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DNA computing: DNA circuits and data storage

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Computation has consistently served as a significant indicator and direction of social development, and volume, speed, and accuracy are critical factors during development. To accelerate this computational process, various advanced technologies and constantly optimized computational methods have been developed, such as upgrading chip design and proposing quantum and photonic computing. Recently, DNA computing, as a unique computational model distinct from traditional methods, offers remarkable advantages and addresses problems that are difficult to solve with conventional computing. By designing DNA molecules and utilizing their spontaneous reactions, specific types of complex problems can be solved, such as combinatorial optimization, traveling salesman, Sudoku and other nondeterministic polynomial time (NP) problems. Based on the spontaneity of reactions, this type of computation exhibits high parallelism, making DNA computing a viable solution for high-complexity problems. This review presents an overview of the theoretical foundations of DNA computing and summarizes three distinct advantages to over traditional computing: high parallelism, efficient storage, and low energy consumption. Furthermore, based on these advantages, we assess the current state of development in two critical branches of DNA computing: DNA circuit and DNA information storage, and provide unique insights for the future development of DNA computing.

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Introduction

Computing is essentially used to perform a series of operations in a set scenario to obtain specific results. In the process of computing, different conditions and operations may lead to changes in the results, but they also affect the space and time required for computing. A permanent pursuit in this field is to adopt appropriate conditions and computing processes for different problems by using small volume spaces to get the desired results quickly. However, efficient computation based on the complex models designed for particular problems remains a significant challenge, necessitating excess utilization of scarce computing resources and data storage. DNA computing provides an effective means in the field of computing in some special application scenarios. In 1994, Professor Leonard Adleman first proposed the concept of DNA computing and demonstrated the potential of DNA computing.[1] The fundamental idea of DNA computing is utilizing DNA molecules as the primary components of computation, whereby varying pieces of information are loaded into the DNA sequences through the programmable property and specificity of DNA molecules, thereby realizing different conditions and computational operations by using their special chemical reactions. Since the proposal of DNA computing, different computing processes and feasibility experiments for different mathematical and logical problems have also appeared, starting a new chapter in computing.

In this review, we summarized three prominent advantages of DNA computing compared to traditional computing: high parallelism, efficient storage and low energy consumption, which is significant for the development of DNA computing. Based on these advantages, DNA computing derives two important development branches, DNA circuits and DNA information storage, which offer innovative concepts and methodologies for addressing intricate scientific challenges. We provide a comprehensive overview of the current state of development in these two domains, aiming to systematically organize and introduce the development of DNA computing and inspire researchers to further understand and reflect on its strengths and weaknesses, potentially promoting the practical application of DNA computing and breakthroughs in technology and design (Fig. 1).

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Advantages of DNA computing

Highly parallel

High parallelism is the most significant advantage of DNA computing (10^{14} to 10^{20} operations per second compared to

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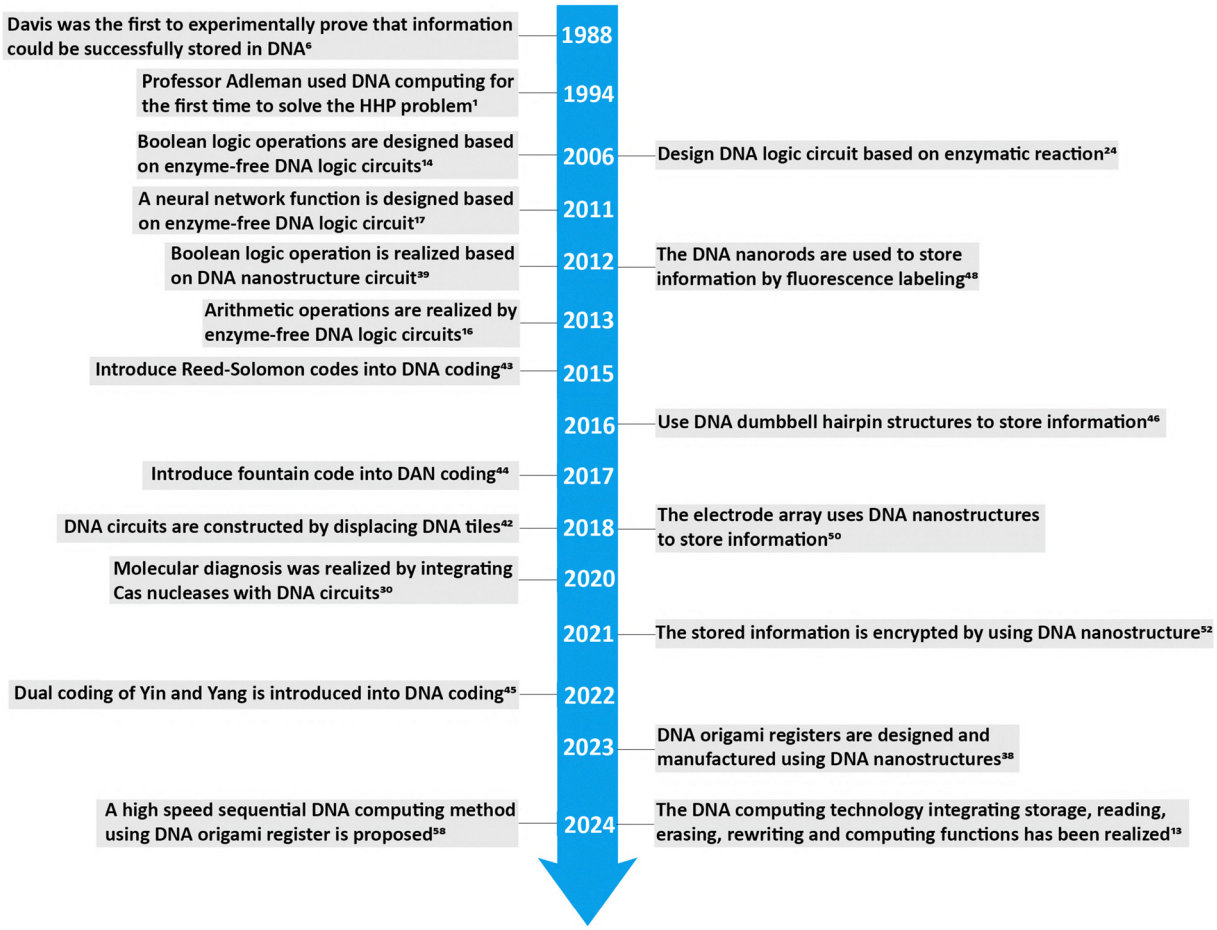

Fig. 1 Timeline of the field of DNA computing, listing the major discoveries and developments.

10^8 to 10^{12} operations per second in modern computers[2]), owing to the high degree of randomness in the chemical reactions that drive DNA strand growth. This allows all the DNA strands in the system to perform simultaneous amplification, denaturation, and base-pairing, which constitute the fundamental principles of DNA computing in addressing complex non-deterministic polynomial time (NP) problems. Therefore, implementing NP-complete problems through DNA computing represents a breakthrough from verifying the correctness of polynomial-time solutions to discovering polynomial-time solutions.[1,3–5] Under high parallelism, DNA computing often yields a large number of results, and one of the key aspects of DNA computing is to filter out a few correct solutions from the vast number of brute-force computational outcomes.

In 1994, professor Adleman first used DNA computing to solve the seven-vertex directed Hamiltonian path problem (HPP), marking the beginning of DNA computing (Fig. 2).[1] In this computation, researchers derived all possible solutions in one step and then refined the results through purification methods. The entire experiment took about seven days. By leveraging the high parallelism of DNA computing, the generation of a solution space that would be computationally

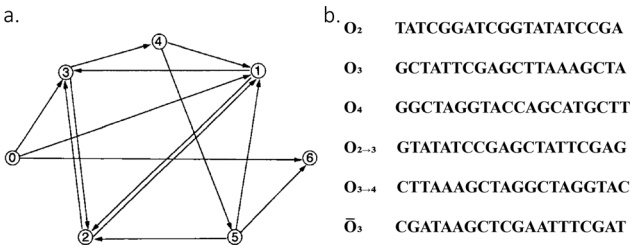

Fig. 2 (a) Illustration of the problem of directed Hamiltonian path with seven vertices. (b) Professor Adleman designed the path points and directions of the Hamiltonian path problem, where each piece of information was expressed in 20 base sequences. Parts (a) and (b) were reproduced with permission from Adlemen[1] Copyright 1994, *Science*.

infeasible in classical electronic computing could be achieved in a single time step. However, the large number of computational results from brute-force methods would lead to an exponential increase in the solution space as the number of vertices in the Hamiltonian path problem increased. In addition to solving NP problems, the parallelism of DNA computing can also be used to simulate the rules of chess,[6] and it shows potential applications in other fields, such as biomedical applications such as biosensing, diagnosis and conditional

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therapy.[7] Early high parallelism relied on the molecular random collisions, with a limited computational scale and a propensity for signal attenuation. In 2022, the Fan Team introduced an innovative DNA-based programmable gate array, which guided the directional transfer of molecules and successfully realized 30 gate-level circuits for the first time. This technology enhanced computational reliability and minimized crosstalk, offering a viable avenue for the pursuit of high parallelism and low-energy biological computing.[8] In the same year, Xiong *et al.* constructed a DNA computing structure of convolutional neural network algorithm, and realized the recognition of up to 32 molecular patterns with lower connectivity and complexity.[9] In 2024, Lin *et al.* constructed a DNA computing structure which can solve simple chess and Sudoku problems.[10] In addition to the exploration of computing power, DNA computing has gradually been applied in the field of pathological diagnosis in recent years, such as the diagnosis system of various pathological causes[11,12] and cancer diagnosis.[13,14]

Efficient storage

DNA serves as a data coding carrier of biology, consisting of a random arrangement and combination of four distinct nucleotide bases. Meanwhile, the advanced synthesis methods of DNA molecules enable the precise arrangement of nucleotide bases, thereby facilitating the encoding of desired information. Moreover, the information storage density of DNA is exceptionally high (one bit per cubic nanometer, compared with three bits per 10^{12} nanometers in modern computers[2]), and the loaded data on DNA can be stored for long periods of time under suitable conditions. In essence, DNA computing is a new solution to data processing and storage that utilizes molecular-level reactions to solve complex problems. Consequently, the data storage is the ultimate outcome of DNA computing.

