

# recipes for future plagues

with great power comes great responsibility

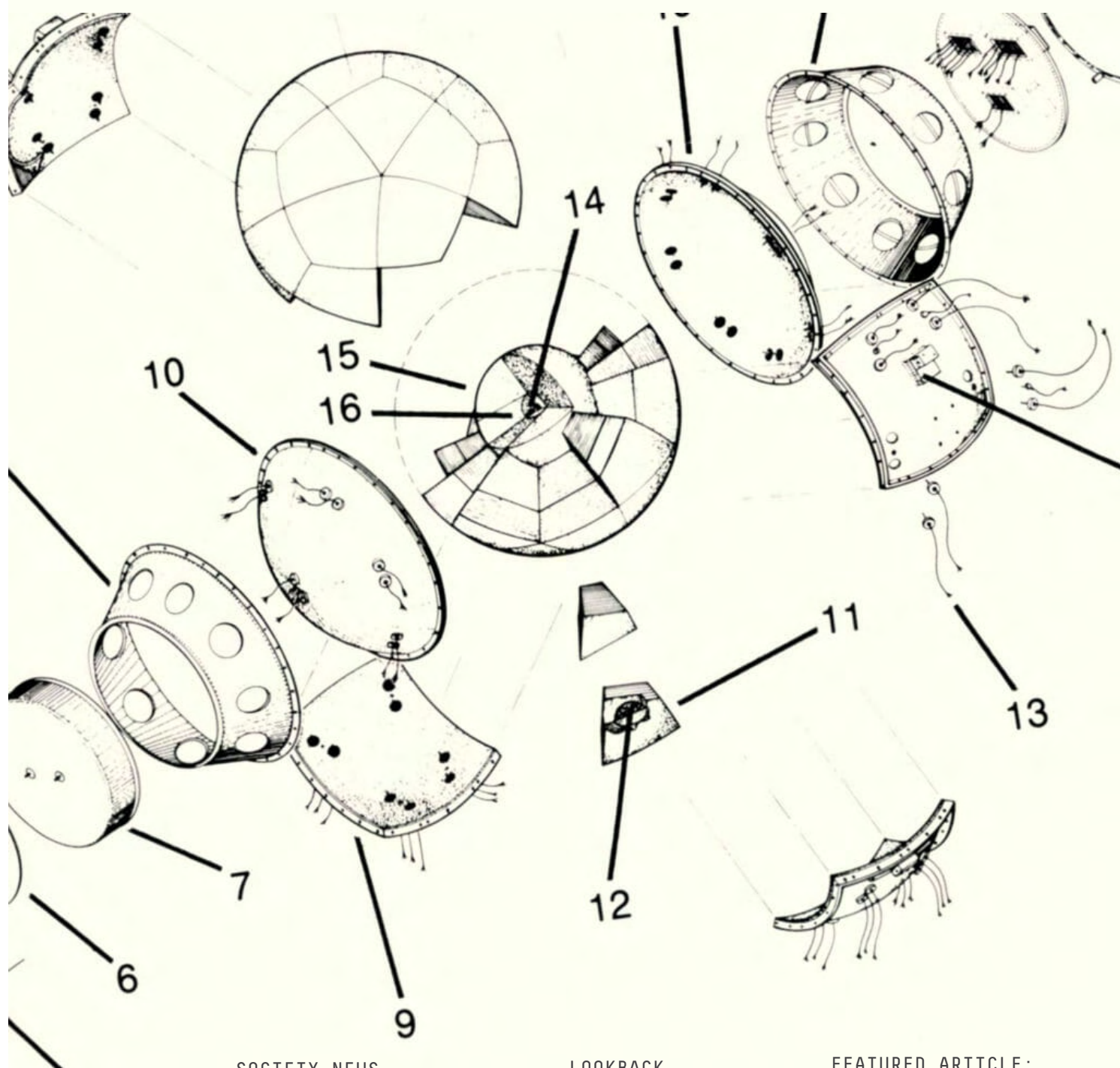


IMAGE SOURCE:  
Mike Wagnon

SOCIETY NEWS  
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BIOINFORMATICS DEBUGGED  
PUB CRAWL  
MERCH COMPETITION

LOOKBACK  
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SUBCOM INDUCTION

FEATURED ARTICLE:  
PANDEMIC PREPAREDNESS

QUOTE  
AMINO ACID OF THE WEEK  
CONTACT

# Society News



# BINFSOC

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## Bioinformatics Debugged.

