

Synthetic DNA for Digital Storage

Brian W. Bramlett <u>bbramlett@twistbioscience.com</u> October 2019

@TwistBioscience #WeMakeDNA

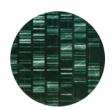
Writing Synthetic DNA on Silicon Platform



KEY ADVANTAGES OF WRITING DNA ON SILICON



MINIATURIZATION 10³⁻⁶ less volume of required reagents



THROUGHPUT 20M oligos/month



LOW COST Driving adoption and new applications



VERSATILE PLATFORM Broad applications

Multiple Large Market Opportunities

TWIST'S PLATFROM TECHNOLOGY ADDRESSES



LARGE MARKET OPPORTUNITIES



- Competitive • **Turnaround Time**
- Lower Cost
- **High Throughput** •
- High Quality
- SHORT TERM GOAL Grow Revenue

LARGE MARKET DRUG DISCOVERY/ DEVELOPMENT

- High Quality Diversity Hits / Leads
- Shorter Time and Cost • from Target to IND

MID TERM GOAL Develop novel therapeutics



IT INDUSTRY DATA STORAGE

- Permanence •
- Density
- Ease of Copying
- Universal Format

LONG TERM GOAL Enter technology market

Synthetic Biology is Rapidly Growing

time and lower costs



NEW APPLICATIONS FOR SYNTHETIC DNA

- Antibodies / TCR
- Vaccines
- Immuno and Cancer Therapies
- Small Molecule Drug Manufacture

Industrial

Healthcare

 Increased population growth impacting the sustainability of finite resources

Better drug development tools to lessen

More effective diagnostic tools for DNA

extraction to lower costs (i.e. NGS)

- Industrial production to address the needs of civilization
- **Agriculture**
- Global population growing with decrease in per capita arable land
- Food security and increased nutrition

- Specialty Chemicals
- Advanced Property **Materials**

We need a new type of DNA supplier to meet demand

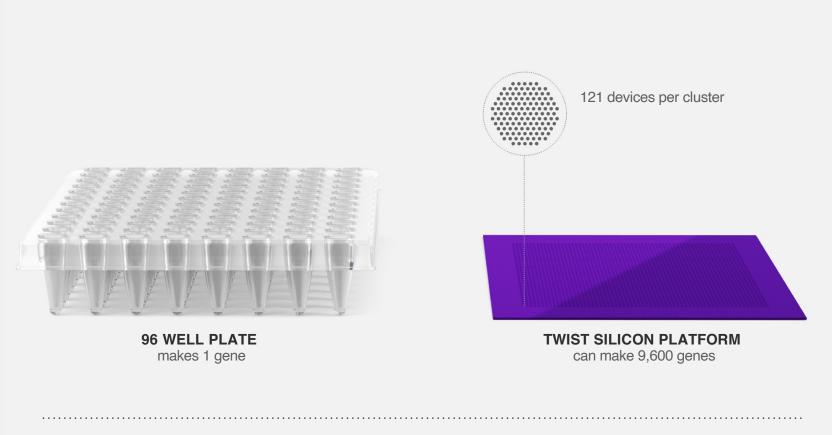
- Self-fertilizing crops
- Oil-Free Fertilizers
- Drought Solutions
- New Disease Protection

NEEDS



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Rewriting DNA with the Power of Silicon



Developing Game-Changing Throughput and Cost through Quality and Speed at Scale

Other Growth Verticals

TWIST'S PLATFROM EXTENDS TO



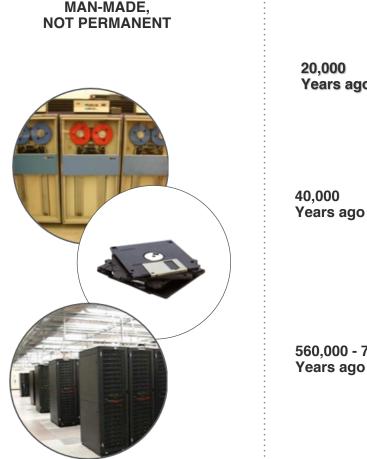




WHY DNA?

