

Metabolomics

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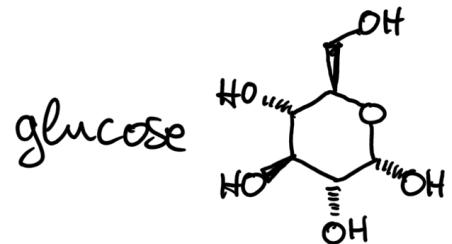
CSAMA 2019

Content

- (Brief) introduction to metabolomics
- Preprocessing of LC-MS data
- Normalization
- Annotation/identification

Metabolite? Metabolism?

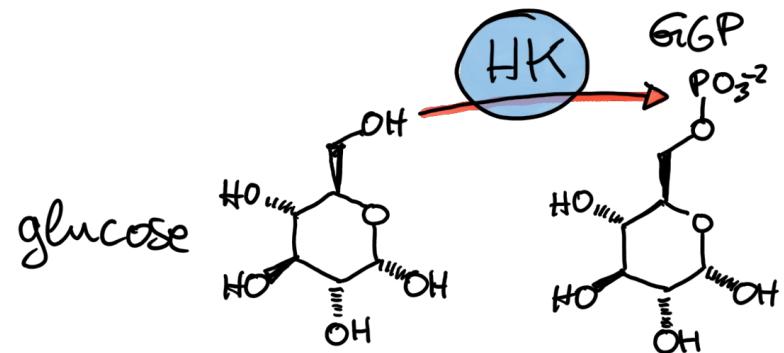
- Glycolysis



- Key metabolic pathways common to all cells.
- Creates energy by converting glucose to pyruvate.

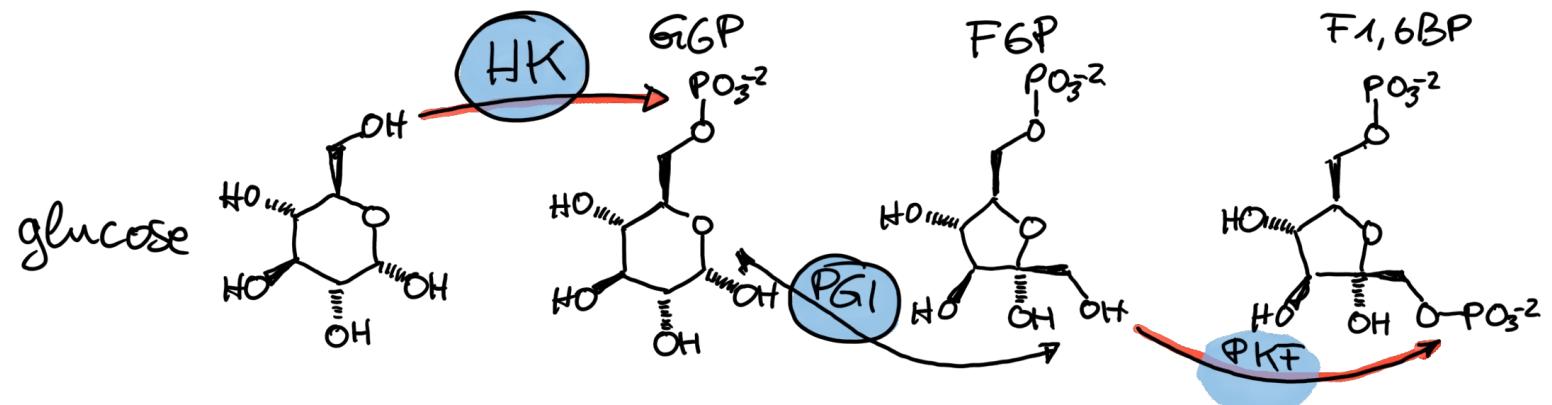
Metabolite? Metabolism?

- Glycolysis



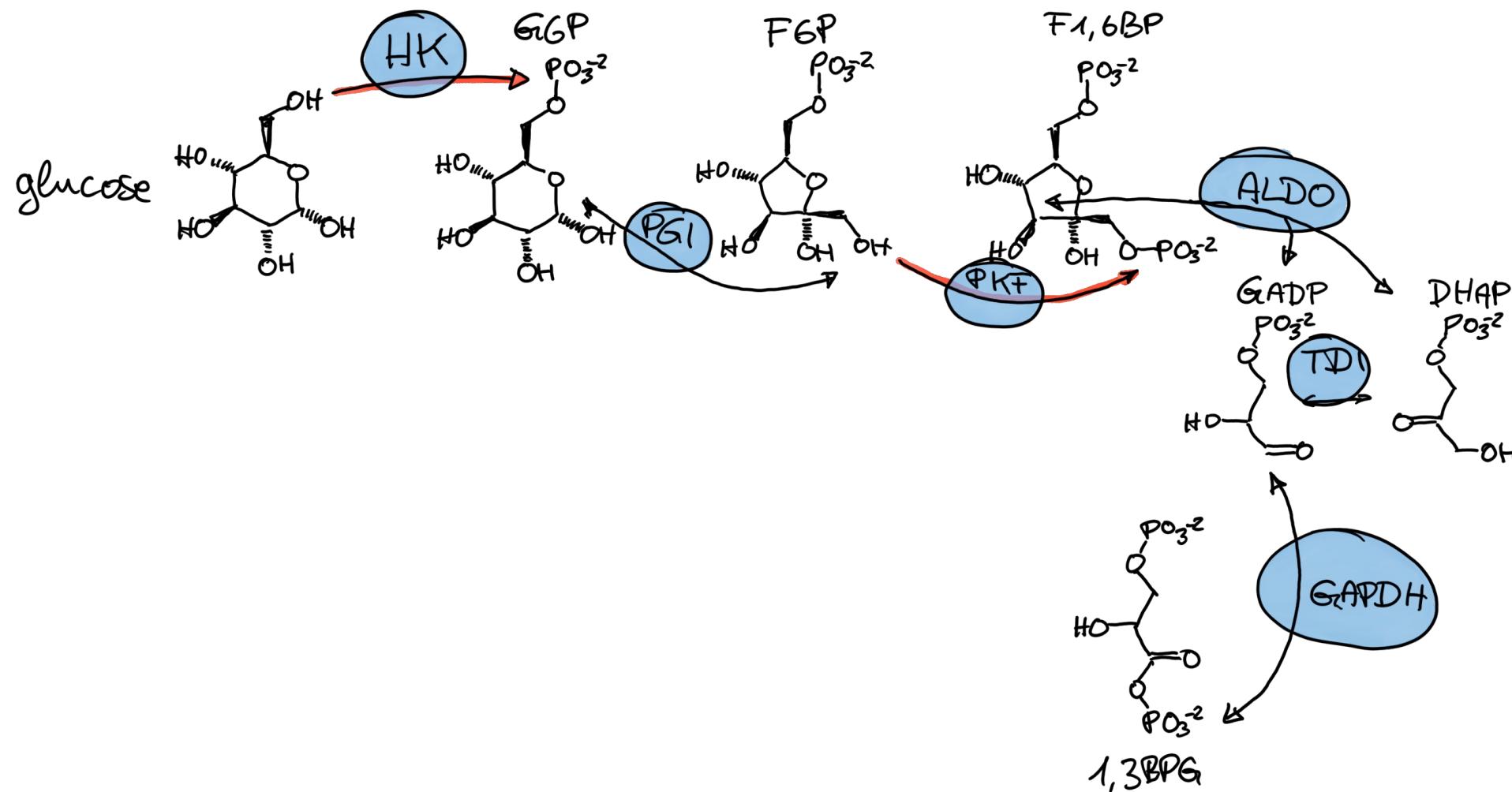
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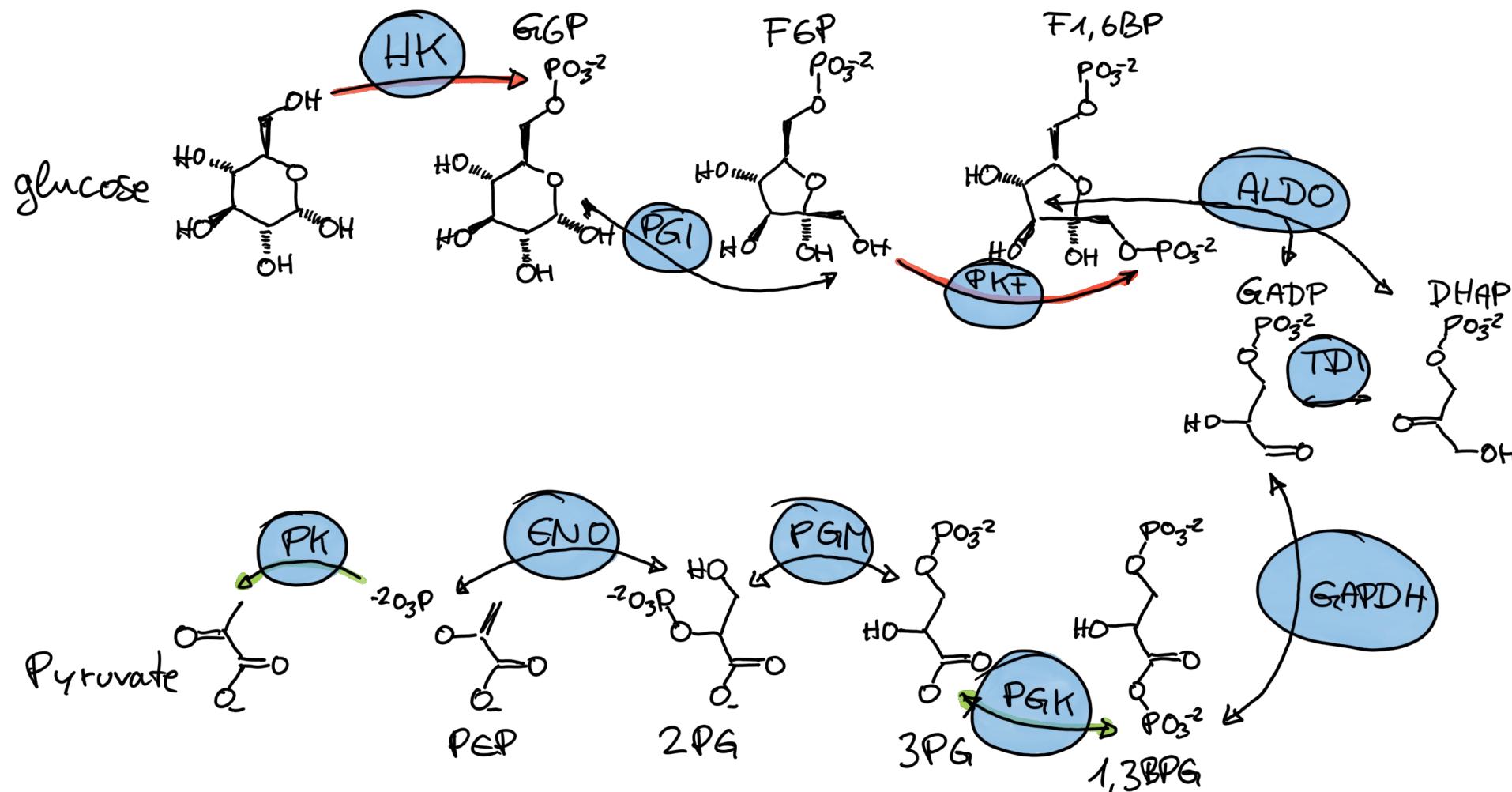
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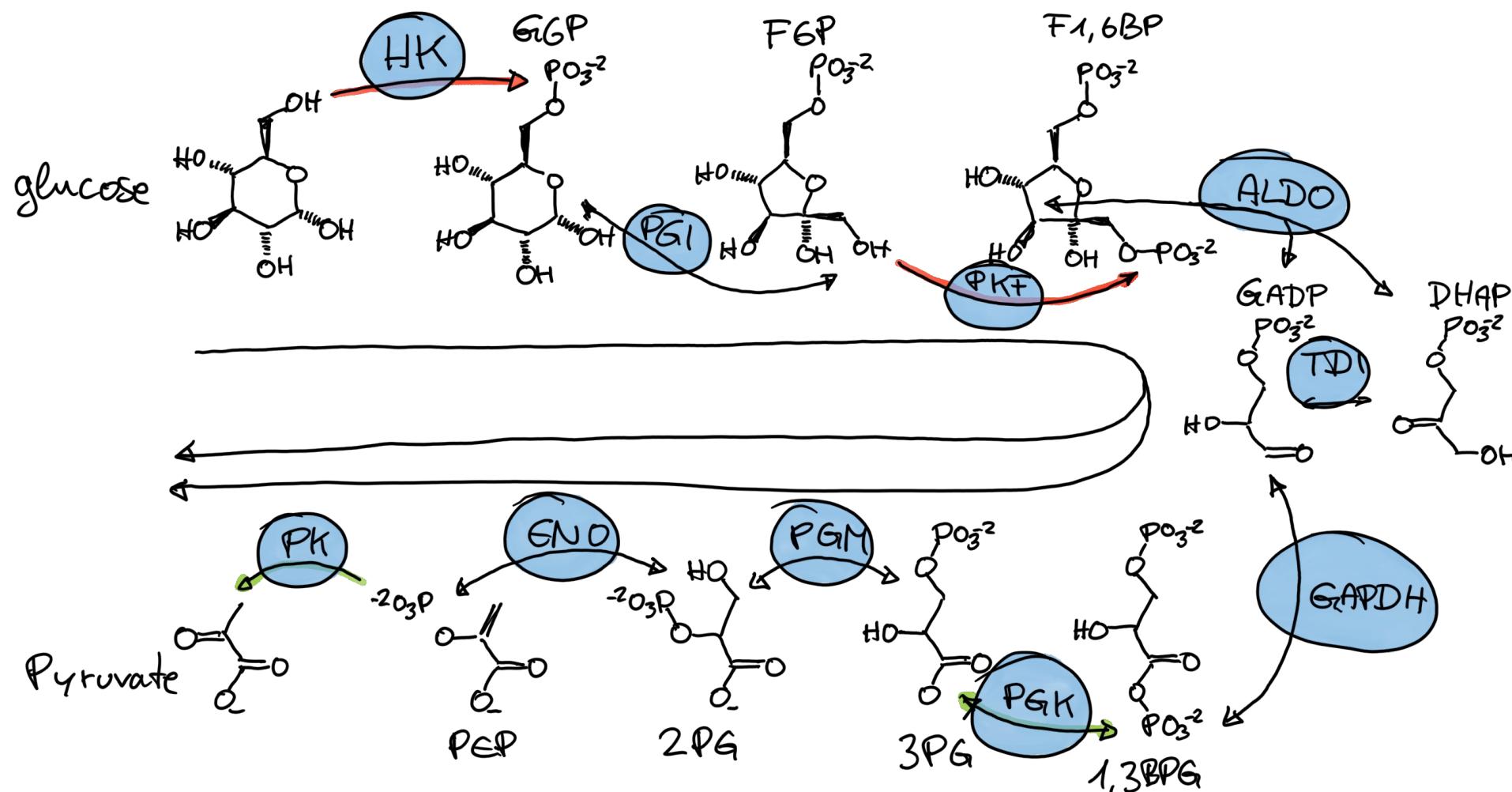
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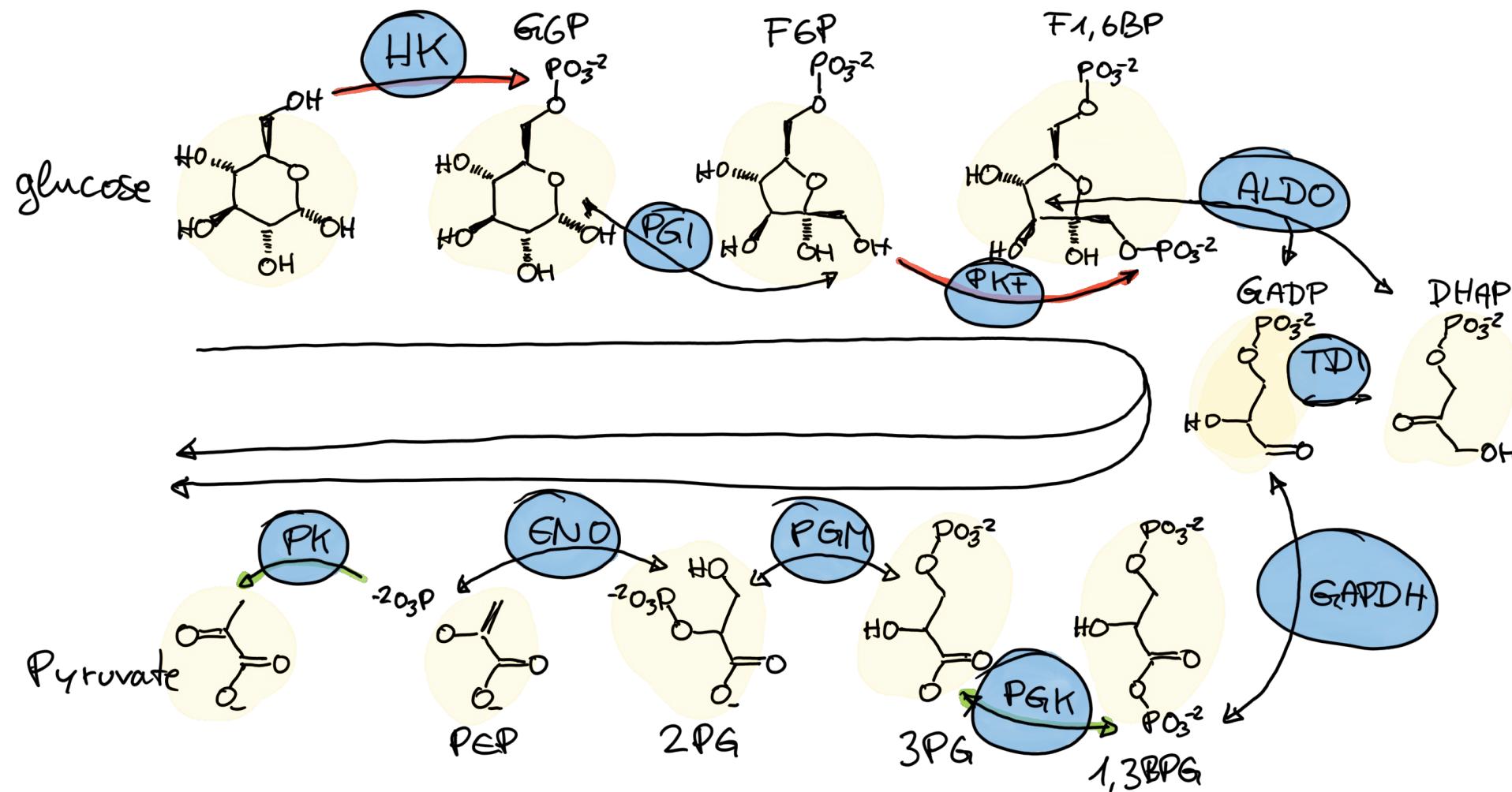
Metabolite? Metabolism?

