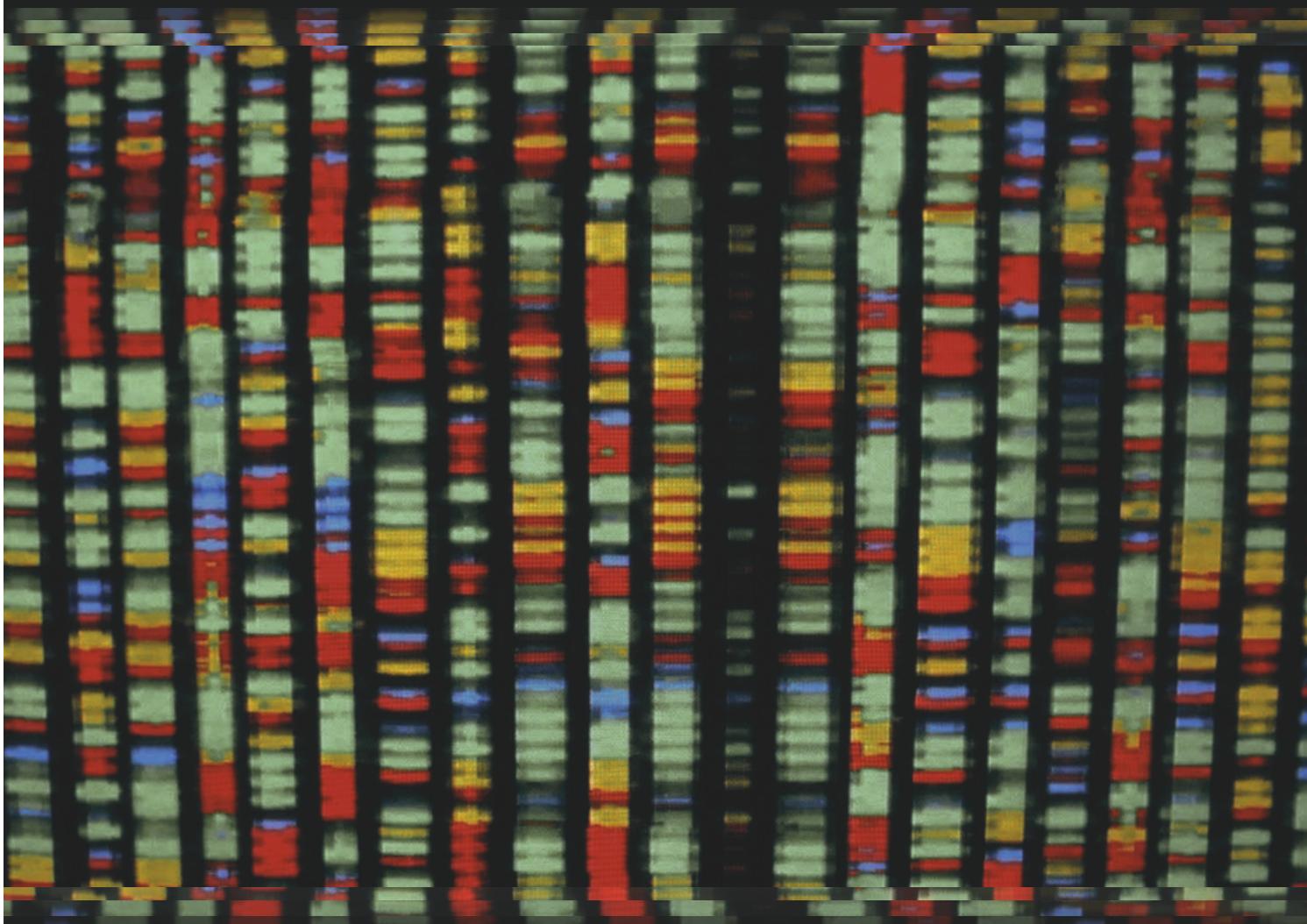


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the next generation DNA and RNA sequencing is here



SOCIETY NEWS

BIOINFORMATICS IN
CONSERVATION

BIOINFORMATICS DEBUGGED

PRESIDENT'S ADDRESS 2023
OUR EXECs: MEET THE TEAM

FEATURED ARTICLE

NANOPORE CONFERENCE:WHAT'S
NEXT?

