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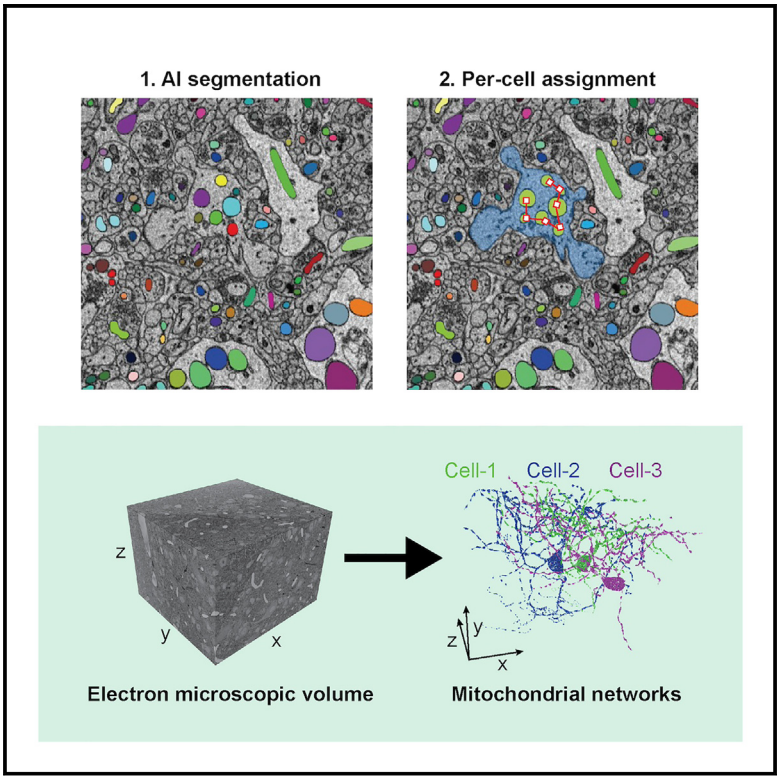
Efficient cell-wide mapping of mitochondria in electron microscopic volumes using webKnossos

Graphical abstract



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In brief

Jiang et al. develop an image analysis procedure for volume electron microscopy. It involves organelle segmentation by a pre-trained artificial neural network and instance assignment using the path-based annotation tool. By doing so, they achieved a highly efficient mapping of cellular mitochondrial networks in various specimens, including brain tissue.

Highlights

- A hybrid procedure for fast analysis of mitochondria in electron microscopic volumes
- webKnossos functions for visualization, annotation, and regrouping of mitochondria
- Cell-wide mitochondrial network reconstruction in various specimens

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Report

Efficient cell-wide mapping of mitochondria in electron microscopic volumes using webKnossos

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MOTIVATION Deep learning models have been developed to automatically infer mitochondrial instances in volume electron microscopic datasets. However, in order to obtain their cellular landscape, individual mitochondria need to be assigned to the host cell. Oftentimes, cell membrane contouring, as a separate task, can be extremely demanding in tissue samples, thereby hindering direct organelle-to-cell assignment based on pixel overlap. In this study, we develop a flexible approach for use-dependent sampling of mitochondrion populations, e.g., in a particular cell type or subcellular compartment.

SUMMARY

Recent technical advances in volume electron microscopy (vEM) and artificial-intelligence-assisted image processing have facilitated high-throughput quantifications of cellular structures, such as mitochondria, that are ubiquitous and morphologically diversified. A still often-overlooked computational challenge is to assign a cell identity to numerous mitochondrial instances, for which both mitochondrial and cell membrane contouring used to be required. Here, we present a vEM reconstruction procedure (called mito-SegEM) that utilizes virtual-path-based annotation to assign automatically segmented mitochondrial instances at the cellular scale, therefore bypassing the requirement of membrane contouring. The embedded toolset in webKnossos (an open-source online annotation platform) is optimized for fast annotation, visualization, and proofreading of cellular organelle networks. We demonstrate the broad applications of mito-SegEM on volumetric datasets from various tissues, including the brain, intestine, and testis, to achieve an accurate and efficient reconstruction of mitochondria in a use-dependent fashion.

