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Comparing Automated Morphology Quantification Software on Dendrites of Uninjured and Injured *Drosophila* Neurons

Carolee Nguyen¹ · Katherine L. Thompson-Peer^{1,2,3}

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Abstract

Dendrites shape inputs and integration of depolarization that controls neuronal activity in the nervous system. Neuron pathologies can damage dendrite architecture and cause abnormalities in morphologies after injury. Dendrite regeneration can be quantified by various parameters, including total dendrite length and number of dendrite branches using manual or automated image analysis approaches. However, manual quantification is tedious and time consuming and automated approaches are often trained using wildtype neurons, making them poorly suited for analysis of genetically manipulated or injured dendrite arbors. In this study, we tested how well automated image analysis software performed on class IV *Drosophila* neurons, which have several hundred individual dendrite branches. We applied each software to automatically quantify features of uninjured neurons and neurons that regenerated new dendrites after injury. Regenerated arbors exhibit defects across multiple features of dendrite morphology, which makes them challenging for automated pipelines to analyze. We compared the performances of three automated pipelines against manual quantification using Simple Neurite Tracer in ImageJ: one that is commercially available (Imaris) and two developed by independent research groups (DeTerm and Tireless Tracing Genie). Out of the three software tested, we determined that Imaris is the most efficient at reconstructing dendrite architecture, but does not accurately measure total dendrite length even after intensive manual editing. Imaris outperforms both DeTerm and Tireless Tracing Genie for counting dendrite branches, and is better able to recreate previous conclusions from this same dataset. This thorough comparison of strengths and weaknesses of each software demonstrates their utility for analyzing regenerated neuron phenotypes in future studies.

Keywords Dendrites · Dendrite arbor · *Drosophila* · Dendrite regeneration · Automated analysis · Software comparison · Dendrite injury

Introduction

The complex architecture of neurons are composed of highly branched dendrites extending from the cell body and a long axon projecting to target cells. The primary function of dendrites is to receive information from the environment or from upstream neurons and to integrate input signals across the

dendrite arbor. Despite their importance, only recently have researchers begun testing the regenerative capacity of dendrites after injury (Song et al., 2012; Stone et al., 2014; Thompson-Peer et al., 2016). Dendrites can be injured in various manners including stroke, traumatic brain injury, and neurodegenerative diseases (Gao et al., 2011; Klapstein et al., 2001). Subsequently, dendrite regeneration is affected by environmental and cellular factors that differ across neuron types and forms of injury. Such circumstances would be expected to create variability in the resulting morphologies of individual regenerated neurons. In order to understand the cellular mechanisms involved in dendrite regeneration, it is necessary to investigate changes in neuron morphologies after injury.

Dendrite regeneration can be assessed by tracing the neuron's architecture. Neuronal tracing, a process which determines the shape and location of axons and dendrites in respect

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55 to the cell body of a neuron, is a computational technique
56 frequently utilized to analyze neuron morphologies.
57 Common parameters used to investigate neuronal phenotypes
58 are total dendrite length and number of dendrite branches,
59 which can reveal changes in dendrite architecture throughout
60 development (Henley et al., 2019). Tracing neurons allows
61 neuroscientists to digitally quantify regeneration and under-
62 stand how different types of injuries affect overall dendrite
63 architecture. However, tracing regenerated neurons is difficult
64 because newly formed dendrite branches are disorganized,
65 exhibit self-avoidance defects, and have a denser arbor com-
66 pared to dendrites of wild type uninjured neurons (Thompson-
67 Peer et al., 2016). This issue is further complicated by the fact
68 that many existing tracing software have been specifically
69 developed and used to quantify healthy, uninjured neurons
70 (Donohue & Ascoli, 2011).

71 A common technique for dendrite analysis involves hand
72 tracing neurons using the Simple Neurite Tracer plug-in of
73 ImageJ software (Longair et al., 2011; Rueden et al., 2017).
74 This semi-manual approach involves identifying the
75 beginning and end points of dendrites and digitally drawing
76 individual branch segments throughout an entire neuron.
77 Previous studies have manually quantified dendritic
78 morphologies to investigate the cellular mechanisms
79 involved in promoting dendrite development and
80 regeneration. For example, Jiang et al. (2019) examined the
81 role of epidermal somatosensory neurite ensheathment on
82 neuron morphogenesis by hand tracing specific classes of no-
83 ciceptive sensory neurons (Jiang et al., 2019). Using a similar
84 technique, DeVault et al. (2018) demonstrated that the regen-
85 erative capacity of dendrites decreases with age but can be
86 compensated by inhibition of matrix metalloproteinase 2
87 (Mmp2) in surrounding tissue (DeVault et al., 2018). A more
88 recent study discovered a novel function of the receptor tyro-
89 sine kinase (RTK) orphan receptor (Ror) for promoting den-
90 drite regeneration as well (Nye et al., 2020). While digital
91 hand tracing remains a popular choice for analyzing neuronal
92 phenotypes, this approach is laborious and is hampered by
93 variability in how researchers distinguish individual dendrite
94 branches (Donohue & Ascoli, 2011).

95 In order to aid with such tasks, many automated algorithms
96 have been developed to address the challenges involved with
97 neuronal tracing (Chen et al., 2015; Kanaoka et al., 2019;
98 Myatt et al., 2012; Peng et al., 2010; Smafield et al., 2015).
99 These software, which have largely been developed by inde-
100 pendent studies, demonstrate the use of self-learning algo-
101 rithms for particular issues at hand. Additionally, several stud-
102 ies have demonstrated the applicability of commercially avail-
103 able software as potential candidates for analyzing dendritic
104 morphologies with minimal user input. Agostinone et al.
105 (2018) reconstructed dendritic arbors to investigate whether
106 an insulin supplement was capable of promoting new branch
107 formation after axon-injury-induced retraction in retinal

ganglion cells (RGCs) (Agostinone et al., 2018). Tapias 108
et al. (2013) studied the effects of neurodegeneration on den- 109
drite morphologies by quantifying neurons subjected to neu- 110
rotoxic treatments (Tapias et al., 2013). The increase in avail- 111
ability of automated tracing software has undoubtedly helped 112
to facilitate such analyses; however, there still remains a need 113
for a standardized neuron tracing protocol. 114

115 A subset of peripheral sensory neurons in *Drosophila*, 116
known as the multidendritic dendritic arbor (md-da) neurons, 117
are often used to investigate dendrite development, in part 118
because of their distinct morphology amongst specific classes 119
(Grueber et al., 2002). *Drosophila* da neurons are categorized 120
based on gene expression and morphology of their dendritic 121
arbors, which vary in branching complexity across different 122
classes (Jan & Jan, 2010). The dendritic arbor of class I da 123
neurons are established in early larval development and have 124
the most simple dendrite architecture. In contrast, class IV da 125
neurons contain several hundred individual dendrite branches, 126
which grow throughout development, making them the most 127
complex class of md-da neurons. *Drosophila* da neurons are 128
ideal for studying dendrite regeneration, because their mor- 129
phology is highly stereotyped from animal to animal, neurons 130
can be easily located across different imaging sessions, and 131
their superficial location makes optical dendrite injuries 132
straightforward (Song et al., 2012; Stone et al., 2014).

133 Several papers have examined various techniques of neu- 134
ron reconstruction primarily on mammalian brain neurons 135
(Acciai et al., 2016; Donohue & Ascoli, 2011; Halavi et al., 136
2012; Meijering, 2010; Parekh & Ascoli, 2013). However, 137
these papers only compared specific features and methodolo- 138
gies of each software, and the accuracy of these programs 139
have yet to be compared comprehensively to hand tracing or 140
to one another when specifically addressing the unique chal- 141
lenges presented by dendrites regenerated after injury. Many 142
automated image quantification software claim to be more 143
efficient than manual hand tracing. Yet, their accuracies are 144
still validated with the golden standard of hand tracing 145
(Donohue & Ascoli, 2011). Given such context, developing 146
a standardized procedure that automates neuron tracing with 147
high accuracy will resolve a significant bottleneck in analyz- 148
ing the complex arbor of regenerated dendrites.

149 In this study, we compared the accuracy and efficiency of 150
various automated image analysis pipelines using the same 151
data set in Imaris, which is commercially available 152
(Bitplane), and DeTerm and Tireless Tracing Genie (TTG), 153
which are both independently developed by researchers (Iyer 154
et al., 2013; Kanaoka et al., 2019). We evaluated the accuracy 155
of these software relative to the hand tracing technique, when 156
applied to uninjured and regenerated *Drosophila* class IV da 157
neurons. In order to streamline the process of neuron tracing, 158
we quantified the duration it takes to accurately trace neurons 159
using each software, which could potentially replace tradition- 160
al hand tracing methods. We expect that one of these

161 automated approaches will yield more accurate results than
 162 the others, closer to hand tracing, but will also be more effi-
 163 cient at analyzing neuron morphologies.