CROSSWORD CORNER

AMINO ACID OF THE WEEK

Society



BINFSOC

News

President's Address.

BINFSOC president Jasmin welcomes the society to another year and introduces the new executive team. Huge thanks to the president and exec team last year who helped shape and grow BINFSOC to the form we see it in today!

Recent Events.

Recently we had our **Scavenger Hunt** where we tasked participants with a series of riddles, puzzles, and guessing games to explore UNSW campus and compete for GYG vouchers. Congratulations to the winners and runners up - and remember this could be you at future events!

During week 6 we put on our **bowling** shoes and lined up to get the perfect strike at Strike in Chatswood. It was great to see everyone gather around and connect with each other while also flexing some truly amazing bowling skills. We hope to see you at our upcoming social events!

Upcoming Events.

Bioinformatics in Conservation:

31 MARCH

6 - 7 PM

Come along to our Bioinformatics in Conservation event where we learn more about how bioinformatics can help save the turtles! Delve further into how we can apply bioinformatics into the conservation and protection of many endangered species and their habitats.

Sign up here: [Bioinformatics in Conservation sign up](#)

Bioinformatics Debugged:

5 APRIL

6 - 7:30 PM

Want to hear more about where bioinformatics can take you? Look no further than BINFSOC's Bioinformatics Debugged where we have a range of professionals coming in to share their experience, insights, and answers for any questions you may have about bioinformatics!

Sign up here: [Bioinformatics Debugged sign up](#)

President's Address



Welcome to T1 2023!

After two amazing years of BINFSOC we are so excited for another year where we can continue to connect students with industry, showcase bioinformatics as a multidisciplinary field, and inspire passionate students to reach their potential with the many events and opportunities we provide.

Last year was one of growth; we expanded our society portfolios to include Sponsorships, and the separation of Digital Branding into Marketing and Pubs/IT, we increased our social media outreach to Instagram, introduced an Industry Mentoring Program, and held many exciting social and career focused events.

We want to thank every member of the bioinformatics community for continuing to support this society by attending events, providing positive and insightful feedback, and supporting each other throughout the year, and hope that we can continue with this energy for the upcoming year!

In 2023 we hope to grow even more and expand our community outwards to form closer bonds with students interested or passionate about all STEM fields. We also introduced a new Education portfolio to increase student learning and help upskill in specialised areas of bioinformatics.

We started off with a bang in the Quad with O-Week 2023, and settled down with some Peer Mentoring, Scavenger Hunts, and Bowling. We've onboarded our new subcommittee members and Pubs/IT executive, and as we approach the end of T1 we are excited for all the new events and opportunities we have lined up!

Our newest event will be Bioinformatics in Conservation where we will learn how we can apply Environmental DNA to the field of conservation and understand the importance of data in protecting endangered species.

Follow along as we continue to explore the opportunities bioinformatics can provide us as well as getting involved with our incredible community and rep our society merch!