INTRODUCTION

Mitochondria are vital organelles for eukaryotic cells, producing the energy-rich compound ATP that is essential for cellular metabolism. *In situ*, mitochondria not only vary in shape, size, and dynamics according to cell type and bioenergy status but also form highly organized networks with subcellular compartment precision to meet local metabolic demands.[1–3] Therefore, spatial mapping of mitochondrial networks provides crucial information about key aspects of mitochondrial biology (such as morphological features, cellular positioning, and fission-fusion ratio) to comprehend the biological relevance of mitochondrial properties under healthy conditions or in disease states.[4]

Recent technical advances in volume electron microscopy (vEM) have enabled high-throughput three-dimensional (3D) imaging of large tissue blocks at nanometer resolutions.[5–7] Using this approach, mitochondrial network organization has been profiled at an unprecedented scale in various cell types, including neurons,[8–10] sensory cells,[11,12] muscles,[13–15] hepatocytes,[16–18] sperm,[19,20] and tumor cells.[21] Currently, despite substantial progress in automated analysis powered by deep learning (DL) algorithms,[22–26] manual annotation and proofreading of hundreds to thousands of instances are required to ensure trustful quantification of mitochondria, likely owing to the complexity and diversity of their morphology as well as prevalent inter-organelle contacts. Moreover, different sample preparations and imaging settings, cell-type-specific mitochondrial heterogeneity, and unseen disease-related phenotypes lead to poor DL model generalization.[22] Thus, most DL pipelines still rely on repeated cycles of use-dependent fine-tuning. Lastly, it is often of interest to investigate the cellular landscapes of mitochondria, in particular those of polarized cells such as neurons,[9]

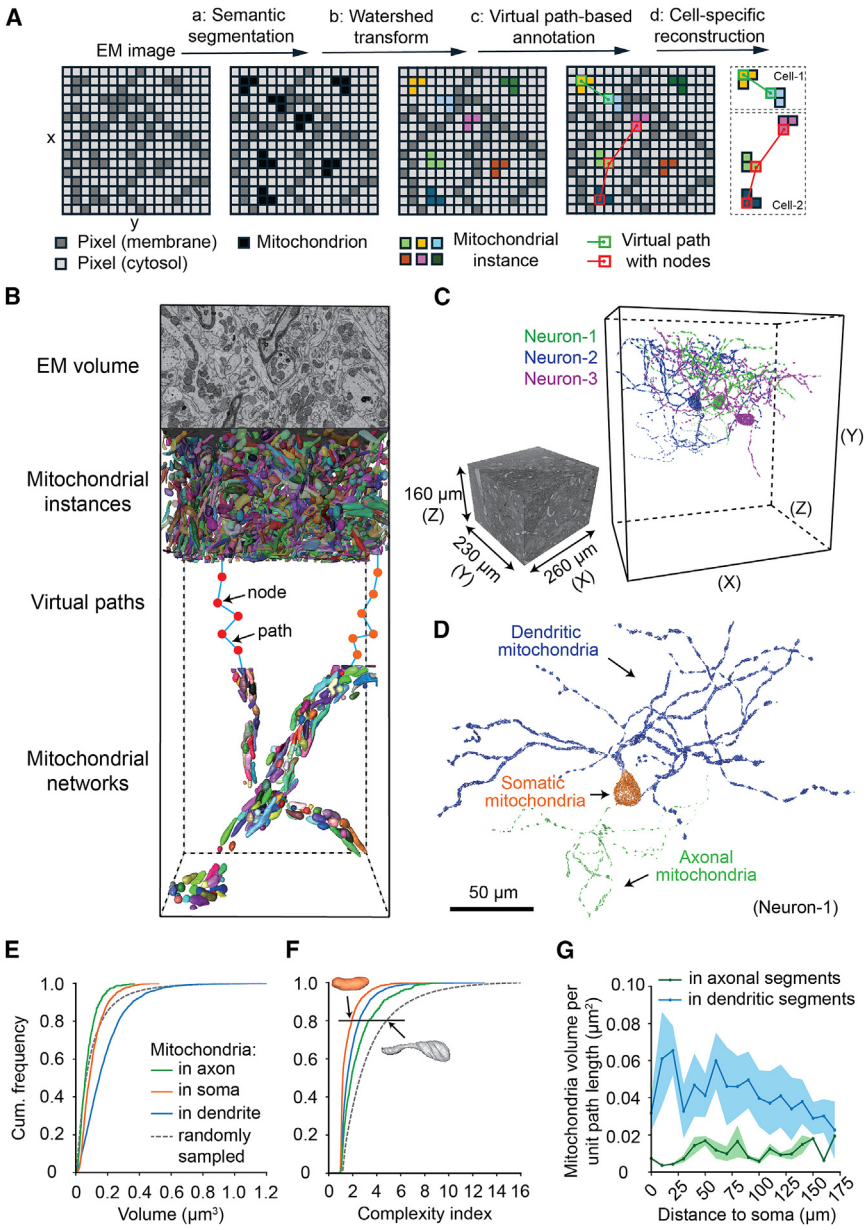

Figure 1. Reconstruction of the mitochondrial network in a neuron

(A) Flowchart of semi-automated analysis for cell-specific mitochondrial reconstruction using webKnossos. For the sake of simplicity, 2D pixel art is used as an example.

(B) Schematic illustration of neuronal mitochondrial network reconstruction.

(C) Dimensions of example SBEM volume acquired from the mouse brainstem (left). 3D rendering of the reconstructed mitochondrial networks (color coded) from three neurons (right).

