

# Tracing the Pandemic

P07 FEATURED ARTICLE

--  
HOW BIOINFORMATICS TOOLS  
ARE HELPING TRACK THE VIRUS

NEWS:  
STUDENT GUIDE

LOOKBACK:  
ARC COMPETITION

OPPORTUNITY:  
ENGG3060

QUOTE

AMINO ACID  
OF THE WEEK

CONTACT

# 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@unswbinfsoc.com](mailto:binfsights@unswbinfsoc.com)

# LOOKBACK

## Peer Mentoring.

BINFSOC's Peer Mentoring program is ongoing, with a recent social event held last week. We are currently preparing for more academic based events, with the first BINF courses for the year running next term at UNSW.

## Arc Clubs Clash Competition.

BINFSOC participated in the recent Arc Clubs Clash events. Whilst we lost the first day in puzzle activities, we displayed our mental fortitude by coming first in the trivia competition, with Bluesat coming close behind. Day 2 saw our execs and subcom show off their strength, coming out in front of EngSoc by winning the sports activities: tug-o-war, yoga poses, and push-up challenges. Shoutout to Jason (our secretary) and Ayra (HR subcom) for performing incredible 3 minute planks, and Michael (DB subcom) for bringing the win home with the push-ups.

Results are still being counted for the final event, the Club Medley with submissions ranging from photos around campus locations, counting the number of Basser steps, and poetry slams.



*Figure 1a* BINFSOC's Yoga skills on display.

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](mailto:challeng@unsw.edu.au)

# Open Position @ UNSW

## PhD student in single cell computational biology



-  
SUPERVISOR

--

Dr. Fabio Zanini  
Data Driven Biomedicine lab @ UNSW Sydney

> [fabilab.org](http://fabilab.org)

ABOUT THE PROJECT

--

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.

-

PLANNED START: third/last quarter of 2021

MORE INFO > [unswbinfsoc.com/phd-position](http://unswbinfsoc.com/phd-position)

“

Nothing in biology  
makes sense except  
in the light of evolution.

— Теодосій Добжанський



# how bioinformatics is tracing the virus

A BRIEF INTRODUCTION TO THE CONCEPT OF PHYLOGENY, AND HOW  
BIOINFORMATICS USES IT TO ANSWER IMPORTANT QUESTIONS  
CONCERNING THE SARS-COV-2 VIRUS, HOW IT SPREAD, WHERE IT CAME  
FROM, AND HOW WE CAN FIGHT IT

*Writer* Cam McMenamie

# Tracing the Pandemic

Despite large amounts of misinformation surrounding the global COVID-19 pandemic, in particular the recent vaccination statistics here in Australia, some hard facts remain. It emerged in China in late 2019. It spread to almost every region on earth except a handful of countries and the International Space Station. It was responsible for 2 million deaths in 12 months.

But the exact origins of the SARS-CoV-2 human coronavirus are a little murkier. The month-long World Health Organisation's investigation has found bats the probable origin; with another animal species posing as an 'intermediate' stepping stone to humans. However, speculation remains. The possibility of a 'leak' from a Wuhan laboratory - either accidentally or deliberately - remains unable to be ruled out by some scientists.

Understanding the origin of the virus is of great importance to epidemiologists, as the knowledge of how it initially spread can inform containment efforts to avoid future outbreaks. Answering the question of the virus' origin will also help inform ecological decisions regarding human-ecosystem interactions; legislation on breeding wild animals; laboratory practises and biosafety regulations.

Regardless of the COVID-19 origin, studying the virus' evolution at the molecular level is also important for microbiologists and pharmaceutical companies alike. Battling the current pandemic is dependent on keeping tabs

on each strain, and each new mutation that brings another adaptation or ability. Even developing the vaccine is limited by the continual branching of virus lineages, often in various parts of the world and at different times. To solve this problem, researchers look to bioinformatics for computational methods that better track changes in the virus's genome and proteome, giving them essential strategies for therapeutic developments and transmission prevention.

A key principle in life sciences is that of evolution. As organisms mutate at the genomic level, they will diverge over time. This process is responsible for the diversity of life we observe today on earth. Whilst sequencing any one organism's genetic code is fairly easy (thanks to next-generation sequencing techniques), the sequence of just one variant is only a piece of the puzzle - not the solution to the puzzle itself. Different organisms can be more similar or more different to each other; and placing them together on some sort of 'hierarchical structure' can be used to infer ancestral origins -- and their descendants. These relationships between organisms -- their 'phylogeny' -- can be visualised best as a tree (see front page). Understanding phylogenies is crucial to tracking and understanding evolution on any scale - be it the origins of the human species, or the rapid mutations of SARS-COV-2.



Since we cannot measure every single change to an organism's DNA as it happens in real time, 'probabilistic' methods that infer the phylogenies of any given set of organisms must be used. One such example is using 'multiple alignment', such as with a bioinformatics tool like clustalw. When various coronavirus genomes are sequenced, each sequence can be input to a computer, and read and compared by an algorithm. Each sequence is compared with every other sequence; and changes in the 4 letter code are noted, stored, and re-calculated. Using mathematical scoring methods and matrices, the computer spits out the result in seconds: a tree that infers the most likely path of evolution for the organisms it was given.

