push their pathway data out into the world," says Conklin. Alexander Pico, lead author on the report, also notes that "for our internal team and our collaboration with [colleagues from] the Netherlands, WikiPathways has made it so much easier to edit and curate content." Evelo describes another important benefit: "Pathways created on WikiPathways are not just representations of knowledge; they can also be used for analysis of new results."

Using a wiki-based platform for managing gene or pathway data is very different from the traditional model, in which researchers submit their data to databases that are curated by a relatively small number of experts (**Fig. 1**). Neither Su's nor Conklin's teams intend their wiki platforms to replace traditional databases, but they both emphasize that wikis can serve as highly complementary resources. "Even the people behind the gene portals recognize that their crew of 50 people can't keep on top of all the literature; … essentially you're empowering a large community to serve as amateur curators," explains Su. However, he stresses that with a wiki platform, "at any moment there may be a misleading statement, or it may be incorrect or incomplete—it's an eternal work in progress," and as such, wikis are not meant to serve as primary sources.

Perhaps one of the main reasons the wiki format works so well for communicating scientific data is because it is so simple and requires little effort to use. In using a wiki platform, Pico says, "an average biologist who's quite busy doesn't notice that at the same time that they're helping themselves they're also helping everyone else."

Allison Doerr

RESEARCH PAPERS

Huss, J.W. *et al.* A gene wiki for community annotation of gene function. *PLoS Biol.* **6**, e175 (2008).

Pico, A.R. *et al.* WikiPathways: pathway editing for the people. *PLoS Biol.* **6**, e184 (2008.)

frequency at which they occur, Steinmetz's group noted good agreement with the DSB map generated by Michael Lichten's team (US National Institutes of Health), providing additional confidence in their approach. Taking a closer look at their maps, the team identified 8 out of 9 previously known so-called recombination hotspots. Centromeres, mating-type loci and ribosomal DNA were, as expected, largely cold (recombination-free).

Notably, DSBs in certain regions of the genome were repaired through crossover events and others as non-crossovers. "There isn't a 50/50 choice in how a DSB is repaired," explains Steinmetz. "We think the chromosomal context influences this decision, … although this is an area that remains to be further investigated."

What is next? Huber's group is working toward a revised version of ssGenotyping that can be used as a general genotyping tool in which mutations can be accurately detected using one reference genome. "We feel based on the performance in this experiment, array-based genotyping based on this platform is reasonable for the detection of single-nucleotide polymorphisms, very short insertions and deletions," says Huber, "providing the basis for rapidly and inexpensively screening novel mutations." Huber and Steinmetz's teams hope to apply their tool to study the budding yeast as it evolves.

Michelle Pflumm

RESEARCH PAPERS

Mancera, E. *et al.* High-resolution mapping of meiotic crossovers and non-crossovers in yeast. *Nature* **454**, 479–485 (2008).

NEWS IN BRIEF

GENOMICS

Mapping the human methylome

Using different reductionist approaches, two groups now map the human methylome at nucleotide resolution. Using reduced representation bisulphate sequencing, Meissner *et al.* charted the methylomes of embryonic stem cells and primary neuronal cells, providing key insights into stem cell differentiation. With the aid of a new computational tool called Batman, Down *et al.* used DNA methylation immunoprecipitation coupled to high-throughput sequencing to chart the methylome of human sperm.

Down, T.A. *et al. Nat. Biotechnol.* **26**, 779–785 (2008).

Meissner, A. *et al. Nature* **454**, 766–770 (2008).

PROTEOMICS

Mice on a SILAC diet

Stable isotope labeling with amino acids in cell culture (SILAC) is a metabolic labeling technique used to quantitatively compare proteomic differences in two cell populations via mass spectrometry. Krüger *et al*. now extend the SILAC method to a mammalian model organism: the mouse. They found that mice could be SILAC-treated for several generations without any detrimental effects, and the labels were incorporated into all organ proteomes.

Krüger, M. *et al*. *Cell* **134**, 353–364 (2008).

GENE TRANSFER

A new strategy for zinc-finger nuclease design

Zinc-finger endonucleases can be custom-engineered to induce gene targeting at a user-specified sequence in the genome, but the strategies available to engineer these potentially very useful tools still have limitations. Maeder *et al.* now present a strategy termed oligomerized pool engineering (OPEN) based on an archive of selected zinc-finger pools and demonstrate its utility by designing nucleases targeting 11 sites in five different genes.

Maeder, M.L. *et al. Mol. Cell* **31**, 294–301 (2008).

MOLECULAR LIBRARIES

A library of histone mutants

As a resource for chromatin researchers, Nakanishi *et al.* present a complete alanine-scanning mutant library of the four core histones in *Saccharomyces cerevisiae*. They used this library to discover 18 core histone residues that are essential for viability and normal growth as well as to determine regulatory residues required for histone H3 Lys4 methylation.

Nakanishi, S. *et al. Nat. Struct. Mol. Biol.* **15**, 881–888 (2008).

PROTEIN BIOCHEMISTRY

Proximity biotinylation

Fernández-Suárez *et al.* report a new concept for detecting protein-protein interactions in live cells using an enzyme-substrate pair, exemplified by attaching the enzyme biotin ligase (BirA) to one protein and an acceptor peptide, which is site-specifically biotinylated by BirA, to the interacting protein partner. If the proteins interact, the acceptor peptide will become biotinylated, which can be detected by streptavidin staining.

Fernández-Suárez, M. *et al. J. Am. Chem. Soc.* **130**, 9251–9253 (2008).