164 Methods

165 Image Acquisition

166 Class IV ddaC da neurons in *Drosophila* larvae were injured
 167 and imaged as previously described (Thompson-Peer et al.,
 168 2016). In this study, we re-analysed the same data from that
 169 manuscript of the heterozygous cross progeny of w^{1118} ; ppk -
 170 $CD4$ -tdGFP^{1b} (Han et al., 2011) adults crossed to w^{1118}
 171 adults. This fly line drives expression of the membrane-
 172 tagged CD4-tdGFP exclusively in the class IV da neurons of
 173 the *Drosophila* peripheral nervous system under the control of
 174 the cell-type specific *ppk* promoter. The *ppk* promoter is rel-
 175 atively strong, and quite specific, which results in an image
 176 with a good signal/noise ratio. Adult flies were allowed to lay
 177 eggs onto grape agar plates with a dot of wet yeast paste for a
 178 short period of time (approx 4 h), and the embryos were then
 179 allowed to develop and eventually hatch for the desired length
 180 of time (hours AEL) at room temperature. At the time of
 181 injury, animals were individually mounted onto agarose pads
 182 on slides, covered with glycerol and a coverslip, and imaged
 183 on a Zeiss LSM 580 microscope equipped with a Chameleon
 184 2-photon laser at 930 nm. In a version of the injury assay that
 185 is a hybrid of the two-photon injury described in Song et al.
 186 (2012) and the total dendrite removal described in Stone et al.
 187 (2014), the two-photon laser was used to first image the
 188 membrane-tagged GFP in the neuron, then focused on the
 189 2–5 branch points closest to the cell body, with higher power
 190 and slower scanning speed, to cut off all the dendrite branches
 191 of these neurons (so-called “balding” the neurons). In order to
 192 eliminate the complicating factor of adjacent neurons invading
 193 the territory, adjacent neurons were ablated when dendrites
 194 were injured at 24, 36, or 48 h AEL. Generally, neurons in
 195 segments T3, A2, A4, and A6 were ablated; neurons in seg-
 196 ments A1 and A3 were balded; and the neuron in segment A5
 197 remained as the uninjured age-matched control neuron. After
 198 injury, animals were housed individually on grape plates with
 199 yeast paste at room temperature, imaged at 24 h later and again
 200 72 h later. Any injured neurons that showed a branch(es) that
 201 had been missed at 24 h after injury were not included in this
 202 analysis. Any neurons or animals that did not survive all the
 203 way through to the final imaging session were also not includ-
 204 ed in this analysis. At 24 h after injury (24 h AI for injured
 205 neurons and 24 h AMI for mock-injured neurons) and 72 h
 206 after injury and after mock injury A(M)I animals were indi-
 207 vidualy mounted again on an agarose pad in glycerol under a
 208 coverslip, and imaged on a Leica SP5 confocal microscope
 209 using an HC PlanAPO 20x/0.75 IMM oil objective and

standard 488 nm laser illumination. Later, after out of focus
 planes were removed, Z stacks were converted to maximum
 intensity projections using ImageJ. Further processing of the
 images, such as background subtraction, was not performed.

Uninjured neurons @24 h after egg laying (AEL) at 24 h ($n =$
 12) and 72 h after mock injury (AMI) ($n = 12$). Injured neurons
 @24 h AEL at 24 h ($n = 8$) and 72 h after injury (AI) ($n = 8$).
 Uninjured @36 h AEL at 24 h ($n = 3$) and 72 h AMI ($n = 3$).
 Injured @36 h AEL at 24 h ($n = 6$) and 72 h AI ($n = 6$).
 Uninjured @48 h AEL at 24 h ($n = 15$) and 72 h AMI ($n = 15$).
 Injured neurons @48 h AEL at 24 h ($n = 16$) and 72 h AI ($n =$
 16). Uninjured @72 h AEL at 24 h ($n = 10$) and 72 h AMI ($n =$
 11). Injured @24 h AEL at 24 h ($n = 13$) and 72 h AI ($n = 13$).

ImageJ Measurements

Manual dendrite tracing was conducted using the Fiji distri-
 bution of Simple Neurite Tracer plug-in (Longair et al., 2011)
 in ImageJ software (using the most recent Fiji version of
 ImageJ (Schindelin et al., 2012) <https://imagej.nih.gov/ij/>).
 Using the previously defined protocol, individual dendrite
 branches of a neuron were traced from an acquired 2D or
 converted 3D image (Thompson-Peer et al., 2016). This
 plug-in allows users to quantify dendrite branch and length
 by tracing and registering individual branches with respect to
 the cell body. Individual dendrite fragments were selected to
 determine the beginning and end of each individual dendrite.
 This process was repeated for all dendrites in each neuron.
 Total dendrite branch number was extracted from ImageJ path
 to data output. Specifically, branch number is the number of
 terminal branch tips. Path lengths of individual dendrites were
 totaled to reveal the total dendrite length of the neuron.

DeTerm Measurements

DeTerm source code and network model was run in Python
 (v3.6.8). Several external python packages, including tensor
 flow, scipy, scikit-image, numpy, and matplotlib were
 installed, as directed by the DeTerm supplementary protocol
 (Kanaoka et al., 2019). Input images for DeTerm were pre-
 processed in ImageJ: raw input images were acquired by
 inverting the lookup table (LUT) and region of interest
 (ROI) input images were acquired by manually selecting a
 ROI in ImageJ software for each original image in our dataset.
 DeTerm software was executed in the command line through
 a series of available python scripts (<https://bitbucket.org/skibbe/determ/wiki/Home>). Raw and ROI input images were
 processed in DeTerm to generate output images and positional
 data. Each generated output image was manually corrected by
 subtracting mis-detected dendrite branch terminals and adding
 undetected terminal points using the multipoint tool in ImageJ
 as false positives and negatives respectively. These points
 were removed or added from the original output of total

| | | |
|-----|--|-----|
| 259 | branch terminals detected by DeTerm accordingly. Thus, | 306 |
| 260 | DeTerm also quantifies the number of terminal branch tips. | 307 |
| 261 | Imaris Measurements | 308 |
| 262 | Imaris software (ver. 9.3.1–9.5.0, Oxford Instruments) provid- | 309 |
| 263 | ed by the UC Irvine Optical Biology Core facility was used for | 310 |
| 264 | image analysis. Neuron images were imported into Imaris | 311 |
| 265 | software as flat 2-D maximum intensity projection images to | 312 |
| 266 | avoid inappropriate z-direction terminal branches and to make | 313 |
| 267 | comparable analyses to the other 2-D software tested. Image | 314 |
| 268 | processing was performed by adjusting threshold levels to | 315 |
| 269 | remove background noise for each image. Images were | 316 |
| 270 | cropped within Imaris to exclude unwanted neighboring neu- | 317 |
| 271 | rons. Neuron reconstruction was performed using automated | 318 |
| 272 | detection by the Filament Tracer tool. The largest and thinnest | 319 |
| 273 | diameters of the neuron were manually determined to generate | 320 |
| 274 | dendrite starting and seed points. The thresholds for these | 321 |
| 275 | points were adjusted in order to cover missed regions on the | 322 |
| 276 | neuron of interest, in which the automated filament was gen- | 323 |
| 277 | erated. Small dendrite branches were reconstructed as though | |
| 278 | they were dendritic spines. The generated filament was edited | |
| 279 | in the creation wizard window to correct mis-detected and | |
| 280 | undetected branches. The semi-automated technique for neu- | |
| 281 | ron reconstruction was used to manually add undetected | |
| 282 | branches. Although Imaris is capable of counting either total | |
| 283 | number of dendrite segments (counting primary branches as | |
| 284 | separate from secondary branches, and so forth), to produce | |
| 285 | data that is comparable to the other algorithms, we only report | |
| 286 | here the number of terminal dendrite tips (marked as total | |
| 287 | branch number). | |
| 288 | Tireless Tracing Genie Measurements | |
| 289 | Tireless Tracing Genie plug-in was installed and ran on ImageJ | |
| 290 | software. An inverted ROI was selected in order to exclude un- | |
| 291 | wanted neighboring neurons. Individual values of the neuron | |
| 292 | skeleton after processing were added using the Cox Sums pro- | |
| 293 | gram provided (Iyer et al., 2013). Instead of directly measuring | |
| 294 | dendrite length, this plug-in utilizes the number of slab voxels for | |
| 295 | each neuron skeleton as an equivalent parameter for total dendrite | |
| 296 | length. The pixel conversion factor (pixels to microns) was ob- | |
| 297 | tained from ImageJ for each individual image to manually con- | |
| 298 | vert the number of slab voxels to total dendrite length in microns. | |
| 299 | TTG uses the number of end point voxels as an equivalent pa- | |
| 300 | rameter for total dendrite branch number, thus also counting the | |
| 301 | number of terminal branch tips. | |
| 302 | Time Calculations | |
| 303 | The time required to trace individual neurons was recorded for | |
| 304 | a handful of neurons analyzed through each pipeline. Pre- | |
| 305 | processing times included the time required to select ROIs, | |
| | adjust brightness and contrast, and apply other image process- | 306 |
| | ing features. Post-processing times included the time required | 307 |
| | to manually edit and correct each image for inaccuracies after | 308 |
| | processing individual images through each pipeline. The | 309 |
| | times required in each pre-processing and post-processing | 310 |
| | step were recorded and added together to sum a total average | 311 |
| | time for each automated software. Each pipeline varied in the | 312 |
| | amount of pre-processing and post-processing required which | 313 |
| | was noted and added when averaging the computing duration | 314 |
| | for neuron reconstruction. The average tracing times of each | 315 |
| | software tested was compared to hand tracing. This process | 316 |
| | was repeated for a small subset of neuron images ($n = 10$ neu- | 317 |
| | rons; $n = 5$ neurons mock injured at 24 h AEL then imaged at | 318 |
| | 24 or 72 h AMI; $n = 5$ neurons bald or mock injured at 48 h | 319 |
| | AEL then imaged at 24 or 72 h A(M)I). Tireless Tracing | 320 |
| | Genie was not included in these time calculations as the time | 321 |
| | it takes the pipeline to analyze each image was nearly instant | 322 |
| | and did not output images for manual correction. | 323 |
| | Statistical Analysis | 324 |
| | The same 124 images were imported and analyzed in each soft- | 325 |
| | ware to obtain parameters of total dendrite branches and total | 326 |
| | dendrite length. These 124 images represent neurons across con- | 327 |
| | ditions of 24 h, 36 h, 48 h, and 72 h after egg laying (AEL), and | 328 |
| | imaged at 24 h and 72 h after injury (AI) or after mock injury | 329 |
| | (AMI) as described. Averages \pm standard deviation error bars are | 330 |
| | shown throughout the manuscript. The statistical significance of | 331 |
| | total dendrite branch number amongst three pairs of methods | 332 |
| | (ImageJ vs DeTerm, ImageJ vs Imaris, and DeTerm vs Imaris) | 333 |
| | was determined using paired two-sample t-tests ($p \leq 0.05$). In | 334 |
| | order to compare the results between ImageJ, DeTerm, and | 335 |
| | Imaris, the statistical significance of total dendrite branches was | 336 |
| | determined using a one-way ANOVA test followed by Tukey's | 337 |
| | multiple corrections test, in Prism 8 (GraphPad, San Diego, CA). | 338 |
| | Biostatistical tests were determined in consultation with the UCI | 339 |
| | Institute for Clinical & Translational Science resources for | 340 |
| | Biostatistics, Epidemiology, and Research Design. Total dendrite | 341 |
| | length between two pairs of methods (ImageJ vs Imaris and | 342 |
| | ImageJ vs Tireless Tracing Genie) was determined using paired | 343 |
| | two-sample t-tests ($p \leq 0.05$). The average tracing times of | 344 |
| | ImageJ, DeTerm, and Imaris was compared using a one-way | 345 |
| | ANOVA test followed by Tukey's multiple corrections test, as | 346 |
| | previously mentioned. | 347 |
| | Results | 348 |
| | DeTerm Requires Significant Manual Correction, but | 349 |
| | Eventually Counts Dendrite Tip Number Accurately | 350 |
| | Our dataset consisted of 124 images of ddaC peripheral ner- | 351 |
| | vous system neurons within abdominal segments A1-A6 in | 352 |

