Whole hippocampus high-resolution optical imaging

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Advanced microscopy methods for neuroscience

Biomedical label-free imaging

Single-molecule biophysics



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Optical techniques: serial two-photon microscopy (STP)



Osten and Margrie, Nat Meth 2013

In serial two-photon imaging the brain is imaged with a scanning two-photon microscope up to a depth of several hundredths of microns, and then sliced away.

Pros

- High resolution
- High sensitivity

Cons

- Limited penetration depth in fixed tissue (about 50-100 μm)
- Sparse axial sampling (1 μm every 50): in fact the initial layers are damaged by the cut, and the deep ones are not imaged clearly.



A new versatile clearing method: 2,2' Thiodiethanol (TDE)



Costantini et al., Sci. Rep., in press

3D reconstruction of TDE cleared hippocampus with two-photon serial sectioning



- Micrometric resolution
- <u>NO loss of information</u>







Scale bar 10 µm

Thy1-GFP-M transgenic mouse

Scale bar 50 µm

3D reconstruction of TDE cleared hippocampus with two-photon serial sectioning

Tracing of single neurons elongating through the entire hippocampus





IHC labeling + STP

1 mm GFP-M mouse brain slice processed with CLARITY, immersed in TDE, and imaged with STP.

The sample was immunostained with an anti-GFP IgG alexa fluor 594 conjugate (FOV=266 x 266 μ m, z-step=5 μ m, depth=400 μ m, λ = 820nm) Acquisition time: 6 minutes

Green channel: GFP Red channel: anti-GFP antibody



Optical techniques: confocal light sheet microscopy (CLSM)



TL = tube lens, L = lens, FF = fluorescence filter

Silvestri et al., Opt. Exp. 2012

CLSM

A new versatile clearing method: 2,2' Thiodiethanol (TDE)

2. Whole-brain clearing in combination with CLARITY

Step 1: hydrogel monomer infusion (days 1-3)

4°C

37 °C

 \ominus



Costantini et al., Sci. Rep., in press

2-3000\$/sample

20-30\$/sample

TDE is a valid alter index matching in TDE is a valid alter index matching in Focus clear TDE is a valid alter index matching in Focus clear

Chung et al., Nature 2013

TDE is a valid alternative to FocusClear for refractive index matching in the CLARITY method.

20\$/ml

0.2\$/ml

Whole-brain imaging with light sheet microscopy



A 2nd generation light sheet microscope has been built <u>S/N improved by a factor 20</u> 3D rendering from a PV-dTomato mouse brain (parvalbuminergic neurons labeled)

Main features:

- Double-side illumination
- Optimized optics for CLARITY solution
- Confocal slit detection
- Multi-color imaging

Whole-brain imaging with light sheet microscopy



PV: PV-dTomato mouse (parvalbuminergic neurons labeled) GAD: GAD-dTomato mouse (GABAergic neurons labeled) PI: propidium iodide staining (all nuclei labeled) Vasc: vasculature filling with FITC-albumin

Scale bar 100 μm

Costantini et al., Sci. Rep., in press

Image management and processing

- 10 Gb/s dedicated connection from LENS to CINECA
- Connection from LENS to Juelich via CINECA (using PRACE infrastructure)
- Data production now: about 2-3 TB per week
- Data production forecast (M18): 20 TB per week

Stitching Teravoxel-sized images: TeraStitcher



Bria et al., BMC Bioinformatics (2012) http://github.com/abria/TeraStitcher

TeraFly

Controls Volume Sur/Moject Othes Volume Mark Market Image Ander And

Peng et al., Nat. Prot. (2014) - a google-maps inspired brain navigation tool Available as plugin of Vaa3D <u>http://www.vaa3d.org/</u>

Automatic cell localization

A point-cloud view of 224222 Purkinje cells in the cerebellum of a mouse.

The software performs a "semantic deconvolution" of the images through a supervised neuronal network to enhance features of interest (cell bodies) and weaken other structures. After this step a **k-means algorithm** is used to localize soma center. The limited memory usage of the software (compared to standard segmentation approaches) makes it highly scalable to large datasets.

