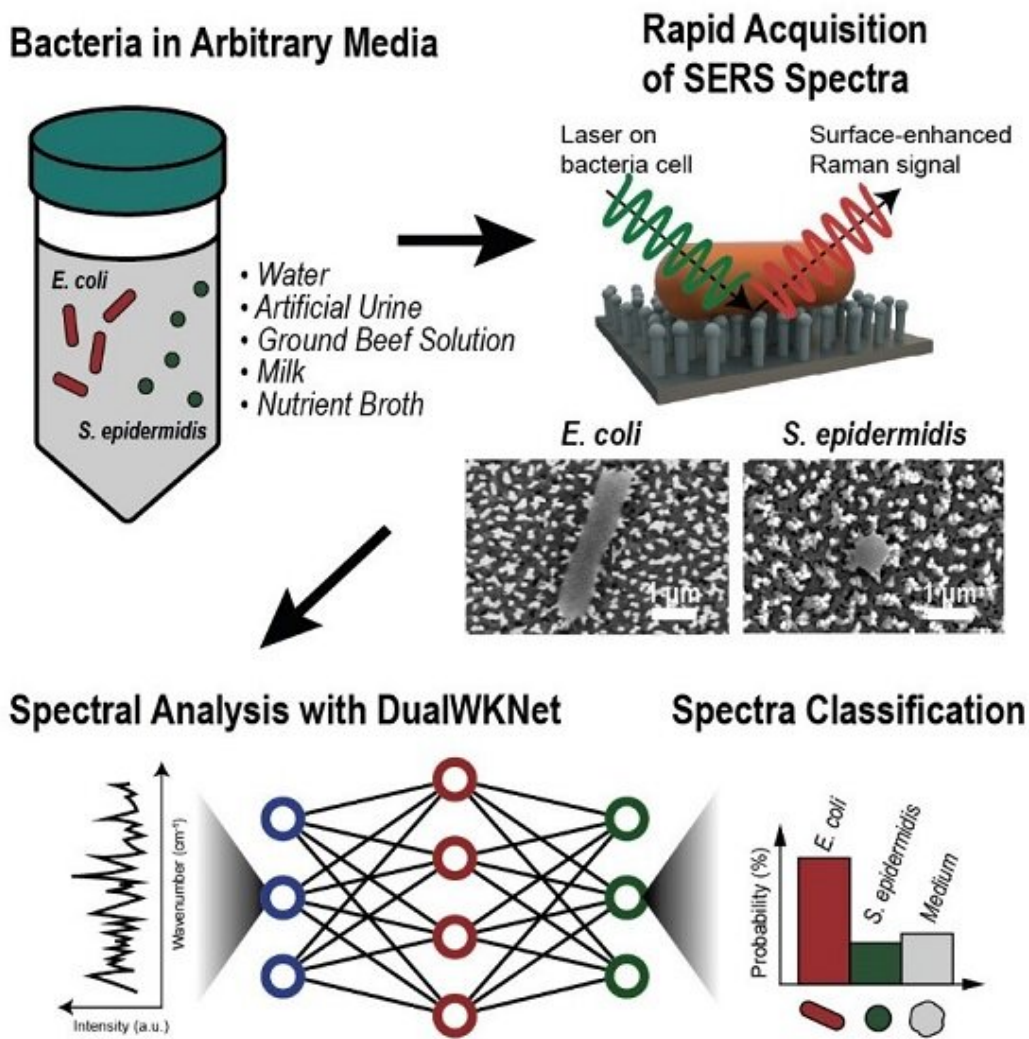


'Fingerprint' machine learning technique identifies different bacteria in seconds

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Schematics of the general process of Raman data collection and analysis where a

single spectrum is attained from a single cell and classified via deep learning.
Credit: The Korea Advanced Institute of Science and Technology (KAIST)

Bacterial identification can take hours and often longer, precious time when diagnosing infections and selecting appropriate treatments. There may be a quicker, more accurate process according to researchers at KAIST. By teaching a deep learning algorithm to identify the "fingerprint" spectra of the molecular components of various bacteria, the researchers could classify various bacteria in different media with accuracies of up to 98%.

Their results were made available online on Jan. 18 in *Biosensors and Bioelectronics*, ahead of publication in the journal's April issue.

Bacteria-induced illnesses, those caused by direct bacterial infection or by exposure to bacterial toxins, can induce painful symptoms and even lead to death, so the rapid detection of bacteria is crucial to prevent the intake of contaminated foods and to diagnose infections from clinical samples, such as urine. "By using surface-enhanced Raman spectroscopy (SERS) analysis boosted with a newly proposed [deep learning model](#), we demonstrated a markedly simple, fast, and effective route to classify the signals of two common bacteria and their resident media without any separation procedures," said Professor Sungho Jo from the School of Computing.

Raman spectroscopy sends light through a sample to see how it scatters. The results reveal structural information about the sample—the spectral fingerprint—allowing researchers to identify its molecules. The surface-enhanced version places sample cells on noble metal nanostructures that help amplify the sample's signals.

However, it is challenging to obtain consistent and clear spectra of bacteria due to numerous overlapping peak sources, such as proteins in cell walls. "Moreover, strong signals of surrounding media are also enhanced to overwhelm target signals, requiring time-consuming and tedious bacterial separation steps," said Professor Yeon Sik Jung from the Department of Materials Science and Engineering.

To parse through the noisy signals, the researchers implemented an artificial intelligence method called deep learning that can hierarchically extract certain features of the spectral information to classify data. They specifically designed their model, named the dual-branch wide-kernel network (DualWKNet), to efficiently learn the correlation between spectral features. Such an ability is critical for analyzing one-dimensional spectral data, according to Professor Jo.

"Despite having interfering signals or noise from the media, which make the general shapes of different bacterial spectra and their residing media signals look similar, high classification accuracies of bacterial types and their media were achieved," Professor Jo said, explaining that DualWKNet allowed the team to identify key peaks in each class that were almost indiscernible in individual spectra, enhancing the classification accuracies. "Ultimately, with the use of DualWKNet replacing the bacteria and media separation steps, our method dramatically reduces analysis time."

The researchers plan to use their platform to study more bacteria and media types, using the information to build a training data library of various bacterial types in additional media to reduce the collection and detection times for new samples.

"We developed a meaningful universal platform for rapid bacterial detection with the collaboration between SERS and deep learning," Professor Jo said. "We hope to extend the use of our [deep learning](#)-based

SERS analysis platform to detect numerous types of [bacteria](#) in additional [media](#) that are important for food or clinical analysis, such as blood."

More information: Eojin Rho et al, Separation-free bacterial identification in arbitrary media via deep neural network-based SERS analysis, *Biosensors and Bioelectronics* (2022). [DOI: 10.1016/j.bios.2022.113991](#)

Provided by The Korea Advanced Institute of Science and Technology (KAIST)

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