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Metabolite? Metabolism?

- Glycolysis



- Metabolites: intermediates and products of cellular processes.

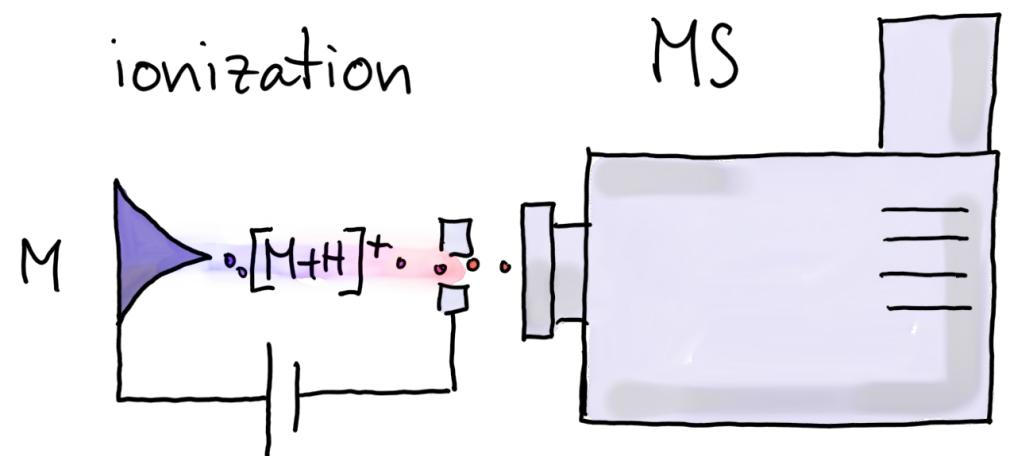
Metabolomics?

- Large-scale study of small molecules (metabolites) in a system (cell, tissue, organism).
- Comparison of the different -omes:
- **Genome**: what can happen.
- **Transcriptome**: what appears to be happening.
- **Proteome**: what makes it happen.
- **Metabolome**: what actually happened.
- Metabolome influenced by genetic **and** environmental factors.

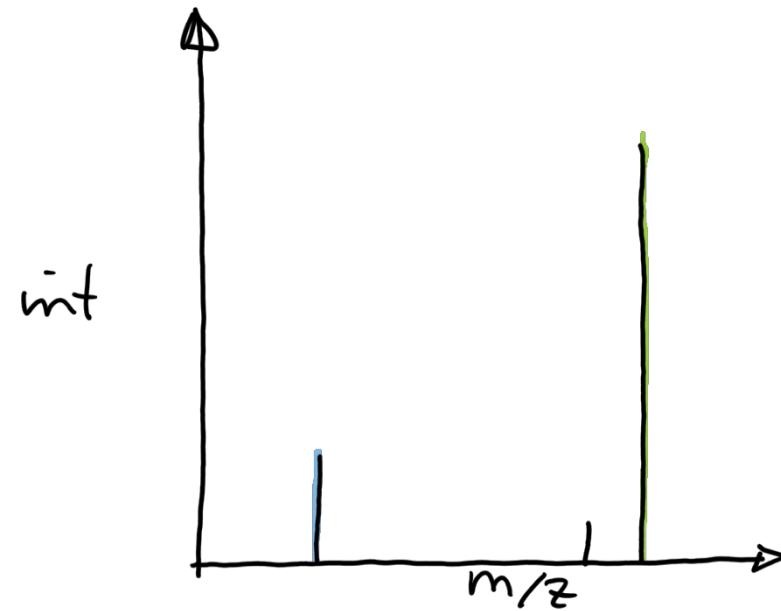
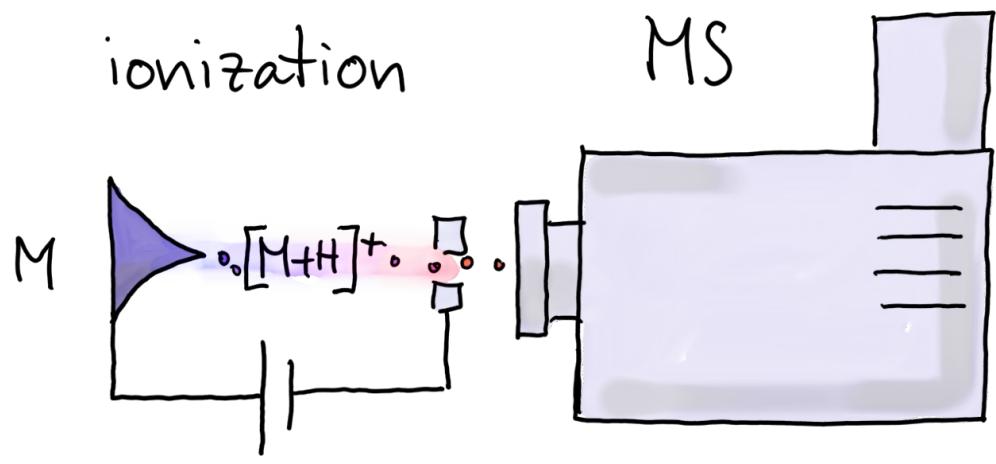
How can we measure metabolites?

- Nuclear Magnetic Resonance (NMR) - not covered here.
- Mass spectrometry (MS)-based metabolomics.
- Metabolites small enough to be directly measured.
- Most metabolites uncharged - need to create ions first.

Mass Spectrometry (MS)



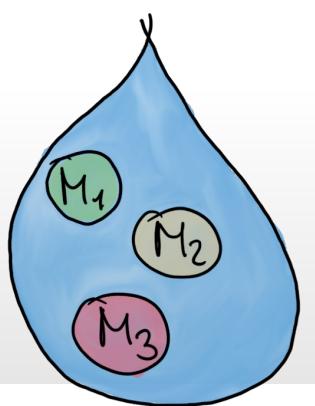
Mass Spectrometry (MS)



- **Problem:** unable to distinguish between metabolites with the same/similar mass-to-charge ratio (m/z).
- **Solution:** additional separation of metabolites prior to MS.

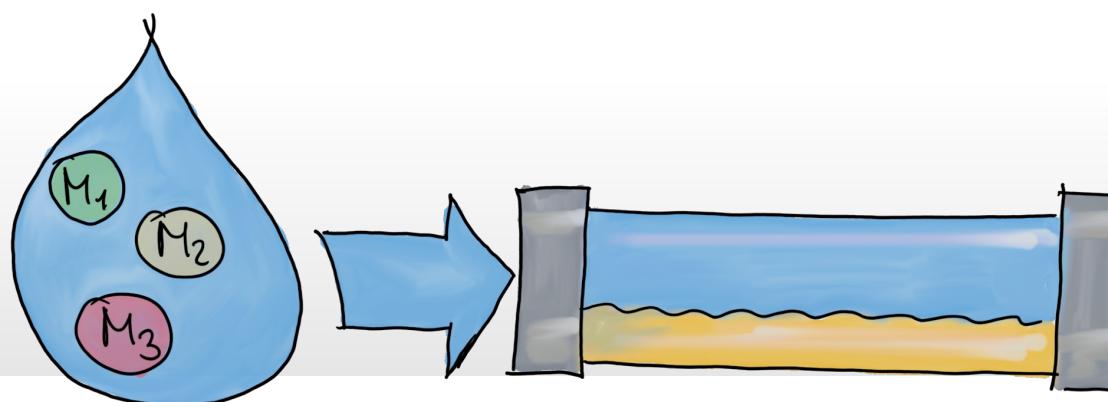
Liquid chromatography

- Sample is dissolved in a fluid (mobile phase).



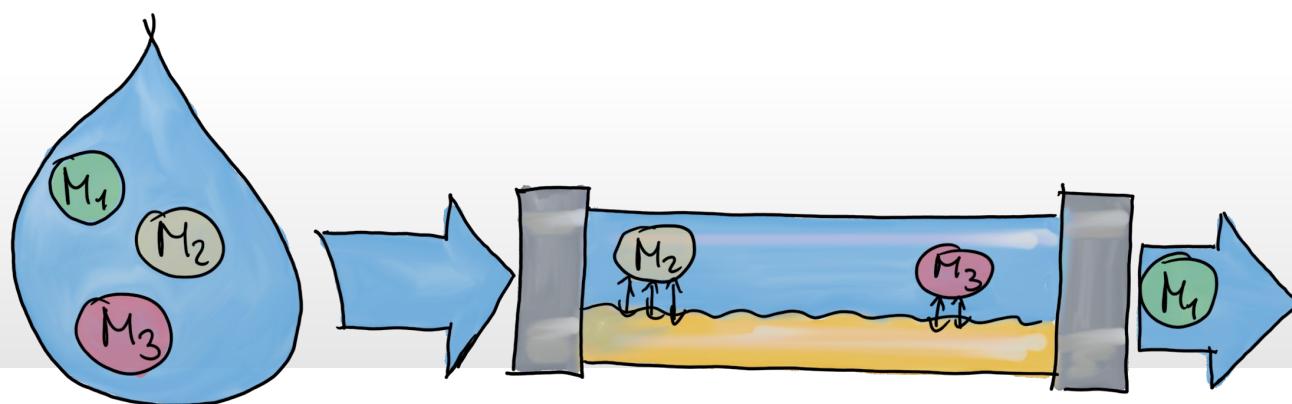
Liquid chromatography

- Sample is dissolved in a fluid (mobile phase).
- Mobile phase carries analytes through column (stationary phase).



