

# Introduction to Mass Spectrometry

by Leo Okkerse

**What is Mass Spectrometry?**

**Does anybody  
have an idea?**

# What is a Mass Spectrometer

***Simplified:***

**A Mass Spectrometer is an Analytical Instrument that measures the weight of molecules.**

# So how does a Mass Spectrometer work?

A Mass spectrometer needs to transfer molecules from either a liquid or gas into **gas phase ions**.

- After the ions are generated in the Ionization region;

The Mass spectrometer moves the ions from the ionization region, either by electrical or magnetic fields. Passing through the analyzer region to a detector.

Where the Detector produces a electronic signal.

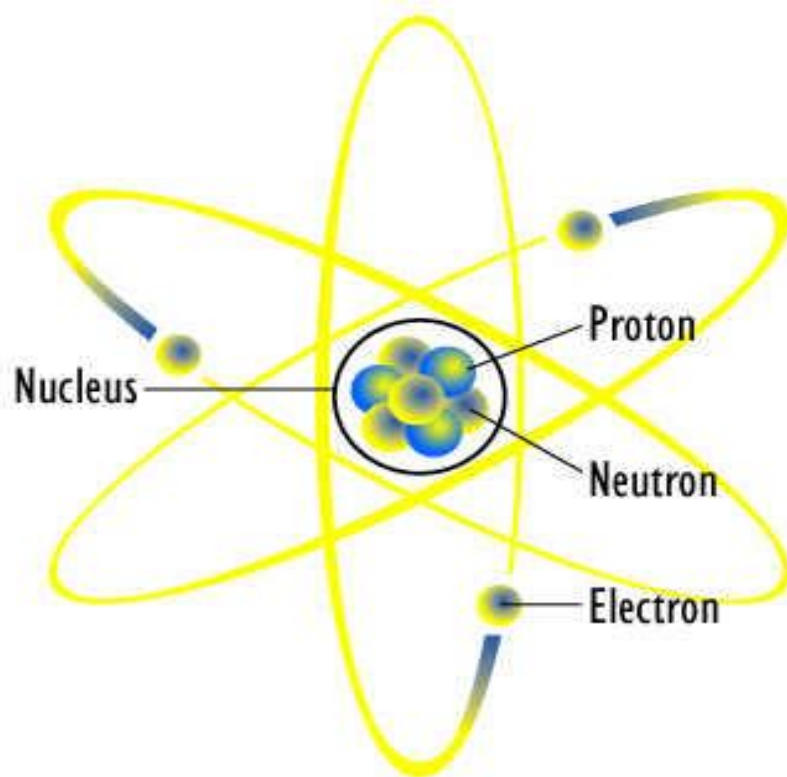
Software will convert the complex signal into a readable



# SO, why a front end

- there is the need for an interface that:
  - will eliminate the solvent
  - generate gas phase ions
  - transfer ions to the Analyzer region
- Even with sophisticated **MS** systems, **HPLC** or **UPLC** is still used to
  - remove interferences from the sample and assist in separating compounds that would impact the ionization process.