(D) A representative cell-wide mitochondrial reconstruction of somatic (orange), dendritic (blue), and axonal (green) subpopulations of a neuron in (C) (neuron-1). Scale bars, 50 µm.

(E and F) Cumulative frequency distribution of mitochondrial instance volume and complexity index in the axons, dendrites, and soma of the neuron shown in (D) (n = 650 axonal, n = 3,890 dendritic, and n = 1,405 somatic mitochondria and n = 192,484 mitochondria in three randomly selected sub-volumes; see Figure S3 for details).

(G) In the same neuron as in (D), dendrites (blue) and axons (green) were binned into 10-µm-long segments, in which mitochondrial volumes were measured, respectively. Data are presented as mean ± SD of mitochondrial volumes in segments at different path lengths away from the soma (see STAR Methods for details).

meaning that all mitochondria belonging to the same host cell are sought to be assigned based on the membrane boundaries of its interior. For intricate tissue systems like the brain, however, cellular volume reconstruction can be more challenging in terms of computational and human labor costs than the mitochondrial segmentation itself,[27] making a high payoff for such analysis only on *ad hoc* densely segmented datasets.

Here, we report the development of a semi-automated analysis procedure (called mito-SegEM) for cell-wide mitochondrial reconstruction in large-scale vEM data. It involves mitochondrial segmentation by a pre-trained artificial neural network and instance assignment using the path-based annotation tool of webKnossos as an alternative to cell membrane contouring, thus achieving a highly efficient mapping of the cellular mitochondrial network in various specimens, including brain tissues.

RESULTS

Based on the online 3D data annotation tool webKnossos,[28] we developed embedded functions that are aimed at facilitating the reconstruction of cellular mitochondrial networks in a semi-automated manner. The workflow (Figure 1A) included (1) automated mitochondrial segmentation, (2) uploading of mitochondrial masks to webKnossos for visualization (Video S1), (3) manual interconnecting of cellular mitochondrial instances by virtual paths (Video S2), and (4) proofreading and downloading of the mitochondrial merges associated with host cells or subcellular compartments (Video S3). Particularly, to enable fast interactive picking up of mitochondrial instances by humans and avoid redundant annotation, all 3D masks of mitochondria are allowed to be hidden, and then each of them can be highlighted with pseudo-color by clicking on the vEM data (demonstrated in Video S2). In addition, on each selected mitochondrion, an annotation node was placed, and interconnected nodes within the cell assembled a virtual path that allows fast indexing of associated mitochondrial merges. Finally, a new keyboard shortcut was implemented in webKnossos to process

all segments that have been picked up by the path of annotation. This tool enables a fast selection of all mitochondria associated with the currently active path and adds them to a new segment group with the meshes automatically loaded for easy handling and 3D rendering (Video S4).

Mapping spatial organization of neuronal mitochondria

We first tested this procedure for neuronal mitochondrial reconstruction in the mouse brainstem tissue (Figure 1B). A dataset containing 3,983 consecutive images with a pixel size of 15 × 15 nm^2 was acquired using serial block-face scanning EM (SBEM)[29] at a nominal thickness of 40 nm, yielding an EM volume of 260 × 230 × 155.7 μm^3 after alignment along the cutting direction (Figure 1C). Automated segmentation of mitochondrial instances was performed using a pre-trained 3D U-net[25] with dataset-specific minor modifications[30] (Figure S1), which generated a map of 3D masks containing 1,048,575 mitochondria in the volume before proofreading. The EM volume, together with the masks, was then uploaded to webKnossos for the inspection and assignment of individual mitochondria to the corresponding host cells. For proof-of-principle purposes, we randomly chose three neuronal cell bodies as starting points for neurite assignments of mitochondrial instances with our new tools.

The quantification revealed that each neuron accommodated 7,495 ± 1,146 (mean ± SD) mitochondrial instances, which was about 0.75% of all the mitochondria in the dataset (Figures 1C and S2). Next, in one neuron, we subdivided the mitochondria into three subpopulations based on cellular positions, i.e., in the soma, dendrites, or axons (Figure 1D), by simply modifying the annotation paths in webKnossos. In contrast to random sampling, our cell-based quantification suggests neuronal compartment-specific differences in the volume and complexity of mitochondria (Figures 1E and 1F). Note that the example cell features an overall higher ratio of simple mitochondria than those from randomly sampled volumes (Figure 1G), implying an intercellular heterogeneity in mitochondrial complexity. Furthermore, we showed distinct spatial distributions of mitochondria in the dendrites and axons (Figure 1H).

