ONLINE MODE

ADVANCED BIOINFORMATICS FOR PROTEOMICS

From data to discovery

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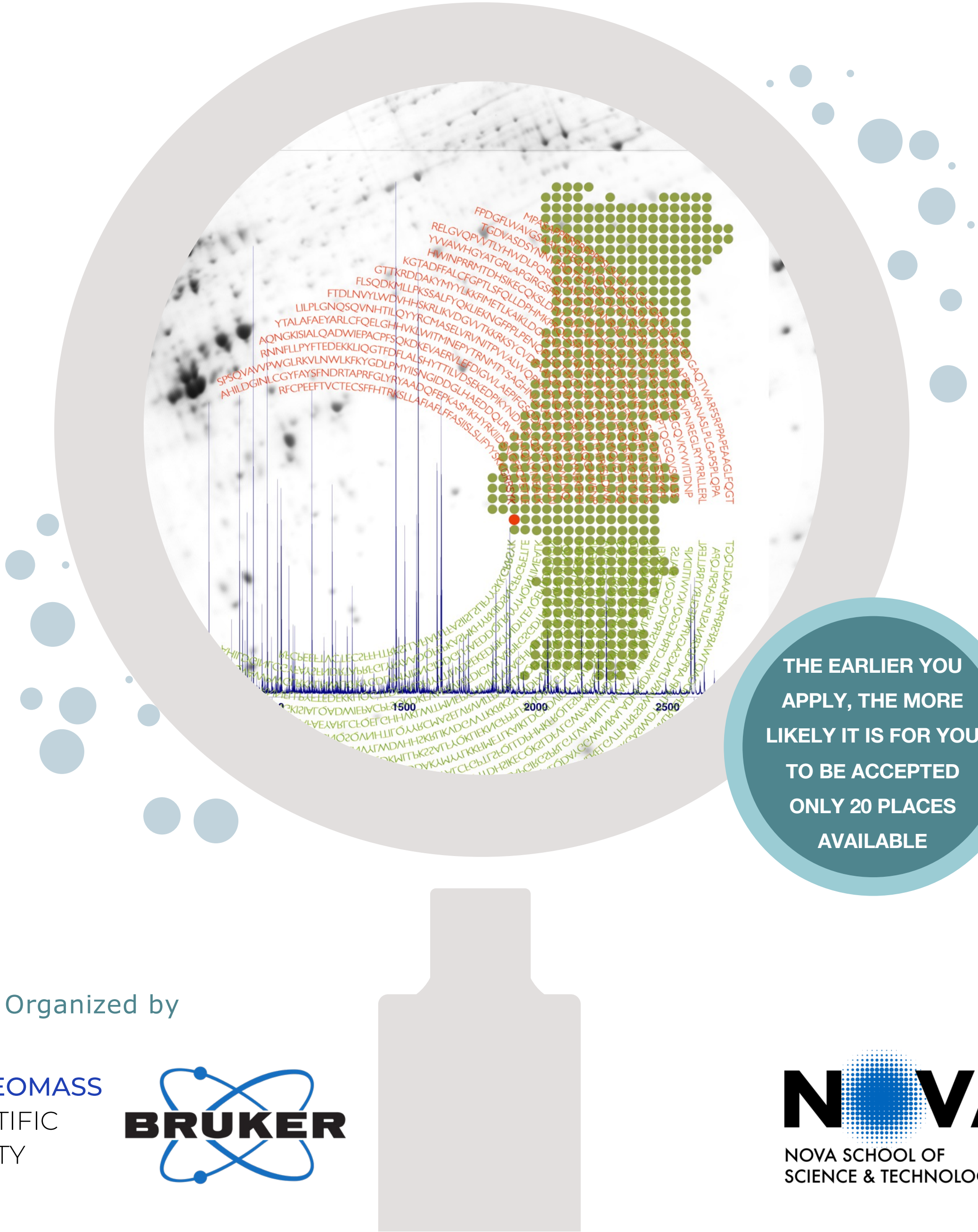
17th – 20th February 2025

NOVA School of Science and Technology (FCT – NOVA), Caparica, Portugal
https://advancedbioinfproteomics.bioscopegroup.org

