

## FEAST - Fast Expectation-Maximization Microbial Source Tracking

Tech ID: 31754 / UC Case 2019-351-0

### SUMMARY

UCLA researchers from the Department of Computer Science have developed a method to analyze large genomic data sets to quickly identify bacteria community imbalances.

### BACKGROUND

Bacterial diseases such as dysbiosis are a widespread and common issue in both medicine and agriculture. Diagnosing the bacterial strain that is causing the disease is a difficult problem to solve as there are a wide variety of bacterial strains that require differing treatments. Current systems can only rapidly identify a small set of bacteria or require expensive, extremely time-consuming processes to identify a bacterial strain. There is a need for a method that can identify a large set of bacteria quickly without decreasing accuracy in identification.

### INNOVATION

UCLA researchers have developed a method that reduces the amount of time for the characterization of bacterial biomes. Fast Expectation-Maximization Microbial Source Tracking (FEAST) can be leveraged for use in medical diagnoses and characterization of agricultural products. It can analyze and identify bacteria accurately up to 300 times faster than conventional identification methods. FEAST can also identify diagnosable differences between biomes from health and sick patients.

### APPLICATIONS

- ▶ Diagnosis tool for various bacteria-based diseases
- ▶ Ecological tool used for studying microorganisms
- ▶ Tracking foodborne illness

### ADVANTAGES

- ▶ Faster identification of bacterial communities
- ▶ Identification of against uncharacterized sources
- ▶ Can be used with significantly larger data sets

### STATE OF DEVELOPMENT

The algorithm has been developed and is ready for use.

### RELATED MATERIALS

- ▶ [Shenhav, L., Thompson, M., Joseph, T. A., Briscoe, L., Furman, O., Bogumil, D., Mizrahi, I., Pe'Er, I., and Halperin, E. \(2019\) FEAST: fast expectation-maximization for microbial source tracking. Nature Methods 16, 627–632.](#)

### PATENT STATUS

Patent Pending

### ADDITIONAL TECHNOLOGIES BY THESE INVENTORS

- ▶ [Automated Biomarker Prediction Using Optical Coherence Tomography](#)

### CONTACT

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### INVENTORS

- ▶ Halperin, Eran

### OTHER INFORMATION

#### KEYWORDS

Gut biome, dysbiosis, Microbiome,  
Microbial source tracking, Sepsis,  
Wine Testing, Agricultural  
microorganisms, genome  
identification, bacteria

#### CATEGORIZED AS

- ▶ [Agriculture & Animal Science](#)
- ▶ [Other](#)
- ▶ [Biotechnology](#)
- ▶ [Bioinformatics](#)

#### RELATED CASES

2019-351-0

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