The concept of DNA as a data carrier can be traced back to the mid-1960s. However, DNA synthesis and sequencing technology were not mature at that time. The initial experimental demonstration occurred in 1988, as evidenced by the studies conducted by Davis.[15] He encoded the light and dark pixels of the image through 0 and 1, and then converted the data into a DNA strand with 28 bases and inserted it into *E. coli*. After nearly 25 years of slow development, DNA information storage technology saw a breakthrough in 2012 when Church's team successfully encoded a 659 kB book using a method called short chain DNA.[16] In 2013, Goldman's team achieved groundbreaking progress in DNA data storage by successfully encoding 739 kB of data.[17] In 2024, Preuss used short sequence combination coding to significantly improve the density of information storage, achieving a DNA information storage density of 1.6 picobits (PB) per gram.[18] In the same year, DNA information storage also began to be effectively integrated with DNA computing on a large scale, developing the capability to repeatedly write, read, erase, reload and compute specific data.[10] At the same time, with the development of random access technology for DNA data storage, the practicability and reliability of DNA storage have also improved.[19,20]

Low-energy

DNA computing is a low-energy computing method. Unlike traditional electronic computers, DNA computing leverages the spontaneous behavior of DNA molecules in chemical reactions, using specific processes such as self-assembly and molecular recognition through enzymatic reactions to perform computational tasks. These reactions typically occur at room temperature, eliminating the need for complex energy supply systems, and the energy consumption of these chemical reactions is significantly lower than that of the electronic operations in traditional computers. Therefore, DNA-mediated computing is more energy-efficient than modern computers. A typical DNA strand reaction in DNA computing consumes 5×10^{-20} joules of energy, compared to 10^{-9} joules in silicon-based computers.[2]

DNA computing has the natural advantage of low energy consumption. By optimizing the operational processes and mechanisms of DNA computing, it can become even more energy efficient. By designing DNA switches and DNA molecular logic gates, the computing amount is reduced to constructing more convenient logic circuit optimization[21,22] (Table 1).

Advances in DNA computing

The above three major advantages have laid the foundation for the advancement of DNA computing, which confirm the potential for the functional and application development. By drawing upon the established framework of traditional electronic computing development, DNA computing has successfully harnessed these advantages to create a range of new functionalities and applications. Traditional electronic computers realize various operations through different combinations of electronic logic gates to receive and process electronic input signals and produce output signals. Therefore, various logic gates based on DNA molecules in DNA computing are the basis of their development, and the DNA-based computing structure using logic gates has become the core architecture of DNA

Table 1 The difference between silicon-based computing and DNA computing. The table was reproduced with permission from Shu *et al.*[2] Copyright 2023, American Chemical Society

Characteristics	Silicon-based	DNA-mediated
Information storage	1 bit per 10^{12} nm^3	1 bit per nm^3
Processing speed	10^8 to 10^{12} operations per second	10^{14} to 10^{20} operations per second (ligation)
Energy efficiency	10^9 operations per Joule	2×10^{19} operations per Joule
Computing architecture	Effective for single operation; multiple cores of CPU for multiple operations at one time (up to six operations)	Ineffective for single operation; naturally effective for massive parallel operations

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computing. In order to realize the logic gate function of different scenarios, DNA circuits currently have four construction methods: only composed of DNA chains, composed of a series of enzymatic reactions, based on DNA nanostructure circuits and compartmentalized DNA circuit structures based on other materials.

Enzyme-free DNA logic circuits

The enzyme-free DNA logic circuit is a kind of computing method developed based on traditional DNA computing, executing complete complex computing operations only through the interaction of DNA molecules. The core idea of the enzyme-free DNA logic circuit is to design specific DNA sequences and reaction steps, so that DNA molecules can spontaneously complete logic operations driven by molecular thermodynamics without enzyme catalysis. The realization of an enzyme-free DNA logic circuit is usually based on two basic strategies of DNA molecular exchange and DNA molecular recognition. In molecular exchange, DNA molecules can spontaneously react with each other through the energy difference of designed base pairing to exchange specific nucleotide pairs and finally realize the exchange of DNA chains. In molecular recognition, the transmission of signals is formed through specific DNA molecular recognition, and the continuous DNA strand displacement controls the output result of the entire circuit (Fig. 3a).[23] Based on the above two strategies, the combination of specially designed DNA sequences that enables DNA computing to perform the same operations as in an electronic computer, such as Boolean logic, is implemented by using a molecular exchange strategy (Fig. 3b),[24,25] and arithmetic operation is implemented by using a molecular recognition strategy (Fig. 3c)[26] and a series of neural network functions.[27] With the development of complex DNA computing systems, more DNA logic circuits are being applied to improve the energy efficiency, computing rate and the stability of computing. In 2018, Wang Boya *et al.* introduced redundant sequences to generate entropy changes that are unfavorable for reaction occurrence, thus constructing an error correction circuit that makes unnecessary reactions less likely to occur.[28] In 2020, Wang Fei *et al.* simulated the switching circuit used in electronic computing to enable DNA circuits to perform operations in a modular and high-speed manner.[23] With the increasing complexity of DNA circuits, higher levels of logic statements have been designed through the cross-design and application of molecular exchange and molecular recognition strategies, such as oscillating,[29] probabilistic switching,[30] buffering[31] and time control.[32]

In the enzyme-free DNA logic circuit, the circuit structure and experimental operation are simple with high system stability. However, due to the single strategy of calculation steps, the computational efficiency and flexibility are limited when dealing with complex tasks. The enzymatic DNA logic circuit compensates for these deficiencies to some extent.

Enzymatic DNA logic circuits

In synthetic biology, DNA structures that are constructed through simple enzymatic reactions exhibit enhanced specificity and superior catalytic capability compared to pure DNA systems.[33,34] Therefore, learning from these successful experiences, DNA logic circuit introduces the enzyme to make DNA computing have a simpler circuit structure to achieve efficient computing and faster computing speed.[22,35] In enzyme-free DNA logic circuits, one of the severe challenges is leakage, caused by multiple strand complexes resulting from defects in sequence design and synthesis errors. In the enzyme-promoted DNA circuit, due to the catalysis of an enzyme, the leakage problem is significantly alleviated by allowing simpler structures to be used as logical statements. For example, Song *et al.* used chain replacement DNA polymerase to achieve signal replacement output through primer polymerization.[22] In his design, the circuit functions of the OR gate (Fig. 4a) and AND gate (Fig. 4b) are realized successfully, and the result can be detected by using a fluorescence signal. The selection of enzymes is one of the most important steps in the enzymatic logic circuit, and the commonly used enzymes include DNA polymerase or splicing enzyme. There are also some promising DNA computing enzymes such as RecA (recognition and excision enzyme), deoxyribozyme, and Cas nucleases.[35] Milligan *et al.* used the RecA in 2015 to increase the reaction rate of DNA circuits by nearly 9 times (Fig. 4c).[36] Cas nucleases can bind to RNA with a complementary base, thus recognizing DNA sequences specifically through specific RNA sequences. Therefore, based on this characteristic of the Cas nuclease, various applications can be achieved by the rational design of different guide RNA and DNA circuits. In 2007, Barrangou *et al.* were able to control the activity of Cas nucleases through DNA circuits to regulate gene expression in living cells.[37] Simultaneously, specific Cas nucleases would exhibit indiscriminate nuclease activity upon binding, leading to non-selective cleavage of all single-stranded nucleic acids. By taking advantage of this indiscriminate catalytic capacity, Cas nucleases can be used to activate fluorescent single-stranded DNA reporters and be integrated with DNA circuits for sensitive molecular diagnostics.[38,39] At the same time, various combinations of polymerases, restriction endonucleases, ligase and nucleases have been gradually integrated into DNA circuits. For example, Kim and Winfree used T7 RNA polymerase to create various types of transcriptional oscillators to produce RNA and used RNaseH to destroy it (Fig. 4d).[40] The addition of enzymes not only brings more strategic choices to DNA circuits in addition to molecular exchange and molecular recognition, but also enables enzymatic DNA circuits to have complex and efficient structures by using the specificity and catalytic control of enzymes.

