

# A matchmaker for microbiomes

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Trent Northen, a Berkeley Lab co-author, analyzes a microbiome sample. Credit: Roy Kaltschmidt/Berkeley Lab

Microbiomes play essential roles in the natural processes that keep the planet and our bodies healthy, so it's not surprising that scientists' investigations into these diverse microbial communities are leading to advances in medicine, sustainable agriculture, cheap water purification

methods, and environmental cleanup technology, just to name a few. However, trying to determine which microbes contribute to an important geochemical or physiological reaction is both incredibly challenging and slow-going, because the task involves analyzing enormous datasets of genetic and metabolic information to match the compounds mediating a process to the microbes that produced them.

But now, researchers have devised a new way to sort through the [information overload](#).

Writing in *Nature Methods*, a team led by UC San Diego describes a [neural network](#)-based approach called microbe-metabolite vectors (mmvec), which uses probabilities to identify the most likely relationship of co-occurring microbes and metabolites. The team demonstrates how mmvec can outperform traditional correlation-based approaches by applying mmvec to datasets from two well-studied microbiomes types—those found in desert soils and cystic fibrosis patients' lungs—and gives a taste of how the approach could be used in the future by revealing relationships between microbially-produced metabolites and [inflammatory bowel disease](#).

"Previous statistical tools used to estimate microbe-metabolite correlations performed comparably to random chance," said Marc Van Goethem, a postdoctoral researcher who is one of three study authors from Berkeley Lab. "Their [poor performance](#) led to the detection of spurious relationships and missed many true relationships. Mmvec is a powerful new tool that accurately links metabolite and microbial abundances to solve this problem. There could be wide-ranging applications from clinical trials to environmental engineering. Ultimately, mmvec will allow us to begin moving away from simple pattern recognition towards unravelling mechanisms."

**More information:** James T. Morton et al. Learning representations of

microbe–metabolite interactions, *Nature Methods* (2019). DOI: [10.1038/s41592-019-0616-3](https://doi.org/10.1038/s41592-019-0616-3)

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