TU DRESDEN, B CUBE – CENTER FOR MOLECULAR BIOENGINEERING
TU DRESDEN, CFAED – CENTER FOR ADVANCING ELECTRONICS DRESDEN
MAX PLANCK INSTITUTE OF MOLECULAR CELL BIOLOGY AND GENETICS, DRESDEN

PRESS RELEASE

25 February 2016

World's First Parallel Computer Based on Biomolecular Motors

A study reports the realization of a parallel computer based on designed nanofabricated channels explored in a massively parallel fashion by protein filaments propelled by molecular motors.

A study published this week in *Proceedings of the National Academy of Sciences* reports a new parallel-computing approach based on a combination of nanotechnology and biology that can solve combinatorial problems. The approach is scalable, error-tolerant, energy-efficient, and can be implemented with existing technologies. The pioneering achievement was developed by researchers from the Technische Universität Dresden and the Max Planck Institute of Molecular Cell Biology and Genetics, Dresden in collaboration with international partners from Canada, England, Sweden, the US, and the Netherlands.

Conventional electronic computers have led to remarkable technological advances in the past decades, but their sequential nature –they process only one computational task at a time– prevents them from solving problems of combinatorial nature such as protein design and folding, and optimal network routing. This is because the number of calculations required to solve such problems grows exponentially with the size of the problem, rendering them intractable with sequential computing. Parallel computing approaches can in principle tackle such problems, but the approaches developed so far have suffered from drawbacks that have made up-scaling and practical implementation very difficult. The recently reported parallel-

computing approach aims to address these issues by combining well established nanofabrication technology with molecular motors which are highly energy efficient and inherently work in parallel.

In this approach, which the researchers demonstrate on a benchmark combinatorial problem that is notoriously hard to solve with sequential computers, the problem to be solved is 'encoded' into a network of nanoscale channels (Fig. 1a). This is done, on the one hand by mathematically designing a geometrical network that is capable of representing the problem, and on the other hand by fabricating a physical network based on this design using so-called lithography, a standard chip-manufacturing technique.

The network is then explored in parallel by many protein filaments (here actin filaments or microtubules) that are self-propelled by a molecular layer of motor proteins (here myosin or kinesin) covering the bottom of the channels (Fig. 3a). The design of the network using different types of junctions automatically guides the filaments to the correct solutions to the problem (Fig. 1b). This is realized by different types of junctions, causing the filaments to behave in two different ways. As the filaments are rather rigid structures, turning to the left or right is only possible for certain angles of the crossing channels. By defining these options ('split junctions' Fig. 2a + 3b and 'pass junctions', Fig. 2b + 3c) the scientists achieved an 'intelligent' network giving the filaments the opportunity either to cross only straight or to decide between two possible channels with a 50/50 probability.

The time to solve combinatorial problems of size N using this parallel-computing approach scales approximately as N^2, which is a dramatic improvement over the exponential (2^N) time scales required by conventional, sequential computers. Importantly, the approach is fully scalable with existing technologies and uses orders of magnitude less energy than conventional computers, thus circumventing the heating issues that are currently limiting the performance of conventional computing.

Attachments:

Press images, video links, press contacts, references, information about collaborating institutes

Press Images

Image Credits: Till Korten, B CUBE; Mercy Lard, Lund University; Falco van Delft, Philips Research

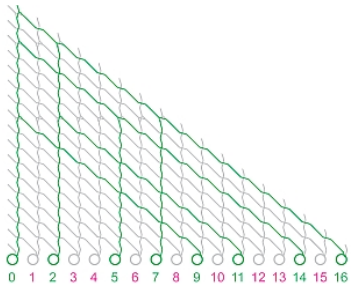

Fig. 1a

Caption: Encoding of the combinatorial Subset Sum Problem into a lithographically defined network of nanoscale channels – green numbers label the problem's solutions at the network's exits.

HiRes Download: http://bit.ly/1TwWnxt

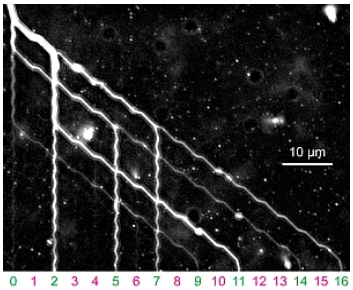

Fig. 1b

Caption: Accumulated paths of Protein filaments exploring the network in a massively parallel fashion to arrive to the problem's solution.