Logic circuits for DNA nanostructures

Whether enzyme-free or enzyme-containing, the stability of DNA circuits primarily depends on the precise pairing and interaction between DNA molecules. This makes them more susceptible to interference or failure when exposed to environmental changes or require precise reactions. In contrast, DNA nanostructures are designed with a certain level of structural stability and redundancy, allowing them to maintain strong stability under specific environmental conditions. In the 1980s, professor Seeman first proposed the scheme to self-assemble DNA strands from the bottom up.[41] In the following 40 years,

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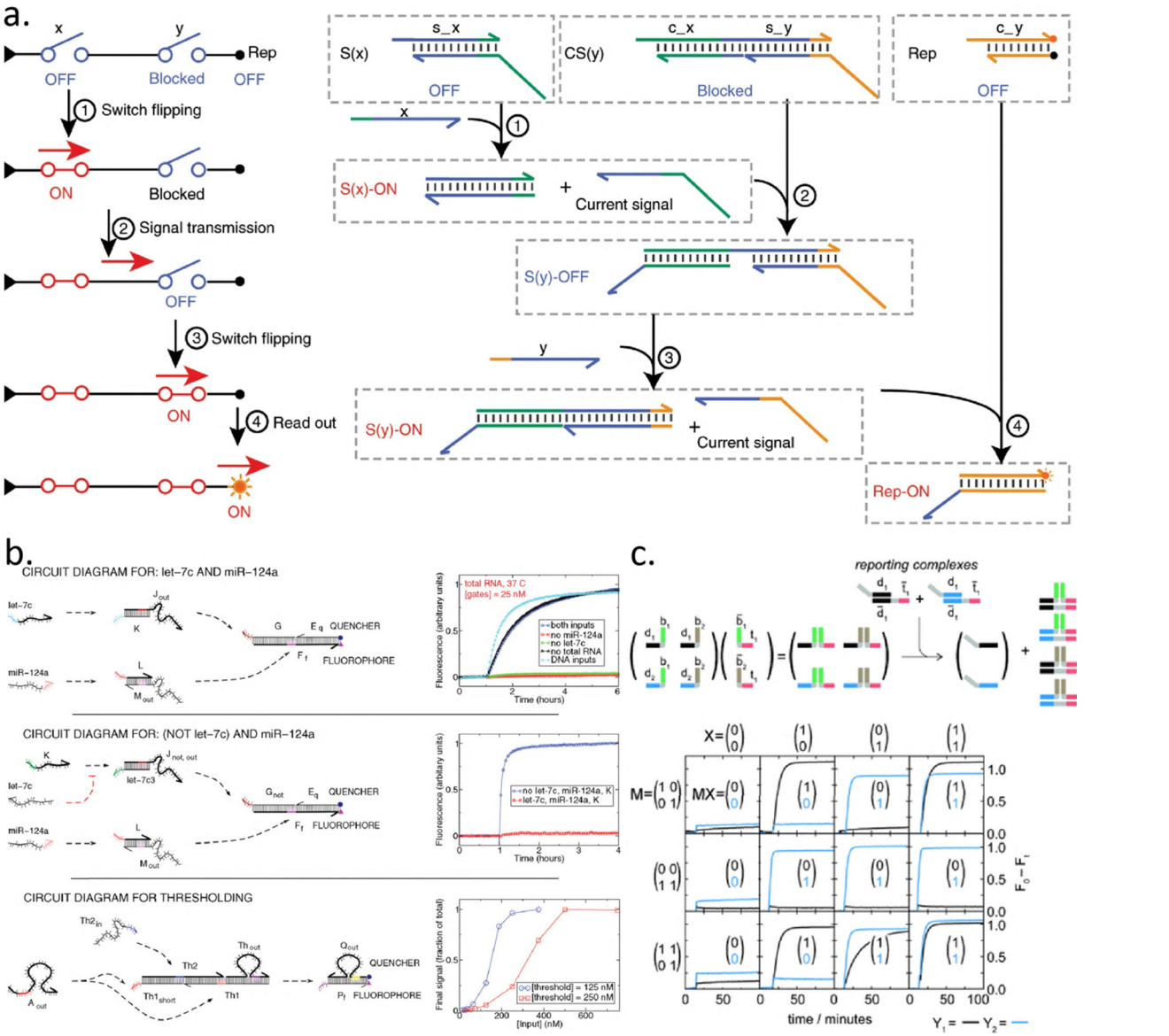

Fig. 3 (a) Schematic diagram of DNA signal conduction in a simple circuit. Using four steps, the circuit process using molecular exchange and molecular recognition strategies is realized through a specially designed DNA sequence. The figure was reproduced with permission from Wang *et al.*[16] Copyright 2020, Nature Publishing Group. (b) Some basic Boolean logic operations are implemented by the specific design of the DNA sequence, which are Translator gates, NOT operation and signal restoration from top to bottom. The figure was reproduced with permission from Seelig *et al.*[17] Copyright 2006, The American Association for the Advancement of Science. (c) Boolean matrix multiplication was performed by the combination and replacement of DNA, and 12 different combinations of products were calculated using the presence or absence of specific DNA chains to represent true (1) and false (0). The figure was reproduced with permission from Genot *et al.*[19] Copyright 2012, John Wiley and Sons.

DNA nanostructures were gradually improved by the initial tiles, extending to DNA brick and DNA origami structures, which can lead to construction of DNA structures with controllable geometry and topology.[42]

At the same time, compared with DNA molecules, a major advantage of DNA nanostructures is that the spatial structure of DNA circuits can be predetermined. Chatterjee realized DNA circuits with predetermined reaction paths by constructing DNA hairpins with certain spatial structures on DNA origami scaffolds (Fig. 5a and b).[43] This highly precise and stable self-assembly design, along with modular DNA circuits, can address specific tasks, such as cargo sorting,[44] maze solving,[45] building limited-state machine[46] and cryptography.[47] Among them, a promising DNA computing device is the DNA origami register, which is designed and manufactured using the addressable characteristics of the DNA nanostructure. This structure can temporarily store the intermediate data of the computing and guide the asynchronous computing of the cascade circuit, thus increasing the scale and circuit depth of the liquid phase DNA digital computing.[8] By designing solid-state DNA origami registers and surface-to-solution adapters to form a heterogeneous integrated architecture, the signal transmission speed between

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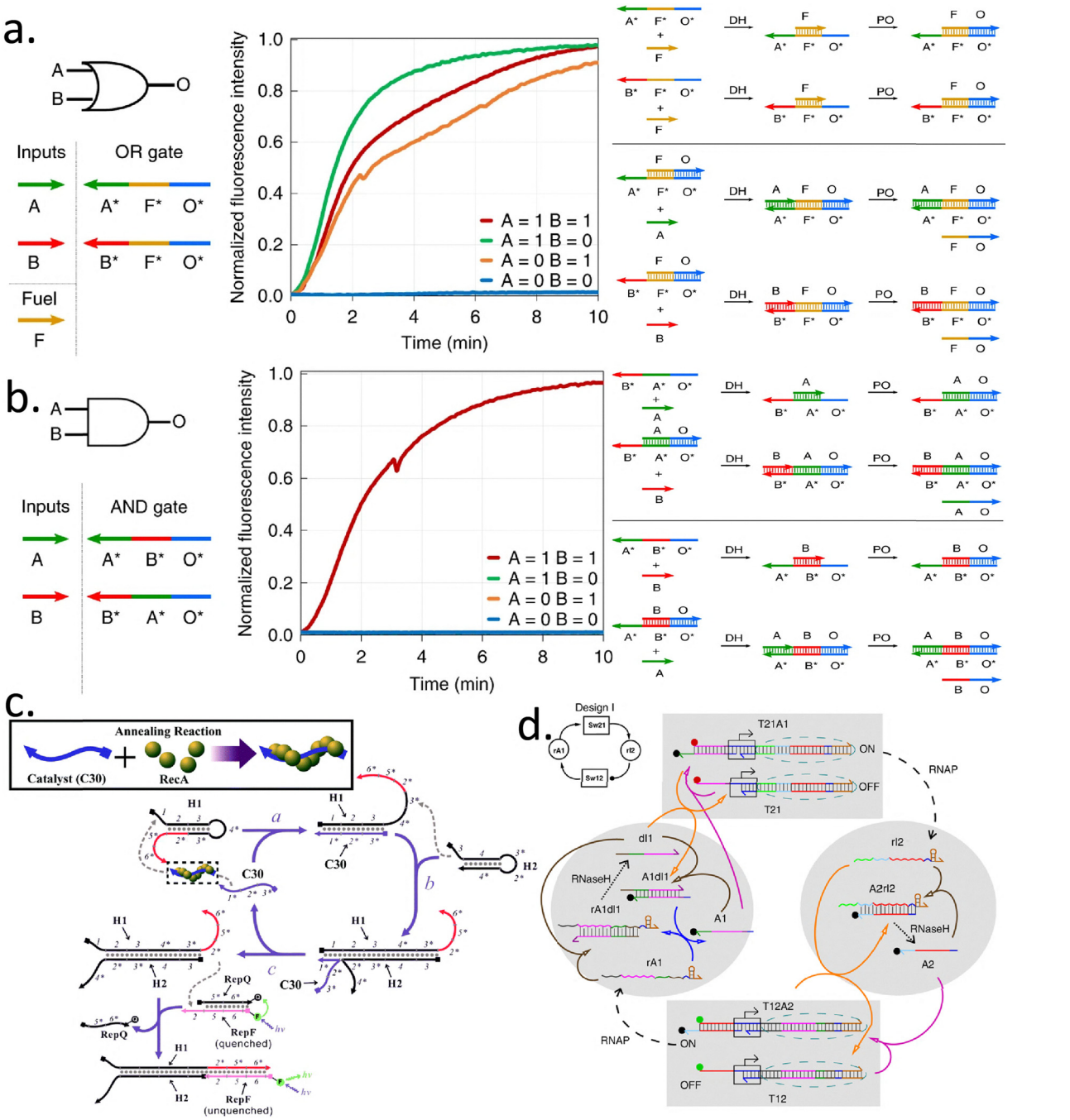

