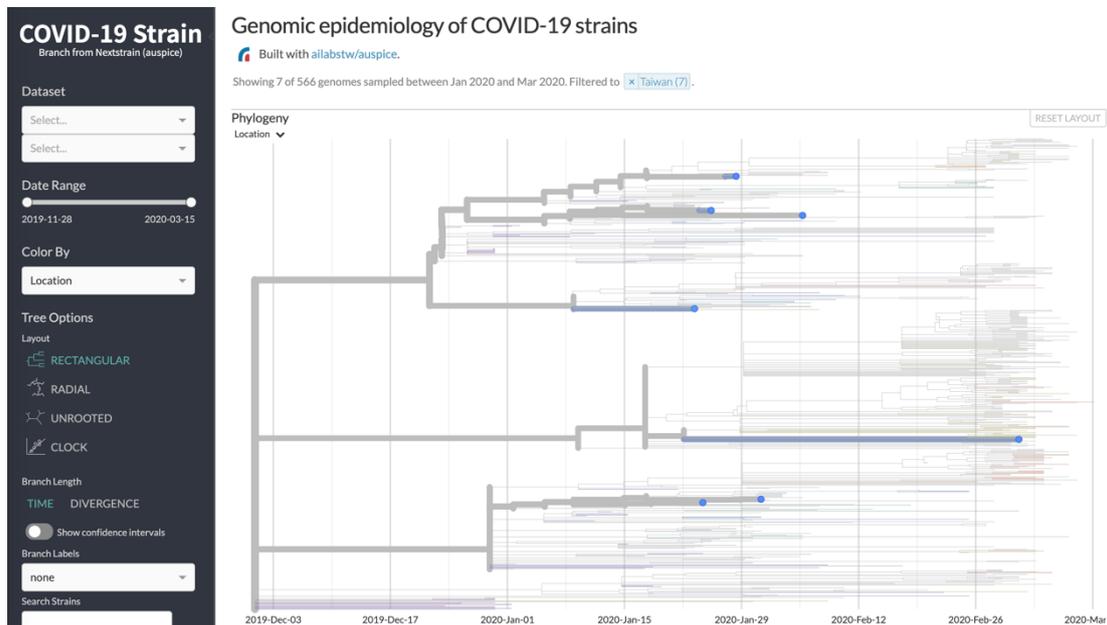


## AI Labs in COVID-19 Executive summary:

- Five Tools Can Help
  1. COVID-19 Strain | Coronavirus Phylogenetic Tree  
Exploring COVID-19 transmissions through genetic tracing with phylogenetic trees (branched from Nextstrain using data from GISAID).
  2. COVID-19 Drugs Screening  
Drug discovery for COVID-19 using computational protein-ligand docking simulations.
  3. variant2literature  
Understanding diseases from medical literature through the application of natural language processing.
  4. TAIGenomics (Taiwan Genomics)  
Practice of precision medicine through an automated genomic analysis platform
  5. TAIMedImg (Taiwan Medical Image)  
The automation of pneumonia detection through deep learning techniques for clinical screening.
- Other ongoing projects
  - Help development of rapid screening for COVID-19 (pneumonia) reagents.
  - Facilitate the process of COVID-19 (Pneumonia) vaccine development

## 1. COVID-19 Strain | Coronavirus Phylogenetic tree

<https://covirus.cc/phylogeny/>



Exploring COVID-19 transmissions through genetic tracing with phylogenetic trees (branched from Nextstrain using data from GISAID).

Since the outbreak of COVID-19 in December, over 200,000 cases have been confirmed, and current death tolls are nearing 10,000. As the number of cases continue to rise, nations across the world have started taking drastic measures as means to contain and control the spread. Currently on GISAID, viral sequences from thousands of patients spanning 38 countries have been made available. From this database, we hope to use the phylogenetic trees built based on sequence mutation information to predict the transmission pathway for each patient. Here we adopted the open-source package Nextstrain to predict a transmission tree connecting each infection to its most likely source. We hope this package can help countries around the world better understand from where and how the virus spread to their country, so that the world can develop a more effective plan for pathogen control.

Users of this package only need to provide their own patient viral sequence, as well as the patient's corresponding information in order to receive a curated transmission tree tracing each of their patient's viral strand to its original source.