Mitochondrial morphologies in mouse intestine and testis tissues

To highlight the general applicability of the mito-SegEM workflow, we analyzed two additional datasets from various mouse tissues. First, an intestinal sample block was cut at a 50 nm step size, and 1,000 consecutive slices were collected using an automated tape-collecting ultramicrotome (ATUM).[31] The SEM images were acquired at a pixel size of 8 × 8 nm^2 and sequentially aligned to yield an EM volume of 41 × 57.3 × 50 μm^3. Likewise, mitochondrial instances were automatically segmented and assigned to eight individual cells located at different regions of the intestinal crypt (Figures 2A and 2B). On average, each cell contained 80 ± 8 (mean ± SD) mitochondria (Figure S4A) with relatively broad size distributions (Figure 2C) and differential degrees of complexity (Figure 2D). Second, we reanalyzed a previously published SBEM dataset[32] (dimension: 49.8 × 66 × 125 μm^3, voxel size: 15 × 15 × 50 nm^3) of mouse testis tissue (Figures 2E and 2F), in which twelve cells were randomly selected for mitochondrial reconstruction (491 ± 322, mean ± SD mitochondria per cell; Figure S4B). This revealed overall small-sized and simple mitochondria in the germ cells with a limited inter-cell difference (Figures 2G and 2H).

Annotation consumption for the mitochondrial assignment to host cells

Assigning individual mitochondria to corresponding host cells was an underestimated task that required accurate segmentation of both mitochondrial and cell membranes to calculate their spatial overlapping. In the mito-SegEM workflow, we employed virtual-path-based annotation to replace unnecessary contouring of the host cell membranes, whose annotation was usually done slice by slice. In neurons, for instance, contouring a small neurite fragment that contained one 1-μm-sized mitochondrion required manual tracing throughout 25 slices of 40 nm cutting thickness, while mito-SegEM simplified this to a single click on the mitochondrion. Thus, we speculated an increase in the annotation speed by one order of magnitude. To quantitatively compare the time costs between membrane contouring and virtual-path-based annotation, we tested both approaches on the same datasets with pre-segmented mitochondria (Figure 3). For the dendrite fragment with a path length of 13.6 μm (Figures 3A–3D), annotation of all 50 mitochondria using mito-SegEM was found to be 48.8 times faster than manual contouring of the membrane. Similarly, we reported a 21.8-fold reduction in the annotation consumption on a 13.3-μm-sized cell containing 77 mitochondria (Figures 3E–3H). The varying degrees of annotation time savings are likely owing to different structural complexity and mitochondrial content between neurites and spherical cells.

Recently developed AI-based tools have enabled saturated segmentation for cortical tissues, making the human annotation consumption rate about 25 times faster on neurite reconstruction.[33] Although direct comparison was not performed, virtual-path-based annotation seemed to be as fast as the focused annotation on AI-segmented neurites, without the need for computational resources and dataset-specific parameter tuning. Thereby, mito-SegEM is currently advantageous over other methods in terms of reconstruction costs in many scenarios and provides a fast alternative for studies whose primary goal is the mitochondrial network instead of dense neurite reconstruction.

DISCUSSION

In the present work, we have developed mito-SegEM to facilitate use-dependent mitochondrial network reconstruction in electron microscopic volumes. By combining automatic mitochondrial segmentation and virtual-path-based annotation, mito-SegEM enabled the efficient assignment of mitochondrial instances rather than individual pixels to the host cell. Besides, this procedure bypassed the contouring of the cell membrane borders that often appear intricate in tissues. We illustrated the broad applicability of our procedure on vEM datasets of the mouse brain containing intermingled neurites (Figure 1C), as well as the intestine and testis (Figures 2B and 2E), in which densely packed cells show less defined membrane borders.

Neurons are polarized cells with anatomically distinct compartments. This feature helps mitochondria maintain microenvironments in support of unique subcellular functions,[1,34] including

