Title: Semi-automated protocol to quantify and characterize fluorescent three-dimensional

vascular images

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17 Abstract

The microvasculature facilitates gas exchange, provides nutrients to cells, and regulates

blood flow in response to stimuli. Vascular abnormalities are an indicator of pathology for

various conditions, such as compromised vessel integrity in small vessel disease and

angiogenesis in tumors. Traditional immunohistochemistry enables visualization of tissue cross-

sections containing exogenously labeled vasculature. Although this approach can be utilized to

quantify vascular changes within small fields-of-view, it is not a practical way to study the

vasculature on the scale of whole organs. Three-dimensional (3D) imaging presents a more

appropriate method to visualize the vascular architecture in tissue. Here we describe the

complete protocol that we use to characterize the vasculature of different organs in mice

encompassing the methods to fluorescently label vessels, optically clear tissue, collect 3D

vascular images, and quantify these vascular images with a semi-automated approach. To

validate the automated segmentation of vascular images, one user manually segmented fifty

random regions of interest across different vascular images. The automated segmentation

results had an average sensitivity of 80±8% and an average specificity of 90±5% when

compared to manual segmentation. Applying this procedure of image analysis presents a

method to reliably quantify and characterize vascular networks in a timely fashion. This

procedure is also applicable to other methods of tissue clearing and vascular labels that

generate 3D images of microvasculature.

Introduction

The microvasculature facilitates gas exchange, provides nutrients to cells, and regulates

blood flow in response to stimuli. Thus, it plays a fundamental role in the survival and health of

tissues and organs. Vascular abnormalities are an indicator of pathology for various conditions,

such as compromised vessel integrity in small vessel disease and angiogenesis in tumors (1,2).

In addition, impaired blood flow to the brain is associated with neurodegenerative diseases such

as Alzheimer's disease (3).

Traditional immunohistochemistry enables visualization of tissue cross-sections

containing exogenously labeled vasculature. Although this approach can be used to quantify

vascular changes within small fields-of-view, it is not a practical way to study the vasculature on

the scale of whole organs. Furthermore, traditional immunohistochemistry requires the

sectioning of tissue into thin (6-40 μm) sections, which effectively limits visualization of features

to planar views and thus impedes facile 3D visualization of vascular architecture.

Volumetric imaging of tissue samples is vital to studying the microvasculature in its

native state. The main limitation to 3D imaging of tissue samples is optical scattering resulting

from the microscopic variations of refractive index occurring in most biological tissues. Organic

solvents and aqueous solvents have been used to reduce tissue turbidity by achieving refractive

index matching (4,5). CLARITY is a popular method used for tissue clearing that involves

embedding of the sample into a hydrogel and using an electric current to remove lipids from the

sample (6). Other tissue clearing procedures have advantages and disadvantages associated

with clearing time, extent of clearing, and preservation of original tissue characteristics (size,

endogenous fluorescence, etc.).

Quantitative analysis of microvasculature is essential to understand how structural

variations in the microvascular network may change for different pathological states (7). The

feasibility of such analysis depends on accurate, ideally automated segmentation methods for

isolating the microvasculature from the background due to the hundreds of gigabytes of data

generated with high-resolution 3D imaging. Various groups have developed automated

algorithms to perform quantitative characterization of vascular images (8,9). Each method varies

in complexity, processing time, and computational requirements.

We currently use iDISCO (immunolabeling-enabled three-dimensional imaging of

solvent-cleared organs) as our primary method of tissue clearing (4,10). Briefly, iDISCO

consists of methanol dehydration, lipid removal with dichloromethane, and refractive index

matching with dibenzyl ether. iDISCO is a fast, simple-to-implement clearing method that

enables deep-tissue imaging. It is compatible with many exogenous labels often used for

traditional immunohistochemistry. We previously demonstrated the effectiveness of iDISCO in

combination with lectin-DyLight-649 for 3D visualization of vasculature in a mouse brain (10).

We also have used Prussian blue labelling of hemosiderin (11–13), a by-product of cerebral

microhemorrhages, with iDISCO-cleared brains and lectin-DyLight-649 labelling.

