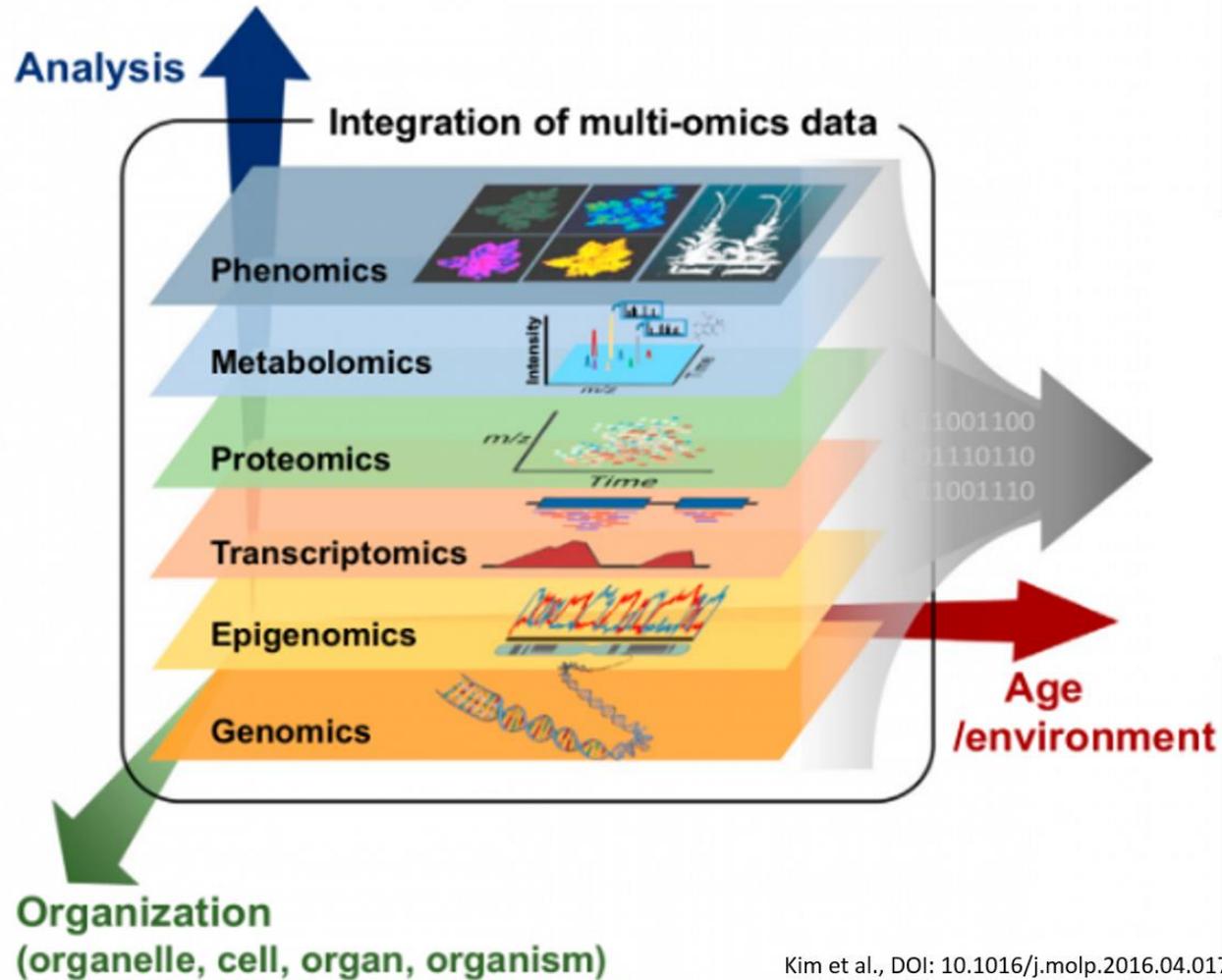


Lipidomics: analytical aspects

Metabolismo y Enfermedades Metabólicas
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Systems biology



Omics

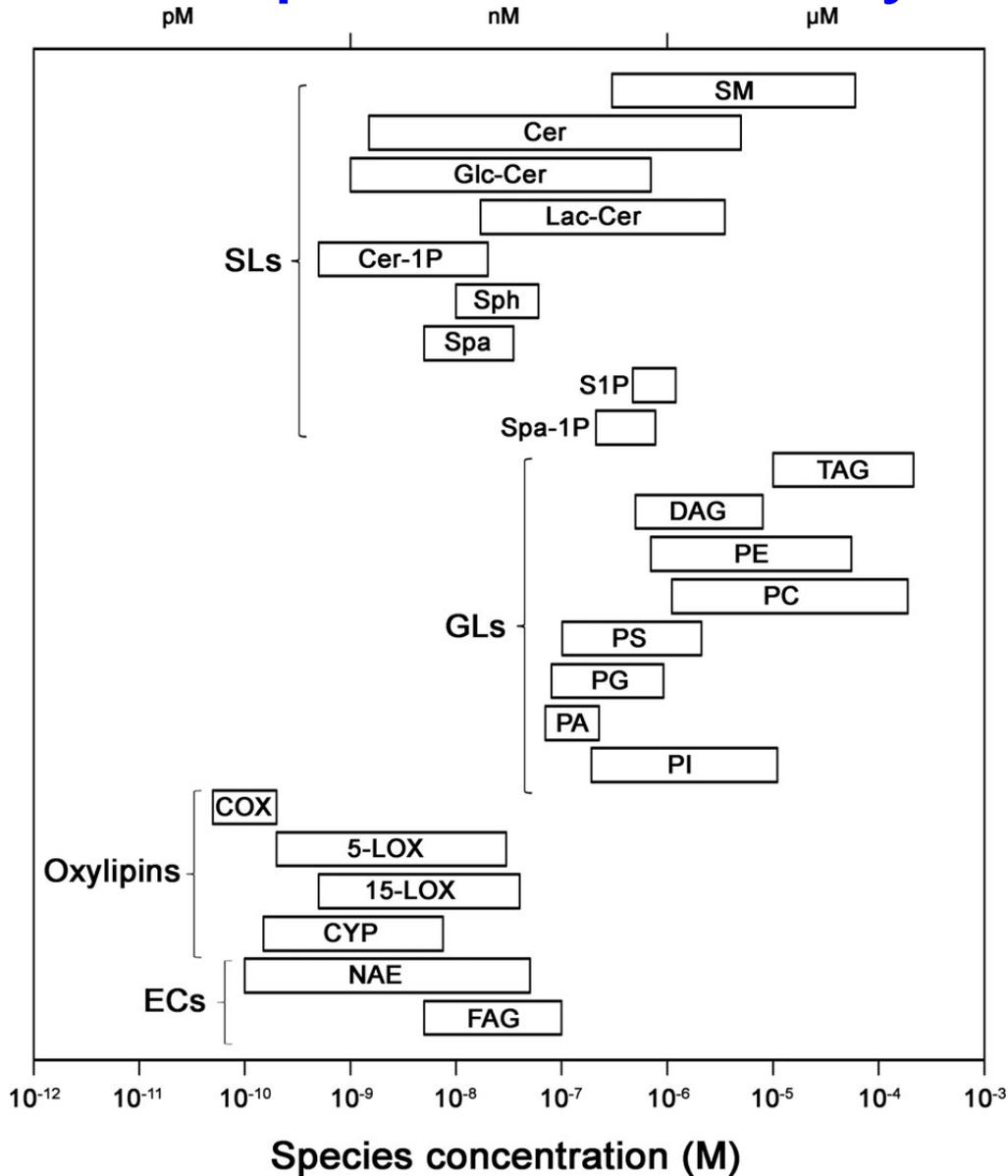
"Omics" refers to **the large-scale study** and analysis of biological molecules or systems within a specific field, such as genomics, proteomics, metabolomics, or transcriptomics. **It involves comprehensive, high-throughput approaches** to characterize and understand the entirety of a particular biological component, such as genes, proteins, metabolites, or RNA molecules, within an organism or system.

