

<sup>1</sup> MotilA – A Python pipeline for the analysis of  
<sup>2</sup> microglial fine process motility in 3D time-lapse  
<sup>3</sup> multiphoton microscopy data

<sup>4</sup> Fabrizio Musacchio  <sup>1</sup>, Sophie Crux<sup>1</sup>, Felix Nebeling<sup>1</sup>, Nala Gockel<sup>1</sup>, Falko  
<sup>5</sup> Fuhrmann<sup>1</sup>, and Martin Fuhrmann  <sup>1</sup>

<sup>6</sup> 1 German Center for Neurodegenerative Diseases (DZNE), Bonn, Germany ¶ Corresponding author

DOI: [10.xxxxxx/draft](https://doi.org/10.xxxxxx/draft)

Software

- [Review](#) 
- [Repository](#) 
- [Archive](#) 

Editor: [Open Journals](#) 

Reviewers:

- [@openjournals](#)

Submitted: 01 January 1970

Published: unpublished

License

Authors of papers retain copyright  
and release the work under a  
Creative Commons Attribution 4.0  
International License ([CC BY 4.0](#)).  
18  
19  
20  
21

<sup>7</sup> **Summary**

<sup>8</sup> *MotilA* is an open-source Python pipeline for quantifying microglial fine-process motility in  
<sup>9</sup> 4D (TZYX) or 5D (TZCYX) time-lapse fluorescence microscopy data, supporting both single-  
<sup>10</sup> channel and two-channel acquisition. It was developed for high-resolution *in vivo* multiphoton  
<sup>11</sup> imaging and supports both single-stack and cohort-scale batch analyses. The workflow  
<sup>12</sup> performs sub-volume extraction, optional registration and spectral unmixing, a maximum-  
<sup>13</sup> intensity projection along the Z-axis, segmentation, and pixel-wise change detection to compute  
<sup>14</sup> the turnover rate (TOR). *MotilA* specifically targets pixel-level process motility rather than  
<sup>15</sup> object tracking or full morphometry. The code is platform independent, documented with  
<sup>16</sup> tutorials and example datasets, and released under GPL-3.0.

<sup>17</sup> **Statement of need**

<sup>18</sup> Microglia are immune cells of the central nervous system and continuously remodel their  
processes to survey brain tissue and respond to pathology ([M. Fuhrmann et al., 2010](#); [Nimmer-  
jahn et al., 2005](#); [Prinz et al., 2019](#); [Tremblay et al., 2010](#)). Quantifying this subcellular motility  
is important for studies of neuroinflammation, neurodegeneration, and synaptic plasticity. Cur-  
rent practice in many labs relies on manual or semi-manual measurements in general-purpose  
tools such as Fiji/ImageJ or proprietary software ([Carl Zeiss Microscopy GmbH, Accessed  
2025](#); [Schindelin et al., 2012](#)). These procedures are time consuming, hard to reproduce, focus  
on single cells, and are sensitive to user bias ([Brown, 2017](#); [Wall et al., 2018](#)). There is no  
dedicated, open, and batch-capable solution tailored to this task.

<sup>19</sup> *MotilA* fills this gap with an end-to-end, reproducible pipeline for 3D time-lapse two-channel  
imaging. It standardizes preprocessing, segmentation, and motility quantification and scales  
from individual stacks to large experimental cohorts. Unlike Fiji/ImageJ macros or proprietary  
packages, *MotilA* provides a fully automated non-interactive workflow in Python that applies  
identical parameters across datasets, logs all intermediate steps, and avoids user-dependent  
adjustments. This ensures reproducible, bias-minimized, and scalable processing of large 3D  
time-lapse datasets, including optional motion correction and spectral unmixing. Although  
optimized for microglia, the approach generalizes to other motile structures that can be reliably  
segmented across time.

<sup>20</sup> To clarify *MotilA*'s novelty relative to existing analysis approaches, the following table summa-  
<sup>21</sup> rizes key differences between *MotilA*, Fiji/ImageJ, and ZEISS ZEN:

<sup>22</sup> **Table 1.** Comparison of MotilA with commonly used alternatives for microglial motility analysis.

