Epitope Prediction Of Swine Flu Virus By Using Bioinformatics Tools

Epitope Prediction

Epitope prediction is part of an antigen that is recognized by the immune system, specifically by antibodies, B cell or T cells. Which are a linear sequences of amino acid. Epitope are often used in proteomics and the study of other gene products.

The epitope of protein antigens are divided into two types :

1. Conformational epitope:- A conformational epitope is composed of discountinous section of the antigens amino acid sequences.
2. Linear epitope:- A linear epitope is formed by a continous sequence of amino acid from antigen.

Improving B- cell epitope prediction and its application to global antigen and antibody docking. Antibodies are the most important class of biopharmaceuticals development of such antibody based drug depends on costly and time consuming screeing campaigns. Computional techniques such as antibody antigen docking hold the screeing to facilitate the screeing process by rapidly providing a list of initial poses that approximate the native complex. EpiPred to rescore the globel docking result of two rigid body docking alogorithms : ZDOCK and ClusPra.

Antigen:

Based upon the ability of antigens to carry out their functions, antigens are of two types: complete antigens and incomplete antigens. macrophages, Dendritic cells and B cells. Antigens are substance (Usually proteins) on the surface of cells, viruses , fungi or bacteria.

Common allergen include:

1. Animal proteins and animal dander.
2. Viruses.
3. Dust.
4. Drugs (Such as antibiotics or medications you put on your skin).
5. Foods (Such as milk, chocolate, Strawberries, wheat).
6. Perfumes.
7. Plants: Mosaic virus .

Viruses

A virus is a small infections particle that can replicate only inside the living cell of an organism. Viruses can infect all types of life forms , such as animals, plants, microorganisms including bacteria and archea. Since Dimitri Lvanovsky’s 1892 article describing a non-bacteria pathogen infection tobacco mosaic Virus by Martinus Beijetinck in 1898, about 5,000 virus species have been described in detail, although there are millions of types . The genetic material made from

either DNA or RNA, long molecules that carry genetic information.

1. A protein coat, called the capsid, which surrounds and protects the genetic material. And in some cases.
2. An envelope of lipids that surrounds the protein coat.

The shapes of these virus particles range from simple helical and icosahedral forms for some virus species to more complex structures for others. Most virus species have virions that are too small to be seen with an optical microscope.

On the basis of viruses in the human body:

- · Smallpox
- · The common cold and different types of flu.
- · HIV, the virus that causes.

“Flu Virus”

Swine Flu Viruses H1N1 Strain

Swine influenza is an infection caused by any one of several types of swine influenza viruses. Swine influenza virus (SIV) or Swine origin influenza virus (S-OIV) is any strain of the influenza family of viruses that endemic in pigs. As of 2009, the known SIV stains include influenza C and the subtypes of Influenza A known as H1N1, H1N2, H2, N1, H3, N1, H3N2 and H2N3.

Influenza (H1N1) virus the subtype of influenza A virus the most common causes of human influenza (Flu) in 2009. And is associated with the 1918 outbreak known as the Spanish flu. It is an orthomyxovirus that contain glycoproteins heamagglution and neuramindase. For the reason, they are described as H1N1, H1N2 etc, depending they express with metabolic energy.

Haemagglutinin causes red blood cells to clump together and binds the virus to infected cell.

Neuraminidase is a type of glycoside hydrolase enzyme which helps through the infected cell and in budding from the host cells.

Some strains of H1N1 are endemic in humans and causes a small fraction of all influenza like illness and a small fraction of all seasonal influenza. Pigs can also become infected with the H4N6 and H9N2 subtype. Other strain of H1N1 are endemic in pigs Swine influenza and in birds (Avian influenza). In June 2009, the world health organization (WHO) declared the new strain of swine – origin H1N1 as pandemic. The Spainsh flu virus infected lung cells, leading to overstimulation of the immune system via release of cytokinese into lung tissue.