353 *Drosophila* larva that came from 16 different conditions
354 (Thompson-Peer et al., 2016). The dendrites of these neurons
355 were either uninjured or injured using a two-photon laser inju-
356 ry method as previously described (Thompson-Peer et al.,
357 2016). The conditions in our dataset are as follows: for injured
358 neurons, dendrites were removed using a two-photon laser at
359 24 h, 36 h, 48 h, or 72 h after egg laying (AEL). Control
360 neurons are uninjured neurons from these same animals. At
361 24 h AEL, 36 h AEL, and 48 h AEL, adjacent neurons were
362 ablated, to reduce invasion of territory from adjacent unin-
363 jured neurons. Neurons are then imaged at both of two differ-
364 ent timepoints: 24 h after injury (AI) or after mock injury
365 (A(M)I) and 72 h (A(M)I). Thus, 4 ages \times 2 treatment options
366 (uninjured or injured) \times 2 imaging time points (24 h A(M)I and
367 72 h A(M)I) results in the 16 conditions represented here
368 (Fig. 1A).

369 As *Drosophila* larvae age, they grow in size, and the terri-
370 tory that each individual neuron is responsible for covering
371 with its dendrite arbor proportionally increases in size as well.
372 The youngest neurons have much smaller dendrite arbors,
373 with much thinner dendrite branches, than the older neurons.
374 For our data set, all images were collected with the same
375 microscope and the same objective. However, the digital
376 zoom is greater for the smaller younger neurons than for the
377 larger older neurons, since the size of those neurons is smaller.
378 Each neuron was imaged with a digital zoom that allowed the
379 dendrite arbor to be captured in a Z stack of a single 1024
380 pixel \times 1024 pixel field of view (without stitching of adjacent
381 images). Thus, while the younger neurons are smaller, and
382 their dendrite branches are thinner, their dendrites are not cap-
383 tured by fewer pixels on the PMT detector of the confocal
384 microscope. After removing Z planes above or below the neu-
385 ron of interest, the maximum intensity projection was gener-
386 ated (Fig. 1B).

387 All 124 neurons had been laboriously hand-traced using
388 the Simple Neurite Tracer (SNT) plug-in in ImageJ (Fig.
389 1C). Hand tracing quantification is labeled as “ImageJ”
390 throughout the study. We had measured the number of termi-
391 nal dendrite tips (annotated as total branch number) and the
392 total dendrite length of all branches summed together.

393 We ran the complete dataset of 124 neurons through the
394 DeTerm pipeline, a freely available software package which
395 detects dendrite terminals based on a machine learning via
396 artificial neural network algorithm (Kanaoka et al., 2019).
397 DeTerm was trained by developers using a dataset of 70
398 wildtype class IV da (ddaC) neurons from wandering 3rd in-
399 star *Drosophila* larvae, where the dendrite tips had been man-
400 ually annotated. After processing our data into the software,
401 DeTerm generated output images of detected branch terminals
402 which were then manually corrected to adjust for false positive
403 and false negative points (Fig. 1D). Manual corrections were
404 required at all time points and across all ages to accurately
405 quantify the image data, including neurons uninjured at 72 h

AEL that were imaged at 72 h AMI, which is most similar to 406
the DeTerm training dataset (Fig. 2A). After manual correc- 407
tion, DeTerm resulted in similar counts of total dendrite 408
branches compared to hand tracing across all conditions 409
($p > 0.05$, $n = 124$), excluding one time point (Fig. 2B). 410
Automatic detection by DeTerm resulted in a statistically 411
higher total count of dendrite branches in neurons uninjured 412
at 48 h AEL that were imaged at 24 h AMI compared to hand 413
tracing ($p < 0.0001$, 221 ± 35 dendrites from ImageJ versus 414
 248 ± 39 dendrites for DeTerm, $n = 8$). Overall, with manual 415
correction, DeTerm performs well for counting total branch 416
number. However, as DeTerm does not measure dendrite 417
length, we could not extract that parameter from our dataset 418
using this pipeline. 419

420 **Imaris Reconstructs Arbors to Correctly Count Branch** 421 **Number but Underestimates Dendrite Length**

422 Next, we ran the complete dataset of 124 images through the 422
commercially available software package Imaris (Oxford 423
Instruments). Unlike DeTerm which only marks dendrite tips, 424
Imaris reconstructs the entire dendrite arbor, allowing for 425
quantification of a variety of features (Fig. 1E). Imaris counted 426
similar numbers of total dendrite branches across all 16 con- 427
ditions compared to hand tracing ($p > 0.05$, $n = 124$) (Fig. 3A). 428
However, automatic detection by Imaris measured significant- 429
ly shorter total dendrite lengths than hand tracing for 11 out of 430
16 ages and conditions (Fig. 3B). For example, in neurons 431
uninjured at 24 h AEL that were reimaged at 24 h AMI, 432
ImageJ measured an average length of $2002 \pm 468.6 \mu\text{m}$, com- 433
pared to $1826 \pm 406.5 \mu\text{m}$ for Imaris ($p < 0.0001$, $n = 12$). This 434
significant under-measurement of dendrite length persisted in 435
these same neurons when they were later re-imaged at 72 h 436
AMI. At these time points, ImageJ and Imaris counted statisti- 437
cally similar numbers of dendrite branches. We wanted to 438
ensure that consistent under-measurement of dendrite length 439
was not simply a calculation error, so we measured the direct 440
distance between two points on three images in Imaris and 441
ImageJ for validation. Both software gave the same measure- 442
ment length, suggesting that the observed difference in total 443
arbor length is not merely a conversion error from pixels to 444
microns (data not shown). Thus, after manual correction, 445
Imaris is able to accurately count branch numbers, but signif- 446
icantly underestimates dendrite length in reconstructed arbors. 447

448 **Imaris is Slightly Better than DeTerm at Counting** 449 **Branch Number**

450 One significant difference between a hand tracing approach 450
and the automated approaches is the need for after-the-fact 451
manual correction of automated image analysis performed 452
by DeTerm and Imaris. Like DeTerm, Imaris also required 453
extensive correction, though since this step is embedded 454

