# eLife digest questions and answers

## What background information would someone who is completely unfamiliar with your field need to know to understand the findings in your paper? (Suggested word limit: 150 words)

Every winter, someone you know will get sick with the flu. They will have a fever, difficulty breathing, and pain throughout their body and may need to go to the hospital. The flu vaccine is the best protection we have against this seasonal illness. The vaccine safely teaches our immune system what the flu virus looks like, so it will be prepared to fight that virus. Unfortunately, the flu virus changes its appearance to our immune system every year and requires us to update the vaccine to match. Since a new vaccine takes almost one year to make, flu researchers must predict which current flu viruses look the most like the viruses of the future. Researchers test the appearance of many current flu viruses with specialized experiments. Researchers also read the genetic code of current viruses and look for changes that might alter the virus’s appearance to our immune system.

## What exact research question did you set out to answer and why? (Suggested word limit: 75 words)

Previous research has shown that mathematical models of changes in flu’s genetic code could accurately make forecasts one year into the future. We wanted to know if including experimental measures of the viruses’s appearance into these models could improve forecasts. If these experimental data improved forecasts, then we could immediately pick better flu vaccines. If these data did not help, then we could save researchers the cost of performing their specialized experiments.

## What are the most important findings of your paper? (Suggested word limit: 100 words)

Using 25 years of historical flu data, we made forecasts one year into the future from all available past seasons. Each forecast predicted what the future virus population would look like using the virus’s genetic code, experimental data, or both. We compared the predicted and observed future populations to find the most useful data types. We found that combining changes from flu’s genetic code with experimental measures of its appearance improved forecasts over previous approaches that only used the genetic code. Importantly, we found that changes in the genetic code are not a replacement for experiments that measure flu’s appearance.

## Who might eventually benefit from the findings of your study, and what would need to be done before we could achieve these benefits? (Suggested word limit: 75 words)

These results specifically help flu researchers focus more on experiments and less on potentially misleading changes in the genetic code. Our open source forecasting tools can immediately provide better forecasts of future flu populations, leading to better flu vaccines and fewer illnesses and deaths from flu. More generally, our results highlight the importance of experimental measurements for any attempts to forecast changes in biological systems.