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OSSI proposal: Paintera

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Motivation

The Paintera tool¹ enables dense annotation of large 3D volumes. It uses the ImgLib2-based BigDataViewer rendering engine² to virtually slice and zoom into arbitrarily large composites of 3D volumes. The N5 API³ is used to store and load large multi-scale raw volumes, labels, and meta-data in HDF5 files, N5 file stores, or in the cloud. Paintera is implemented in Java⁴ and Kotlin⁵ and uses JavaFX⁶ for its user interface which provides hardware accelerated 3D rendering on all major platforms. At this time, Paintera features 2D and 3D label brushes and interactive shape interpolation in arbitrarily re-sliced orientations, tools for manual superpixel agglomeration, and on-the-fly mesh generation and interactive display with adaptive level of detail (LoD) and smoothing.

Paintera evolved from a series of ad-hoc solutions to urgent real world issues and therefore has an organic history. Initially, the Saalfeld lab, in collaboration with then visitor Jan Funke and the Bock lab, needed a tool to rapidly annotate dense ground truth for neuron and synapse segmentation in non-isotropic serial section transmission electron microscopy (ssTEM) of the *Drosophila* brain (Zheng et al. 2018). We had first used FlyEM's Raveler tool⁷ to annotate a sample with mostly orthogonally sectioned neurons. Raveler, however, does not include 3D visualization, reslicing, and other means to assess 3D continuity of 2D annotations and therefore the labels included a large number of annotation errors. We then contracted a commercial annotation service provider whose undisclosed workflow improved upon Raveler generated labels but still contained too many obvious errors to be practically useful. We reasoned from ongoing communication with the service provider that, at the time, they were unable to handle larger volumes efficiently and had no effective tool to validate 3D continuity of labels. We therefore used BigDataViewer as a platform to develop the annotation tool BigCAT⁸ which uses the HDF5 storage format for raw volumes, labels, and annotations and can lazily load only the parts of the raw volume that are in the field of view (FoV). We developed manual agglomeration tools to interactively merge and split segmentation fragments, and 2D and 3D label brush and fill tools. BigCAT

¹Paintera: <https://github.com/saalfeldlab/paintera>

²ImgLib2: Pietzsch, Preibisch, Tomančák, and Saalfeld 2012, <https://imglib2.net/>; BigDataViewer: Pietzsch, Saalfeld, Preibisch, and Tomancak 2015, <https://github.com/bigdataviewer/bigdataviewer-core>.