The genetic material of the virus; they code for one or two proteins. Each RNA segment as they are called consists of RNA joined with several protein shown in the B1, PB1, PA, NP. These RNA segments are the genes of the influenza virus. Both Influenza A and B viruses have 8 RNA segments, while the influenza virus have been 7. Influenza viruses are called (-) strand, RNA viruses of the polarity RNA that is carried in the virion.

Influenza A Strain :

1. 1. H1N1 - 2009.
2. 2. H3N2 - 1968 Return 2018.
3. 3. H5N9 -
4. 4. H7N1 - 2017 Return 2018.

History :

Swine flu, also called Hog or Pig Flu, is an infection caused by any one of the several types of Swine influenza virus (SIV) which is common throughout pig population worldwide. The term 'influenza' derived from the Italian word' influence' was coined in 1357 AD as the disease was thought to be caused by influence of stars.

Influenza pandemics are believed to have occurred at unpredictable intervals for many centuries. Outbreaks of swine flu are common and cause significant economical losses. Influenza, the flu, is believed to have been around for a few thousand years. Hippocrates, who is considered to be the father of modern medicine, has described the symptoms of the flu in 412 B.C at Printouts in North Greece.

1. In 855 Ebn al atir mentions a virulent epidemic resembling flu that started in Central Asia and spread across Persia.
2. In 1485 an illness with flu like symptoms killed thousands of people in Britain, including the mayor.
3. In 510 a flu pandemic originated in Africa and spread across Europe.
4. In 1580 a pandemic originated in the North Africa during summer, spread to Sicily, and then up through Italy, through Europe and to North America. It had a high mortality rate and killed 9000 people in Rome alone.
5. In 1688, an outbreak, described as being like the plague because of the death toll, swept through England, Ireland and Virginia.
6. In 1699 an influenza outbreak occurred in Europe and America and Massachusetts. The sickness extended to almost all families
7. In 29 a pandemic originated in Russia, and re-emerged in Sweden in September and in Vienna in October. In November it spread across Europe, and reached America in 1732. Deaths were most numerous amongst the elderly and pregnant women.
8. In 1781-82 an influenza pandemic afflicted two-thirds of the people of Rome and three-quarters of the population of Britain Influenza also spread widely in North America, the West Indies and Spanish America.
9. In 1789 influenza epidemic hit England, New York and Nova Scotia. Most deaths appeared to have been from secondary pneumonia.
10. In 1830-33 a pandemic spread out from China. The infection rate was high (20- 25%), but mortality was low.
11. In 1847-1848 an epidemic swept through the Mediterranean to southern France and thence elsewhere in Western Europe.
12. 1889 a pandemic began in May in Bokara, Central Asia and traveled west to Russia and Western Europe after a pause of several months.
13. In 1900: a major epidemic was reported in North America, England and Wales.
14. In 1918-19 the worst pandemic, so-called 'Spanish flu” affected nearly one third of the world's population and caused 50 million plus deaths worldwide.
15. In 1957-58 avian influenza originated in China, with deaths worldwide estimated at

between one and four million. In 1968, Hong Kong flu caused some million deaths worldwide, particularly among the elderly.

16. In 1976, a variant of H1N1, known as A/New Jersey/ 1976 caused death of a army recruit at Fort Dix New Jersey USA. But it did not spread beyond Fort Dix.
17. In 1977 a pandemic." Russian Flu' spread across Siberia and European part of Russia. In 1988, swine flu killed a 32 year old, otherwise healthy pregnant woman, Barbaran Ann Wieners in Wisconsin, USA after she visited a pig exhibition.
18. In 1997 Avian Flu outbreak originated from the New Territories Region in northern Hong Kong. In this area, chickens had been dying and routine testing of poultry had verified the presence of the Avian Flu virus - subtype H5N1.

