

OrNet - a Python Toolkit to Model the Diffuse Structure of Organelles as Social Networks

Mojtaba Fazli^{1,*}, Marcus Hill^{1,*}, Andrew Durden¹, Rachel Mattson², Allyson T. Loy³, Barbara Reaves⁴, Abigail Courtney³, Frederick D. Quinn⁴, Chakra Chennubhotla⁵, and Shannon Quinn^{1,6}

1 Department of Computer Science, University of Georgia, Athens, GA 30602 USA **2** Institute for Artificial Intelligence, University of Georgia, Athens, GA 30602 USA **3** Department of Microbiology, University of Georgia, Athens, GA 30602 USA **4** Department of Infectious Diseases, University of Georgia, Athens, GA 30602 USA **5** Department of Computational and Systems Biology, University of Pittsburgh, Pittsburgh, PA 15232 USA **6** Department of Cellular Biology, University of Georgia, Athens, GA 30602 USA * The two first authors made equal contributions.

DOI: [10.21105/joss.01983](https://doi.org/10.21105/joss.01983)

Software

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

Editor: [Anisha Keshavan](#) ↗

Reviewers:

- [@serine](#)
- [@vc1492a](#)

Submitted: 19 November 2019

Published: 18 March 2020

License

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

Summary

Fluorescent microscopy videos are vital for analyzing the morphological changes that sub-cellular protein structures undergo after exposure to external stimuli. Changes in organelle structures offer crucial insight into the manner in which cells respond to viral or bacterial infections, cellular invaders, or even the organelles themselves malfunctioning (Stavru & Cossart, 2011). Generally, modeling organellar structures involve manually inspecting each video then denoting time points and regions that demonstrate anomalous behavior. However, manual analyses lack objective metrics to assess morphological changes, and thus hinder the ability to perform secondary analyses and quantitative comparisons. Thus, arises the need to find a methodology that generates quantitative models capable of accurately describing the data (Eliceiri KW, 2012). Prior works have demonstrated success in the generation of static models for subcellular modeling (Chen et al., 2018; Murphy, 2015; Ruan et al., 2019). Such advancements have inspired us to propose a novel framework, OrNet, that models both the spatial and temporal morphology changes that organelles undergo as dynamic social networks.

OrNet is an open-source python package (Rossum, 1995) that is built-upon the libraries of Scikit-Learn (Pedregosa et al., 2011), NumPy (Oliphant, n.d.), SciPy (Virtanen et al., 2019), and Matplotlib (Hunter, 2007). Our tool accepts as input microscopy videos of cells with fluorescently tagged organelles, and outputs quantitative descriptions of the morphological changes. Modeling these dynamic structures is no trivial task because many organelles are amorphous, and the lack of rigidity renders traditional shape-based, parametric modeling techniques ineffective. Our framework addresses such difficulties by modeling organelles as social networks to capture the spatio-temporal relationships via a dynamic edge management process. The graphs are constructed by fitting gaussian mixture models to every frame of an input video; the final means become the vertices, while a divergence metric is applied to every combination pair of mixture components to create the edges. Once graphs are created for each frame, spectral decomposition is utilized to track the leading eigenvalues to understand the time-points and frame regions where organellar structures are demonstrating significant changes.

The viability of OrNet has been illustrated by (Durden, 2019) when the framework was utilized to model mitochondria found in HeLa cells that were exposed to various stimuli. We hope that our tool will be utilized by any project seeking to model subcellular organelles.

Acknowledgements

The project that yielded this software was supported in part by a grant from the National Science Foundation (#1458766).

We gratefully acknowledge the support of NVIDIA Corporation with the donation of the Titan X Pascal GPU used for this research.

