Analyzing gut bacteria more accurately to make diagnosis

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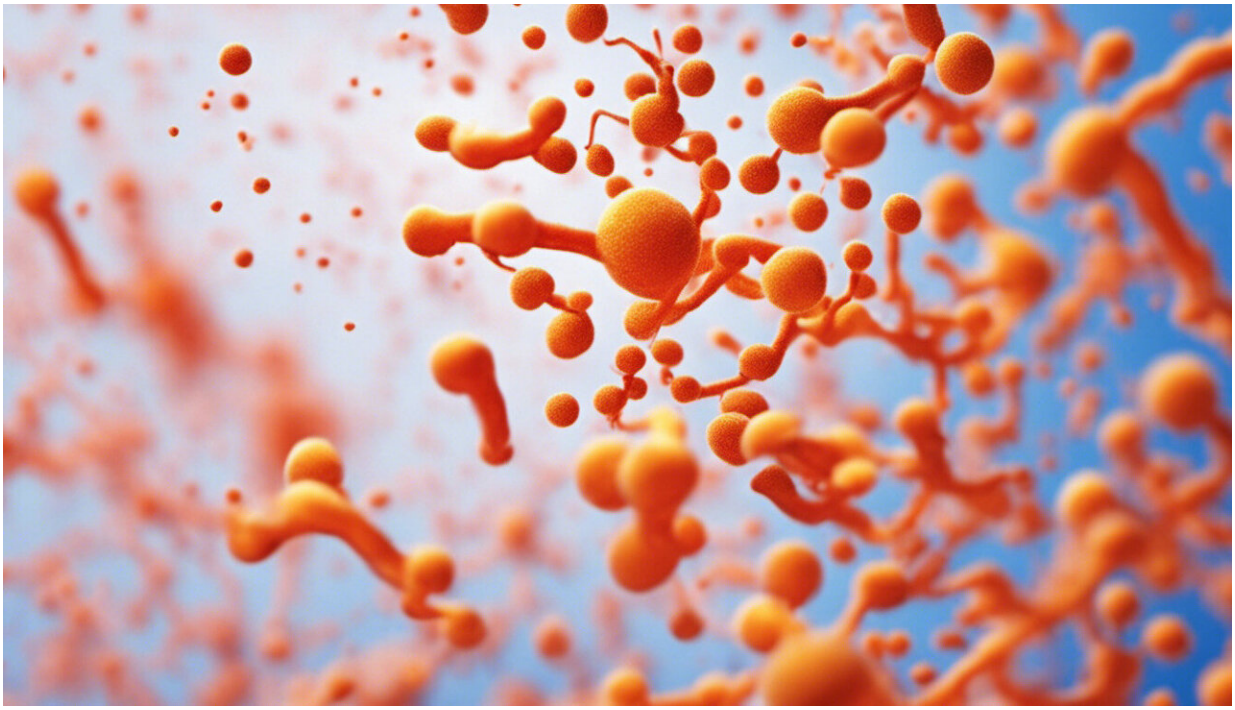