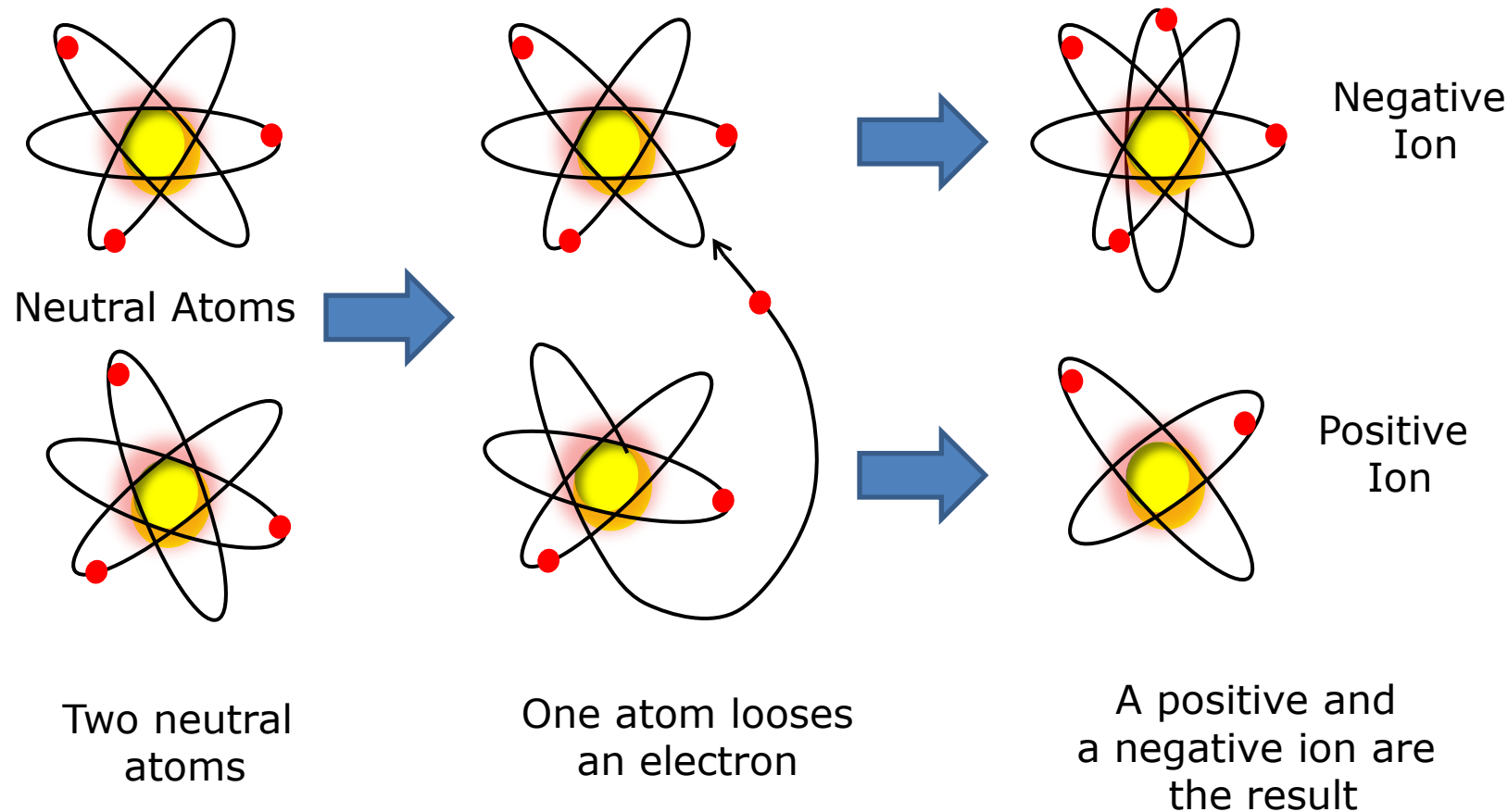


**Nucleus of an atom  
consists of Protons and  
Neutrons**

- 1. Protons have a positive charge.**
- 2. Electrons have a negative charge.**
- 3. Neutrons are neutral meaning they have no charge**

- An **ion** is an **atom** which has lost or gained one or more **electrons**, giving it a positive or negative electrical charge.
- A negatively charged ion, which has **more electrons** in its **electron shell** than it has **protons** in its **nuclei**, is known as an **anion**.
- A positively charged ion, which has fewer electrons than protons, is known as a **cation**.

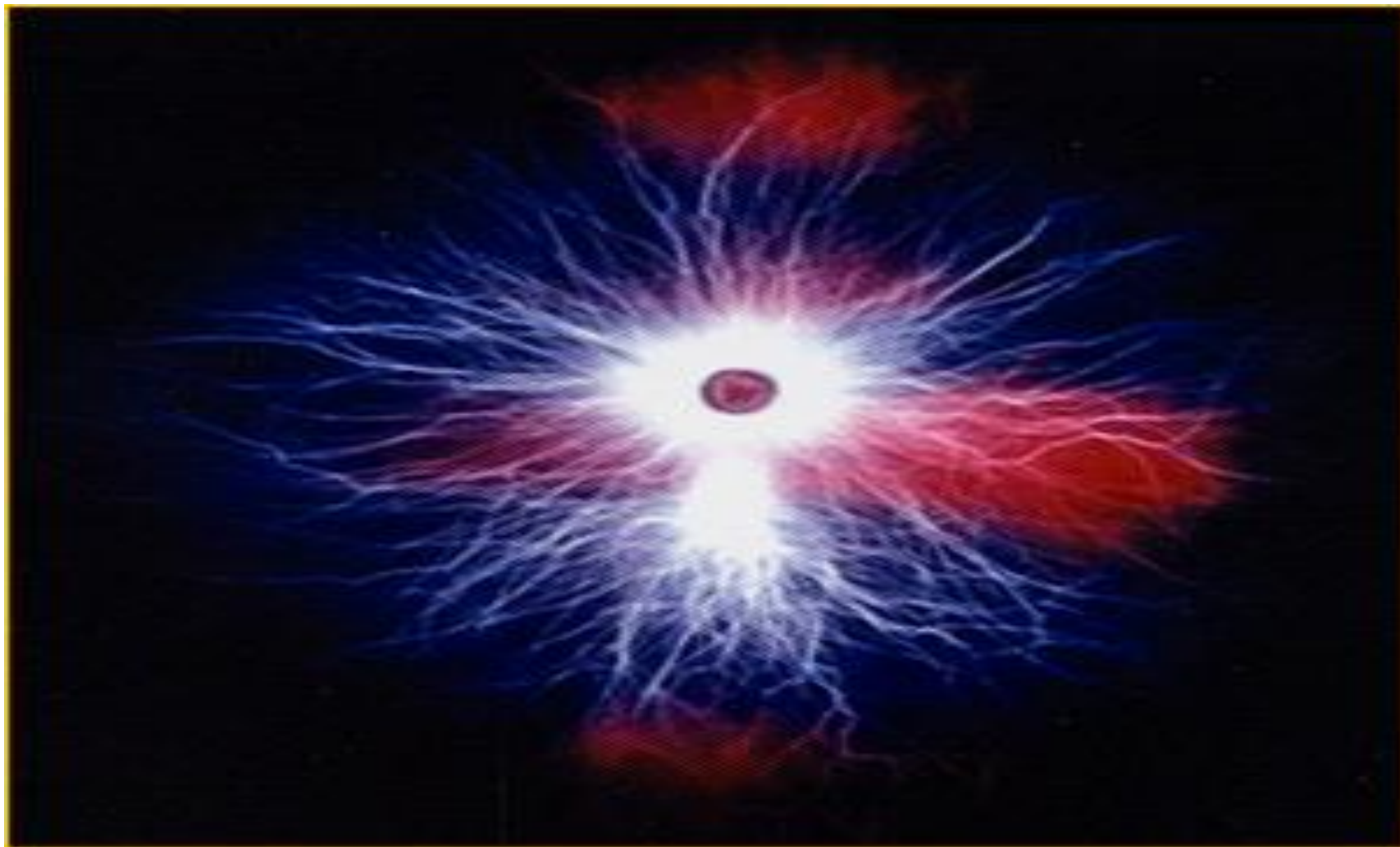






# Negative Ion

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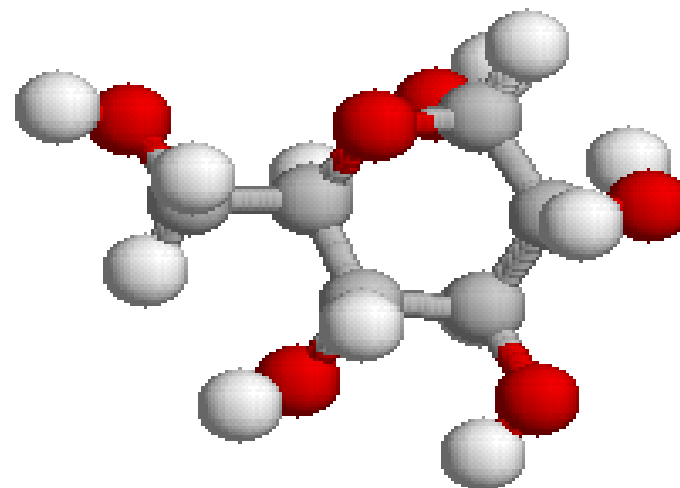


# So, what is a Molecule

- A **molecule** is defined as a sufficiently stable **electrically** neutral group of at least two **atoms** in a definite arrangement held together by very strong **chemical bonds**.
- It can also be defined as a unit of two or more atoms held together by covalent bonds.
- In **organic chemistry** and **biochemistry**, the term *molecule* is used less strictly and also is applied to charged **organic molecules** and **biomolecules**.