Fig. 4 (a) The design and testing of OR gate DNA polymerase enzymatic DNA circuits, which involve two types of DNA hybridization (DH) and polymerization (PO) reactions in the OR gate. (b) The design and testing of AND gate DNA polymerase enzymatic DNA circuits, which involve two types of DNA hybridization and polymerization reactions in the AND gate to generate output strands. The above two figures were reproduced with permission from Song *et al.*[15] Copyright 2019, Nature Research. (c) The use of RecA, a molecular sliding enzyme, to form catalytic complexes with DNA, enhancing the reaction rate in DNA circuit reactions. The figure was reproduced with permission from Milligan *et al.*[29] Copyright 2015, Royal Society of Chemistry. (d) The design and construction of a bistable negative feedback oscillator using T7 RNA polymerase and RNaseH. The figure was reproduced with permission from Kim *et al.*[33] Copyright 2011, European Molecular Biology Organization.

sequential cascaded circuits is improved, realizing high-speed sequential DNA computing (Fig. 5c).[48] Apart from DNA origami registers, DNA nanostructure itself can also be used as a unit of DNA computing. The carefully designed DNA nanostructure can be used to interact with biomolecules, and the computing can simulate Boolean logic in living cells *in vitro*.[49–51] In addition to programming a single DNA nanostructure, it is also possible to organize and coordinate multiple nanostructures to form DNA circuits, and then construct complex self-assembly circuits for DNA computing. DNA computing circuits

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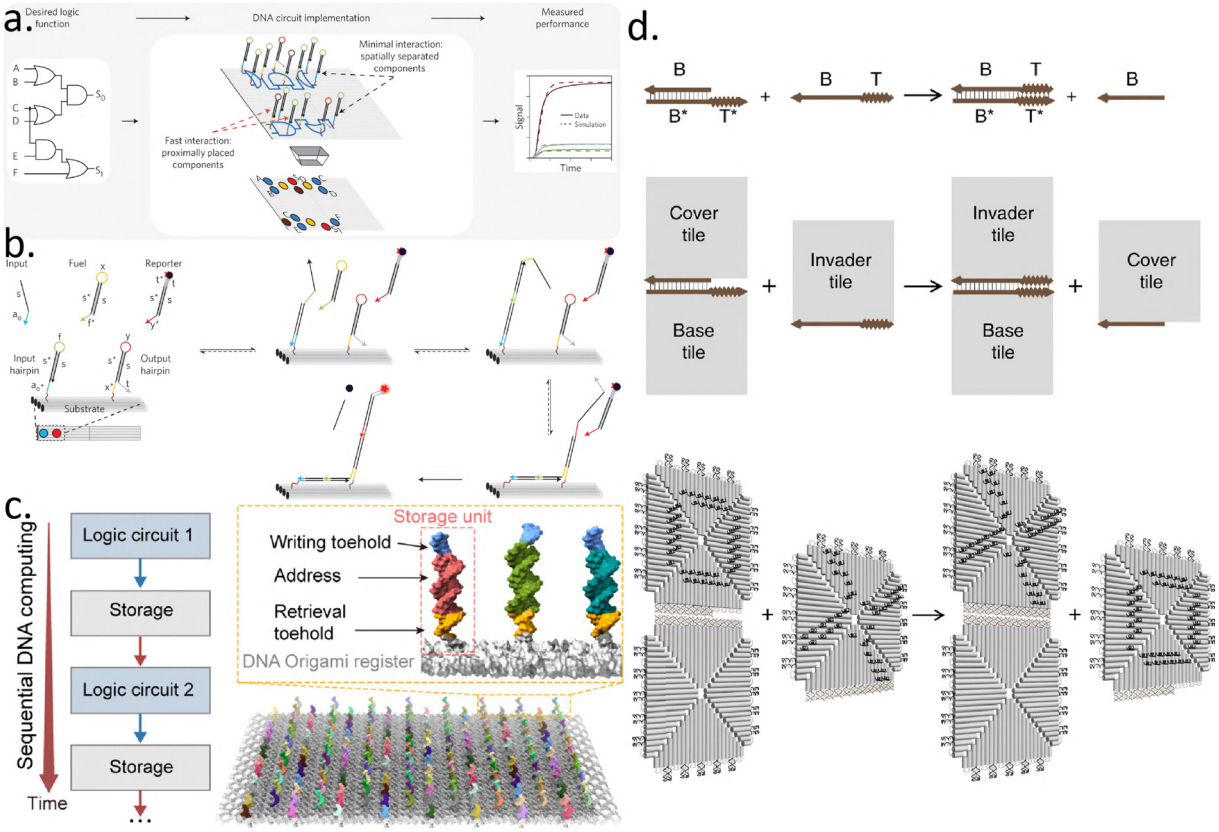

Fig. 5 (a) An abstract logic circuit (left) is implemented using DNA hairpin components arranged on the DNA origami, and a top view (middle and bottom) of the circuit on the origami shows that there are four basic hairpins in the circuit, which is tested experimentally to test the structure of the circuit (right). (b) The reaction mechanism of the four basic DNA hairpins on DNA origami. The above two figures were reproduced with permission from Chatterjee *et al.*[36] Copyright 2017, Nature Research. (c) The left figure shows the sequential calculation of data exchange between liquid circuit and solid-state DNA origami register, while the right figure shows the molecular details of the DNA origami record that can work on the surface. The gray box shows the molecular details of the storage unit. The figure was reproduced with permission from Zhang *et al.*[41] Copyright 2024, American Chemical Society. (d) Schematic diagram of the three scenarios of DNA chain replacement reaction at the level of DNA strand, domain and DNA nanostructure are realized by DNA tiles. The figure was reproduced with permission from Petersen *et al.*[45] Copyright 2019, Nature Publishing Group.

can be constructed through the interaction between DNA nanostructures, such as Petersen *et al.* constructed DNA circuits by the displacement of DNA tiles in 2018 (Fig. 5d).[52] In addition to building DNA circuits, the nuclease resistance of the DNA nanostructure may be used to realize the long-term stable DNA circuit in cells, so as to realize the living application of DNA computing. Whether it is an enzyme-free or enzyme-containing DNA circuit or a logic circuit of DNA nanostructure, there are always biological molecules diffusing and mixing in the solution, so it is difficult to control the inherent random collision of molecules.[53] To deal with this problem, researchers proposed a method to construct compartmentalized DNA circuit using other materials.

Compartmentalized DNA circuit

The compartmentalized DNA circuit is a strategy to provide an alternative for the positioning of DNA circuits by using other materials or structures besides DNA nanostructures, such as colloid, lipid, protein, vesicle, *etc.*, so as to reduce the accidental crosstalk in the solution system after the attachment or encapsulation of DNA circuit. For example, Kim and colleagues constructed DNA logic circuits by loading DNA-functionalized nanoparticles onto lipid bilayers, using the hybrid state of these nanoparticles as a signal (Fig. 6a).[54] However, the reaction rate is slow, especially between particles, due to the very small amount of DNA on such 2D surfaces.[55] This issue can be addressed by encapsulating DNA circuits in vesicles or oil-in-water droplets. For vesicle encapsulation, the vesicle membrane is modified with nanopores to create a compartmentalized space for single-stranded DNA (Fig. 6b)[56] or absorbable aggregates.[57] For oil-in-water droplet encapsulations, the signal changes are determined by the random distribution of key components such as internal enzymes,[58] making them ideal for optimizing DNA circuits in a large parameter space. Additionally, the small volume of the droplets enables single-molecule level DNA computations, making them suitable for constructing highly sensitive sensing devices.[59]

Currently, compartmentalized DNA circuits have not been widely applied in the construction of DNA computing. Their potential to achieve computational reaction specificity

