The Japanese monkey (Macaca fuscata) is a medium-sized monkey species of the genus Macaca. There is an international trend toward not using anthropoid apes such as chimpanzees and gorillas for invasive experiments and research in the future, and macaques are the closest relatives to humans among animals that are used for experiments and research. In particular, many brain science researchers have used Japanese monkeys for their research in Japan. One reason is that the Japanese monkeys that have been caught to prevent crop raiding are provided free of charge to researchers. Other reasons include their gentleness, which makes them easy to handle as experimental animals, and their high intelligence quotient, which many researchers think makes them suitable for higher brain function research. At present, animals caught from their natural habitats are almost impossible to use for experiments and research. Because the National BioResource Project (NBRP) has established a system to supply macaques bred for research, brain science research can now be smoothly pursued.

Humans and other higher primates are said to have explosively evolved after acquiring the ability to move fingers skillfully. The ability to skillfully move each finger individually is considered to have been acquired because the motor areas of the cerebral cortex are directly connected with the motor nerve cells in the spinal cord, which control muscles. However, in animals whose finger development is primitive and finger movement is unskillful, such as cats and rats, motion command output from the cerebral cortex is indirectly connected with the motor nerve cells in the spinal cord through interneurons in the spinal cord. This “indirect pathway” still remains in primates, but its purpose has not been clearly elucidated. Is the “old pathway” that has been left behind in the evolutionary process used in the brain of higher animals or restrained because it is obstructive? This issue has been discussed many times but has not been resolved.

Recently, a joint research team comprising Professor Tadashi Isa and Assistant Professor Masaharu Kinoshita of the NIPS, National Institutes of Natural Sciences, Professor Kazuto Kobayashi of Fukushima Medical University, and Professor Dai Watanabe of Kyoto University combined two types of new viral vectors to develop a new method of pathway-selective gene transfer (the double-gene transfer method). By using this method, the team succeeded in selectively restraining spinal interneuronal systems (proprispinal neurons) that relay the indirect pathway (Fig. 1).
When the spinal interneuronal systems were selectively restrained, skillful movements of fingers were clearly impaired by the second day after the restraint (Fig. 2). However, functional compensation rapidly occurred through other pathways, and skillful movements of fingers had almost entirely recovered at the fifth day after the restraint. Therefore, the ‘indirect pathway’ was revealed to play an important role in skillful finger movements. Thus, this long-term question was finally settled.

The key element in the above research was the combination of two types of new viral vectors to develop a new technology to selectively and reversibly interrupt a specific neural circuit.

Previously, a specific neural circuit could be selectively manipulated in mice, in which genetic modification was possible in the germ cells, but could not be selectively manipulated in primates. The newly developed method enabled the selective manipulation of a neural circuit in animal species, whose genetic modification had been difficult, so the method has attracted the interest of researchers worldwide. In addition, because of the above-mentioned research achievements, Professor Isa, Professor Watanabe, and Professor Kobayashi received the Commendation for Science and Technology by the Minister of Education, Culture, Sports, Science and Technology 2013.

Let’s visualize data (using D3.js)

Research data has become massive and complex in recent years, and data visualization tools that use graphs and charts are becoming increasingly important to represent data that continuously changes over time, and to facilitate the quick identification of target data. In this edition, I would like to introduce “D3.js,” a useful visualization tool for such scenarios.

What is D3.js?

D3.js or Data Driven Document (http://d3js.org) is a JavaScript library for manipulating HTML documents based on data, and it facilitates the interactive representation of data. In addition, the official website (Fig. 1) has samples of complex graphs, figures, and animations, most of which can be rendered at sufficient speeds even when they are viewed on a smartphone.

Let’s give it a try

On the gallery website (Fig. 2), you can experiment with a variety of samples. When writing your own programs, you can refer to the source codes which are available for most examples.


How to Use D3

You need to include the D3.js library for manipulating HTML documents using DOM(1). In addition, you also need to define data and select a design for visualization when using D3.

Dynamically create interactive elements through DOM

Example 1: Co-occurrence Graph

Example 2: Partition Layout

D3 stand for Document Object Model and it is a convention for programmatically interacting with HTML elements (tags) such as div and img.

Fig. 1: Official website

Fig. 2: Gallery website

You can use DOM and D3.js to create websites which displays data that changes continuously over time. It can be difficult to use this tool initially because it involves some programming. However, once you have familiarized yourself with the tool, it is easy to create beautiful graphs and other visual representations.

National BioResource Project “Yeast”

DB name: NBRP Yeast
URL: http://yeast.lab.nig.ac.jp/nig/index_en.html
Language: Japanese, English

Original contents:
Yeast resources for research
- Fission yeast (strains, plasmids, libraries, full length cDNA, genomic DNA clones)
- Budding yeast (strains, plasmids, genomic DNA clones, gTOW6000)
- Yeast information from literature
- Paper information on resource development and research achievements using resources

Other contents:
- GenomeViewer (fission yeast, budding yeast), BLAST
- Resources can be ordered from the website.
- Resources can be accessed from Viewer
- YeastDB construction group: NBRP Yeast, NBRP Information Management organization: Genetic Resource Center, NIG

Comment from a practicing developer: The NBRP Yeast includes globally top-class information on the abundant resources conserved in the Yeast Genetic Resource Center. The number of resource species has steadily increased. We have received many resource orders and inquiries, so we feel that the NBRP Yeast is an effective database. The database working group has a plan to rewrite the website based on the large amount of insights accumulated during the operation of the database for nearly 10 years.

BioResource Information

(NBRP) www.nbrp.jp/
(SHIGEN) www.shigen.nig.ac.jp/
(WGR) www.shigen.nig.ac.jp/wgr/
(JGR) www.shigen.nig.ac.jp/wgr/jgr/jgrUrlList.jsp

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