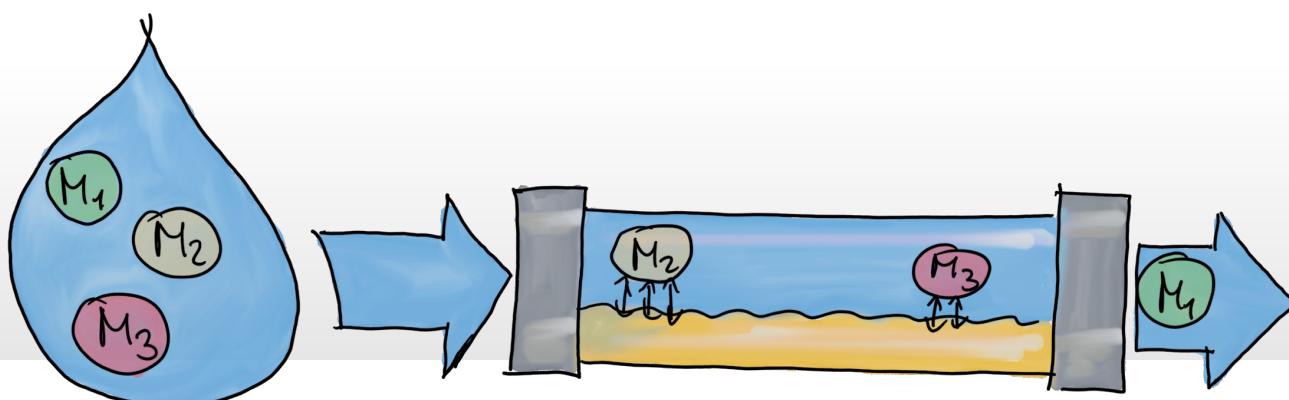
Liquid chromatography

- Sample is dissolved in a fluid (mobile phase).
- Mobile phase carries analytes through column (stationary phase).
- Separation based on affinity for the column's stationary phase.

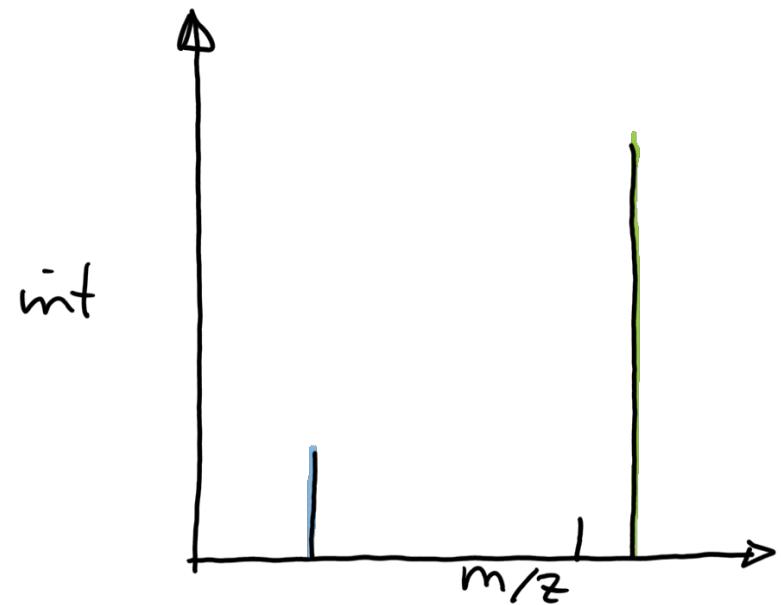
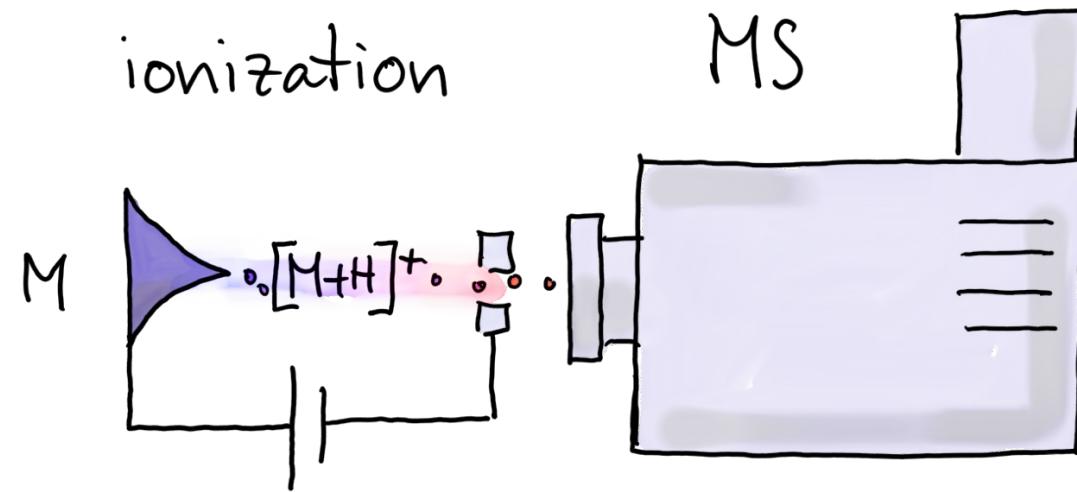


Liquid chromatography

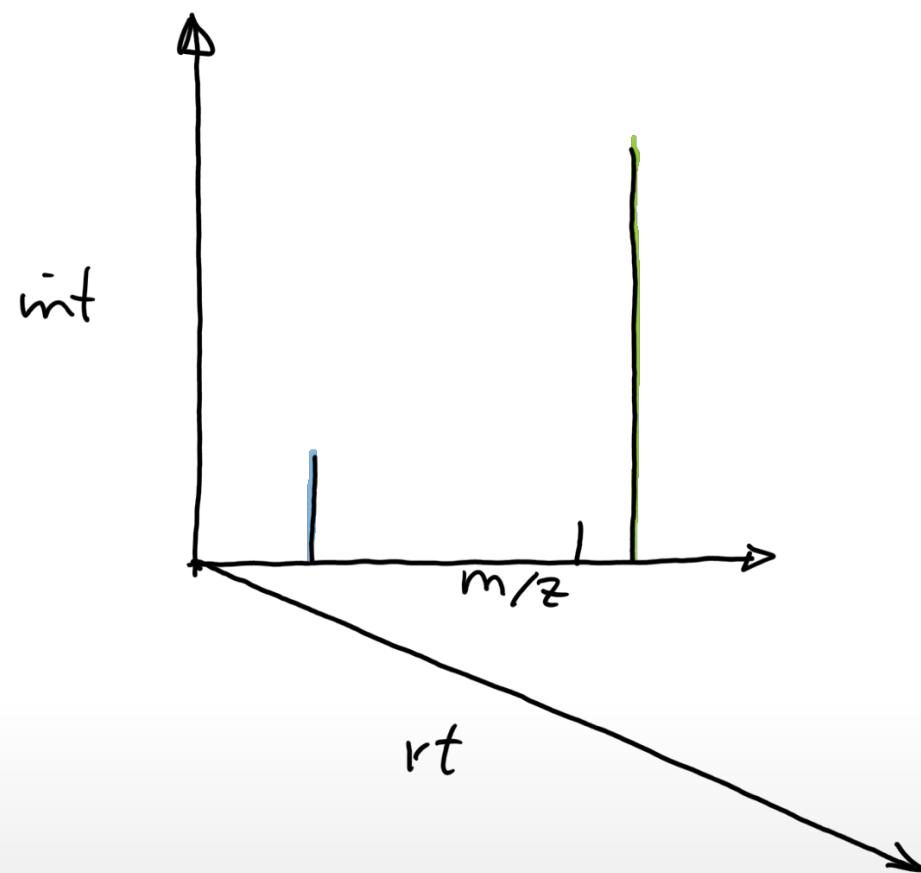
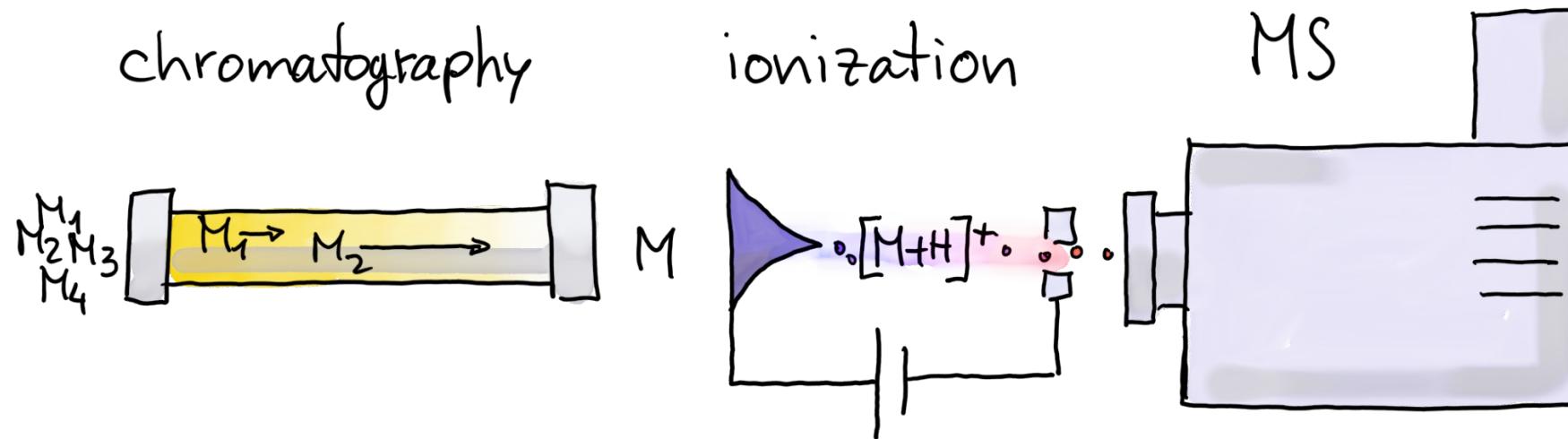
- Sample is dissolved in a fluid (mobile phase).
- Mobile phase carries analytes through column (stationary phase).
- Separation based on affinity for the column's stationary phase.
- HILIC (hyrophilic liquid interaction chromatography):
 - Hydrophilic, polar stationary phase.
 - Analytes solved in mobile phase.
 - Analytes separated by polarity: compounds with low polarity elute first, with high polarity later.



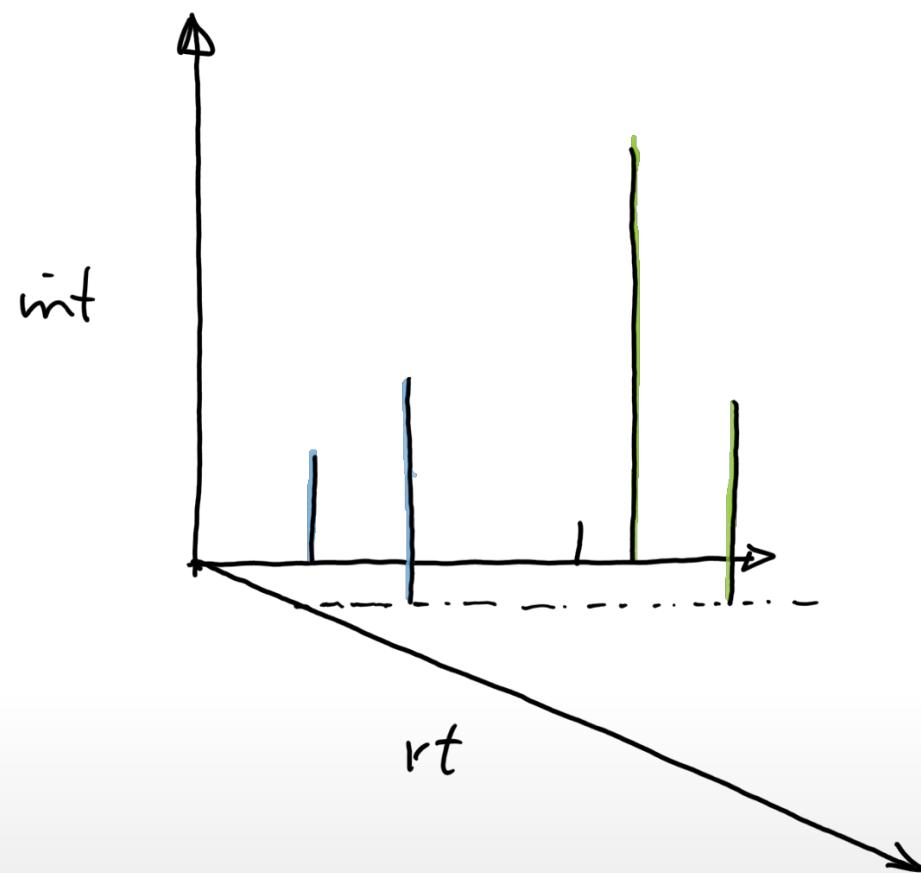
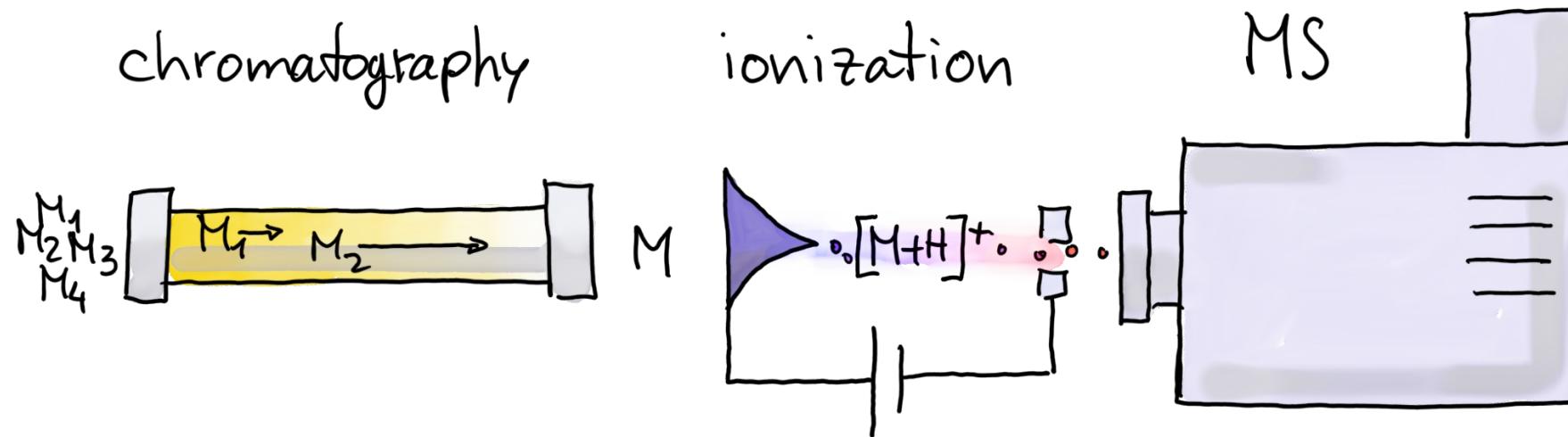
Liquid Chromatography Mass Spectrometry (LC-MS)