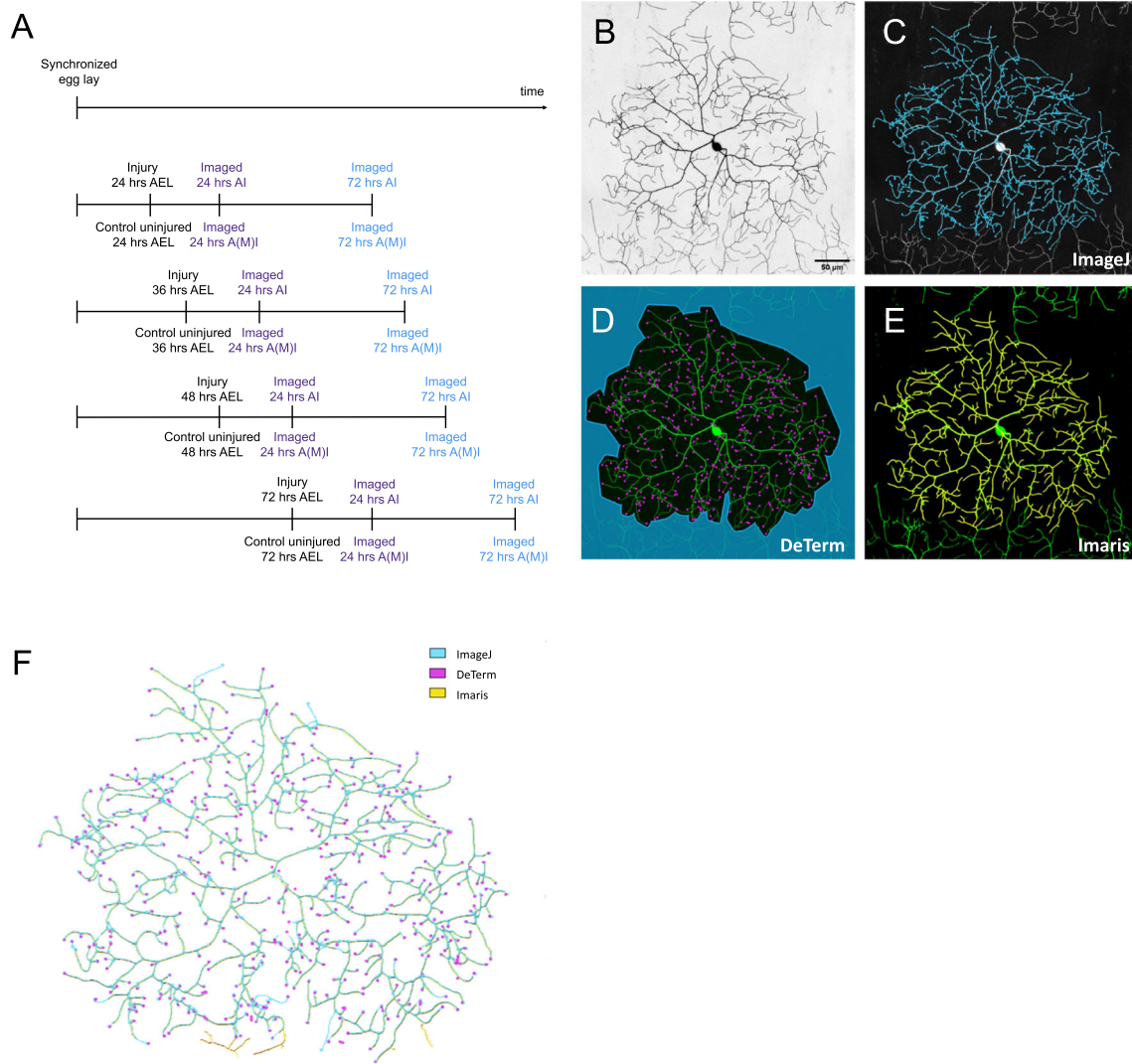


Fig. 1 Timeline of the complete data set that is reiteratively processed through data analysis pipelines. **A** Timeline for experiments. After a synchronized egg lay, neurons are injured (or not injured, in the case of control uninjured neurons) at 24, 36, 48, or 72 h after egg laying (AEL). Animals are then recovered, and continue to develop. Neurons are imaged at 24 h after injury (AI) or after mock injury (for uninjured neurons, A(M)I) and again at 72 h A(M)I. **B** Representative image of an injured & regenerated neuron, balded at 24 h AEL and imaged at 72 h AI. **C**

ImageJ hand tracing analysis of the neuron in panel **B**. **D** DeTerm analysis of neuron in panel **B**. Purple dots are branch tips counted by DeTerm before manual correction. Blue shading indicates the area marked as outside the dendrite arbor. **E** Imaris reconstruction of neuron in panel **B**. **F** ImageJ (blue) hand tracing analysis overlaid above DeTerm terminal branch detection (pink) output and Imaris neuron reconstruction (yellow). Branches traced by both ImageJ and Imaris appear green

455 within the pipeline, we were unable to count the number of
 456 corrections made. The types of neuron features that required
 457 manual correction were observed to be similar for both auto-
 458 mated pipelines (Fig. 4A). In cases where the fluorescent sig-
 459 nal for neurons was poorly contrasted by a bright autofluorescent
 460 background, both DeTerm and Imaris excluded branches entirely,
 461 or only partially reconstructed the arbor (Fig. 4A). Autofluorescence
 462 from background structures such as the denticle belt could be mis-
 463 interpreted as dendrites by automated approaches. If the animal
 464 moved slightly during image acquisition, which resulted in dupli-
 465 cating branches by a double shadow, the software would erroneously
 466 double count branches in the final projection image. Finally,
 467

468 automated approaches would trace the axon in many cases
 469 as well, since the proximal region of the axon is in a nearby
 470 Z-plane. In these cases, the axon was manually removed and
 471 not included as part of dendrite architecture. Manual correc-
 472 tion allows users to remedy these errors where branches are
 473 either over- or under-counted by automated pipelines, that of
 474 which would be correctly traced by hand. Having manually
 475 corrected the Imaris reconstructions for dendrite branch num-
 476 ber, we investigated potential reasons for the significant
 477 under-measurements of dendrite length in those reconstructed
 478 neurons. Upon closer inspection, only a number of small ter-
 479 minal branches were partially captured (Fig. 4B). Presumably,
 480 if enough branches are incompletely captured, this may

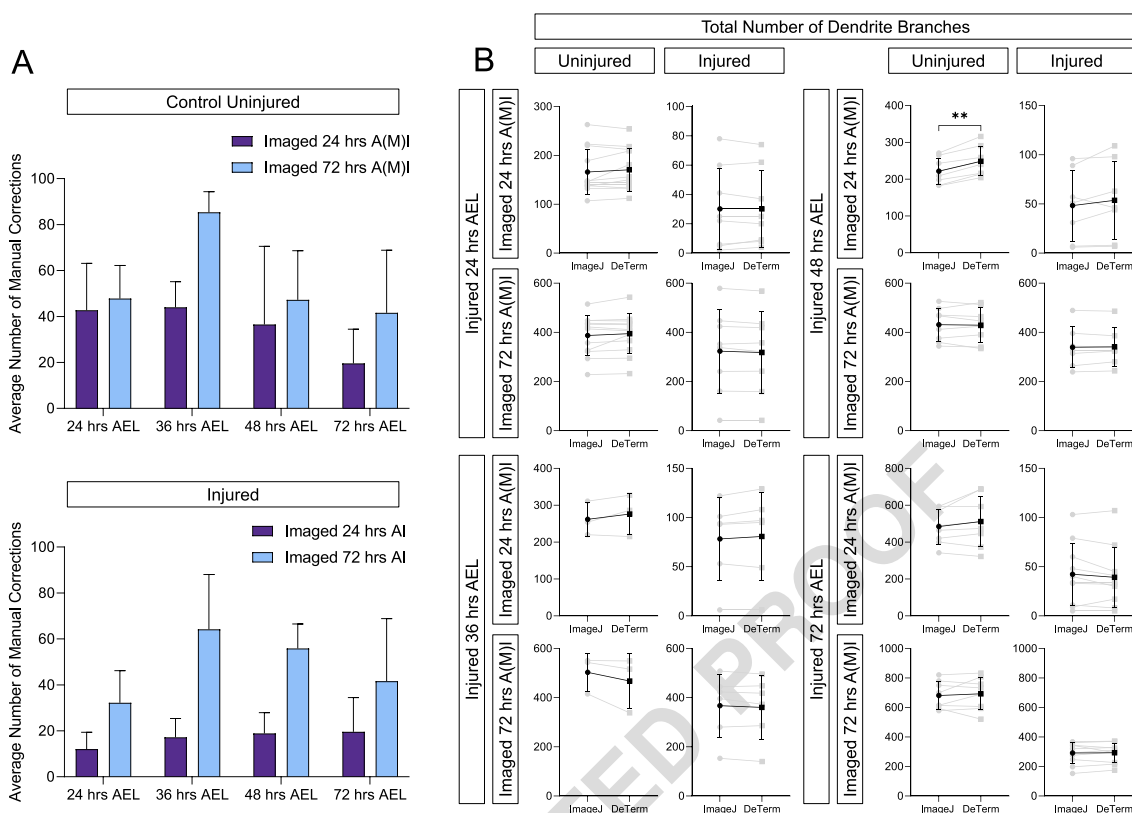


Fig. 2 With significant manual correction, DeTerm generally counts the correct number of dendrite branch tips, but does not measure total dendrite length. **A** Average number of manual corrections required for neurons at each stage, whether uninjured (top) or injured (bottom), imaged 24 h A(M)I (blue) and 72 h A(M)I (gray), \pm standard deviation error bars. **B** For neurons either injured at 24 h AEL, 36 h AEL, 48 h

AEL, or 72 h AEL or uninjured controls, imaged at 24 h A(M)I (after injury or after mock injury) or 72 h A(M)I, the total number of branches counted by hand tracing in ImageJ or DeTerm is shown. Individual neurons are shown in gray (line connects the quantification of the same neuron), average \pm standard deviation error bars are in black. ** $p < 0.01$ by paired t-test

481 subtract from the total length of the dendrite arbor observed
482 while maintaining accurate values of total dendrite branches.