³N5: <https://github.com/saalfeldlab/n5>

⁴OpenJDK: <https://openjdk.java.net/>

⁵Kotlin: <https://kotlinlang.org/>

⁶JavaFX: <https://openjfx.io/>

⁷Raveler: <https://wiki.janelia.org/wiki/display/RAV/Raveler>

⁸BigCAT: <https://github.com/saalfeldlab/bigcat>

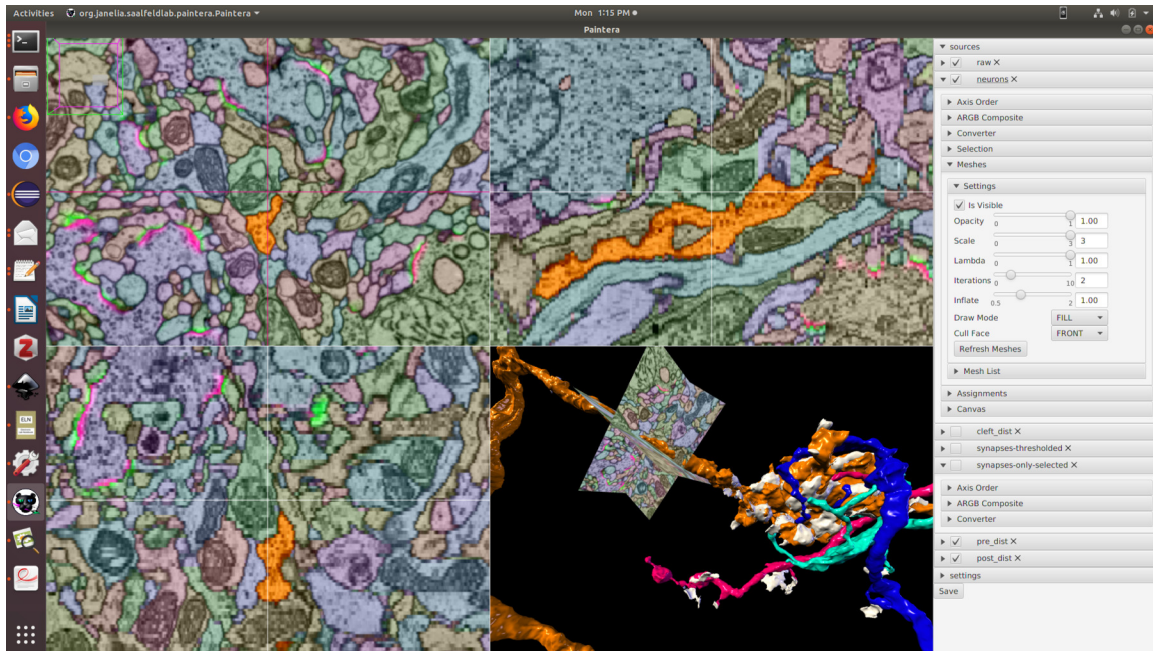


Figure 1: Paintera running on the Ubuntu Linux desktop was used to proofread automatic neuron segmentations and pre- and post-synaptic contact predictions in non-isotropic ssTEM of the *Drosophila* brain to improve the CREMI challenge.

was used by a small number of annotators in the lab and associated groups to finalize the annotations at a significantly smaller error rate than before and we eventually used it to host the CREMI challenge.⁹

The CREMI challenge data enabled several groups to dramatically improve the performance of neuron segmentation pipelines¹⁰ and the detection of synaptic contacts¹¹ which, in turn, revealed that more and even better curated training labels are required to train and validate machine learning based reconstruction methods. In parallel, other groups, e.g. the COSEM team,¹² started using BigCAT to fine-tune their training labels for cellular organelles in isotropic FIB-SEM. BigCAT lacked three main features to support these efforts more efficiently: (1) lazy-loading and -writing support for multi-scale labels, (2) interactive 3D rendering of selected labels, (3) 2D label brushes and fill tools that work in arbitrary orientation instead of just the orthogonal axes, (4) interactive interpolation between arbitrarily oriented shape profiles labeled at a distance. For its platform independent support of hardware accelerated 3D rendering, we switched to the JavaFX platform and developed the Paintera tool which now supports all of those features. We also replaced the HDF5 backend by the N5 API which makes it easier to use Paintera on both file-based backends (including HDF5) and cloud storage. Paintera has been used successfully to densely proofread volumes that were more than 100× larger than the CREMI challenge volumes

⁹CREMI: <https://cremi.org/>

¹⁰Plaza and Funke 2018; Cerrone, Zeilmann, and Hamprecht 2019; Luther and Seung 2019; Lee et al. 2019; Funke et al. 2019; Li et al. 2019; Bailoni et al. 2019; Linsley, Kim, Berson, and Serre 2020; Lee, Lu, Luther, and Seung 2021.

¹¹Heinrich et al. 2018; Buhmann et al. 2021.

¹²Heinrich et al. 2020.

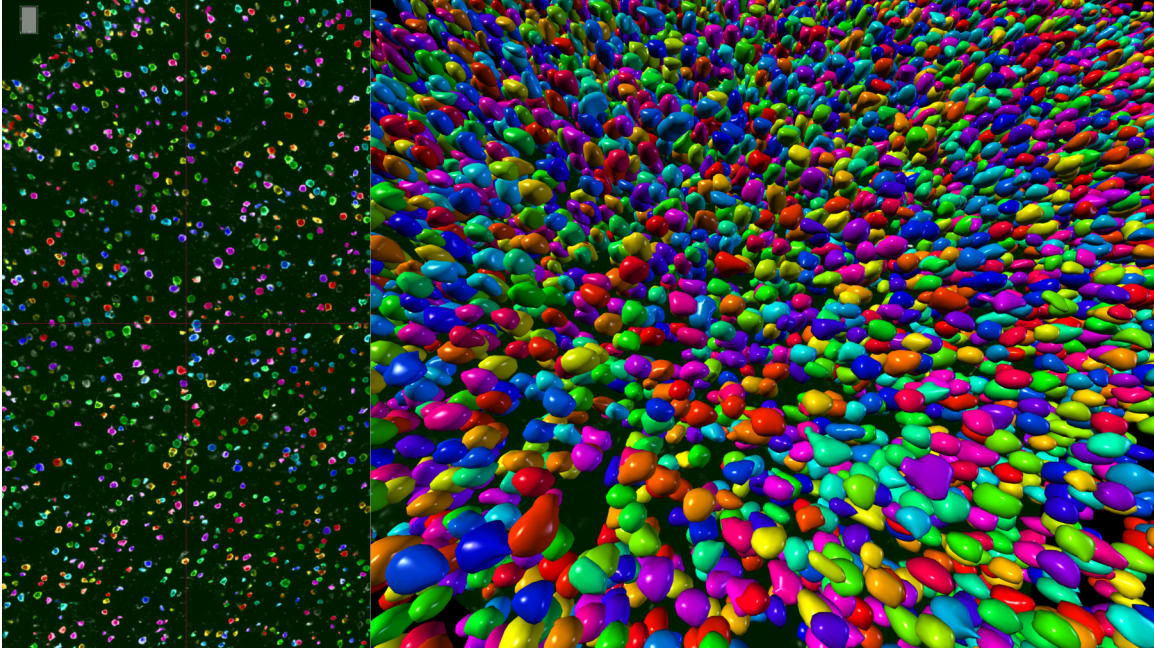


Figure 2: Paintera running on the Windows desktop was used to generate training labels for Starfinity cell body segmentation in large light sheet microscopy volumes from mouse cortex and to visualize and proofread the results.