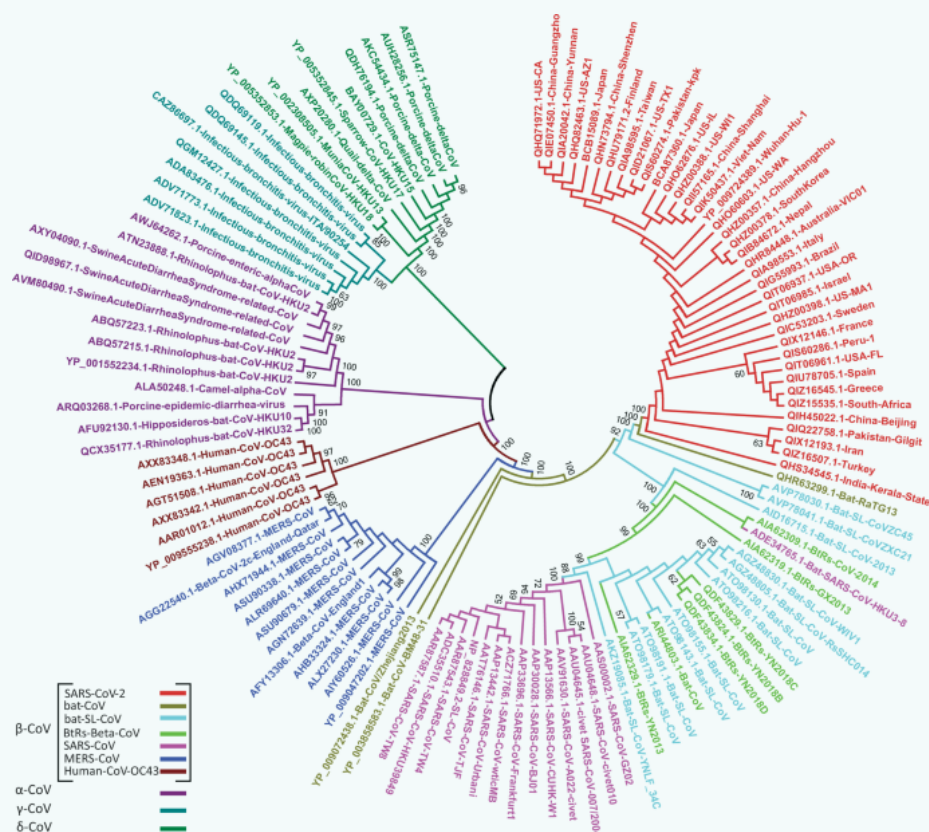
These phylogenies can be re-used and re-calculated for different sets of input data. If another strain of CoV-2 is detected in some other animal species, it could be compared with the known bat-strains, and humans -- and could confirm the leap to humans. Governments also

use phylogenetic trees to track various strains of the virus by location, telling them who's spreading which strain, and from where. This information can be used to better target containment efforts, or understanding where a hotspot has originated from.

Further research is needed to properly understand the mechanics of the virus, and the bioinformatics tools needed won't be gone anytime soon. The investigations being conducted are vital to understanding how the virus spread, how it mutates and adapts to environmental factors, and even whether or not its origin was natural or synthetic.

In order to keep up with the research efforts to combat the spread, bioinformatics tools will have to be multiplied, changed, and adapted -- much like the virus itself.

**Figure 2a:** Phylogenetic tree comparing SARS-CoV-2 (COVID-19) with other coronaviruses. The length of each 'branch' reflects the amount of genetic change.



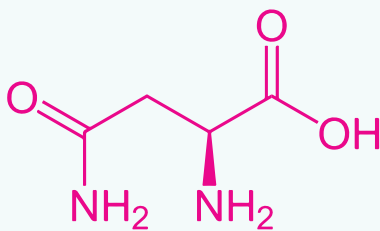
## AMINO ACID OF THE WEEK

-----

-  
[ASPARAGINE]

### CHEMICAL STRUCTURE

--



## ASPARAGINE

N

Asn

132.12

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

SULFUR CONTAINING.

DISCOVERED: 1806  
POLAR: YES  
CRYSTAL STRUCTURE: ORTHORHOMBIC

FIRST ISOLATED FROM ASPARAGUS JUICE. FIRST AMINO ACID TO BE ISOLATED.

NON-ESSENTIAL (CAN BE MADE BY BODY)

MAMMALIAN PROTEINS ONLY USE L-STEREISOIMER.

### USES

-- Used in biosynthesis of glycoproteins. 'Storage' form of aspartate (precursor for DNA, RNA and ATP synthesis). Required for development and function of Central Nervous System (CNS). Important for metabolising ammonia (toxic to body).

# Contact us



IF YOU HAVE ANY COMMENTS or feedback regarding BINFsights, please write to us at [binfsights@unswbinfsoc.com](mailto: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](http://unswbinfsoc.com/binfsights)

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

-- The BINF SOC Team

**BINF**  
sights.