Statistical Physics Can Help Build a Better Flu Vaccine

A new way to study the effectiveness of flu vaccines is to use the tools of statistical physics, according to Rice University's Michael Deem. Deem has taken the random energy or spin glass models originally used to describe nuclear cross-sections and applied them to epidemiology. At the APS March Meeting, he described how this method could provide a better prediction of a particular flu vaccine's efficacy in a given year. A higher efficacy means that fewer vaccinated individuals get the flu relative to unvaccinated individuals.

Influenza epidemics are a major concern that affects a large majority of the world's population, killing between 250,000-500,000 people every year; the US mortality rate alone is more than 40,000 per year, with estimated annual costs in lost work days and health care topping $10 billion in the US.

Early each year, the World Health Organization in Geneva recommends which three strains to include in the next winter's flu vaccine for both hemispheres. The three chosen strains are then grown in chicken eggs before being tested for safety and distributed nationwide. The shot contains killed versions of the three strains, which means it has to closely match the strains that are circulating among the populace.

Some of the most common strains are not always easy to grow, so similar strains are chosen with higher growth rates. But these are often not similar enough. As a result, the efficacy of flu vaccines among the elderly has only been between 30% and 40% over the last few years. Deem's calculations revealed an even lower efficacy rate: between 8% and 20%.

Sometimes there is even negative efficacy. It turns out that a shot one year and not the next may actually increase your risk of getting the flu the following year. This is known in epidemiological circles as original antigenic sin: it's when a vaccination against a disease can actually make you more susceptible. The body's first exposure to an antigen defines the antibody response. The second exposure, to a new antigen, generates a response only to those coat proteins it has in common with the first antigen.

To measure efficacy, researchers examine each strain's hemagglutinin (H) protein, the major protein on the surface of influenza A virus that is recognized by the immune system. In one standard approach, researchers study all the mutations in the entire H protein from one season to the next. In another approach, researchers study the ability of antibodies produced in ferrets to recognize either the vaccine strain or the mutated flu strain, which had been thought to be a good method for predicting flu vaccine efficacy in humans.

However, these approaches are only modestly reliable indications of the vaccine's efficacy. Deem and his Rice University colleagues point out that each H protein has five "epitopes," antibody-triggering regions mutating at different rates. The Rice team refers to the one that mutates the most as the "dominant" epitope Drawing upon theoretical tools originally developed for nuclear and condensed-matter physics–specifically, spin-glass models–the researchers focus on the fraction of amino acids that change in the dominant epitope from one flu season to the next.

Analyzing 35 years of epidemiological efficacy data, the researchers believe that their focus on epitope mutations correlates better with vaccine efficacy than do the traditional approaches. Deem and his colleagues Vishal Gupta and Robert Earl believe that this new measure may prove useful in designing the annual flu vaccine and in interpreting vaccine efficacy studies.

For instance, last year's flu shot included a strain called Wyoming, but Deem's model suggested that a related strain called Kumamoto might have been more effective. Next year's shot will replace Wyoming with an emerging strain called California, a decision his research supports. Deem and his colleagues are hoping to get more recent data from the CDC to further confirm their findings and validate their statistical method.

zero gravity
The Lighter Side of Science

Riordon's Lament

Ed. Note: *The following is based on an incident that occurred late one night, after a hard day's work at the APS March Meeting. A few staff members were sitting around when the subject of the proper spelling of Maxwell's name came up.*

Listen my children and shortly you'll hear
How Jimmy C. Maxwell cost me some beer
It happened the day I decided to bet
On spelling his name, which I now do regret.

I'd heard the name spoken, and, clear as a bell
It sounded exactly like James Clark Maxwell.
"I know how to spell that," I thought, "I'm no jerk,
The name is spelled Clark, and it cannot be Clerk."

But what I forgot was that Maxwell was British,
And spelling in Britain is, at its best, skittish.
I don't take it lightly, but view it quite darkly,
That something spelled Berkeley is verbalized "Barkley".

Driving to Louisville, you can quite sure be
That you will witness the Kentucky Derby.
Driving to Ascot, if you in your car be,
Brings you—surprise!—to a race called the "Darby".

In England the way that they spell is perverse;
In Scotland, if anything, it's even worse.
Jimmy C.'s middle name's spelling is queer,
And that's why I owe everybody a beer.

–Alan Chodos