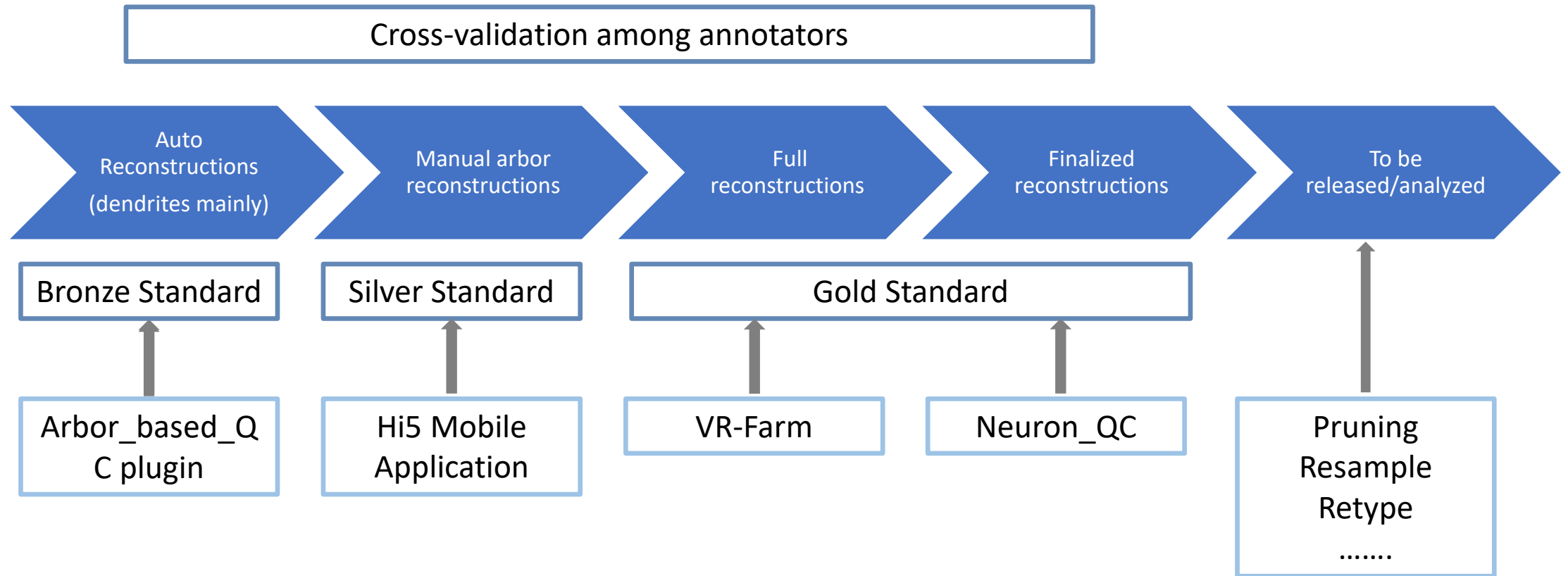


# Quality Control for Neuron Reconstructions

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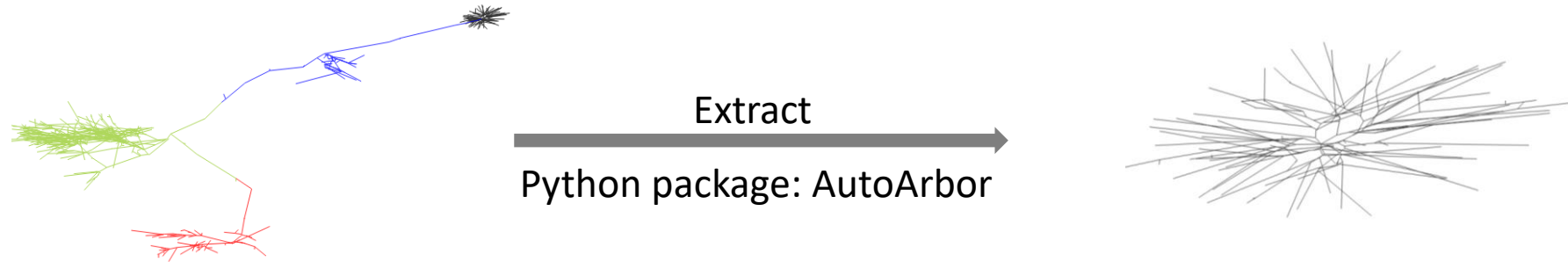
2021-10-20