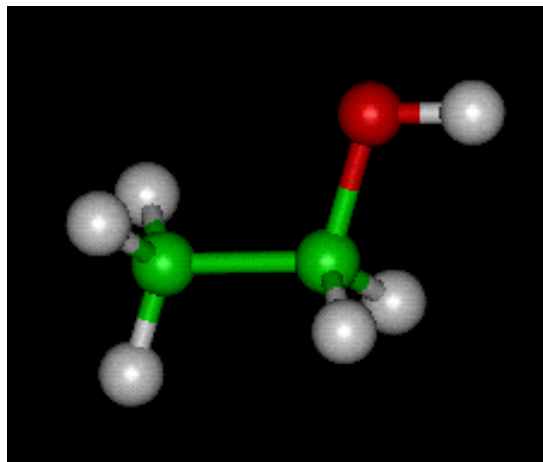
# Carbohydrate Molecule

- Carbohydrates are molecules that are composed of the elements carbon (C), hydrogen (H), and oxygen (O).
- Commonly, these molecules are known as sugars.
- Carbohydrates can range in size from very small to very large. Like all the other biomolecules, carbohydrates are often built into long chains by stringing together smaller units.



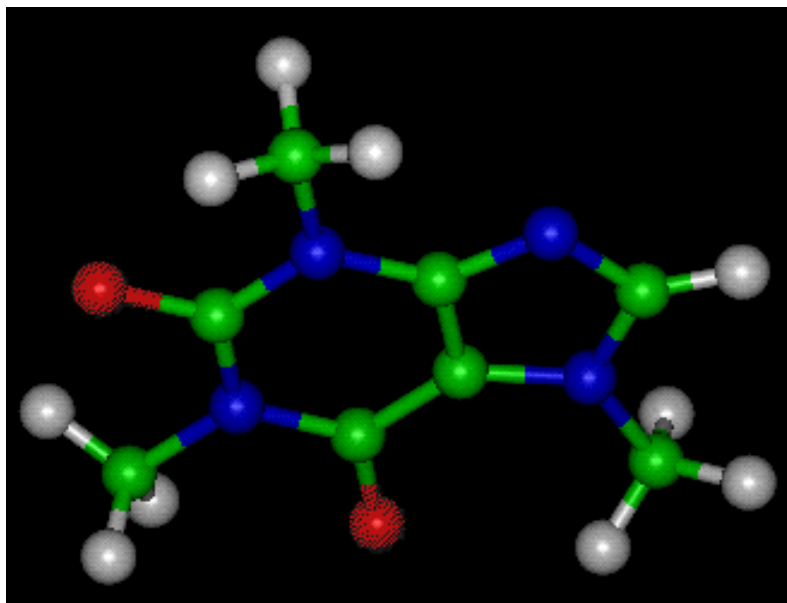
Glucose

# Molecules that are essential for life



Ethanol =  $C_2H_5OH$   
( $2 \times 12 + 5 \times 1 + 16 + 1$ )  
mass = 46

Or



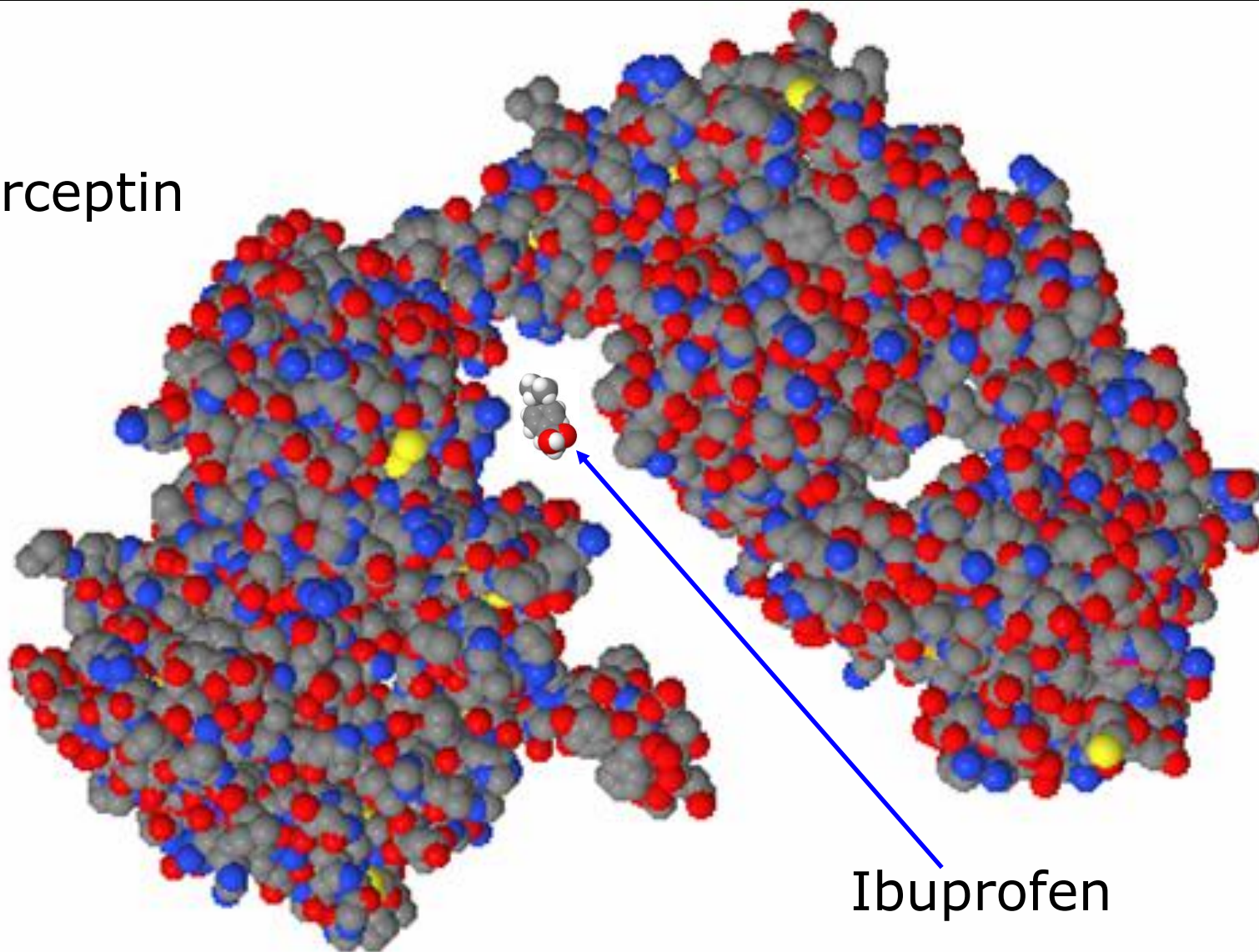
Caffeine =  $C_8H_{10}N_4O_2$   
( $8 \times 12 + 10 \times 1 + 4 \times 14 + 2 \times 16$ )  
mass = 194