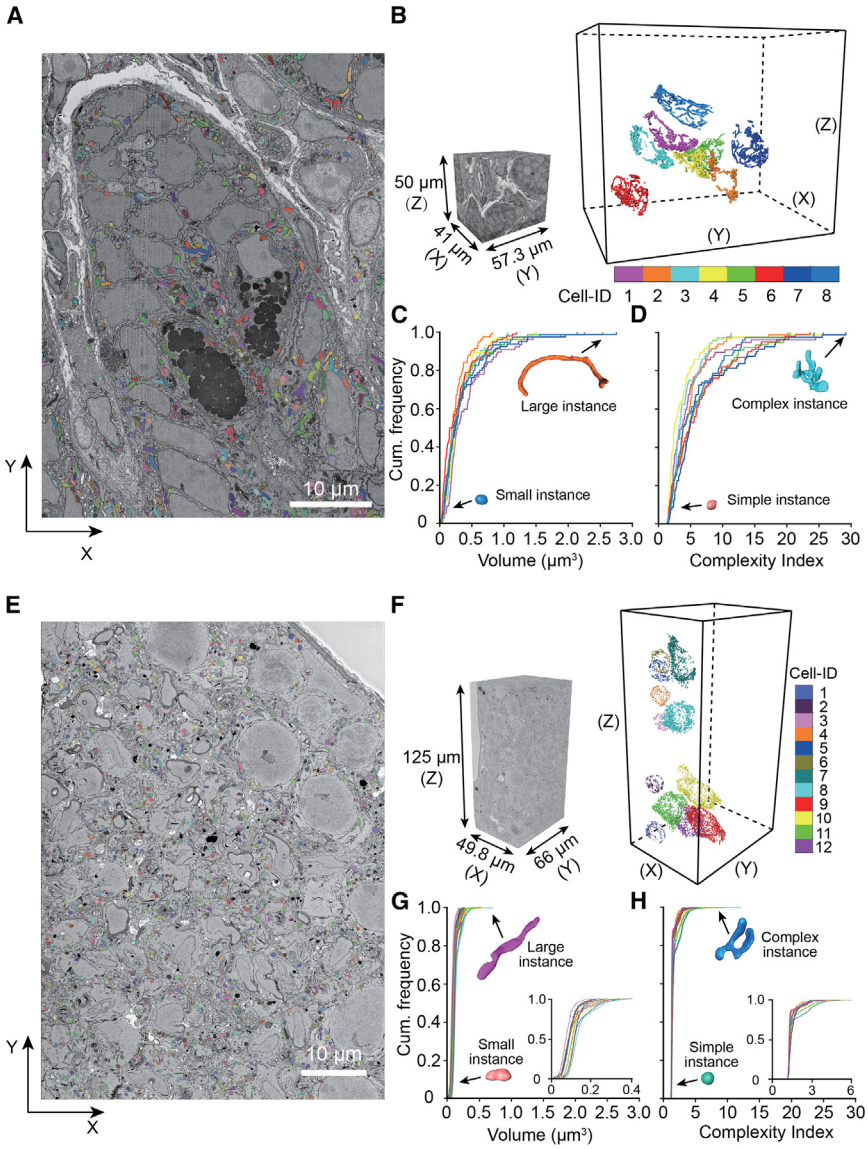

Figure 2. Cell-type-specific differences in mitochondrial morphology

(A) EM image of a single ultra-thin slice from the mouse intestinal tissue. Mitochondria were automatically segmented and labeled with pseudo-colors. Scale bar, 10 μm.

(B) Volume of the acquired ATUM dataset (left), in which eight cells (color coded) were randomly selected for mitochondrial reconstruction (right).

(C and D) Cumulative frequency distributions of the volume and complexity index of mitochondrial instances per cell were computed from the reconstructions in (B).

(E) Example EM image with mitochondrial segmentations (pseudo-colored) of the mouse testis tissue block. Scale bar, 10 μm.

(F) SBEM volume (left) and 3D rendering of the mitochondrial reconstruction in twelve randomly selected cells.

(G and H) Same as (C) and (D) but for cumulative frequency distributions of mitochondrial instance volume and complexity index from the cellular reconstructions shown in (F). Insets: same plots but with an expanded x axis.

synaptic plasticity,[35–37] axonal branching,[38,39] and presynaptic release.[39–41] Thus, it is of particular significance for both basic neuroscience and clinical studies to quantitatively characterize the compartment-specific mitochondrial morphologies in healthy individuals and disease models. While recent progress in vEM methods provides an unprecedented opportunity to visualize the cellular landscape of mitochondrial networks at nanometer resolution in 3D,[9] a fast extraction of this information relies on existing full-volume reconstructions of neurites, to which individual mitochondria could be automatically assigned. Just like SegEM,[42] our procedure, which profits from well-established neuronal mitochondrial segmentation and efficient skeleton annotation, can presumably achieve a 20- to 50-fold reconstruction efficiency gain (Figures 3D and 3H) and make a neurite-specific mapping of mitochondrial morphology affordable in most laboratories (Figure 1C). In addition, the skeleton-like annotation not only allows a real-time update of assigned mitochondria upon split and merge operations of neurites during proofreading in webKnossos but also enables a spatial correlation of the mitochondrial network with numerous published neurite tracings and synapse annotations.[43–46] Moreover, it has been recently shown that mitochondria can be used to facilitate neurite tracing in a focused annotation mode due to their elongation and ubiquitous presence in a neuron.[47]

Much progress has been made in improving the accuracy of mitochondrial segmentation using an adaptive template transformer (ATFormer) combined with a hierarchical attention learning mechanism for the simultaneous identification of the mitochondrial mask and contour.[25,26] Moreover, it has been recently demonstrated that promising inference results of mitochondrial segmentation can be readily delivered by a generalist DL model trained on massive EM datasets.[22] However, given the structural diversity and different imaging settings, quantifications of mitochondrial morphologies without proofreading would not be granted in most case studies. In principle, the mito-SegEM procedure will allow transfer learning of a generalist model through human-in-the-loop annotation of mitochondria within the cells of interest only, bypassing the excessive requirement of model perfection for datasets with intermixed cell types or cells at different phases. Another advantage of this analysis routine is that the result from path annotation can be applied to the same dataset with mitochondrial masks inferred by different DL models, allowing the assignment of mitochondria with progressively improved segmentation outcomes. In order to enhance this function, further work will incorporate special nodes to interactively correct false split or merge errors.