483 Since DeTerm does not measure total dendrite length, we
484 could not compare this parameter across all tested approaches.
485 However, each automated approach was able to extract values
486 of dendrite branch number. DeTerm and Imaris resulted in
487 similar counts of total dendrite branches compared to hand
488 tracing across all injury conditions ($p > 0.05$, $n = 124$), except
489 for one (Fig. 5). DeTerm counted significantly more dendrite
490 branches than ImageJ and Imaris in control uninjured neurons
491 at 48 h AEL and imaged at 24 h AMI ($p = 0.0019$ compared to
492 ImageJ, $p = 0.0007$ compared to Imaris, $n = 8$). For this same
493 condition, DeTerm averaged a greater number of total dendrite
494 branches ($\mu = 248.5 \pm 39.2$ dendrites) compared to ImageJ ($\mu = 221.6 \pm 35.0$ dendrites) and Imaris ($\mu = 218.6 \pm 43.1$ dendrites). For the remaining 15 conditions, there were no significant differences observed amongst ImageJ, Imaris, and DeTerm for counting dendrite branch number ($p > 0.05$).

499 Do the different algorithms perform differently on simpler
500 versus more complex arbors? We compared each algorithm
501 against hand-tracing by calculating the relative error output for
502 each neuron compared to hand tracing, and then normalized

503 that to the number of branches for that neuron (Fig. S3). For
504 example, if ImageJ counted 200 branches on a given neuron,
505 but Imaris counted 210 branches, the relative error would be
506 $(200 - 210) / 200$, or -5% for that neuron. For uninjured control
507 neurons, DeTerm's relative error is sometimes positive (when
508 it underestimates the number of branches) and sometimes nega-
509 tive (when it overestimates the number of branches), while
510 Imaris' relative error is usually positive, but both are generally
511 small. However, the size of the relative error for both DeTerm
512 and Imaris is larger and more variable when calculated for
513 neurons regenerating after injury (Fig. S3B). This supports
514 our assertion that the automated pipelines perform more like
515 hand tracing on uninjured control neurons, but that quantifi-
516 cation of regenerated neurons after injury is a greater chal-
517 lenge for these software.

518 Due to the dependence of researchers to identify every
519 starting and end point of individual dendrites, it took an aver-
520 age of 21 min to hand trace individual neurons from our
521 dataset (Table 1). DeTerm and Imaris, which required both
522 preprocessing and postprocessing steps, added to the amount
523 of time on each image amongst automated approaches.
524 DeTerm averaged about 7 min to process each image

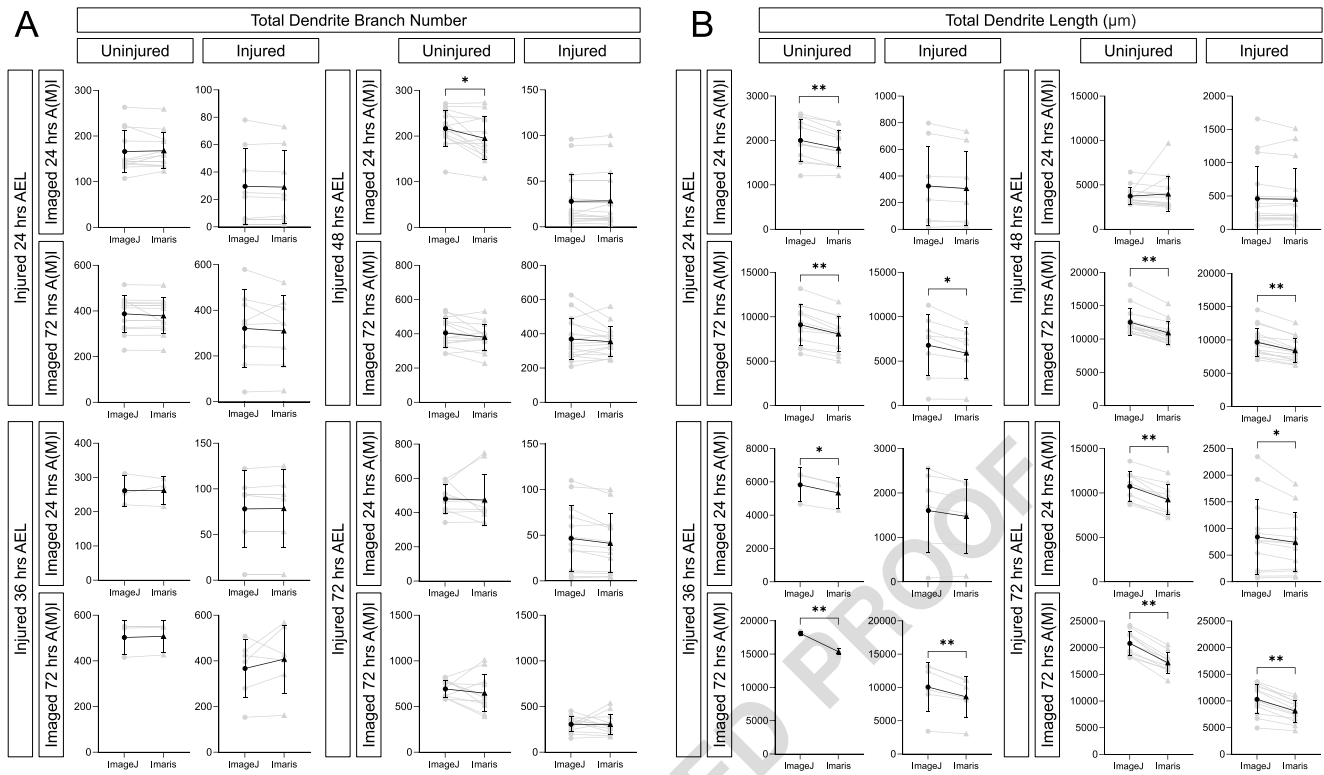


Fig. 3 With manual correction, Imaris counts the correct number of dendrite branch tips, but significantly underestimates total dendrite length. **A** Total number of branches counted by hand tracing in ImageJ or by reconstruction in Imaris is shown. Individual neurons are shown in gray (lines connect the quantification of the same neuron), average \pm standard deviation error bars are in black. None of the pairwise

comparisons are significantly different. **B** Total dendrite length measured by hand tracing in ImageJ or by reconstruction in Imaris is shown. * $p < 0.05$, ** $p < 0.01$ statistically significant difference by pairwise t-test. Absence of an asterisk indicates no significant difference was observed

525 including preprocessing and postprocessing, which is significantly
 526 quicker than manual hand tracing by ImageJ
 527 ($p < 0.0001$, $n = 10$). Similarly, Imaris required around 5 min
 528 per each image, which was significantly quicker than ImageJ
 529 as well ($p < 0.0001$, $n = 10$). However, both DeTerm and
 530 Imaris were not significantly quicker than each other ($p >$
 531 0.05 , $n = 10$). As previously mentioned, Tireless Tracing
 532 Genie was not included in these time calculations as the time
 533 it takes the pipeline to analyze each image was nearly instant.
 534 Since this approach did not output images for manual

correction, we could not compare post processing times 535
 against the other software tested. 536

Tireless Tracing Genie under-Estimates Dendrite Branch Number and over-Estimates Dendrite Length 537 538

Unlike DeTerm and Imaris, Tireless Tracing Genie does not 539
 offer the function to view processed images for manual cor- 540
 rection. Due to this, we were unable to manually edit the 541
 analysis of dendrite architecture to add missed branches, 542