Feature	Fiji/ImageJ	ZEISS ZEN	MotilA
<b>Automation</b>	Limited. User-recorded macros; complex workflows often require manual steps and must be split across several macros.	None. Full user interaction required.	Full. End-to-end non-interactive workflow.
<b>Batch processing</b>	Limited. Macros can process several files in one folder, but they cannot navigate nested directory structures or manage multi-step 3D multi-channel time-series pipelines.	None. Each dataset processed manually.	Full. Metadata-driven cohort processing.
<b>Reproducibility</b>	Moderate. Requires complete manual logging; interactive tuning reduces reproducibility.	Low. Manual adjustments introduce strong user bias.	High. Full parameter logging and deterministic runs.
<b>Scalability</b>	Low. Full-stack RAM loading; no chunked I/O for large 3D data.	Low-medium. Efficient viewing but no automated processing for large time-lapse datasets.	High. Chunked I/O for multi-gigabyte 3D two-channel stacks.
<b>Open-source</b>	Yes (GPL-3.0).	No (proprietary).	Yes (GPL-3.0).

### <sup>39</sup> Implementation and core method

<sup>40</sup> Input is a 5D stack in TZCYX or a 4D stack in TZYX order, where T is time, Z is depth, C is channel, and YX are spatial dimensions. *MotilA* does not assume a fixed channel order. Users <sup>41</sup> specify which channel contains microglia and which, if present, provides a structural reference <sup>42</sup> signal, such as a neuronal label. Although the reference channel does not enter the motility <sup>43</sup> computation, it is commonly acquired in microglial imaging because it offers stable features <sup>44</sup> that support robust pre-processing registration of the 3D stack before it is passed to *MotilA*. <sup>45</sup> The additional channel may also be used for optional spectral unmixing in the presence of <sup>46</sup> bleed-through.

<sup>47</sup> For each time point, *MotilA* extracts a user-defined z-sub-volume, optionally performs 3D <sup>48</sup> motion correction and spectral unmixing, and computes a 2D maximum-intensity projection <sup>49</sup> along the Z-axis to enable interpretable segmentation. After thresholding, the binarized <sup>50</sup> projection  $B(t_i)$  is compared with  $B(t_{i+1})$  to derive a change map <sup>51</sup>

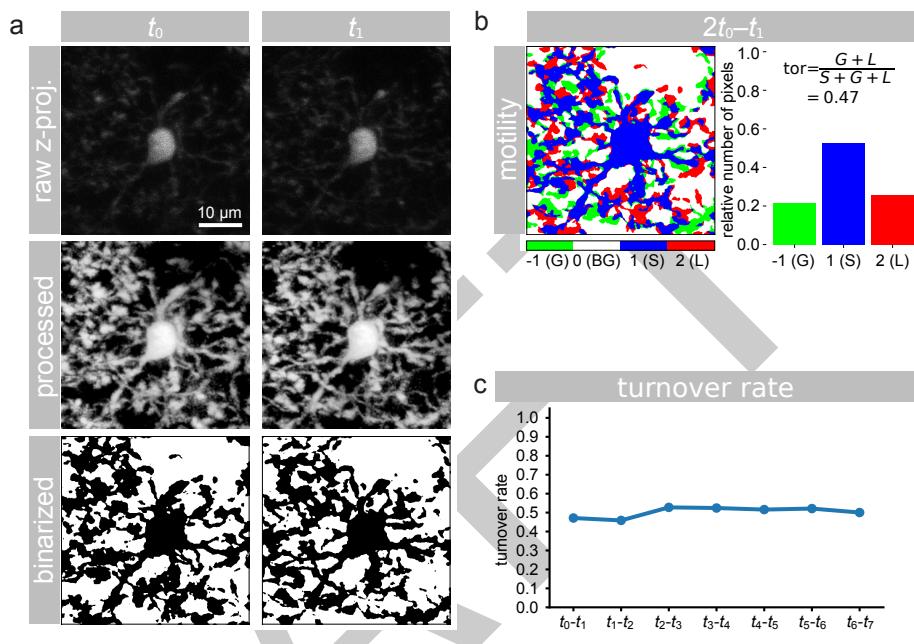
$$\Delta B(t_i) = 2B(t_i) - B(t_{i+1}).$$