Are you pursuing a Bioinformatics Degree with little to no understanding of what it actually is? Or have you just always wanted to learn more about the field and the career opportunities coming with this major?

BINFSOC presents Bioinformatics Debugged 2.0, a great opportunity for students to interact with a range of professionals who have studied bioinformatics or are currently in the field, to discuss the wide career opportunities available to aspiring bioinformaticians such as industry research or software development and data analysis. Get a greater understanding of the exciting field of bioinformatics through people who have gone through a similar journey!

EVENT LINK: <https://fb.me/e/2uvh3lsEL>

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## Pub Crawl.

Still recovering from midterms? Flex-week wasn't long enough? Well here's your chance to let loose at the INTER-SOC PUB CRAWL!

Hosted with BABSOC x CEUS x BINFSOC x SOCS. Epic deals will be up for grabs! Get your friends, and make your way across the city – everyone is welcome! We will post updates for locations on this event as the evening progresses. Feel free to join at any time.

### EVENT DETAILS:

Date: Thursday 7th April

Time: 4pm onwards

Dress Code: Anything neon or bright. Free glow sticks available.

LINK: <https://fb.me/e/1jD5xSqQB>

Click GOING and stay tuned for updates!

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## Merch Comp.

If flexi week wasn't enough time for you to procrastinate, then channel your creative energy and create the next image for BINFSOC! The winner of our design competition will receive a free merch item.

SIGNUP: <https://forms.gle/D66aq1VJvrg9vGBM6>

SUBMISSIONS CLOSE SUNDAY 3rd APRIL 11.59PM

Details: Design for front and/or back only. Feel free to submit the design on a mock-up. Ensure you have a high-res PNG of your design in case you win. UNLIMITED ENTRIES PERMITTED

# B Subcom Induction

A warm welcome to all our new subcommittee members! Our induction was held on the 24th and we are excited to have the new team on board. With more members than last year and a new sponsorships portfolio, it's exciting to see BINFSOC grow for our 2nd year running.

## MEMBERS LIST

### HR:

Gavin Li  
Cate Timso

### Marketing:

Andrea Dobles  
Donren Leung  
Anish Sanghvi

### Events:

Naomi Warren  
Sabena Bhadri  
Sophie Khov  
Ethan Dichiara  
Neysa Ngo

### Sponsorship:

Derrick Lin  
Sasha Graham

### Publications/IT

Thomas Parish  
Dan Shea  
Anna Do



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The fact that there was no catastrophic pandemic in recent history does not mean there won't be another one. And we are certainly not prepared for the next pandemic.

— Bill Gates, 2017

# recipes for future plagues

A NEW GOVERNMENT PROGRAM: THE SOLUTION TO  
FUTURE PANDEMICS? OR THE PATH TO CATASTROPHE?

*Writer* Cam McMenamie

# pandemic preparedness

IN THE INFORMATION AGE OF TODAY, there's no doubt that much of our technology and ways of life have changed to incorporate rapid collection, storage, and dissemination of data at massive scale. In just a few generations, we have gone from a handful of TV channels to conglomerate streaming platforms such as Netflix. Our reliance on the internet for our entertainment, social interaction, news and even navigation is clear. It may come as no surprise, therefore, that biology has similarly been revolutionised by information technology.

## Sequencing

This has been highlighted by the ongoing COVID-19 pandemic, in which scientists in independent labs from most nations on earth rushed to sequence, document, and upload viral genome sequences to the internet in order to understand how SARS-CoV-2 mutates and spreads. This open sharing of data of genome sequences is one of the cornerstones of bioinformatics, and is thanks to the rapidly declining cost of sequencing technology. For perspective, the current estimate for a per-specimen whole genome sequence of SARS-CoV-2 is around USD \$33.8. That's roughly a 30kb-long RNA sequence. The human genome in comparison is approximately 3.2 billion base pairs long, and has gone from around USD \$1bil to less than \$1000 (and taking a lot less time). Of course, the sequencing hardware wouldn't be able to obtain rapid, accurate sequence reads without the onboard computation as pioneered by the bioinformatics field.