DNA: Nature's Choice for Data Storage





20,000 Years ago

STABLE FOR 1000s of YEARS

Sequencing the nuclear genome of the extinct woolly mammoth

Webb Miller¹, Daniela I. Drautz¹, Aakrosh Ratan¹, Barbara Pusey¹, Ji Qi¹, Arthur M. Lesk¹, Lynn P. Tomsho¹, Michael D. Packard¹, Fangqing Zhao¹, Andrei Sher²[‡], Alexei Tikhonov³, Brian Raney⁴, Nick Patterson⁵, Kerstin Lindblad-Toh⁵, Eric S. Lander⁵, James R. Knight⁶, Gerard P. Irzyk⁶, Karin M. Fredrikson⁷, Timothy T. Harkins⁷, Sharon Sheridan⁷, Tom Pringle⁸ & Stephan C. Schuster¹

A Draft Sequence of the **Neandertal Genome**

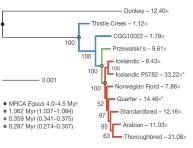
Richard E. Green,¹*†‡ Johannes Krause,¹†§ Adrian W. Briggs,¹†§ Tomislav Maricic,¹†§ Udo Stenzel, 1+§ Martin Kircher, 1+§ Nick Patterson, 2+§ Heng Li, 2+ Weiwei Zhai, 3+11 odo Jeneze, jy matin Antier, jy nick rateson, jy neig L, j Weier Lina, ji Markus Hsi-Yang Fritz, ⁴N Fansey, F Kansen, ² Frir Y. Durand, ³† Anna-Sapfo Malaspinas, ³† Jeffrey D, Jensen, ⁶† Tomas Marques-Bonet, ⁷¹³† Can Alkan, ⁷ Kay Prüfer, ¹† Matthias Meyer, ¹† Hernán A. Burbano, ¹† Jeffrey M. Good, ^{1,6}† Rigo Schultz, ¹Ayinuer Aximu-Petri, ¹Anne Butthof, ¹ Barbara Höber,¹ Barbara Höffner,¹ Madlen Siegemund,¹ Antje Weihmann,¹ Chad Nusbaum, Eric S. Lander,² Carsten Russ,³ Nathaniel Novok,⁴ Jason Affouriti,⁴ Michael Egholm,⁹ Christine Verna,²¹ Pavao Rudan,³⁰ Dejana Brajkovi,¹¹ Željko Kucan,³⁰ Ivan Guši,¹⁰ Vladimir B. Doronichev,¹² Liubov V. Golovanova,³² Carles Lalueza-Fox,³³ Marco de la Rasilla,¹⁴ Javier Fortea,¹⁴ Antonio Rosa,³⁵ Ralf W. Schmitz,^{16,17} Prilip L. F. Johnson,²⁴ E tvan E. Eichler,⁴ T Daniel Falush, 19 + Ewan Birney, 4 + James C. Mullikin, 5 + Montgomery Slatkin, 3 + Rasmus Nielsen, 3 Janet Kelso, 1+ Michael Lachmann, 1+ David Reich, 2,20*+ Svante Pääbo1*+



560,000 - 780,000 Years ago

Recalibrating Equus evolution using the genome sequence of an early Middle Pleistocene horse

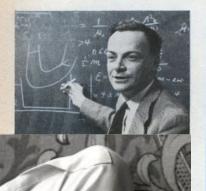
Ludovic Orlando¹*, Aurélien Ginolhac¹*, Guojie Zhang²*, Duane Froese³, Ant Enrico Cappellini¹, Bent Petersen⁶, Ida Moltke^{4,7}, Philip L. F. Johnson⁶, Matt Thorfinn Korneliussen¹, Anna-Sapío Malaspinas¹, Josef Vogt⁶, Damian Szkla Andrei Dolocan¹², Jesper Stenderup¹, Amhed M. V. Velazquez¹, James Cahill Grant D. Zazula¹¹, Andaine Seguin-Orlando¹¹⁴, Cecilie Mortensen¹¹⁴, Kim J Jacobo Weinstock¹⁰, Kristian Gregersen^{1,17}, Knut H. Roed¹⁸, Véra Elsenman Douglas F. Antezak²¹, Mads F. Bertelsen²², Søren Brunak^{6,23}, Khaled A. S. A John Mundy²⁶, Anders Krogh^{1,4}, M. Thomas P. Gilbert¹, Kurt Kjær¹, Thomas Jesper V. Olsen¹⁰, Michael Hofreiter³⁷, Rasmus Nielsen³⁸, Beth Shapiro⁵, Jun

