# A METHOD FOR ESTIMATING SAMPLE IMAGE RESOLUTION

Ryuta Mizutani[1], Rino Saiga[1], Susumu Takekoshi[2], Chie Inomoto[2], Naoya Nakamura[2], Makoto Arai[3], Kenichi Oshima[3], Masanari Itokawa[3], Akihisa Takeuchi[4], Kentaro Uesugi[4], Yasuko Terada[4], and Yoshio Suzuki[5]

*1Department of Applied Biochemistry, Tokai University, Hiratsuka, Kanagawa 259-1292, Japan*
*2Tokai University School of Medicine, Isehara, Kanagawa 259-1193, Japan*
*3Tokyo Metropolitan Institute of Medical Science, Setagaya, Tokyo 156-8506, Japan*
*4Japan Synchrotron Radiation Research Institute (JASRI/SPring-8), Sayo, Hyogo 679-5198, Japan*
*5Graduate School of Frontier Sciences, University of Tokyo, Kashiwa, Chiba 277-8561, Japan*

**Abstract**

Spatial resolution is a fundamental parameter in structural sciences. Although edge profile are used for estimating the spatial frequency response of optics, the resolution of the sample image depends on a number of experimental factors, including stage drift and sample condition. Therefore, the resolvability of the sample image should be determined from the sample image itself. In this paper, we report a method for estimating the spatial resolution of a sample image without defining a noise level criterion [1].

Test images were generated by convolving a Gaussian point-spread function (PSF) and the original images. The test images were then analyzed by plotting logarithmic intensities of their Fourier transforms. The results indicated that the full width at half maximum (FWHM) of the applied PSF is proportional to the slope of the plots.

Imaging x-ray microtomography using Fresnel zone-plate optics was examined with this method. A cross section of square-wave test patterns [2,3] visualized with imaging microtomography indicated that patterns up to 100-120 nm pitch were resolved (Figure 1). The logarithmic intensity plot was calculated from a tomographic cross section of brain tissue. The FWHM of the point-spread function estimated from the plot was 118 nm (Figure 2), which coincides with the resolution determined from the test patterns.

The resolutions of real images have been estimated from the detection limit of signals against the noise level in the Fourier domain, although there are a number of variations in noise level criteria and hence the resultant resolution. In contrast, the logarithmic intensity plot provided a sound estimate without explicitly defining any criterion. We suggest that the logarithmic intensity plot in the Fourier domain provides a resolvability measure regardless of visualization modality.

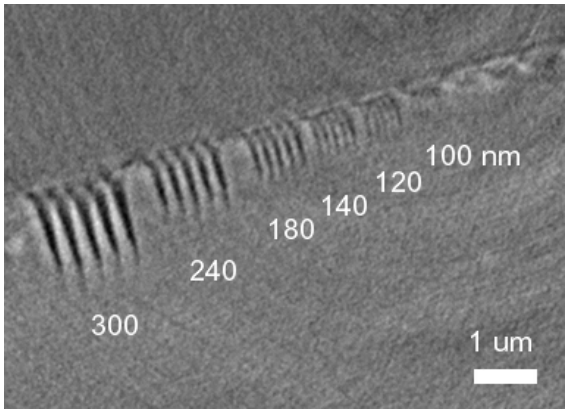


**Figure 1:** X-ray microtomographic cross section of aluminum square-wave patterns with pitches of 300, 240, 180, 140, 120 and 100 nm.

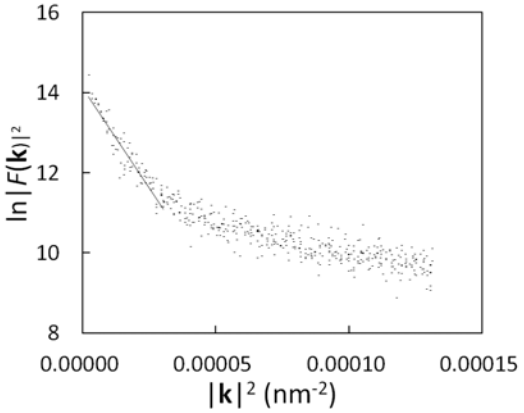


**Figure 2:** Logarithmic intensity plot of brain tissue image. The linear correlation at the left end can be regarded as representing a Gaussian PSF with 118-nm FWHM.

