Different Model for DNA Computation

Type	Nodes	Strands	Computation	Input Concentration	Input Type	Chemistry	Input Number
Logic	5 gates	33	miRNA pattern classification	>10 nM	miRNA	TMSD	6
Logic	12 gates	130	4-bit square root circuit	>10 nM	ssDNA	TMSD	4
Logic	7 gates	ND	2 inputs classification	>μM	Metabolites	TMSD	2
Logic	10 gates	34	4-bit square root circuit	>nM	ssDNA	Polymerase-driven SD	4
Logic	1 gate	ND	Glucose and NOx classifier	>μM	Metabolites	In-cellulo genetic circuit	2
Logic	7 gates	ND	miRNA pattern classification	fM to pM	miRNA	In-cellulo genetic circuit	6
Logic	8 gates	1	RNA transcript classifier	ND	RNA transcripts	In-cellulo TMSD + TXTL	12
Logic	7 gates	24	4-bit square root circuit	>μM	ssDNA	TMSD	4
Logic	7 gates	100	Even–odd number sorting	100 nM	ssDNA	Tile assembly	6
Neural	4 neurons	112	4-neuron Hopfield NN	>10 nM	ssDNA	TMSD	4
Neural	6 neurons	305	Handwritten digit recognition	>10 nM	ssDNA	TMSD	100
Neural	1 neuron	≈20	Healthy vs. lung cancer	>nM	Circular ssDNA	TMSD	4
Neural	2 neurons	62	Bacterial vs. Viral infection	>nM	mRNA	TMSD	7
Neural	1 neuron	ND	AND, OR, or MAJORITY	ND	DNA genes	TXTL	3

Neural	1 neuron	ND	4-input linear classifier	>μM	Metabolites	TXTL	4
Neural	1 neuron	13	Majority voting	>nM	ssDNA	PEN-DNA	10
Neural /Logic	2 neurons, 1 gate	13	Nonlinear space partitioning	pM-nM	miRNA	PEN-DNA	2
Neural	1 neuron	ND	Spatial pattern recognition	>μM	Metabolites	Multicellular genetic network	2
Neural	2 neurons	250	Handwritten symbol recognition	>10 nM	ssDNA	TMSD	144
Neural	8 neurons, 1 gate	512	Handwritten symbol recognition	>10 nM	ssDNA	TMSD	148

Other Research Papers

Paper: Implementing Digital Computing with DNA-Based Switching Circuits
Link: https://www.nature.com/articles/s41467-019-13980-y.pdf

Objective: To develop DNA-based circuits capable of performing digital computations, mimicking traditional electronic logic gates.
Key Idea: Utilizes DNA strand displacement reactions to create switching circuits that can execute basic logic operations, paving the way for molecular-scale computing.

Paper: Three-Input Logic Gate Based on DNA Strand Displacement Reaction
Link: https://www.nature.com/articles/s41598-023-42383-9.pdf

Objective: To design and construct a DNA-based logic gate capable of processing three distinct inputs, enhancing the complexity of molecular computations.
Key Idea: Employs DNA strand displacement mechanisms to build a three-input logic gate, demonstrating the scalability of DNA-based logic systems for complex decision-making processes.

Paper: Neural Network Execution Using Nicked DNA and Microfluidics
Link: https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0292228

Objective: To execute neural network computations using nicked DNA strands within a microfluidic environment, integrating molecular computing with microfluidic technology.
Key Idea: Combines DNA strand nicking enzymes with microfluidic systems to perform neural network operations, demonstrating a novel approach to in-memory molecular computing.

Paper: Training DNA Perceptrons via Fractional Coding
Link: https://ieeexplore.ieee.org/document/9048931?denied=

Objective: To develop a method for training DNA-based perceptrons (simple neural network units) using fractional coding techniques.
Key Idea: Introduces a fractional coding scheme where variables are represented by pairs of DNA molecules, enabling the training of DNA-based perceptrons through molecular reactions, bridging the gap between stochastic logic in electronics and molecular computing.

Paper: Rewireable Building Blocks for Enzyme-Powered DNA Computing Networks
link: https://www.pure.ed.ac.uk/ws/portalfiles/portal/474251479/manuscript_JACS_final.pdf

The main focus of the paper is the development of Rewireable Enzyme-Powered (REPO) neurons, a modular system for DNA-based neural networks. These neurons aim to enhance scalability and efficiency by reducing the number of nucleic acids required for computation. The study explores three strategies to improve DNA computing: enzymatic synthesis, spatial patterning of neurons, and universal single-stranded DNA backbones. This approach demonstrates better scalability, reduced noise, and modular rewiring for neural motifs like cascading and fan-in circuits.