Bioinformatics plays a crucial role in omics studies by providing **computational tools and methods to manage, analyze, and interpret the vast amounts of data**, enabling researchers to derive meaningful insights from complex biological datasets

Lipidomics

Integrated in metabolomics, lipidomics studies all lipid types in a system, exploring their roles, amounts, and interactions. It uses advanced tools like mass spectrometry and bioinformatics for comprehensive lipid analysis and interpretation.

Lipidomics: analytical challenges



-Structural variability

-Big range of concentrations

Analytical technique: RMN vs MS

Aspect	Nuclear Magnetic Resonance (NMR)	Liquid Chromatography coupled to Mass Spectrometry (LC-MS)
Principle	Measures magnetic properties of atoms in molecules.	Analyzes ionized molecules based on mass-to-charge ratio.
Sensitivity	Moderate sensitivity, requires larger sample amounts.	High sensitivity , can detect low amounts of lipids.
Resolution	Limited resolution for complex lipid mixtures.	High resolution , can identify and quantify diverse lipids.
Throughput	Lower throughput, time-consuming for analysis.	Higher throughput , faster analysis of multiple samples.
Quantification	Absolute quantification	Semiquantitative or Relative quantification
Sample Prep	Minimal sample preparation, non-destructive method.	More extensive sample prep, potential for ionization bias.
Structural Info	Provides limited structural information.	Offers detailed structural insight, including isomers.
Reproducibility	Strong among laboratories	Low even intralaboratory

MS lipidomics: Analytical process

Aim: to obtain separated lipids ionized in gas phase to be detected

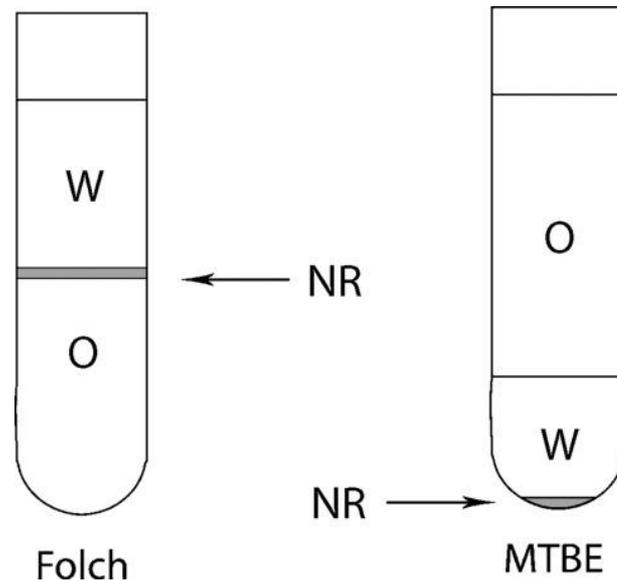
The most general elements:

- Sample preparation
- Chromatographic separation
- Ionization
- m/z analyzer
- detector



MS lipidomics: Sample prep

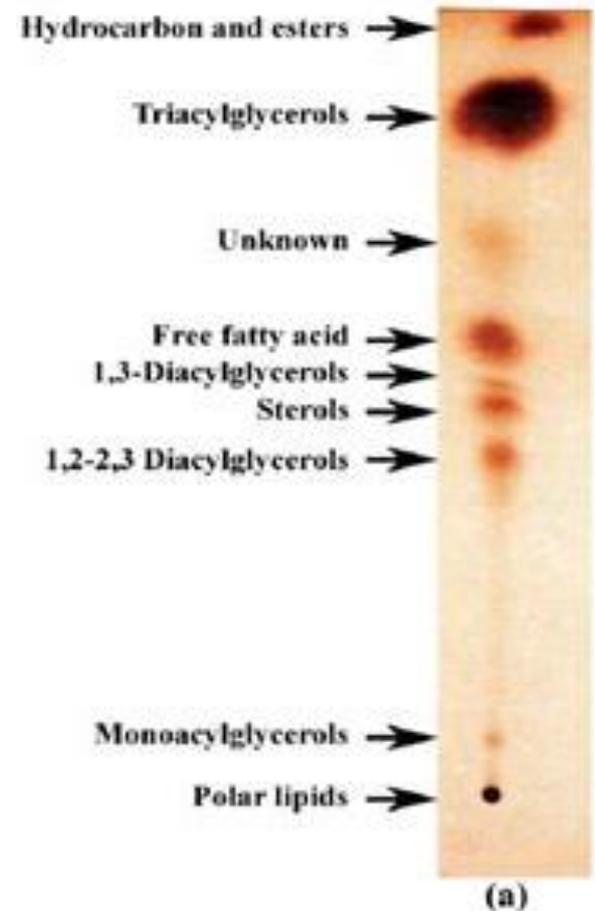
- + Solid phase extraction (SPE): oxylipins
- + Protein precipitation with organic solvents
- + Folch and Bligh & Dyer methods: mixtures of chloroform, methanol and water
- + Matyash: mixtures of methyl-tert-butyl ether (MTBE)



