

# **E5020 – Analysis of nontarget MS data**

0 - Organization

# What are we going to do?



Lectures – **theoretical** understanding of the **concepts**, methods and algorithms



Practical – **applying** tools implementing those **methods** to process data using Galaxy

# Course Objectives

At the end of this course, you will:

- know different approaches to separation and detection of molecules with a focus on liquid and gas chromatography
- know the principles of mass spectrometry (MS) instrumentation
- know basic MS data formats and related terminology
- know which steps are involved in processing untargeted MS data
- based on data type, methodology used and molecule type, select and apply methods for data processing
- be able to work with software for MS data analysis using Galaxy

# Agenda

Date	Topic	Class	Teacher
20.02.	<b>Organization and Introduction</b>	Lecture	Helge Hecht
27.02.	<b>Instrumental Analysis – Chromatography, Mass Spectrometry &amp; Acquisition methods</b>	Lecture	Thomas Contini
05.03.	<b>Introduction to -omics</b>	Lecture	Elliott Price
12.03.	<b>Introduction to untargeted mass spectrometry data &amp; pre-processing</b>	Lecture	Helge Hecht
19.03.	<b>Getting started with Galaxy, exploring the data and pre-processing Feature detection from instrumental data</b>	Practical Lecture	Helge Hecht
26.03. & 02.04.	<b>No classes</b>		
09.04.	<b>Feature detection from instrumental data</b>	Practical	Thomas Contini
16.04.	<b>From features to spectra (deconvolution)</b>	Lecture	Helge Hecht
23.04.	<b>From features to spectra (deconvolution)</b>	Practical	Helge Hecht
30.04.	<b>Annotation – from spectra to compounds</b>	Lecture	Helge Hecht
07.05.	<b>Annotation – from spectra to compounds</b>	Practical	Helge Hecht
14.05. & 21.05.	<b>TBA</b>	TBA	TBA

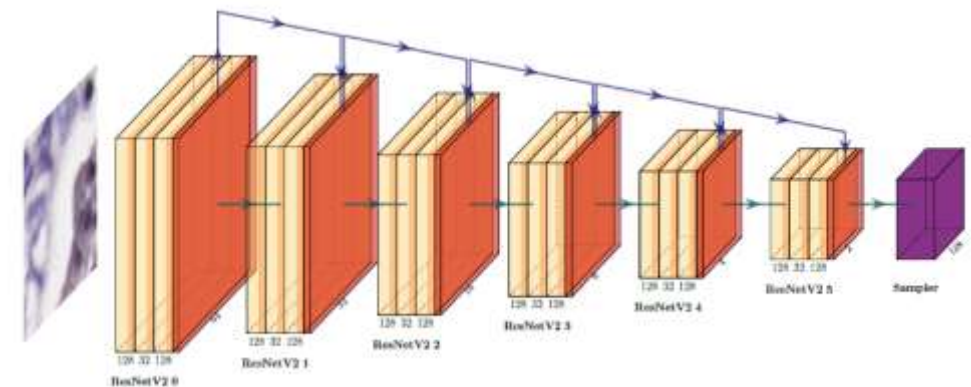
# General Information

- Contact the course coordinator: [eva.budinska@recetox.muni.cz](mailto:eva.budinska@recetox.muni.cz)
- Contact me: [helge.hecht@recetox.muni.cz](mailto:helge.hecht@recetox.muni.cz)
- Course information & (interactive) syllabus available in IS
- Interactive syllabus contains
  - a summary of each session
  - accompanying slides after each lesson
  - link to anonymous feedback form
- Attendance is not compulsory (but highly encouraged!)
- Assessment via written exam based the slides (100%)
- Additional information and examples are linked in the slides