INNOVATION. COLLABORATION. BEYOND SCIENCE



THE EARLIER YOU APPLY, THE MORE LIKELY IT IS FOR YOU TO BE ACCEPTED ONLY 20 PLACES AVAILABLE

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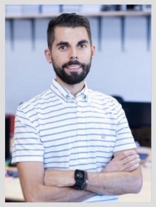
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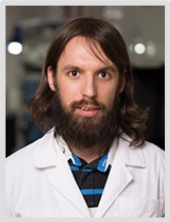
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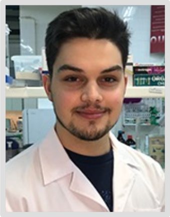
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THE HISTORY OF...

PROTEOMICS

1971
Automated Edman sequencing, ELISA technique

1977
DNA Sequencing (Sanger Method)

1979
First software for DNA sequence assembly

1988
MALDI-TOF (>10 kD), phage display, DNA pyrosequencing invented

1994
Introduction of the concept of Proteome. Correlation of tandem MS data with protein databases

1996
Yeast PROTEOME (MALDI/ESI), real-time DNA pyrosequencing. Data-controlled automated LC-MS/MS

2002
Yeast phosphoproteome,
SILAC labelling, PAI

2005
454 pyrosequencing, emPAI

2008
Absolute SILAC

2010
Aptamer-based multiplexed proteomics

2015
Advancements in Data-Independent Acquisition (DIA) Mass Spectrometry

2016
Trapped Ion Mobility Spectrometry

2018
Parallel accumulation-serial fragmentation (PASEF)

2023
Prescriptomics

BRUKER BIOINFORMATICS

1960
Bruker Physik-AG founded, focusing on NMR spectrometers

1969
The world’s first Fourier Transform NMR spectrometer

1980
Bruker enters mass spectrometry field with ‘Bruker-Franzen Analytik’

1982
First installations of FT-ICR mass spectrometry systems

1997
Acquisition of Siemens analytical X-ray division

2008
Introduction of the maXis $^{\text{TM}}$ QTOF mass spectrometer for proteomics

2015
Launch of the Impact II$^{\text{TM}}$ QTOF, enhancing sensitivity for proteomics research

2017
Introduction of the timsTOF Pro with PASEF ® technology, revolutionizing proteomics worksflows

2019
Release of the timsTOF flex, combining MALDI imaging with PASEF for spatial proteomics

2020
Introduction of 4D-Proteomics$^{\text{TM}}$ workflow, leveraging CCS values for improved selectivity

2022
Launch of timsTOF Ultra and timsTOF HT systems for high-throughput proteomics

2024
Advancements in CCS-enabled 4D-proteomics, including improved software for immunopeptidomics and glycoproteomics

> “... With the sequencing of the human genome, personalized medicine is becoming a reality. In the future, medical treatments will be tailored to the individual genetic needs of each patient...”
>
> **James D. Watson**

THE COURSE

COURSE OUTLINE

Introduction to Bioinformatics

- Overview of bioinformatics in proteomics
- Importance of data analysis in proteomics

Data acquisition & Processing

- Peptide and protein analysis (case study)
- Quantification methods
- Parameter optimization, output files type and interpretation
- Mass-Up for MALDI Applications

Statistical analysis & Data extrapolation (Perseus for advanced analysis)

- Data filtering/normalization
- Statistical tests for differential expression
- Clustering and principal component analysis
- Volcano plots and other visualization

Network analysis (Cytoscape for protein interaction)

- Importing protein-protein interactions data
- Network visualization and layout algorithm
- Topological analysis of networks
- Integration of expression data with networks

THE COURSE

Advanced approaches

Total protein approach (TPA)

- Principles of TPA
- Absolute protein quantification
- Applications and limitations of TPA

Differential Personalized Pathway Index (dPPi)

- Concept and methodology
- Identifying differential interactions
- Biological interpretation of dPPi results

Integration with other OMICS data

- Combining proteomics with metabolomics
- Multi-omics data visualization

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Caparica Campus

Take a look at this ⟶ **https://www.youtube.com/watch?v=8DAZq40wmMo**

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REGISTRATION FEE INCLUDES:

- Manual with theoretical classes
- Certificate of participation