<sup>52</sup> Pixels are classified as stable “S” ( $\Delta B = 1$ ), gained “G” ( $\Delta B = -1$ ), or lost “L” ( $\Delta B = 2$ ). <sup>53</sup> From these counts, the turnover rate is defined as

$$TOR = \frac{G + L}{S + G + L},$$

<sup>54</sup> representing the fraction of pixels that changed between consecutive frames. This pixel-based <sup>55</sup> strategy follows earlier microglial motility work (M. Fuhrmann et al., 2010; Nebeling et al., <sup>56</sup> 2023) while providing a fully automated and batchable implementation with parameter logging <sup>57</sup> and diagnostics.

58 The pipeline exposes options for 3D or 2D registration, contrast-limited adaptive histogram  
59 equalization, histogram matching across time to mitigate bleaching, and median or Gaussian  
60 filtering (Pizer et al., 1987; Virtanen et al., 2020; Walt et al., 2014). Results include segmented  
61 images, G/L/S/TOR values, brightness and area traces, and spreadsheets for downstream  
62 statistics. Memory-efficient reading and chunked processing of large TIFFs are supported via  
63 Zarr (Miles et al., 2025).



**Figure 1:** Example analysis with MotilA. **a)** z-projected microglial images at two consecutive time points ( $t_0$ ,  $t_1$ ), shown as raw, processed, and binarized data. **b)** pixel-wise classification of gained (G), stable (S), and lost (L) pixels used to compute the turnover rate (TOR). **c)** TOR values across time points from the same dataset, illustrating dynamic remodeling of microglial fine processes.

## Usage

64 *MotilA* can be called from Python scripts or Jupyter notebooks. Three entry points cover  
65 common scenarios: `process_stack` for a single stack, `batch_process_stacks` for a project  
66 folder organized by dataset identifiers with a shared metadata sheet, and `batch_collect` to  
67 aggregate metrics across datasets. All steps write intermediate outputs and logs to facilitate  
68 validation and reproducibility. *MotilA*'s GitHub repository provides tutorials and an example  
69 dataset to shorten onboarding.

## Applications and scope

71 *MotilA* has been applied to quantify microglial process dynamics in several *in vivo* imaging  
72 studies and preprints (Crux et al., 2024; F. Fuhrmann et al., 2024; Gockel et al., 2025). Typical  
73 use cases include baseline surveillance behavior, responses to neuroinflammation or genetic  
74 perturbations, and deep three-photon imaging where manual analysis is impractical. The  
75 binarize-and-compare principle can in principle be adapted to other structures such as dendrites  
76 or axons when segmentation across time is robust.

## Limitations

78 Using 2D projections simplifies processing but sacrifices axial specificity and can merge  
79 overlapping structures. Segmentation quality determines accuracy and can be affected by

vessels, low signal-to-noise ratios, or strong intensity drift. The current spectral unmixing is a simple subtraction; advanced approaches may be needed for some fluorophores. *MotilA* targets pixel-level process motility rather than object-level tracking or full morphometry.

Using 2D Z-projections confines motility quantification to the XY plane, but this reflects practical constraints of two-photon microglial imaging. Axial resolution degrades with imaging depth, yielding elongated point-spread functions and reduced contrast along Z, which makes voxel-wise 3D segmentation of thin microglial processes unreliable. Maximum-intensity projection increases effective signal per pixel and follows established practice in earlier microglial motility work (see, e.g., M. Fuhrmann et al. (2010); Nebeling et al. (2023)). This approach necessarily sacrifices axial specificity and can merge structures that overlap in Z, particularly in densely populated regions, which are best avoided by selecting a sub-volume with minimal axial overlap. Fully 3D motility analysis would require volumetric segmentation, morphological reconstruction, and substantially higher memory and computational resources and is therefore out of scope for the current version of *MotilA*.

Beyond the inherent limitations of Z-projection, segmentation quality critically affects accuracy and can be influenced by blood vessels, low signal-to-noise ratios, and strong intensity drift across time. The current spectral unmixing is implemented as a simple subtraction and may be insufficient for fluorophores with complex spectral overlap. *MotilA* targets pixel-level process motility rather than object-level tracking or full morphometry, and its interpretability depends on reliable and consistent segmentation across frames.