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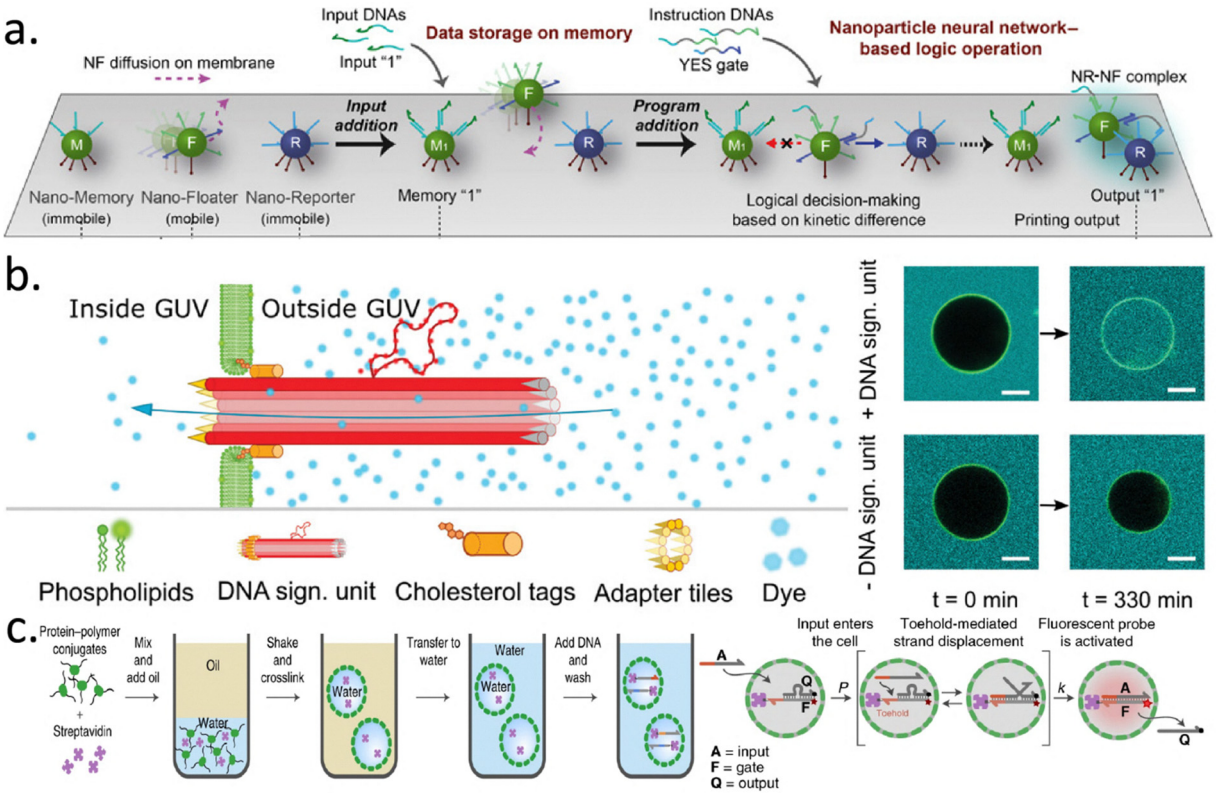

Fig. 6 (a) Three types of DNA-modified nanoparticles, memory, floating and reporting, are attached to the lipid bilayer. Memory and reporting nanoparticles are fixed, while floating nanoparticles can diffuse and react with DNA in the solution to change the hybridization state of nanoparticles. The figure was reproduced with permission from Kim *et al.*[47] Copyright 2020, American Association for the Advancement of Science. (b) By inserting cholesterol-tagged DNA origami signal units (DOSUs) into the surface of the vesicles, a transmission channel through which fluorescent molecules can be transported was constructed. The figure on the right shows the vesicles containing DOSUs (first row) and those without DOSUs (second row) in a fluorescent solution. The figure was reproduced with permission from Jahnke *et al.*[49] Copyright 2024, Wiley. (c) Oil-in-water droplets containing DNA can be prepared using protein polymer conjugates and streptavidin for DNA computing. The figure was reproduced with permission from Joesaar *et al.*[54] Copyright 2019, Nature Research.

by attaching or encapsulating DNA circuits remains to be explored. This approach could lead to a breakthrough in the flexibility of DNA computing by preventing unnecessary interactions (Fig. 6c).[60] In such a system, the diffusion of biomolecules no longer causes circuit crosstalk; instead, it facilitates circuit operation. Theoretically, this system allows for the construction of complex DNA computations using only identical and simple circuits.[61]

DNA computing structure

Currently, DNA logic circuits have been successfully constructed using different reaction principles and basic structures. When constructing DNA computing systems using these different DNA logic circuits, there are typically two approaches. The first approach involves achieving specific functions through the unique recognition capabilities of DNA. A prime example is the development of various DNA-based sensors that detect changes in parameters such as fluorescence, current, or absorbance intensity. These sensors achieve high sensitivity by designing specific DNA sequences to target molecules. To date, nearly infrared voltage sensors,[62] magnetic sensors,[63] cisplatin sensors based on fluorescent DNA,[64] and a series of enzyme sensors have been successfully developed.[65] In the field of bioengineering, DNA biosensors are widely used in environmental monitoring and clinical diagnosis. However, most DNA computations currently focus on the outside of cell membranes, with applications within cells limited to relatively simple circuits.[66] Therefore, developing DNA biosensors that can function normally in living cells is crucial for further advancements. First, it is necessary to develop DNA circuits with long-term stability, such as using DNA nanostructures to enhance the stability of DNA circuits in living cells.[67] The second type is an integrated DNA computing structure designed for large-scale parallel computing and problem-solving. In 2001, the Benenson's team constructed a programmable finite automaton using DNA and DNA polymerase.[68] In 2018, Cherry *et al.* developed a winner-take-all neural network based on DNA strand displacement reactions and an extended seesaw DNA gate motif,[25,69] which enabled information memory and utilization.[70] In 2023, Fan *et al.* designed a highly scalable DNA-based programmable gate array (DPGA) and integrated three layers of DPGA to create a universal DNA integrated circuit (DIC) capable of solving binary equations, thus overcoming the limitations of circuit scale and depth in DNA molecular computing.[8]

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Progress in DNA data storage

The DNA circuit is the main framework of DNA computing. Its development is very important, but as the input signals and output signals of the ends of computing, information storage is also a key component that cannot be avoided in the development of a DNA computer. The rapid development of DNA data storage began in 2012, when the Church Team first realized large-scale data storage in DNA molecules.[16] After nearly 12 years of development, DNA data storage has made impressive achievements in the design of data coding algorithms and data storage modes.

DNA data coding algorithm

The first key point of data storage is the coding of data. In the coding design of data, the storage capacity and recoverability of data are mainly considered. However, there are some special obstacles in the DNA data storage due to the synthesis and nature of DNA, including base mutation, sequence loss, sequence duplication, and generating unsatisfactory secondary structures. Therefore, in the development of DNA data storage there is an urgent need for algorithm optimization. In 2015, Grass *et al.* first introduced the Reed–Solomon code for error correction in the data field into the DNA data storage system (Fig. 7a),[71] thus successfully solving the error problems such as base mutation and sequence loss, laying the foundation for DNA data storage applications. From this advance, DNA storage started to develop towards storage capacity. In 2017, Erlich and Zielinski introduced the fountain code, successfully achieving a high data density of 1.57 bits per nucleotide (Fig. 7b).[72] In 2022, Ping *et al.* used two sets of coding rules to encode and convert two binary messages, with their intersection forming the final sequence (Fig. 7c).[73] This coding scheme realized high density and high stability of information storage, and increased the storage density to 1.778 bits per nucleotide. The algorithm of Yin–Yang dual encoding realizes high density and high stability of data storage, and the storage density per nucleotide reached 1.778 bits. Meanwhile, the data recovery rate of Yin–Yang dual encoding was nearly two orders of magnitude higher than that of the fountain code. In 2024, Esra Satır proposed a lossless compression method based on spatial coding, which encoded and decoded the vectors of DNA bases in each two-bit space