- Jasmin Yip

BINFSOC President

B

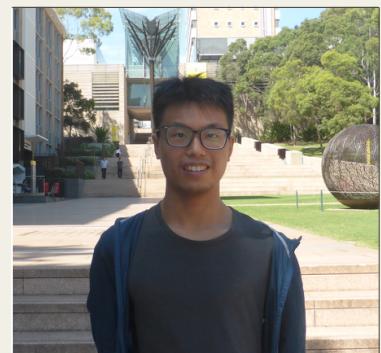
Meet the team

BINFSOC Execs and Subcommitee 2023



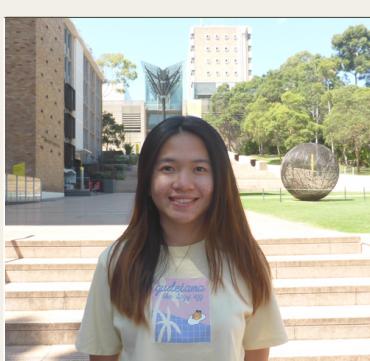
Jasmin

President



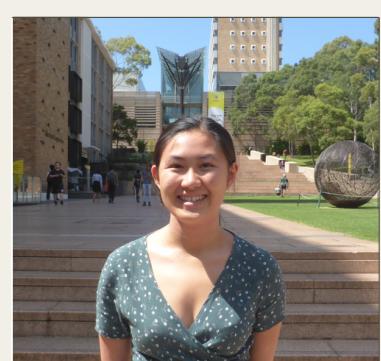
Jason

Vice President



Neysa

General Secretary



Sophie

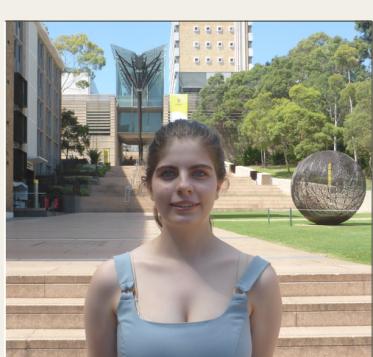
Treasurer

Following this year's first Extraordinary General Meeting, we've elected a new Pubs/IT executive, Elisabeth who will be carrying on with publishing BINFSights and maintaining our website.



Hanan

Education



Elisabeth

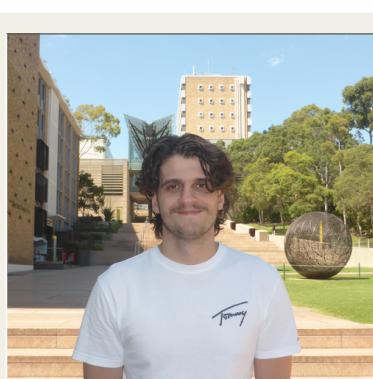
Publications/IT



Education Portfolio: Vibhuti, Hanan, Maria



Pubs/IT Portfolio: Elisabeth, Vibhuti

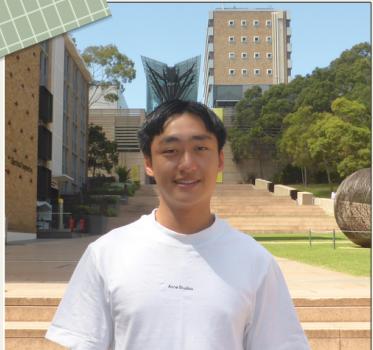


Ethan

Events



Events Portfolio: Alex, Ethan, Larissa, Sarina

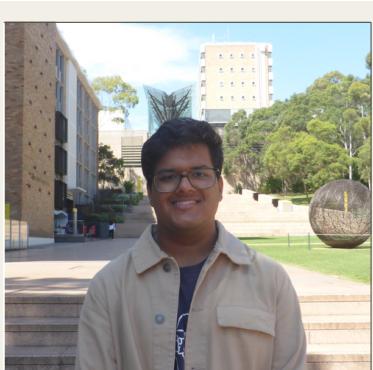


David

Human Resources

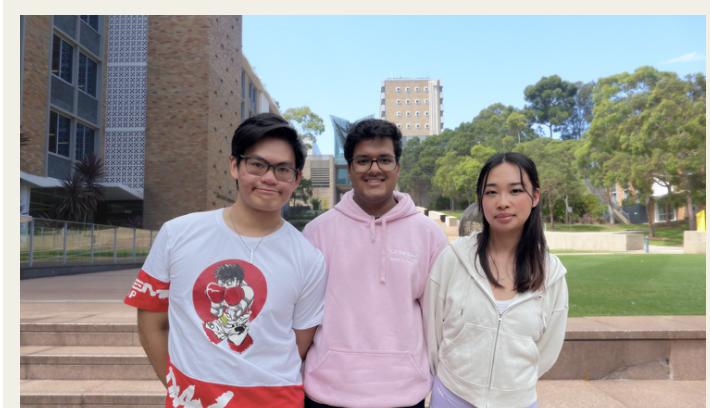


HR Portfolio: David, Keshiga, Jason Y (Not pictured)