# QC flowchart



# Bronze: arbor\_based\_QC

- Definition of an arbor: dense cluster structure

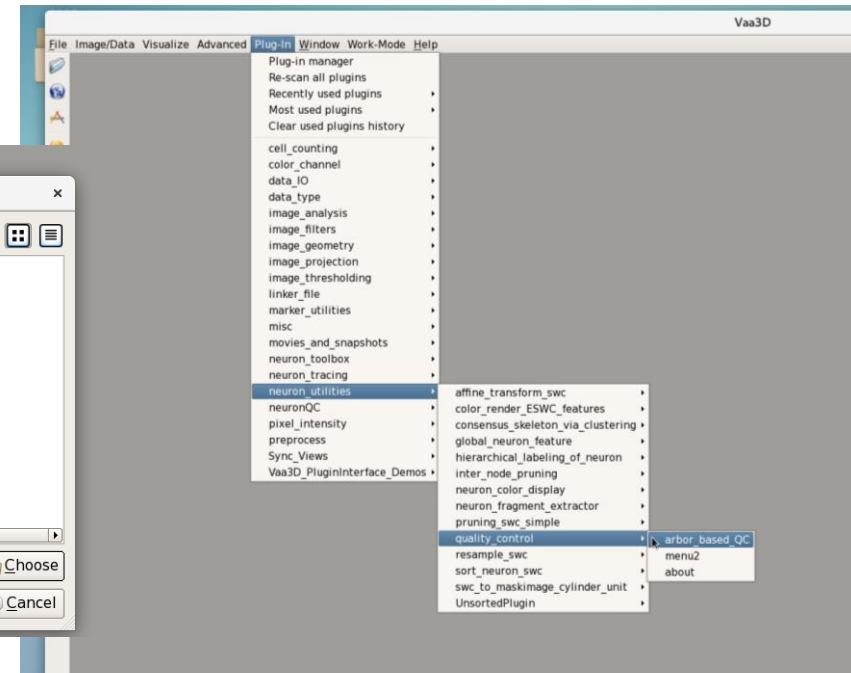
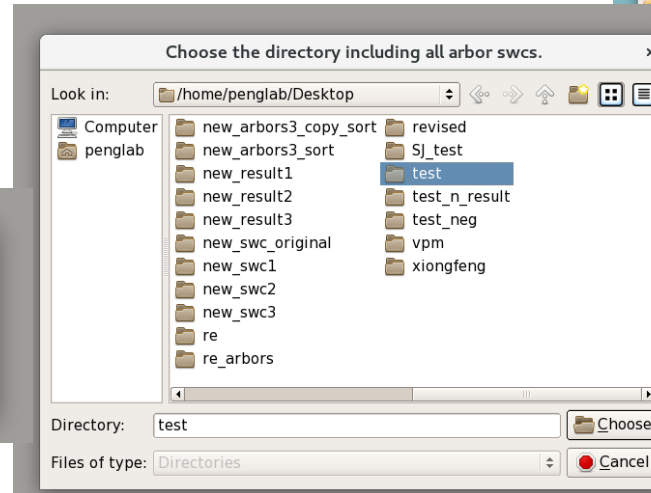
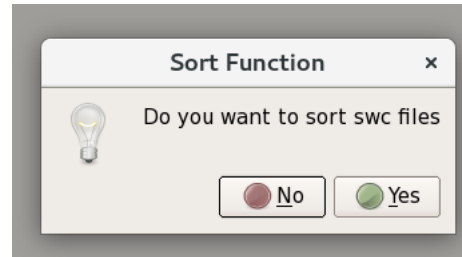