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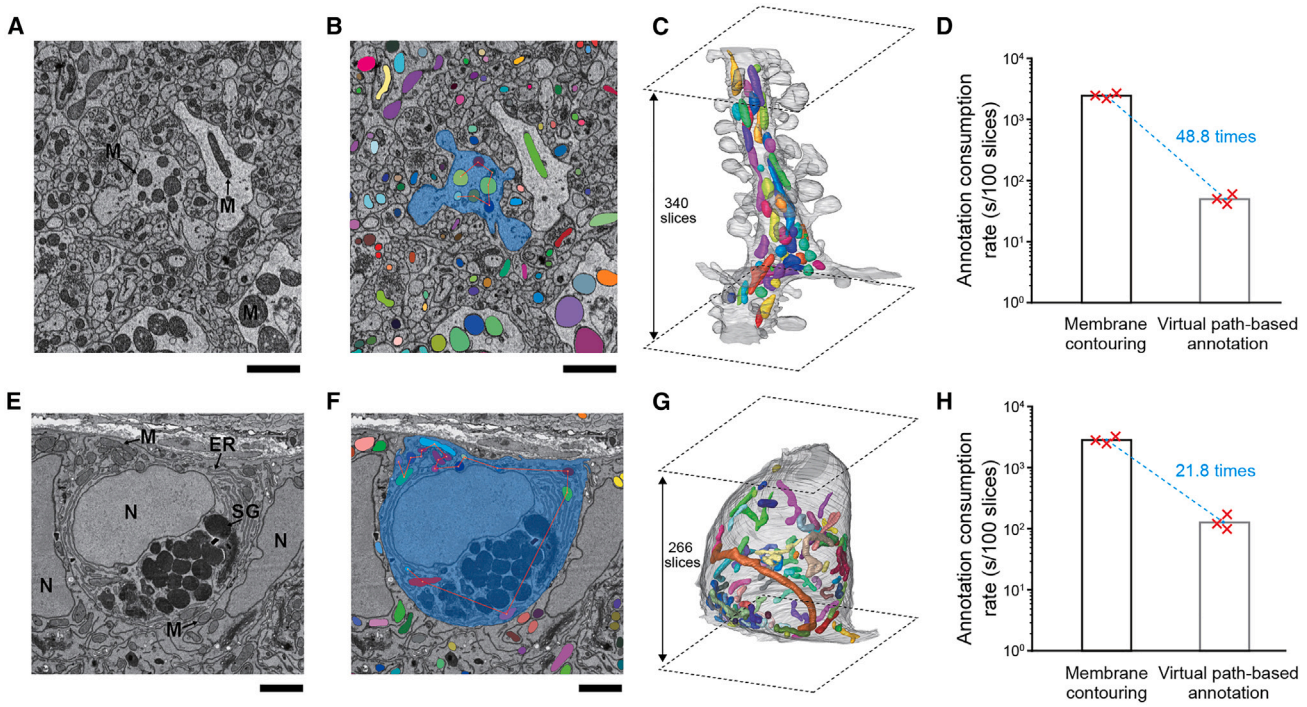

Figure 3. Annotation consumption needed for mitochondrial assignment

(A) Cropped EM image of the analyzed dendrite fragment from the mouse brainstem dataset. M, mitochondrion. Scale bar, 2 μm.

(B) AI-segmented mitochondrial masks were labeled with pseudo-colors and overlaid on the raw image. Membrane contours of the dendrite (blue) were manually traced, within which annotated virtual paths were indicated as red lines.

(C) The dendrite fragment (throughout 340 consecutive slices cut at a thickness of 40 nm) containing 50 mitochondria (colored) was rendered in 3D.

(D) The normalized annotation durations required for slice-by-slice membrane contouring and annotation of mitochondria with virtual paths only.

(E and F) An example cell was chosen from the mouse intestinal dataset. N, nucleus; ER, endoplasmic reticulum; M, mitochondrion; SG, secretory granule. The raw EM image (E) and its overlap (F) with mitochondrial masks (color coded), the cell mask (blue), and virtual paths (red lines) are shown. Scale bar, 2 μm.

(G) 3D rendering of the analyzed cell (throughout 266 consecutive slices, 50 nm thick) containing 77 mitochondria (colored).

(H) Required annotation consumption for cell membrane contouring and virtual-path-based mitochondrial annotation.