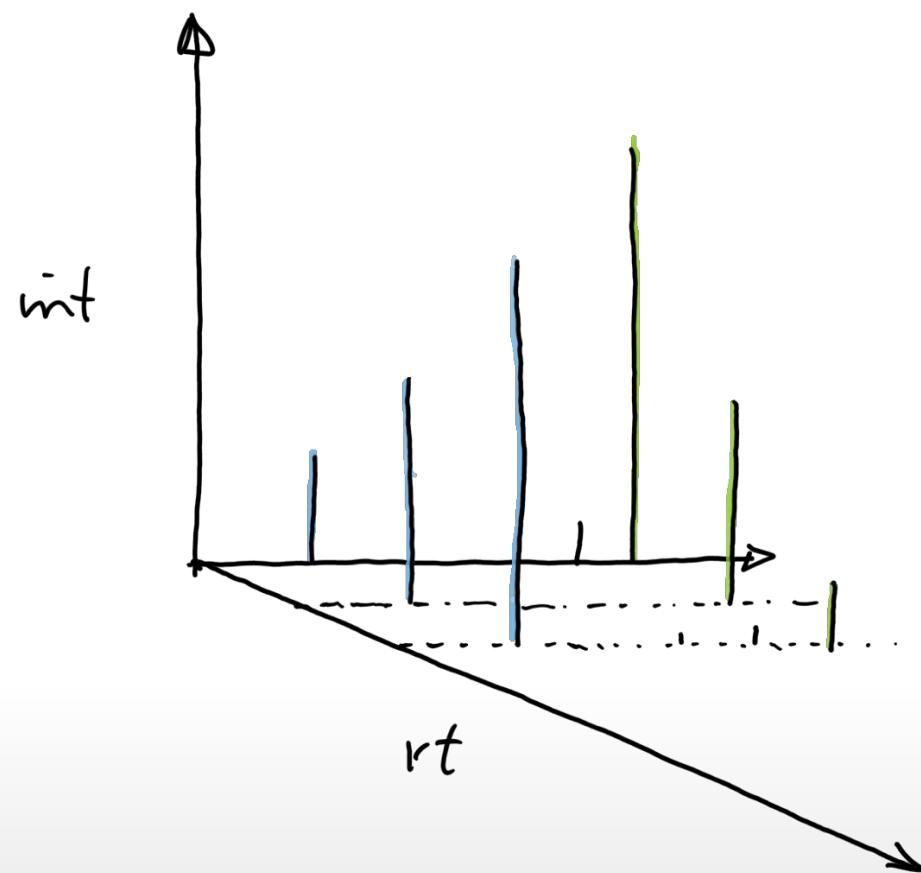
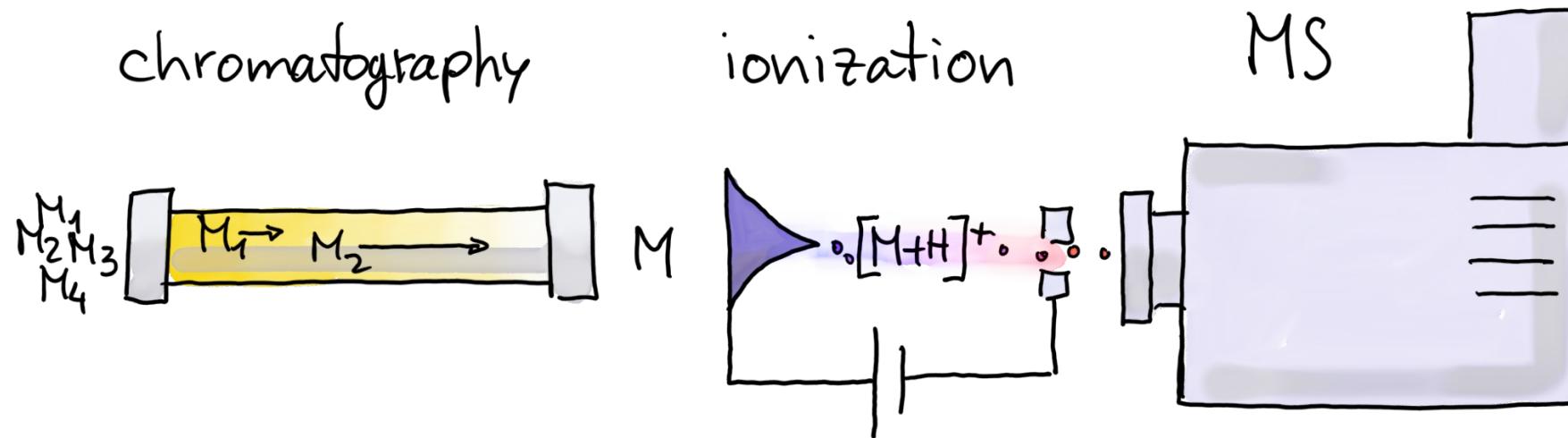
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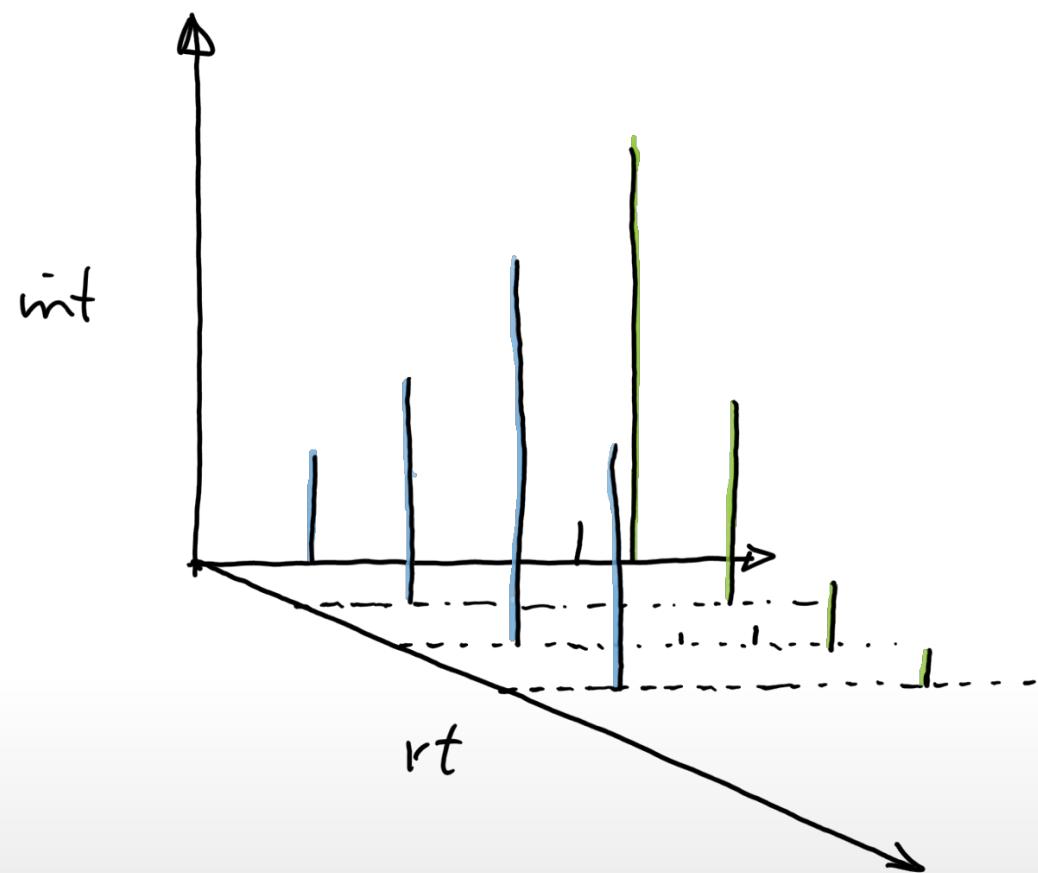
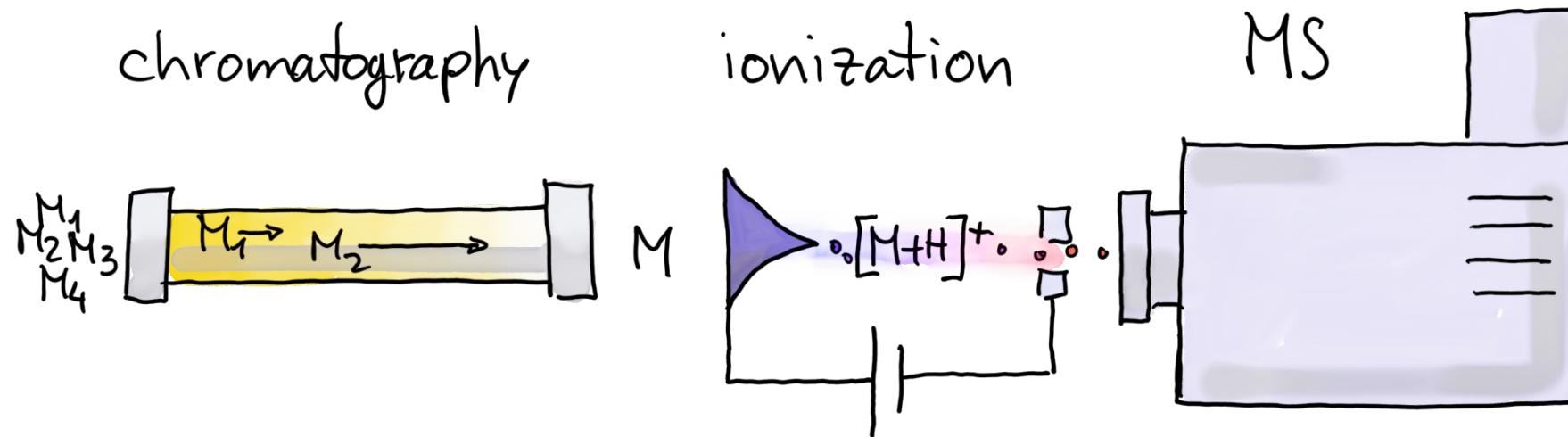
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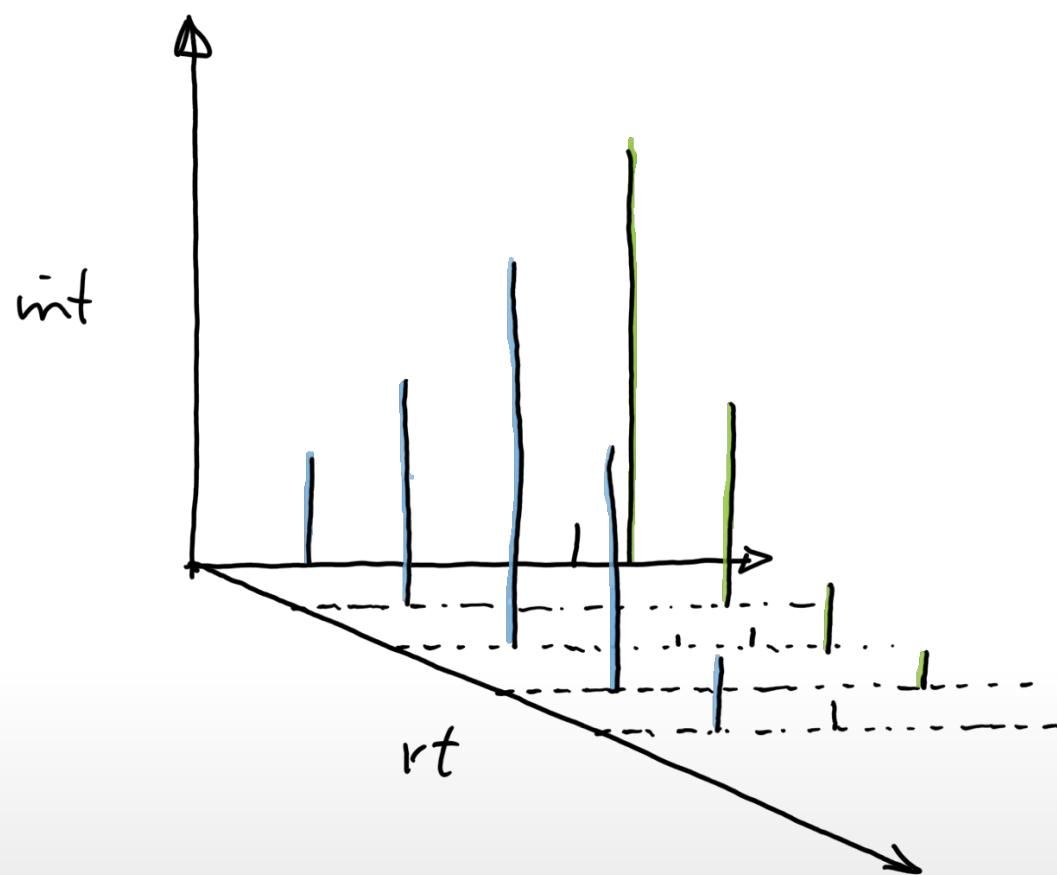
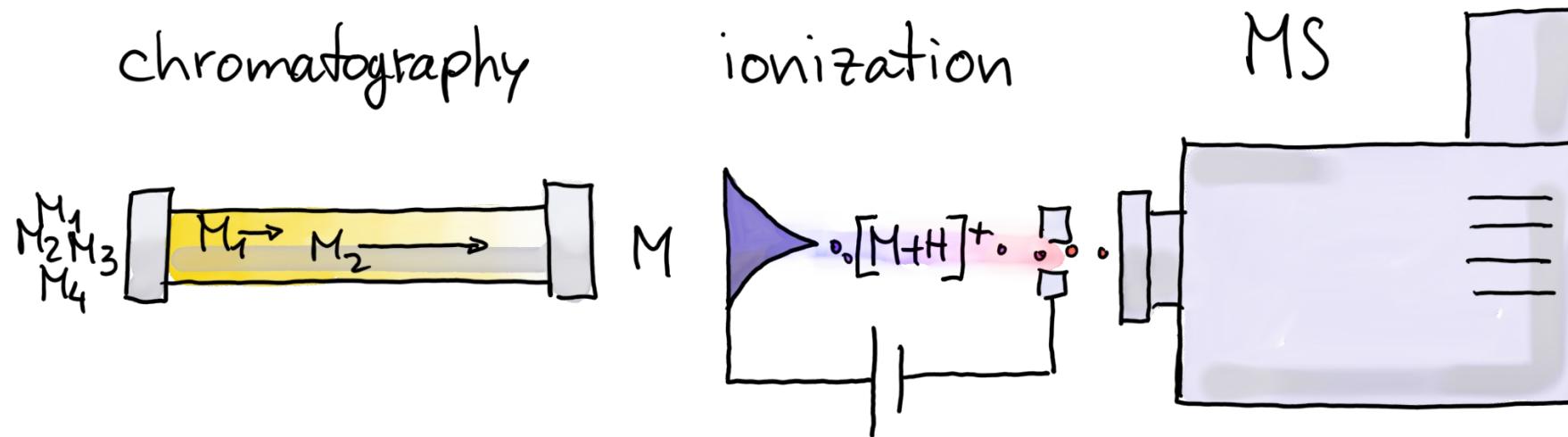
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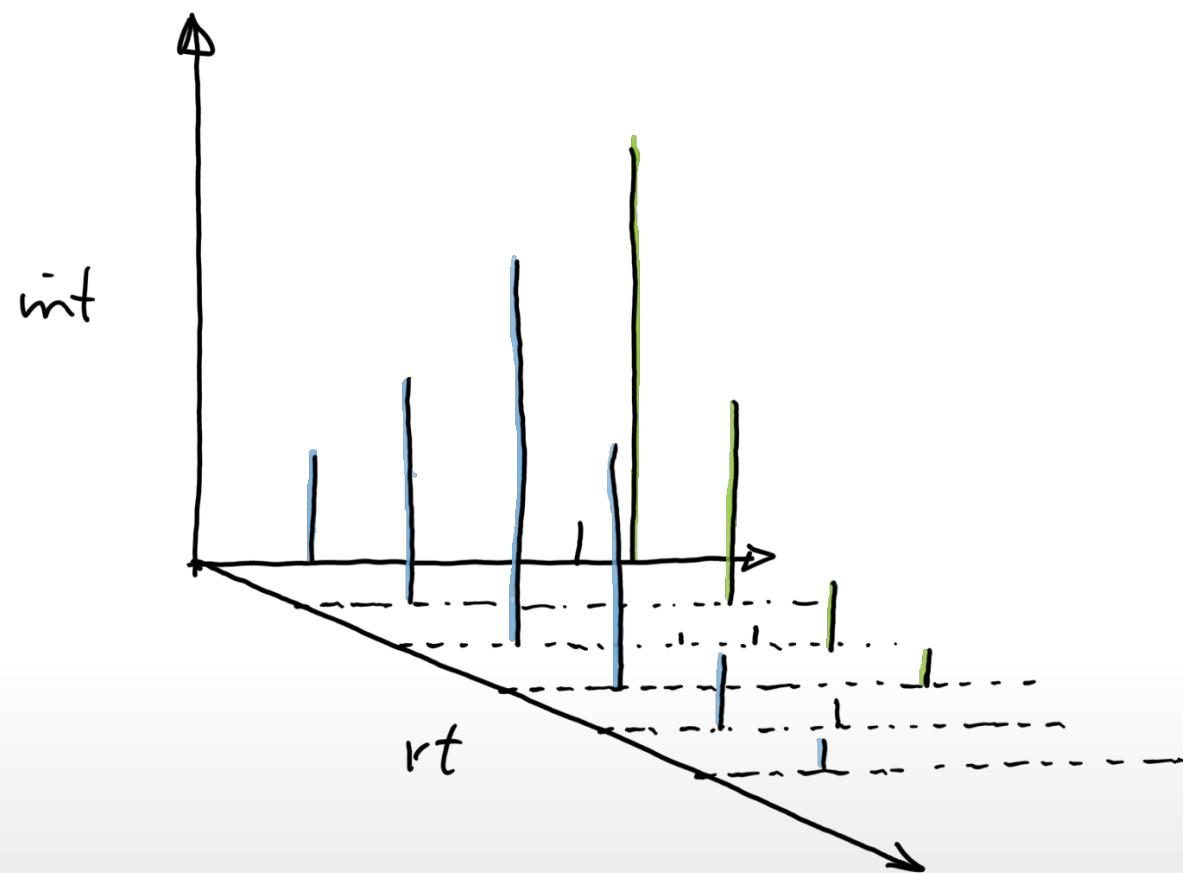
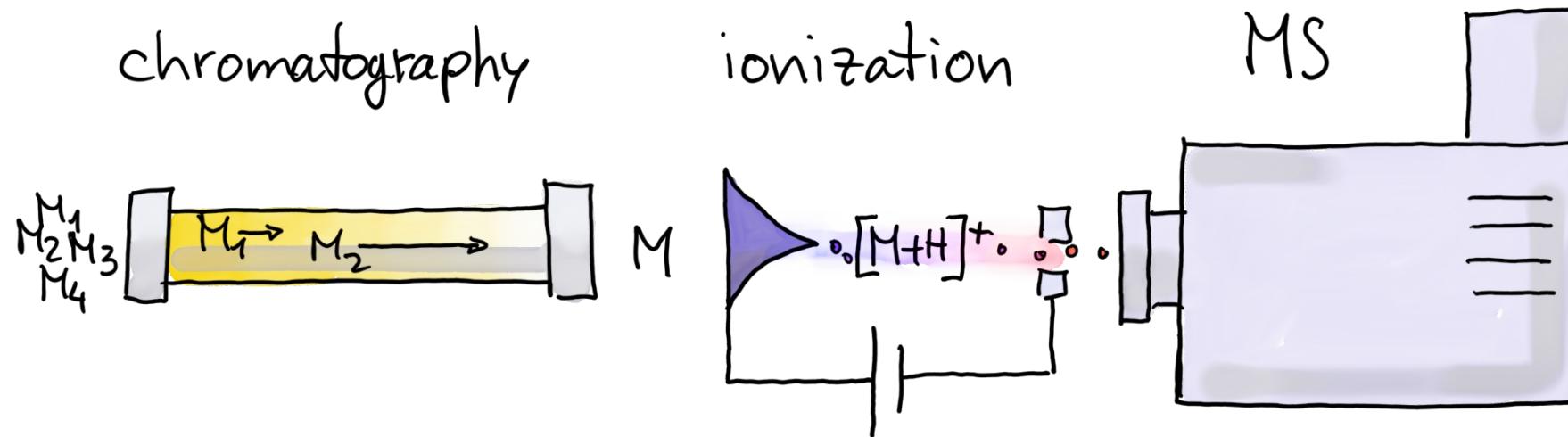
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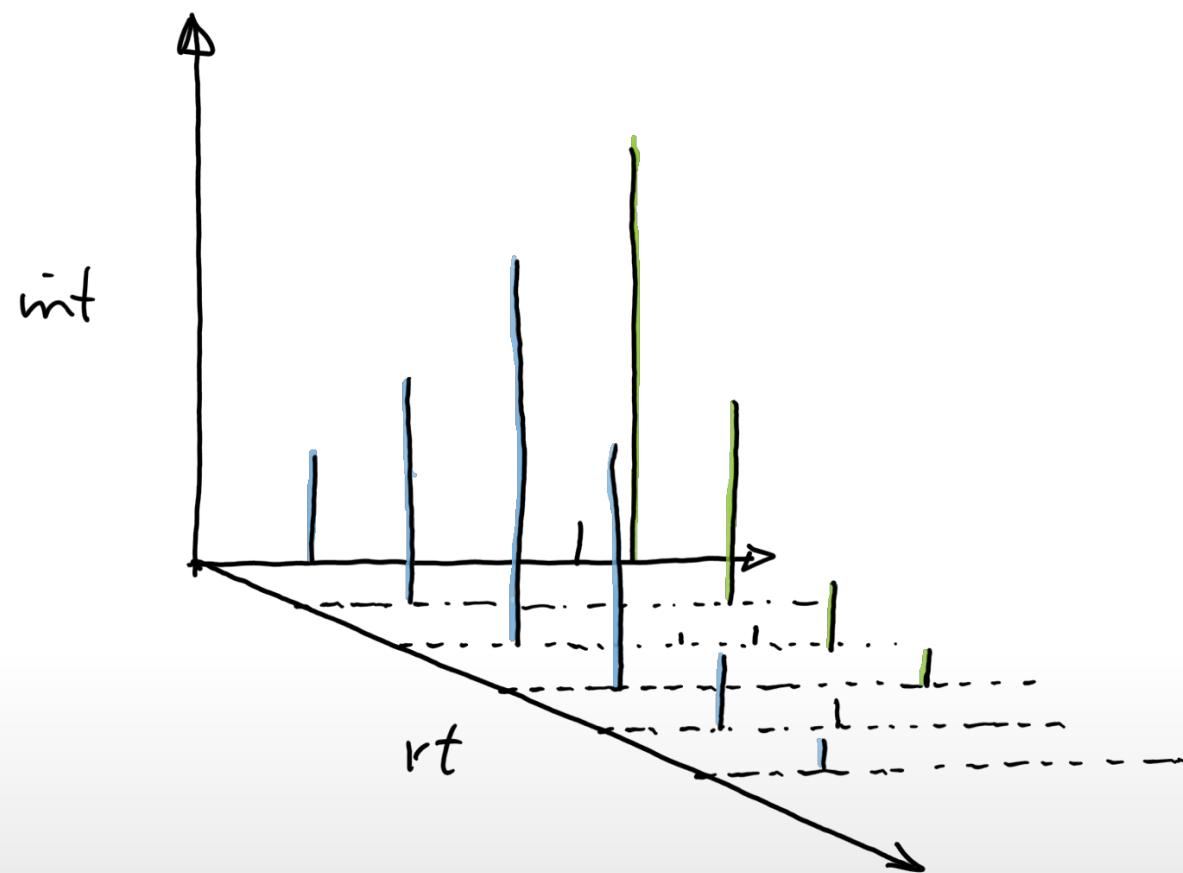
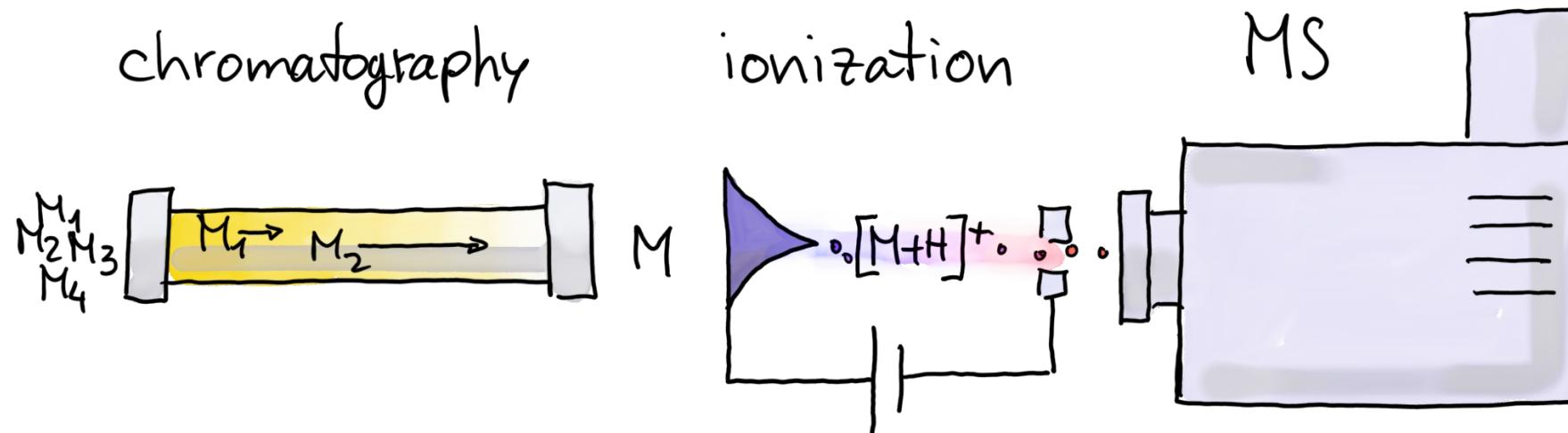
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Liquid Chromatography Mass Spectrometry (LC-MS)