MS lipidomics: TLC

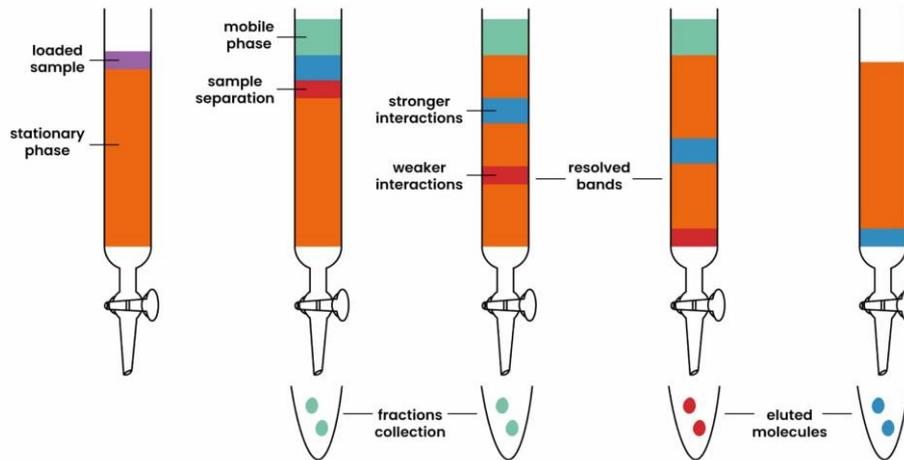
Thin layer chromatography (TLC)

- Normal phase (the more polar the more retained)
- Non-high-throughput
- Reserved for specific analyses



MS lipidomics: LC

Liquid chromatography (LC)



Columns in chromatograph:

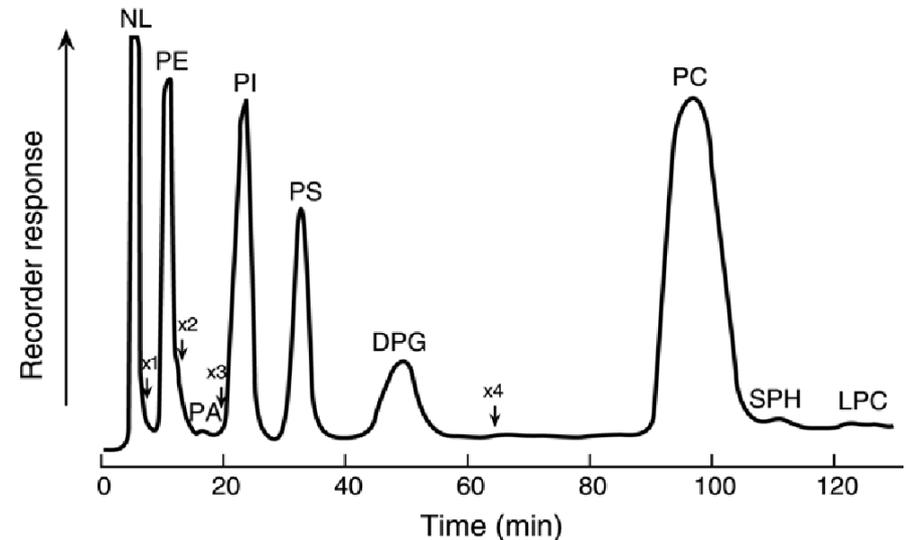
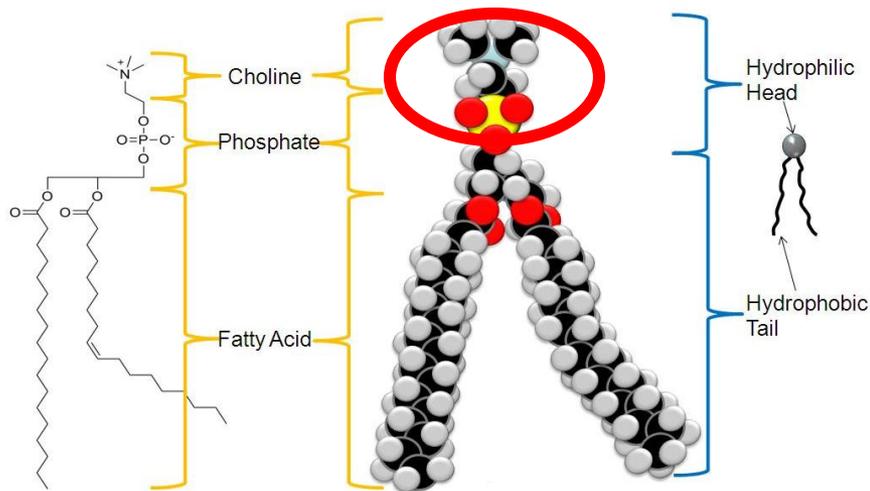
- High pressure (HPLC)
- Ultra high pressure (UHPLC)



MS lipidomics: NPLC

Normal phase Liquid chromatography (NPLC)

- Stationary phase more polar than the mobile phase.
- The more polar the more retained (higher retention time)
- Phospholipids mainly separated by the polar headgroup



MS lipidomics: RPLC

Reversed phase Liquid chromatography (RPLC, *fase inversa* in Spanish)

- Stationary phase more apolar than the mobile phase.**
- The more polar the less retained (lower retention time)**

