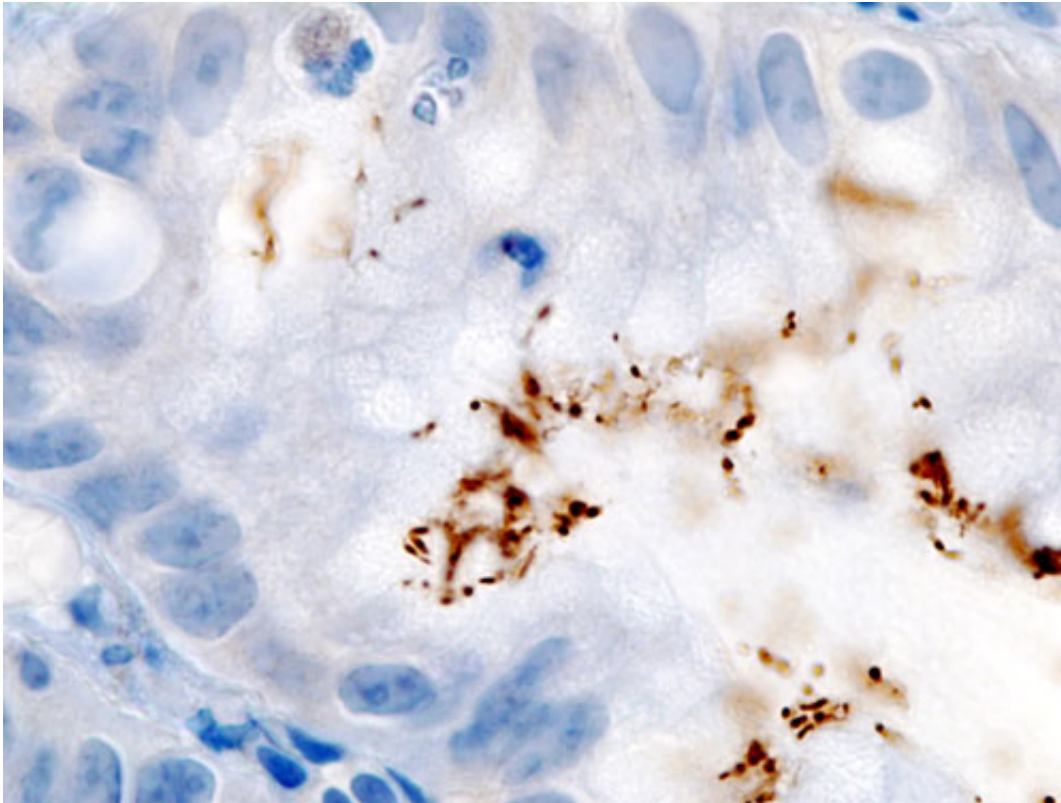


Antibiotics through machine learning

August 2 2019, by David Bradley



Histopathology of *Helicobacter pylori* infection in a gastric foveolar pit demonstrated in endoscopic gastric biopsy. Credit: Wikipedia.

Machine learning techniques can be used to search for new drugs for one of the most insidious causes of stomach ulcers and other gastrointestinal problems, the bacteria known as *Helicobacter pylori*.

Ulcers are like open sores in the wall lining the stomach into which

stomach acid can eat. These so-called peptic ulcers can be very painful and are a major risk factor for stomach cancer. In the late 1980s, Australian scientists demonstrated that the corkscrew-shaped *H. pylori*. This was the subject of the 2005 Nobel Prize for Medicine as it overturned decades of received wisdom regarding the nature of ulcers. It suggested that a multi-billion dollar drug industry based on acid inhibitors and other such agents was no longer needed as a course of antibiotics might suffice. This later proved to be the case in treating [ulcers](#) caused by *H. pylori*.

Unfortunately, bacteria quickly evolve resistance to antibiotics, so there is always a need to find new ones that can keep us one step ahead of the infectious pathogens. Now, work published in the *International Journal of Bioinformatics Research and Applications*, points the way to a new approach to finding antibiotics to treat conditions associated with *H. pylori* infection.

The approach taken by Surekha Patil and Shivakumar Madagi of the Department of Bioinformatics at Karnataka State Women's University, Jnanashakti Campus in Karnataka, India, could truncate the drug discovery pipeline significantly in this area of medicinal chemistry. The researchers discuss which algorithms work best to screen a database of small molecules against the target proteins associated with the bacterium. Specifically, the enzyme peptide deformylase is the focus of the work. As candidates emerge from the computer, those that have the most promise can be screened in the laboratory against the target, before further testing against *H. pylori* in laboratory animals and then humans.

More information: Patil, S. and Madagi, S.B. (2019) 'Application of machine learning techniques towards classification of drug molecules specific to peptide deformylase against *Helicobacter pylori*', *Int. J. Bioinformatics Research and Applications*, Vol. 15, No. 3, pp.221–242. [DOI: 10.1504/IJBRA.2019.101206](https://doi.org/10.1504/IJBRA.2019.101206)

Provided by Inderscience

Citation: Antibiotics through machine learning (2019, August 2) retrieved 6 May 2024 from <https://medicalxpress.com/news/2019-08-antibiotics-machine.html>

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