

The Race for the Vaccine

P07 FEATURED ARTICLE

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THROUGH THE BIOINFORMATICS
PIELINE: HOW THE
SCIENTIFIC WORLD BROUGHT
COMPUTATIONAL BIOLOGY TO
THE FIGHT



Society News



BINFSOC

Arc Competition.

Congratulations to our execs and subcom who brought home the win for the Arc Clubs Clash competition. Thanks to the other societies who participated for their sportsmanship and spirit – we'll see you again next year!

Discord.

As T1 comes to a close and exams draw nearer, BINFSOC has opened our Discord for focused study sessions over the coming weeks. Feel free to register and come along to be held accountable for exam study before taking scheduled breaks with everyone else there.

When you're not studying, you can use the server to find other bioinformatics students, ask advice on BINF courses, and meet our execs and subcom.

Networking Night.

We've got another career event in the pipeline planned for week three next term. Stay tuned to our Facebook and LinkedIn pages for updates and registration details. We've also got more social events planned for T2 and we can't wait to see more BINFSOC members there!

Student Guide.

We are now in the planning stages of a Student Guide for first year bioinformatics students. We're aiming to include info about degree structure, where to find help and advice regarding your courses, and a general overview on what to expect from the bioinformatics world. If you're interested in giving us advice on what to include, as someone thinking of changing to bioinformatics or as a past student who wishes they had been told something about their journey beforehand, contact us at binfsights@unswbinsoc.com

ENGG3060

Maker Games: Activation Hub

Biomechanics of Physical Rehabilitation



Activation Hub gives engineering students nearing the end of their studies the chance to work with real clients on real problems, all while fitting into their degree program. For third and fourth year Bioinformatics Engineering students, this fits in nicely as a discipline elective!

The redesigned course focuses on intimately involving the end-user for whom you are designing the product in the entire design process, as they ultimately are the experts in the things that they need. You will be working in diverse teams to prototype and develop assistive technologies that make an impact on the lives of clients with a disability.

It is all part of a larger initiative to engage students in exciting, real-world, project-based opportunities as well as to connect students from various technical disciplines.

Keen to see how you can use your disciplinary skills to make a difference? Enrol now. No prior knowledge is required.

If you have any questions, please reach out to

> challeng@unsw.edu.au

Open Position @ UNSW

PhD student in single cell computational biology



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SUPERVISOR

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Dr. Fabio Zanini
Data Driven Biomedicine lab @ UNSW Sydney

> fabilab.org

ABOUT THE PROJECT

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While Physics has a standard model that explains most phenomena in the universe in terms of interactions between elementary particles, such a model is still missing in biology. To fill this gap, we are looking for a talented PhD student to create a standard model of cell biology.

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PLANNED START: third/last quarter of 2021

MORE INFO > unswbinfsoc.com/phd-position

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When you think about it, caring for patients is 99 percent information and 1 percent intervention, so it's clear that with or without genomics, the paradigm is shifting. Bioinformatics brings a cutting edge capacity to healthcare.

— Christopher G. Chute

Bioinformatics and the COVID Vaccine

In the early stages of the COVID-19 Pandemic, the World Health Organisation (WHO) in partnership with COVAX, laid out the goal to leave the initial phase of the pandemic by addressing three key concerns. The first of these spoke of the “speeding up the development of safe and effective vaccines against COVID-19”.

A little over a year after the pandemic began, we are seeing seven different vaccines being rolled out globally, with an additional 200 vaccines in developmental stages.

This is a very positive direction forward since having many different vaccines in development, each having slightly different targets and generating slightly different responses in the human body, increases the chance that there will be at least one safe, efficacious, and successful vaccine among the candidate vaccines, according to WHO.

The average person might pause and reflect on the incredible speeds at which these candidate vaccinations are being developed, considering the long and complex processes commonly associated

with vaccine development.

This has partly been due to the improved cooperation between administrative and research bodies. However, those with an interest in bioinformatics may be inclined to pause and reflect on the impact that bioinformatics pipelines have had on the speedy development of vaccines.

One key consideration in vaccine development is choosing of viral strain(s) most representative of the ones that currently circulating within a given population (or most likely to emerge in the future) in order to increase the efficiency of our response to outbreaks. A team at CSIRO, led by Dr. Denis Bauer, have been using and developing novel bioinformatics tools in order to address this question.

One of the projects involved collating large volumes of data of viral genomes and using machine learning techniques to build a visualisation tool. This did not use traditional bioinformatics techniques based on point-to-point alignment and phylogeny, but rather genome-wide

genomic signatures to show the relationship between many different viral strains. This offered a fluid view of the way that different viral strains were developing.

Another project proposed a server-less platform which would enable the global community to de-identify and share data such as genomic viral sequences and their associated clinical symptoms, in a way that would allow upscaling of the project to accommodate more data and continuous analyses on the nature and spread of different strains.

At the same time, other groups have investigated immunoinformatics pipelines to fly through to the vaccine stage by rapidly identifying the proteins crucial in triggering the immune response. As a refresher, WHO provides an excellent summary on how vaccines work.

In brief, a pathogen, such as a virus, can be recognised by your body's immune system through molecules called antigens, which are generally present on and unique to any particular virus. This is what vaccines intend to use to train your immune system to better recognise and defend against that virus.

However, finding these specific antigens can be difficult given the large amount of information captured in cells and genomes.

One method used a bottom-up approach and looked at the genomic information of the virus and used bioinformatics software and databases to identify open reading frames , or regions of DNA, that may potentially encode antigenic proteins - that is, those that elicit an immune response. This significantly refined the number of important proteins to be studied and significantly streamlined the process.

Other methods, involving patients who had

already developed antibodies to the virus that causes COVID-19, looked at all of the genes and proteins of the cells involved in the immune response and used machine learning algorithms and statistical methods to predict the specific sites on the antigen proteins to which immune cells are binding. Structural bioinformatics could then be used to gauge whether the candidate proteins are structurally stable to be used in a vaccine.

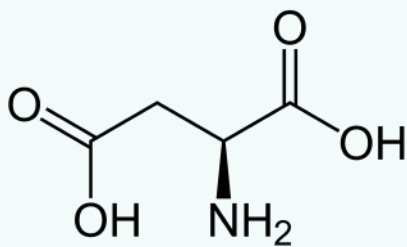
While there are caveats in interpreting the predictions being generated by bioinformatics tools and approaches, it is clear that at the intersection of computation, statistics, and a range of disciplines of biology, bioinformatics has played an enormous role in both vaccine development and intelligent monitoring of the pandemic.

AMINO ACID OF THE WEEK

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[ASPARTIC ACID]

CHEMICAL STRUCTURE

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ASPARTIC ACID

D

Asp
133.10

> DNA CODONS **G A T** **G A C**

DISCOVERED: 1827

FIRST ISOLATED FROM HYDROLYSIS OF ASPARAGINE USING LEAD HYDROXIDE.

NON-ESSENTIAL (CAN BE MADE BY BODY)

MAMMALIAN PROTEINS ONLY USE L-STEREISOIMER.

USES

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Building block of proteins. Aspartate (the conjugate base) used at NMDA receptors as neurotransmitter. Donates amino groups to form urea. Important in the fertilizer industry to improve nitrogen uptake. Used in biodegradable superabsorbent polymers, for use in nappies and feminine hygiene.

Contact us



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



TO VIEW PAST AND PRESENT issues of BINFsights, check out our website at unswbinfsoc.com/binfsights

Stay tuned on our Facebook page for updates regarding events and society news.

-- The BINF SOC Team

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