LC-MS data has 3 dimensions:

- m/z , retention time, intensity.

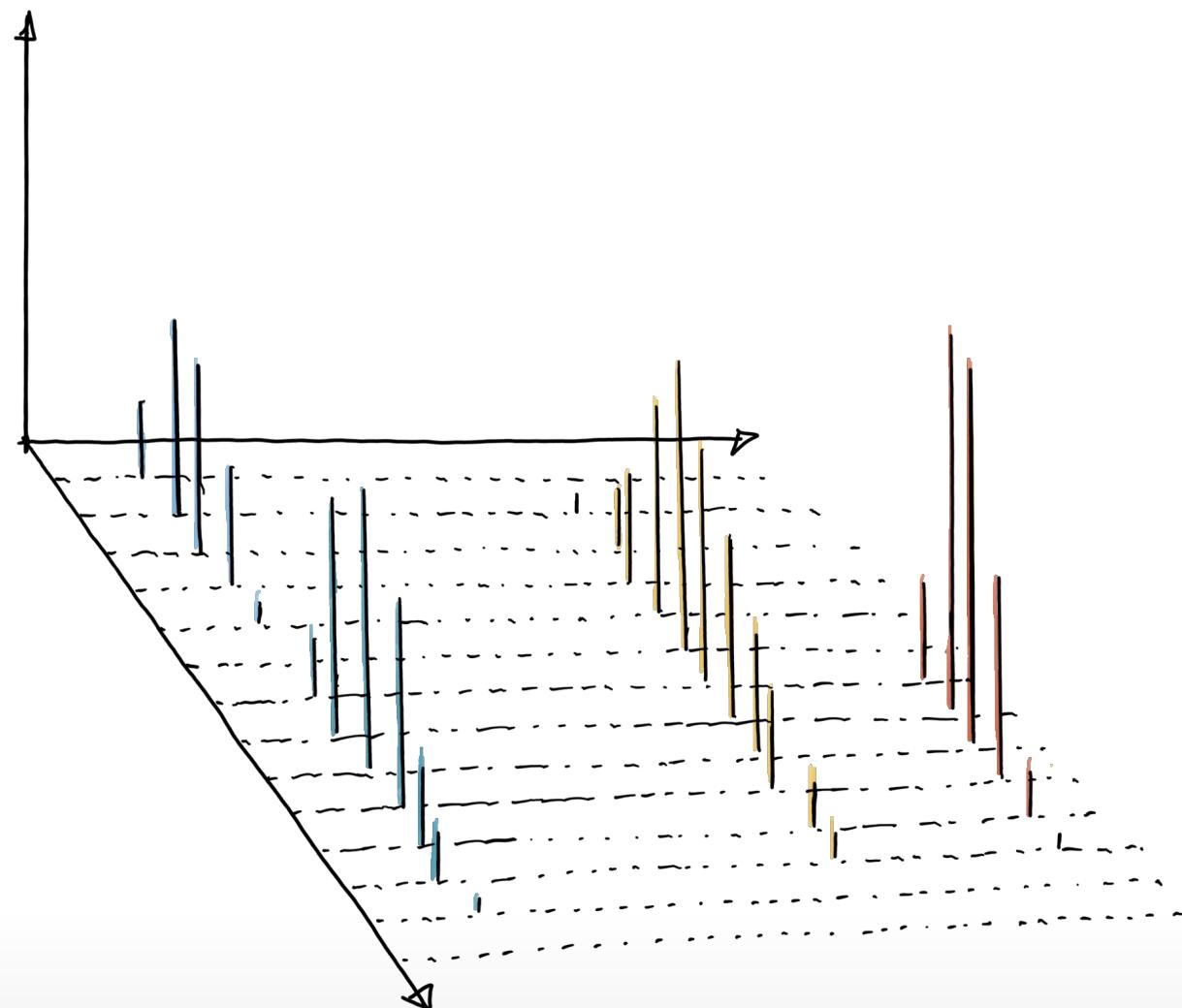
Analyze data along rt.