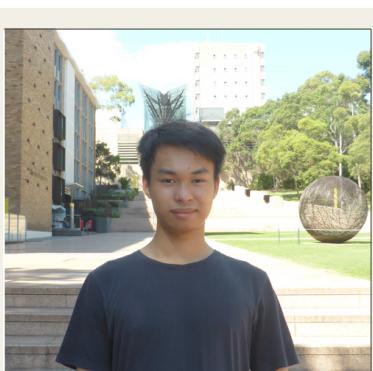


Anish

Marketing



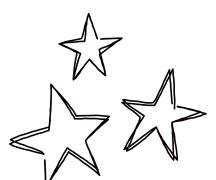
Marketing Portfolio: Simon, Anish, Annie

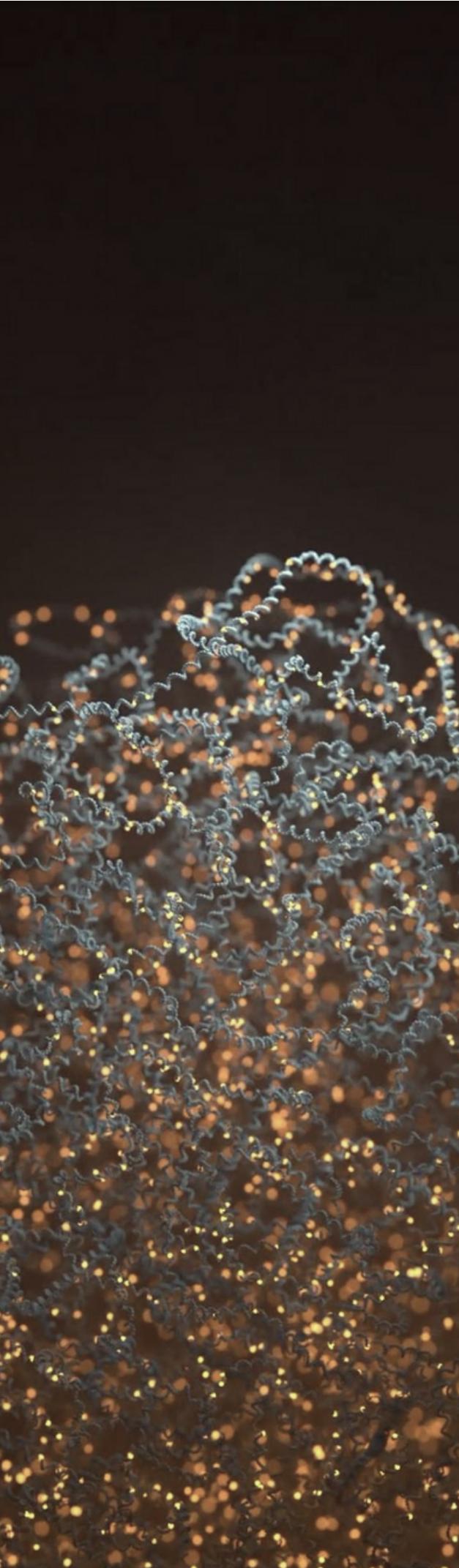


Donren

Sponsorships

A big congratulations to the subcommittee members joining BINFSOC. Looking forward to seeing great success from everyone.





hidden code

how nanopore sequencing is the future to
DNA/RNA sequencing

| findings from the 2022 Nanopore Community Meeting |

author: Gavin Li

compiled: Elisabeth Cola, Vibhuti Nandel

a deep dive into the technology that is transforming how we look into the human genome

THE NANOPORE COMMUNITY MEETING conference recently took place in New York between the 5th-7th of December of 2022. With more than 4000 people registering for the conference, it inevitably brings up the question - *what is nanopore sequencing and why is it useful in the field of bioinformatics?*

Revolutionising Sequencing

Nanopore sequencing is a technology that has revolutionised DNA sequencing. Developed under Oxford Nanopore Technologies, the genetic molecule of interest is first passed through a nanopore protein that is embedded in a membrane. The DNA is subsequently split into two single strands before it is passed through the membrane. Each nanopore acts like an electrode which, upon interacting with the DNA base, produces a signal (or more commonly known as a squiggle) indicating the position of the base. As different bases have different physical properties such as shape and sizes, its interaction with the nanopore will be different. Therefore, the nature of each signal provides insight into the identity of the base at each position.