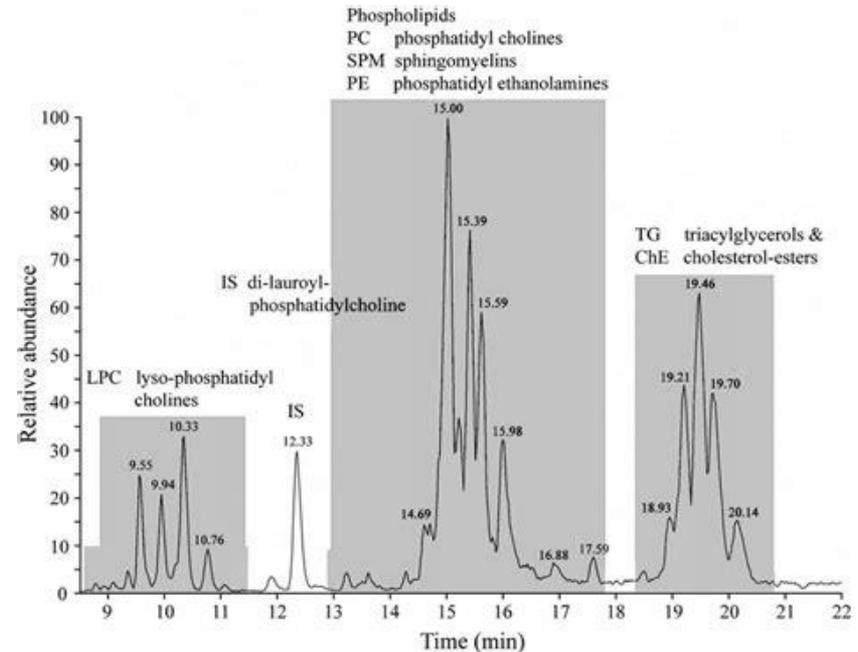
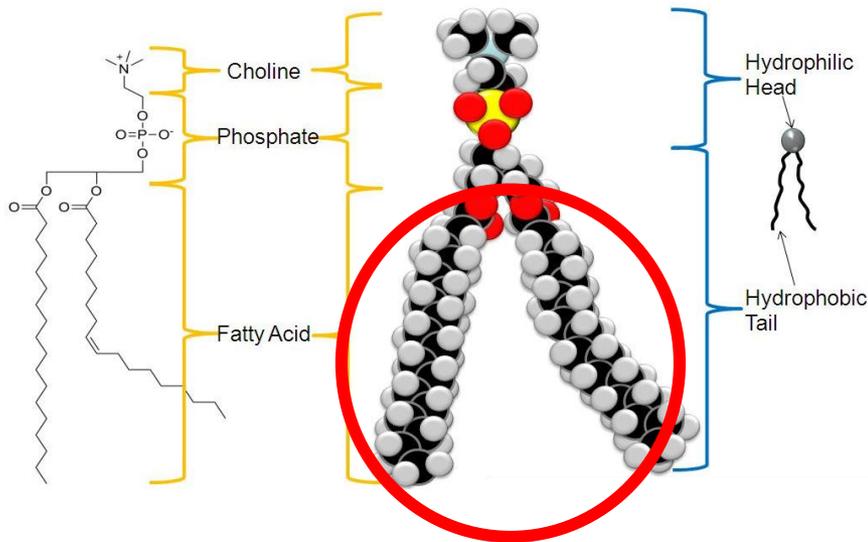
NPLC vs RPLC:

<https://www.youtube.com/watch?v=MLoitPJQH3g>

MS lipidomics: RPLC

Separation of lipids by a combination of:

- Number of acyl chains (fatty acids)
- Polar headgroup
- Length of the fatty acids
- Number of the double bonds (unsaturations)



MS lipidomics: Quality Control

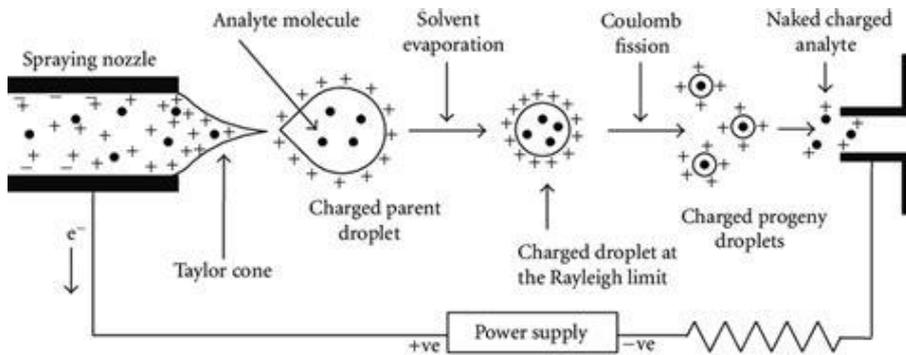
Quality control in lipidomics/metabolomics ensures data accuracy by using **reference samples** to detect and correct instrument variability.

Usually, it is a mixture of the samples that are going to be injected

Of special importance when the number of samples is high and **multiple batches** of injection are required

MS lipidomics: ionization

The most common ionization is electrospray (ESI)



Two polarities that determine how the lipid ionize:
positive | negative

We obtain ions that are transported to low pressure!

MS lipidomics: analyzers



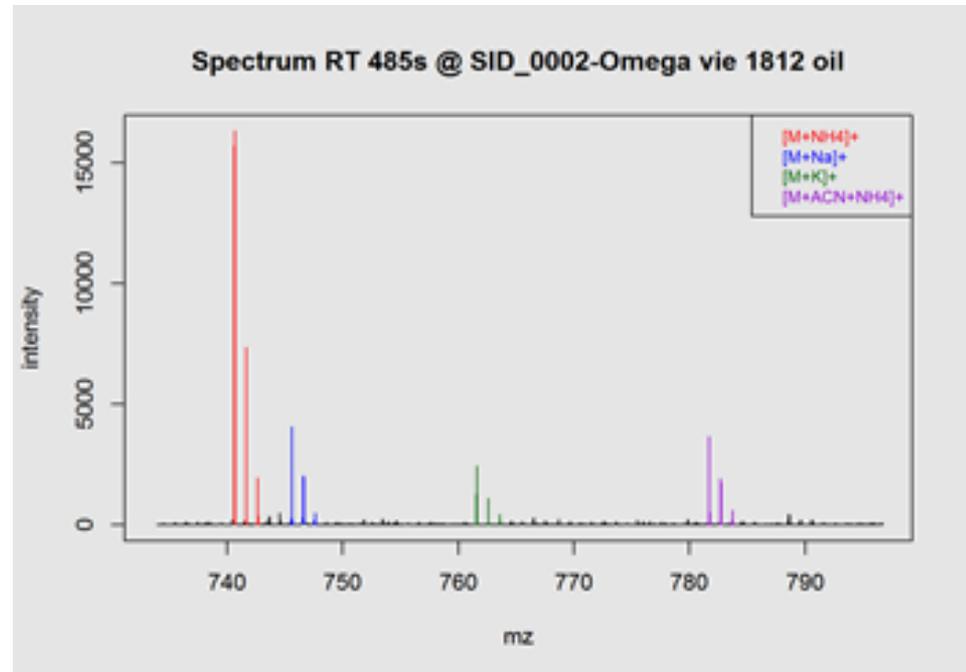
Different types

+Single quadrupole (SQ)

+Triple quadrupole (TQ)

+Time of flight (ToF)

+Orbitrap (Orbi)