**References**

[1] R. Mizutani et al., J. Microsc. 261, 57-66 (2016).
[2] R. Mizutani et al., J. Synchrotron Radiat. 15, 648-654 (2008).
[3] R. Mizutani et al., Nucl. Instrum. Methods Phys. Res A621, 615-619 (2010).

# MOUSE BRAIN NETWORK VISUALIZED WITH X-RAY MICROTOMOGRAPHY

Rino Saiga[1], Masato Ohtsuka[2], Masato Hoshino[3], Akihisa Takeuchi[3], Kentaro Uesugi[3], and Ryuta Mizutani[1]

*1Department of Applied Biochemistry, Tokai University, Hiratsuka, Kanagawa 259-1292, Japan*
*2Tokai University School of Medicine, Isehara, Kanagawa 259-1193, Japan*
*3Japan Synchrotron Radiation Research Institute (JASRI/SPring-8), Sayo, Hyogo 679-5198, Japan*

**Abstract**

The brain is composed of a large number of neurons, which constitute a 3D network. The first step to understanding brain function is to determine the network structure. We report here a 3D analysis of a murine brain network by x-ray microtomography.

Soft tissues are composed of light elements, which produce little contrast in a hard x-ray image. Therefore, contrast should be enhanced to visualize cellular structures. We have reported a number of methods for labeling cellular structures with high-Z elements [1,2]. Another way to visualize cellular structure is lowering the intensity of the surrounding extracellular matrix, giving a contrast between the target structure and its background. This can be achieved by removing water from the tissue. In this study, murine brain hemispheres were immersed in t-butyl alcohol and then subjected to lyophilization so as to reduce the intensity of the background matrix. The resultant brain was visualized with x-ray microtomography at the BL20B2 beamline of SPring-8.

A cutaway section of the obtained 3D structure is shown in Figure 1. Fibrous structures were clearly observed in the striatum (Figure 2), indicating that axonal tracts can be visualized with this method. The tracts were traced to build a network model of the brain. Further analysis of this network should be able to delineate the functional mechanisms of the murine brain.

**Figure 1:** A coronal cutaway rendering of murine brain hemisphere. X-ray attenuation coefficients were gray-scaled from 0.9 $cm^{-1}$ (black) to 3.4 $cm^{-1}$ (white). Anterior view.

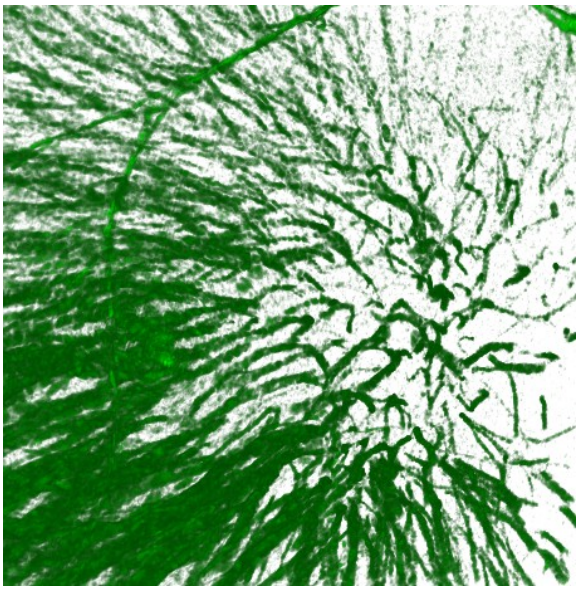

**Figure 2:** Axonal tracts observed in the striatum. X-ray attenuation coefficients in a 1.0 x 1.0 x 0.4 mm volume were rendered from 1.6 $cm^{-1}$ to 3.4 $cm^{-1}$. Posterior view.

**References**

[1] R. Mizutani et al., J. Synchrotron Radiat. 15, 374-377. (2008).
[2] R. Mizutani et al., Cerebral Cortex 20, 1739-1748 (2010).