(see Fig. 1) and to create training labels for Starfinity cell segmentation in near isotropic light sheet microscopy volumes¹³ (see Fig. 2).

Goals and milestones

While Paintera has been demonstrated to be useful as is, it carries some historical legacy and lacks useful features to make it an even better tool and to enable its inclusion as a module for future active machine learning tools for ongoing projects for CellMap and the 4D Cellular Physiology research area.

Database for indices: Paintera maintains indices to accelerate caching, mesh generation, updates, and search queries over labels and fragment agglomeration. These indices are currently stored as N5 datasets but the N5 format is not ideal for this purpose because it creates a significant number of files and/ or has high latency for search operations when stored in the cloud. We have hesitated to add more indices that would be useful to support targeted proofreading workflows because of these technical difficulties. The appropriate store for these indices is an SQL database such as SQLite, PostgreSQL, or MySQL.¹⁴ Paintera should connect to and use an SQL database to maintain its indices and other relational data. Ideally, a Paintera project without a dedicated database server would store a compressed dump of the database content in its project N5 file and create and fill a local SQLite instance when

¹³Wang et al. 2021.

¹⁴SQL databases: <https://www.sqlite.org/>, <https://www.postgresql.org/>, <https://www.mysql.com/>

the project is loaded. Projects that connect to a dedicated database server will store the necessary account information.

Improve mesh generation: Paintera supports interactive mesh generation with view dependent LoD. Meshes are generated for label blocks, not for objects, and smoothed to improve visual appearance. Label blocks currently overlap significantly to guarantee visual continuity. This overlap is not required if mesh smoothing operates on sufficient padding to guarantee that corresponding vertices undergo the same operation. Furthermore, the current implementation does not re-use vertices for adjacent polygons but naively duplicates them. This leads to a more than 6× inflated memory demand on the GPU. Lastly, the parameters for mesh smoothing do not currently consider the LoD at which the mesh is being rendered. This leads to over-smoothing at lower LoD and inconsistent appearance of the meshes at detail level transitions. We have already implemented the improved smoothing method including LoD dependency and adjusted the code to re-use vertices instead of duplicating them, however, this code has not been integrated into Paintera yet. Integration is not entirely trivial because details of the previous method are deeply mixed with other components of the tool, so some careful testing and refactoring will be required.

Modularize: Paintera’s current tool set and UI are rather monolithic and almost all components interact with each other. This simple design makes it easy to serialize and deserialize the state of a project but it is difficult to use individual components of Paintera in other projects. We plan to better separate individual components and their interfaces, to separate tools and UI control elements, and to make the UI more flexible. We will convert control elements that are currently statically associated with properties of sources, meshes, and tools into re-usable components that can be connected to groups of elements. This will make it simpler to e.g. share mesh property controls for several mesh sources and to de-clutter the UI. We will also convert the currently static UI arrangement to a flexible tile tree like in the CATMAID window manager.¹⁵

Tools: Paintera is currently a single stateful annotation tool that enables label painting, manual fragment agglomeration, and label profile interpolation simultaneously. For label profile interpolation, the capabilities of this global tool need to be managed because both navigation and interaction with source controls must be constrained while profiles are being selected. Anticipating the development of more tools, we will introduce explicit control modes for stateful tools instead of depending on tools to manage the entire UI. This will not only make the operation of the current set of tools and states simpler but it will enable us to quickly add simple new tools that have long been missing. We will start by adding contrast based magic wands, interactive thresholding, seeded level sets, and label shape smoothing. We will also add an alternative label shape interpolator that uses polygonal re-sampling of the label shapes instead of boundary distances. This shape interpolation mode will make it simpler to annotate fine structures like microtubules and thin membranes.

Deployment and integration: Currently, Paintera is released through conda, including a JGO based launcher. We would like to switch to a more OS native release of both Paintera and future integration with other tools and have submitted a parallel pro-

¹⁵Saalfeld, Cardona, Hartenstein, and Tomančák 2009, <https://catmaid.readthedocs.io/en/stable/>.

posals to improve the deployment of JVM based tools at Janelia and in the open source community. As Painter is becoming more modular, it will be even more relevant to release its components and build and release various tools that re-use these components.