## GISAID Database

The data-sharing efforts seen in the pandemic have been staggering, and only increase exponentially with each year. The popular data platform GISAID (Global Initiative on Sharing Avian Influenza Data, as featured in the lab exercises from the BINF3XXX courses) hit 1 million coronavirus sequences from 172 countries in April 2021. The sequence data has been important for understanding the origins of the virus, mapping its spread and transmission across earth, and understanding the new functions or abilities gained through evolution. The data has also been vital to creating vaccines (particularly the spike 'S' protein sequence), and observing the effect of vaccination on viral strains and epidemiological changes.

The success of genome sharing seen with GISAID has also surprised many scientists who have in the past speculated that the openness of data may prove a barrier to those wishing to retain the credit for publication. The non-for-profit team at GISAID have also helped educate other users around the world to contribute to the repository. One team in West Africa that lacked bioinformatics know-how were able to learn skills such as sequence analysis from workshops hosted in Senegal by a GISAID-affiliated scientist.



Positive COVID tests are prepared for sequencing to study variants at the University of Maryland in Baltimore. Credit: Michael Robinson Chavez/The Washington Post via Getty



## The USAID Program

If the COVID-19 pandemic has highlighted anything, it has certainly been the importance of responding to the impacts of viruses well before they emerge as fully-fledged threats to human health and impact global society. Understanding the coronavirus now is clearly important; but perhaps more importantly is understanding potential threats before they become issues. For this reason, the United States Agency for International Development (USAID) is currently in the planning stages of a global effort to identify and understand many pandemic-capable threats; particularly those that may emerge from wildlife and transmit to human populations. Discovery & Exploration of Emerging Pathogens - Viral Zoonoses (DEEP VZN), a five-year, approximately \$125 million project will work with partner nations and research institutions to detect and categorise novel pandemic-grade viruses that have a chance of uprooting society as we have seen the last few years. USAID's announcement comes at a time where "advancing global health security, international pandemic preparedness, and global health resilience" is a key focus in the eyes of world governments, and particularly the Biden administration. The United States government is no doubt well aware of the economic costs faced during the COVID-19 outbreak, despite the effects of the coronavirus being about as mild as they could have been (considering the lethality of pandemics in the past). As viral outbreaks do not adhere to national or geographic boundaries, the threat of an emerging pandemic-grade virus on global security, population health and economic prosperity is, in a way, being treated as a concern of national security and understanding rather than any other health crisis.

## A Strategic Error?

For these reasons, USAID's announcement of the VZN program ([usaid.gov](https://www.usaid.gov)) may seem to many like an appropriate and much-needed action on behalf of all those affected by COVID-19 and any potential pandemics. However, there may be a dark side to the project that a few academics have already found alarming. Some have even called for the immediate scrapping of the project entirely, or at least to limit the public and open-source nature of the data collected.

In the interests of pandemic preparedness, new strains and genome sequences are being uploaded at an increased rate. As mentioned previously, this is thanks to the advances in bioinformatics and sequencing technology. Whilst the people behind the USAID project undoubtedly have the best interests in mind, a potentially catastrophic effect may emerge as an unforeseen consequence, argues Kevin M. Esvelt, an assistant professor of the MIT Media Lab (<https://www.sculptingevolution.org/kevin-m-esvelt>). Esvelt is known for his work on 'gene drive' systems as utilised by CRISPR, and has been an outspoken advocate for research sharing in the interests of public safety to the expense of research credit and getting results published. Having received his PhD from Harvard for synthetic microbial ecosystems, he contributed to the development of CRISPR (a popular tool for engineering genomes). Since then his work has involved finding early-warning systems for catastrophic biological threat detection, utilising methods from cryptography (such as those found in Bitcoin) to secure the screening of DNA synthesis, and advising policymakers on biological risk mitigation. He has had articles published in *Nature* and *Science*, and been covered in the *New York Times* and *Washington Post*.

