

A CONVERSATION WITH NICK GOLDMAN

# Double Helix Serves Double Duty



European Molecular Biology Laboratory

Nick Goldman, a molecular biologist at the European Bioinformatics Institute in Hinxton, England, used a technique with error-correction software to store and retrieve data in synthetic DNA molecules.

By JOHN MARKOFF  
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Last Wednesday, a group of researchers at the European Bioinformatics Institute [reported in the journal Nature](#) that they had managed to store digital information in synthetic DNA molecules, then recreated the original digital files without error.

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The amount of data, 739 kilobytes all told, is hardly prodigious by today's microelectronic storage standards: all 154 of Shakespeare's sonnets, a scientific paper, a color digital photo of the researchers' laboratory, a 26-second excerpt from the Rev. Dr. Martin Luther King Jr.'s "I have a dream" speech and a software algorithm. Nor is this the first time digital information has been stored in DNA.

But the researchers said their new technique, which includes error-correction software, was a step toward a digital archival storage medium of immense scale. Their goal is a system that will safely store the equivalent of one million CDs in a gram of DNA for 10,000 years.

If the new technology proves workable, it will have arrived just in time. The lead author, the British molecular biologist [Nick Goldman](#), said he had conceived the idea with a colleague, Ewan Birney, while the two sat in a pub pondering the digital fire hose of genetic information their institute is now receiving — and the likelihood that it would soon outpace even today's chips and disk drives, whose capacity continues to double roughly every two years, as predicted by Moore's law.

The telephone interview with Dr. Goldman, from his laboratory in Hinxton, near Cambridge, has been edited and condensed.

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## Does your experiment suggest that DNA is a reasonable alternative for archiving digital information?

It's too far beyond us at the moment because of the price. I don't know if there are enough machines to write DNA in big quantities. I suspect not. The experiment we did converted about three-quarters of a megabyte of information off a hard disk drive into DNA. We showed it worked on a large scale, and part of what we published is an analysis of how that might scale up, at least theoretically. But we couldn't do the scale-up experiments.

### You've proved something. What's next?

We've got a couple of ideas to pursue to make this a bit more likely to be something to turn up in the real world. One is to improve the coding and the decoding to see if we can get more information into the same amount of DNA. Hopefully if we can store twice as much information, that will halve our costs.

We were quite conservative in the approach we took. We really wanted to make sure that it worked, and so we used quite a lot of error-correction code. We could maybe sacrifice less to the error-correction part and use more actual information.

The other thing to make it work on a scale that the world would really be interested in is to automate and miniaturize. All the technologies exist — they're all commercially available. But they're not all in one place, and they're not designed to work with each other as such.

If you wanted to do it properly you'd invest in the site, you'd have DNA synthesis at the site, you'd have the storage there, you'd have the reading back in one place, and you'd miniaturize it all. You'd have micro-fluidics to do what is currently lab science — even to the level of having robots to do the filing of the test tubes onto shelves. Robots are used in magnetic tape archive centers now, and you'd just want a smaller version of the same.

### How similar is what you've done to what is involved in today's gene-sequencing systems, which read and store the proteins in a DNA molecule?

The sequencing, or reading it back, that we did is exactly the same. We designed it that way. We designed it so that it would work in the standard protocols that we and our laboratory collaborators are familiar with, day in day out. It is really exactly the same process. We use an Illumina sequencing machine.

The writing of the information is a technology I'm a little bit less familiar with. But Agilent Technologies, whom we worked with, is one of the world leaders in developing this, and it is, I believe, very much like an inkjet printing system. But you're not using colored dyes on paper — you're using chemical solutions that include in them the nucleotides, the basis of DNA, fired very accurately onto a glass slide so that each little spot on the slide you build up is a separate sequence.

### Is there a category of information you were most interested in archiving?

A version of this interview appeared in print on January 29, 2013, on page D3 of the New York edition with the headline: Double Helix Serves Double Duty.

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