Background of Work / Problem :

In 2009, scientists recognized a particular strain of flu virus known as H1N1. This virus is actually a combination of viruses from pigs, birds and humans. During the 2009-10 flu season, H1N1 caused the respiratory infection in humans that was commonly referred to as swine flu.

Flu vaccine:- The seasonal flu vaccine protects against the 3 strains of flu virus recommended by the World Health Organization (WHO) as the strains most likely to be circulating this season. You should get your flu vaccination from September to be covered for flu season. The viruses change each year. The pandemic began to taper off in November 2009,and by May 2010, the number of cases was in steep decline. On 10 August 2010, the Director-General of the WHO, Margaret Chan, announced the end of the H1N1 pandemic and announced that the H1N1 influenza event has moved into the post-pandemic period. According to the latest WHO statistics (as of July 2010), the virus has killed more than 18,000 people since it appeared in April 2009, however they state that the total mortality (including deaths unconfirmed or unreported) from the H1N1 strain is 'unquestionably higher'. Critics claimed the WHO had exaggerated the danger, spreading 'fear and confusion' rather than 'immediate information '.The WHO began an investigation to determine] it had 'frightened people unnecessarily '.A flu follow-up study done in September 2010, found that 'the risk of most serious complications was not elevated in adults or children.' In a 5 August 2011 PLoS ONE article, researchers estimated that the 2009 H1N1 global infection rate was 11% to 21%, lower than what was previously expected.

Review of Literature :

Related past work/research paper:

1. An Introduction to B-Cell Epitope Mapping and In Silico Epitope Prediction Lenka Potocnakova, Mangesh Bhide, and Lucia Borszekova Pulzova ,
2. T-cell epitope content comparison (EpiCC) of swine H1 influenza A virus hemagglutinin. Gutiérrez AH1, Rapp-Gabrielson VJ2, Terry FE3, Loving CL4, Moise L, Martin WD,

De Groot AS informatic comparison of T-cell epitopes contained in novel swine-origin influenza A (H1N1) virus with epitopes in 2008-2009 conventional influenza vaccine.De Groot AS1, Ardito M, McClaine EM, Moise L, Martin WD.

Classification of swine flu :

- · Influenza A:

Swine influenza is known to be caused by influenza A subtypes H1N1, H1N2, H2N3, H3N1, and H3N2. In pigs, three influenza A virus subtypes (H1N1, H1N2, and H3N2) are the most common strains worldwide. In the United States, the H1N1 subtype was exclusively prevalent among swine populations before 1998; however, since late August 1998, H3N2 subtypes have been isolated from pigs. As of 2004, H3N2 virus isolates in US swine and turkey stocks were triple reassortants, containing genes from human (HA, NA, and PB1), swine (NS, NP, and M), and avian (PB2 and PA) lineages.

According to the National Center for Immunization and Respiratory Diseases (NCIRD), Influenza A viruses are divided into subtypes based on two proteins on the surface of the virus: the hemagglutinin (H) and the neuraminidase (N). There are 16 different hemagglutinin subtypes and 9 different neuraminidase subtypes. Influenza A viruses can be further broken down into different strains.

- · Influenza B:

Influenza B viruses are only known to infect humans and seals, giving them influenza. This limited host range is apparently responsible for the lack of Influenza virus B caused influenza pandemics in contrast with those caused by the morphologically similar Influenza virus A as both mutate by both genetic drift and reassortment.

- · Influenza C:

Influenza C viruses infect both humans and pigs, but do not infect birds. Transmissions between pigs and humans have occurred in the past. For example, influenza C caused small outbreaks of a mild form of influenza amongst children in Japan and California. Because of its limited host range and the lack of genetic diversity in influenza C, this form of influenza does not cause pandemics in humans.