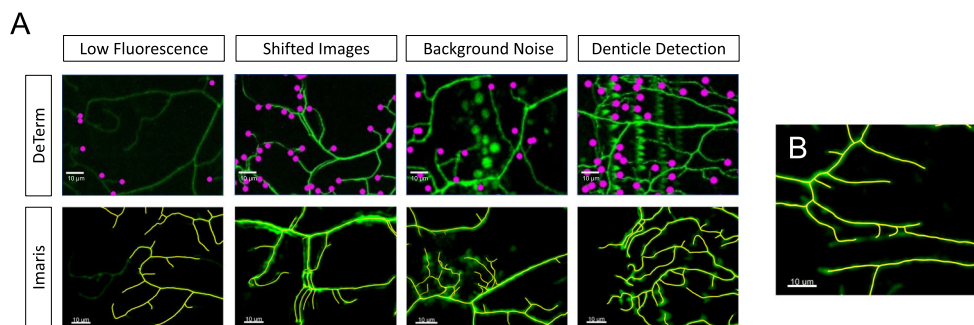
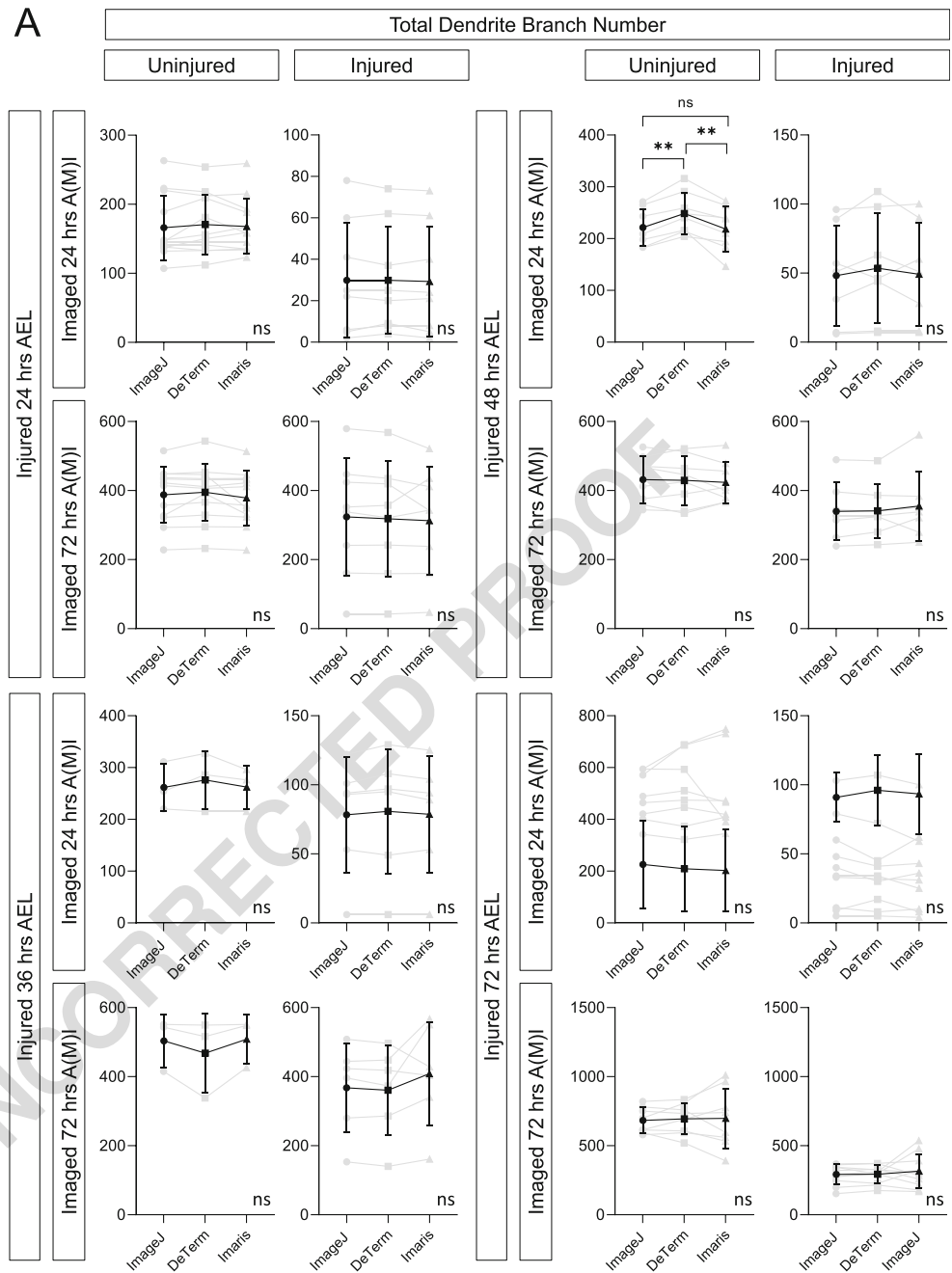


Fig. 4 Manual correction of common errors in both DeTerm and Imaris. **A** These errors include adding in areas of low fluorescence, accounting for animal movement during image collection, removing high background detection, and removing detection of the denticle belt. **B**

Looking closely at the Imaris reconstructed arbor, inappropriate shortening of small dendrite branches may account for the under-measurement of total dendrite arbor length

Fig. 5 DeTerm and Imaris both generally count the correct number of dendrite branches on average, though DeTerm overcounts in one condition. Total number of branches counted by hand tracing in ImageJ or by automated analysis in DeTerm or by reconstruction in Imaris is shown. Individual neurons are shown in gray (lines connect the quantification of the same neuron), average \pm standard deviation error bars are in black. $** p < 0.01$ by one-way ANOVA with Tukey's multiple corrections test, otherwise no statistical difference was found



t1.1 **Table 1** Average Tracing Times
 t1.2 ($n = 10$). Hand tracing takes
 significantly longer than Imaris or
 DeTerm

| Software | Pre-processing Time (min:sec. 1/100 s) | Tracing Time (min:sec. 1/100 s) | Post-processing Time (min:sec. 1/100 s) | Total (min:sec. 1/100 s) |
|----------|--|---------------------------------|---|--------------------------|
| ImageJ | N/A | 20:58.4 | N/A | 20:58.4 |
| DeTerm | 01:05.7 | 01:52.3 | 04:06.3 | 07:09.5 |
| Imaris | 00:30.0 | 01:48.8 | 02:41.0 | 04:29.8 |

Pre-processing, automated tracing time, and manual editing time are shown for the same 10 neurons to go through ImageJ, DeTerm, and Imaris. These neurons were not chosen to be representative of all 16 conditions, but the relative time involved should be comparable across approaches

Q3

t1.3
 t1.4
 t1.5

543 remove inappropriate branches, or extend partially traced
 544 branches. We examined two output parameters in order to
 545 determine the total number of branches: *branches* and *end*
 546 *point voxels*, which is equivalent to the number of endpoints.
 547 The *branches* output reports the number of branch segments,
 548 so a single dendrite branch may have many segments, which is
 549 not comparable to the ImageJ branch tip number. The *end*
 550 *point voxels* output significantly underestimated the number
 551 of branches, and varied across all conditions (Fig. S1). Total
 552 dendrite length was extracted from Tireless Tracing Genie as
 553 *total slab voxels*, which the developers reported as nearly
 554 equivalent to total length. We individually converted each
 555 output length from pixels to microns, in order to determine
 556 total dendrite length in microns. After doing so, we found that
 557 total dendrite length was overestimated in nearly all cases
 558 except two (Fig. 6).

559 **Only Imaris, among all the Automated Approaches,**
 560 **Reproduced Essential Conclusions of ImageJ Manual**
 561 **Analysis**

562 This data set is a subset of the experiments generated for
 563 Thompson-Peer et al., 2016, where conclusions from the manual
 564 analysis were first described. At any age, branch number
 565 and branch length is less at 24 h after injury compared to
 566 uninjured neurons. There were four primary conclusions from
 567 this subsection of the data in that manuscript when neurons
 568 were imaged 72 h after injury, depending on the age at the

time of injury (Table 2). For neurons injured at 48 h AEL, 569
 when they were imaged at 72 h AI, dendrite branch number 570
 had regenerated enough to not be significantly different from 571
 uninjured age-matched controls, but total dendrite length 572
 remained significantly shorter. For neurons injured slightly 573
 later in development, at 72 h AEL, when they were imaged 574
 at 72 h AI, dendrite branch number and total dendrite length 575
 were both significantly less than age-matched uninjured controls. 576
 We performed these same comparisons on the data as 577
 quantified by DeTerm (Fig. S2A), Imaris (Fig. S2B), and 578
 Tireless Tracing Genie (Fig. S2C), summarized in Table 2. 579

At 24 h after (mock) injury, the differences between recently 580
 injured versus uninjured neurons are striking and should be 581
 obvious by any method of quantification. Only Imaris detected 582
 the obvious decrease in dendrite number and total length in 583
 neurons imaged 24 h after injury compared to age-matched 584
 uninjured controls. DeTerm detected the decrease in dendrite 585
 number but does not measure branch length, and Tireless 586
 Tracing Genie detected the decrease in length but failed to 587
 detect the decrease in branch number (in neurons injured at 588
 72 h AEL, and detected the decrease in neurons injured at 48 h 589
 AEL with less significance than ImageJ hand tracing). 590

By 72 h after injury, injured neurons have regenerated sig- 591
 nificantly, but still fall short of uninjured control neurons in 592
 many important ways. DeTerm produced an novel slight but 593
 significant decrease in branch number of neurons injured at 594
 48 h AEL, and recapitulated the same significant decrease in 595
 branch number of neurons injured at 72 h AEL; as DeTerm 596