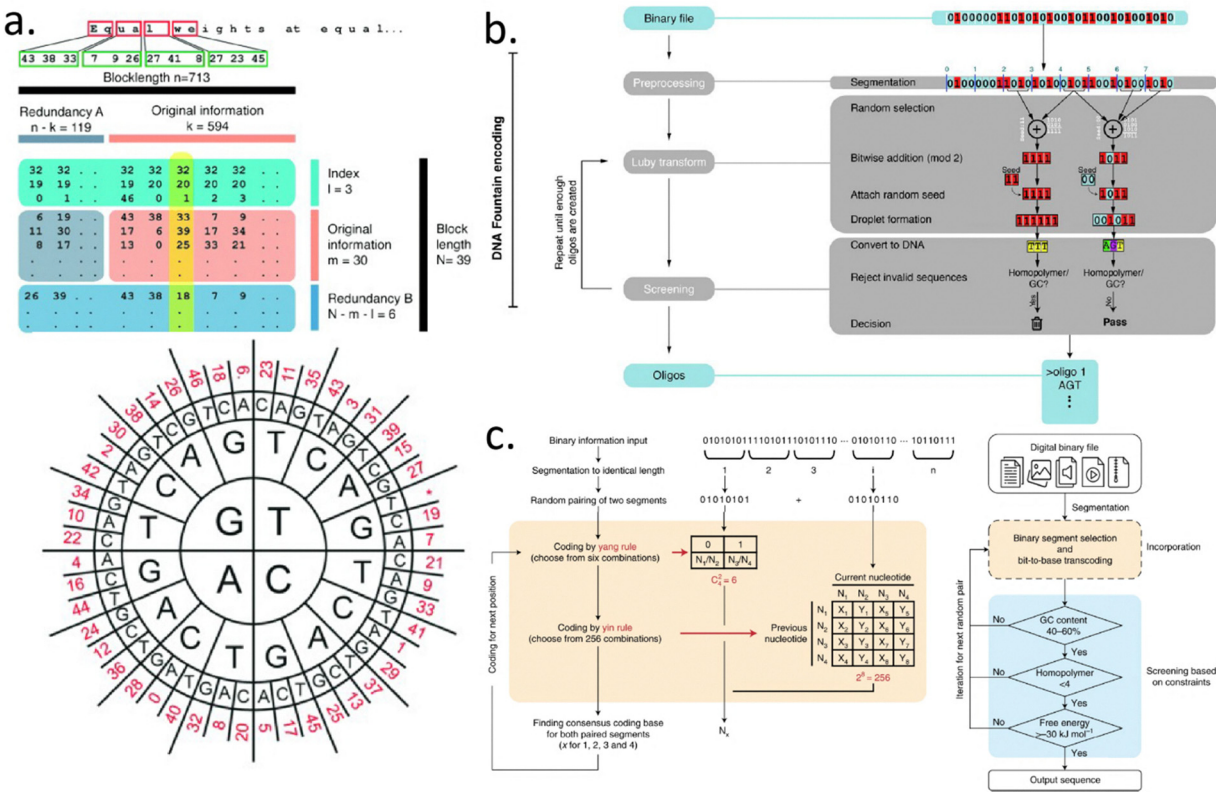

Fig. 7 (a) As illustrated in the figure above, two letters or bytes from the text file are mapped to three elements of a Galois field, which is 47 in size, through a base conversion (from the square of 256 to the cube of 47). The Reed–Solomon (RS) code, as illustrated in the middle figure, is used to add redundancy A to each block. Each column is indexed, and redundancy B is generated through a second (internal) RS encoding step. Finally, by mapping GF (47) to the DNA encoding wheel depicted below, each element is mapped to three nucleotides, ensuring that no base is repeated more than three times. The figure was reproduced with permission from Grass *et al.*[65] Copyright 2015, John Wiley and Sons. (b) The 32-bit small file uses the fountain code to divide into eight four-bit segments, and introduces a two-digit seed code, used only for display purposes. The figure was reproduced with permission from Erlich *et al.*[66] Copyright 2017, The American Association for the Advancement of Science. (c) As shown in the left figure, the YYC code is used to split and compile the same information by combining two sets of Yin and Yang coding strategies. The process of realizing the right figure is shown by YYC coding. The figure was reproduced with permission from Ping *et al.*[67] Copyright 2022, Nature Research.

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domain to improve the efficiency and density of data storage, achieving a storage density increase of 1.99 bits.[74] Recently, DNA storage systems predominantly utilize a substantial quantity of short DNA strands within a DNA pool. The process of data writing is dependent on the synthesis of DNA array, while data reading is facilitated through DNA sequencing technologies. Therefore, the faster speed and greater density of data writing and reading are apparently the further development of DNA data storage technology. In recent years, with the advancement of DNA nanostructure technology, which can write data at multiple sites in three-dimensional space and provides a larger storage capacity, DNA nanostructures have emerged as a new type of DNA information storage medium, avoiding the data read/write limitations associated with short-strand DNA.

Data storage in DNA nanostructures

DNA nanostructures provide the potential to optimize these problems through the three-dimensional multi-site writing and more macroscopic data storage space. The main types of DNA nanostructures in current DNA information storage technologies are linear DNA, DNA origami, and other structures. Linear DNA structures encode information through differences in DNA nodes, such as using enzymes to create deletions at specific sites (Fig. 8a),[75] designing DNA sequences to create dumbbell hairpin structures (Fig. 8b)[76] or using biotin for modification.[77] Such linear DNA structures store information *via* nanopore reading. The key feature of using DNA origami for information storage compared to linear DNA is that the information can be stored not just in the DNA sequences but directly in the three-dimensional origami structure, where information is encoded through the deformation or asymmetry of the origami structure. Additionally, under this storage model, more cost-effective methods like fluorescence microscopy can be used to read the information. Lin *et al.* achieved asymmetric labeling on nanorods using multicolor fluorescence, which exponentially increases coding capacity with the number of fluorophores and labeled regions, while also enabling information reading with super-resolution microscopy (Fig. 8c).[78] Pan *et al.* similarly labeled DNA nanorods with fluorescence and introduced varying amounts of fluorophores as an intensity variable, enhancing its coding capability.[79] Moreover, DNA can also form unique structures on other substrates for information storage, such as fluorescently modified DNA strands loaded onto electrode arrays (Fig. 8d)[80] and DNA chains are wound around carbon nanotubes (CNTs) to form tubular nucleic acids (TNAs).[81] At the same time, the characteristics of self-assembly of DNA nanostructures endows them with unique advantages in data encryption. The self-assembly properties of DNA nanostructures provide unique advantages in information encryption. Many information storage systems that utilize DNA nanostructures have achieved

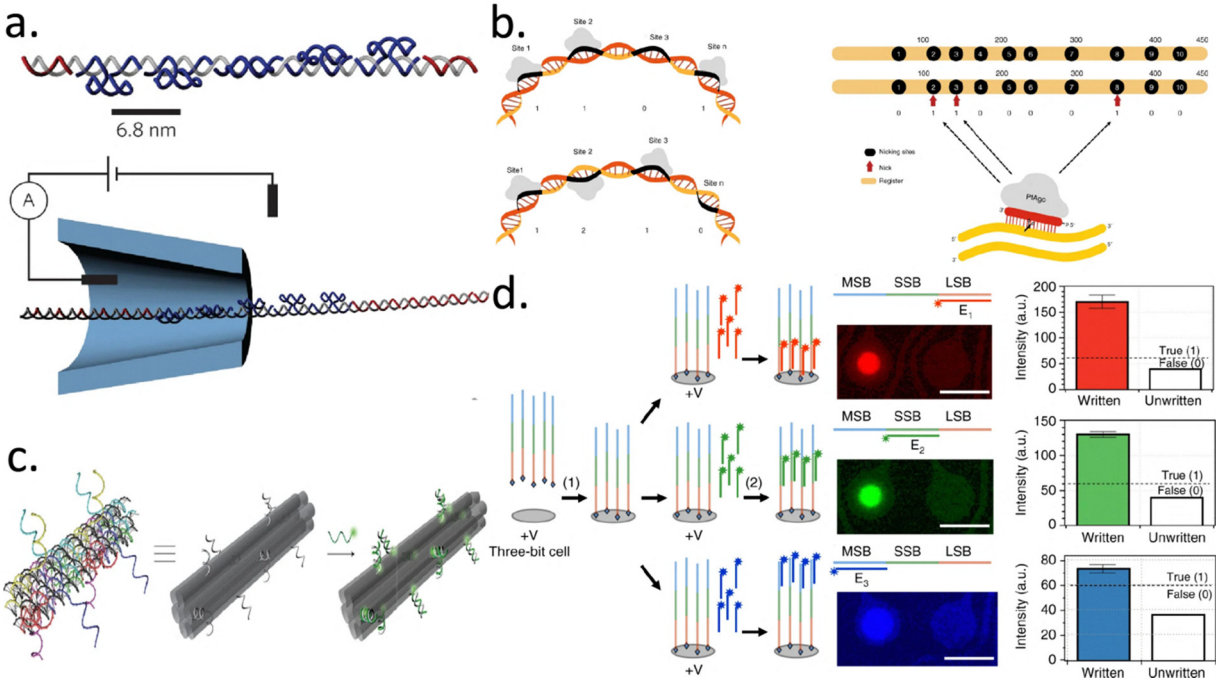

Fig. 8 (a) Different numbers of DNA dumbbell structures were inserted into a segment of the long DNA chain, resulting in different current signals under the same potential in the nanopore. The torsion angle between each DNA dumbbell unit was 34.3°. The process of realizing the right figure is shown by YYC coding. The figure was reproduced with permission from Tabatabaei *et al.*[69] Copyright 2020, Nature Publishing Group. (b) The DNA-guided programmable restriction enzyme Pyrococcus furiosus Argonaute (PfAgo) creates gaps at specific sites on linear DNA as sites for information storage. The figure was reproduced with permission from Bell *et al.*[70] Copyright 2016, Nature Research. (c) Different sites that can be loaded with fluorescein were extended on the DNA nanorods, and barcodes based on DNA nanorods were created by introducing a variable number or type of fluorescein. The figure was reproduced with permission from Lin *et al.*[72] Copyright 2012, Nature Research. (d) Three different types of information were recorded on a single electrode array unit, with different bits represented by different fluorophores. The figure on the right shows the fluorescence readings for the three different bits. The figure was reproduced with permission from Song *et al.*[74] Copyright 2018, Nature Publishing Group.

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information encryption. By removing or replacing key elements, the self-assembly structure of DNA nanostructures can become more complex and secure. For example, Zhu used linear DNA structures to store information by reserving specific ends at each site, allowing for the addition of invasion chains to alter specific information and achieve encryption.[82] Talbot used DNA switches to create small DNA loops within linear DNA structures, achieving both information storage and encryption.[83]

In recent years, research studies on DNA information storage have primarily focused on the development of static systems. When storing information, the inability to precisely control individual bases in DNA makes it difficult to modify its structure, thus the stored data is fixed at that moment. Further developing DNA computing may require dynamic information storage systems capable of reading, erasing, and writing information.