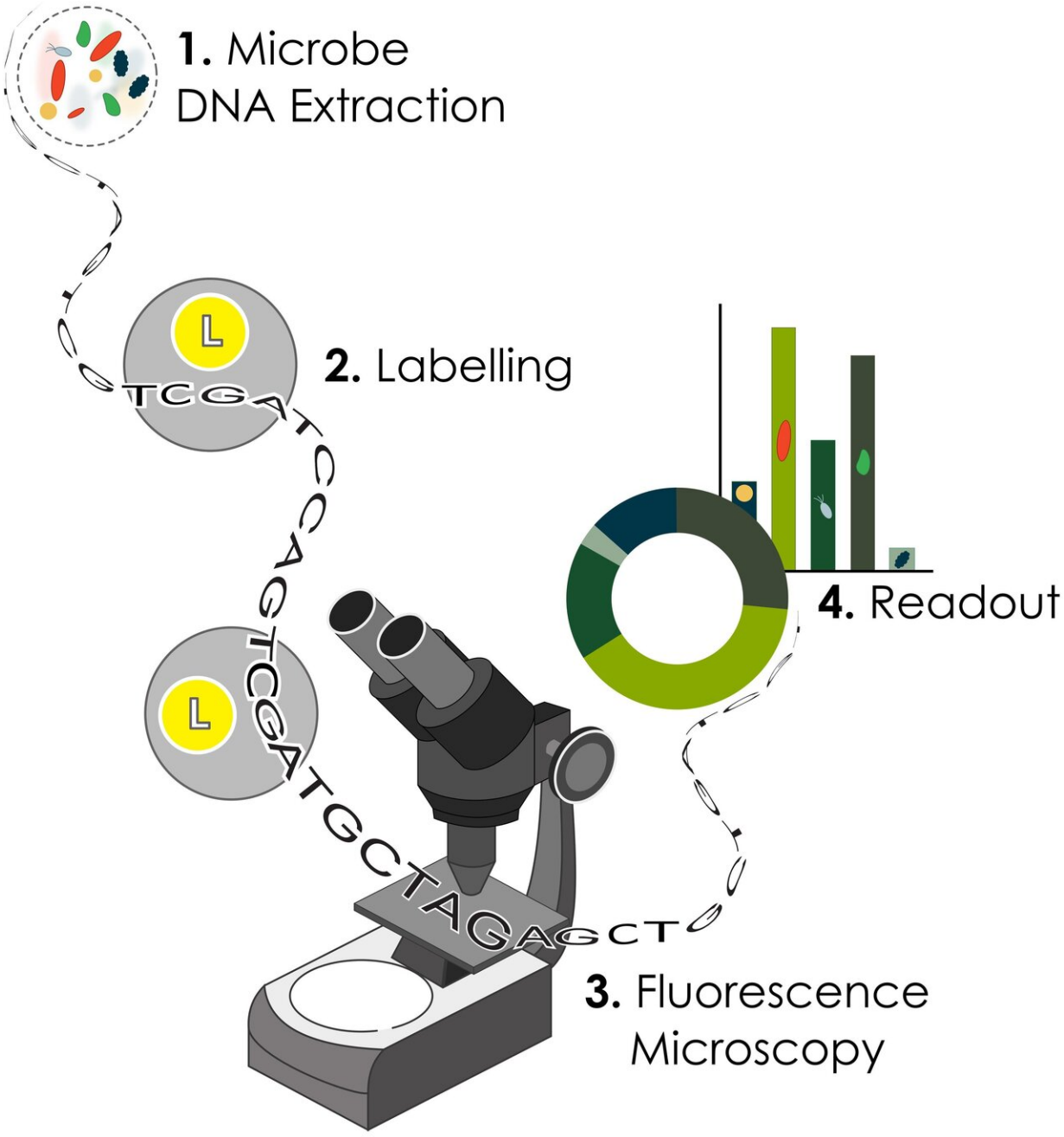
Credit: AI-generated image (disclaimer)

The microorganisms in our intestines could be linked to certain diseases such as Alzheimer's and diabetes. Researchers from the AD-gut consortium have developed a novel method—combining optical DNA mapping and statistics—for accurately distinguishing and rapidly identifying the various species in the microbiota.

Is there a link between the bacteria in our gastrointestinal tract and diseases such as Alzheimer's and diabetes? Recent scientific advances suggest that this is an area that should be explored.

To better explore this possibility, teams led by Prof. Johan Hofkens (KU Leuven), Prof. Aleksandra Radenovic (EPFL / school of Engineering), Prof. Dimitri Van De Ville (EPFL / School of Engineering) and Prof. Theo Lasser (EPFL / School of Engineering) joined forces to develop a robust statistical framework that would enable the use of DNA mapping in microbiome-based diagnostics. The related research paper has been published in *NAR Genomics and Bioinformatics*.

The researchers showed that their method was effective by correctly identifying in a mouse model of Alzheimer's disease, single DNA strands coming from a mixture of two different chromosomes of Vibrio Harveyi, a known gut bacterium. It was a complex challenge. "Real-life samples contain millions of different bacterial species, and we are usually only interested in a dozen of them," explains Raffaele Vitale, one of the study's co-authors. "With our method, we considerably accelerate microbiome analysis in settings where single base level analysis is not required or would not be cost efficient."



Credit: Ecole Polytechnique Federale de Lausanne

In DNA mapping, a microscope image is made from stretched DNA molecules that are specifically labeled with a fluorescent marker,

resulting in sort of "DNA barcodes." To identify where such DNA barcodes came from, they need to be compared to reference maps generated from the bacteria's known genomic sequences. The analysis method then generates a score for every one of these comparisons and uses it to calculate an empirical p-value for the reliability of each match.

Until now, the most common method for analyzing microbiota involved looking for the genes common to all life, such as ribosomal DNA. However, this method suffers from certain drawbacks, such as a potential bias in the readout and the inability to both differentiate between closely related species and to recognize species that do not have these genes (such as bacteriophages). Another option would be for researchers to sequence everything in the sample. But this approach is computationally very intensive, and it has troubles with closely related species. The new method developed within the AD-gut consortium will enable researchers to identify microbial species more quickly and effectively.

More information: Arno Bouwens et al. Identifying microbial species by single-molecule DNA optical mapping and resampling statistics, *NAR Genomics and Bioinformatics* (2019). DOI: 10.1093/nargab/lqz007

Provided by Ecole Polytechnique Federale de Lausanne