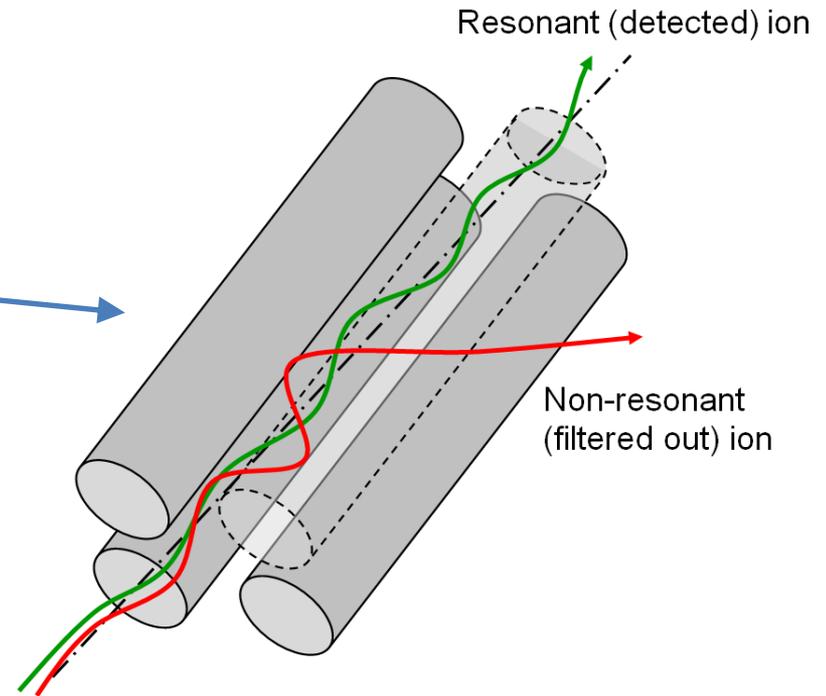
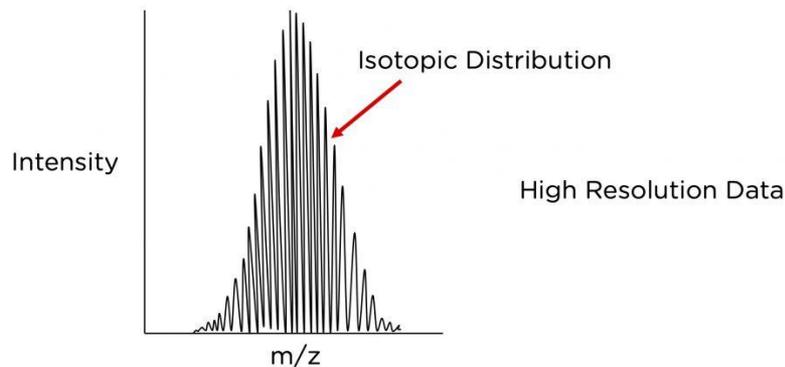
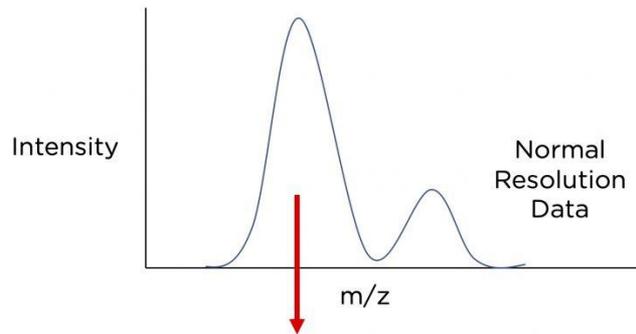
MS lipidomics: SQ analyzer

Properties

+Non efficient for scanning

+ion filter

+low resolution

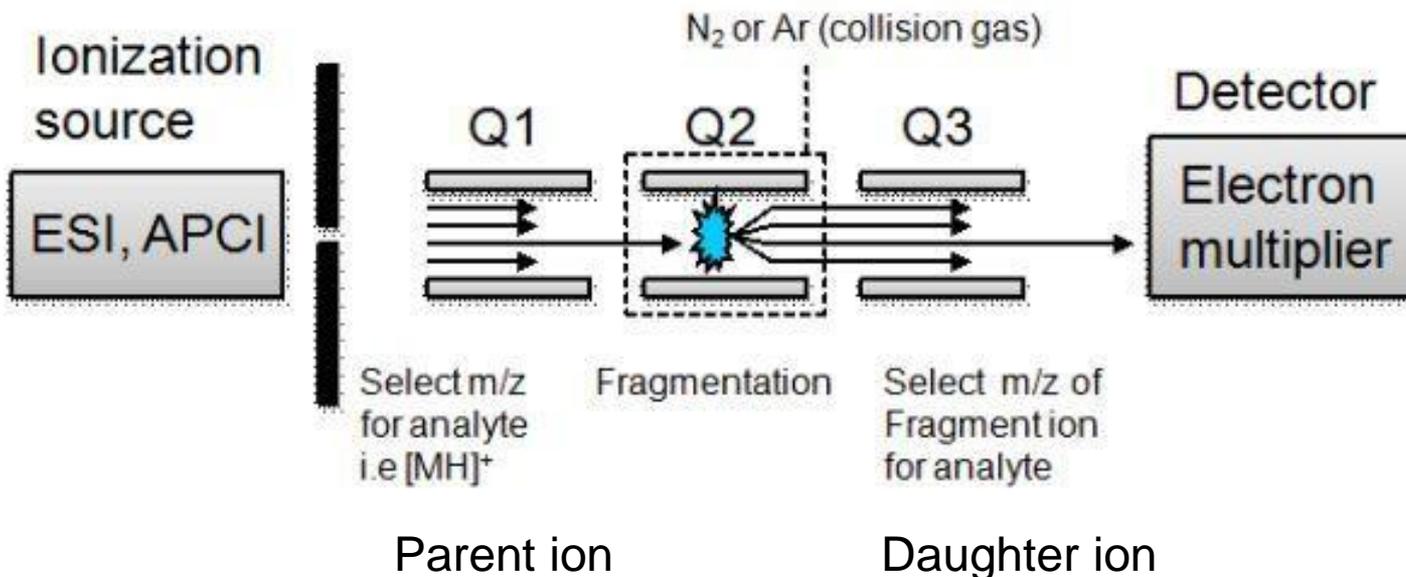


Low selectivity

MS lipidomics: TQ analyzer

Properties

- Ion filter + collision cell + Ion filter
- Low resolution but increased selectivity
- High dynamic range (linear response)