## 2. Drug screen search

<https://covirus.cc/drugs>

**COVID-19 Drugs Screen Search**

Taiwan NHI Drugs 1,811    FDA Approved Drugs 1,615

Try an example:  
Drug Name: [Fungizone](#)

**Top 10 Drugs List**

#	Drug Name	Docking Score	Protein Type	Popular Views	Drug From
1	Fungizone	-11.98	3CL-Pro	3	FDA
2	Fungizone	-11.37	RdRp	3	FDA
3	Fungizone	-10.97	Helicase	3	FDA
4	(4S,6S,8S,11R,12S,1...	-12.46	3CL-Pro	0	FDA
5	Digoxin	-11.86	3CL-Pro	0	FDA NHI
6	Venetoclax	-11.85	3CL-Pro	0	FDA NHI
7	(4S,6S,8S,11R,12S,1...	-11.84	3CL-Pro	0	FDA
8	Trypan blue	-11.75	3CL-Pro	0	FDA
9	(4S,6S,8S,11R,12S,1...	-11.67	RdRp	0	FDA
10	Trypan blue	-11.55	Helicase	0	FDA

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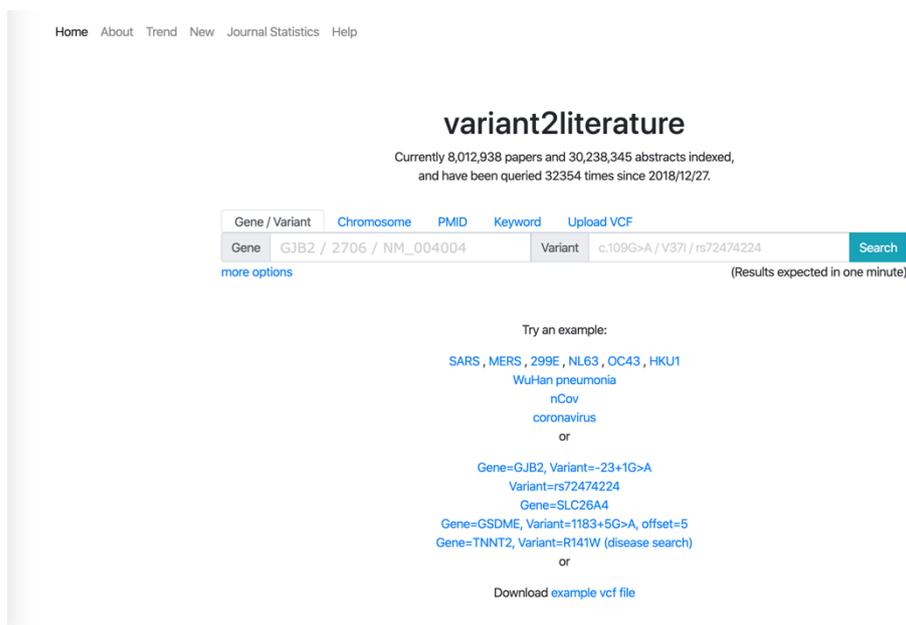
Drug discovery for COVID-19 using computational protein-ligand docking simulations.

Perhaps equally as important as virus containment is how to effectively treat patients confirmed with the disease. Currently, the process of developing a new drug requires a painfully long procedure of animal and clinical testing, a policy inherently ignorant to the urgency of the current situation. During virus outbreaks, the next best option is to use previously approved medication that possess the appropriate viral restraining mechanisms as means to control the virus. Here we used computational docking to predict and score the viral replication restraining abilities of different small molecule drugs in order to quickly select high potential drugs for clinical testing. We have also released docking scores for all FDA approved drugs to be used as reference.

If you have any other drug of interest that is not currently listed in our database, please provide us with the drug's structure, and we will add your desired information into our database.

### 3. variant2literature

<https://v2l.taigenomics.com>



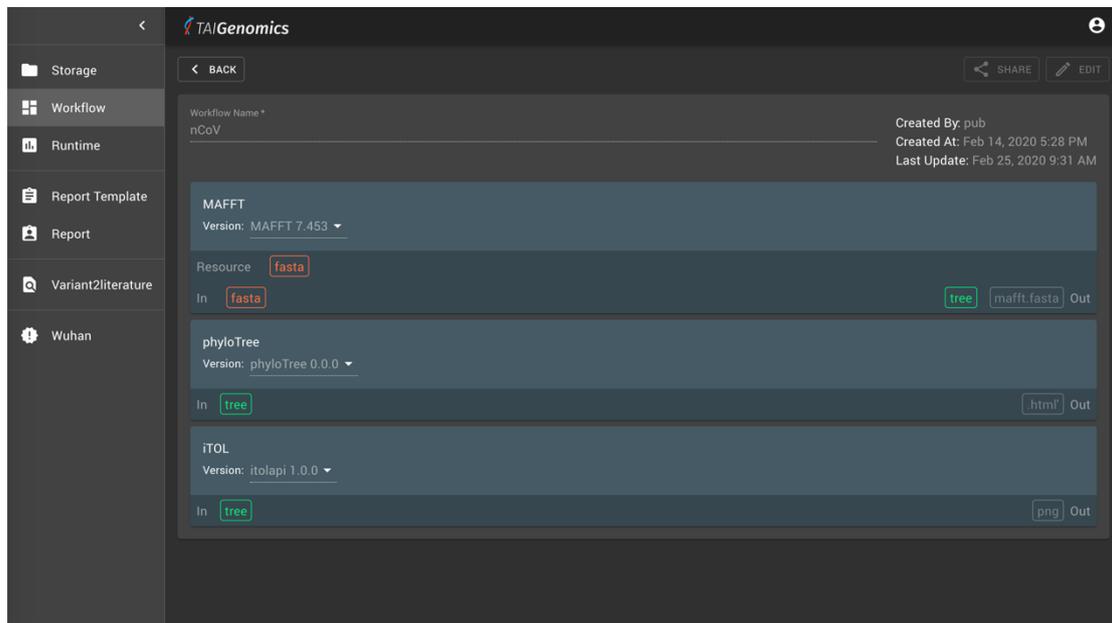
Understanding diseases from medical literature through the application of natural language processing.