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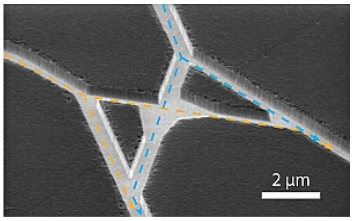

Fig. 2a

Scanning electron microscopy (SEM) capture of a split junction.

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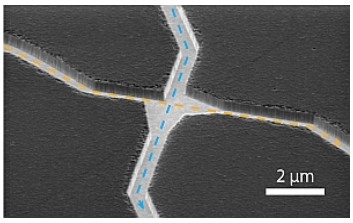

Fig. 2b

Scanning electron microscopy (SEM) capture of a pass junction.

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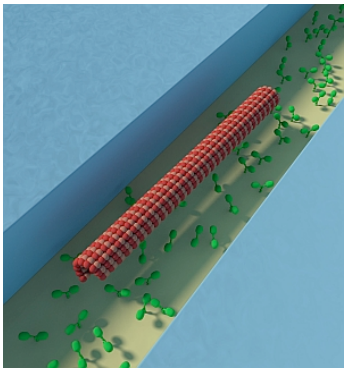

Fig. 3a

Microtubule in channel.

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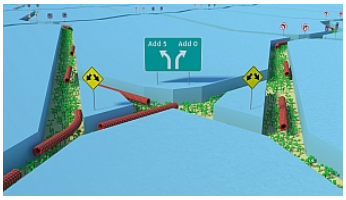

Fig. 3b

Split junction overview. Illustration of protein filaments (red) propelled by molecular motors (green) arriving at a junction where they perform a calculation operation (adding 3 or adding 0).

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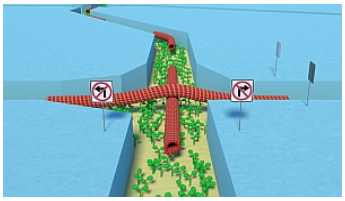

Fig. 3c

Microtubules crossing at pass junction.

HiRes Download: http://bit.ly/1QeaTcE

Videos:

https://www.youtube.com/watch?v=IhwOSS9w72Q (Animation)

https://www.youtube.com/watch?v=mR3Y5pwnX5U

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Reference:

Dan V. Nicolau Jr., Mercy Lard, Till Korten, Falco van Delft, Malin Persson, Elina Bengtsson, Alf Månsson, Stefan Diez, Heiner Linke, Dan V. Nicolau, ***Parallel computation with molecular motor-propelled agents in nanofabricated networks***, *DOI: 10.1073/pnas.1510825113*
Link to paper: http://www.pnas.org/content/early/2016/02/17/1510825113.full#sec-2

Acknowledgements:

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Information About Collaborating Institutes:

B CUBE

The Center for Innovation Competence (ZIK) B CUBE – Center for Molecular Bioengineering at the Technische Universität Dresden was founded in 2008 in conjunction with funding by the BMBF-program „Unternehmen Region". The center is dedicated to investigate and engineer biological materials along the three main axes BioProspecting, BioNano Tools and Biomimetic Materials, thereby contributing significantly to the profile of the Technische Universität Dresden in the fields of modern biotechnology and biomedicine.
www.bcube-dresden.de

cfaed

cfaed is a microelectronics research cluster of the German Excellence Initiative. It comprises 11 cooperating institutes in Saxony. About 300 scientists from more than 20 countries investigate completely new technologies for electronic information processing. These technologies are inspired by innovative materials such as silicon nanowires, carbon nanotubes or polymers or based on completely new concepts such as the chemical chip or circuit fabrication methods by self-assembling structures e.g., DNA-Origami. The orchestration of these new devices into heterogeneous information processing systems with focus on their resilience and energy-efficiency is also part of cfaed's research program which comprises nine different research paths.
www.cfaed.tu-dresden.de

MPI-CBG

The Max Planck Institute of Molecular Cell Biology and Genetics (MPI-CBG) is one of 83 institutes of the Max Planck Society, an independent, non-profit organization in Germany. The Institute has a core staff of about 500 scientists, who form a network of 25 research groups covering different topics at the interface of cell biology, developmental biology, and systems biology including research investigating illnesses such as cancer, Alzheimer's disease, or retinal degeneration.
www.mpi-cbg.de