# A little about myself

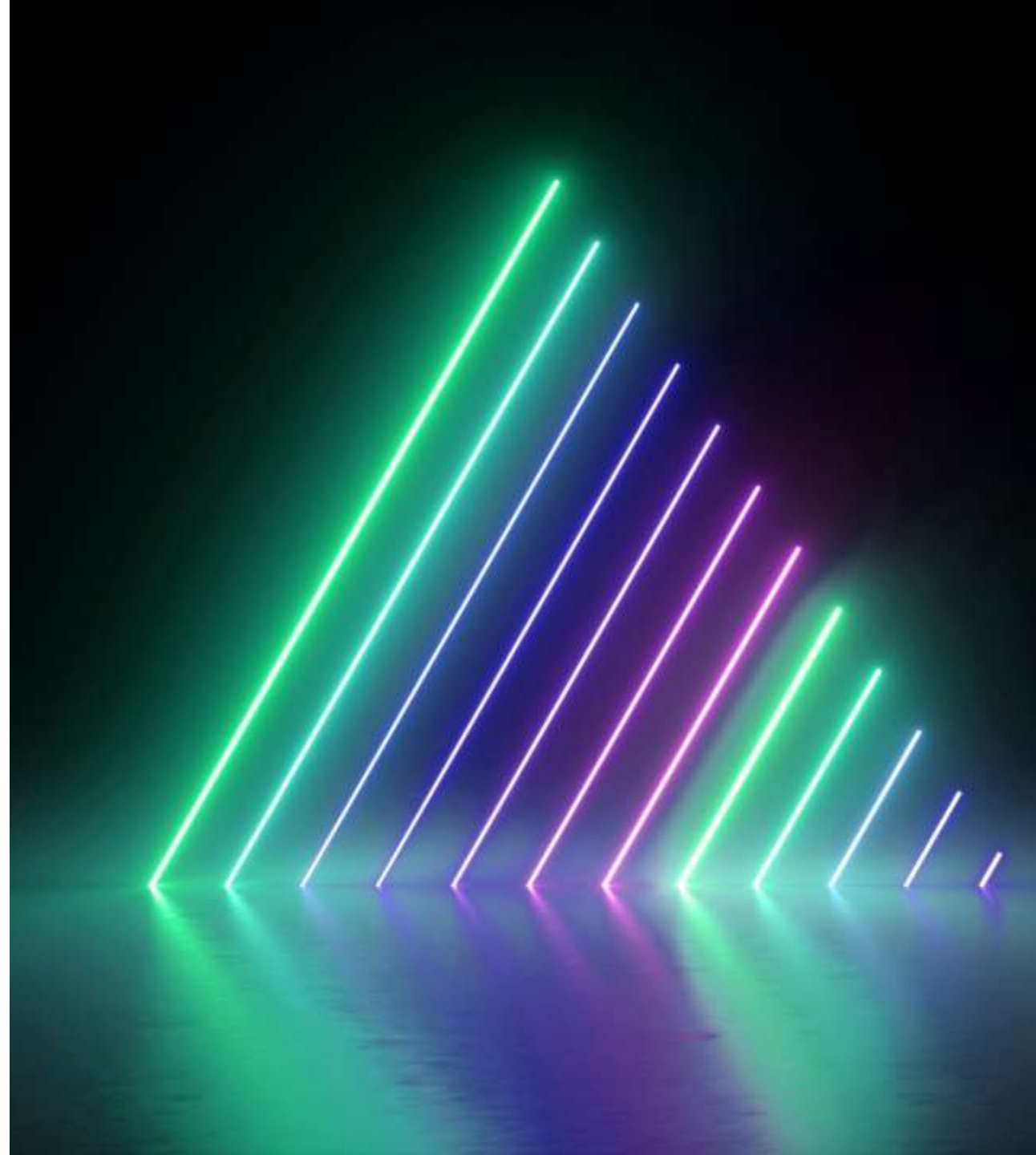
Helge Hecht – Spectrometric Data Processing & Analysis Research Infrastructure (SpecDatRI)

- BSc in **Informatik: Games Engineering**
- MSc in **Computer Science (TUM)**
- **Research assistant** working with Building Information Modeling (BIM)
- **Software engineer** in Thermo Scientific
- **PhD student** at RECETOX with Jana Klánová & Elliott James Price
- Developing tools for **mass spectrometry data processing** in the RECETOX RI