The current rate of scientific publications far exceeds the amount that a single individual can read and digest. In order to efficiently sort through relevant information contained within all these papers, we utilized modern natural language processing techniques to do this task for us. Our platform, variant2literature, attempts to extract the most relevant information from top publications regarding a variant in order to find a potential cure. Our database currently contains 30 million publications, including nearly 8,000,000 full length papers. Based on the relationship between a disease and its corresponding genetic variant, we hope our platform can help users identify the most successful treatment mechanisms. Specifically for COVID-19, we are fully invested in helping to identify a cure, and will be continuously adding relevant papers to our database daily.

To use variant2literature, simply enter a variant or keyword to get the results from all relevant publications. You can also perform a search using sequencing data directly.

## 4. TAIGenomics

<https://www.taigenomics.com/console>



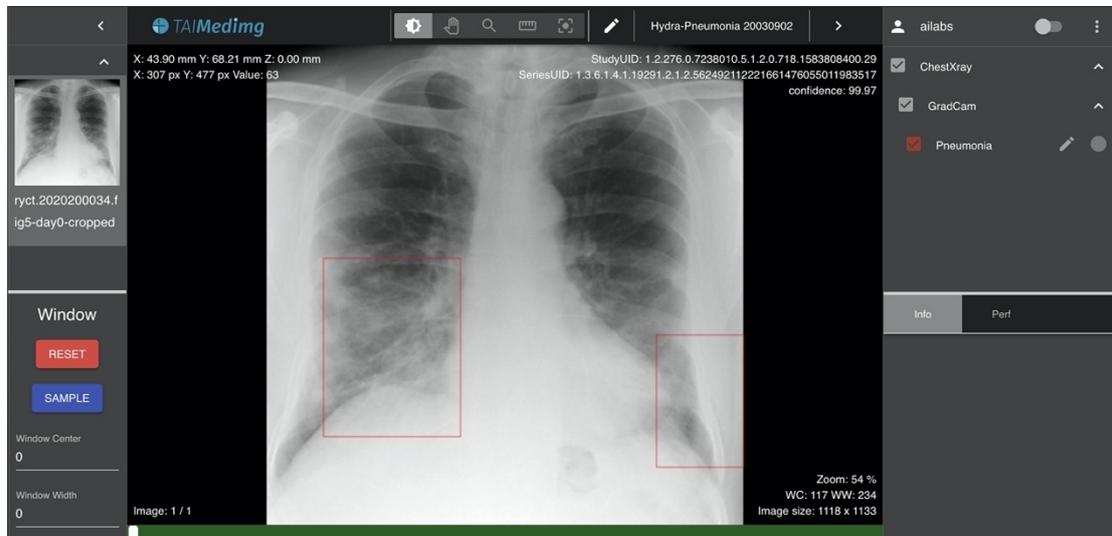
Practice of precision medicine through an automated genomic analysis platform.

In the ever improving medical world, the study of individual genetic variants is the key to modern precision medicine. Here we developed a platform, TAIGenomics, that can perform various analyses based on the patient's unique genetic sequence. Current analyses tools include the detection of rare diseases, risk prediction of diseases, cancer classification and prognosis, clinical drug guides, Immunotherapy prediction, as well as a variety of other analyses tools.

