eBot: An image bank of Australian flora

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*e*Bot is an initiative of the University of Sydney Faculty of Science, School of Biological Sciences and the University of Sydney Library. *e*Bot supports the use of images for research, teaching and learning in the plant sciences, with a specific focus on the Australian context. To date, images have been submitted by members of the university community. All content is freely available to the wider community as web-ready or powerpoint-ready objects. Images are metatagged according to botanical conventions with plant 'family' as a mandatory field for plant images. The collection is presented, indexed and navigated using the eXtensible Text Framework (XTF). XTF can be adapted to suit diverse metadata, and this flexibility offers a way of accommodating future phylogenetic changes. We believe that this way of organising and tagging biological images could serve as a model for sister repositories in the sciences.

Keywords: digital object repository, plant science, *e*learning in biology

*e*Bot is a partnership initiative of the Faculty of Science, School of Biological Sciences and the University of Sydney Library. *e*Bot was designed to support the use of plant sciences images within a tertiary educational environment, but it has potential to be used in other educational sectors. At this stage all images have been contributed by members of the university community. We envisage that future development would enable a wider global community to contribute to *e*Bot. Creators of each image object retain copyright, and, with their permission, digital representations of works can be used by third parties to enrich learning and teaching programs and aid scholarly research. Collection access is provided by the University of Sydney Library, while editorial oversight is managed by the academic partners. *e*Bot provides one model for the management of digital assets important to learning and teaching in science.

*e*Bot uses a descriptive framework based on the Herbarium Information Standards and Protocols for Interchange of Data (HISPID). HISPID was developed collaboratively by a committee of representatives from Australian Herbaria. Adherence to standards, such as HISPID, supports interoperability (van Prooijen, 2006), allowing links with other services to be made in the future. We have expanded on the HISPID framework to include metadata relating to how the digital objects were generated (*e.g.* for micrographs, the type of microscopy used). To allow images to be closely examined on screen, *Zoomify* (http://www.zoomify.com/) software has been incorporated into the repository. Images are available for download in sizes appropriate for powerpoint presentations and for incorporation into websites. For a more extensive description of the assets in the repository and their importance to plant science refer to Quinnell *et al.* (2008). For a screen shot of the site see Figure 1.

It is through being able to 1) identify vegetative and reproductive structures and 2) identify shared characteristics that students of botany learn how to discriminate between taxa, particularly at the level of family (Quinnell *et al.,* 2008). Table 1 shows the alignment of *e*Bot content to tiers of digital content management. Tagging images with the taxa they represent supports object *connectedness* allowing images from the same taxa to be examined and compared. The phylogenetic underpinning of the images allows individual plant taxa to be gathered together into a group of objects representing diverse aspects of the plant represented and provide the students with an holistic overview.

The site was developed by Rowan Brownlee, using the eXtensible Text Framework (XTF), a highly customisable content presentation framework developed at the California Digital Library and capable of incorporating a variety of media including text, image and video

(http://www.cdlib.org/inside/projects/xtf/). XTF's capacity to accommodate diverse metadata provides a model for use with other biological collections of images important to the study of animals, fungi, the protists and prokaryotes.

Table 1: The alignment of *e*Bot to tiers of digital content management

Tier of content organisation		*e*Bot content
Asset	Images as .tiff	
Object	Phylogenetic	Image + plant "family" mandatory for most image types
Connectedness	metatags	Images representing the same taxa (*e.g.* family) can be grouped
Learning activity		Images representing the same taxa (*e.g.* family) can be compared to each other highlighting shared characteristics
Learning design		Implicit to learning in biology is being able to link to the phylogenetic framework.

What we have achieved to date offers a possible solution for those managing digital assets in science that can be aligned to the digital content tiers (Table 1). Our next step is to monitor site access, downloads and potential use of the images. We will benchmark against guidelines from organisations such as the Advanced Distributed Learning initiative in the USA, which has developed the Sharable Content Object Reference Model (accessibility, interoperability, durability and reusability). We are in the process of designing survey instruments for students and staff so that we can assess the effectiveness of the repository as a way to manage learning, teaching and research assets important to biology.
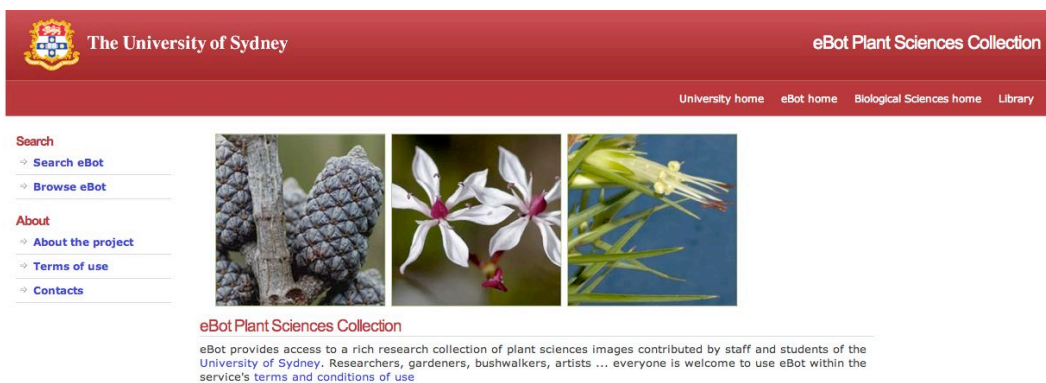

Figure 1: Screenshot of eBot homepage http://eBot.library.usyd.edu.au/

Acknowledgments

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