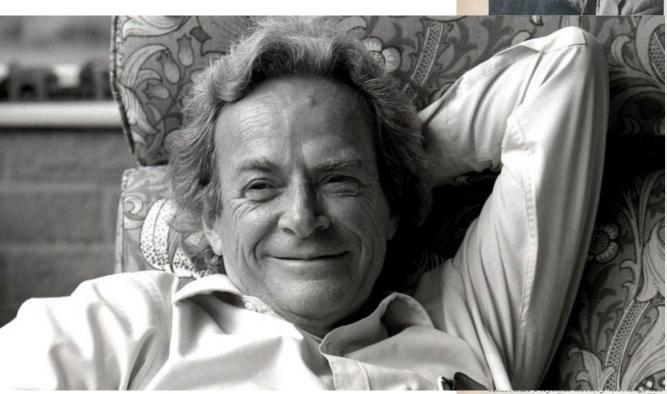


First record: 1959

Richard Feynman Lecture There's Plenty of Room at the Bottom There's plenty of room at the bottom, says noted scientist as he reveals-

How to Build an Automobile





the Pasadena Rotary luncheon). The full transcript appeared in "Engineering and Science Magazine," published at the California Institute of Technology.

14 POPULAR SCIENCE NOVEMBER 1960

Exploring the fantastic possibilities of the very small should pay off handsomely and provide a lot of fun, too

By Richard P. Feynman Professor of Theoretical Physics, California Institute of Technology

PEOPLE tell me about miniaturization, about electric motors the size of the nail on your small finger. There is a device on the market by which you can write the Lord's Prayer on the head of a pin. But that's nothing. That's the most primitive, halting step.

Why not write the entire 24 volumes of the "Encyclopaedia Britannica" on the head of a pin?

Let's see what would be involved. The head of a pin is a sixteenth of an inch across. If you magnify it 25,000 diameters, the area of the head of the pin is equal to the area of all pages of the encyclopedia. All it is necessary to do is to reduce the writing in the encyclopedia 25,000 times. Is that possible? One of the little dots on the fine halftone reproductions in the encyclopedia, when you demagnify it by 25,000 times, still would contain in its area 1,000 atoms. So, each dot can easily be adjusted in size as required, and there is no question that there is enough room on the head of a pin to put all of the "Encyclopaedia Britannica."

I MAGINE that it is written in raised letters of metal that are 1/25,000 ordinary size. How would we read it?

We would press the metal into plastic and make a mold; peel the plastic off very carefully; evaporate silica into the plastic to get a very thin film; then shadow it by evaporating gold at an angle against the silica so that all the little letters appear clearly; dissolve the plastic away from the silica film; and then look through it with an electron microscope.





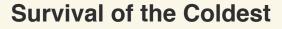
• Terminal media format,

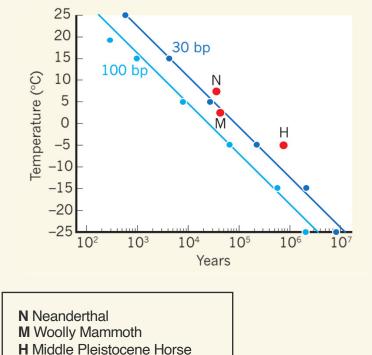
independent of read or write platform

- Permanence
- Density
- Copying
- Data Transfer



The rate of DNA decay varies with environmental conditions





Millar and Lambert, Nature 499, p 34-35, 2013

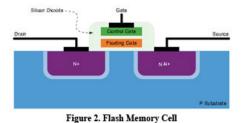
The Molecular Weight of Information

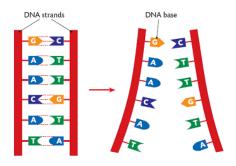


Compare Three Storage Media

- Hot Storage: Flash
 - 10¹⁰ Atoms per bit
- Cold Storage: Tape
 - 10¹⁰ Atoms per bit
- NAM: Nucleic Acid Memory
 - 14 Atoms per Bit