In this paper, we first review different methods for vascular labeling in conjunction with

optical clearing that have been published by other groups. Next, we describe the complete

protocol that we use for imaging the vasculature in different organs in mice. Specifically, we

report on sample collection and perfusion of lectin-DyLight-649 followed by application of

additional labels as desired and optical clearing. We then describe our procedure to obtain 3D

confocal microscopy images. Finally, we describe our semi-automated approach to process the

resulting images and quantify the vascular architecture in three dimensions.

Vascular imaging with various vessel labels and optical clearing techniques

Through reviewing the literature on 3D vascular imaging of cleared tissue, one will

quickly realize the large variability in methodology across different experiments (see Table 1 for

specific references). For example, blood vessels can be visualized with transgenic animals

expressing a fluorescent protein in endothelial cells, labeled *in vivo* with intravascular dyes, or

labeled *ex vivo* with immersion-based antibody labelling. In addition, tissue preparation can vary

from thick tissue sections and whole organs to whole-mount specimens, depending on the

purpose of an experiment. Finally, clearing procedures can be grouped into aqueous solvents

(14–19), organic solvents, and hydrogel-based.

When selecting a clearing procedure, it is essential to consider its compatibility with the

chosen vascular label. Endogenous fluorescence intensity is known to be reduced when using

the iDISCO protocol; hence, an alternative vascular label would be preferred. Imaging of cleared

samples is typically performed with confocal microscopy or light-sheet microscopy. Lastly,

vascular-related metrics, such as vessel diameters and vessel density, are quantified with

existing software such as FIJI and Imaris, or custom-designed software such as ClearMap 2.0.

We have reviewed several optical clearing methods utilized to image vasculature. They

are organized in Table 1 by clearing method, tissue type, vessel label, and quantification.

Vascular images in cleared tissue from select publications are included in Fig 1B-D. FDISCO is

an organic solvent-based clearing method derived from the 3DISCO method. In developing

FDISCO, Qi *et al.* found that they could achieve superior fluorescent signals of CD31-labelled

vessels by optimizing temperature and pH conditions (Fig 1B, 1B') (20,21). Moy *et al.* visualized

vessels with an intravascular fluorescent dye along with FocusClear (Figure 1C, 1C') (8). They

were able to quantify functional vascular density in different regions of cardiac tissue with a

custom MATLAB algorithm (21). With a polyethylene glycol-associated solvent system

(PEGASOS), researchers developed a clearing technique that preserved both hard and soft

tissue structures (Fig 1D, 1D') (22), allowing for vascular imaging throughout an entire

specimen.

Fig 1. A) Illustrations of the critical steps and workflow for vascular visualization in cleared tissue. B-D)

Examples of vascular visualization in literature. B) Visualization of CD31-labeled mouse kidney

vasculature with FDISCO (20). B') Magnified view of 1B. C) Visualization of DiI-labeled mouse heart

vasculature with FocusClear (8). C') Magnified view of 1C. D) Visualization of liver vasculature from *Tie2-*

Cre mouse model with PEGASOS (22). D') Magnified view of 1D).

117   **Table 1.** Summary of different approaches to visualize 3D microvasculature in optically cleared tissues.