Discussion

The emergence of DNA computing offers a new approach to the field of computation. By leveraging its high parallelism and efficient information storage, DNA computing demonstrates superior efficiency in solving large-scale complex problems compared to electronic computing. Additionally, due to its high-specific programmability, DNA computing can also achieve functional designs such as biological monitoring. Based on the scale of application, DNA computing can be divided into two main development directions: one is the integrated DNA computing system designed for large-scale complex operations, and the other is the small-scale DNA computing structure designed for specific functions. Regardless of the direction chosen, the core focus remains on the customized design of DNA circuits and the flexible use of DNA information storage. In the design of DNA circuits and DNA information storage, DNA origami has demonstrated unique advantages. When constructing DNA computing structures, biomolecular components diffuse and mix in a solution, and the inherent random collisions of molecules,[53] which are difficult to control, hinder the development of scalable and programmable biological computing devices. To address this issue, DNA origami registers have been developed, offering a possibility for large-scale and even small-scale ordered DNA computing.[8,48] Currently, the development of DNA origami structures is still focused on the self-assembly of superstructures[84–86] and biomedical applications such as drug loading and targeted recognition.[87,88] However, the multi-site and three-dimensional spatial structure of DNA origami structures in DNA circuits and DNA information storage indicates greater potential for development.

Challenges and prospects

The high programmability and biocompatibility of DNA computing, among other features, make its potential for development undeniable. However, practical applications face significant challenges due to the high costs of DNA synthesis and sequencing, the low computational efficiency compared to electronic computing, and the instability of computational results. The large-scale application of DNA computing still faces numerous challenges. The development of DNA computing shares similarities with traditional electronic computing, including the need to explore new computational models, optimize computational processes, and enhance DNA circuit design. Additionally, it has its unique direction, which involves adapting to the characteristics of DNA by upgrading and iterating DNA synthesis and sequencing technologies, thereby breaking the limitations on information reading and writing.

In the face of the potential of DNA computing, we need to face up to the gap with traditional electronic computing and explore its advantages. We need to accurately identify the location of DNA computing to fully realize its potential capabilities. The excellent biocompatibility of DNA computing provides a solid foundation for biological detection. At present, most of the DNA computing concentrates on the cell membrane and the outside of the cell, and the intracellular application is only relatively simple circuit, so the development of DNA circuits that can function in living cells is the key to further development, which needs to improve long-term stability for DNA circuit in the cells. Additionally, compared to traditional computing, DNA computing has very high computational power, but due to the limited read and write speeds, this potential has been difficult to fully explore. Therefore, the data read and write potential of DNA nanostructure should be further developed, and the enhanced programmability of the system should be leveraged to develop a DNA data storage solution characterized by high data storage density and the capability for data modification.

DNA computing is still a long way from developing into an integrated computer. For a real computer, circuits form its fundamental framework, and information storage marks the beginning and end of its computations. However, integrating DNA circuits with DNA information storage has been a significant challenge in DNA computing. The primary issue is the limited controllability of DNA. Although DNA is highly programmable, accurately controlling individual bases within it remains a significant challenge after synthesis. Consequently, it is difficult to overwrite DNA circuits and information storage at the single-base or short-chain level. Although a functional DNA computer structure capable of storing, retrieving, computing, erasing, and rewriting DNA data is preliminarily constructed, this system still has vast potential for improvement in terms for speed and information capacity, and further advancements are needed to integrate DNA circuits with DNA information storage.

In the case that the breakthrough of DNA computing to electronic computing cannot be realized in the short term, the combination of DNA computing and electronic computing and the efficient conversion of DNA computing and data signals are the greatest possibility for the practical investment of DNA computing. In the future, by making full use of the advantages of DNA computing and the combination with electronic computing or living organisms, for example, enhancing the directionality and speed of DNA computing by activating different

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small-scale segmented DNA circuits with electrical signals, or achieving comprehensive and efficient detection by combining the biocompatibility and diversity of DNA sensors with the conversion between DNA signals and electrical signals, we may see a huge technological upgrade.

Author contributions

Conceptualization and supervision: H. X., Y. Y., and Y. T. Investigation, resources, and visualization: H. X. and Y. Y. Writing – original draft: H. X. Writing – review and editing: H. X., Y. Y., X. Y., Z. Z., P. L., S. L., and Y. T.

Conflicts of interest

There are no conflicts to declare.

Data availability

No primary research results, software or code have been included and no new data were generated or analysed as part of this review.

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References

1 L. M. Adlemen, Molecular computation of solutions to combinatorial problems, *Science*, 1994, **266**, 1021–1024.
2 J. J. Shu, *et al.*, Programmable biomolecule-mediated processors, *J. Am. Chem. Soc.*, 2023, **145**, 25033–25042.
3 R. J. Lipton, DNA solution of hard computational problems, *Science*, 1995, **268**, 542–545.
4 D. F. Li, Is DNA computing viable for 3-sat problems?, *Theor. Comput. Sci.*, 2003, **290**, 2095–2107.
5 M. Darehmiraki and H. M. Nehi, A surface-based DNA algorithm for the solving binary knapsack problem, *Appl. Math. Comput.*, 2007, **188**, 1991–1994.
6 X. Chen, *et al.*, Massively parallel DNA computing based on domino DNA strand displacement logic gates, *ACS Synth. Biol.*, 2022, **11**, 2504–2512.
7 S. S. Jia, *et al.*, DNA-based biocomputing circuits and their biomedical applications, *Nat. Rev. Bioeng.*, 2025, **3**, 535–548.
8 H. Lv, *et al.*, DNA-based programmable gate arrays for general-purpose DNA computing, *Nature*, 2023, **622**, 292–300.
9 X. W. Xiong, *et al.*, Molecular convolutional neural networks with DNA regulatory circuits, *Nat. Mach. Intell.*, 2022, **4**, 625–635.
10 K. N. Lin, *et al.*, A primordial DNA store and compute engine, *Nat. Nanotechnol.*, 2024, **19**, 1654–1664.
11 Q. Ma, *et al.*, An automated DNA computing platform for rapid etiological diagnostics, *Sci. Adv.*, 2022, **8**, eade0453.
12 L. H. Zhang, *et al.*, A multi-input molecular classifier based on digital DNA strand displacement for disease diagnostics, *Adv. Mater.*, 2025, **37**, 2413198.
13 D. R. Kong, *et al.*, DNA logical computing on a transistor for cancer molecular diagnosis, *Angew. Chem., Int. Ed.*, 2024, **63**, e202407039.
14 H. Y. Zhao, *et al.*, DNA molecular computing with weighted signal amplification for cancer mirna biomarker diagnostics, *Adv. Sci.*, 2025, **12**, 2416490.
15 J. Davis, Microvenus, *Art J.*, 1996, **55**, 70–74.
16 G. M. Church, *et al.*, Next-generation digital information storage in DNA, *Science*, 2012, **337**, 1628.
17 N. Goldman, *et al.*, Towards practical, high-capacity, low-maintenance information storage in synthesized DNA, *Nature*, 2013, **494**, 77–80.
18 I. Preuss, *et al.*, Efficient DNA-based data storage using shortmer combinatorial encoding, *Sci. Rep.*, 2024, **14**, 7731.
19 Y. Zhou, *et al.*, Advances and challenges in random access techniques for in vitro DNA data storage, *ACS Appl. Mater. Interfaces*, 2024, **16**, 43102–43113.
20 S. Yang, *et al.*, DNA as a universal chemical substrate for computing and data storage, *Nat. Rev. Chem.*, 2024, **8**, 179–194.
21 P. J. Shi, *et al.*, Ph-controlled DNA switching circuits with multi-state responsiveness for logic computation and control, *Chem. – Eur. J.*, 2025, **31**, e202404541.
22 T. Q. Song, *et al.*, Fast and compact DNA logic circuits based on single-stranded gates using strand-displacing polymerase, *Nat. Nanotechnol.*, 2019, **14**, 1075–1081.
23 F. Wang, *et al.*, Implementing digital computing with DNA-based switching circuits, *Nat. Commun.*, 2020, **11**, 121.
24 G. Seelig, *et al.*, Enzyme-free nucleic acid logic circuits, *Science*, 2006, **314**, 1585–1588.
25 L. Qian and E. Winfree, Scaling up digital circuit computation with DNA strand displacement cascades, *Science*, 2011, **332**, 1196–1201.
26 A. J. Genot, *et al.*, Combinatorial displacement of DNA strands: application to matrix multiplication and weighted sums, *Angew. Chem., Int. Ed.*, 2013, **52**, 1189–1192.
27 L. Qian, *et al.*, Neural network computation with DNA strand displacement cascades, *Nature*, 2011, **475**, 368–372.
28 B. Wang, *et al.*, Effective design principles for leakless strand displacement systems, *Proc. Natl. Acad. Sci. U. S. A.*, 2018, **115**, E12182–E12191.
29 N. Srinivas, *et al.*, Enzyme-free nucleic acid dynamical systems, *Science*, 2017, **358**, eaal2052.
30 D. Wilhelm, *et al.*, Probabilistic switching circuits in DNA, *Proc. Natl. Acad. Sci. U. S. A.*, 2018, **115**, 903–908.
31 Dominic Scalise, *et al.*, DNA strand buffers, *J. Am. Chem. Soc.*, 2018, **140**, 12069–12076.
32 A. P. Lapteva, *et al.*, DNA strand-displacement temporal logic circuits, *J. Am. Chem. Soc.*, 2022, **144**, 12443–12449.
33 J. Kim, *et al.*, Construction of an in vitro bistable circuit from synthetic transcriptional switches, *Mol. Syst. Biol.*, 2006, **2**, 68.
34 K. Montagne, *et al.*, Programming an in vitro DNA oscillator using a molecular networking strategy, *Mol. Syst. Biol.*, 2011, **7**, 466.