The media is the information





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Data Transfer



Amazon Snowmobile — up to 100 PB

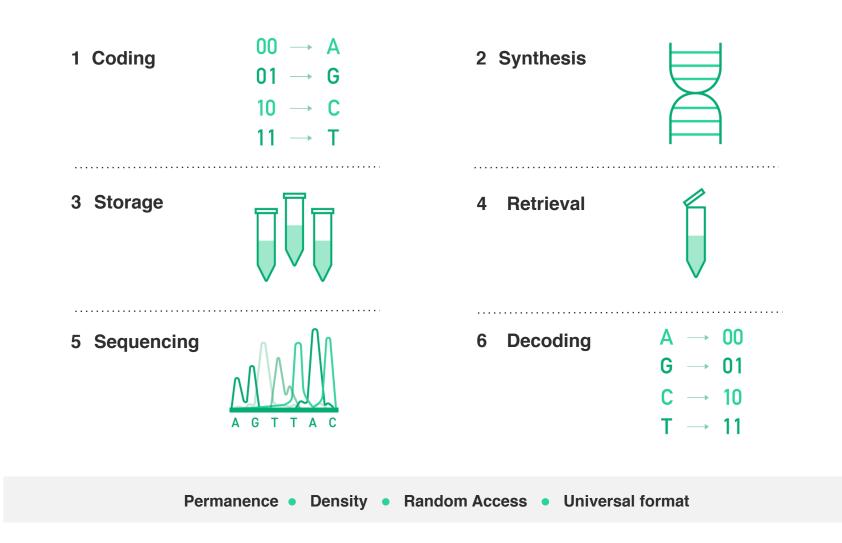




HOW?

Data Storage in DNA









- Transform Binary information to Nature's code
- Information Theory ECC's adapted to correct for errors and provide redundancy

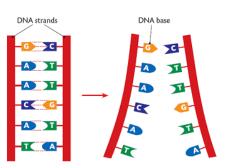
 $\begin{array}{ccc} 00 \rightarrow A \\ 01 \rightarrow G \\ 10 \rightarrow C \\ 11 \rightarrow T \end{array}$

Synthesis (Write)

- Artificially assemble DNA from the chemical building blocks
- Molecule is identical to DNA occurring in living organisms but is created synthetically
- Similar to assembling Lego® blocks from 4 colors
- We exploit the molecules' complementary nature





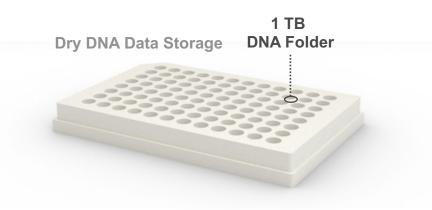


Storage



- Only requires a cool dry vessel to keep the data viable for hundreds of years
- Thousands of times more compact than current media

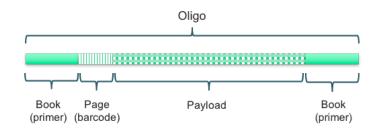




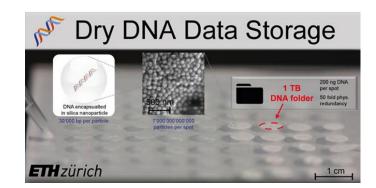




Pools of DNA Molecules with Barcode



Addressable Objects for Storage



Sequencing (Read)









Decoding



- Reconstruct the digital file from sequences of DNA
- Computational methods remove errors that may be introduced in from the synthesis (write) and sequencing (read)

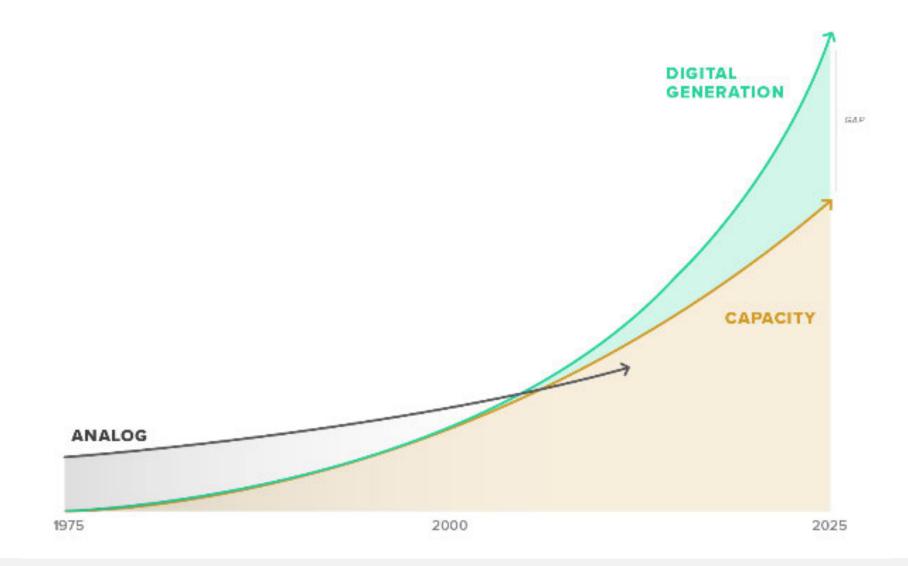
 $\begin{array}{c} A \rightarrow 00 \\ G \rightarrow 01 \\ C \rightarrow 10 \\ T \rightarrow 11 \end{array}$