Clearing agent(s)	Organ(s)	Vascular label	Quantification Method/Tool	Quantified Metrics
MACS (14)	brain, heart, lung, spleen, femur, kidney, spinal cord, embryo, entire body	DiI, tetramethylrhodamine-conjugated dextran	Custom algorithm via Python, Imaris: surface function	glomerulus number and glomerulus volume; general metrics (imaging depth, size change, fluorescence intensity)
SeeDB, SeeDB2, 3DISCO, uDISCO, iDISCO, CUBIC, simplified CLARITY method, 75% v/v glycerol, Ce3D, FRUIT (23)	lymph nodes	CD31	Imaris: surface function, ImageJ	general metrics (imaging depth, size change, fluorescence intensity)
sodium dodecyl sulfate/sodium deoxycholate with Sca*l*eCUBIC-2 (24)	brain	RITC-Dex-GMA, Texas red lectin, CD31, αSMA	N/A	capillary diameters, signal-to-noise ratio
iDISCO (4)	brain, peripheral nervous system, kidney, muscle, heart, whisker pad, entire embryo	PeCAM	N/A	N/A
iDISCO with CUBIC (25)	ovary	endomucin	N/A	N/A
FDISCO (20)	brain, kidney	AlexaFluor647, CD31, lectin-DyLight-649	Imaris, ImageJ	general metrics (size change, imaging depth, fluorescence quantification)
Sca*l*eS (15)	brain	Texas Red lectin	custom C++, commercial Volocity, commercial Igor Pro	microglia and Aβ plaques with custom C++, distance between microglia and Aβ plaques
3DISCO (26)	brain	FITC albumin-gelatin hydrogel	Imaris, ImageJ	vessel density, vessel diameter
thiazone with PEG-400 (27)	dorsal skin	N/A (imaged blood flow via LSI)	N/A	bloodflow via LSCI
iDISCO (28)	brain	Dye-conjugated secondary antibodies	ClearMap	Aβ deposits

CLARITY, TDE (29)	brain	lectin-FITC, gel-BSA-FITC, gel-BSA-TRITC	Markov random field based algorithm, ImageJ, Amira 5.3 software	automatic segmentation, vessel diameter, vessel length
FACT (30)	brain, spinal cord, heart, lung, adrenal gland, pancreas, liver, esophagus, duodenum, jejunum, ileum, muscle, bladder, ovary, uterus	CD31, auto fluorescence	Imaris	segmentation
CUBIC, BABB (16)	heart	FITC-lectin, 649-lectin, CD31	N/A	N/A
BABB (31)	heart	PECAM1	N/A	N/A
DBE, SCALE, CLARITY, CUBIC (32)	heart and embryo	GFP		
vDISCO (33)	whole mouse	GFP, lectin	ImageJ, ClearMap	signal level, microglia distribution
3DISCO (34)	brain	tomato lectin	N/A	N/A
CLARITY (35)	brain	fluorescein-conjugated tomato lectin	Amira	area, volume, perimeter, and length of stained vessel
CLARITY with ScaleA2 (36)	ovary, uterus, lung, liver	tdTomato	Ilastik, Imaris	segmentation, total vessel length, vessel mean diameter, vessel straightness, total number of branching points
PEGASOS (22)	whole mouse	αSMA, GS-IB4 isolectin dye, collagen IV	Imaris	vessel density
iDISCO (9)	brain	CD31, podocalyxin, collagen IV, smooth muscle actin, transgelin, von Willebrand factor	ClearMap 2.0, TubeMap	vascular density, vascular orgnaization, vascular remodeling
ethyl-cinnamate (37)	liver, skin, lung, heart, muscles, pancreas, brain, kidney	In-house developed NIR fluorescent dye (MHI148-PEI)	Leica LAS X	segmentation, volume of glomerulus
X-CLARITY (38)	placenta	DiI	Imaris, Image-Pro Premier	N/A

CLARITY, iDISCO (39)	brain	lectin-DyLight, lectin-FITC, anti-CD31	Imaris, segmentation	number of branches, total vessel length, total vessel volume, total vessel area, diameter of single segments per volume, distance between cells and nearest vessel
PEGASOS (40)	bone, teeth	tdTomato	Imaris	blood vessel volume
ScaleS (17)	pancreas	lectin-DyLight	N/A	N/A
CLARITY (41)	retina	Griffonia lectin	Angiotool, ImageJ, Vaa3D, MATLAB, APP-2.0	network tracing, vessel percentage area, total number of junctions, junction density, total vessel length, average vessel length, total number of endpoints, mean lacunarity
No clearing approach (42)	retina, heart	DiI	N/A	N/A
FocusClear (18)	small intestine	DiI	N/A	N/A
FocusClear, ScaleSQ, RIMS, sRIMS (19)	brain	Lectin-Dylight649	MATLAB	optical properties, vascular density
FRUIT 100 (43)	brain tumor	DiI	N/A	N/A
FocusClear (44)	brain	DiI	N/A	optical properties
FocusClear (45)	brain	DiI	MATLAB	functional vascular density

Three-dimensional quantitative analysis of microvasculature imaged in thick tissue sections

Microvascular labeling is performed with an injection of a lectin conjugated to a fluorophore. In our work, we have focused on the DyLight-649 fluorophore. As the lectin travels through the circulatory system, it binds to glycoproteins adjacent to endothelial cells of the vascular wall. This binding allows for labeling of the vascular network within every organ of the body.

