

¹ Cardiotensor: A Python Library for Orientation Analysis and Tractography in 3D Cardiac Imaging

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

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Submitted: 01 January 1970

Published: unpublished

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Summary

Understanding the architecture of the human heart requires analyzing its microstructural organization across scales. With the advent of high-resolution imaging techniques such as synchrotron-based tomography, it has become possible to visualize entire hearts at micron-scale resolution. However, translating these large, complex volumetric datasets into interpretable, quantitative descriptors of cardiac organization remains a major challenge. Here we present cardiotensor, an open-source Python package designed to quantify 3D cardiomyocyte orientation in whole- or partial-heart imaging datasets. It provides efficient, scalable implementations of structure tensor analysis, enabling extraction of directional metrics such as helical angle (HA), intrusion angle (IA), and fractional anisotropy (FA). The package supports datasets reaching teravoxel-scale and is optimized for high-performance computing environments, including parallel and chunk-based processing pipelines. In addition, cardiotensor includes tractography functionality to reconstruct continuous cardiomyocyte trajectories. This enables fiber-level visualization and structural mapping of cardiac tissue, allowing detailed assessments of anatomical continuity and regional organization.

Statement of Need

Despite major advances in high-resolution 3D imaging, there is a lack of open-source tools to analyze cardiomyocyte orientation in large volumetric datasets. Most established frameworks were developed for diffusion tensor MRI (DT-MRI), where orientation is inferred from water diffusion. Examples include MRtrix3 (Tournier et al., 2019), DIPY (Garyfallidis et al., 2014), and DSI Studio (Yeh, 2025). While powerful for diffusion-based neuro and cardiac applications (Mekkaoui et al., 2017), these packages are not designed to handle direct image-gradient-based orientation estimation or the teravoxel-scale datasets produced by synchrotron tomography, micro-CT, or 3D optical microscopy.

For non-diffusion imaging modalities, researchers have historically relied on custom structure tensor implementations to estimate fiber orientation directly from image intensity gradients. However, most of these are in-house codes, often unpublished or not generalizable. For example, structure tensor analysis has been applied in the heart using micro-CT (Reichardt et al., 2020), optical microscopy (Dileep et al., 2023; Garcia-Canadilla et al., 2022), and synchrotron tomography (Dejea et al., 2019), but these methods were tailored to specific datasets and lacked scalability or public availability. Existing tools like OrientationJ (Fiji) and OrientationPy (Python) enable 2D and 3D structure tensor analysis for microscopy (Navaee

et al., 2023). However, they are not optimized for teravoxel-scale datasets, do not compute classical cardiac microstructure descriptors such as HA and IA, and are not integrated with tractography. Cardiotensor uniquely provides all of these capabilities for large-scale cardiac imaging.

For non-diffusion imaging modalities, such as micro-CT (Reichardt et al., 2020), optical microscopy (Dileep et al., 2023; Garcia-Canadilla et al., 2022), and synchrotron tomography (Brunet et al., 2024; Dejea et al., 2019), researchers have historically relied on custom structure tensor implementations to estimate fiber orientation directly from image intensity gradients. However, most of these are in-house codes, often unpublished or not scalable. Existing tools like OrientationJ (Fiji) and OrientationPy (Python) enable 2D and 3D structure tensor analysis (Navaee et al., 2023), but they are not optimized for teravoxel-scale datasets, do not compute classical cardiac microstructure descriptors such as HA and IA, and do not allow tractography.

Cardiotensor addresses this gap by providing an open-source Python package specifically tailored to structure tensor analysis of large cardiac volumes. Rather than relying on diffusion modeling, cardiotensor infers tissue orientation directly from image intensity gradients, making it applicable across a wide range of modalities. Previous studies have demonstrated strong agreement between structure tensor-based orientation and DT-MRI-derived metrics when applied to the same human hearts (Teh et al., 2016). The package supports full pipelines from raw image stacks to fiber orientation maps and tractography. Its architecture is optimized for large datasets, using chunked and parallel processing suitable for high-performance computing environments.