Unlike traditional platforms used for DNA sequencing that required short lengths of DNA, nanopore sequencing is able to read DNA strands between 10-300 kilobases long. This allows for repetitive sequences to be better read and analysed, ultimately allowing for base modifications (i.e methylation) to be detected without amplification of the original strand. Essentially, nanopore sequencing allows the study of gene expression to enhance the study of heritable phenotypic changes and base modifications, the latter of which is associated with diseases such as cancer.

Throughout the years, the portability and affordability of nanopore sequencing has improved significantly. In the 1990s The Human Genome Project was launched in order to isolate and analyse a human genome and cost around \$2 billion dollars and the collective effort of thousands of scientists. Currently nanopore technologies include MinION, a pocket-sized device from only \$1000 that yields real-time sequencing data at an ideal speed of 420 bases/second. Ultimately, the time-efficiency of this technology allows it to be used in pathogen identification, a notable example being the sequencing of SARS-CoV-2 virus responsible for the COVID-19 pandemic. Developments around nanopore technology has also allowed its base calling algorithm to increase in accuracy of approximately 99.5%, allowing reliable data to be generated in a quick amount of time.

“ *The Future of DNA Sequencing Will Be in the Palm of Your Hand*

- James D. Watson

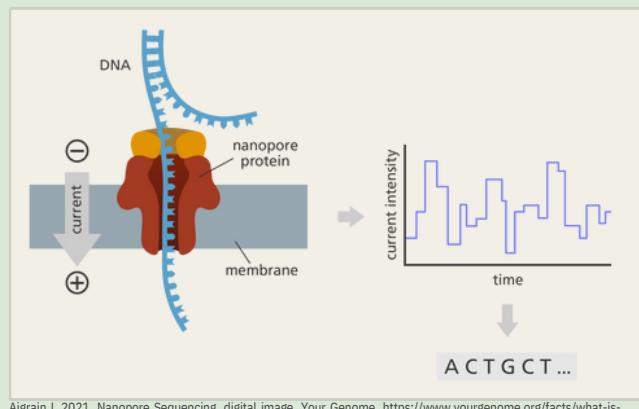
Applications

So what is one application of nanopore sequencing in scientific research?

Meet Dr Karen Miga, an eminent guest speaker in the 2022 Nanopore Community Meeting. As an Assistant Professor in the Biomolecular Engineering Department at the University of California, Dr Miga is also a co-founder of the Telomere-to-Telomere (T2T) consortium. In creating this institution, Dr Miga and her team is able to use nanopore sequencing to generate and obtain the first complete assembly of a human genome - a holistic and gapless assembly of all 22 autosomes plus the sex chromosomes X and Y.

Prior to the works of Dr Miga, the Human Genome Project (HGP) used genome sequencing to successfully sequence most of human euchromatin DNA, a loosely folded DNA that contains nearly all the genes that are actively coding for proteins. However, as euchromatin DNA consists of 90% of all human DNA, the remaining 10% is human heterochromatin DNA. This refers to the tightly-packed repetitive DNA located towards the ends (telomeres) and centers (centromeres) of chromosomes. As the repetitive bases span across hundreds of kilobases and are different for each individual, its sequencing is often overlooked by geneticists.

To obtain data from human heterochromatin DNA, the T2T consortium used MinION nanopore sequencing. Unlike the traditional methods of DNA sequencing, nanopore sequencing works by directly interacting with the DNA through probing, with long reads of DNA providing deeper insights into the epigenetic patterns on individual molecules.



