Web watch

COMPLETE DARWIN ON THE WEB

• http://darwin-online.org.uk

From October 19th, anyone with an internet connection can now browse the entire body of work of Charles Darwin.

The web site was the idea of a science historian, John van Wyhe, from the University of Cambridge, UK, who realized that the works of Darwin that were already on the web were scattered across different web sites with no obvious editorial standards. Many institutions and individuals have contributed to the project, which started in 2002. So far, over 50,000 searchable text pages and 40,000 images have been uploaded, making the web site the most comprehensive bibliography of Darwin's work ever published.

The repository contains all of Darwin's books, publications and manuscripts, as well as 'ancillary works' — a collection of reviews describing the naturalist's work. The web site also contains unpublished material, such as the notes that Darwin took on the ship the Beagle during his famous journey around the globe.

Alongside the fully searchable electronic text one can view original documents, including invaluable drawings. There are also links to freely accessible audio files and translations in several languages. By 2009, the bicentenary of Darwin's birth, the web site aims to host everything he wrote apart from his private letters, which are being collected on the web by the Darwin Correspondence Project.

And if a project in Wales goes according to plan, the Beagle will not only 'sail on the web', but on the ocean waves. The Beagle Project Pembrokeshire, which was founded by David Lort-Phillips (a descendant of one of the crew members of the Beagle), aims to build a replica of the ship, blending old-fashioned and modern technologies, to retrace its famous journey with a crew of scientists and students.

Francesca Pentimalli

HUMAN GENETICS

Haplotype maps go global

The HapMap project has raised high hopes for mapping genetic determinants of complex human disease, but questions have been raised by some about how universally HapMap data can be used. Two papers represent the most thorough investigation of this concern so far, and conclude that HapMap data will be valuable for mapping studies in human populations around the world.

The HapMap project has characterized haplotype structures across the genome for four human populations with the goal of enabling genome-wide sets of SNPs to be picked for whole-genome association studies. The general principle is simple — if two or more SNPs are in strong linkage disequilibrium (LD), just one of these variants (known as a tagSNP) needs to be genotyped to capture information on all of them. But are haplotype structures similar enough in populations other than those covered by the HapMap to allow successful mapping studies?

This is one question addressed in the study by Conrad, Jakobsson and Coop *et al.*, who looked at SNP variation across the genome in 927 people from 52 populations. Although they found marked differences in the extent of LD, they also revealed correlations in the positioning of recombination hot spots between different populations. Furthermore, there was extensive haplotype sharing between the HapMap populations and the 52 populations that this study assessed — good news for mapping studies using tagSNPs.

As expected, haplotype sharing with the HapMap was generally correlated to geographical closeness to a HapMap population. Consistent with this, the best tagging of common variants from non-HapMap populations was achieved using tagSNPs from the nearest HapMap sample. Some populations were more difficult to tag than others, notably African populations, in which the extent of LD is reduced. The authors also describe how tagging can be improved in the case of some admixed populations by combining tagSNP sets from different HapMap populations.

De Bakker, Burtt and Graham *et al.* also looked at how well HapMap tagSNPs cover common variants in other populations, testing the approach on 11 non-HapMap samples. Furthermore, they carried out simulations of whole-genome association mapping using these tags specifically to determine how powerful such studies are likely to be. Good coverage and statistical power of greater than 80% were achieved using HapMap tagSNPs for non-HapMap populations.

These authors also showed how more effective studies could be carried out by combining tagSNPs from different groups. For a non-HapMap African-American population, power was increased to 80–90% by using some tags from the Caucasian HapMap set, rather than just using a set from the African population that was sampled by the HapMap.

Altogether, these studies confirm the potential of the HapMap, combined with information about the history of individual populations, as a powerful tool for mapping common variants in human populations.

Louisa Flintoft

ORIGINAL RESEARCH PAPERS
Conrad, D. F. *et al.* A worldwide survey of haplotype variation and linkage disequilibrium in the human genome. *Nature Genet.* 22 October 2006 (doi:10.1038/ng1911) | de Bakker, P. I. W. *et al.* Transferability of tag SNPs in genetic association studies in multiple populations. *Nature Genet.* 22 October 2006 (doi:10.1038/ng1899)
FURTHER READING Hirschhorn, J. N. & Daly, M. J. Genome-wide association studies for common diseases and complex traits. *Nature Rev. Genet.* **6**, 95–108 (2005) | Wang, W. Y. S. *et al.* Genome-wide association studies: theoretical and practical concerns. *Nature Rev. Genet.* **6**, 109–118 (2005)
WEB SITE
The International HapMap Project: http://www.hapmap.org