






## Molecular evidence for evolution 4: Viral evolution

### Components

	NAME	DESCRIPTION	AUDIENCE
	<i>Viral evolution</i> teachers guide	This guide explains how to use bioinformatics tools within the Influenza Research Database to build students' understanding of molecular evidence for evolution.	teachers
	<i>Influenza</i> background sheet	This background sheet for teachers describes the structure and reproduction of influenza viruses.	teachers
	<i>Investigating influenza</i> background sheet	This background sheet for teachers describes how influenza viruses evolve, and mechanisms of antigenic drift and shift. It also provides an introduction to bioinformatics and the Influenza Research Database.	teachers
	<i>Fighting the 'flu</i> fact sheet	This fact sheet describes the structure of influenza viruses and how they evolve through antigenic shift and drift.	students
	<i>Influenza – an evolving problem!</i> worksheet	This activity sheet guides students through interactive use of the Influenza Research Database.	students

### Purpose

Students develop an understanding of how databases may be used to map changes in influenza viruses as they evolve.

### Outcomes

Students understand that:

- there are different types of influenza virus that affect different animal species;
- evolution can occur rapidly in viruses, through mechanisms of antigenic drift and antigenic shift;
- mutations or changes in nucleotide sequences of viruses mean hosts may not recognise a virus; and
- online databases, such as the Influenza Research Database, enable scientists to track strains of viruses and map evolutionary changes, as they occur.

### Activity summary

ACTIVITY	POSSIBLE STRATEGY
Students read the fact sheet, <i>Fighting the 'flu</i> , to provide background information for an online database activity.	individually or in pairs
Students work through the activity, <i>Influenza – an evolving problem!</i> , answering questions.	individually or in pairs

## Teacher notes on the Influenza Research Database

The Influenza Research Database used in *Influenza – an evolving problem!* is an authentic research tool. It is used to determine directions of influenza evolution and to identify emerging new strains. As the database is complex it is recommended that teachers work through the activity before giving it to students. The activity is structured and includes screen shots to make the database straightforward to use.

Each student will need to log into the database and set up a workbench. Teachers may want to demonstrate this.

Influenza type A, segment 4, has been selected for this activity. This segment of RNA codes for the protein haemagglutinin, which is a surface protein used to identify influenza strains. After completing the activity, another phylogenetic tree may be generated using segment 6 which codes for neuraminidase.

Students answer questions as they work through the database and produce a phylogenetic tree for selected strains of influenza. Their phylogenetic tree will reveal how genetically different, due to antigenic shift, the 2009 strains of influenza were from earlier strains, thus explaining why so many people became sick. Immune memory is raised in the introduction to the activity. It may be necessary to elaborate on this topic, focusing on immunisation and why it's recommended that influenza vaccination is repeated each year.

Students should be able to complete the activity in the worksheet, *Influenza – an evolving problem!* in about one hour.

### Technical requirements

The teachers guide, background sheets, worksheet, and fact sheet require Adobe Reader (version 5 or later), which is a free download from [get.adobe.com/reader/](http://get.adobe.com/reader/).

The Influenza Research database requires a compatible Javascript-enabled web browser. Minimum browser requirements are Internet Explorer 6.0, Netscape 8.0, Firefox 1.5 or Safari 1.2.

Check with your IT support person if Java is enabled on your computers, as it is required to display aligned sequences and phylogenetic trees. A message 'Missing plug-in' or a blank space where data should be displayed probably indicates problems with your version of Java or security settings. Macintosh users may find Firefox less restrictive than Safari.

You can check that the browser you are using supports Java by going to <http://www.java.com/testjava/>

## Acknowledgements

Grateful thanks are extended to Yun Zhang, Burke Squires, Brett Pickett, and Jyothi Noronha from Richard Scheuermann Bioinformatics Laboratory at the University of Texas Southwestern Medical Centre at Dallas, USA for their help, feedback and support in developing this activity.

The Influenza Research Database Bioinformatics Resource Centre has been wholly funded with federal funds from the National Institute of Allergy and Infectious Diseases, National Institutes of Health, Department of Health and Human Services, USA, under Contract No. HHSN266200400041C.

banner image: A/CA/4/09 swine flu virus by Center for Disease Control / C S Goldsmith and A Balish

Designed and developed by the Centre for Learning Technology, The University of Western Australia. Production team: Anton Ball, Pauline Charman, Jan Dook, Alwyn Evans, Dan Hutton, Bec McKinney, Emma Pointon, Paul Ricketts, Jodie Ween and Michael Wheatley with thanks to Bob Fitzpatrick, Jenny Gull and Wendy Sanderson.

### More information

World Health Organisation, Influenza (Seasonal), fact sheet number 211, April 2009, retrieved January 2013 from [www.who.int/mediacentre/factsheets/fs211/en/](http://www.who.int/mediacentre/factsheets/fs211/en/)

Virus WAch is a weekly electronic publication by the Communicable Disease Control Directorate (CDCD) and key collaborators. It provides a brief summary of General Practice and sentinel surveillance data on influenza-like and other illnesses to alert health care workers in WA to important circulating viruses. [www.public.health.wa.gov.au/3/487/3/virus\\_watch\\_homepage.pm](http://www.public.health.wa.gov.au/3/487/3/virus_watch_homepage.pm)

### SPICE resources and copyright

All SPICE resources are available from the Centre for Learning Technology at The University of Western Australia ("UWA"). Selected SPICE resources are available through the websites of Australian State and Territory Education Authorities.

Copyright of SPICE resources belongs to The University of Western Australia unless otherwise indicated.

Teachers and students at Australian and New Zealand schools are granted permission to reproduce, edit, recompile and include in derivative works the resources subject to conditions detailed at [spice.wa.edu.au/usage](http://spice.wa.edu.au/usage).

All questions involving copyright and use should be directed to SPICE at UWA.

Web: [spice.wa.edu.au](http://spice.wa.edu.au)  
Email: [spice@uwa.edu.au](mailto:spice@uwa.edu.au)  
Phone: (08) 6488 3917

Centre for Learning Technology (M016)  
The University of Western Australia  
35 Stirling Highway  
Crawley WA 6009

## Associated SPICE resources

*Molecular evidence for evolution 4: Viral evolution* may be used in conjunction with related SPICE resources to teach the topic of molecular evidence for evolution.

DESCRIPTION	LEARNING PURPOSE
<i>Molecular evidence for evolution (overview)</i>	
<p><i>Molecular evidence for evolution 1: Mammal evolution</i></p> <p>A card game engages student interest in evidence used to determine evolutionary relationships between eutherians (placental mammals).</p>	<b>Engage</b>
<p><i>Molecular evidence for evolution 2: Primates</i></p> <p>Students use interactive learning objects to explore how anatomical evidence may be used to determine relatedness.</p>	<b>Explore</b>
<p><i>Molecular evidence for evolution 3: Evolutionary trees</i></p> <p>The use of molecular evidence to determine relatedness between species is explained. Students draw evolutionary trees to represent relatedness.</p>	<b>Explain</b>
<p><i>Molecular evidence for evolution 4: Viral evolution</i></p> <p>Students use the Influenza Research Database to investigate virus evolution. This bioinformatics database is an authentic research tool used to compare genetic sequences of virus strains, and to construct cladograms to draw conclusions about their relatedness.</p>	<b>Elaborate</b>