Aigrain L 2021, Nanopore Sequencing, digital image, Your Genome, <https://www.yourgenome.org/facts/what-is-oxford-nanopore-technology-ont-sequencing/>

An advantage of this approach is the ability to simultaneously measure the sequence of the bases as well as the epigenetic state of the DNA, which ultimately paved the way for high-resolved methylation maps of DNA repeats in the arms of the chromosomes. To generate such high resolution methylation maps of DNA repeats, the CHM13 dNA is subjected to CpG methylation processing. Being DNA regions where a cytosine nucleotide is directly followed by a guanine nucleotide, CpG sites are the only site for DNA methylation in mammalian somatic cells. Therefore, the location and frequency of CpG methylation is crucial to the study of methylation which gives rise to human heterochromatin DNA.

From generating a CpG methylation map of satellite DNA, the T2T-CHM13 assembly is able to resolve faps and correct previously vague bases in the CRCh38 region. Resultantly, T2T is able to successfully acquire data into the newly-acquired repetitive regions of DNA, notable examples of which include telomere-associated repeats, pericentromeric repeats and monomeric sequences. As these repetitive regions previously cause issues for short-read alignments, the use of k-mer assisted mapping is able to take care of this issue as the size of k is dependent on the length of the aligned sequence read.

In turn, T2T is able to take care of insertions and indels in the reads whilst simultaneously changing the k-mer size according to how long of the reference genome a specific read spans. In consideration of the genetic diversity of cell lines from different individuals, the ability to accurately detect insertions and deletions is a crucial consideration in nanopore sequencing.

Future

So what comes next?

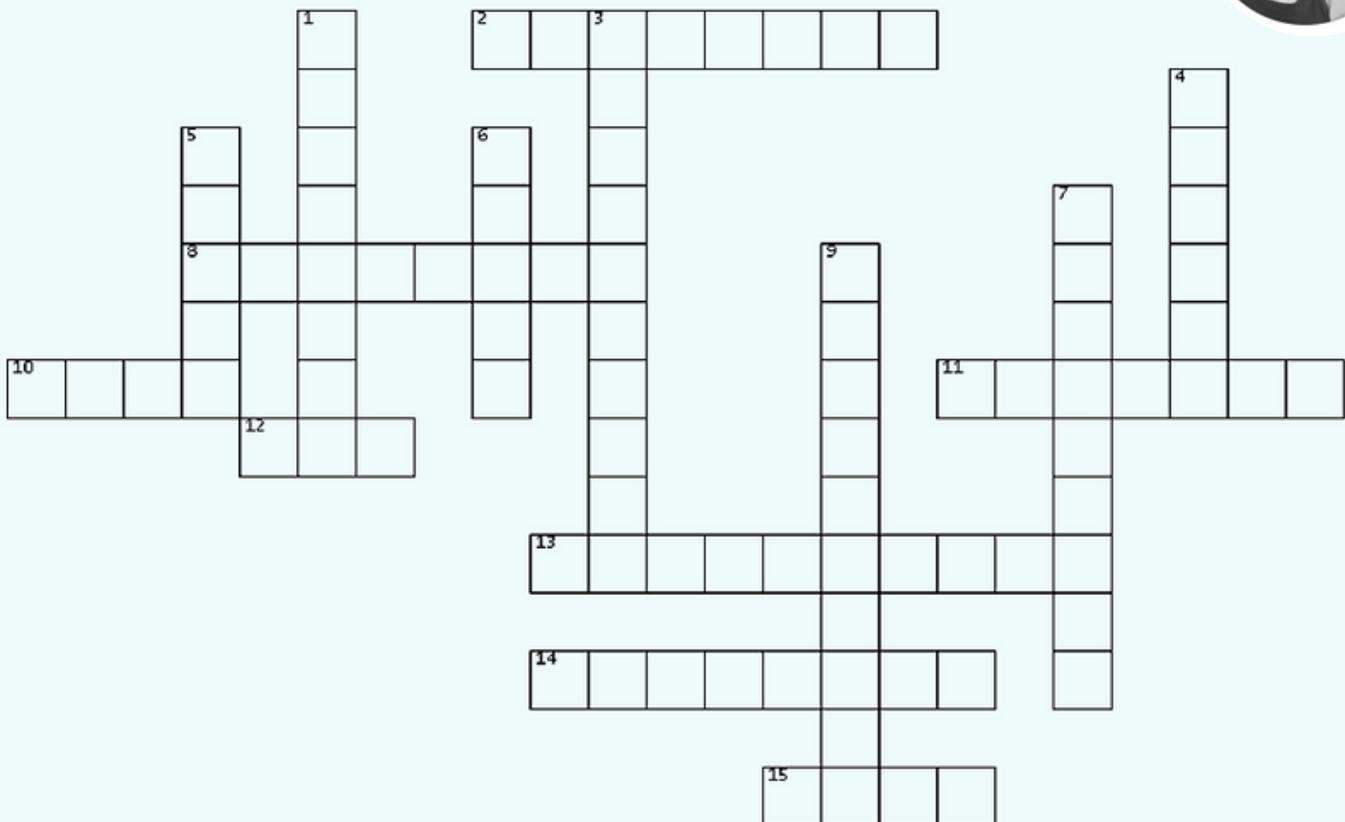
In the words of Dr Miga, the work of T2T using nanopore sequencing ‘has only begun to scratch the surface of [understanding the further details and functions of these heterochromatin sequences]. The discovery of these regions also paved the way for further epigenetic research as well as studying the basis of genetic diseases. Ultimately, the advancements in nanopore sequencing will inevitably become evident in subsequent years, when later researchers enhance the discoveries of T2T.