Requirements and synergies

Currently, the Saalfeld lab is developing Painter as a tool to support ongoing projects in the lab and associated projects such as COSEM and CellMap. We cover development, user support, and deployment with one full time software developer and occasional associated work by other lab members. In particular the developments on high impact infrastructure components is secondary to urgent daily needs in the lab (this has not been the case for the last year but will become an issue as we transition back into normal research operations). The utility and applicability of Painter would therefore strongly benefit from additional support by which the tool can become a very flexible component for semi-automatic proofreading methods on large volumes that we plan to develop in collaboration with the Funke lab. This will be particularly relevant for the CellMap project associated with 4DCP, and improved neuron and synapse reconstruction and classification for MCN.

We would appreciate support by developers with strong experience with the Java programming language and the JVM in general. Knowledge of the N5 API, ImgLib2, BigDataViewer, and the Kotlin programming language can be helpful but can be acquired along the way.

References

- Bailoni, A. et al. (2019). "A Generalized Framework for Agglomerative Clustering of Signed Graphs applied to Instance Segmentation". In: *arXiv:1906.11713 [cs]*.
- Buhmann, J. et al. (2021). "Automatic detection of synaptic partners in a whole-brain Drosophila electron microscopy data set". In: *Nature Methods* 18.7, pp. 771–774.
- Cerrone, L., A. Zeilmann, and F. A. Hamprecht (2019). "End-To-End Learned Random Walker for Seeded Image Segmentation". In: *2019 IEEE/CVF Conference on Computer Vision and Pattern Recognition (CVPR)*. Long Beach, CA, USA: IEEE, pp. 12551–12560.
- Funke, J. et al. (2019). "Large Scale Image Segmentation with Structured Loss Based Deep Learning for Connectome Reconstruction". In: *IEEE Transactions on Pattern Analysis and Machine Intelligence* 41.7, pp. 1669–1680.
- Heinrich, L. et al. (2018). "Synaptic Cleft Segmentation in Non-isotropic Volume Electron Microscopy of the Complete Drosophila Brain". In: *Medical Image Computing and Computer Assisted Intervention – MICCAI 2018*. Ed. by A. F. Frangi et al. Lecture Notes in Computer Science. Springer International Publishing, pp. 317–325.
- Heinrich, L. et al. (2020). "Automatic whole cell organelle segmentation in volumetric electron microscopy". In: *bioRxiv*, p. 2020.11.14.382143.
- Lee, K., R. Lu, K. Luther, and H. S. Seung (2021). "Learning and Segmenting Dense Voxel Embeddings for 3D Neuron Reconstruction". In: *IEEE Transactions on Medical Imaging*, pp. 1–1.
- Lee, K. et al. (2019). "Convolutional nets for reconstructing neural circuits from brain images acquired by serial section electron microscopy". In: *Current Opinion in Neurobiology*. Machine Learning, Big Data, and Neuroscience 55, pp. 188–198.
- Li, P. H. et al. (2019). "Automated Reconstruction of a Serial-Section EM Drosophila Brain with Flood-Filling Networks and Local Realignment". In: *Microscopy and Microanalysis* 25.S2, pp. 1364–1365.

- Linsley, D., J. Kim, D. Berson, and T. Serre (2020). “Robust neural circuit reconstruction from serial electron microscopy with convolutional recurrent networks”. In: *arXiv:1811.11356 [cs]*.
- Luther, K. and H. S. Seung (2019). “Learning Metric Graphs for Neuron Segmentation In Electron Microscopy Images”. In: *arXiv:1902.00100 [cs]*.
- Pietzsch, T., S. Preibisch, P. Tomančák, and S. Saalfeld (2012). “ImgLib2—generic image processing in Java”. In: *Bioinformatics* 28.22, pp. 3009–3011.
- Pietzsch, T., S. Saalfeld, S. Preibisch, and P. Tomancak (2015). “BigDataViewer: visualization and processing for large image data sets”. In: *Nature Methods* 12.6, pp. 481–483.
- Plaza, S. M. and J. Funke (2018). “Analyzing Image Segmentation for Connectomics”. In: *Frontiers in Neural Circuits* 12, p. 102.
- Saalfeld, S., A. Cardona, V. Hartenstein, and P. Tomančák (2009). “CATMAID: Collaborative Annotation Toolkit for Massive Amounts of Image Data”. In: *Bioinformatics* 25.15, pp. 1984–1986.
- Wang, Y. et al. (2021). *Expansion-Assisted Iterative-Fish Defines Lateral Hypothalamus Spatio-Molecular Organization*. SSRN Scholarly Paper ID 3797275. Rochester, NY: Social Science Research Network.
- Zheng, Z. et al. (2018). “A Complete Electron Microscopy Volume of the Brain of Adult *Drosophila melanogaster*”. In: *Cell* 174.3, 730–743.e22.