- Bronze Standard: Dendritic part mainly

Region	Number of Tips	Overall Width	Overall Height	Overall Depth	Total Length	Max Branch Order
VPM	[29,93]	[5.48,13.759]	[7.189,19.258]	[5.153,15.497]	[93.281,402.169]	[5,14]
VPL	[31,108]	[5.916,14.946]	[7.662,17.703]	[4.611,15.628]	[95.924,369.248]	[6,15]
LGd	[47,82]	[6.816,13.477]	[3.949,18.641]	[5.125,16.95]	[126.229,358.143]	[7,11]
MG	[34,79]	[6.149,14.498]	[7.059,22.429]	[6.26,14.093]	[120.773,318.078]	[6,16]
Other Thalamus cells	[29,111]	[6.132,19.839]	[7.010,21.136]	[6.29,21.51]	[118.877,499.613]	[5,20]
CP	[26,109]	[5.942,21.221]	[3.806,22.034]	[5.486,18.734]	[81.289,344.946]	[4,18]
	[40,208]	[13.271,66.578]	[12.03,72.919]	[11.288,54.891]	[263.618,1312.98]	[8,29]
Other CNU cells	[1,67]	[2.665,20.478]	[2.687,32.034]	[0.956,20.952]	[6.028,263.969]	[1,12]
CTX	[22,121]	[6.77,31.354]	[6.683,46.143]	[6.36,35.99]	[71.317,585.043]	[5,30]
Others	[21,125]	[6.132,38.328]	[6.353,46.256]	[5.592,39.227]	[68.434,662.401]	[5,29]

# arbor\_based\_QC plugin

- Plugin Interface



- Command line

Vaa3D -x quality\_control -f arbor\_qc -i swc\_file -o csv\_file

- Output — an excel table

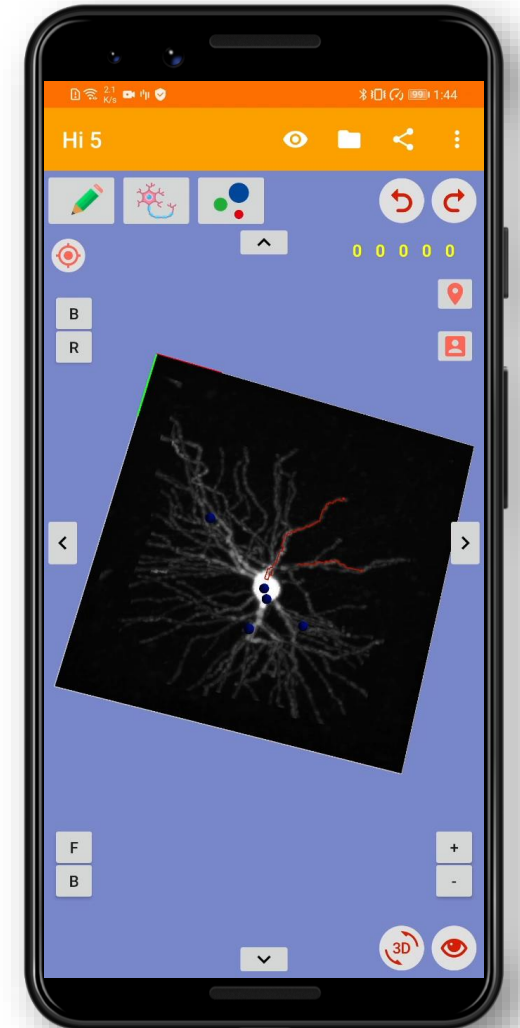
Name	Region	Celltype_Rough	Tips	Width	Height	Depth	Length	MaxBranchOrder	QC_result
17300_00056	CP	CNU	20	21.555	15.634	9.788	202.66	10	0
17300_00057	VISpor	CTX	21	10.651	9.543	15.282	126.12	5	0
17300_00058	CP	CNU	9	9.138	6.744	6.182	58.205	6	0
17300_00073	SSs	CTX	30	18.984	10.553	14.456	179.46	7	1

