

## Handlebar: a flexible, web-based inventory manager for handling barcoded samples

Tim Booth<sup>1</sup>, Jack Gilbert<sup>2</sup>, Josh D. Neufeld<sup>3</sup>, Jon Ball<sup>4</sup>, Milo Thurston<sup>1</sup>, Kevin Chipman<sup>5</sup>, Ian Joint<sup>2</sup>, and Dawn Field<sup>1</sup>

<sup>1</sup>NERC Centre for Ecology and Hydrology, Oxford, <sup>2</sup>Plymouth Marine Laboratory, Plymouth, <sup>3</sup>University of Warwick, Coventry, <sup>4</sup>University of Exeter, Exeter, and <sup>5</sup>University of Birmingham, Birmingham, UK

*BioTechniques* 42:300-302 (March 2007)  
doi 10.2144/000112385

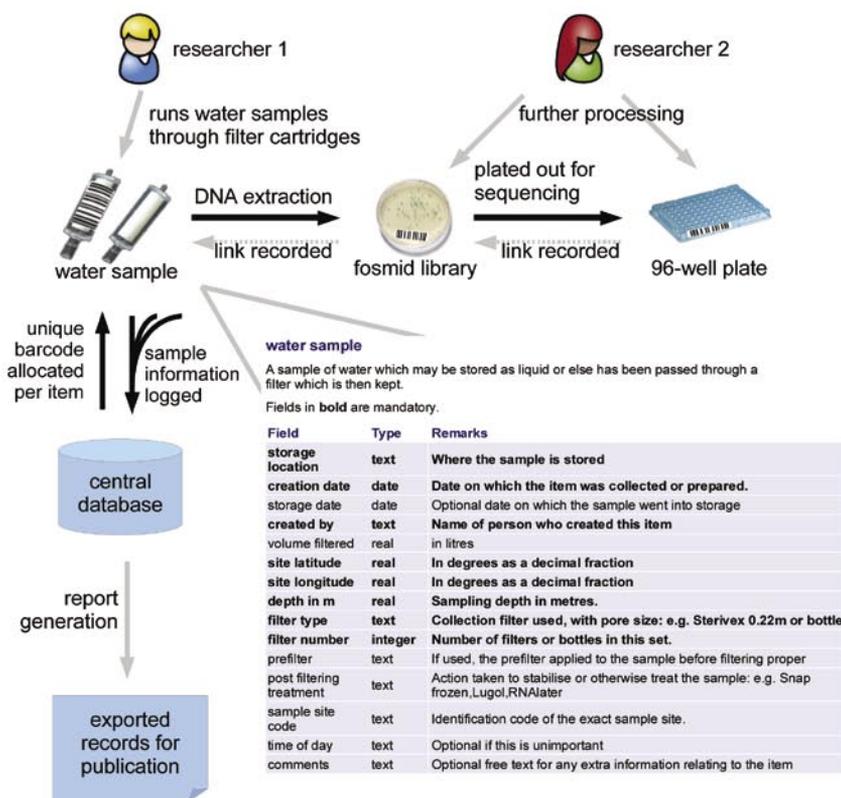
Researchers are increasingly calling for more effective approaches to managing multi-institutional projects as the size and scope of such collaborative endeavors increases. It is therefore essential to build and use tools that help unite virtual communities of geographically dispersed research groups (1). The management of physical samples is an example of a common practice across laboratories, and the coordination of an effective barcoding approach can greatly improve the ease with which samples can be stored, referenced, manipulated, and redistributed (2,3). While a Laboratory Information Management System (LIMS) is the preferred option for handling large quantities of sample data in a routine way ([www.limsources.com](http://www.limsources.com)) (4), the cost to maintain a commercial LIMS system can be prohibitive, and open-source solutions tailored for a particular type of work might not be available. Still, even the smallest projects can benefit from orderly handling of samples through barcoding.

Here we present Handlebar, version 2.0, a freely available, web-based barcode handling system that makes it possible for a group of collaborators to work together to barcode their collective physical resources. We developed this system in response to the requirements of two large collaborative groups working in microbial metagenomics ([www.genomics.ceh.ac.uk/mm](http://www.genomics.ceh.ac.uk/mm)) and fish ecotoxicogenomics ([www.biosciences.bham.ac.uk/fishtoxicogenomics](http://www.biosciences.bham.ac.uk/fishtoxicogenomics)) to simplify and standardize the management of their physical samples. We started by convening a working group of collaborating members to examine current work practices across

participating labs. Handlebar was designed to be compatible with any computer available to the user, deployed rapidly over multiple sites with no onsite support, and be user-friendly for students, postdoctoral research fellows, and principal investigators. A centrally

managed, web-based solution with a simple focus on inventory logging met these requirements.

When faced with the task of handling a large batch of samples, most researchers will choose to use spreadsheets, since they are familiar, easily edited, and readily shared. Handlebar builds upon the familiar spreadsheet environment by adding a central database to allocate identifiers (i.e., barcodes), standardizing the spreadsheet layout, providing usage notes, holding a definitive copy of each spreadsheet, validating incoming data, managing ownership, recording disposals, defining links between samples, logging activity, and providing rich searching and reporting (Figure 1). Users enter data into the system through their chosen spreadsheet software package and download



**Figure 1. Usage of Handlebar.** Handlebar was used to log over 1400 physical samples from a complex mesocosm experiment involving 20+ researchers working for 1 month to study ocean acidification ([www.genomics.ceh.ac.uk/mm](http://www.genomics.ceh.ac.uk/mm)). The example shows a water sample from which DNA is being extracted for eventual sequencing. The definition of the water sample item type is shown. The first researcher allocates barcodes and logs his water samples into the central database. When processing the sample, the second researcher can call up these records and enter her own barcode record for the fosmid library, linking it back to the original sample code. When the barcoded 96-well plate is sent for sequencing, all relevant information about the origin of the sample is available to be added as annotation to sequence files when they are submitted to public databases (e.g., latitude and longitude).

and upload information as required to an online database that all members of the project can access. The resulting system is a lightweight solution for managing barcodes that can be run by individual research groups and service providers. The Handlebar system acts as both an inventory of freezer contents and as an electronic complement to records kept in a lab book.