LC-MS data preprocessing

- Chromatographic peak detection
- Alignment
- Correspondence

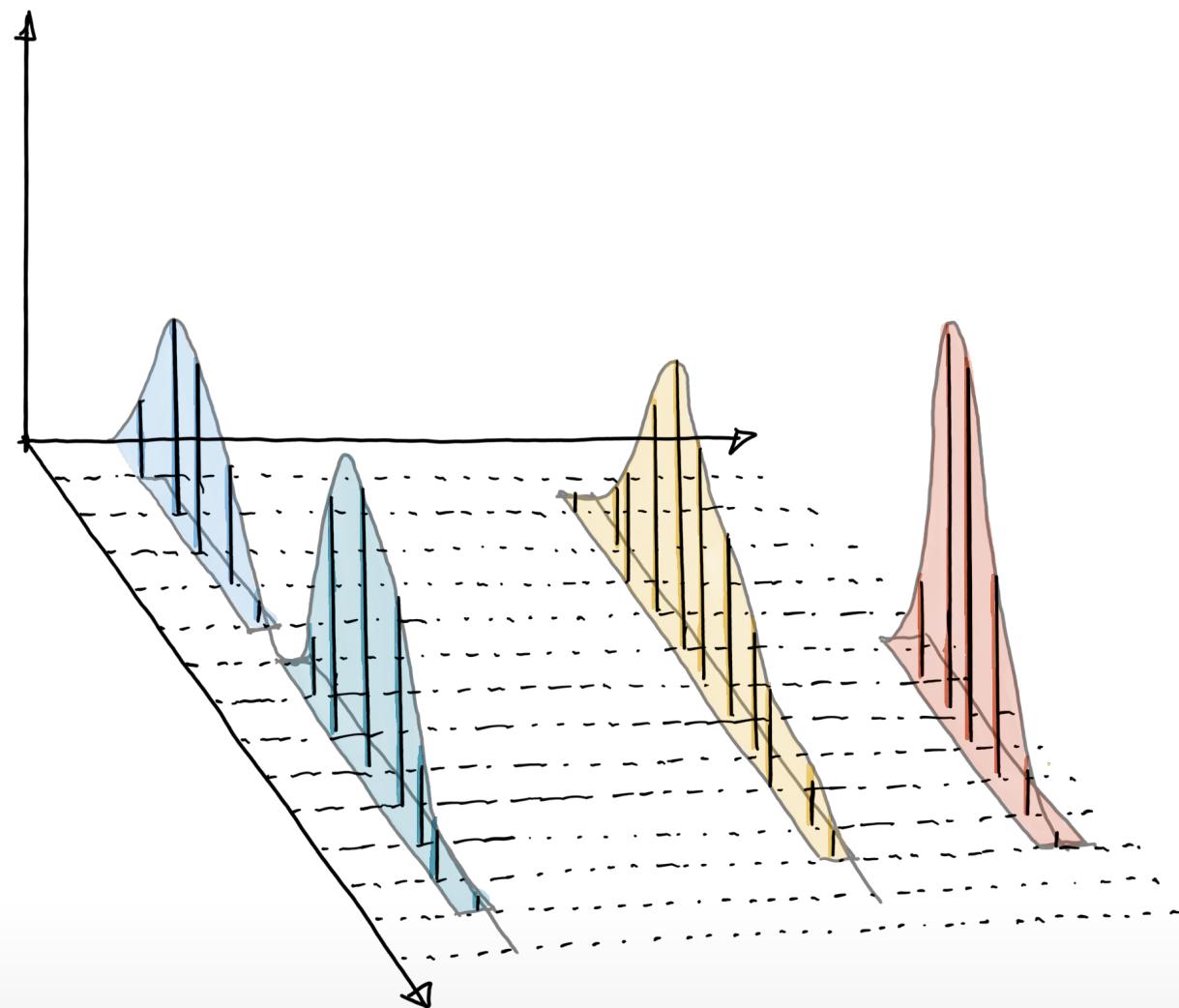
Chromatographic peak detection

- **Aim:** identify chromatographic peaks in the data.



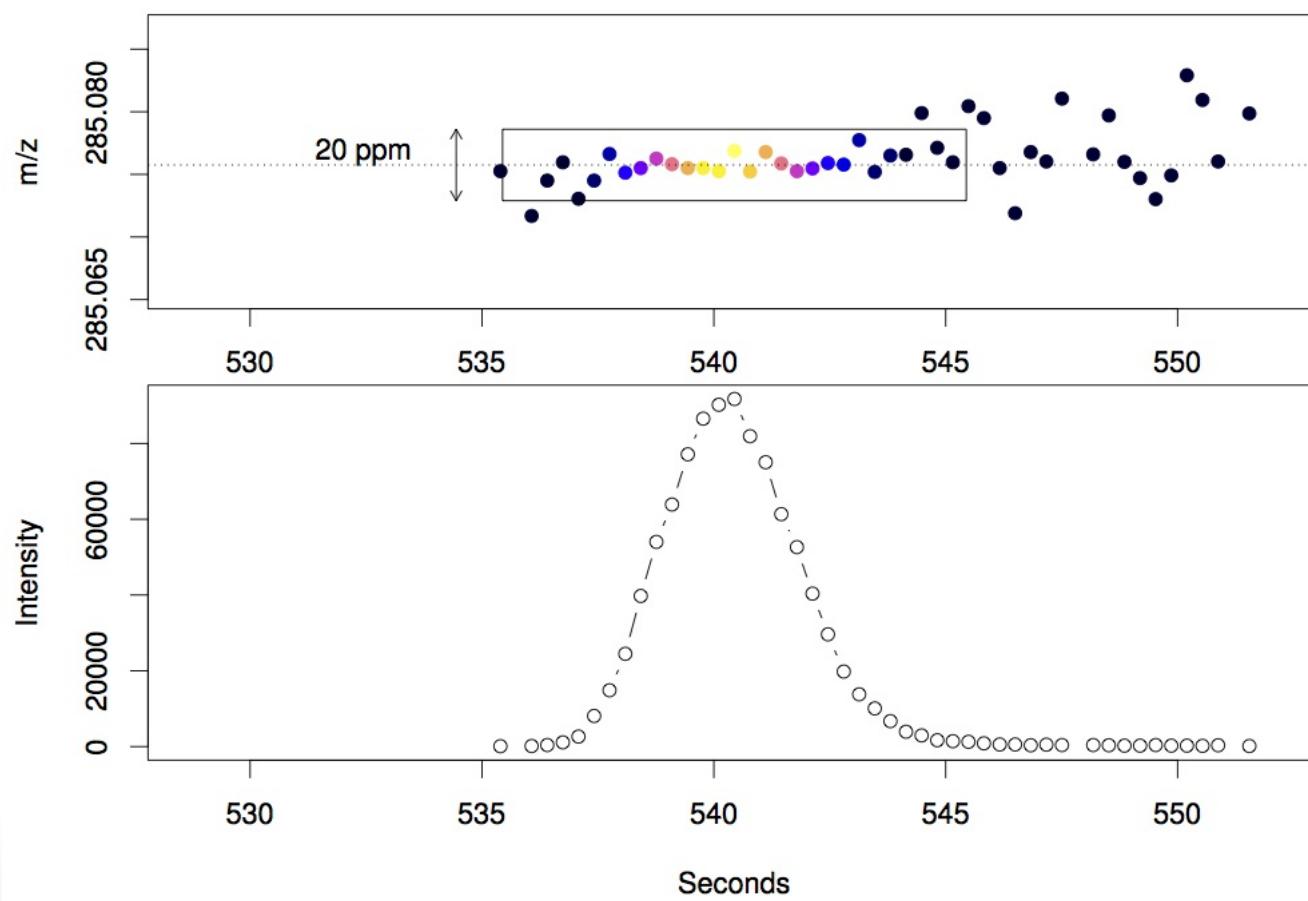
Chromatographic peak detection

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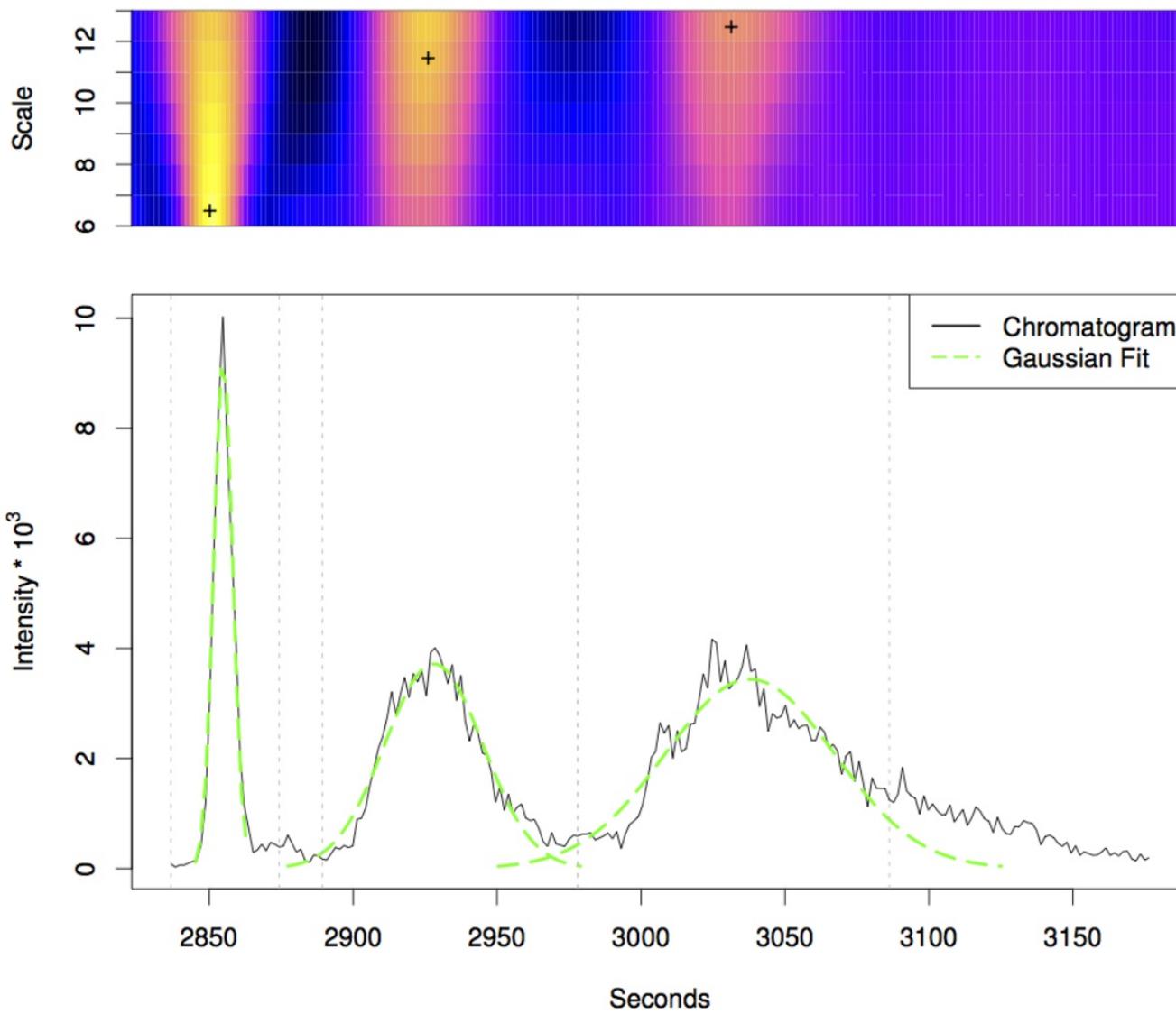
Chromatographic peak detection

- **centWave** [Tautenhahn et al. BMC Bioinformatics, 2008]:
- Step 1: identify regions of interest.



Chromatographic peak detection

- Step 2: peak detection using continuous wavelet transform.
- Allows detection of peaks with different rt widths.



Chromatographic peak detection

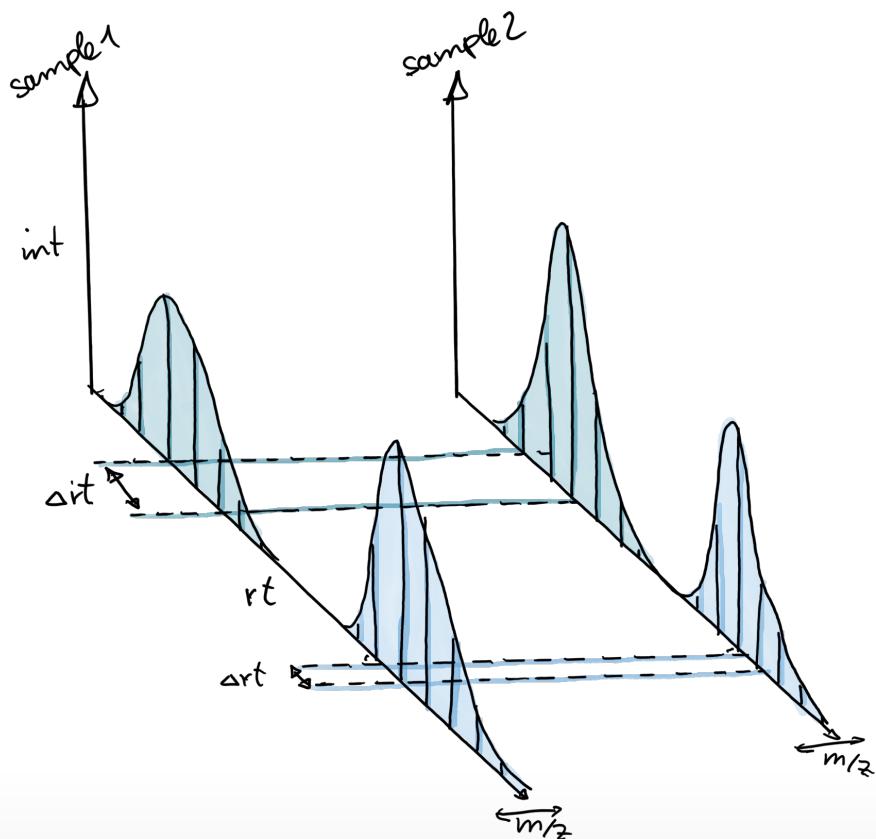
- `MSnbase`: data import with `readMSData`.
- `xcms`: peak detection with `findChromPeaks` and algorithm-specific parameter object.

```
cwp <- CentWaveParam(peakwidth = c(2, 10), snthresh = 5)
data <- findChromPeaks(data, param = cwp)
head(chromPeaks(data), n = 3)
```

```
##          mz    mzmin    mzmax      rt    rtmin    rtmax     into     intb
## CP001 114.0907 114.0899 114.0929  1.954  0.280  3.907 1559.829 1555.923
## CP002 114.0913 114.0884 114.0929  5.860  4.465  8.650 1890.221 1885.757
## CP003 114.0914 114.0899 114.0929 10.882  8.650 13.114 1950.953 1946.210
##          maxo   sn sample
## CP001 584.9510 584       1
## CP002 601.8881 601       1
## CP003 691.9580 691       1
```

