

## Problema

Proteomics is an analytical technique that allows the identification and quantification of proteins from a biological system in the search for greater understanding at the molecular level. The method helps in the discovery of new biomarkers and the development of drugs. However, complex samples such as biological fluids, tissues, biopsies, or cell cultures are analyzed by mass spectrometry, generating a collection with thousands of spectra that cannot be interpreted manually. This limits the accuracy and reliability of the data generated by the technique.

## Solução

The solution proposes the creation of computational software that enables the analysis of the spectra for proteomic experiments to allow statistical analysis and accurate biological interpretation. The solution offers a series of new modules, as well as an easy graphical interface. The program is robust and stands out when compared to several competitors when evaluated in data from proof-of-concept experiments.

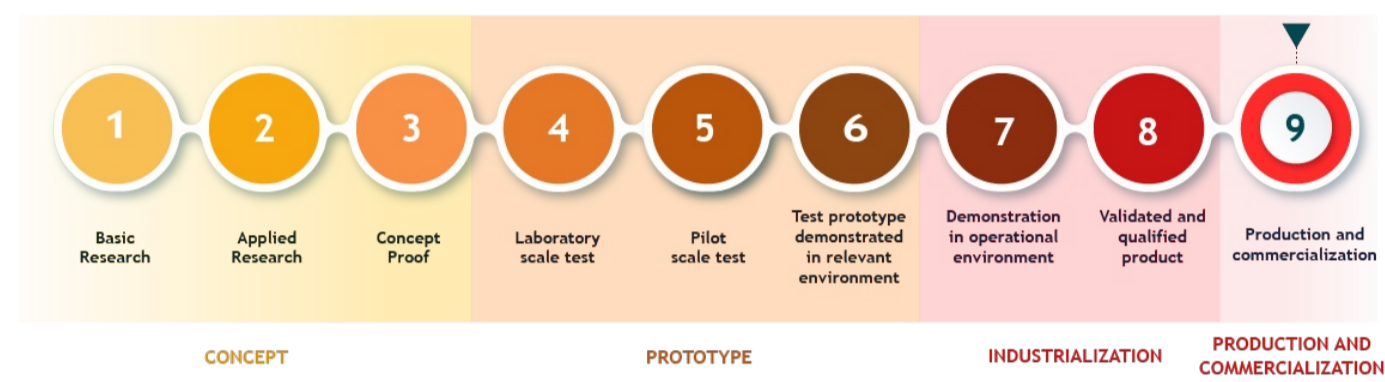
## Diferencial

New computing environment

Preciso

User-friendly graphical interface

## Estágio de Desenvolvimento



## O que buscamos?

Licensing for companies, platforms, or research groups that use mass spectrometry for proteomic analysis. We also offer on-site training, analyzing customer data.

WANT MORE INFORMATION? CONTACT US!

## Inventores

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