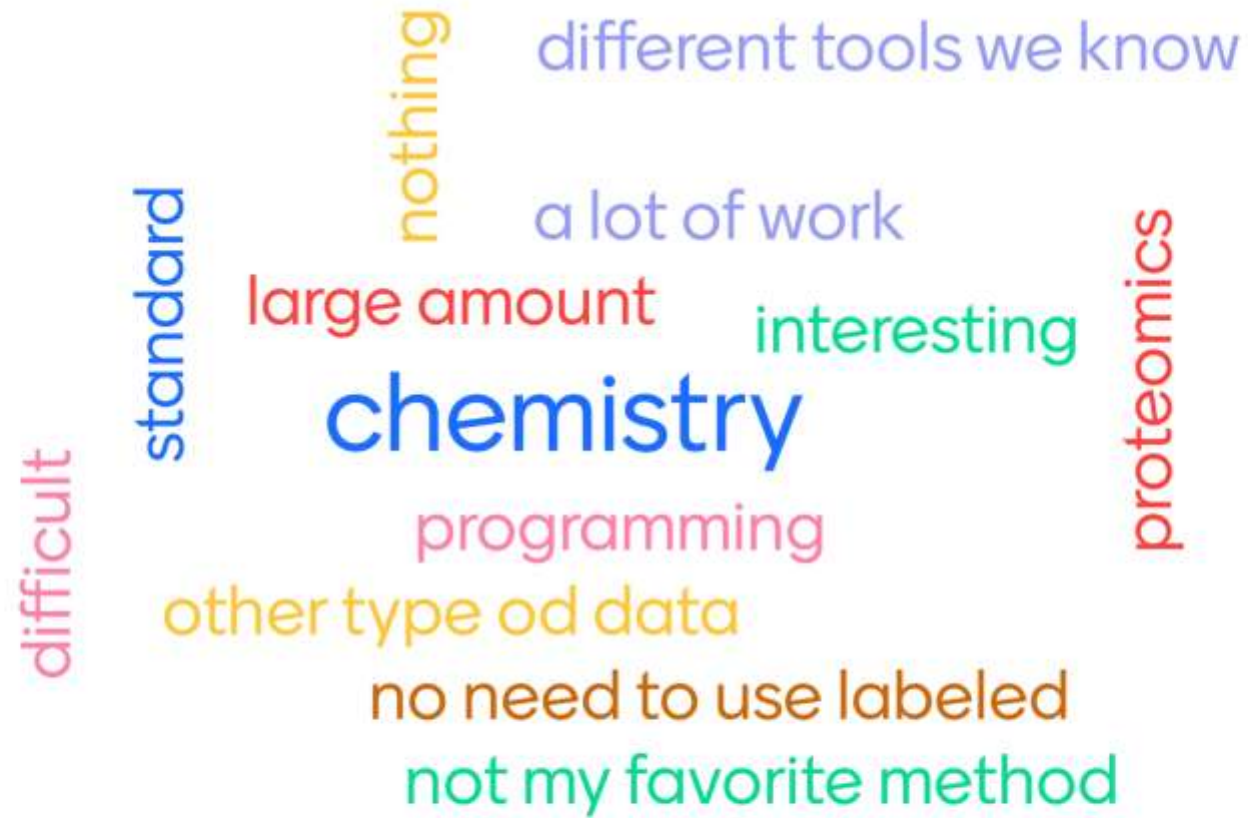
## Discussion

[menti.com 4133 9615](https://menti.com/41339615)



What do you think of when you hear "Analysis of non-targeted mass spectrometry data"?