WHY NOW?

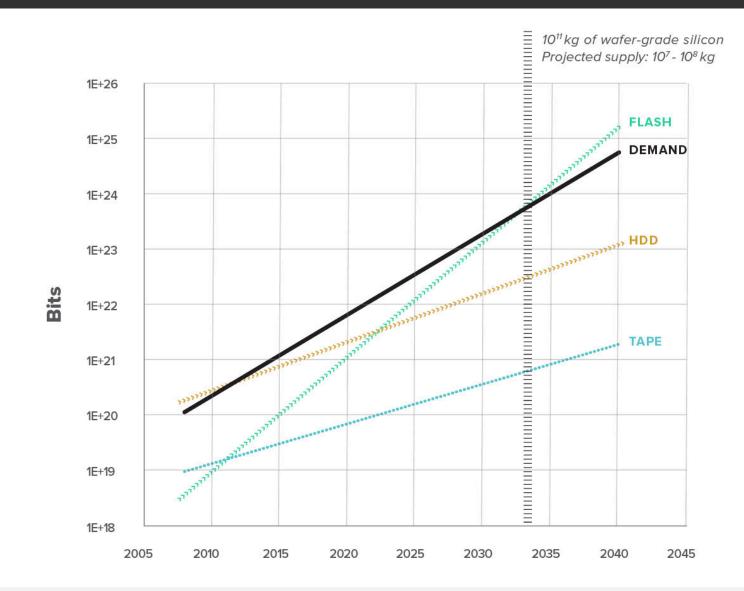
Storage Capacity





Storage Capacity

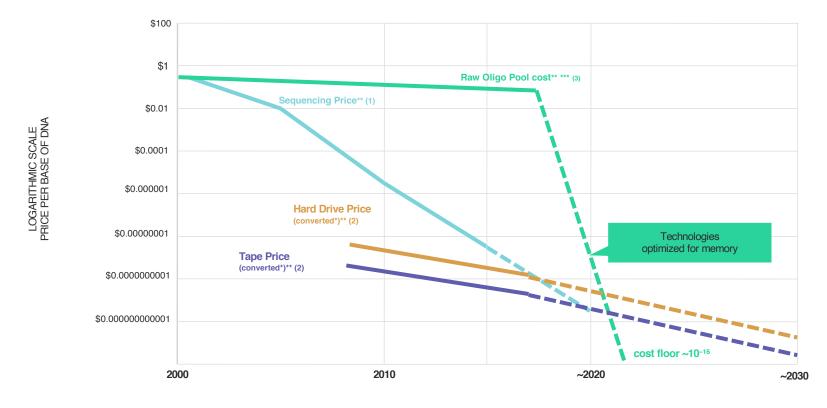




DNA Data Storage Trends and Projections



We believe new DNA technologies and cost efficiencies could surpass mature IT hardware solutions in 3–5 years