Limitations of the study

Here, we demonstrated an efficient procedure for pre-cell analysis of mitochondria in vEM datasets. Since it still relies on human annotation, the workload linearly increases with dataset size. Nevertheless, it provides an additional option when AI-based full segmentation is not required or is unaffordable for the labs. Besides mitochondria, content-rich vEM datasets enable investigations of various organelles, for instance, endoplasmic reticula, lipid droplets, and lysosomes, as well as inter-organelle contact sites.[16,17,48,49] Our subsequent work will extend this analysis routine to a multi-organelle approach by parallelizing reconstructions of different organelles with specialist DL models, serving as a powerful tool for nanoscale mapping of a comprehensive cell atlas.

RESOURCE AVAILABILITY

Lead contact

Further information and requests for resources and reagents should be directed to and will be fulfilled by the lead contact, Yunfeng Hua (yunfeng.hua@shsmu.edu.cn).

Materials availability

This study did not generate new unique reagents.

Data and code availability

- Raw EM image data and segmentations supporting the current study are publicly available on EMPIAR (ID: EMPIAR-12535) or via the links listed in the key resources table.
- All original codes are publicly available as of the publication date (https://doi.org/10.5281/zenodo.14742225).
- Any additional information required to reanalyze the data reported in this paper is available from the lead contact upon request.

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AUTHOR CONTRIBUTIONS

Y.H. conceived and supervised the study; Y.J. conducted the experiments with critical inputs from H.W. and K.M.B.; N.R. developed the software; F.W.

acquired the EM datasets; and Y.H. wrote the manuscript with contributions from all authors.

DECLARATION OF INTERESTS

N.R. is a founder of Scalable Minds GmbH.

STAR★METHODS

Detailed methods are provided in the online version of this paper and include the following:

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SUPPLEMENTAL INFORMATION

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STAR★METHODS

KEY RESOURCES TABLE

REAGENT or RESOURCE	SOURCE	IDENTIFIER
Deposited Data		
Brainstem dataset	This paper	https://wklink.org/7813
Intestine dataset	This paper	https://wklink.org/9127
Testis dataset	This paper	https://wklink.org/3287
Software and algorithms		
Codes used for analysis	This paper	https://doi.org/10.5281/zenodo.14742225
Codes of mitochondrial segmentation	Wei et al.[25]	https://github.com/zudi-lin/pytorch_connectomics
ImageJ	Schindelin et al.[52]	https://imagej.net/software/fiji/
TrakEM	Cardona et al.[53]	https://imagej.net/plugins/trakem2/
webKNOSSOS	Boergens et al.[28]	https://webknossos.org
Amira	Thermo Scientific, Inc	release 2019.2
MATLAB and Statistics Toolbox	MathWorks, Inc	release 2021a

EXPERIMENTAL MODEL AND STUDY PARTICIPANT DETAILS

Adult C57BL/6 male mice were used to generate the vEM datasets for this paper. Experiments were conducted at Shanghai Institute of Precision Medicine. All procedures were approved by the Institutional Authority for Laboratory Animal Care of Shanghai Ninth People's Hospital (SH9H-2020-A65-1).

METHOD DETAILS

Volume electron microscopy datasets

The mouse brainstem SBEM dataset contained 3983 single images (16000 × 16000 pixels) that were acquired at 15 nm pixel size and 40 nm cutting thickness using a field-emission scanning electron microscope (SEM, Gemini300, Carl Zeiss) equipped with an in-chamber ultramicrotome (3ViewXP, Gatan). The mouse intestine dataset was produced by SEM imaging on 50-nm-thick serial sections collected by a commercial ATUM setup (RMC Boeckeler, ATUMtome), yielding 1000 images of 6000 × 8000 pixels at 8 nm pixel size. The mouse testis dataset was previously reported,[32] which was acquired using SBEM and contained 2500 50-nm-spaced single tiles of 10000 × 4000 15-nm-sized pixels.

Image alignment and cubing

The alignment of both SBEM datasets (brainstem and testis) was performed offline using a script developed in our lab in MATLAB (MathWorks, US) to compute image offsets based on the cross-correlation maximum between consecutive sections.[45] For the intestine dataset, a coarse-to-fine strategy was adopted to align the serial sections owing to nonlinear distortion. In detail, coarse alignment was performed by extracting the corresponding points between adjacent images using an affine transformation model, followed by fine alignment that involved pairwise correspondence extraction between adjacent images by SIFT flow,[50] global adjustment of correspondence positions, and image wrapping through the moving-least-square method.[51]

After alignment, all datasets were cubed in 3D using a Python script included in the webKnossos toolkit (https://github.com/scalableminds/webknossos-libs) and uploaded to webKnossos for browsing and annotation.