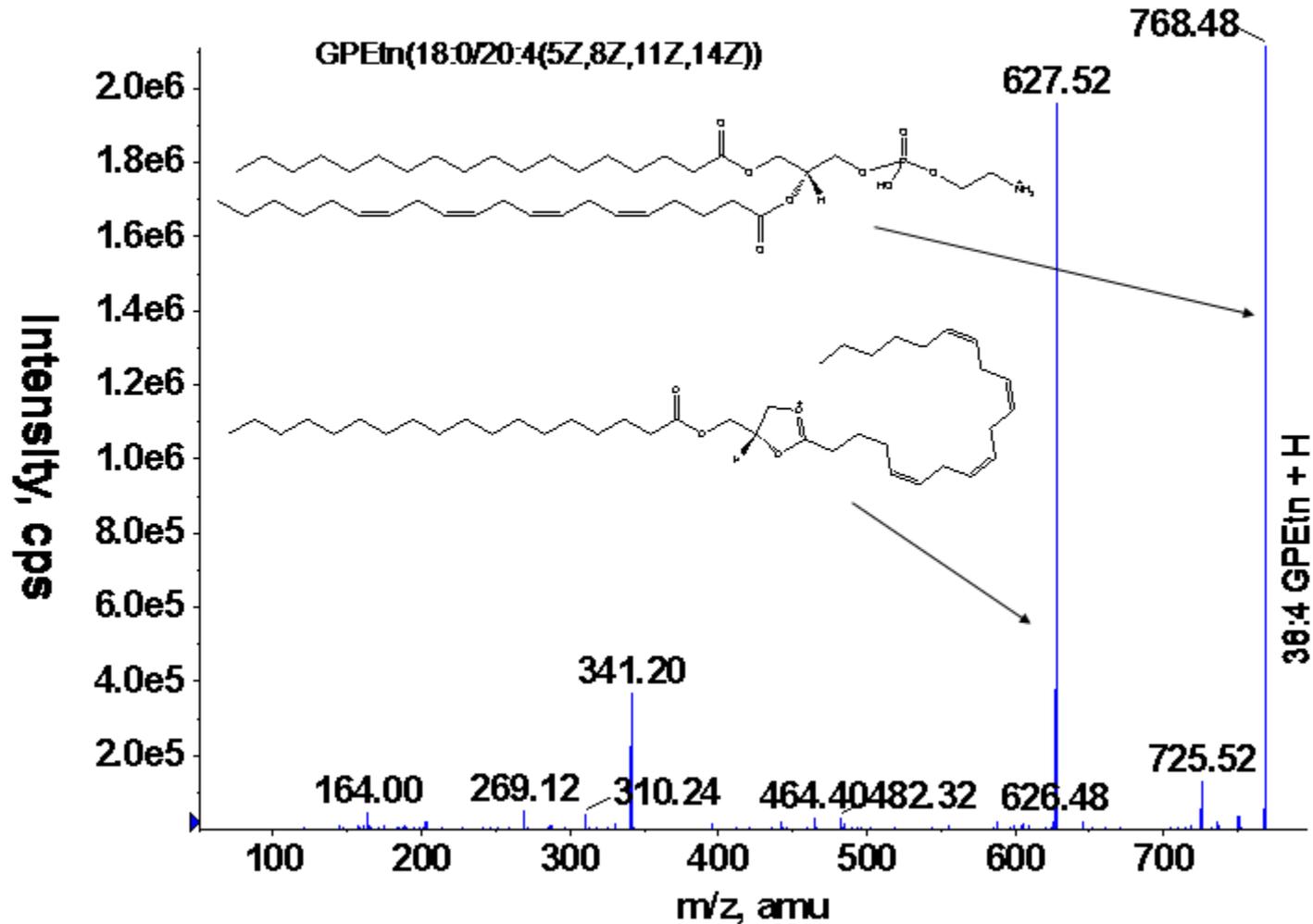
<https://www.youtube.com/watch?v=Jc1uC6EbMCs>

MS lipidomics: Fragmentation

PE 18:0_20:4 in positive mode

■ +EPI (768.30) CE (30): 6 MCA scans from Sample 1 (pos 768 38_4PE) of pos 768 38_4PE.wiff (T...

Max. 2.1e6 cps.