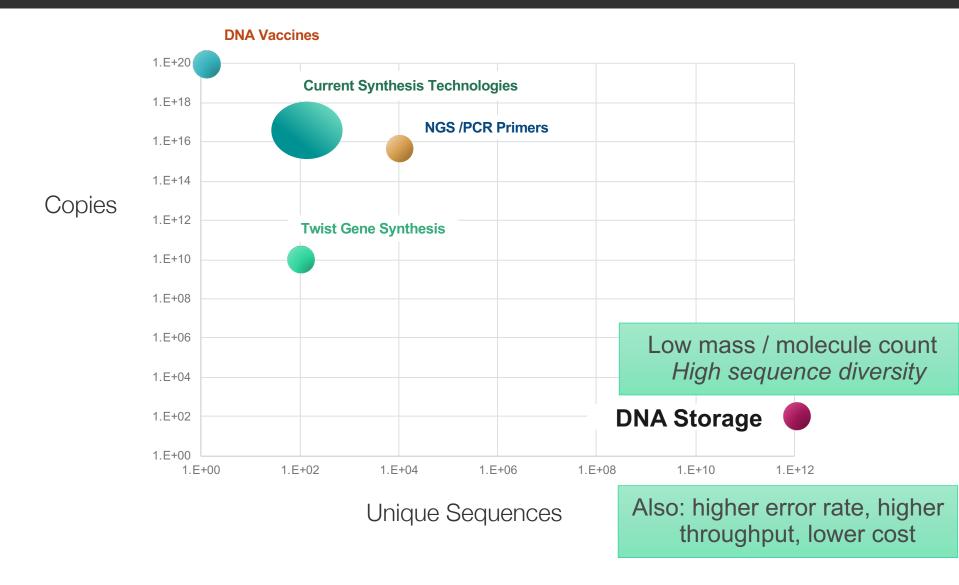


* DNA bases per byte for hard drive and tape shown at typical published encoding ranges from about 5:1 to 6.25:1

** All dotted lines represent extrapolations and assumes continued trajectory of historical trends, and that there will be continued decrease in price as technology improves. *** Raw oligo pool cost extrapolation based on DARPA and another anticipated government-sponsored grant project objectives, both at specified time points

(1) www.genome. Gov. (2) Bob Fontana, IBM Systems, Storage Media Overview, May 4,2016 (3) Bioeconomy Capital, Rob Carlson, January 20, 2018, www.synthesis.cc

How is DNA for Memory different from Genes





RECENT PROGRESS



2012–13 first papers & experiments on DNA memory (including our CEO)

- 2013 SRC establishes SemiSynBio (3 years, \$2.5M) Twist Founded in April
- 2014-16 NIST-funded SemiSynBio Industry Roadmap (\$0.5M)
- 2016 IARPA/SRC workshop on Exascale DNA Memory Twist engagement with Microsoft through SRC meeting
- 2017 DARPA program on Molecular Computing announced IARPA/SRC workshop to develop MIST program
- 2018 IARPA MIST program formally announced IARPA MIST proposal submission

Twist Selected & Awarded for DARPA program \$2.5M IARPA subcontract in process

Encoding at Scale: first Papers (2012/2013)



Harvard & EBI

dealing with not just putting information into DNA, but techniques of recovery



Ross England | January 26, 2013

Nick Goldman, Ewan Birney, and their colleagues at the EMBL-European Bioinformatics Institute have, incredibly, developed a way to store data in synthetic DNA, the biochemical material that carries cellular genetic information.

Most data storage mediums require a consistent electricity supply, and those that don't often rapidly degrade. Goldman and his associates realized that DNA might pose a solution to this problem. DNA, with the capacity to carry the vast genetic information of all of earth's life forms, can store enormous



amounts of data. It is also incredibly long-lasting—samples drawn from 10,000-year-old biological matter are still "readable" using modern DNA sequencing techniques. As Goldman explains, DNA contains other desirable characteristics: "It's also incredibly small, dense, and does not need any power for storage, so shipping and keeping it is easy."

Semiconductor Research Corporation

R

February 2013 SRC establishes SemiSynBio (3 years, \$2.5M)