Aspect	Details
Title	Rewireable Enzyme-Powered (REPO) neurons for DNA-based neural networks
Strategies	Enzymatic synthesis, spatial neuron patterning, universal DNA backbone
Applications	Neural network motifs (cascading, fan-in), portable diagnostics, autonomous decision-making
Advantages	Scalability, reduced signal noise, modularity
Techniques	Polymerase-actuated DNA synthesis, microfluidic automation

Potential Impact	Enhanced DNA computing power for diagnostics, data storage, and lab-on-chip devices

Peper: Cancer diagnosis with DNA molecular computation

The paper titled "Cancer diagnosis with DNA molecular computation" presents a novel method for diagnosing non-small cell lung cancer (NSCLC) by analyzing microRNA (miRNA) profiles in serum samples using DNA-based computational classifiers.
NATURE

This approach enables accurate differentiation between NSCLC patients and healthy individuals, offering a promising tool for early cancer detection.

Diagnostic Method	Lung cancer diagnostic accuracy	Invasiveness	Result analysis requirements	Time required for diagnosis	Instrumentation requirements	Cost
Computed tomography (CT)	>80% [2,3]	Non-invasive	Manual	1- 3 days	High	$$
Pathological biopsy	~100% [4]	Highly invasive	Manual	3- 5 days	Moderate	$$$
Bronchoscopy	>80% [5]	Invasive	Manual	1- 3 days	High	$$
DNA computation	~85%	Non-invasive	Automatic	6 hours	Minimal	$
Quantitative PCR	NA*	Non-invasive	Manual and Automatic	6-12 hours	Minimal	$
High throughput sequencing	NA*	Non-invasive	Manual and Automatic	1 day	High	$$$

Paper: Scaling down DNA circuits with competitive neural networks
Link: https://doi.org/10.1098/rsif.2013.0212

Objective: To demonstrate how the winner-take-all (WTA) computational effect, driven by competition for limited enzymatic resources, enables robust nonlinear computations in DNA circuits with a reduced number of DNA strands.
Key Idea: The paper presents WTA DNA circuits that classify patterns with minimal strand usage by leveraging nonlinearity, competition, and compactness. It introduces both hybrid DNA/enzyme and DNA-only systems capable of performing robust classification tasks, including handling corrupted inputs. The study highlights how biochemical competition simplifies circuit design and improves scalability for molecular computation.

Paper: A molecular multi-gene classifier for disease diagnostics
Link: https://par.nsf.gov/servlets/purl/10060829

Objective: To develop a molecular computation framework for analyzing complex gene expression signatures without requiring expensive instrumentation, enabling low-cost diagnostics and classification of diseases, such as cancer and respiratory infections.
Key Idea: The study combines an in silico classifier trained on labeled gene expression data with engineered DNA probes that process RNA inputs through molecular interactions. This approach enables gene expression analysis and classification of unknown samples, demonstrating its potential in early cancer diagnostics and distinguishing viral from bacterial infections.

Paper: An automated DNA computing platform for rapid etiological diagnostics
Link: https://pmc.ncbi.nlm.nih.gov/articles/PMC9699674/

Objective: The objective of this study is to develop an automated, DNA computation-based platform that can accurately and rapidly classify the etiology of acute respiratory infections (ARI) as bacterial or viral. The platform is designed to overcome the challenges of traditional diagnostic methods, such as long turnaround times and high costs, and aims to provide an efficient, low-cost, and automated solution for diagnosing ARI in emergency departments or point-of-care clinics.
Key Idea:The key idea of this study is the integration of DNA-based molecular computation to implement an in silico trained classifier model that uses seven mRNA expression markers for distinguishing between bacterial and viral ARI. The DNA computation platform automates the entire diagnostic process, including sample loading, marker amplification, classifier implementation, and results reporting, eliminating the need for computer or laboratory technician intervention. This system is able to classify ARI etiology within four hours, achieving high diagnostic accuracy (87%) in clinical samples, thus offering a rapid and cost-effective solution for ARI diagnosis.