Cardiotensor has already been successfully applied in published work to characterize 3D cardiomyocyte architecture in healthy and diseased human hearts using synchrotron tomography (Brunet et al., 2024) to datasets over a terabyte in size. While cardiotensor was conceived for cardiac imaging, the package is modality- and tissue-agnostic. Any volumetric dataset exhibiting coherent fibrous microstructure can be analyzed, including brain white matter, skeletal muscle, and tendon. This generality makes the library useful for both cardiovascular and broader anatomical or histological studies.

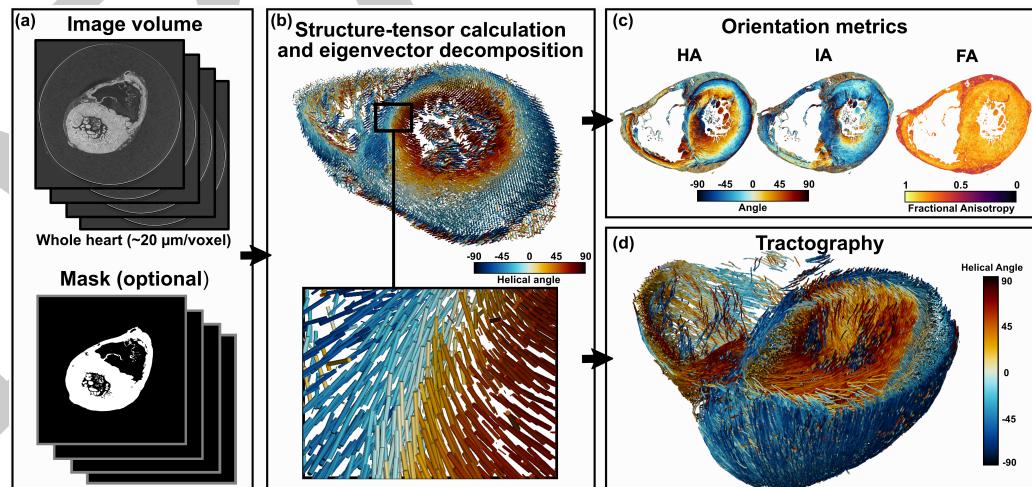


Figure 1: Cardiotensor pipeline for 3D cardiac orientation analysis and tractography. (a) Input whole- or partial-heart volume with optional myocardial mask. (b) Local cardiomyocyte orientation estimated via 3D structure tensor and eigenvector decomposition. The third eigenvector field (smallest eigenvalue) is visualized as arrows color-coded by helical angle (HA); inset shows structure tensor orientation in the ventricular septum. (c) Transformation to a cylindrical coordinate system enables computation of voxel-wise helical angle (HA), intrusion angle (IA), and fractional anisotropy (FA) maps. (d) Streamline tractography reconstructs continuous cardiomyocyte trajectories, color-coded by HA.

70 Implementation

71 Cardiotensor is implemented in Python and designed to efficiently process very large 3D cardiac
72 imaging datasets. It relies primarily on NumPy ([Van Der Walt et al., 2011](#)) for numerical
73 computation, with I/O accelerated by tifffile ([Gohlke, 2025](#)), Glymur ([Evans, 2025](#)), and
74 OpenCV ([Bradski, 2000](#)). Dask ([Rocklin, 2015](#)) is used exclusively to parallelize file reading,
75 while the core computations rely on Python's multiprocessing module for local parallelism.
76 The package builds on the structure-tensor library ([Jeppesen et al., 2021](#)) to calculate the 3D
77 structure tensor and eigenvector decomposition.

78 The package supports multiple use cases:

- 79 ▪ Command-line workflows, which automate batch processing from a configuration file of
80 terabyte-scale heart volumes and produce results as live plots or files saved to disk.
- 81 ▪ Embedded use in larger Python analysis workflows, enabling flexible scripting and scalable
82 execution on cluster environments.

83 Efficient computation is achieved through a chunk-based processing strategy with padding,
84 which avoids edge artifacts. This architecture allows parallelization across computing clusters by
85 splitting volumes into independent jobs, enabling cardiotensor to process whole-heart volumes
86 in hours rather than days while maintaining practical memory requirements.