# Biopharmaceuticals vs. small molecule pharmaceuticals

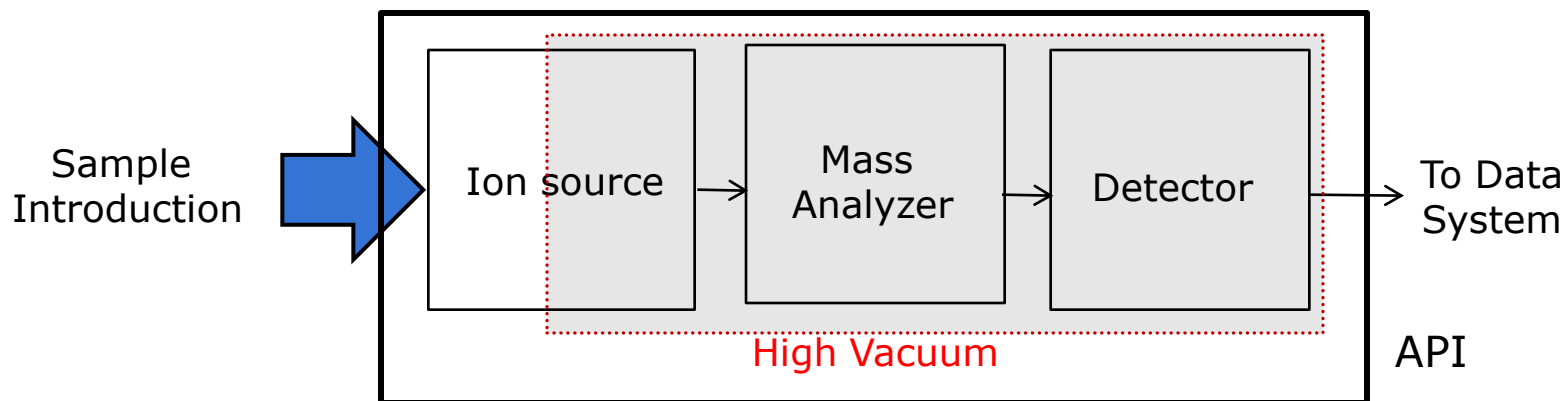
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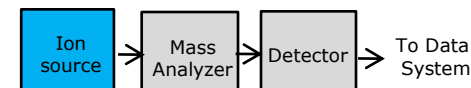


Mass spectrometers can be divided into three fundamental parts

1. the **Ionization source**
2. the **Analyzer**
3. the **Detector**



- The analyzer and detector are under high vacuum allowing the ions to travel from one end of the mass spectrometer to the other without colliding with any air or other interferences (molecules). The source region is mostly at atmospheric pressure but can be under vacuum as well.

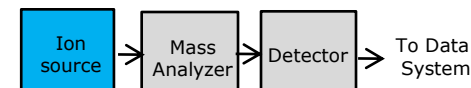


## Methods of sample ionization:

- Most instruments now use a atmospheric pressure ionization (**API**) technique where solvent elimination and ionization steps are combined in the source and take place at atmospheric pressure.
- Here are the most commonly used **API** techniques:
  - **ESI**      Electrospray Ionization (LC technique)
  - **APCI**    Atmospheric Pressure Chemical Ionization (LC technique)
  - **APPI**    Atmospheric Pressure Photo Ionization (LC technique)

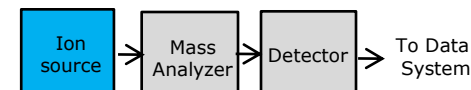


# Other Techniques available



## ■ Here are some more commonly used techniques:

- **MALDI** Matrix Assisted Laser Desorption Ionization- (LC-MS technique)
- **EI** Electron Impact ( GC technique)
- **CI** Chemical Ionization ( GC technique)
- **Nanospray**



- Electrospray ionization **ESI** is a **API**(atmospheric pressure ionization technique)
- Electrospray is a method of generating a very fine liquid aerosol through electrostatic charging
- ESI is used for:
  - Polar compounds
  - mass range from less than 30Da up to more than 100KDa
  - flow rates between 1ul/min. up to 1 ml/min.

