Northwestern SCIENCE CAFE

A Billion-Piece Puzzle:

Completing the Human Protein Project Would Revolutionize Understanding of Health and Disease

presented by Neil Kelleher,
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The first whole human genome cost about $2.7 billion to sequence in 2003. Today, anyone with $1,000 can learn about the entirety of their DNA, while $99 can offer clues on a person's health and ancestry.

While the field of genetics has exploded, early detection of disease using protein markers has remained elusive. Global leaders like Northwestern's Neil Kelleher are attempting to change that paradigm.

Wednesday
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6:30 - 8:00pm

The Firehouse Grill
750 Chicago Avenue
Evanston

"Like the Genome Project at the turn of the century, developing a cheap protein sequence is the major measurement challenge of our day," says Kelleher. "Mapping the universe of protein molecules will allow researchers to further pursue biomedical research goals like 'designer organs,' personalized drugs, and truly precise and early detection of human disease."

Proteomics is the large-scale study of proteins. Until the 2000's, proteomics relied on breaking a protein into small pieces, analyzing it using mass spectrometry, and piecing the information back together to learn their look and function. Alternatively to that traditional, or bottom-up, approach, Cornell's Fred McLafferty developed the field of top-down proteomics. One major advantage of the top-down strategy is the potential access to the complete protein sequence.. Kelleher, who has established one of the leading groups in the world studying intact proteins, was a graduate student in McLafferty's lab.

"Imagine trying to do a puzzle where you don't have the picture on the box of what it's supposed to be, and you're missing over half the pieces, and there are pieces of other puzzles in the box too," says Kelleher. "That's bottom-up proteomics, and that's what the world uses." By looking at whole proteins, Kelleher and his team understand "the picture on the box" and then make sure they have all the pieces.

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