## Example dataset

The repository includes two *in vivo* two-photon stacks from mouse frontal cortex formatted for use with *MotilA* (Gockel et al., 2025). Each stack contains eight time points at five-minute intervals, two channels for microglia and neurons, and approximately sixty z-planes at one micrometer steps in a field of view of about 125 by 125 micrometers. The example reproduces the full analysis, including projections, segmentation, change maps, brightness traces, and TOR over time, and serves as a template for cohort-level workflows.

## Availability

Source code, documentation, tutorials, and issue tracking are hosted at: <https://github.com/FabrizioMusacchio/motila>. The software runs on Windows, macOS, and Linux with Python 3.9 or newer and standard scientific Python stacks. It is released under GPL-3.0, and contributions via pull requests or issues are welcome.

## Acknowledgements

We thank the Light Microscopy Facility and Animal Research Facility at the DZNE, Bonn, for essential support. This work was supported by the DZNE and grants to MF from the ERC (MicroSynCom 865618) and the DFG (SFB1089 C01, B06; SPP2395). MF is a member of the DFG Excellence Cluster ImmunoSensation2. Additional support came from the iBehave network and the CANTAR network funded by the Ministry of Culture and Science of North Rhine-Westphalia, and from the Mildred-Scheel School of Oncology Cologne-Bonn. Animal procedures followed institutional and national regulations, with efforts to reduce numbers and refine conditions.

## References

- Brown, D. L. (2017). Bias in image analysis and its solution: Unbiased stereology. *Journal of Toxicologic Pathology*, 30(3), 183–191. <https://doi.org/10.1293/tox.2017-0013>
- Carl Zeiss Microscopy GmbH. (Accessed 2025). *ZEISS ZEN Microscopy Software*. <https://www.zeiss.com/metrology/en/software/zeiss-zem-core.html>.