## Advantages:

- Ionic/polar analyte
- Low temperature, no degradation
- High Molecular weight determination
- Volatile and non-volatile solutes
- Good for Quantitative method and sensitivity

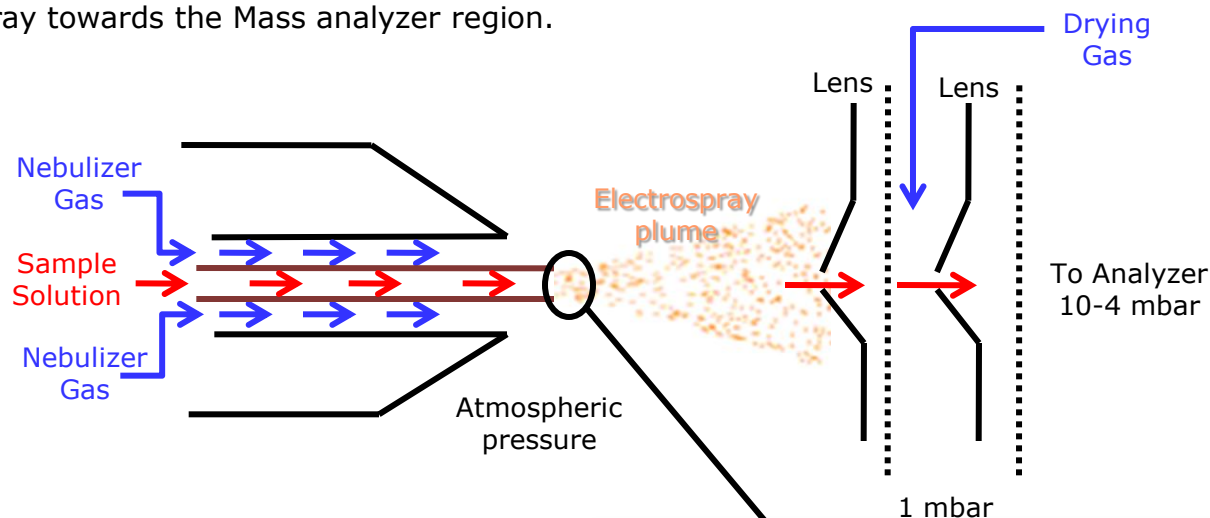
## Disadvantages:

- Must form ions in solution
- High salt conditions can suppress ionization
- LC mobile phase additives may affect ionization, TFA for example
- Low flow rates

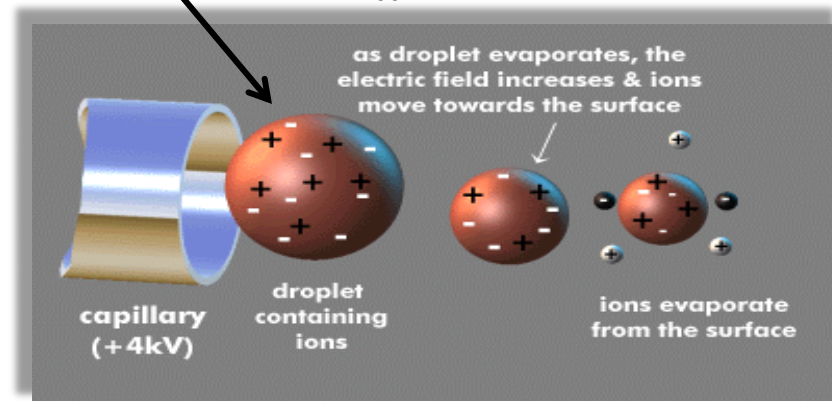
# Electrospray ionization

## ■ How it works.

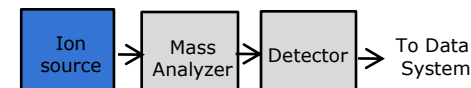
The sample is introduced through a narrow stainless steel or fused silica capillary (~50-100 micron i.d.), with an appropriate flow rate. A high voltage is applied to the tip of the probe. As a result of the high electric field, the sample emerges from the tip as an aerosol of highly charged droplets. The nebulizing gas helps with directing the spray towards the Mass analyzer region.



The **charged droplets** diminish in size due to solvent evaporation, assisted by the drying gas. Eventually, **charged sample ions**, free from solvent, are created and some of them will pass through the lenses into the higher vacuum region.



# Atmospheric Pressure Chemical Ionization (APCI)



## Characteristics:

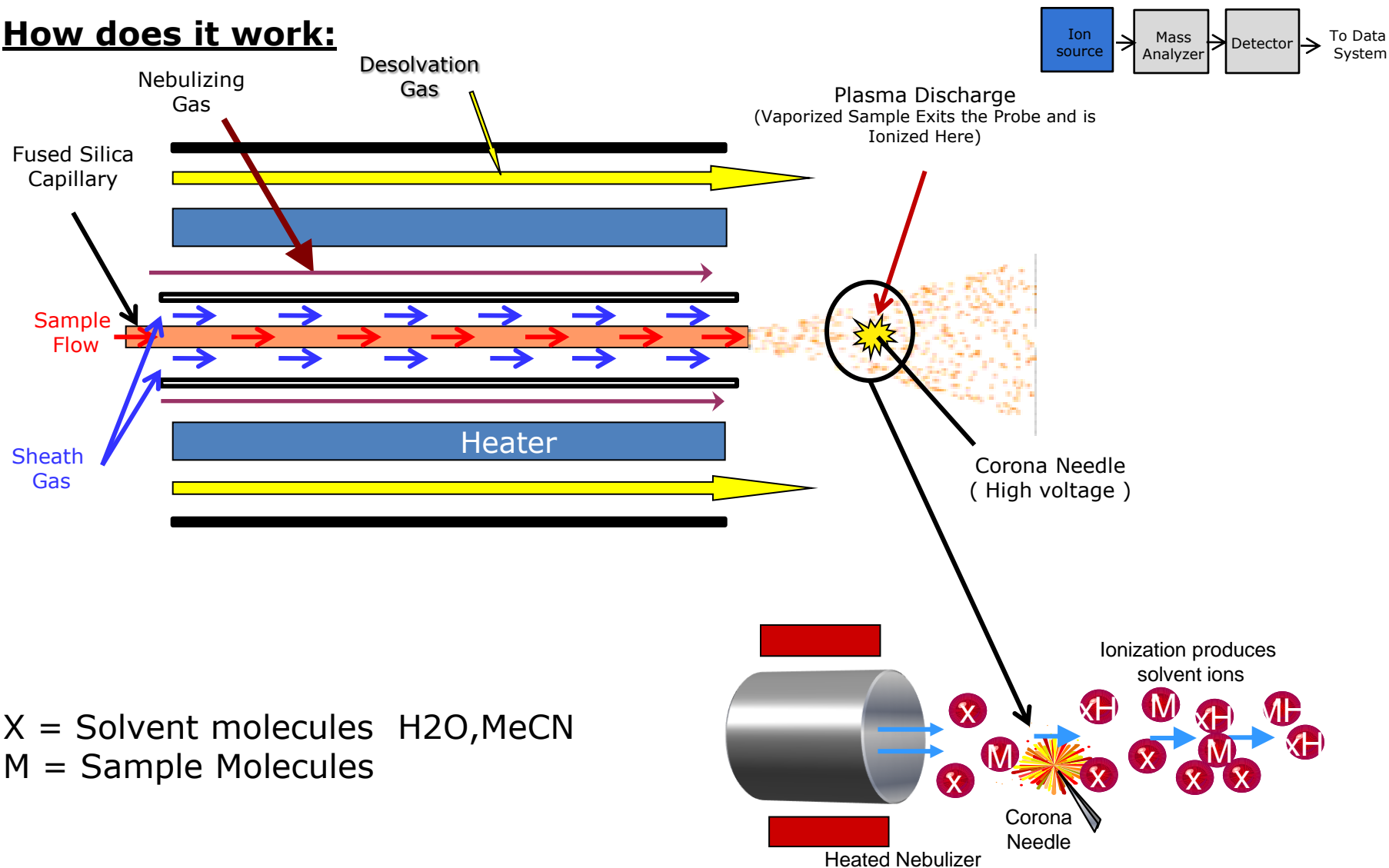
- Higher temperature, more aggressive ionization
  - Solvent molecules are in the gas phase
  - Ionization takes place in the plasma
  - Potentially more sensitive than electrospray with some non-polar molecules
- 
- Positive Ion APCI
    - Ions similar to those formed in positive ion electrospray are formed as:  
 $(M + H)^+$  or  $(M + Na)^+$
  - Negative Ion APCI
    - $(M - H)^-$  ion formed in negative ion electrospray is also produced
    - Free electrons are formed by the corona pin
      - Certain types of molecules can pick up a free electron and become negatively charged without a change in mass. This process is sometimes referred to as  $M+\bullet$