An overview of our workflow is outlined below in Fig 2. We administer lectin-DyLight-649 via retroorbital injection. The lectin is allowed to circulate throughout the body prior to cardiac perfusion with saline followed by formalin. Mouse brains are then extracted, bisected into hemispheres, and sectioned into thick (0.5-1.0mm) sections. Each section is then imaged using confocal microscopy to generate image stacks of the complete section throughout its entire thickness. Segmentation is performed by a custom MATLAB (MathWorks, Natick, MA) script. Finally, neuTube, an open-source neuron tracing software, is used to extract diameter measurements of the vessel structures (46). Below, we describe in detail the materials and methods we use.

Fig 2. Workflow for 3D visualization and quantitation of microvasculature in thick tissue sections. A)

Vasculature is labeled via retroorbital injection of lectin-DyLight-649. Brains are then sectioned and

cleared. B) Depiction of z-stack imaging and tile stitching to visualize an entire sample in 3D via confocal

microscopy. C) From left to right: representative example of a raw image of the vasculature, segmented

vasculature via MATLAB, and traced vasculature via neuTube.

Methods

Equipment and supplies

Reagents:
- Saline solution (Aspen Veterinary Resources, NDC No. 46066-807-50)
- 10% formalin solution (Sigma-Aldrich Product Code HT50-1-1)
- PBS with 0.02% sodium azide solution (Syringa Lab Supplies, Part No. 11001)
- Potassium ferrocyanide (Sigma: P3289-500G)
- Hydrochloric acid (Fisher: A144-212)
- Methanol (Fisher: A412S)
- Deionized water
- Dichloromethane (Sigma: 270997-100ML)

153    ● Dibenzyl ether (Sigma: 108014-1KG)
154
155  *Equipment:*
156    ● 2x 10 mL syringes (Sigma-Aldrich: Z683604)
157    ● 1x 23G x ¾ x 12" butterfly needle (Vaculet, 26766)
158    ● 3x hemostat clamps (Excelta: 37SE)
159    ● 1x bone scissors (Fine Science Tools: 91604-09)
160    ● 1x forceps (Fine Science Tools: 11000-12)
161    ● 1x scissors (Excelta: 290)
162    ● 1x angled scissors (Fine Science Tools: 15010-10)
163    ● 1x spatula (Fine Science Tools: 10089-11)
164    ● 1x syringe pump (Harvard Apparatus Model 11 Plus)
165    ● 1x 20 mL glass scintillation vial (Grainger: 3LDT2)
166    ● Aluminum foil
167    ● Tape
168    ● Liquid absorbent mats
169    ● Isoflurane chamber (E-Z Systems: EZ-178)
170    ● Nose cone (E-Z Systems: EZ-103A)
171    ● Magnetic stir plate with stir bar (Corning PC 353 Stirrer)
172    ● Orbital shaker (Scilogex: SK-D1807-E)
173    ● Scale
174    ● Weigh boats
175    ● Pipette controller (Grainger: 49WF85)
176    ● Serological pipette tips
177    ● 1.5 mL opaque microcentrifuge tube (Argos Technologies: 06333-80)
178    ● Microcentrifuge tube rack
179    ● Pipettes
180    ● 18-gauge needle
181    ● Leica TCS SP8 microscope
182
183  *Software:*
184    ● MATLAB (https://www.mathworks.com/)
185    ● FIJI (https://imagej.net/Fiji)
186    ● neuTube (https://www.neutracing.com/)
187
188  *Reagent setup:*
189    ● *10% potassium ferrocyanide (PF) solution*
190      ○ Dissolve the appropriate amount of PF in deionized water (DIW) (10 g of PF per
191       100 mL of DIW) to create a 10% PF solution. Use a magnetic stir bar and
192       magnetic stir plate to dissolve potassium ferrocyanide.
193    ● *20% hydrochloric acid (HCl) solution*
194      ○ Dilute the appropriate amount of stock HCl solution in DIW (20 mL of stock HCl
195       per 80 mL of DIW) to create 20% HCl solution. Perform this step under a fume
196       hood.
197    ● *Potassium ferrocyanide/hydrochloric acid working solution*
198      ○ Mix 1 part 10% potassium ferrocyanide solution per 1 part 20% HCl solution
199