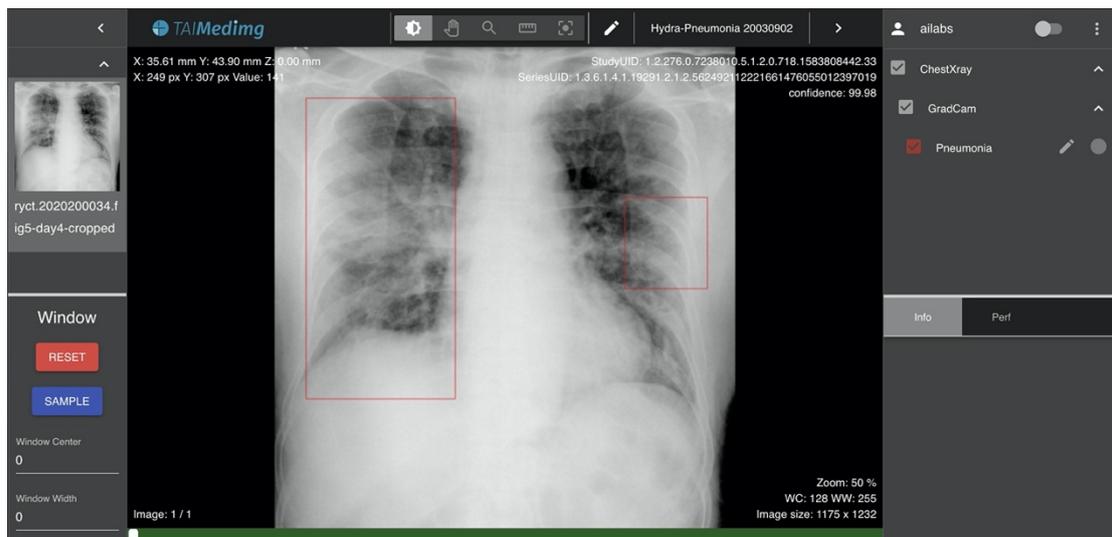
To use TAIGenomics, the users can simply upload a genomic data acquired through next generation sequencing or microarrays, as well as the corresponding patient information in order to start your analysis.

## 5. Pneumonia Detection

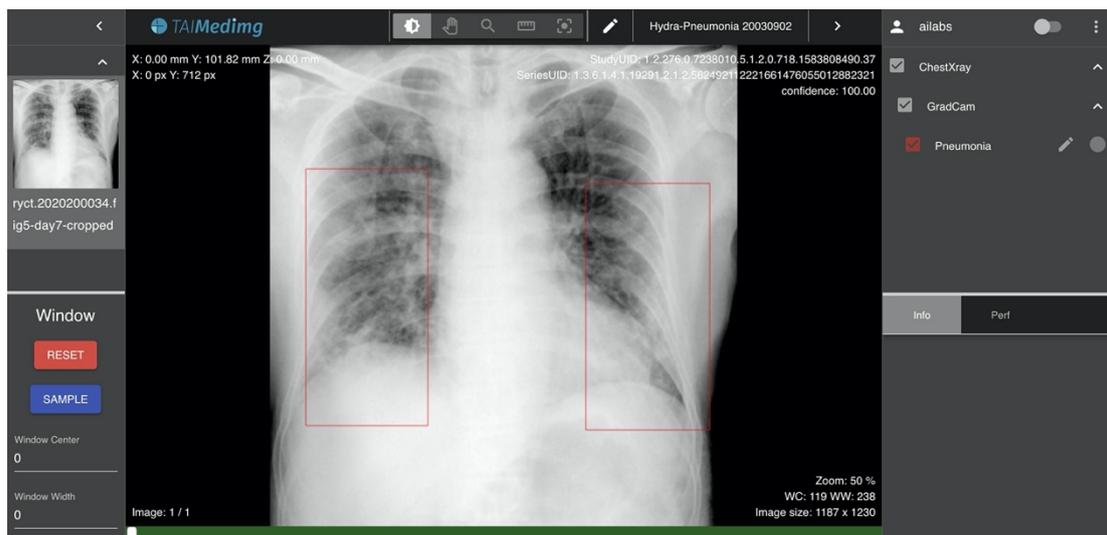
Day 0



Day 4



Day7



The automation of pneumonia detection through deep learning techniques for clinical screening.

To improve the efficiency of disease quarantine, using AI to assist physicians in image interpretation is an indispensable part.

We first developed an automated pneumonia detection system based on the X-ray imaging open dataset. This not only helps doctors to determine the area and severity of pneumonia in the X-ray films, but also acts as a triage system to refer patients with suspected severe pneumonia to receive early and detailed diagnosis and treatment. In addition, in response to COVID19, we collected the COVID19 X-ray imaging open dataset to optimize our pneumonia detection system. With such effort, the system can both determine whether the patient has pneumonia and provide the correlation between the pneumonia and COVID19, thereby improving the quarantine quality and efficiency of COVID19.

If you have any questions, please contact us:

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