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35 H. M. Su, *et al.*, High-efficiency and integrable DNA arithmetic and logic system based on strand displacement synthesis, *Nat. Commun.*, 2019, **10**, 5390.
36 J. N. Milligan and A. D. Ellington, Using reca protein to enhance kinetic rates of DNA circuits, *Chem. Commun.*, 2015, **51**, 9503–9506.
37 R. Barrangou, *et al.*, Crispr provides acquired resistance against viruses in prokaryotes, *Science*, 2007, **315**, 1709–1712.
38 K. Shi, *et al.*, A crispr-cas autocatalysis-driven feedback amplification network for supersensitive DNA diagnostics, *Sci. Adv.*, 2021, **7**, eabc7802.
39 J. J. Shen, *et al.*, Sensitive detection of a bacterial pathogen using allosteric probe-initiated catalysis and crispr-cas13a amplification reaction, *Nat. Commun.*, 2020, **11**, 267.
40 J. Kim and E. Winfree, Synthetic in vitro transcriptional oscillators, *Mol. Syst. Biol.*, 2011, **7**, 465.
41 N. C. Seeman, Nucleic-acid junctions and lattices, *J. Theor. Biol.*, 1982, **99**, 237–247.
42 P. W. K. Rothemund, Folding DNA to create nanoscale shapes and patterns, *Nature*, 2006, **440**, 297–302.
43 G. Chatterjee, *et al.*, A spatially localized architecture for fast and modular DNA computing, *Nat. Nanotechnol.*, 2017, **12**, 920–927.
44 A. J. Thubagere, *et al.*, A cargo-sorting DNA robot, *Science*, 2017, **357**, eaan6558.
45 J. Chao, *et al.*, Solving mazes with single-molecule DNA navigators, *Nat. Mater.*, 2019, **18**, 273–279.
46 L. Liu, *et al.*, A localized DNA finite-state machine with temporal resolution, *Sci. Adv.*, 2022, **8**, eabm9530.
47 Y. N. Zhang, *et al.*, DNA origami cryptography for secure communication, *Nat. Commun.*, 2019, **10**, 5469.
48 Q. Zhang, *et al.*, High-speed sequential DNA computing using a solid-state DNA origami register, *ACS Cent. Sci.*, 2024, **10**, 2285–2293.
49 S. M. Douglas, *et al.*, A logic-gated nanorobot for targeted transport of molecular payloads, *Science*, 2012, **335**, 831–834.
50 B. Groves, *et al.*, Computing in mammalian cells with nucleic acid strand exchange, *Nat. Nanotechnol.*, 2016, **11**, 287–294.
51 Y. J. Chen, *et al.*, DNA nanotechnology from the test tube to the cell, *Nat. Nanotechnol.*, 2015, **10**, 748–760.
52 P. Petersen, *et al.*, Information-based autonomous reconfiguration in systems of interacting DNA nanostructures, *Nat. Commun.*, 2019, **9**, 5362.
53 Y. Benenson, Biomolecular computing systems: principles, progress and potential, *Nat. Rev. Genet.*, 2012, **13**, 455–468.
54 S. Kim, *et al.*, Nanoparticle-based computing architecture for nanoparticle neural networks, *Sci. Adv.*, 2020, **6**, eabb3348.
55 S. Piranej, *et al.*, Chemical-to-mechanical molecular computation using DNA-based motors with onboard logic, *Nat. Nanotechnol.*, 2022, **17**, 514–523.
56 K. Jahnke, *et al.*, DNA origami signaling units transduce chemical and mechanical signals in synthetic cells, *Adv. Funct. Mater.*, 2024, **34**, 2301176.
57 T. Mashima, *et al.*, DNA-mediated protein shuttling between coacervate-based artificial cells, *Angew. Chem., Int. Ed.*, 2022, **61**, e202115041.
58 M. Weitz, *et al.*, Diversity in the dynamical behaviour of a compartmentalized programmable biochemical oscillator, *Nat. Chem.*, 2014, **6**, 453.
59 G. Gines, Isothermal digital detection of micrornas using background-free molecular circuit, *Sci. Adv.*, 2020, **6**, eaay5952.
60 A. Joesaar, *et al.*, DNA-based communication in populations of synthetic protocells, *Nat. Nanotechnol.*, 2019, **14**, 369–378.
61 R. Carlson, The pace and proliferation of biological technologies, *Biosecurity Bioterrorism*, 2003, **1**, 203–214.
62 G. Giammanco, *et al.*, DNA-based near-infrared voltage sensors, *ACS Sens.*, 2023, **8**, 3680–3686.
63 P. J. Hore, A DNA-based magnetic sensor, *ACS Cent. Sci.*, 2018, **4**, 318–320.
64 T. Jantarat, *et al.*, A label-free DNA-based fluorescent sensor for cisplatin detection, *Sens. Actuators, B*, 2021, **326**, 128764.
65 N. Dai and E. T. Kool, Fluorescent DNA-based enzyme sensors, *Chem. Soc. Rev.*, 2011, **40**, 5756–5770.
66 J. Li, Engineering nucleic acid structures for programmable molecular circuitry and intracellular biocomputation, *Nat. Chem.*, 2017, **9**, 1056–1067.
67 A. R. Chandrasekaran, Nuclease resistance of DNA nanostructures, *Nat. Rev. Chem.*, 2021, **5**, 225–239.
68 Y. Benenson, *et al.*, Programmable and autonomous computing machine made of biomolecules, *Nature*, 2001, **414**, 430–434.
69 A. J. Thubagere, *et al.*, Compiler-aided systematic construction of large-scale DNA strand displacement circuits using unpurified components, *Nat. Commun.*, 2017, **8**, 14373.
70 K. M. Cherry and L. L. Qian, Scaling up molecular pattern recognition with DNA-based winner-take-all neural networks, *Nature*, 2018, **559**, 370–376.
71 R. N. Grass, *et al.*, Robust chemical preservation of digital information on DNA in silica with error-correcting codes, *Angew. Chem., Int. Ed.*, 2015, **54**, 2552–2555.
72 Y. Erlich and D. Zielinski, DNA fountain enables a robust and efficient storage architecture, *Science*, 2017, **355**, 950–953.
73 Z. Ping, *et al.*, Towards practical and robust DNA-based data archiving using the yin-yang codec system, *Nat. Comput. Sci.*, 2022, **2**, 234–242.
74 E. Satir, A DNA data storage method using spatial encoding based lossless compression, *Entropy*, 2024, **26**, 1116.
75 S. K. Tabatabaei, *et al.*, DNA punch cards for storing data on native DNA sequences via enzymatic nicking, *Nat. Commun.*, 2020, **11**, 1742.
76 N. A. W. Bell and U. F. Keyser, Digitally encoded DNA nanostructures for multiplexed, single-molecule protein sensing with nanopores, *Nat. Nanotechnol.*, 2016, **11**, 645–651.
77 K. K. Chen, *et al.*, Nanopore-based DNA hard drives for rewritable and secure data storage, *Nano Lett.*, 2020, **20**, 3754–3760.
78 C. X. Lin, *et al.*, Submicrometre geometrically encoded fluorescent barcodes self-assembled from DNA, *Nat. Chem.*, 2012, **4**, 832–839.

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79 V. Pan, *et al.*, Monochromatic fluorescent barcodes hierarchically assembled from modular DNA origami nanorods, *ACS Nano*, 2021, **15**, 15892–15901.
80 Y. Song, *et al.*, DNA multi-bit non-volatile memory and bit-shifting operations using addressable electrode arrays and electric field-induced hybridization, *Nat. Commun.*, 2018, **9**, 281.
81 Y. Y. Zhang, *et al.*, Encoding carbon nanotubes with tubular nucleic acids for information storage, *J. Am. Chem. Soc.*, 2019, **141**, 17861–17866.
82 J. B. Zhu, *et al.*, Image encoding using multi-level DNA barcodes with nanopore readout, *Small*, 2021, **17**, 2100711.
83 H. Talbot, *et al.*, Encoding, decoding, and rendering information in DNA nanoswitch libraries, *ACS Synth. Biol.*, 2023, **12**, 978–983.
84 X. H. Yan, *et al.*, Dynamically reconfigurable DNA origami crystals driven by a designated path diagram, *J. Am. Chem. Soc.*, 2023, **145**, 3978–3986.
85 Y. F. Yu, *et al.*, Fast synthesis of DNA origami single crystals at room temperature, *Chem. Sci.*, 2025, **16**, 793–801.
86 Z. Y. Zhou, *et al.*, Phase behavior modulation of a unary DNA origami system through allosteric stimuli, *Nano Lett.*, 2024, **24**, 12263–12270.
87 L. Z. Dai, *et al.*, DNA origami: an outstanding platform for functions in nanophotonics and cancer therapy, *Analyst*, 2021, **146**, 1807–1819.
88 X. X. Hu, *et al.*, Tunable multivalent aptamer-based DNA nanostructures to regulate multiheteroreceptor-mediated tumor recognition, *J. Am. Chem. Soc.*, 2024, **146**, 2514–2523.

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