## SCORECARD

**San Francisco's offices** Mayor Gavin Newsom has banned bottled water for thirsty city workers, who will now be offered only environmentally friendly water from the tap.

**TV remote controls** Even the humble remote might soon feel too much like hard work. Japanese firm Hitachi has unveiled a 'brain interface' that it hopes will ultimately allow users to change channels just by thinking about it.

## ON THE RECORD

**"The conservation of the bald eagle is a true reflection of the concern Americans have for the environment."**

George Fenwick, president of the American Bird Conservancy, is pleased by the news that the nation's emblem is to be removed from the Endangered Species Act's list of threatened species.

**"It's the same as you feel after a plate of spaghetti."**

Alessandro Sannino, Italian researcher and inventor of the 'fill pill', explains how his invention, which is made out of the same absorbent material as nappies, helps dieters by expanding to take up space in the stomach.

## OVERHYPED

**The iPhone**
Yes it's beautiful. Yes it's multifunctional. But ultimately it's only a telephone, and therefore not worth camping out for days on end to get your hands on.

*Sources: Reuters, Fox News, American Bird Conservancy, Daily Mirror, Associated Press*

APPLE


C. RUSS, BROAD INST.

Sequencing machines such as the 1G are revolutionizing the speed at which DNA is analysed.

# Faster still and faster

A new generation of sequencing machines is broadening horizons for users. Various groups have recently performed epigenetic studies — looking at modifications to the genome that control its expression — that would have been utterly impractical using old technologies.

The latest approach fishes out all the DNA associated with a given marker, such as one of the histone proteins used to package genes in chromosomes. Then, instead of comparing each piece of DNA with a library of previously isolated sequences, as used to be done, scientists simply sequence the whole lot.

The key to this approach is new technology such as that sold by Solexa, a company that earlier this year merged with Illumina of San Diego. "The amount of DNA sequence being produced by these machines is staggering," says Steven Jones, associate director of the Genome Sciences Centre at the British Columbia Cancer Agency in Vancouver. Working flat out, a Solexa 1G machine could triple the total amount of DNA sequence contained in the GenBank database in just one year.

Jones's group looked at histone changes that control which regions of DNA can be read[1]. Meanwhile, scientists from the Broad Institute in Cambridge, Massachusetts, and Massachusetts General Hospital in Boston used a Solexa machine to examine two types of histone modification in mouse cells. Their paper[2], published online in *Nature* on 1 July, describes how these modifications change during development, and how such changes can either keep cells poised to switch fates, or close down their future options.

"The excitement about this paper is that we now have a means of studying cellular state in a high-throughput manner," says Bradley Bernstein, a pathologist at Massachusetts General Hospital who co-led the work with Broad director Eric Lander. "We certainly couldn't have done this on a genome-wide scale before." (See 'Sequencing revolution ushers in new era'.)

This advance is already unveiling new biology, says Keji Zhao of the US National Heart, Lung and Blood Institute in Bethesda, Maryland. Zhao's group has used it to decipher the messages encoded by two types of epigenetic mark produced by adding methyl groups to DNA[3]. Zhao says scientists' ability to take large-scale, complete snapshots means it might one day be possible to catalogue all the non-genetic alterations that control how genes are expressed in various cells and at all stages of development. And progress could be breakneck: Zhao's group took delivery of its first Solexa machine in January and published its results in May.

Beyond epigenetics, says Lander, other ambitious projects beckon. For example, this May, the genome of genomics pioneer James Watson was bared to the world[4] after being sequenced using technology from 454 Life Sciences, a company based in Branford, Connecticut, that has

PUNCHSTOCK

**WORLD HERITAGE LIST GETS BIGGER**

News@nature.com rounds up key decisions from last week's conference on UNESCO's wonders of the world.

**www.nature.com/news**

just been acquired by Roche Diagnostics. This got institutions such as the US National Human Genome Research Institute thinking seriously about sequencing the complete genomes of hundreds or even thousands of people. The technology might also be used to identify new organisms, such as obscure bacteria living in complex microbial communities.

But Lander cautions that all this will take a lot of work as scientists map out how best to use the latest advances. The new technologies typically read out much shorter stretches of DNA than the older generation of sequencers did. And new methods must be developed for preparing samples and assembling these short reads into whole genomes. "It's going to be a nightmare for a year or two, as we try to fit old or important applications to these strange new platforms," Lander says. "But the return is going to be tremendous." ■

**Erika Check**


1. Robertson, G. *et al. Nature Methods* doi:10.1038/nmeth1068 (2007).
2. Mikkelsen, T. S. *et al. Nature* doi:10.1038/nature06008 (2007).
3. Barski, A. *et al. Cell* **129,** 823–837 (2007).
4. *Nature* **447,** 358–359 (2007).


## Sequencing revolution ushers in new era

The genome sequencing centre at the Broad Institute in Cambridge, Massachusetts, has long been what ecologists call a monoculture: rows of identical sequencing machines, namely the trusty Applied Biosystems 3730s on which much of the human genome was sequenced. But all that is beginning to change.

First came two new types of machine, one made by 454 Life Sciences and the other by Solexa (see main story). Both use modified versions of the 'Sanger' sequencing method used by the old ABI workhorses, but add new wrinkles that allow vast numbers of short fragments to be sequenced in parallel.

In June, the Broad Institute and several other major sequencing centres received the first shipments of a new ABI sequencer that uses a sequencing chemistry that is fundamentally different from that of Solexa and 454. These machines read the cutting of DNA strands as opposed to their synthesis when sequencing. This technique requires serious computing power, as it produces terabytes of data at a time.

What all three instruments have in common is speed: Both the Solexa and ABI technologies claim to be able to identify 1 billion bases of sequence in a single run, taking just days to produce the equivalent of one-third of the human genome. 454 technology produces runs of about half that size.

Chad Nusbaum, co-director of the Broad's sequencing programme, says this is just the start. Other companies are developing even faster technologies that they're not discussing publicly yet. The new entries are changing the way sequences are harvested at the Broad and other large sequencing centres, such as those at Washington University in St Louis, Missouri, and the Wellcome Trust Sanger Institute in Hinxton, Cambridge, UK.

"This is a very aggressive horse race," Nusbaum says. "Companies are working on new techniques that in two or five years might dramatically rewrite the state of the technology, and that's a great thing for science." **E.C.**