Shelf-Life Prediction based on Peptidomics in combination with Deep Learning Applications – A Modell Approach

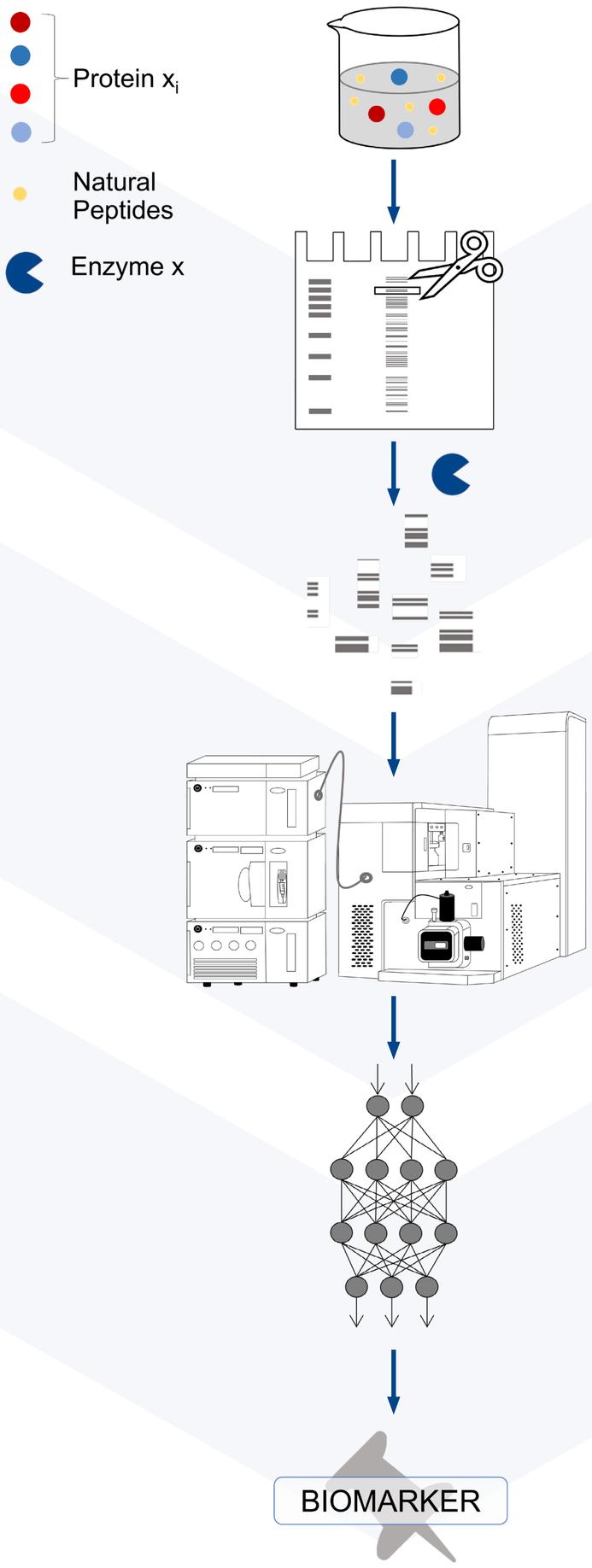
Lisa-Carina Class[1,2], Gesine Kuhnen[1,3], Sascha Rohn[2,3] and Jürgen Kuballa[1]

[1] GALAB Laboratories GmbH, Am Schleusengraben 7, 21029 Hamburg
[2] Hamburg School of Food Science, Institute of Food Chemistry, University of Hamburg, Grindelallee 117, 20146 Hamburg, Germany
[3] Department of Food Chemistry and Analysis, Institute of Food Technology and Food Chemistry, Technische Universität Berlin, Gustav-Meyer-Allee 25, 13355, Berlin, Germany

Corresponding authors: lisa-carina.class@galab.de, gesine.kuhnen@galab.de

MOTIVATION

The accurate prediction of shelf-life is a relevant topic in food analytics.[1] An approach to prevent food waste is the precise prediction of the shelf-life. The reduce of food waste is crucial, especially regarding the growth of population and the limitation of resources.[2] One way to predict the best-before-date of food is the study of the proteome. It is strongly affected by exogenous natural or anthropogenic factors e.g., proteolysis by enzymes.[3,4] Highlighting changes in the proteome during food storage and identifying shelf-life markers could help determine shelf-life more accurately. In the following, the main steps for the shelf-life prediction based on Peptidomics in combination with Deep Learning are presented. The goal is to develop and establish a method for the prediction of shelf-life based on Peptidomics and integrating Deep Learning to this workflow. The aim of this approach is to identify peptide biomarkers which indicate food spoilage and enables an accurate shelf-life prediction. With the outlook that this can be one way to prevent the waste of food.



SAMPLE PREPARATION

To analyse the proteins and the peptides of e.g., milk regarding to determine the shelf-life with HRMS technologies, firstly the proteins have to be separated. In this approach the proteins in the sample are separated by size on a SDS-PAGE gel in an electric field. After the individual protein is available an enzymatic in-gel digestion will be performed.

LC-HRMS

The received peptide-mix is than ready to get analysed with a Liquid Chromatography High Resolution Mass Spectrometry (LC-HRMS) system. After the information about the peptides such as the mass-to-charge ratio, drift time and quantity of each peptide in the mix can be obtained, the data processing can be performed.

DEEP LEARNING

Deep Learning (DL) is a type of Machine Learning, it can be used to detect and learn patterns in datasets. No manual feature extraction and effectiveness with big data are advantages of DL. DL is based on artificial neural networks (NN), different architectures of these are used to fit the task. Besides the common use for language processing and pattern recognition, it can be used for de-novo peptide sequencing.[5] By integrating this application, the identification of peptide biomarkers for e.g., shelf-life determination can be performed effectively and more accurate. Essential parts of the development process are the encoding of amino acids, data conversion, the training (Supervised, Unsupervised or Reinforcement Learning), testing and validation.

References:
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