Cardiac perfusion protocol and sample preparation

Cardiac perfusion

Begin by anesthetizing a mouse using an isoflurane chamber with 1.5 L/min of oxygen

and 4.0% isoflurane. Once the mouse is anesthetized, remove it from the chamber and place its

snout in a nose cone at 1.5 L/min oxygen and 1.5% isoflurane. Administer a solution of lectin-

DyLight-649 (200 µL, 25% lectin-DyLight and 75% saline) via retroorbital injection (see Fig

3A,B) (47,48). Allow the solution to circulate for about 20 minutes before proceeding with the

cardiac perfusion (49).

Fig 3. Key steps for animal procedures. A,B) Retroorbital injection diagram. Correct needle placement is

shown. C) Incision points for opening the chest cavity. A lateral incision beneath the diaphragm and a

vertical incision along both sides of the chest opens the chest cavity. The right atrium of the heart is cut,

and a needle is inserted into the left ventricle (47,50).

It is recommended to perform the cardiac perfusion on a surgical tray or similar platform

to contain the exsanguinated blood. Confirm that the mouse is at an appropriate plane of

anesthesia using toe and/or tail pinches. Next, open the chest cavity by performing a horizontal

incision beneath the rib cage and a vertical incision along both sides of the chest (see Fig 3C)

(47). Use hemostats to assist with holding the chest open to access the heart. Then, perform a

small incision on the right atrium of the heart to allow blood to exit the body. This is followed by

inserting a butterfly needle into the left ventricle of the heart. Use a syringe pump to perfuse 10

221 mL of saline into the heart at a rate of 2 mL/min. Afterwards, perfuse 10 mL of formalin at a rate

222 of 2 mL/min.

224 **Brain extraction**

225  Remove the head by cutting caudal of the skull with scissors (bone scissors or large

226 scissors preferred). Cut the scalp to create two folds and expose the cranium. Using angled

227 microscissors, gently cut upwards from the foramen magnum to approximately the location of

228 bregma on the brain. Using a set of scissors, perform a lateral cut directly rostral to the olfactory

229 bulbs. This cut should split the remainder of the skull down the centerline beyond bregma. Use

230 fine tweezers or a spatula to pry open each hemisphere of the skull. Gently separate the brain

231 from the base of the skull with a spatula. Sever any nerves connecting the brain to the skull.

232 Place the brain in ~10 mL of 10% formalin to completely submerge the brain. After 24h, store

233 the brain in PBS with 0.02% sodium azide at 4°C until further tissue processing.

235 **(Optional) Exogenous labeling of hemosiderin with Prussian blue for**

236 **cerebral microhemorrhage visualization**

237  The following procedures are based on 1-mm thick coronal sections of a bisected brain.

238 Volumes and times may need to be adjusted for tissues of different sizes.

239  Prepare a working solution of 10% w/v of potassium ferrocyanide (10 g of potassium

240 ferrocyanide per 100 mL of DIW). Use a magnetic stir plate to mix the solution for at least 20

241 minutes. Next, prepare a working solution of hydrochloric acid that is 20% of stock hydrochloric

242 acid. Mix the solutions of potassium ferrocyanide and hydrochloric acid in a 1:1 ratio.

243 Approximately 5 mL of the mixed solution is used per sample. This solution should be prepared

244 prior to each staining session.