Automated mitochondrial segmentation

The pre-trained mitochondrial segmentation model[25,30] was based on a residual 3D U-Net architecture with four-down/four-up layers (See Figure S1 for more details of the network architecture), which was provided by PyTorch Connectomics (https://connectomics.readthedocs.io/en/latest/). The model was trained to classify each voxel of the input stack (17 consecutive 256 × 256 pixel-sized images) into the "background", "mitochondrial mask", and "mitochondrial contour" categories. The model output was a two-channel image stack with the same format as the input, including the predicted probability maps of mitochondrial masks and contours. The overall loss function was

$$L_{total} = L_{mask} + L_{contour} + \alpha\left(L_{mask\_dice} + L_{contour\_dice}\right),$$

where L_{mask} and $L_{contour}$ were the binary cross-entropy losses calculated for the mask and contour of mitochondrial segmentation, respectively. L_{mask_dice} and $L_{contour\_dice}$ were the Dice losses calculated for the mask and contour segmentation of mitochondria, respectively. α was a constant value and was set to 0.5.

Model training and evaluation

The PyTorch deep learning framework (https://pytorch.org/) was employed for model training. The training datasets were randomly cropped from the raw image stacks. For the brainstem dataset three sub-volumes (1000 × 1000 × 100 voxels); for the intestine dataset four sub-volumes (one 1000 × 1000 × 100 voxels and three 2000 × 2000 × 100 voxels); and for the testis dataset two sub-volumes (1500 × 1500 × 100 voxels) were used. The ground-truth labels of mitochondria for the training datasets were generated by human experts using the Fiji[52] plugin trakEM2.[53] For model training, the training datasets were pre-processed by padding and cutting pixel-by-pixel into small patches (256 × 256 × 17 voxels), which were randomly selected as inputs to conduct data augmentation, including rotation, flip, motion blur, noise addition, small region missing, and section missing. In addition, batch normalization was carried out during training, and the batch size was set to 4 due to hardware limitations. The model was trained for 300,000 iterations with a base learning rate of 0.04 using WarmupCosineLR (https://github.com/facebookresearch/detectron2) and asynchronous stochastic gradient descent on a single NVIDIA TITAN RTX GPU.

IOU and F1-score were used for model evaluation on three test datasets, which were cropped randomly from the raw data and labeled manually. The model-predicted values and human ground truth were compared, yielding an IOU of 0.88 and an F1-score of 0.94 for the test dataset of the brainstem. For the intestine and testis cases, an IOU of 0.92 and an F1-score of 0.96 as well as an IOU of 0.90 and an F1-score of 0.95 were obtained.

To generate mitochondrial instance masks, the seeds of mitochondria (or markers) were determined with a high mask probability and low contour probability by thresholding. Then, the marker-controlled watershed transform algorithm (part of the scikit-image library) was employed to generate high-quality instance masks of mitochondria with the seed locations and the predicted probability map of the masks.

Mitochondria assignment by a virtual path

The segmentation of mitochondria was imported into the webKnossos using Python scripts. Next, in the "toggle merger mode" and with the option "hide the unmapped segmentation" selected, a start point was seeded and associated mitochondria were annotated one after another through the mouse right-clicks within individual instances. Upon each valid assignment, the corresponding mitochondrial instance would become visible with a pseudo-color and linked by an active node, so that missing and multiple annotations of mitochondrial instances could be minimized. Note that the "toggle merger mode" does not allow a mouse click outside the segments and ignores redundant annotations of a single segment. Finally, the assembly of the nodes was utilized to specify the associated mitochondrial instances that could be then operated as a defined group with i.e., self-written Python scripts.

Quantitative analysis

Mitochondrial volume and surface area were calculated from the image stack using a Python script developed in our lab. The mitochondrial complexity index (MCI) was calculated using the formula[13] as below:

$$\mathrm{MCI} = \frac{\text{surface area}^3}{16\,\pi^2\,\text{volume}^2}$$

The skeleton for each neuron was split according to its compartment to generate individual sub-skeletons for the dendrites and axons. For each sub-skeleton, the nodes closest to the soma surface were chosen as the source nodes, and all other leaf nodes were marked as target nodes. The shortest path length from the source node to each target node was computed using Dijsktra's algorithm. Each mitochondrion of the dendrite and axon was assigned to the closest skeleton node by calculating the distance between the mitochondrial centroid and the skeleton node. The mitochondrial volume per unit length was calculated by dividing the total mitochondrial volume within 10 μm of the dendritic or axonal path length by the 10 μm.

Comparison of annotation consumption

In two separate annotation tasks, three independent human annotators were asked to trace the cell boundaries as well as annotate the mitochondria using the virtual path-based way for the same dendrite fragment (340 slices) and intestinal cell (266 slices) in webKnossos. The required durations could be directly readout from the saved annotation files containing the time points of each tracing or node placing (Tables S1 and S2).

QUANTIFICATION AND STATISTICAL ANALYSIS

The pipeline to compute mitochondrial segmentation is described above in the corresponding methods subsection Automated mitochondrial segmentation. Mitochondrial morphological quantification is described in the corresponding methods subsection Quantitative analysis. The procedure for evaluating the annotation consumption is provided in the relevant figure legends and results section.