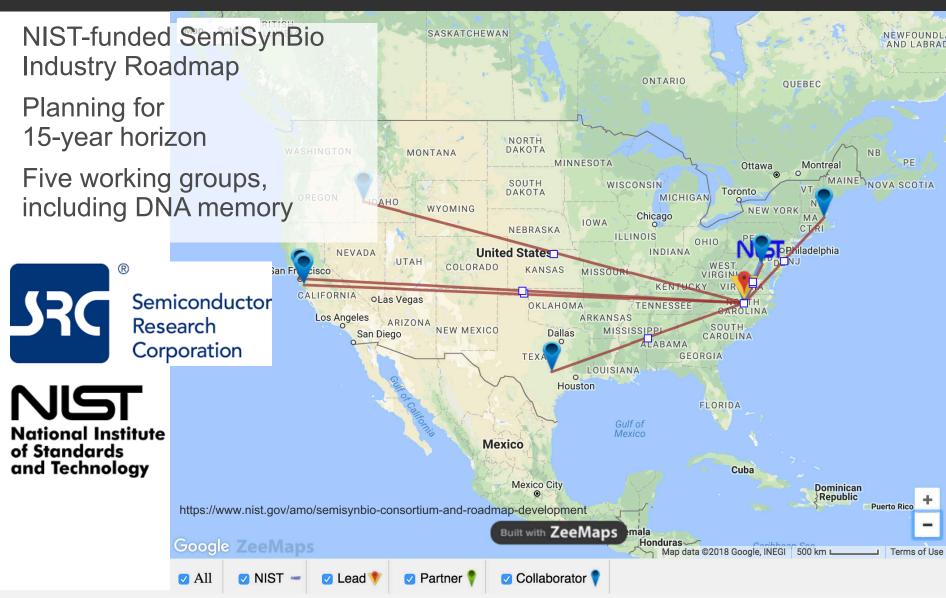
Pre-competitive academic research, intersection of synthetic biology and semiconductors/computing

Five topics, including DNA memory

Second generation of funding with NSF started (\$4.5M)

SRC Roadmap (2014–2016+)





SRC/IARPA Workshop (April 2016)



Feasibility of Exascale storage system Pre-cursor to MIST program (2018)

http://spectrum.ieee.org/biomedical/devices/tech-companies-mull-storing-data-in-dna

Tech Companies Mull Storing Data in DNA

As conventional storage technologies struggle to keep up with big data, interest grows in a biological alternative

By <u>Eliza Strickland</u> Posted 20 Jun 2016 | 16:00 GMT





Photo: Getty Images Test Tube Bits: Biology's data-storage method, DNA, might work for our data, too.

It was the looming sense of crisis that brought them together. In late April, technologists from IBM, Intel, and Microsoft joined an intimate gathering of computer scientists and geneticists to discuss the big problem with big data: Our data storage requirements are rapidly exceeding the capacity of today's best storage technologies: magnetic tape, disk drives, and flash memory.

The <u>closed-door meeting</u> in Arlington, Va., was convened to explore the potential of a new storage technology that is actually as old as life itself. The experts came together to weigh the merits of DNA data storage, which makes

DARPA Molecular Informatics

Announced April 2017, Awarded 2018





The Molecular Informatics program brings together a collaborative interdisciplinary community to explore completely new approaches to store and process information with molecules. Chemistry offers an untapped, rich palette of molecular diversity that may yield a vast design space to enable dense data representations and highly versatile computing concepts outside of traditional digital, logic-based approaches.

Given radical advances in tools and techniques to sense, separate, and manipulate at the molecular scale, what innovations can be injected into information technology, and what will the resulting systems be able to "compute"?

By addressing a series of mathematical and computational problems with moleculebased information encoding and processing, Molecular Informatics aims to discover and define future opportunities for molecules in information storage and processing.

#MemoriesInDNA

Program Goals 100 MB read/write in 1 day from archive of 1GB

https://www.darpa.mil/program/molecular-informatics https://www.darpa.mil/news-events/2017-03-23





The goal of the MIST program is to develop deployable storage technologies that can eventually scale into the exabyte regime and beyond with reduced physical footprint, power and cost requirements relative to conventional storage technologies.