0: unqualified  
1: qualified

# Silver Standard — arbors

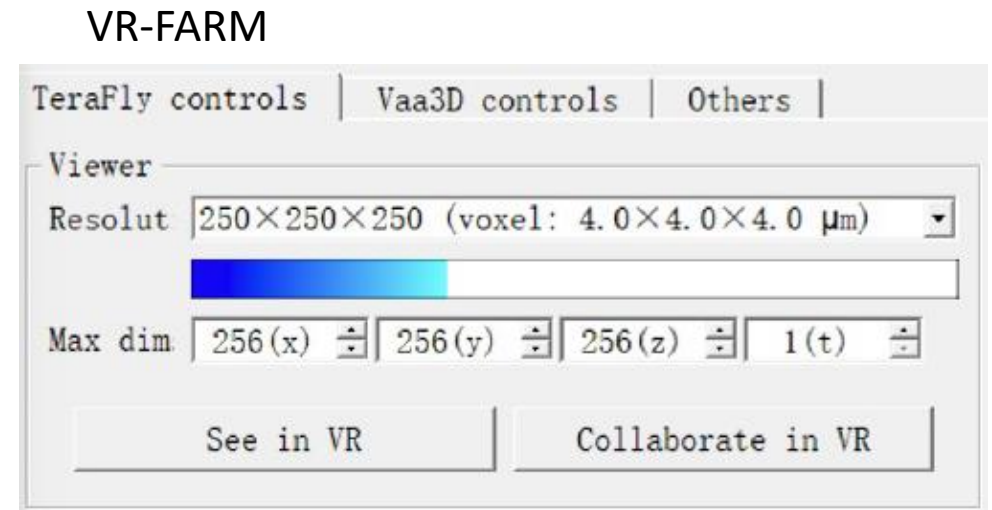
- Fully cover the 3D space of the actual arbor
- Missing branches are less than 1/3
- No jumping to neighboring neurons
- No over-tracing into background

Hi5 Mobile Platform



# Gold Standard — complete neurons

- Soma denoted as type '1'
- Primary branches start at soma node
- No missing branches
- No crossing
- No over-tracing
- No gaps
- No loops or multifurcations



# Finalized: NeuronQC

- Command Line:

Vaa3D -x nueronQC -f neuronQC\_batch -i `swc_file` -o `csv_file` -p 10 4 1

Parameters: short branch length threshold;  
node-to-node length threshold;  
whether to check loops & trifurcations

- Output — an excel table

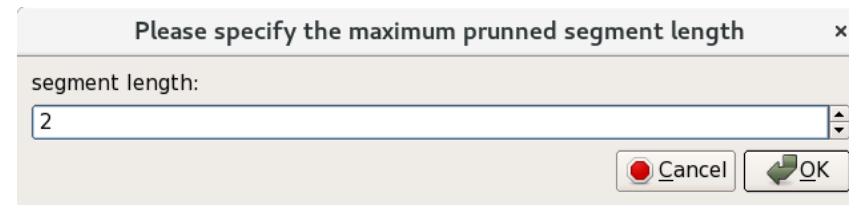
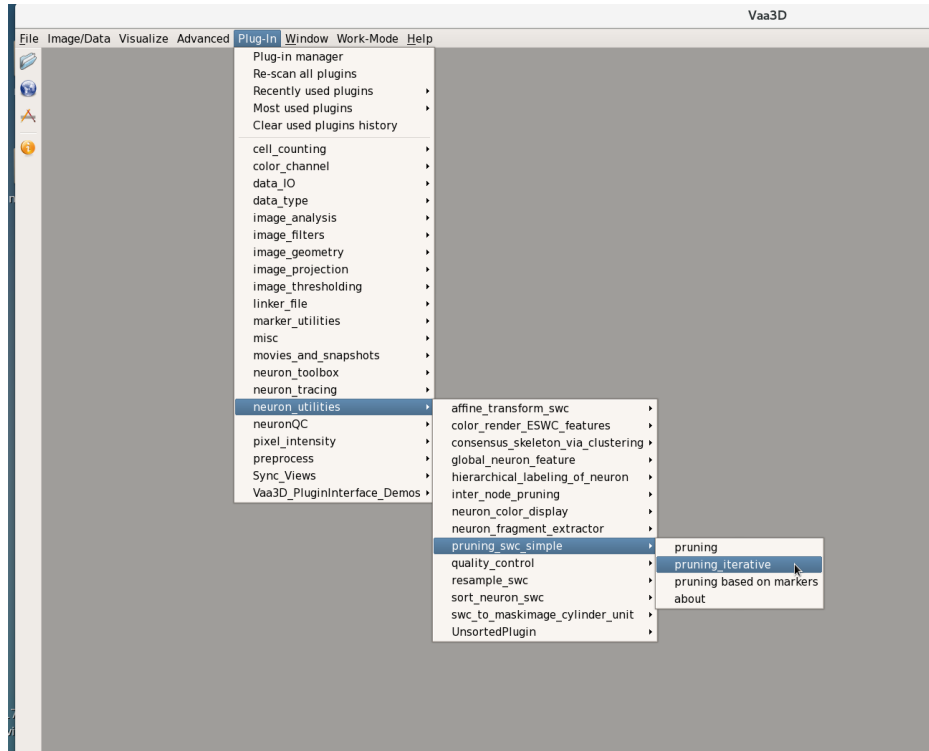
neuronId	loop	loop Info	threeBifurcation	threeBifurcation Info	isSort	isSort Info	somaType	somaType Info	gap	nodeLength Info	isQualified
17781_00001	1	number of key points of loop: 0	1	0	1	continuous	1	1	1	minLength = 4.000003 maxLength = 6.471980	0
17781_00003	1	number of key points of loop: 0	0	1	1	continuous	1	1	1	minLength = 4.000135 maxLength = 6.473404	0