- 127 Crux, S., Roggan, M. D., Poll, S., Nebeling, F. C., Schiweck, J., Mittag, M., Musacchio, F.,  
128 Steffen, J., Wolff, K. M., Baral, A., Witke, W., Gurniak, C., Bradke, F., & Fuhrmann,  
129 M. (2024). Deficiency of actin depolymerizing factors ADF/Cfl1 in microglia decreases  
130 motility and impairs memory. *bioRxiv*. <https://doi.org/10.1101/2024.09.27.615114>
- 131 Fuhrmann, F., Nebeling, F. C., Musacchio, F., Mittag, M., Poll, S., Müller, M., Giovannetti, E.  
132 A., Maibach, M., Schaffran, B., Burnside, E., Chan, I. C. W., Lagurin, A. S., Reichenbach,  
133 N., Kaushalya, S., Fried, H., Linden, S., Petzold, G. C., Tavosanis, G., Bradke, F., &  
134 Fuhrmann, M. (2024). Three-photon *in vivo* imaging of neurons and glia in the medial  
135 prefrontal cortex with sub-cellular resolution. *bioRxiv*. <https://doi.org/10.1101/2024.08.28.610026>
- 137 Fuhrmann, M., Bittner, T., Jung, C. K. E., Burgold, S., Page, R. M., Mitteregger, G., Haass,  
138 C., LaFerla, F. M., Kretzschmar, H., & Herms, J. (2010). Microglial Cx3cr1 knockout  
139 prevents neuron loss in a mouse model of alzheimer's disease. *Nature Neuroscience*, 13(4),  
140 411–413. <https://doi.org/10.1038/nn.2511>
- 141 Gockel, N., Nieves-Rivera, N., Druart, M., Jaako, K., Fuhrmann, F., Rožkalne, R., Musacchio,  
142 F., Poll, S., Jansone, B., Fuhrmann, M., & Magueresse, C. L. (2025). *Example datasets for*  
143 *microglial motility analysis using the MotilA pipeline*. Zenodo. <https://doi.org/10.5281/zenodo.15061566>
- 145 Miles, A., jakirkham, Hamman, J., Orfanos, D. P., Stansby, D., Bussonnier, M., Moore,  
146 J., Bennett, D., Augspurger, T., Rzepka, N., Cherian, D., Verma, S., Bourbeau, J.,  
147 Fulton, A., Abernathey, R., Lee, G., Spitz, H., Kristensen, M. R. B., Jones, M., &  
148 Schut, V. (2025). *Zarr-developers/zarr-python: v3.0.6* (Version v3.0.6). Zenodo. <https://doi.org/10.5281/zenodo.3773449>
- 150 Nebeling, F. C., Poll, S., Justus, L. C., Steffen, J., Keppler, K., Mittag, M., & Fuhrmann,  
151 M. (2023). Microglial motility is modulated by neuronal activity and correlates with  
152 dendritic spine plasticity in the hippocampus of awake mice. *eLife*, 12, e83176. <https://doi.org/10.7554/eLife.83176>
- 154 Nimmerjahn, A., Kirchhoff, F., & Helmchen, F. (2005). Resting microglial cells are highly  
155 dynamic surveillants of brain parenchyma *in vivo*. *Science*, 308(5726), 1314–1318. <https://doi.org/10.1126/science.1110647>
- 157 Pizer, S. M., Amburn, E. P., Austin, J. D., Cromartie, R., Geselowitz, A., Greer, T., Haar  
158 Romeny, B. ter, Zimmerman, J. B., & Zuiderveld, K. (1987). Adaptive histogram equaliza-  
159 tion and its variations. *Computer Vision, Graphics, and Image Processing*, 39(3), 355–368.  
160 [https://doi.org/10.1016/S0734-189X\(87\)80186-X](https://doi.org/10.1016/S0734-189X(87)80186-X)
- 161 Prinz, M., Jung, S., & Priller, J. (2019). Microglia biology: One century of evolving concepts.  
162 *Cell*, 179(2), 292–311. <https://doi.org/10.1016/j.cell.2019.08.053>
- 163 Schindelin, J., Arganda-Carreras, I., Frise, E., Kaynig, V., Longair, M., Pietzsch, T., Preibisch,  
164 S., Rueden, C., Saalfeld, S., Schmid, B., & others. (2012). Fiji: An open-source platform  
165 for biological-image analysis. *Nature Methods*, 9(7), 676–682. <https://doi.org/10.1038/nmeth.2019>
- 167 Tremblay, M.-È., Lowery, R. L., & Majewska, A. K. (2010). Microglial interactions with  
168 synapses are modulated by visual experience. *PLOS Biology*, 8(11), 1–16. <https://doi.org/10.1371/journal.pbio.1000527>
- 170 Virtanen, P., Gommers, R., Oliphant, T. E., Haberland, M., Reddy, T., Cournapeau, D.,  
171 Burovski, E., Peterson, P., Weckesser, W., Bright, J., Walt, S. J. van der, Brett, M.,  
172 Wilson, J., Millman, K. J., Mayorov, N., Nelson, A. R. J., Jones, E., Kern, R., Larson, E., ...  
173 Contributors, S. 1.0. (2020). SciPy 1.0: Fundamental algorithms for scientific computing  
174 in python. *Nature Methods*, 17, 261–272. <https://doi.org/10.1038/s41592-019-0686-2>
- 175 Wall, E., Blaha, L. M., Paul, C. L., Cook, K., & Endert, A. (2018). Four perspectives on

<sup>176</sup> human bias in visual analytics. In G. Ellis (Ed.), *Cognitive biases in visualizations* (pp.  
<sup>177</sup> 29–42). Springer International Publishing. [https://doi.org/10.1007/978-3-319-95831-6\\_3](https://doi.org/10.1007/978-3-319-95831-6_3)

<sup>178</sup> Walt, S. van der, Schönberger, J. L., Nunez-Iglesias, J., Boulogne, F., Warner, J. D., Yager,  
<sup>179</sup> N., Gouillart, E., Yu, T., & contributors, the scikit-image. (2014). Scikit-image: Image  
<sup>180</sup> processing in python. *PeerJ*, 2, e453. <https://doi.org/10.7717/peerj.453>

DRAFT