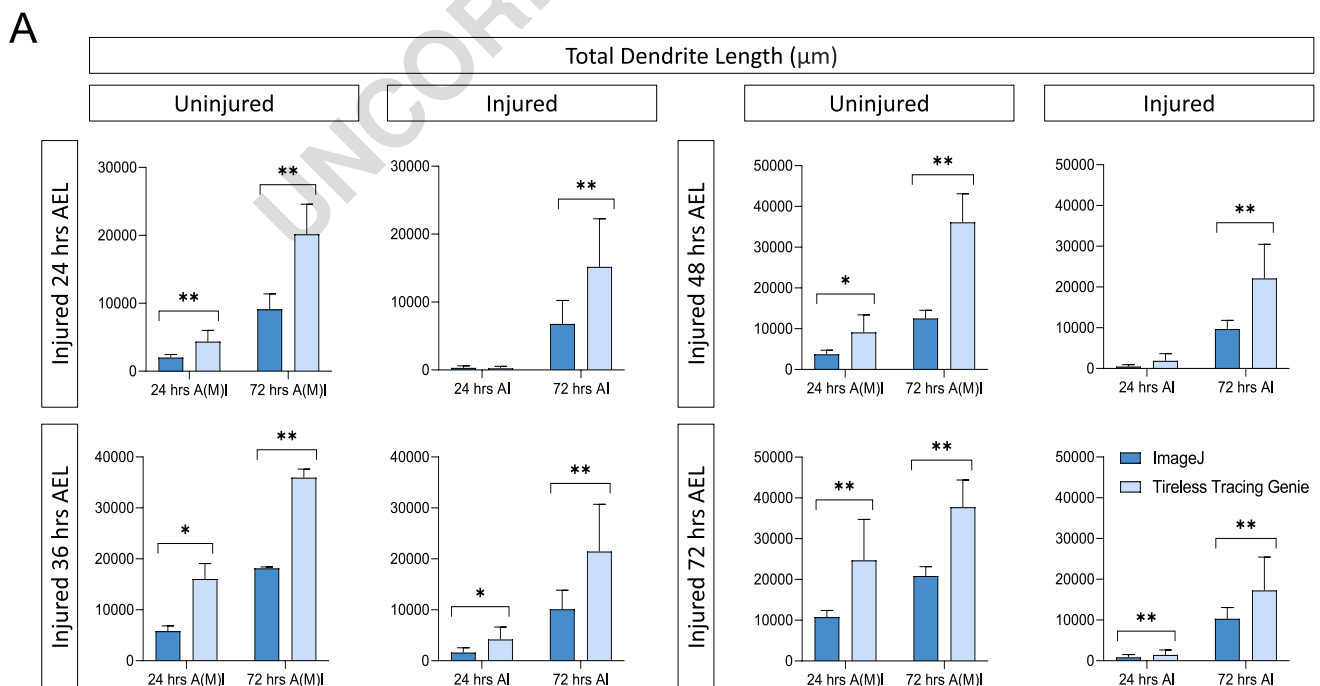


Fig. 6 Tireless tracing genie consistently overestimates dendrite length. Average total dendrite length measured by hand tracing in ImageJ or by Tireless tracing genie is shown \pm standard deviation. * $p < 0.05$, **

$p < 0.01$ statistically significant difference by pairwise t-test. Absence of an asterisk indicates no significant difference was observed.

t2.1 **Table 2** Comparison to Thompson-Peer et al. (2016). Automated pipelines compared to manual tracing in their ability to detect major similarities and differences between uninjured and regenerated neurons

| t2.2 | Hours AEL | Observation | ImageJ | DeTerm | Imaris | Tireless Tracing Genie |
|-------|------------------|---|--------|--------|--------|------------------------|
| t2.3 | Injured 48 h AEL | At 24 h A (M) I, injured neurons have fewer branches than uninjured neurons | ** | ** | ** | ** |
| t2.4 | | At 72 h A(M)I, injured neurons have fewer branches than uninjured neurons | ns | ** | ns | ns |
| t2.5 | | At 24 h A(M)I, injured neurons have shorter total length than uninjured neurons | ** | n/a | ** | **** |
| t2.6 | | At 72 h A(M)I, injured neurons have shorter total length than uninjured neurons | ** | n/a | ** | ** |
| t2.7 | Injured 72 h AEL | At 24 h A (M) I, injured neurons have fewer branches than uninjured neurons | ** | ** | ** | ns |
| t2.8 | | At 72 h A(M)I, injured neurons have fewer branches than uninjured neurons | ** | ** | ** | ns |
| t2.9 | | At 24 h A(M)I, injured neurons have shorter total length than uninjured neurons | ** | n/a | ** | ** |
| t2.10 | | At 72 h A(M)I, injured neurons have shorter total length than uninjured neurons | ** | n/a | ** | ** |

Each approach was tested in their ability to recreate the major conclusions of how injury alters dendrite architecture. Neurons were (mock) injured at 48 or 72 h AEL, then at 24 h and 72 h later, mock uninjured control neurons were compared to injured neurons. Among the 3 automated pipelines, Imaris best supports biological conclusions similar to what is seen for ImageJ. * $p < 0.05$ statistical difference detected, in the direction indicated by the statement. ** $p < 0.01$ statistical difference detected, in the direction indicated by the statement. NS: no statistical difference was found. N/A: quantification is not an available output of the software. See also Fig. S2

597 does not measure dendrite arbor length, it was unable to sup-
 598 port conclusions about differences in dendrite length that were
 599 in the original manuscript. Imaris was able to successfully
 600 replicate all the findings previously observed with ImageJ.
 601 Tireless Tracing Genie detected the decreases in branch length
 602 for neurons injured at both 48 h AEL and 72 h AEL, relative to
 603 uninjured age-matched controls. While TTG replicated the
 604 finding that branch number regenerates to match age-
 605 matched controls in neurons injured at 48 h AEL, it failed to
 606 detect the significant impairment in branch number regenera-
 607 tion in neurons injured at 72 h AEL.
 608 Overall, DeTerm would have allowed us to come to the
 609 same conclusions about branch number, but would not have
 610 been able to provide any insight into branch length. Tireless
 611 Tracing Genie would not have allowed us to come to the same
 612 conclusions about branch number, and significantly
 613 overestimates dendrite length. While Imaris underestimates
 614 dendrite length, this is consistent enough that it would have
 615 supported the same conclusions we came to in our earlier
 616 manuscript, while offering significantly faster data
 617 quantification.

618 **Discussion**

619 While many automated software exist to aid with neuron trac-
 620 ing, different neuron types present various challenges for these
 621 software to adapt to. Our results highlight how each software
 622 analyzes morphological differences in dendrite architecture
 623 between wildtype uninjured and regenerated neurons. Since
 624 the morphology of an elaborate dendrite arbor determines how
 625 it functions as a receptive structure, it is important to examine
 626 how automated approaches capture the subtle differences

caused by injury. Analyzing changes in dendrite morphology
 can help researchers identify cellular mechanisms involved in
 regeneration of dendrite architecture. As the field of dendrite
 regeneration continues to grow, the development of a reliable
 automated tracing software will be highly valued.

In this study, we compared how three publicly available
 automated neuron tracing software performed, both on unin-
 injured and regenerated class IV *Drosophila* neurons. We eval-
 uated the performance of DeTerm, Imaris, and Tireless
 Tracing Genie to accurately and efficiently quantify total den-
 dendrite length and number of dendrite branches. We determined
 that both DeTerm and Imaris counted a similar number of
 dendrite branches, though a great extent of manual correction
 was required. The Tireless Tracing Genie significantly
 underestimated the total number of dendrite branches across
 all conditions. Unfortunately, none of the software we tested
 were capable of accurately extracting total dendrite length
 even following manual correction. DeTerm currently does
 not extract total dendrite length from images, and therefore,
 could not be compared to the other software. Tireless Tracing
 Genie overestimated length in almost every condition, despite
 proper conversion of pixels to microns. In contrast, Imaris
 significantly underestimated dendrite length in a vast majority
 of cases. Underestimations similar to that seen in Imaris have
 been previously reported by other studies. Meijering et al.
 (2004) observed underestimation of total dendrite length in a
 semi-automated approach, likely due to the algorithm
 shortcutting sharply bending segments (Meijering et al.,
 2004). Similarly, Smafield et al. (2015) attributed their under-
 estimation of total dendrite length to disregard of dim
 branches and reciprocal overestimation of dendrite length in
 other parts of the neuron (Smafield et al., 2015). As shown in
 our study, automated reconstruction of dendrite branches by

660 Imaris only captured a number of small terminal branches,
661 which may be attributed to similar reasons as those seen in
662 previous studies.

663 While none of the automated approaches are a perfect
664 quantification of the dendrite arbor, limitations in reliability
665 due to misquantification may be offset by increases in effi-
666 ciency. The average neuron tracing time was determined by
667 adding the time it took to prepare each image before tracing
668 and the time it took for the software to trace both manual and
669 automated approaches. Hand tracing by ImageJ took the lon-
670 gest time with an average of 21 min per image. DeTerm was
671 significantly quicker than ImageJ with an average tracing time
672 of 7 min. Likewise, Imaris' average tracing time of 5 min was
673 quicker than ImageJ, but was not significantly quicker than
674 DeTerm. Our sample size consisted of mostly uninjured neu-
675 rons imaged at 24 h AMI, which had the most simple arbors
676 across all our conditions, and are certainly simpler than their
677 injured counterparts and neurons in older animals. Regen-
678 erated neurons have disorganized branches, exhibit
679 self-avoidance defects, and have denser arbors after injury
680 compared to uninjured neurons. These defects exhibited by
681 regenerating dendrites make analysis more complicated com-
682 pared to uninjured neurons. Thus, the analysis times that we
683 reported represent the shortest possible analysis time with
684 each approach. Analysis of more complex arbors in older
685 animals and an increased number of dendrite branches would
686 expect to take proportionally longer with each approach.