0: unqualified  
1: qualified

# For release/analysis

## 1. Pruning

### V3D interface



### Command line

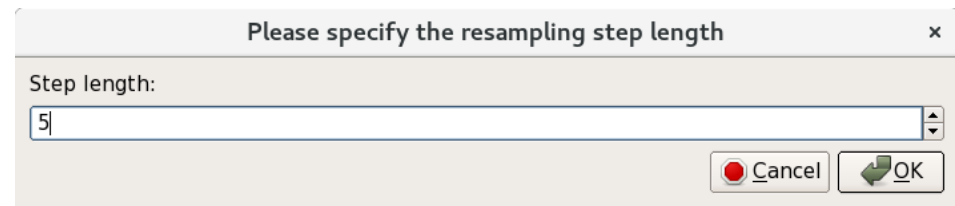
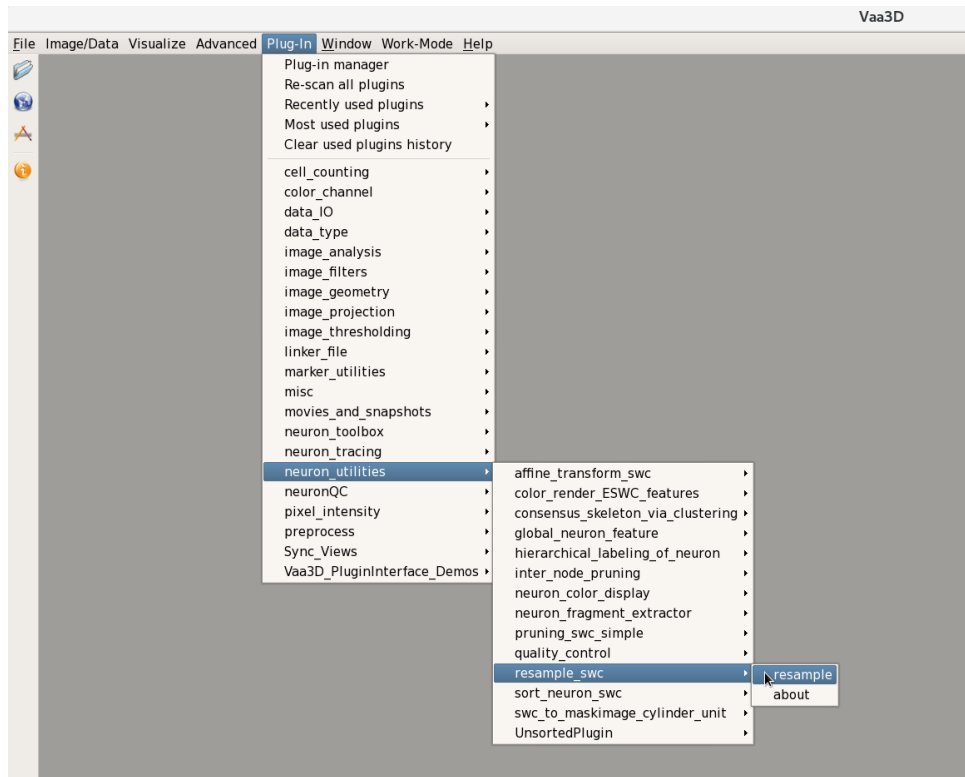
```
vaa3d -x pruning_swc_simple -f pruning_iterative -i swc_file -o swc_file -p 2
```



