

BioResource Now!

Issue Number 7 October 2011

Announcements
 The 34th Annual Meeting of the Molecular Biology Society of Japan
NBRP Panel Exhibitions with Realia: "Full Array of Bioresources"
 Date : Date: December 13 (Tue.) -16 (Fri.), 2011.
 9:00 - 17:00 (until 14:00 on the final day)
 Place : NBRP section at the poster exhibition site (Exhibition Hall at Pacifico Yokohama)

News from Resource Information Center

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News from Resource Information Center

We announced the initiation of the 2nd stage of the National BioResource Project (NBRP) in the April 2007 issue; however, presently, NBRP is already in the latter half of the last year of the 2nd stage and about to enter the 3rd stage. The resources and databases of the project have been well-developed, and in this newsletter, I would like to introduce recent events regarding the NBRP.

R Representative institutions for 27 model organisms participated in the NBRP. The 27 organisms include animals (mice, rats, *Xenopus tropicalis*, zebrafish, medaka, *Ciona intestinalis* and *Oryzomanthus japonicus*, silkworms, *Drosophila*, *Caenorhabditis elegans*, and Japanese macaques); plants (rice, wheat, barley, *Arabidopsis*, tomato, *Lotus* and *Glycine*, morning glory, *Chrysanthemum*, and algae); microorganisms and others (cellular slime molds, yeast, prokaryotes [*Escherichia coli* and *Bacillus subtilis*], pathogenic microorganisms, general microbes; human embryonic stem cells; animal cells; and DNA material). These organism groups were selected primarily on the basis of the frequency of use in basic scientific research, the number of individuals involved in research on these organisms, and the indigenesness to Japan. Our information center was collaborating with all the resource institutions to spread the knowledge gained from research to the scientific community at large and to promote the application of this knowledge.



R As of October 2011, a total of approximately 5.5 million resources were maintained for the NBRP (Fig. 1-A: 2 million resources maintained in 2007), and the NBRP database had approximately 170,000 users per month (100,000 users existed in 2007). In the 2nd stage of the NBRP, we particularly focused on collecting research articles written by using the NBRP resources and have so far collected 7,700 papers (Fig. 1-B). This is the result of cooperation from the users and the enthusiastic information-gathering activity of the resource institutions; however, the collection percentage of the articles is not necessarily high, and thus, additional efforts need to be taken. All the information, including "Evaluation Reports," is available at the NBRP publication website (www.nbrp.jp).

R All the databases have been well-developed. I would like to introduce each database in a separate issue of the newsletter next year, since the space is too limited for introduction of all the databases at once. Therefore, in this issue, I will give an overview of the project and the resource integrated search site, Bio Resource World (BRW), which has been provided by the information center.

R Readers may wonder specifically about the kind of resource information available. The center provides information on available resources (what), their locations (where), and procedures to obtain them (how). Information on "what" includes the name of each resource, identification code, history, genetic background, DNA sequence, related gene information, morphological characteristics (including images), related journal articles, and handling procedures. The available information is different for different species and also varies depending on the resource type, even in case of same species. A database containing resource types in columns and resource information in rows, is expanded by resource institutions primarily by accumulating the information contained in the rows. The information center mainly focuses on facilitating the cross-sectional use of information across the columns that is called the BRW. In the NBRP homepage, users can search information both by rows (Fig. 1-C) and columns (Fig. 1-D).

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Fig. 1 - A **Fig. 1 - B** **Fig. 1 - C** **Fig. 1 - D**

Fig. 1 : NBRP Information website

Fig. 2-1 **Fig. 2-2** **Fig. 2-3** **Fig. 2-4**

Fig. 2 : NBRP BRW

R Through BRW, we currently provide 4 types of services: keyword search (Fig. 1-D, Fig. 2-1), DNA sequence-based homology search (Fig. 2-2), search by gene ontology (GO) (Fig. 2-3), and references search (Fig. 2-4). Although we are still in the process of collecting information for the GO and references search and available information is considered inadequate, the usability of these services can probably be expanded to a great extent in the future for the following reasons. For example, keyword search is often ineffective for finding 2 or more genes that have the same function but are named differently depending on the species; however, the GO search in which such genes are tagged with a single ID that represents their common function (or meaning) allows users to search genes with a common function by using any of the gene names for these genes from among the organisms contained in the database.