687 DeTerm's automated detection of dendrite branch number
688 performed better in its original study compared to our study
689 relative to manual tracing (Kanaoka et al., 2019). The differ-
690 ence in the results obtained from Kanaoka et al. (2019) and this
691 study may be attributed to the original dataset used to train
692 DeTerm's artificial neural network. Their dataset consisted of
693 70 wildtype class IV da neurons of wandering 3rd instar
694 *Drosophila* larvae while ours contained images of uninjured
695 and injured neurons acquired at earlier time points. Thus, it is
696 difficult to determine DeTerm's applicability to younger ani-
697 mals or on regenerated neurons as we tested in this study.
698 Wandering 3rd instar larvae are at least 96 h AEL compared
699 to the larvae examined in this study, which are between 24 and
700 72 h AEL. Class IV da neurons grow throughout larval devel-
701 opment, therefore the number of dendrite terminals detected by
702 DeTerm in wandering 3rd instar larvae in the original study is
703 much higher than the number we report here for younger neu-
704 rons. Additionally, DeTerm was originally applied to neurons
705 of varying nutritional conditions, which altered dendrite mor-
706 phology, whereas the two-photon laser injury assay was used in
707 our study. Differences in the intensity of each injury method
708 may have resulted in varying regenerated morphologies. This
709 may explain why DeTerm performed better at quantifying den-
710 dritic branches in wildtype as well as neurons subjected to
711 minor injuries but struggled to accurately quantify complex
712 regenerated dendrite arbors without manual correction.

713 Similarly, the original Tireless Tracing Genie study detect-
714 ed several thousand branches on average for each genetic
715 condition analyzed and did not apply the program to simpler
716 uninjured neurons utilized in our dataset (Iyer et al., 2013).
717 Our results show that Tireless Tracing Genie significantly
718 overestimates total dendrite length in almost every condition,
719 making it difficult to assess its applicability for this purpose.
720 Tireless Tracing Genie was originally used to quantify den-
721 drite morphology of neurons in various genetic mutants,
722 which had a greater number of dendrite branches and
723 total arbor length compared to our samples. Given such,
724 our results are not simply due to errors in the applica-
725 tion, but rather due to differences in the morphologies
726 of neurons utilized in each dataset.

727 Out of the three automated approaches tested, Imaris best
728 suits our goal to study dendrite regeneration on both uninjured
729 and regenerated dendrite. Our results demonstrate that purely
730 automated methods do not yield accurate results, and manual
731 correction is required to correct errors in resulting output
732 traces. Imaris mitigates this issue by incorporating a strategy
733 that combines automated reconstruction and user editing,
734 through a semi-manual construction method similar to
735 Simple Neurite Tracer. In contrast, DeTerm requires users to
736 manually correct for missed and overcounted dendrite
737 branches using an external software. While this step greatly
738 enhances the accuracy of DeTerm, it also increases the amount
739 of time required to effectively trace each image, which is
740 important to consider when quantifying large datasets.
741 Tireless Tracing Genie, while simple to install and execute,
742 could not output annotated images from input images, making
743 it difficult to assess the validity of the software's performance.
744 The choice of tracing method is an essential element in opti-
745 mizing efficiency. DeTerm is operated via the command line,
746 and thus requires knowledge on setting up programming en-
747 vironments, installing external libraries, and running Python
748 scripts. On the other hand, Imaris's user interface has a crea-
749 tion wizard that guides users through the tracing pipeline step-
750 by-step. In addition, users can choose between various tracing
751 strategies ranging from manual to automatic, and given such,
752 Imaris' customizable user interface could be considered more
753 user-friendly. Moving forward, user-interface and program
754 features will be significantly important to maximize the effi-
755 ciency of automated neuron tracing software for studying den-
756 drite regeneration.

757 While this study only tested three applicable software for
758 quantifying regeneration in *Drosophila* neurons, we acknowl-
759 edge that other image analysis techniques exist for this partic-
760 ular issue at hand. Sheng et al. (2019) and Satoh et al. (2012)
761 both utilized a combination of time lapsed video imaging with
762 image analysis software to observe and quantify the develop-
763 ment of uninjured and regenerated *Drosophila* neurons, res-
764 pectively (Satoh et al., 2012; Sheng et al., 2019). Many studies
765 have utilized the commercial software, NeuroLucida (MBF 766

766 Bioscience), for neuron image analyses as well (Dickstein et al.,
767 2016; Egger et al., 2012; Ghosh et al., 2011; Sohn et al., 2016).
768 Previous studies have also identified the need for automated
769 analysis of complex neuron morphologies. Similar to DeTerm,
770 Soltanian-Zadeh et al. (2019) developed an algorithm based on a
771 convolutional neural network (CNN) architecture for neuron image
772 segmentation (Soltanian-Zadeh et al., 2019). While these
773 studies demonstrate the applicability of machine learning soft-
774 ware for neuron image quantification, they have only been illus-
775 trated to be useful for their own unique dataset. This issue of
776 applicability of algorithms to external datasets is widely investi-
777 gated, and a software that could successfully be applied to vari-
778 ous types of neurons is desired for the future. It is also important
779 to note that these results may not fully apply to other neuronal
780 systems, or the same neuronal systems visualized using different
781 methods. Images with poorer signal-to-noise ratios will be harder
782 to quantify automatically, such as imaging on other microscopes,
783 or with dimmer fluorophores, or deeper dendrites that are farther
784 from the imaging coverslip.

785 Unlike automated approaches, hand tracing requires re-
786 searchers to determine the starting and end points of individual
787 dendrites themselves. While this completely eliminates post-
788 processing times, it significantly adds to the time spent directly
789 analyzing each image. On the other hand, state-of-the-art auto-
790 mated neuron tracing approaches still require intensive manual
791 correction after algorithmic processing (Peng et al., 2011). While
792 automated approaches significantly reduce the amount of time to
793 trace dendrites, the time dedicated to manual correction could
794 potentially render this advantage impractical. In fact, the online
795 neuron morphology database Neuromorph.org primarily consists
796 of neuron reconstructions using manual approaches most likely
797 due to this reason (Ascoli et al., 2007). Therefore, it is important
798 to consider that faster analyses may not necessarily be the most
799 efficient. Additionally, pre-processing images by adjusting image
800 quality and removing interfering signals can improve the perfor-
801 mance of each software tested. Imaris allows users to adjust
802 imaging settings within the software, while DeTerm and
803 Tireless Tracing Genie require images to be pre-processed using
804 external software, ImageJ. For Imaris, Image processing was
805 performed by adjusting threshold levels to remove background
806 noise for each image. Images were then cropped within Imaris to
807 exclude unwanted neighboring neurons. While the imaging set-
808 tings were not altered for DeTerm and Tireless Tracing Genie, it
809 is possible that their performances may improve with image
810 quality. Increasing the neuron signal may have allowed
811 DeTerm and Tireless Tracing Genie to detect dendrite branches
812 that would have otherwise been undetected. Similarly, removal
813 of background noise may reduce the instances in which branches
814 are falsely misdetected by both software. It is important to con-
815 sider all facets of automated techniques, as no software is going
816 to perfectly quantify these features of a dendritic tree. The infor-
817 mation we present here should help researchers in this
818 cost/benefit analysis, to determine if the increase in efficiency

819 afforded by automated pipelines compensates for the particular
820 decrease in reliability of any individual measurement.

821 For this manuscript, we focused on extracting two specific
822 measurements from these automated pipelines: branch num-
823 ber and total dendrite length. We focused on these parameters
824 because they were important for the conclusions of our previ-
825 ous work, and because most of the software could deliver
826 these quantifications, allowing us to cross compare the output
827 results. However, these are only a few of the many important
828 parameters that determine dendrite architecture. In addition to
829 branch number and total length, other important parameters
830 include dendrite branch order (the number of primary versus
831 secondary versus terminal branches), branching location, and
832 overlap with other branches of the same neuron (self-
833 avoidance) or adjacent neurons (tiling). These features are
834 frequently quantified using Sholl analysis and overlap mea-
835 surements (O'Neill et al., 2015; Sholl, 1953). While Sholl
836 analysis was not conducted or compared amongst the tested
837 software in this study, the neuronal reconstructions of both
838 ImageJ hand tracing and Imaris are capable of generating this
839 valuable metric (along with a variety of other morphological
840 parameters). Tireless Tracing Genie and DeTerm are not ca-
841 pable of supporting automated Sholl analysis. Thus, for ques-
842 tions where the Sholl analysis would prove useful, our con-
843 clusion that the Imaris pipeline best facilitates automated ex-
844 traction of the features that can be manually extracted by hand
845 tracing holds true. None of the approaches automatically mea-
846 sure crossing over (of other branches of the same neuron, as
847 defects in self-avoidance, or of other branches of other neu-
848 rons, as defects in tiling), but the measurements of dendrite
849 length is necessary for the normalization of crossing over
850 events per 1000 μm of dendrite length, and this data is reliably
851 generated by ImageJ and Imaris (but not TTG nor DeTerm).
852 This study presents a simplified analysis of the performance of
853 several methods available for neuron tracing, which included
854 parameters of total dendrite branches and total dendrite length,
855 for studying dendrite architecture when comparing a wild-
856 type to abnormal arbor.

Information Sharing Statement 857

858 Most of the hand tracing analysed in this manuscript was
859 previously uploaded to NeuroMorpho.org, as part of the
860 Thompson-Peer et al., 2016 manuscript. Any hand tracing
861 not previously uploaded to the repository as part of the prior
862 publication will be added to that repository.

863 DeTerm and TTG were previously published by their de-
864 velopers (Iyer et al., 2013; Kanaoka et al., 2019). Imaris is
865 available commercially from Oxford Instruments.

- 866 **Supplementary Information** The online version contains supplementary
868 material available at <https://doi.org/10.1007/s12021-021-09532-9>.
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