Alignment

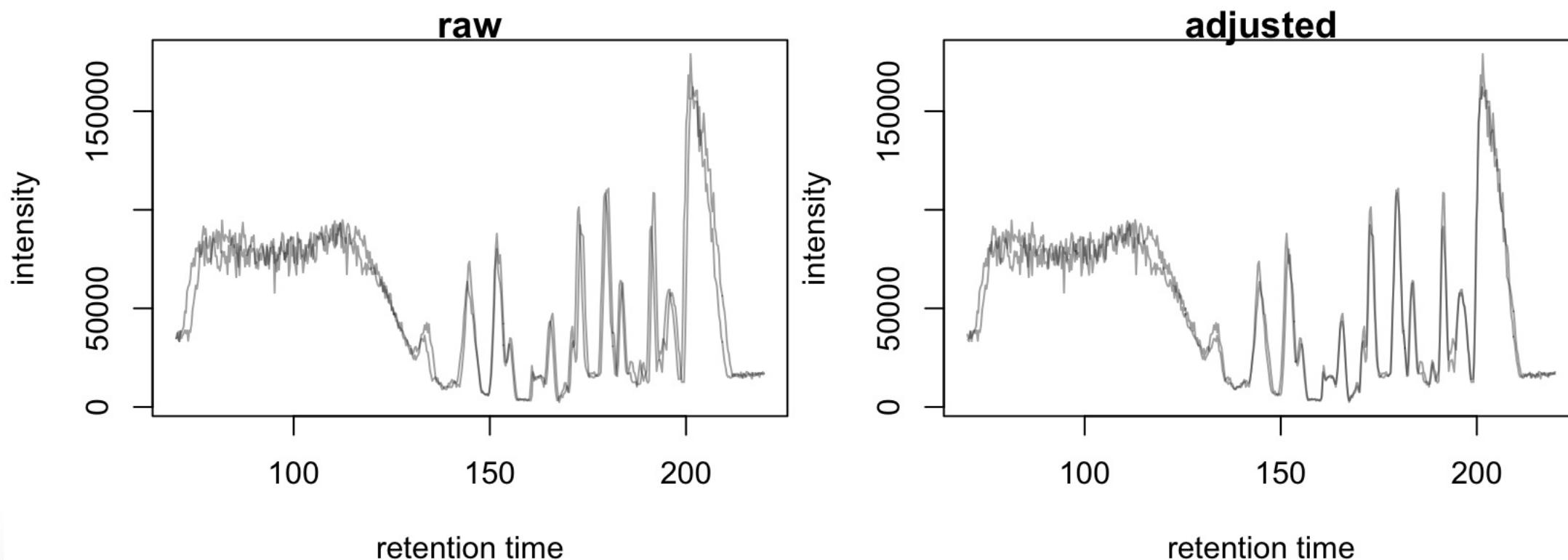
- **Aim:** adjust differences in retention times between samples.
- Same analyte elutes at slightly different time between measurements.



- **Why?** Age of column, temperature ...

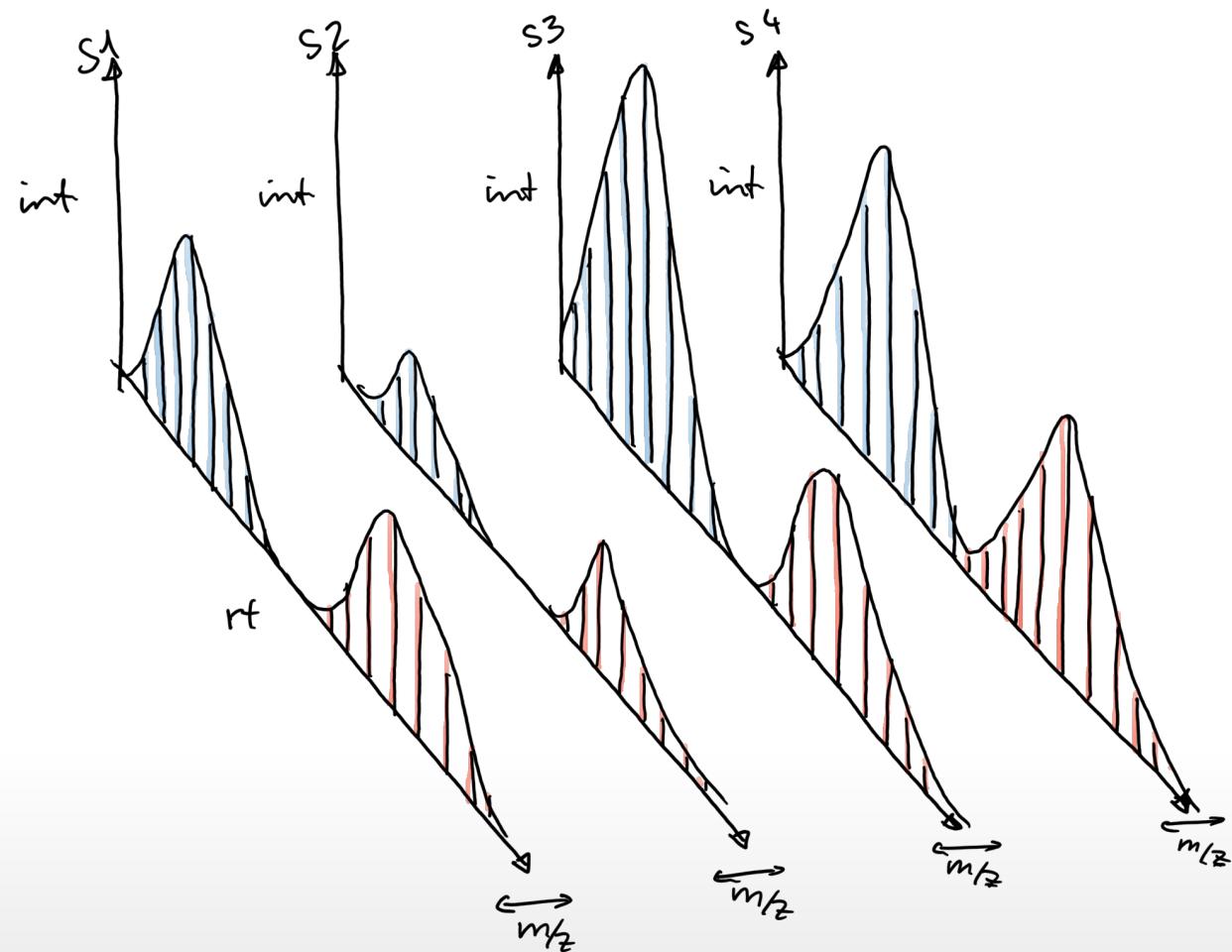
Alignment

- Many algorithms available [Smith et al. Brief Bioinformatics 2013]
- xcms: `adjustRtime` function with `PeakDensityParam` [Smith et al. Anal. chem. 2006] or `ObiwarParam` [Prince et al. Anal. chem. 2006].



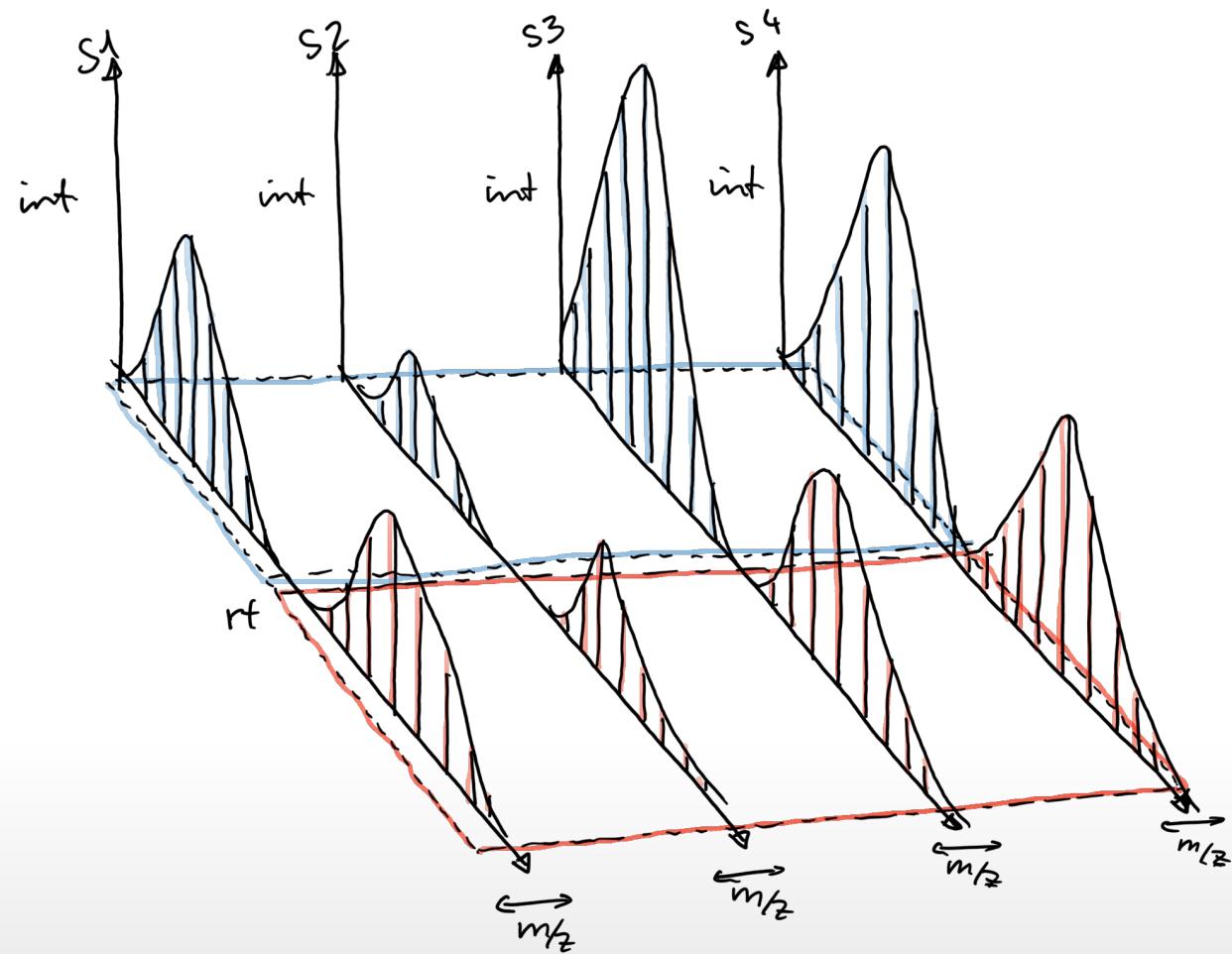
Correspondence

- **Aim:** group peaks representing same ion species across samples.
- **Result:** matrix of abundances, rows *features*, columns samples.



