

Detecting lung infections with breath analysis and machine learning

ZonaIT



IBEC researchers, together with clinicians from Sant Pau Hospital and Hospital Clinic in Barcelona, use “electronic noses” and machine learning to analyse the breath of patients, identifying with high accuracy those with lung infections of *P. aeruginosa*, a multidrug resistant pathogen. This method could represent a non-invasive and efficient tool to diagnose and monitor patients with a bacterial lung infection, offering a faster alternative to standard sputum cultures.

Bronchiectasis is a chronic lung condition that causes frequent infections and trouble breathing. Although it is more common in women and older patients, it affects individuals of all ages and genders and tends to worsen with time if not treated properly.

Traditionally, lung infections are diagnosed by a time-consuming procedure: collecting a sputum sample that is used firstly to grow the bacteria in the lab, and then identifying the disease-causing microorganism.

In this context, breath analysis is currently being explored as an alternative tool to diagnose, monitor, and triage patients. It offers advantages over other diagnostic techniques in that there is an unlimited sample supply, samples can be collected non-invasively, and analysis results can be delivered quickly. However, breath is a complex biofluid containing thousands of compounds at very small concentrations. Additionally, there are no standardized methods for breath sampling, and breath differences can be due to multiple factors. While chemical analysis of breath has reached clinics in a limited number of biomedical diseases such as asthma and sucrose intolerance or abnormal bacterial growth in the small intestine, expanding it to a wider range of biomedical diseases is challenging.

The Group of [Santiago Marco](#), leader of the [Signal and information processing for sensing systems](#) group at the Institute for Bioengineering of Catalonia (IBEC) and Professor at the University of Barcelona (UB), aims to bring a better methodology to monitor lung infections in bronchiectasis patients and bring this technique closer to the clinic. Luciana Fontes de Oliveira and other colleagues from Santiago Marco’s group, in collaboration with researchers from the University of Barcelona, Hospital de la Santa Creu i Sant Pau and Hospital Clínic – IDIBAPS publish a paper presenting how to detect lung infections with breath analysis.

Comparing breath analysis techniques

The researchers studied two breath analysis techniques that have been widely explored in the literature: electronic noses (e-nose) and gas chromatography-mass spectrometry (GC-MS). An electronic nose is a sensing device that analyzes the pattern of volatile organic compounds in the subject's exhaled breath. A number of systems have been proposed for breath analysis. In this study, the researchers used a device called Cyranose 320® (Sensigent, CA, USA). GC-MS is considered the gold standard technique to analyze and potentially identify substances in a gaseous test sample. This technique combines the capacity of the gas chromatography to separate molecules with the mass spectrometer's ability to provide a mass fingerprint that sometimes allows the chemical identification of the VOCS

In previous studies, the electronic nose has proven effective in identifying *Pseudomonas aeruginosa* infection in bronchiectasis patients – a common bacterial lung infection in these patients. In this study and for the first time, the same samples have been analyzed by both techniques, hoping that GC-MS could provide the chemical identity of putative biomarkers of infection in bronchiectasis patients.

Given that this condition is more common in women, they analyzed three female-only groups: bronchiectasis with no infection, bronchiectasis with known current *Pseudomonas aeruginosa* infection, and healthy controls. Samples were collected in the hospital and e-nose and GC-MS measurements were carried out the same day.

“We found that the e-nose together with proper machine learning software was able to correctly classify healthy controls versus bronchiectasis patients with *Pseudomonas Aeruginosa* infection 100% of the validation cases,” explains Santiago Marco. The technique was also capable of discriminating Bronchiectasis from healthy controls at 95% accuracy and Bronchiectasis PA from Bronchiectasis in 87% of the cases.

The analysis by GC-MS was instead unreliable, and no biomarkers were found. Despite the higher analytical power of GC-MS the complexity and richness of the produced data hindered the discovery of the discriminant biomarkers.

“What this study shows is that the application of standard workflows for the analysis of GC-MS data is not sufficient. The richness of GC-MS data makes biomarker discovery as difficult as finding a needle in a haystack,” adds Marco. “The positive results obtained by the electronic nose indicate that a more sophisticated data analysis with a larger sample size could yield positive results.”

Although breath analysis has clear advantages over other analysis techniques, such as rapidity, the results of this study are still at a very early stage and more research will need to be carried out before it can reach the clinic. “In future studies, we will need to confirm our findings with more patients and more centres, and also to confirm that there is analytical robustness,” concludes Marco.

Breath analysis offers an interesting alternative for the diagnosis of *Pseudomonas Aureoginosa* infection in Bronchiectasis patients, that is accurate and faster than sputum cultures. However, the discovery of the chemical biomarkers behind the observed differences require further studies. Professor Santiago Marco, IBEC

This research field is very important for the diagnosis in an early and non-invasive way of of bronchial infection, since they have a big impact on quality of life, the prognosis and treatment of patients.

Oriol Sibila, Hospital Clínic de Barcelona