Pathophysiology:

Influenza viruses and the 2009 pandemic virus the influenza viruses are enveloped viruses with segmented negative-stranded RNA genomes. They are classified in three genera – A, B and C. The influenza A viruses contain eight genome segments that encode ten different viral proteins, of which nine are part of the virus structure. These include the surface haemagglutinin (HA), neuraminidase (NA) and M2 ion channel proteins, the M1 matrix protein, the nucleocapsid protein (NP) that packages the RNA genome and the replication complex comprising the PA, PB1 and PB2 proteins.

Some viruses also encode a protein called PB1-F2 from an alternate reading frame within the PB1 gene; this protein is also produced during infection and is associated with increased virulence and pathogenicity.

Influenza viruses are named on the basis of their surface proteins – HA, which is required for virus binding to the target cell, and NA, which is required for virus release from infected cells. For influenza A viruses 16 HA serotypes (H1–H16) and 9 NA serotypes (N1–N9) are known, of which only the H1, H2, H3 and H5 viruses, and rarely the H7 and H9 viruses have been found to infect humans.

Influenza viruses evolve through ‘antigenic drift’, and occasionally by ‘antigenic shift’. The viral RNA dependent RNA polymerase (replicase) lacks proof reading activity and is therefore unable to correct random errors introduced in the genome during replication.

The effects of this are most obvious in the HA protein, which shows high rates of amino acid substitutions in its epitopes. And for which the ratio of non-synonymousto synonymous substitutions is 1.This indicates a positive selection, which is directly related to evasion of host immunity.’ Antigenic drift’ changes the HA protein enough to render immunity acquired during an influenza season, either through infection or vaccination, ineffective in the next season. A more serious problem occurs when two different influenza viruses infect the same host.

This leads to reassortment of genome segments and the generation of novel progeny viruses. If this reassortment takes place between viruses originating from different species. It can generate viruses with pandemic potential, which include HA and/or NA proteins from the avian or swine influenza viruses against which humans have no preexisting immunity.

This introduction of completely new HA serotypes into circulating human influenza viruses is called ‘antigenic shift’.

Epidemiology:

· Historical perspective :

Illness with influenza in pigs was first recognized during the influenza pandemic of 1918 to 1919, and a swine influenza virus was first isolated from a human in 1974 Between 1958 and 2005, 37 cases of swine influenza among civilians were reported . Six cases (17 percent) resulted in death.

· United States:

On February 5, 1976, a conscript soldier at Fort Dix said that he felt exhausted and weak. He died the following day and four of his companions were hospitalized.

· The Maxio:

In April 2009 there was an outbreak of swine flu in humans, in Mexico, which caused over 20 deaths. On April 24, 2009 the government of Mexico City and the State of Mexico shut down temporarily, with the support of the Ministry of Education, schools from kindergarten to university level in order to prevent the disease from spreading to a wider area.

· Effects in India India:

has had over 1,000 confirmed cases of swine flu so far that’s roughly one case per every million people in the nation. The first case of death had its epicenter in Pune. Schools and Colleges were closed and all were running to the nearby clinics to buy mask, where the price of mask had a excitation all over the nation. From the normal cost of Rs.5 or 10 it went to Rs.100 to 150.

Application:

- · The cause of the 2009 swine flu was an influenza A virus type designated as H1N1. In 2011, a new swine flu virus was detected. The new strain was named influenza A (H3N2)
- · Only a few people (mainly children) were first infected, but officials from the U.S. Centers for Disease Control and Prevention (CDC) reported increased numbers of people infected in the 2012-2013 flu season. Currently, there are not large numbers of people infected with H3N2v. Unfortunately, another virus termed H3N2 has been detected and caused flu, but this strain is different from H3N2v. In general, all of the influenza A viruses have a structure similar to the H1N1 virus; each type has a somewhat different H and/or N structure.

Aims and objective :

To review and study of swine flu.

Objective:

- · To collect the information on swine flu(Literature survey).
- · To survey the status and severity of disease all over the world.
- · To describe the Epidemiology of disease.
- · To study the life cycle of virus.
- · To explain prevention and treatment of swine flu.
- · To analyze all the parameters related to the swine flu.
- · To aware people about swine flu.
- · Summarization of the information and writing project.