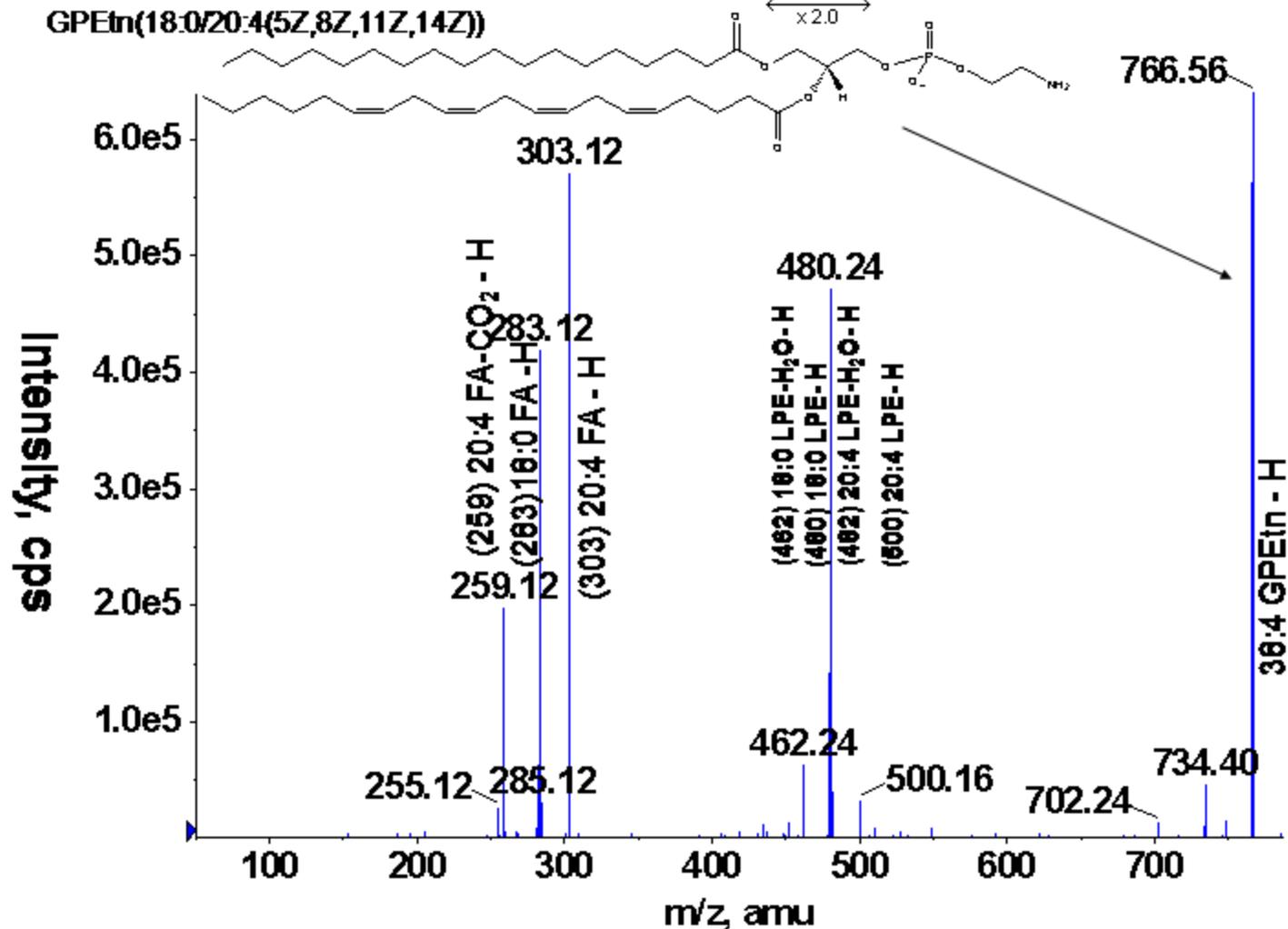


MS lipidomics: Fragmentation

PE 18:0_20:4 in negative mode

■ -EPI (766.30) CE (-41): 5 MCA scans from Sample 1 (766_38_4PE) of 766_38_4PE.wiff (Turbo Spr...

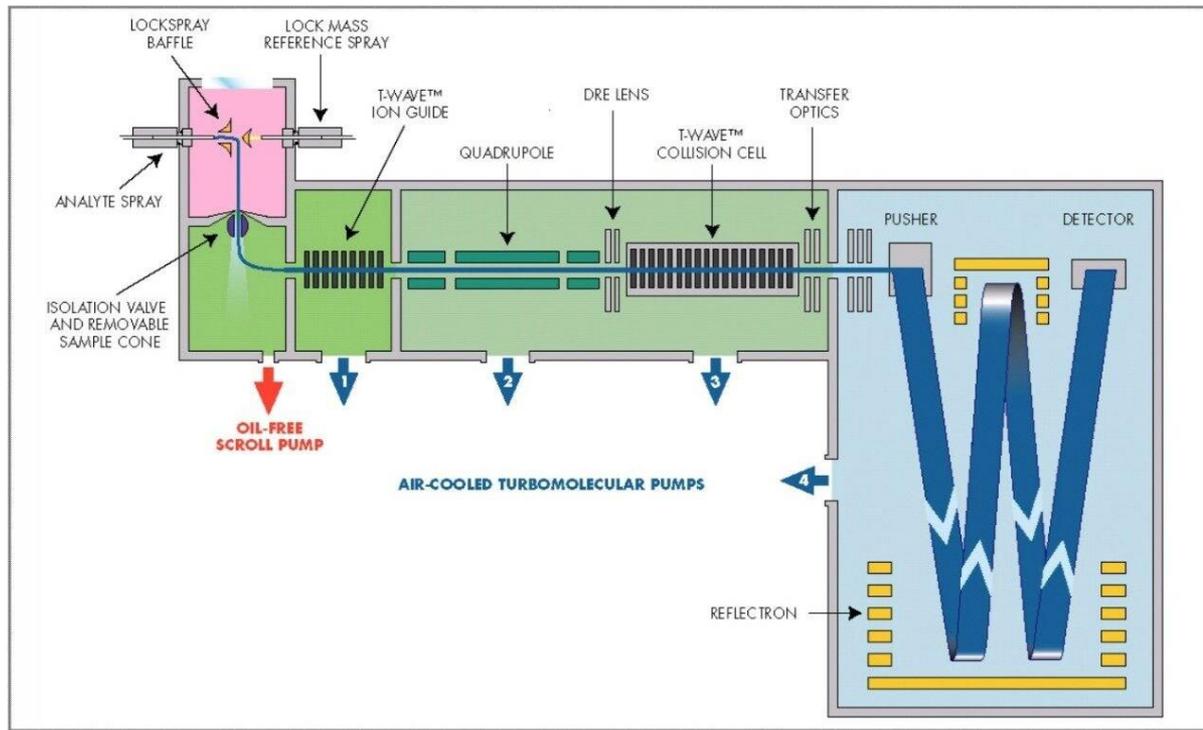
Max. 6.4e5 cps.



MS lipidomics: Q-ToF analyzer

Properties

- Ion filter + collision cell + Time of Flight
- ToF: medium-high resolution but lower dynamic range

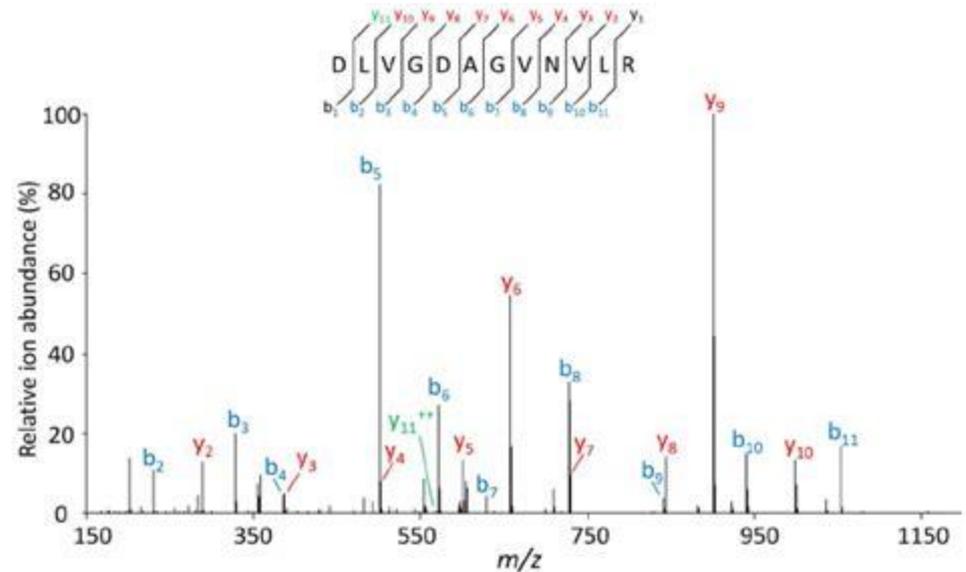
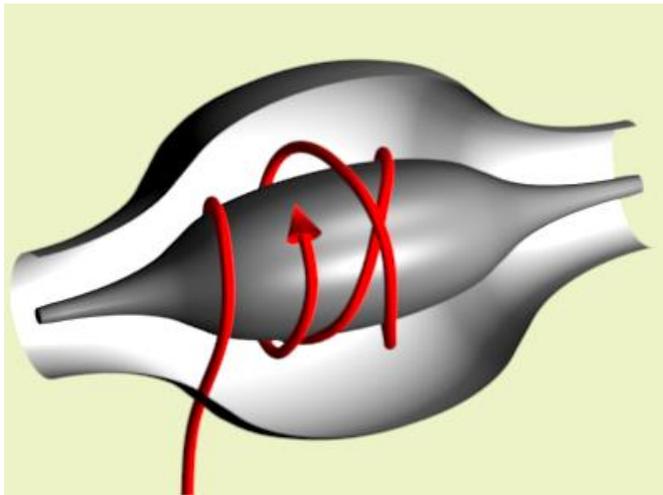