This dataset is being integrated into the HBP mouse brain atlas

Measured performance: Precision [TP/(TP+FP)] 95% Recall [TP/(TP+FN)] 97%

TP = True Positives FP = False Positives FN = False Negatives

Frasconi et al., Bioinformatics (2014)

An integrated pipeline for Big Data analysis



Data (2-3 TB per single imaging dataset) are physically stored @ CINECA. Software tools for data processing, information extraction and atlasing are deployed there (a new HPC machine dedicated to Big Data analytics – PICO – has just been set up). Data will be accessible outside through the HBP portal.

Human brain tissue preparation

Uncleared brain



After polymerization



After passive clearing



- Passive CLARITY protocol treating (hydrogel incubation, degassing and passive clearing) of a human brain block of a patient with hemimegalencephaly (HME) (~ 0,8 x 0,8 x 0,4 cm)
- Performing immunostaining protocol with different antibodies
- Clearing the sample with TDE 47%
- Imaging with two-photon fluorescence microscope

3D reconstruction of neurofilaments in human brain

Tracing of fibers, immunostained with anti-PV antibody, elongating through a volume of 1 mm³



STP + optical clearing

- Imaging of moderately large areas (imaging the whole hippocampus takes about 2 weeks)
- Molecular specificity (transgenic animal or IHC)
- Manual morphology discrimination
- Manual long-tract axonal tracing (not for all axons)
- ✓ Automatic cell counting
- × Morphology reconstruction
- ✗ Non-fluorescence labeling

Light sheet microscopy

Imaging of whole mouse brains (about 2 days per samples)

Molecular specificity (transgenic animal)
– ICH over whole mouse brains requires months

- Manual morphology discrimination
- Manual bundle tracing
- Automatic cell counting
- X Morphology reconstruction
- ✗ Non-fluorescence labeling

People involved and collaborations

Florence: LENS and University

Francesco Saverio Pavone (Principal Investigator) Leonardo Sacconi (light sheet microscopy and serial two-photon) Anna Letizia Allegra Mascaro (serial two-photon) Marie Caroline Muellenbroich (light sheet microscopy) Irene Costantini (clearing methods) Antonino Paolo di Giovanna (serial two-photon) Paolo Frasconi (automatic cell localization)

Rome: University Campus Bio-medico

Giulio Iannello (image stitching) Alessandro Bria (image visualization)

École Polytechnique Fédérale de Lausanne

Jean-Pierre Ghobril (vasculature and brain mapping) Henry Markram (brain mapping)

University of Zurich

Bruno Weber (vasculature mapping) Matthias Schneider (vessel segmentation)

University of Edinburgh

Fei Zhu (synaptic puncta mapping) Seth Grant (synaptyic puncta mapping)

Seattle: Allen Institute for Brain Sciences

Hanchuan Peng (image visualization)

Florence: Meyer Paediatric Hospital

Renzo Guerrini (human brain samples) Valerio Conti (human brain samples)

Juelich: Forschungszentrum

Katrin Amunts (human brain mapping) Karl Zilles (human brain mapping)

Human brain imaging

Immunostaining with antibodies against parvalbumin (**PV**) and glial fibrillary acidic protein (**GFAP**) and **DAPI**. Double labelling with the combination of them

PV in red; GFAP in magenta; DAPI in green . Scale bar = $50 \mu m$

Human brain imaging

Human brain sample: nuclei in green (DAPI), neurofilament in red (anti-PV/Alexa 568)

(FOV=1 x 1 mm, z-step=2 μ m, depth=400 μ m, λ = 800nm)

Multi round immunostaining

PV and DAPI GFAP and DAPI Scale bar = 300 μm

Human brain imaging

1 mm³ thick block of a formalin-fixed tissue of a patient with hemimegalencephaly (HME), treated with passive CLARITY protocol, PV immunostained and cleared with TDE 47% (20X Scale objective).

Scale bar = 50 μ m

Synaptic puncta density measurement with STP

Mouse brain tissue cleared with TDE and imaged with STP. This is a transgenic mouse in which PSD95 is labeled with GFP, so synaptic puncta becomes visible.

Voxel size 0.26x0.26x1 µm³

Possible 3D density map reconstruction over large volumes (whole hippocampus)

Data obtained in collaboration with Fei Zhu and Seth Grant, Univ. of Edinburgh