Although, so far, searching only by keywords in titles is available in the references search, we can use medical subject headings (MeSH: ontology of terminologies) provided by PubMed for purposes such as grouping of the articles focusing on similar subjects and also to correlation of the field of research with the resources used.

R The information center is also planning to introduce additional search functions so that users can search by phenotype ontology, genes related to human diseases, metabolic maps, or images, thereby providing multiple ways for the users to access resource information. I hope that external databases will also make up for the limitations in our database.

R In fact, answers to questions raised by users exist in the resources. Thus, resources provide clear answers to the users if used efficiently but will provide only passable solutions if not. In this respect, resources exhibit limitless possibilities. User knowledge will be enhanced depending on how much information is extracted from the resources; nevertheless, newly obtained knowledge would help fill gaps in existing knowledge, and thus, the user knowledge as a whole will be systematized for better understanding. It might be interesting to scrutinize information from different perspectives.

(Yukiko Yamazaki)



Commands for Editing Image Files in Mac

Among general users, the Windows operating system (OS) usually holds an overwhelming share; however, many people appear to use Mac OS in the academic field. In this issue, I will introduce commands for performing simple editing of images in Mac OS.

Mac OS users typically use the iPhoto software (available with Macintosh computers), commercially available software, or free software to edit images. However, because the OS was changed from Mac OS X to a UNIX-based OS, commands of the Scriptable Image Processing System (SIPS) are now available for editing images. By using the commands in SIPS, users can change image formats, resize or rotate images, and invert images vertically or horizontally; of these, I would like to explain commands for the resize function.

Here, we assume that the image to be resized is located in a folder "images" on the desktop.

Let us use commands to resize an image!

First, from the Finder menu select "Go," followed by "Utilities," and "Terminal."



Next, input "cd<space>" to access the "images" folder on the desktop and drag and drop the "images" folder from the desktop to the terminal. This command will input the path of the "images" folder (Fig. 1 - ①).

```
gozaemon$ cd /Users/gozaemon/Desktop/images ①
images gozaemon$ sips -Z 600 IMG4954.JPG --out new.jpg ②
```

Fig. 1

Input the command in the format, "sips -Z <number of pixels> <image file name to be resized> -out <image file name after resized>."

Fig. 1 - ② shows how the image was resized to fit a square of 600 pixels. A horizontally long image file will have 600 pixels in the horizontal direction and vice versa for a vertically long image file, and the corresponding vertical or horizontal size will be automatically scaled while the aspect ratio of the original image will be retained (Fig. 2).



Fig. 2 : Resized image file

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To resize multiple image files, input a command in the format, "sips -Z <number of pixels> <wild card> --out <output folder>."

Fig. 3 - ① shows how all the JPEG files (*.JPG) in the "images" folder on the desktop will be resized to the square of 600 pixels and output in the "resize" folder preliminarily made in the "images" folder (Fig. 4).

```
gozaemon$ cd /Users/gozaemon/Desktop/images ①
images gozaemon$ sips -Z 600 *.JPG --out /Users/gozaemon/Desktop/images/resize
```

Fig. 3 : Resizing multiple files

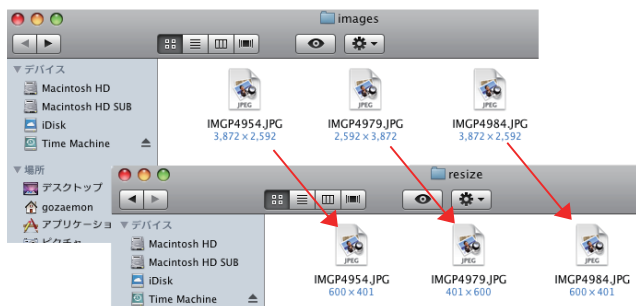


Fig. 4: Multiple image files output in the "resize" folder

Some readers of this newsletter may maintain resources with photos. Because of the increases in the image file size (owing to the improvement of pixels in digital cameras), resizing of images will be especially required when resource images are released on the Web. Please check the usefulness of the function for resizing images en bloc regardless of whether they are in portrait or landscape.

(Masakazu Saga, Center for Genetic Resource Information)



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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