Despite his strong views on collaboration and data sharing, Esvelt has made it clear that the VZN project's plan to collect 800,000 samples in Asia, Africa and Latin America to identify 8,000 to 12,000 new viruses, including some in the same family as SARS-CoV-2, is a catastrophic misstep.

Whilst it intuitively makes sense that we should keep tabs on what viruses are out there that might make the leap to humans and cause another outbreak, might we inadvertently in the process of producing this information cause one? In the interests of preventing a potential pandemic in the future, may we pave the way for one that need not have occurred to inevitably occur in the present?

### **Great Power**

Whilst speculation about lab leaks in Wuhan and revelations of U.S.-funded “gain of function” studies on pandemic-grade viral strains is certainly alarming, and should no doubt be investigated as they stand, the emerging threat seen by Esvelt and other academics is not that of an accidental escape from laboratory. Rather, the potential threat is far more insidious: Esvelt estimates that currently, around 30,000 individuals across the world with access to the necessary equipment and biotechnological know-how could, if they wished, create a pandemic outbreak of their own through simply having the genomic sequence itself. This number of 30,000 will only increase over time – many futurists predict that biotechnology will soon become as easily accessible as a motor vehicle or other device. The rapid advance of sequencing technology with exponentially smaller costs as mentioned earlier is an indication of what is still yet to come. Esvelt's research area of focus, CRISPR-initiated “gene drives”, may also play a role in an engineered

virus: irreversible effects may spread rapidly through a population as demonstrated with malaria-carrying capability in mosquitoes.

“With great power comes great responsibility” – with the increasing ease to wield such biological powers, more and more individuals will have the opportunity to utilise the amazing advances in biotechnology – just as those same individuals have the ability to exploit and misuse it.

Unlike previously discussed misuses of biological technology (previous issue of BINFsights, “bioinformatics in defence”) where the entire biotechnology capability of a rogue state or adversary may be responsible for an attack or provocation, the capability may rest in the hands in a lone-wolf attacker or extremist group that has the biological knowledge – or access to someone that does.

It is for this reason that Esvelt argues that the VZN project, while well-intentioned, should be re-evaluated, and that pandemic-grade virus sequences should be kept secretive and governments and scientific institutions alike have the shared responsibility of keeping the information secure and safe for the community at large.

Esvelt drives this point home with a stark analogy: “you wouldn't expect to find the plans for a nuclear weapon on the internet.”

If you are concerned about the USAID Deep VZN program, you can contact them directly at <https://www.usaid.gov/contact-us>



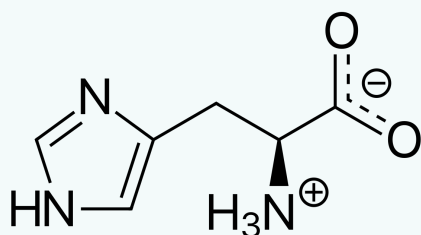
## AMINO ACID OF THE WEEK

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[ HISTIDINE ]

## CHEMICAL STRUCTURE

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## HISTIDINE

H

His

155.1546

DNA CODONS

C A Y

### POLARITY:

DEPENDS ON pH

POSITIVELY CHARGED AT PHYSIOLOGICAL pH

### DISCOVERY:

ISOLATED IN 1896 BY PHYSICIAN Albrecht Kossel AND Sven Gustaf Hedin

PROTEINOGENIC - BUILDING BLOCK OF PROTEINS.

PRECURSOR TO HISTAMINE, IMPORTANT AS AN INFLAMMATORY AGENT IN THE IMMUNE SYSTEM.

CAN FORM COMPLEXES WITH MANY METALLIC IONS

IMIDAZOLE SIDECHAIN SERVES AS A LIGAND IN METALLOPROTEINS, NOTABLY ATTACHING TO Fe (IRON) IN HEMOGLOBIN (PROTEIN FOR OXYGEN TRANSPORT IN RED BLOOD CELLS)

# 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

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