# Atmospheric Pressure Chemical Ionization (APCI)

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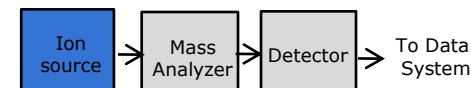
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## How does it work:





# ESI vs. APCI which technique?



## ■ Electrospray

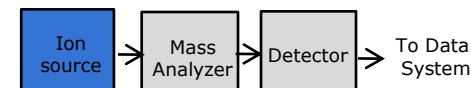
- Ionization in solution
- Reverse phase or normal phase with post column solvent modifications
- Ionization
- Probe not heated
- Capillary voltage
- Strong mobile phase effect
- Polar compounds
- Thermolabile compounds

## ■ APCI

- Gaseous phase ionization
- Reverse and normal phase
- Ionization
  - Heated probe
  - Corona pin
- Low matrix effect
- Less polar compounds



# Atmospheric Pressure Photo Ionization (APPI)

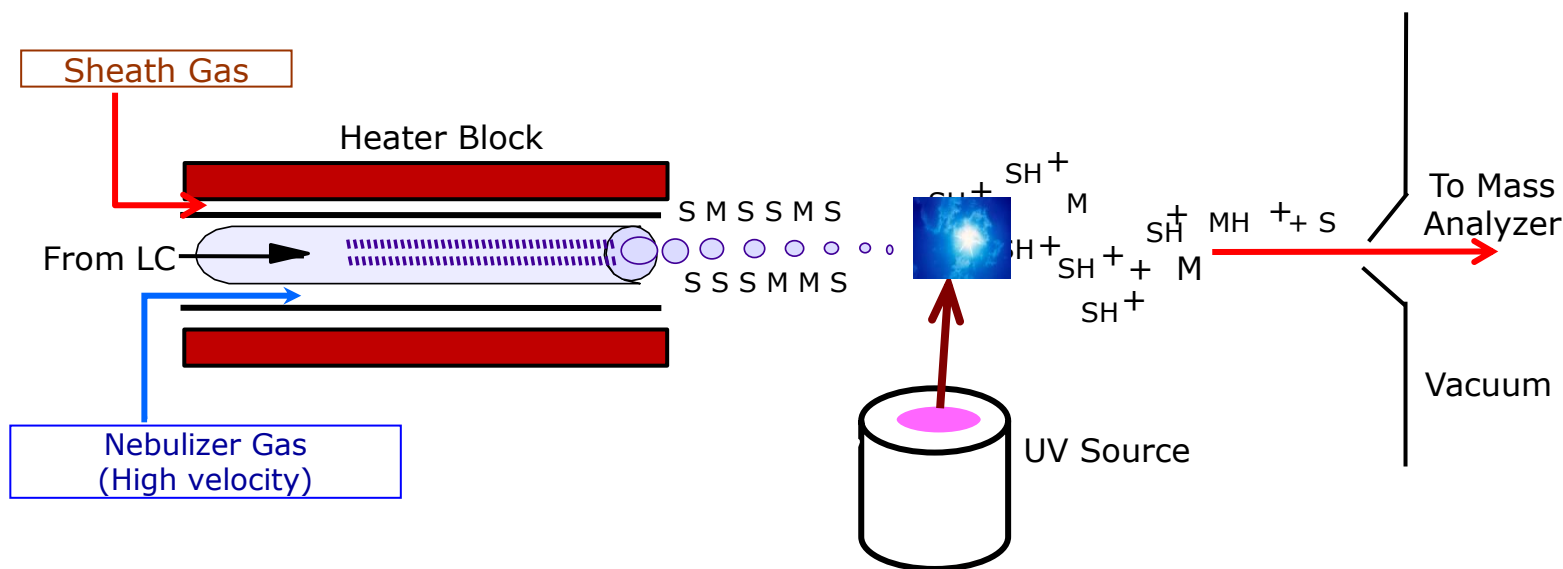
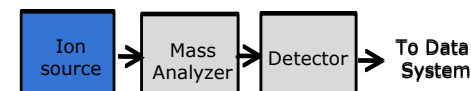