# For release/analysis

## 2. Resample

### V3D interface



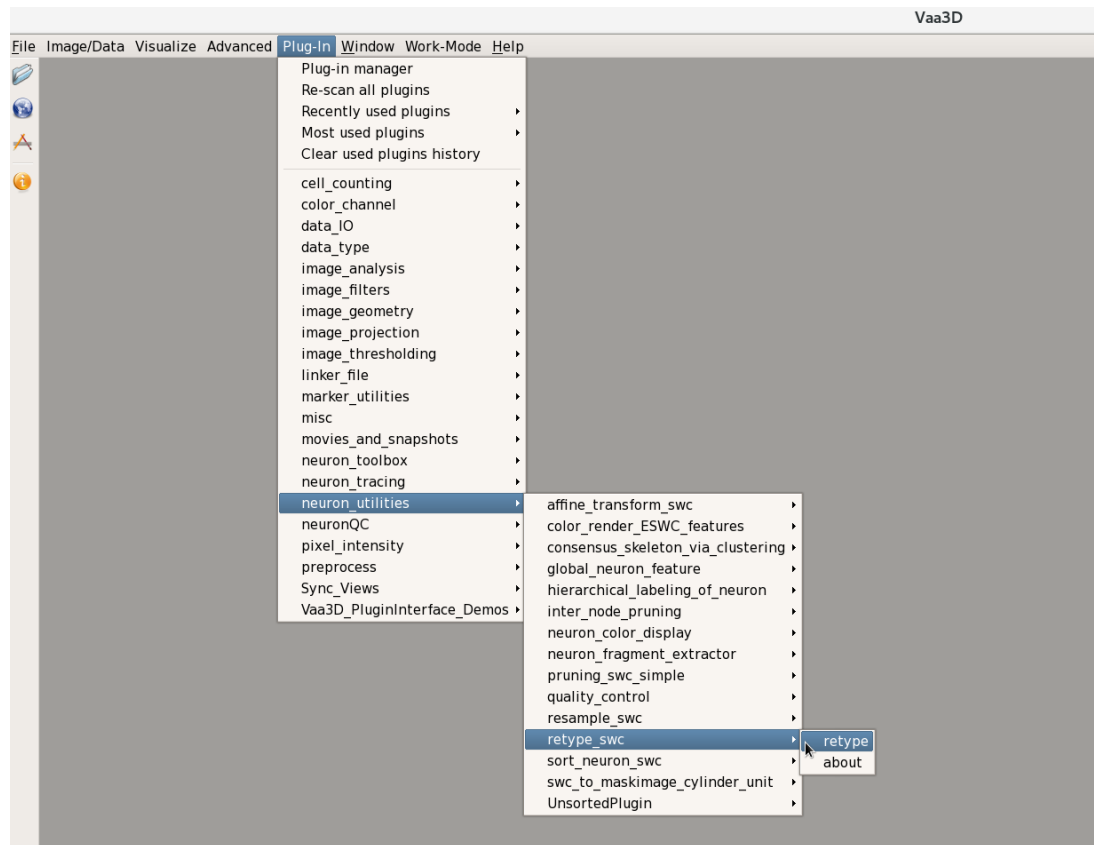
### Command line

```
vaa3d -x resample_swc -f resample_swc -i swc_file -o swc_file -p 5
```

# For release/analysis

## 3. Retype

V3D interface



Command line

```
vaa3d -x retype_swc -f retype -i swc_file -o swc_file
```

**Thank You!**