87 Architecture

88 Cardiotensor is organized into five main modules, designed for clarity and scalability:

- 89 ▪ **orientation**: Computes local cardiomyocyte (or other texture feature) orientation using
90 a chunked 3D structure tensor pipeline, including eigenvalue decomposition, cylindrical
91 coordinate rotation, and calculation of helical angle (HA), intrusion angle (IA), and
92 fractional anisotropy (FA).
- 93 ▪ **tractography**: Generates and filters streamlines tracing cardiomyocyte trajectories from
94 the orientation field for fiber-level reconstruction and analysis.
- 95 ▪ **analysis**: Provides a GUI for regional quantification and plotting transmural profile.
- 96 ▪ **visualization**: Supports interactive 3D visualization of vector fields and streamlines,
97 HA color-coding, and export to VTK/ParaView for large-scale rendering.
- 98 ▪ **utils**: Contains general utilities for I/O, image preprocessing, configuration parsing,
99 and vector math, supporting the entire pipeline.

100 This modular architecture ensures reproducibility, maintainability, and easy integration into
101 larger cardiac imaging workflows.

102 Documentation and Usage

103 The documentation for cardiotensor is available online at:

104 <https://josephbrunet.github.io/cardiotor>

105 The main components of the documentation are:

- 106 ▪ Step-by-step walkthroughs for installation, first steps, and a guided example covering all
107 available commands. A small example dataset and its corresponding mask are provided
108 with the package.
- 109 ▪ In-depth explanations of the core algorithms used in cardiotensor, including structure
110 tensor theory, helical angle calculation, fractional anisotropy (FA), and tractography
111 integration.
- 112 ▪ Reference guides for the command-line interface, configuration file format, and public
113 API.

Acknowledgements

- 114 The authors would like to thank David Stansby for his guidance on the Python package
115 structure, documentation framework, and best practices for scientific software development.
- 116
- 117 This work was supported in part by the Chan Zuckerberg Initiative DAF (grant 2022-316777),
118 the Wellcome Trust (310796/Z/24/Z), and the Additional Ventures Single Ventricle Research
119 Fund (grant 1019894).
- 120 The authors gratefully acknowledge ESRF beamtimes md1290 and md1389 on BM18 as sources
121 of the data.
- 122 Peter D. Lee is a CIFAR MacMillan Fellow in the Multiscale Human program and acknowledges
123 funding from a RAEng Chair in Emerging Technologies (CiET1819/10). This research is also
124 based on work supported by a CIFAR Catalyst Award.
- 125 AC's research is enabled through the Noé Heart Centre Laboratories, which are gratefully
126 supported by the Rachel Charitable Trust via Great Ormond Street Hospital Children's Charity
127 (GOSH Charity). The Noé Heart Centre Laboratories are based in The Zayed Centre for
128 Research into Rare Disease in Children, which was made possible thanks to Her Highness
129 Sheikha Fatima bint Mubarak, wife of the late Sheikh Zayed bin Sultan Al Nahyan, founding
130 father of the United Arab Emirates, as well as other generous funders.

References

- 131
- 132 Bradski, G. (2000). The opencv library. *Dr. Dobb's Journal: Software Tools for the Professional*
133 *Programmer*, 25(11), 120–123.
- 134 Brunet, J., Cook, A. C., Walsh, C. L., Cranley, J., Tafforeau, P., Engel, K., Arthurs, O.,
135 Berruyer, C., Burke O'Leary, E., Bellier, A., Torii, R., Werlein, C., Jonigk, D. D., Ackermann,
136 M., Dollman, K., & Lee, P. D. (2024). Multidimensional Analysis of the Adult Human
137 Heart in Health and Disease Using Hierarchical Phase-Contrast Tomography. *Radiology*,
138 312(1), e232731. <https://doi.org/10.1148/radiol.232731>
- 139 Dejea, H., Garcia-Canadilla, P., Cook, A. C., Guasch, E., Zamora, M., Crispi, F., Stampanoni,
140 M., Bijnens, B., & Bonnin, A. (2019). Comprehensive Analysis of Animal Models of
141 Cardiovascular Disease using Multiscale X-Ray Phase Contrast Tomography. *Scientific*
142 *Reports*, 9(1), 6996. <https://doi.org/10.1038/s41598-019-43407-z>
- 143 Dileep, D., Syed, T. A., Sloan, T. F., Dhandapani, P. S., Siddiqi, K., & Sirajuddin, M. (2023).
144 Cardiomyocyte orientation recovery at micrometer scale reveals long-axis fiber continuum
145 in heart walls. *The EMBO Journal*, 42(19), e113288. <https://doi.org/10.15252/embj.2022113288>
- 146
- 147 Evans, J. G. (2025). *Quintusdias/glymur*. <https://github.com/quintusdias/glymur>
- 148 Garcia-Canadilla, P., Mohun, T. J., Bijnens, B., & Cook, A. C. (2022). Detailed quantification
149 of cardiac ventricular myocardial architecture in the embryonic and fetal mouse heart
150 by application of structure tensor analysis to high resolution episcopic microscopic data.
151 *Frontiers in Cell and Developmental Biology*, 10, 1000684. <https://doi.org/10.3389/fcell.2022.1000684>
- 152
- 153 Garyfallidis, E., Brett, M., Amirbekian, B., Rokem, A., Van Der Walt, S., Descoteaux, M.,
154 Nimmo-Smith, I., & Dipy Contributors. (2014). Dipy, a library for the analysis of diffusion
155 MRI data. *Frontiers in Neuroinformatics*, 8. <https://doi.org/10.3389/fninf.2014.00008>
- 156 Gohlke, C. (2025). *Tifffile*. <https://github.com/cgohlke/tifffile>
- 157 Jeppesen, N., Mikkelsen, L. P., Dahl, A. B., Christensen, A. N., & Dahl, V. A. (2021). Quan-
158 tifying effects of manufacturing methods on fiber orientation in unidirectional composites