14 responses





## How do you usually process data?

Statistics and visualization  
in R

Clean, normalize, visualize

Genome data analysis  
using Python, specifically  
Numpy

Control, edit, perform  
analysis

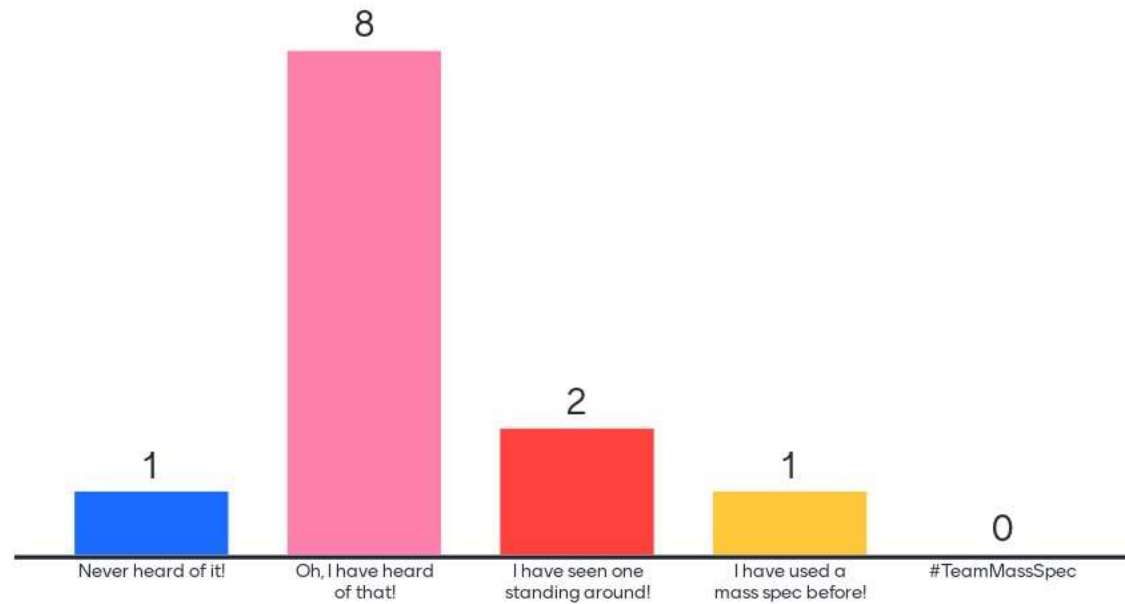
I look at them, try to  
understand them and then  
based on my goal I use  
corresponding tools to process  
the data

In R software or Python -  
gene or genome analysis

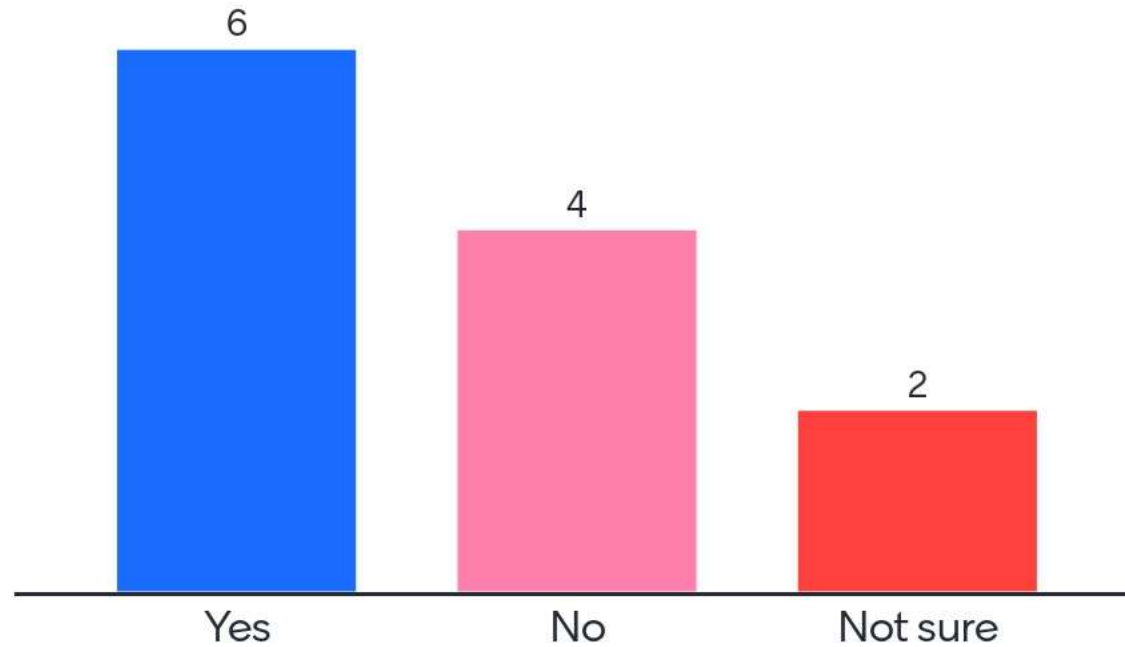
By my scripts or validated  
tools

Obtained (measurements) -  
clean up - visualise

# How familiar are you with mass spectrometry?



# Have you heard of the Galaxyproject before?



# Introduction - Lectures

## **Lectures – theoretical understanding of the concepts, methods and algorithms**

- Learning the instrumental analytical platforms
- Experiment design and research questions – introduction to (mass spectrometry based) –omics
- Understanding of the data and related terminology
- Algorithms and methods behind data processing software