- Photo ionization is a process in which ions are generated from a molecule when it interacts with low energy photons being emitted from a light source.
- **Applicability:**
  - APPI is said to allow the ionization of compounds which cannot be ionized with APCI or ESI.
  - To be compatible with flow rates down to 100  $\mu\text{l}/\text{min}$ , and to be quantitative.
  - Molecule < 2000 m/z
  - Ionizable, polar and mid-polarity molecules
  - Available on all MS types
  - Sensitive technique for compounds with high proton affinity when using dopant compounds
  - Can ionize extremely nonpolar compounds not amenable to ionize by APCI
  - Positive and negative ionization modes

# Atmospheric Pressure Photo Ionization (APPI)

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## ▪ Ionisation mechanism:

- through a dopant (acetone, or toluene)
- Direct APPI:  $M + h\nu \rightarrow M^+$
- Dopant APPI:  $D + h\nu \rightarrow D^+ + D[-H]$   
 $D^+ + M \rightarrow MH^+$

# Which source to use?

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100 000

**Mass**

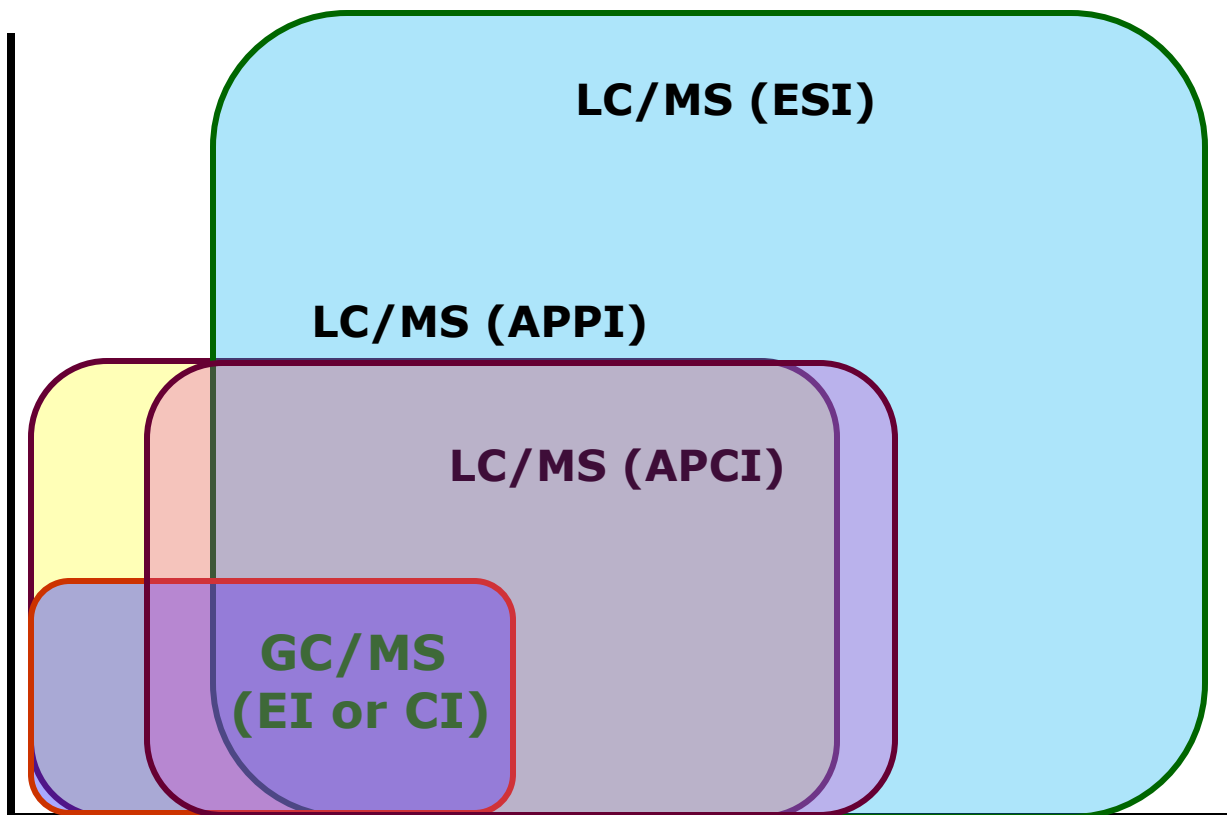
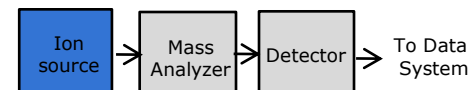
10 000

1000

Non-polar

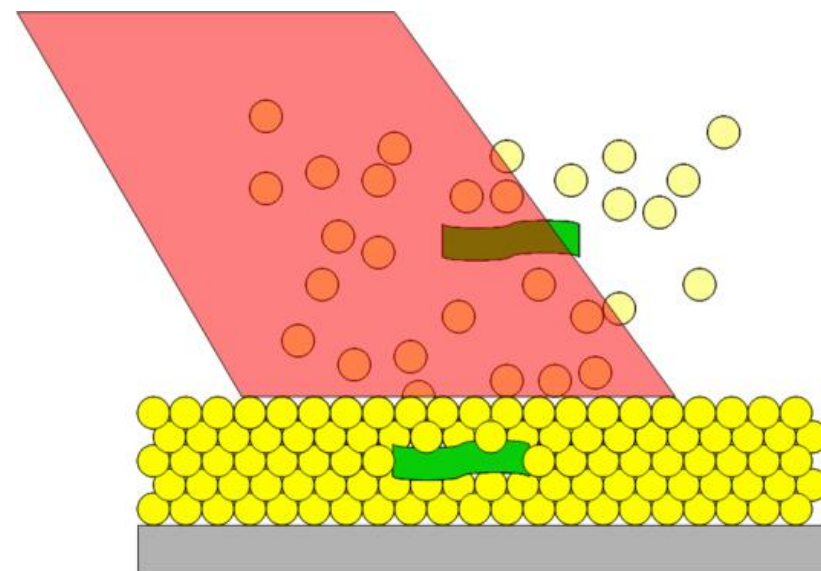
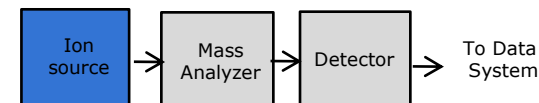
**Polarity**

Very Polar



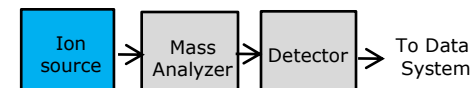
# Matrix Assisted Laser Desorption Ionization (MALDI)

- Matrix absorbs uv laser radiation and rapidly breaks down. It then expands into the gas phase and at the same time carries with it undamaged analyte molecules.
- The high matrix to analyte ratio serves to reduce associations between analyte molecules and provides protonated and free radical species that ionize the sample molecules.
- In positive ionization mode the protonated molecular ions  $(M+H)^+$  are usually the dominant species (sometimes with salt adducts).