<https://youtu.be/W-DRL-V2Rkg?t=29>

MS lipidomics: Orbitrap analyzer

Properties

- High resolution
- Very expensive, reserved for proteomics

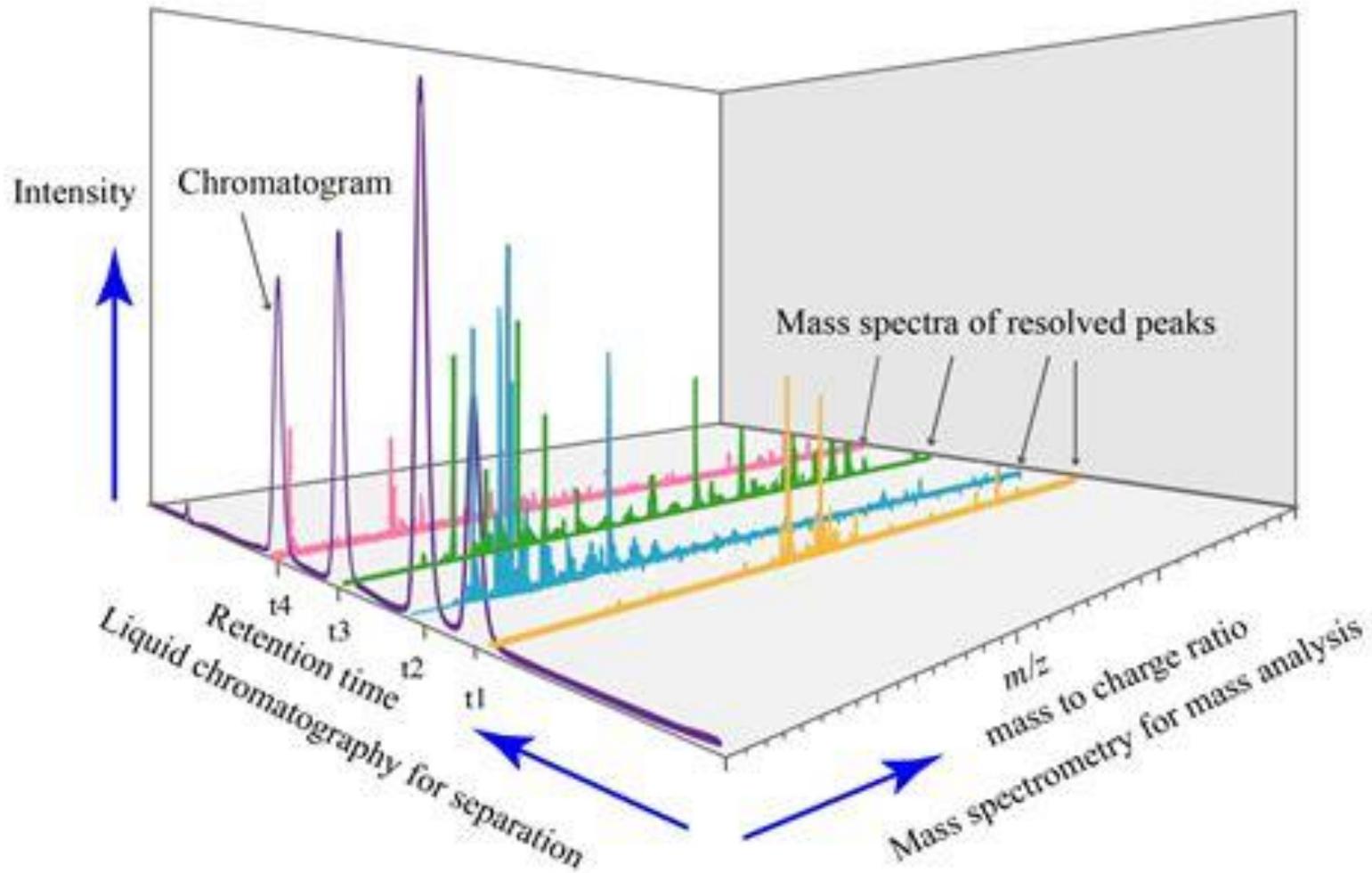


<https://www.youtube.com/watch?v=K1VSYjuw6os>

MS lipidomics: Analyzer Comparison

Aspect	Triple Quadrupole (Triple Quad, TQ)	Q-ToF (Quadrupole-Time of Flight)	Orbitrap
Principle	Selective mass transitions using multiple quads.	Accurate mass measurement with TOF analyzer.	High-resolution mass analysis with ion trapping.
Sensitivity	High sensitivity for targeted analysis.	Medium sensitivity for accurate quantification.	Medium sensitivity and resolving power.
Quantitation	Excellent for targeted quantitation.	Accurate quantitation and identification.	Accurate quantitation for complex samples.
Selectivity	Exceptional selectivity for specific analytes.	Offers high selectivity and comprehensive analysis.	High selectivity for complex samples.
Speed	Fast analysis for high-throughput assays.	Fast acquisition rates for high-resolution analysis.	Moderate acquisition speeds with high resolution.
Fragmentation	Limited MS/MS capabilities for targeted analysis.	Excellent MS/MS fragmentation for structural elucidation.	Versatile MS/MS capabilities for comprehensive analysis.
Common lipidomics applications	Targeted: minor lipids and oxylipins	Glycerolipidome and sphingolipidome	Glycerolipidome and sphingolipidome
Price	Low to medium range.	Medium to high range.	High range.

MS lipidomics: Multidimensional spectrum



MS lipidomics: Analytical developments

- **Coupling to Ion Mobility Spectrometry**
- **Better limits of detection**
- **Bigger dynamic range**
- **Integration of MS scans and MS/MS (fragmentation)**