Materials and methods:

Epitope Prediction Software And Tools

- Databases : NCBI
- Template search: FASTA format
- Sequence Alignment: BLAST
- Verification: IEDB – Immune Epitope Databases Analysis Resource.

Methods

Database:

NCBI

The National Centre for Biotechnology Information (NCBI) is part of the United States National Library of Medicine (NLM), a branch of the National Institutes of Health (NIH). The NCBI is located in Bethesda, Maryland and was founded in 1988 through legislation sponsored by Senator Claude Pepper.

The NCBI houses a series of databases relevant to biotechnology and biomedicine and is an important resource for bioinformatics tools and services. Major databases include GenBank for

DNA sequences and PubMed, a bibliographic database for the biomedical literature. Other databases include the NCBI Epigenomics database. All these databases are available online through the Entrez search engine.

NCBI was directed by David Lipman, one of the original authors of the BLAST sequence alignment program and a widely respected figure in bioinformatics. He also led an intramural research program, including groups led by Stephen Altschul (another BLAST co-author), David Landsman, Eugene Koonin, John Wilbur, Teresa Przytycka, and Zhiyong Lu. David Lipman stood down from his post in May 2017.

Template Search

Fasata Format

In bioinformatics and biochemistry, the FASTA format is a text-based format for representing either nucleotide sequences or amino acid (protein) sequences, in which nucleotides or amino acids are represented using single-letter codes. The format also allows for sequence names and comments to precede the sequences. The format originates from the FASTA software package, but has now become a near universal standard in the field of bioinformatics.

The simplicity of FASTA format makes it easy to manipulate and parse sequences using text-processing tools and scripting languages like the R programming language, Python, Ruby, and Perl.

Sequence Alignment

Blast

In bioinformatics, BLAST (basic local alignment search tool) is an algorithm for comparing primary biological sequence information, such as the amino-acid sequences of proteins or the nucleotides of DNA and/or RNA sequences. A BLAST search enables a researcher to compare a query sequence with a library or database of sequences and identify library sequences that resemble the query sequence above a certain threshold.

Different types of BLASTs are available according to the query sequences. For example, following the discovery of a previously unknown gene in the mouse, a scientist will typically perform a BLAST search of the human genome to see if humans carry a similar gene; BLAST will identify sequences in the human genome that resemble the mouse gene based on similarity of sequence. The BLAST algorithm and program were designed by Stephen Altschul, Warren Gish, Webb Miller, Eugene Myers, and David J. Lipman at the National Institutes of Health and was published in the Journal of Molecular Biology in 1990 and cited over 75,000 times.

Verification

IEDB: Immune Epitope Database Analysis Resource.

The Immune Epitope Database and Analysis Resource (IEDB) is a project hosted by scientists at the La Jolla Institute for Allergy and Immunology (LIAI), with support from the National Institute of Allergy and Infectious Diseases (NIAID), a part of the National Institutes of Health (NIH), and Department of Health and Human Services (HHS). The focus is dissemination of

immune epitope information to facilitate the generation of new research tools, diagnostic techniques, vaccines and therapeutics. The IEDB contains data related to antibody and T cell epitopes for humans, non-human primates, rodents, and other animal species. Curation of data relating to NIAID Category A, B, and C priority pathogens (including Influenza) and NIAID Emerging and Re-emerging infectious diseases is of highest priority and is being continuously updated. The database also contains MHC binding data from a variety of different antigenic sources and immune epitope data from the FIMM (Brusic), HLA Ligand (Hildebrand), TopBank (Sette), and MHC binding (Buus) databases. These databases and their investigators are hereby acknowledged as major contributors to the IEDB.

Conclusion :

From the above study, I conclude that the Epitope prediction based Swine flu virus to compare two antigens by using IEDB Software has find out the obtained result.

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