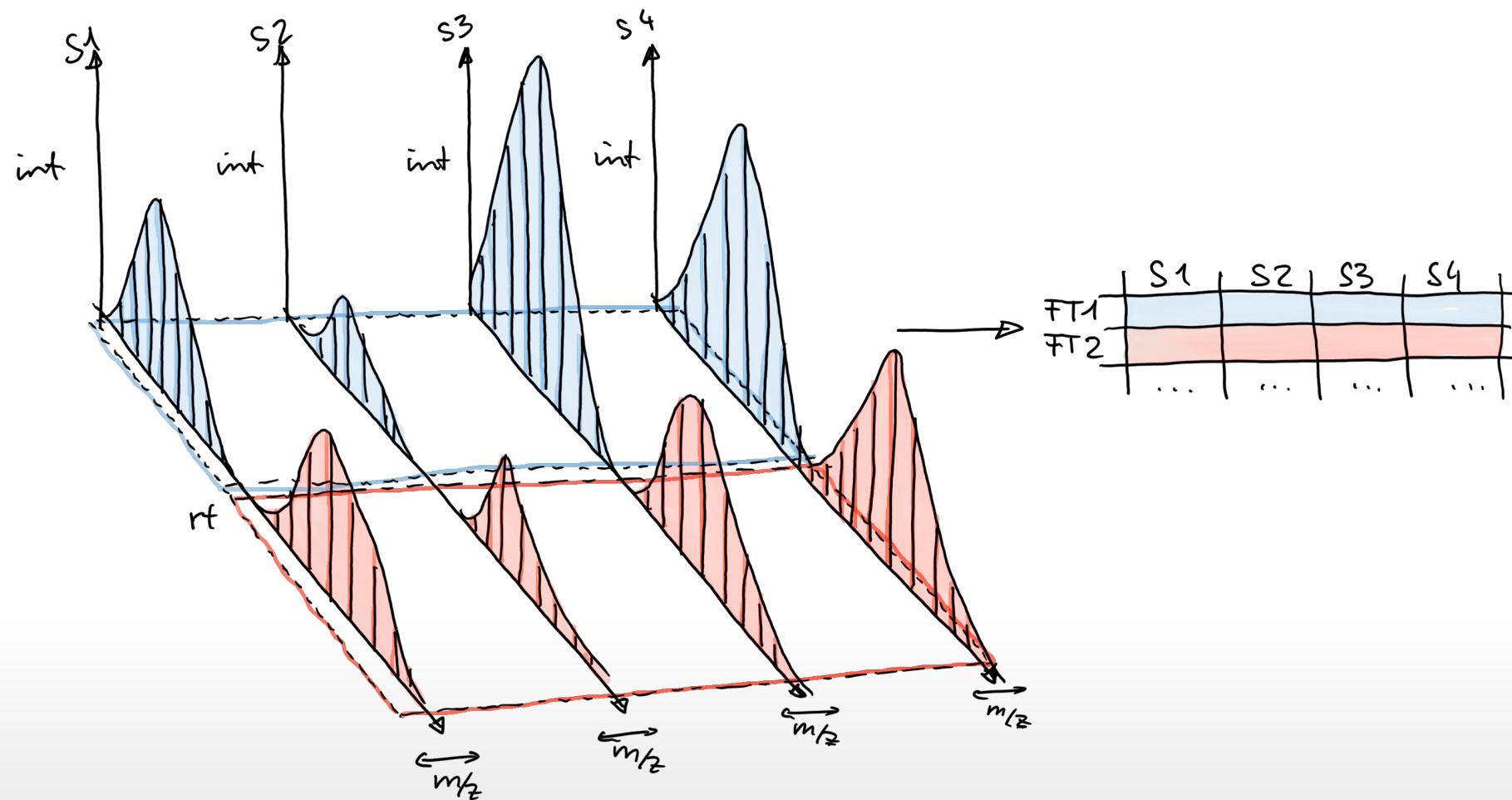
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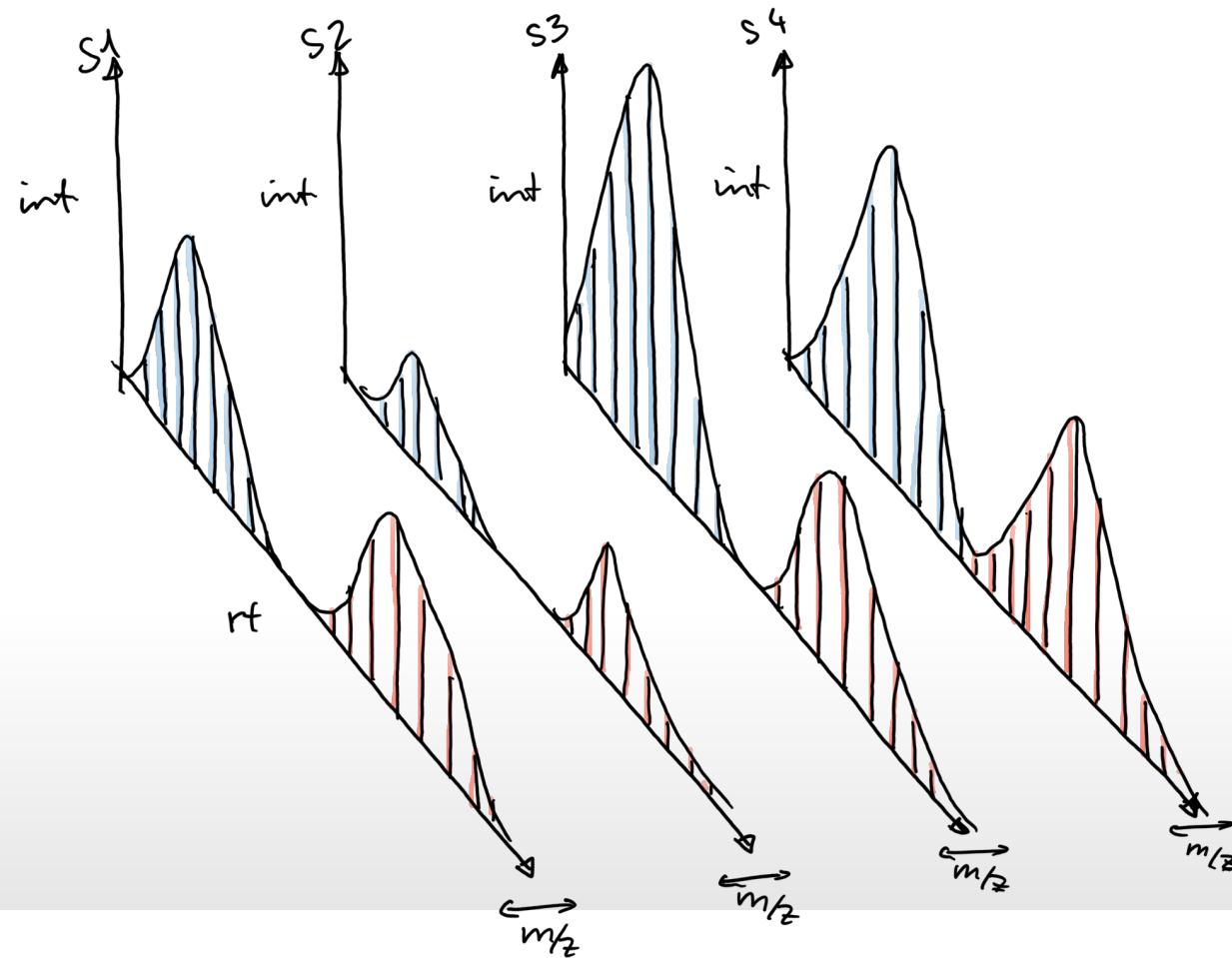
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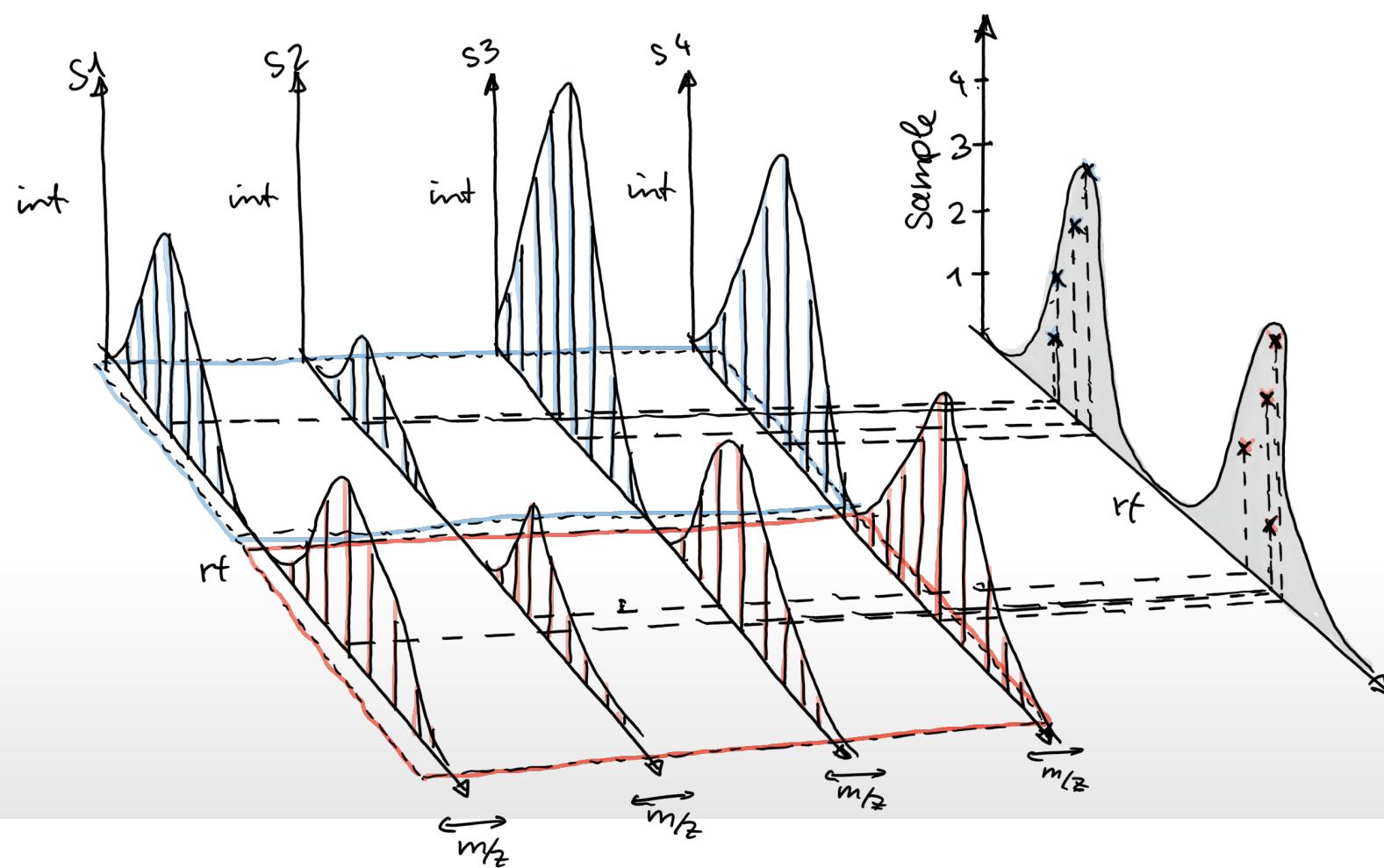
Correspondence

- xcms: `groupChromPeaks` with `NearestPeaksParam` [Katajamaa et al. Bioinformatics 2006] and `PeakDensityParam` [Smith et al. Anal. chem. 2006].
- peak density approach (for a given m/z slice):



Correspondence

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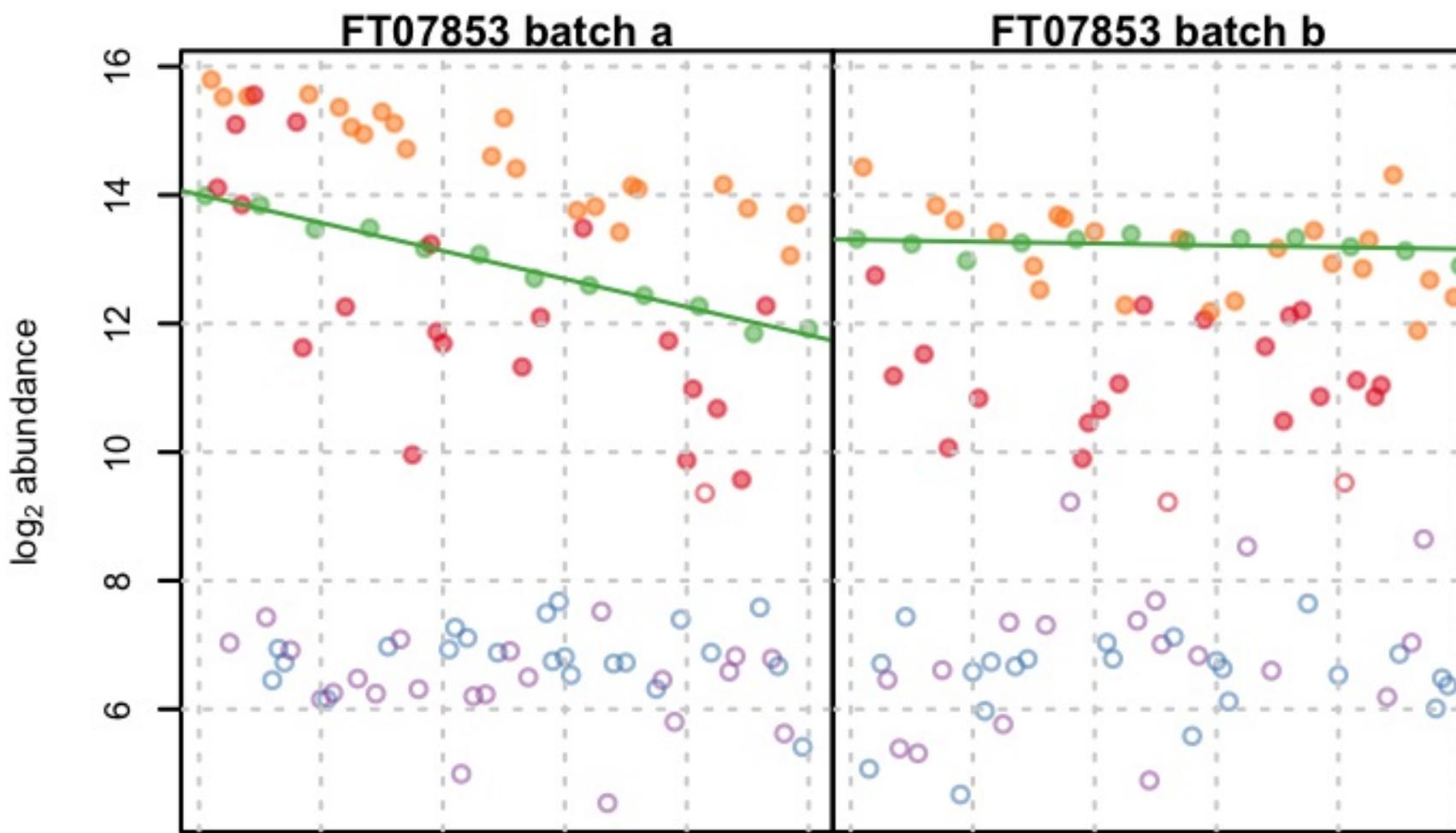


Preprocessing result

- Numeric matrix with *abundances*.
- Normalization.
- Identification of features of interest.
- Annotation.

Normalization

- Sample-specific effects.
- Effects related to batch/measurement run.
- LC-dependent effects: seem to affect each metabolite in a different way.



Normalization

- Good practice:
 - QC samples measured repeatedly.
 - Internal standards.
 - Replicates.
 - Measurement of study samples in randomized order.
- Popular normalization methods:
 - RUV [De Livera et al. Anal. Chem. 2015]
 - linear models [Wehrens et al. Metabolomics 2016]
 - linear and higher order models [Brunius et al. Metabolomics 2016].

Annotation/Identification

- Feature != metabolite.

```
## DataFrame with 4 rows and 4 columns
##           mzmed          rtmed        POOL_1        POOL_2
##           <numeric>      <numeric>      <numeric>      <numeric>
## FT001 105.041814839707 167.96077773118 229.490739260736 3093.75184315684
## FT002 105.041653033614 157.082078655729 4762.39872227773 6601.45091358641
## FT003 105.069636149683 31.8109676438667 699.723986763237 1033.23232267732
## FT004 105.11027064078 63.7514649484463 20211.2633706294 15839.5504368189
```

- Feature characterized by m/z and retention time.

Annotation based on m/z matching

- Match mass against database.
 - The Human Metabolome Database (HMDB): <https://hmdb.ca>
 - Chemical Entities of Biological Interest: <https://www.ebi.ac.uk/chebi>
 - PubChem <https://pubchem.ncbi.nlm.nih.gov>
 - ...
- Will result in many hits.
- m/z is **not** the mass.
- Mass of an $[M+H]^+$ ion: m/z - mass of 1 hydrogen.
- Different ions from the same compound: $[M+H]^+$, $[M+Na]^+$, ...

Improved Annotation

Annotate features based on m/z **and**:

- **retention time**: requires measurement of compound/standard on the same LC-MS setup.
- **MS2 spectrum**:
 - Requires LC-MS/MS data (DDA or DIA).
 - Reference spectrum has to be available in database.
 - GNPS: spectral similarity network: group spectra/compounds into classes.

Afternoon metabolomics lab

- LC-MS data handling (MSnbase).
- LC-MS data preprocessing using xcms.