245  Wash samples in 5 mL of DIW with shaking. Submerge each sample into 5 mL of the

246 working potassium ferrocyanide/hydrochloric acid solution for 1 hour. Afterward, perform a final

247 DIW wash for 5 minutes. Store the samples in PBS with 0.02% sodium azide at 4 C°.

Tissue clearing

The following procedure is modified from the established iDISCO protocols (4). Wash

durations were modified for 1-mm thick coronal sections of a bisected brain.

Perform a series of methanol washes (20%, 40%, 60%, 80%, 100%, and 100%, balance

DIW) each for 20 minutes with shaking. Microcentrifuge tubes of 1.5 mL (or larger for larger

samples) are recommended. Fill the tubes fully to minimize exposure to oxygen. Next, incubate

the samples in a solution of 66% dichloromethane and 33% methanol for one hour with shaking.

The sample may be stored overnight in this situation if desired, without shaking. Next, incubate

the sample in dichloromethane twice for 15 minutes with shaking. Lastly, store the samples in

dibenzyl ether at 4°C until imaging.

Imaging with confocal microscopy

When imaging samples that have been cleared following the iDISCO protocol, it is

recommended to image the sample while submerged in dibenzyl ether. There are various

methods to safely house a sample with dibenzyl ether and protect the imaging objective. A

straightforward method is to create an epoxy well on a cover glass to surround the sample and

hold the dibenzyl ether.

To image the vasculature labeled with the lectin-DyLight-649, use an appropriate

wavelength (633 nm can work) with an emission band of approximately 650-750 nm. To

visualize microhemorrhages labeled with Prussian blue, locate regions of Prussian blue

positivity using a white light source. Simultaneously collect a fluorescent image of the

vasculature and a transmittance image to co-register the vascular fluorescence with cerebral

microhemorrhages. This workflow along with representative images are depicted in Fig 4.

Fig 4. Workflow for 3D visualization of cerebral microvasculature cerebral microhemorrhage in thick

tissue sections. A) Vasculature is labeled via retroorbital injection of lectin-DyLight-649. Brains are then

sectioned, stained, and cleared. B) Depiction of z-stack imaging and tile stitching for a fluorescence

channel and a transmission channel via confocal microscopy. C) From left to right: fluorescent image of

microvascular network in a 70 µm thick tissue region, transmission image of cerebral microhemorrhage in

the same tissue region, overlayed image of both imaging channels, eyepiece view of Prussian blue

positive cerebral microhemorrhage. Scale bars are 100 µm.

In addition to imaging brain microvasculature, the combination of iDISCO and lectin-

DyLight-649 enables visualization of the microvascular network of other organs. Light-sheet

microscopy can be used as an alternative to confocal microscopy to rapidly generate 3D

reconstructions of the vascular network with minimal photobleaching. Fig 5 shows

representative images of different labeled and cleared organs imaged with confocal microscopy

and light-sheet microscopy.

Fig 5. Lectin-DyLight-649 labeling and iDISCO optical clearing enable detailed visualization of mouse

organ microvasculature. A) Confocal image of a 1-mm thick coronal hemisection of the brain. A')

Magnified view of A. B) Light-sheet image of a mammary gland with a lymph node. B') Magnified view of

B. C) Light-sheet image of a bladder. C') Magnified view of C.

Vascular segmentation

There are various segmentation methods to isolate the fluorescent vasculature from the

image background. The iterative selection thresholding method was implemented to binarize the

fluorescent images (Fig 6) (51). This algorithm was selected due to its simplicity and objectivity

and was performed using custom-written code in MATLAB. Vessel parameters such as vascular

density and tortuosity can be calculated from the resulting segmented images. An open-source

neuron tracing software known as neuTube was used to quantify vessel sizes.

Fig 6. Schematic of iterative selection thresholding method for images of fluorescent vasculature. An

initial threshold is selected as the average of the maximum and minimum voxel intensities present in the

image. The subsequent iteration assigns voxels to group A_n if a voxel has an intensity greater than the

threshold of the previous iteration, or to group B_n if a voxel has an intensity less than the threshold of the

previous threshold. Next, the average intensity within each group is calculated, and the average of those

two values determines the new threshold. This process is repeated until the change in threshold is less

than one intensity value. Scale bar is 25 µm.