- 159 using structure tensor analysis. *Composites Part A: Applied Science and Manufacturing*,
160 149, 106541. <https://doi.org/10.1016/j.compositesa.2021.106541>
- 161 Mekkaoui, C., Reese, T. G., Jackowski, M. P., Bhat, H., & Sosnovik, D. E. (2017). Diffusion
162 MRI in the heart. *NMR in Biomedicine*, 30(3), e3426. <https://doi.org/10.1002/nbm.3426>
- 163 Navaee, F., Khornian, N., Longet, D., Heub, S., Boder-Pasche, S., Weder, G., Kleger, A.,
164 Renaud, P., & Braschler, T. (2023). A three-dimensional engineered cardiac in vitro model:
165 Controlled alignment of cardiomyocytes in 3D microphysiological systems. *Cells*, 12(4),
166 576.
- 167 Reichardt, M., Töpperwien, M., Khan, A., Alves, F., & Salditt, T. (2020). Fiber orientation
168 in a whole mouse heart reconstructed by laboratory phase-contrast micro-CT. *Journal of
169 Medical Imaging*, 7(02), 1. <https://doi.org/10.1117/1.JMI.7.2.023501>
- 170 Rocklin, M. (2015). *Dask: Parallel Computation with Blocked algorithms and Task Scheduling*.
171 126–132. <https://doi.org/10.25080/Majora-7b98e3ed-013>
- 172 Teh, I., McClymont, D., Zdora, M.-C., Whittington, H. J., Davidou, V., Lee, J., Lygate,
173 C. A., Rau, C., Zanette, I., & Schneider, J. E. (2016). Validation of diffusion tensor
174 MRI measurements of cardiac microstructure with structure tensor synchrotron radiation
175 imaging. *Journal of Cardiovascular Magnetic Resonance*, 19(1), 31. <https://doi.org/10.1186/s12968-017-0342-x>
- 177 Tournier, J.-D., Smith, R., Raffelt, D., Tabbara, R., Dhollander, T., Pietsch, M., Christiaens,
178 D., Jeurissen, B., Yeh, C.-H., & Connelly, A. (2019). MRtrix3: A fast, flexible and open
179 software framework for medical image processing and visualisation. *NeuroImage*, 202,
180 116137. <https://doi.org/10.1016/j.neuroimage.2019.116137>
- 181 Van Der Walt, S., Colbert, S. C., & Varoquaux, G. (2011). The NumPy Array: A Structure
182 for Efficient Numerical Computation. *Computing in Science & Engineering*, 13(2), 22–30.
183 <https://doi.org/10.1109/MCSE.2011.37>
- 184 Yeh, F.-C. (2025). DSI Studio: An integrated tractography platform and fiber data hub for ac-
185 celerating brain research. *Nature Methods*. <https://doi.org/10.1038/s41592-025-02762-8>