# Introduction - Practical

## applying tools implementing those methods to process data using Galaxy

- Getting familiar with the Galaxy platform
- Learn about existing tools implementing the concepts discussed in the lectures
- Use those tools to process example data
- Each practical is based on a [Galaxy Training Network](#) Tutorial which can be studied also independently at home

# Introduction – Practical – Galaxy Servers



**62,000+**  
registered users



<b>3,100</b> tools	<b>170+</b> reference genomes
<b>54M</b> jobs	<b>94M</b> datasets
<b>270K</b> workflow executions	<b>1.1M</b> histories

**109** countries

**3,600** active users per month

**DISTRIBUTED HETEROGENEOUS COMPUTE**

useGalaxy  
Pulsar node

**12**  
Pulsar Network partners

**300+** tutorials  
training.galaxyproject.org

**1300+** ELIXIR AAI users

**350+** events  
**14K+** trainees  
 Training Infrastructure as a Service

**11K+** publications citing Galaxy



**... and many more!**  
**MUNI | RECETOX**

# Introduction – Practical - TlaaS

- T**rain**I**n**I**n**f**ra**s**tr**u**ct**u**r**e** **a**s **a** **S**ervice
- dedicated environment for teaching
  - registration link for each practical in the interactive syllabus in IS
  - no own device or software setup required
  - all data and steps are recorded and accessible from any device with a web browser

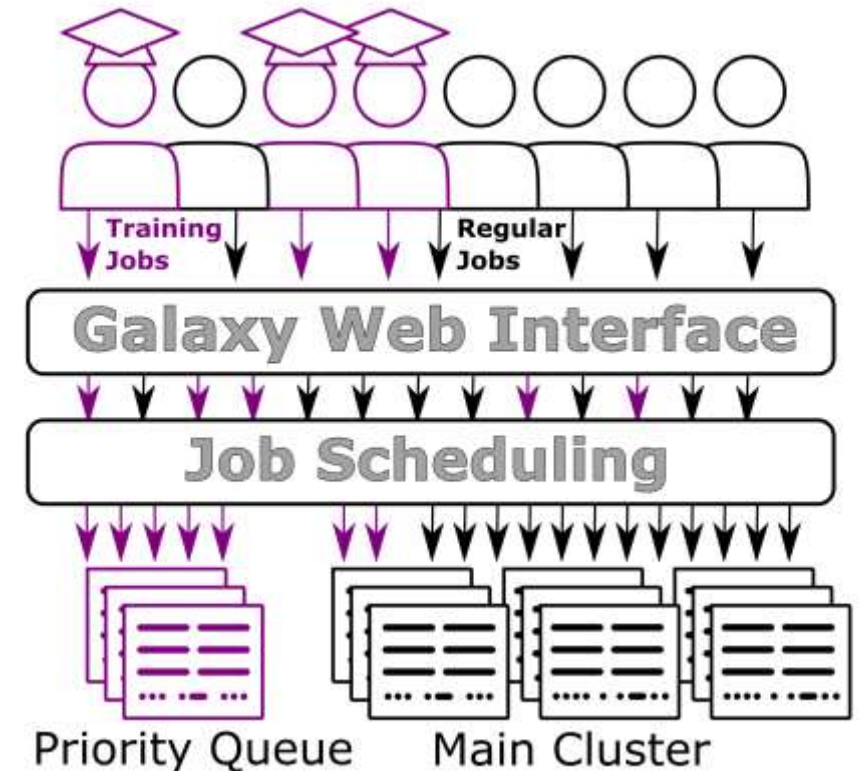


Figure taken from [10.1093/gigascience/giad048](https://doi.org/10.1093/gigascience/giad048)



# Next time...

We are talking about

1. Chromatography
2. Mass Spectrometry
3. Data Acquisition Methods

with Thomas Contini.