Using MATLAB, a 3x3x1 median filter removes noise within the image data. The iterative

selection threshold method is applied by selecting an initial threshold value, T_0. The initial value

is the average value of the maximum intensity and the minimum intensity of all voxels of an

image.

314
$$T_0 = \frac{Max + Min}{2} \quad (1)$$

All voxels within an image are separated into two groups: group A_n if a voxel has an intensity

equal to or greater than the threshold value of the previous iteration, or group B_n if a voxel has

an intensity below the threshold value of the previous iteration.

$$A_n \geq T_n, B_n < T_n \quad (2)$$

The threshold value of the subsequent iteration is calculated as the average value of the

average intensity within groups A_n and B_n.

$$T_n = \frac{\overline{A_n} + \overline{B_n}}{2} \quad (3)$$

This threshold value is compared to the threshold value of the previous iteration. If the

difference between the two values is less than 1, the procedure is complete, and the current

threshold value is selected. If the difference between the two values is greater than or equal to

1, the procedure repeats for another iteration.

$$If \ |T_n - T_{n-1}| < 1, then \ stop \quad (4)$$

Optional morphological operations can be applied to the resulting binarized image to

adjust segmentation results further. The exact parameters for these steps will vary with image

acquisition parameters (particularly resolution).

For example, size filtering is performed by removing objects with a volume less than ~50

μm^3 (the exact voxel size will vary based on image resolution) based on an 18-point connectivity

scheme. Morphological closing using a spherical structural element with a radius of 1 is applied

to close gaps throughout the image. Vascular density can be quantified through built-in

MATLAB functions to generate a skeletonized structure, a single-pixel width line along the

centerline of vessels, of the vascular image (21). From there, density can be calculated by

dividing the total length of the skeleton by a given area. Vessel tortuosity can be calculated by

dividing the shortest distance between two endpoints of a vessel and the total length of the

vessel (52). A complete vessel is defined as the length of the vessel between two branch points.

neuTube tracing to quantify vessel diameters

neuTube is an open-source neuron tracing software that can be applied to tracing

tubular structures, such as vasculature (46). Automated tracing can be performed on binarized

vasculature images in TIF file format. neuTube will output information in an SWC format where

tubular structures are simplified into individual nodes with x, y, z coordinates, a radius, and node

connectivity information. Each node will be a 'parent' to an adjacent 'child' node which provides

the necessary information to understand how these nodes are connected in space.

Nodal connectivity is used to identify individual vessels based on specific rules. Nodes

are defined as branch nodes if they serve as the parent of two different nodes. A node is

defined as an end node if it lacks a child node. Individual vessels are defined as a series of

nodes bordered by two branch nodes or one branch node and an end node, including the nodes

at the borders. The diameter of an individual vessel is defined as the average diameter of all

nodes that make up an individual vessel.

Anticipated results

The procedures detailed herein present a simple method for producing optically-cleared

(>1-mm thick) tissue samples with fluorescently labeled vasculature. Samples can then be

imaged to generate 3D images of the microvasculature. Our presented results are primarily from

brain samples, but the procedures can be easily translated to other organs. The described

segmentation method using custom MATLAB scripts and neuTube presents an automated

method to convert the fluorescent images into binary images. The binary images can then be

used to characterize microvasculature by quantifying vessel density and vessel sizes. The

procedures here can be enhanced by using additional histology dyes or immunohistochemistry

to label biomarkers or other structures of interest in tissue. In doing so, one can visualize and

quantify the microvasculature surrounding these biomarkers to gain insight into their relationship

to each other.

372 Validation

373 Segmentation results

Manually segmented images were used as a ground truth comparison of automated

segmented images. Images from various brain sections across three different animals were

used. Each section was imaged by collecting a stack of images that spans the entire thickness

of the section. Automated segmentation was performed on each image stack. In addition,

manual segmentation was performed on 50 randomly generated ROIs across all images. Each

ROI was presented as a maximum intensity projection (MIP) image of a 50x50x5 voxel

(113x113x38 µm) region. A MIP is used to present a 2D image that is more feasible for tracing.