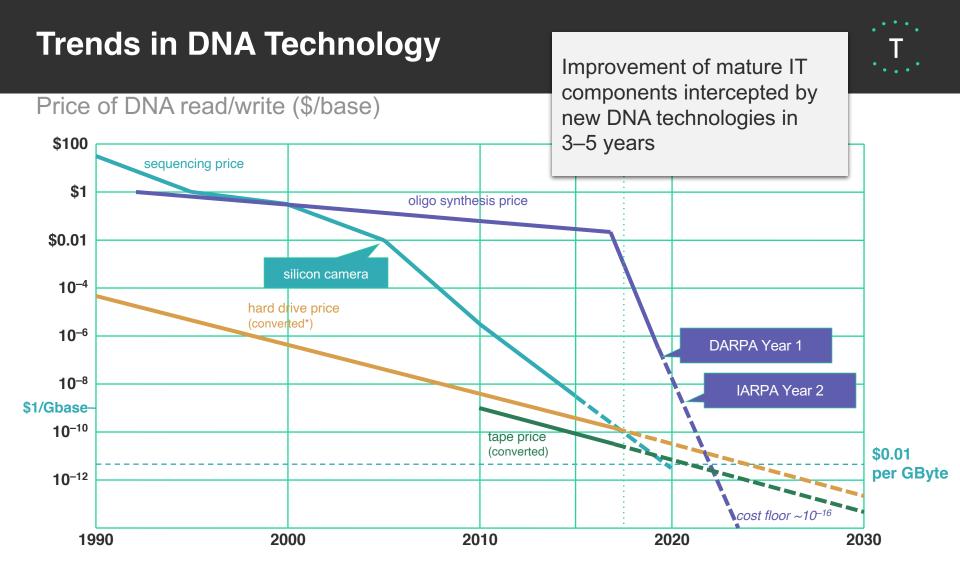
MIST seeks to accomplish this by using sequence-controlled polymers as a data storage medium, and by building the necessary devices and information systems to interface with this medium.

Technologies are sought to optimize the writing and reading of information to/from polymer media at scale, and to support random access of information from polymer media archives at scale.

Program Goals 2 years: 10GB write, 1TB read 4 years: 1TB write system

https://www.iarpa.gov/index.php/research-programs/mist

+ PB/EB scalability plan



* DNA bases per byte conversion shown at typical published encoding ranges from about 5:1 to 6.25:1



PROJECT HIGHLIGHTS

Memory of the World

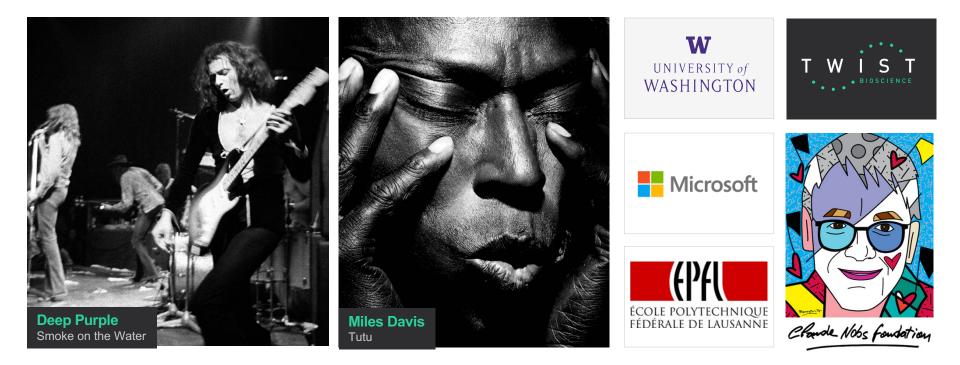




The Treasures that Record our History from 1700 BC to present day

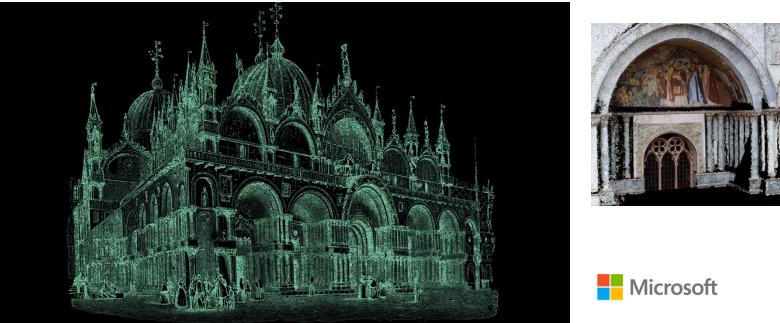
Our Cultural Heritage





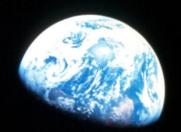
Digitized Three-Dimensional Map of St Mark's Basilica Preserved in DNA





Time Machine St Mark's Basilica UNIVERSITY of WASHINGTON





Arch Mission Foundation Announces Digital Data Stored in DNA headed to the Lunar Library





Powering the Synthetic Biology Revolution