To illustrate the system to users in our group and beyond, we have set up an online demonstration database ([nebc.nox.ac.uk/cgi-bin/test\\_barcode/bc](http://nebc.nox.ac.uk/cgi-bin/test_barcode/bc)). Upon entry to the web site, potential users are presented with a variety of options. New users must register with the system to allocate blocks of barcodes. Once a block of barcodes has been allocated (e.g., 100 barcodes), the user downloads a spreadsheet with column headings appropriate for the requested item type and the 100 codes listed down the left hand column. Guidance notes explain what information is required in each column (Figure 1). Handlebar enables barcodes to be traced through subsequent manipulations of any physical sample. This is done by including a parent barcode in the description of each subsequently barcoded sample. The user can fill in data against some or all codes and, when ready, upload the data. The same web interface offers the ability to download and query the database, as well as a function to generate printer command files to lay out labels in a standard format. A key benefit of this approach is flexibility. Based on user recommendations, the project (database) administrator can define any item type for barcoding. Each item type corresponds to a spreadsheet template with appropriate column headings and formatting and a table in the underlying database.

Handlebar is also integrated with a second tool, GenQuery, which provides a general query interface to any relational database. This component is preconfigured to provide several useful views of the data and makes it possible for an administrator to add custom queries to the interface which can be bookmarked and downloaded as comma-separated values (CSV). To access GenQuery, click on the report maker link in the Handlebar main menu.

A new group wishing to deploy our system would need to purchase a barcode printer (e.g., a Zebra TLP 2824; Zebra Technologies, Buckinghamshire, UK) and any autodiscriminating USB barcode reader for convenience. The group would also need to work to define a suitable set of item types to populate the database with spreadsheet templates. Once a particular item type has been agreed upon within the working group (e.g., through exchange of a prototype spreadsheet), the system administrator makes the item type live by creating a table in the underlying database, after which Handlebar will automatically support the allocation of appropriate barcodes. If more than one Handlebar database is used at a site, the administrator can configure the system to ensure that all barcodes remain unique by setting different prefixes on the codes. A discussion of issues regarding unique identifiers may be found on the web site.

The system requires a web server running Apache, Perl, and PostgreSQL ([www.developer.com/open/article.php/3560296](http://www.developer.com/open/article.php/3560296); Shining a Light on LAMP). The software comprises a set of Perl scripts to run on the web server and a database schema to be loaded into PostgreSQL. For users of Debian GNU/Linux ([www.debian.org](http://www.debian.org)), we provide both Handlebar and GenQuery as packages. Full instructions for installation and maintenance of the system can be found online in the deployer guide ([nebc.nox.ac.uk/projects/handlebar](http://nebc.nox.ac.uk/projects/handlebar)). In addition, a Handlebar demonstration is available on a live DVD ([nebc.nox.ac.uk/live\\_dvd.html](http://nebc.nox.ac.uk/live_dvd.html)). Using the live DVD or the online demonstration database allows a full evaluation of the software without installing the system on a dedicated server. The Handlebar source code has been deposited at SourceForge, and it is the intention of the Natural Environment Research Council (NERC) Environmental Bioinformatics Centre (NEBC) to support this project in the public domain as open-source software well into the future. Feature requests and bug reports can be made through this site, and users can join the Handlebar mailing list for help and further information.

## ACKNOWLEDGMENTS

*We gratefully thank the NERC Post-Genomics and Proteomics Science Programme for funding this work and the NERC Data Management Coordinator for funding T.B. J.D.N. acknowledges support from the Natural Sciences and Engineering Research Council of Canada. We thank Dr. Daniel Swan, Institute for Cell and Molecular Biosciences, University of Newcastle-upon-Tyne, for testing the software on a Mac OS X and providing an installation guide. We also thank all current users of Handlebar for their support and feedback.*

## COMPETING INTERESTS STATEMENT

*The authors declare no competing interests.*

## REFERENCES

1. Field, D., B. Tiwari, T. Booth, S. Houten, D. Swan, N. Bertrand, and M. Thurston. 2006. Open source software for biologists: from famine to feast. *Nat. Biotechnol.* 24:801-803.
2. Nichols, J.H., C. Bartholomew, M. Brunton, C. Cintron, S. Elliott, J. McGirr, D. Morsi, S. Scott, et al. 2004. Reducing medical errors through barcoding at the point of care. *Clin. Leadersh. Manag. Rev.* 18:328-334.
3. Pennisi, E. 2005. National Science Foundation. Boom in digital collections makes a muddle of management. *Science* 308:187-189.
4. Sanchez-Villeda, H., S. Schroeder, M. Polacco, M. McMullen, S. Havermann, G. Davis, I. Vroh-Bi, K. Cone, et al. 2003. Development of an integrated laboratory information management system for the maize mapping project. *Bioinformatics* 19:2022-2030.

Received 3 August 2006; accepted 27 November 2006.

*Address correspondence to Tim Booth, NERC Environmental Bioinformatics Centre, CEH Oxford, Mansfield Road, Oxford OX1 3SR, UK. e-mail: [tbooth@ceh.ac.uk](mailto:tbooth@ceh.ac.uk)*

*To purchase reprints of this article, contact: [Reprints@BioTechniques.com](mailto:Reprints@BioTechniques.com)*