One author [DFX] was tasked with using MATLAB to outline every object within the image that

the author determined to belong to a vessel. The corresponding 50x50x5 voxel region MIP from

the automated segmented image was compared. Four representative examples of this are

depicted in Fig 7. Across the 50 ROIs, the average sensitivity was 80±8%, and the average

specificity was 90±5%. The Dice similarity coefficient between manually segmented and

automated segmented images was calculated across all ROIs. This coefficient can measure

similarity between two sets of Boolean data and ranges between 0 and 1, where 1 represents

identical data, and 0 represents opposite data (53). The average Dice similarity coefficient

across 50 ROIs was 0.71±0.07.

Fig 7. Manual and automated segmentation results. Four examples of different 50x50 pixel regions are

shown. Scale bar is 25 µm.

Diameter results with neuTube

Manually measured diameters of individual vessels were used as a ground truth

comparison for neuTube approximated vessel diameters. Images from various brain sections

across three different animals were used. One author (DFX) was presented with a randomly

generated 50x50x5 voxel (113x113x38 µm) size region as a MIP. Within the image, the user

was tasked with using MATLAB to estimate the diameter of a single vessel in the image at five

different points along the vessel by drawing lines approximately perpendicular to the centerline

of the vessel. In neuTube, five nodes along the corresponding vessel were selected. The

average of the five manual diameter measurements via MATLAB and the five automated

diameter measurements via neuTube were compared. Two representative examples of this are

depicted in Fig 8. The absolute difference between diameter measurements was 1.16±0.73 µm

(n=50 vessels of diameters ranging from 1.78 µm to 3.19 µm).

Fig 8. Manual and neuTube diameter results. Two different 50x50 pixel regions are shown,

where one vessel is selected for manual measurement. Scale bar is 25 μm.

Potential applications

As angiogenesis occurs in organs, endothelial cells respond to local signals to adapt

vessels to the surrounding environment (54). Angiogenesis plays an essential role in tumor

formation. In tumors, angiogenesis directly impacts tumor growth and metastasis.

Overexpression of proangiogenic factors leads to uncontrolled vascular growth in tumors (55).

As a result, anti-angiogenic drugs are frequently used as a potential treatment option for cancer.

Lectin-DyLight-649 combined with iDISCO presents a robust procedure for labeling the

microvasculature in all areas in the body, including tumors. Changes in vessel density,

tortuosity, and diameters can be quantified to evaluate the efficacy of novel anti-angiogenic

treatments.

Ischemic strokes occur when there is a significant drop in cerebral blood flow due to

occlusion in a cerebral artery. A major consequence of such an event is necrosis of neurons

due to deficient blood supply (56). A method to visualize the microvascular network and the

surrounding neurons, astrocytes, and glial cells can provide a detailed 3D snapshot of the brain

in response to an ischemic stroke and monitor potential treatments over time.

In addition to visualizing cerebral microhemorrhages within the surrounding

microvascular network and providing improved capability to estimate size range of these

lesions, our approach can provide enhanced imaging for other disease entities. For example, a

growing body of literature suggests a contribution of dysfunctional regulation of cerebral blood

flow and various types of cognitive impairment (3). The ability to visualize the cerebral

microvasculature in three dimensions offers a new gateway potentially leading to the

identification of novel treatment targets for neurological disorders.

Disclosures

434 The authors do not have any competing interests to disclose.

Acknowledgements

This work was supported in part by the Arnold and Mabel Beckman Foundation and the National

Institutes of Health (Nos. R21AG066000, 5TL1TR001415-07, P41EB015890, R01NS020989,

and R21NS111984). This study was made possible in part through access to the Optical

Biology Core Facility of the Developmental Biology Center, a shared resource supported by the

Cancer Center Support Grant (CA-62203) and Center for Complex Biological Systems Support

Grant (GM-076516) at the University of California, Irvine

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