References

- Alex Clark, A. K., Andrew Murray. (2016). *Pillow*. doi:[10.5281/zenodo.44297](https://doi.org/10.5281/zenodo.44297)
- Almar Klein, A. T., Steven Silvester. (2019). *Imageio*. doi:[10.5281/zenodo.3475011](https://doi.org/10.5281/zenodo.3475011)
- Behnel, S., Bradshaw, R., Citro, C., Dalcin, L., Seljebotn, D. S., & Smith, K. (2011). Cython: The best of both worlds. *Computing in Science Engineering*, 13(2), 31–39. doi:[10.1109/MCSE.2010.118](https://doi.org/10.1109/MCSE.2010.118)
- Bradski, G. (2000). The OpenCV Library. *Dr. Dobbs's Journal of Software Tools*.
- Chen, J., Ding, L., Viana, M. P., Hendershott, M. C., Yang, R., Mueller, I. A., & Rafelski, S. M. (2018). The allen cell structure segmenter: A new open source toolkit for segmenting 3D intracellular structures in fluorescence microscopy images. *bioRxiv*. doi:[10.1101/491035](https://doi.org/10.1101/491035)
- da Costa-Luis, C. (2019). *Tqdm: A fast, extensible progress meter for python and cli*. *Journal of Open Source Software*. doi:[10.21105/joss.01277](https://doi.org/10.21105/joss.01277)
- Durden, A. (2019). Modelling diffuse subcellular protein structures as dynamic social networks. Retrieved from <http://arxiv.org/abs/1904.12960>
- Durden, T Loy, Reaves, Fazli, Courtney, D Quinn, Chennubhotla, S. Chakra, et al. (2018). Dynamic Social Network Modeling of Diffuse Subcellular Morphologies. In Fatih Akici, David Lippa, Dillon Niederhut, & M. Pacer (Eds.), *Proceedings of the 17th Python in Science Conference* (pp. 1–7). doi:[10.25080/Majora-4af1f417-000](https://doi.org/10.25080/Majora-4af1f417-000)
- Eliceiri KW, G. I., Berthold MR. (2012). Biological imaging software tools. *Nature Methods*.
- Eric A. Hagberg, D. A. S., & Swart, P. J. (2008). Exploring network structure, dynamics, and function using networkx. *Proceedings of the 7th Python in Science Conference (SciPy2008)*, 11–15.
- Gregory R. Lee, F. W., Ralf Gommers. (2019). *PyWavelets: A python package for wavelet analysis*. *Journal of Open Source Software*. doi:[10.21105/joss.01237](https://doi.org/10.21105/joss.01237)
- Hunter, J. D. (2007). Matplotlib: A 2D graphics environment. *Computing in Science & Engineering*, 9(3), 90–95. doi:[10.1109/MCSE.2007.55](https://doi.org/10.1109/MCSE.2007.55)
- Kiwisolver. (2018, May).
- McGuire, P. (2007). *Getting started with pyparsing* (First.). O'Reilly.
- Murphy, R. (2015). Building cell models and simulations from microscope images. *Methods (San Diego, Calif.)*, 96. doi:[10.1016/j.jymeth.2015.10.011](https://doi.org/10.1016/j.jymeth.2015.10.011)
- Oliphant, T. (n.d.). NumPy: A guide to NumPy. USA: Trelgol Publishing. Retrieved from <http://www.numpy.org/>
- Pedregosa, F., Varoquaux, G., Gramfort, A., Michel, V., Thirion, B., Grisel, O., Blondel, M., et al. (2011). Scikit-learn: Machine learning in Python. *Journal of Machine Learning Research*, 12, 2825–2830.

- Rossum, G. van. (1995). *Python tutorial, technical report cs-r9526*. Centrum voor Wiskunde en Informatica (CWI).
- Ruan, X., Johnson, G. R., Johnson, I. B., Nitschke, R., Boerries, M., Busch, H., & Murphy, R. F. (2019). Image-derived Models of Cell Organization Changes During Differentiation of PC12 Cells. *BioRxiv*. doi:[10.1101/522763](https://doi.org/10.1101/522763)
- Stavru, F., & Cossart, P. (2011). Listeria infection modulates mitochondrial dynamics. *Communicative & integrative biology*, 4, 364–6. doi:[10.4161/cib.4.3.15506](https://doi.org/10.4161/cib.4.3.15506)
- Stéfan van der Walt, J. N.-I., Johannes L. Schönberger, & contributors. (2014). *Scikit-image: Image processing in python*. doi:[10.7717/peerj.453](https://doi.org/10.7717/peerj.453)
- Virtanen, P., Gommers, R., Oliphant, T. E., Haberland, M., Reddy, T., Cournapeau, D., Burovski, E., et al. (2019). SciPy 1.0—Fundamental Algorithms for Scientific Computing in Python. *arXiv e-prints*, arXiv:1907.10121. Retrieved from <http://arxiv.org/abs/1907.10121>