The 2023 Nanopore Community Meeting will take place between 17-19th of May in London, United Kingdom. The event format will be a hybrid of in-person and online attendees. For more information, check out <https://nanoporetech.com>, and for more insights into all the exciting applications this technology has, look here: <https://nanoporetech.com/applications>.

Further Reading and References

Jain, M., Olsen, H.E., Paten, B. *et al.* The Oxford Nanopore MinION: delivery of nanopore sequencing to the genomics community. *Genome Biol* 17, 239 (2016). <https://doi.org/10.1186/s13059-016-1103-0>

Crossword Corner



ACROSS

2. Study of organisms genes
8. organized collection of biological data from experiments, literature etc.
10. part of gene present in final mature RNA post RNA splicing
11. different versions of same gene in species of an organism
12. ribonucleic acid (abbreviation)
13. amino acid coded by start codon
14. sequences sharing common ancestors
15. hereditary unit of life

DOWN

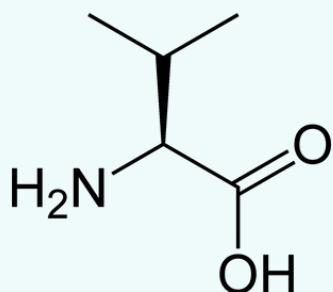
1. variation/change in DNA of an organism
3. phosphate group bonded to a ribose sugar and a nitrogenous base
4. base present only in RNA
5. set of 3 bases of code
6. tool for finding local similarity between 2 or more sequences
7. tree-like diagrams used to study evolutionary relationships
9. a threadlike structure of nucleic acids

Would you like be the Winner of the crossword and be mentioned in the next edition ? Drop-in your answers at binfsights@unswbinfsoc.com!

AMINO ACID OF THE WEEK

[VALINE]

CHEMICAL STRUCTURE



VALINE

V

Val

117.1463

POLARITY:

NONPOLAR

NEUTRAL CHARGE

DISCOVERY:

ISOLATED IN 1901 BY Hermann Emil Fischer

BRANCHED-CHAIN ESSENTIAL AMINO ACID CANNOT BE SYNTHESISED
IN THE BODY, THEREFORE OBTAINED THROUGH DIET

B



Contact us



IF YOU HAVE ANY COMMENTS or feedback regarding BINFsights, please write to us at
binfo@unswbinfsoc.com

We also encourage anyone to share with us anything you'd like us to take a look at, be it a bioinformatics tool that you have made or find useful; or news in the bioinformatics world that you'd like to see written about in future issues.



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-- The BINFSOC Team