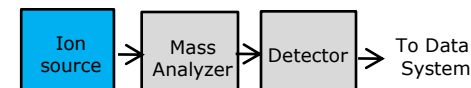
Yellow = Matrix  
Green = Sample  
Red = Laser beam

# Matrix Assisted Laser Desorption Ionization (MALDI)



- MALDI is a “soft” ionization method and so results predominantly in the generation of singly charged molecular-related ions.
- Very versatile technique, biggest application to-date protein identification due to the fact that we can easily ionize large molecules
- Common matrix to sample ratio: 100 ~ 10,000
- No precipitation after mixing sample and matrix
- Close solubility for sample and matrix needed in the solvent or solvent system
- Common solvent for both sample and matrix

# Matrix Assisted Laser Desorption Ionization (MALDI)



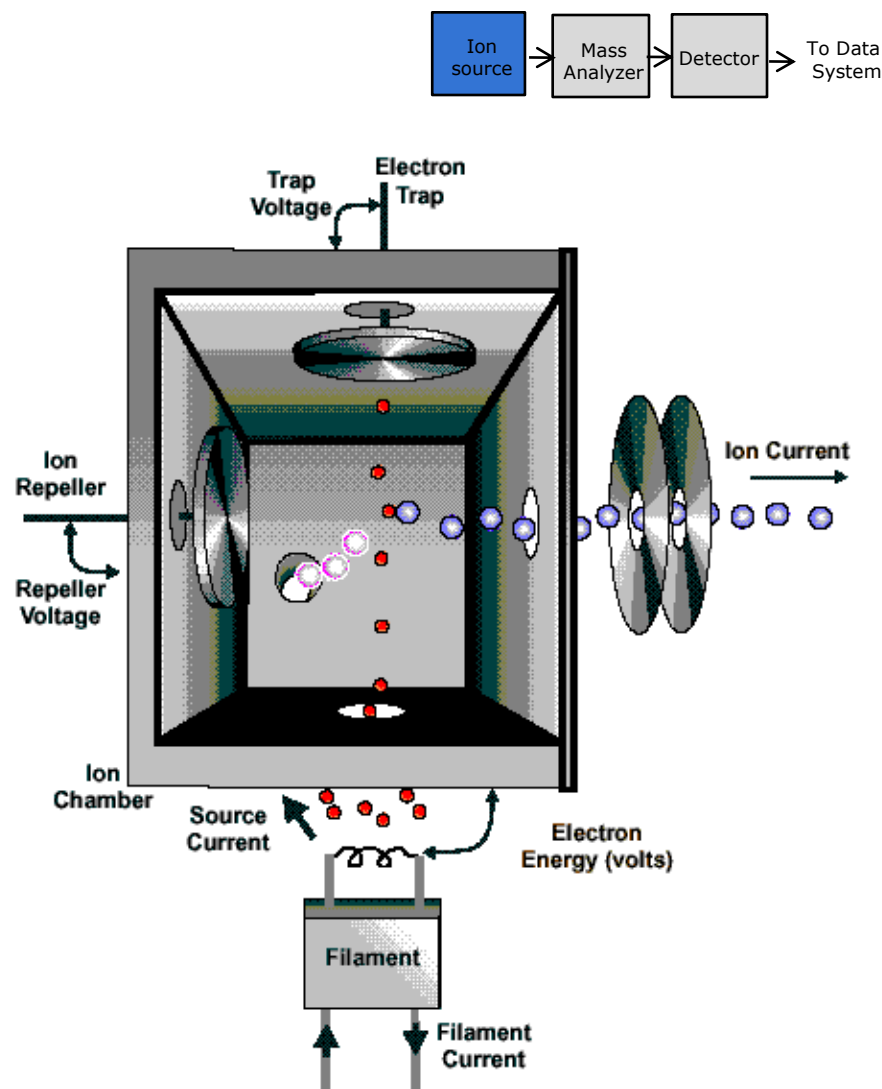
## How it works

- Sample mixed with small uv absorbing organic acid for example:  $\alpha$ -cyano-4-hydroxycinnamic acid, 2,5-dihydroxy benzoic acid (DBA).
- Sample/matrix mixture allowed to air dry.
- Matrix forms crystals which contain sample molecules.
- Matrix absorbs uv laser radiation and rapidly breaks down. It then expands into the gas phase and at the same time carries with it undamaged analyte molecules.
- The high matrix to analyte ratio serves to reduce associations between analyte molecules and provides protonated and free radical species that ionise the sample molecules.



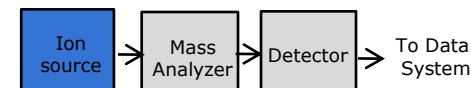
# Electron Impact ionization (EI)

- Sample molecules are admitted to the electron impact source via the GC interface, the solids insertion probe or the reference inlet system. The source is heated to ensure sample vaporization, and the resulting gas phase molecules are ionized in collisions with high-energy electrons released from the white-hot filament. Ions are extracted from the source and pushed into the analyzer by the ion repeller and the focusing lenses. This very energetic process, produces fragmentation in nearly all cases. Molecular ions, if present at all, created by EI are of the form  $M^+$ , making them odd electron ions.
- This diagram does not show the permanent magnets above and below the source which help collimate the beam of electrons from the filament to the trap.

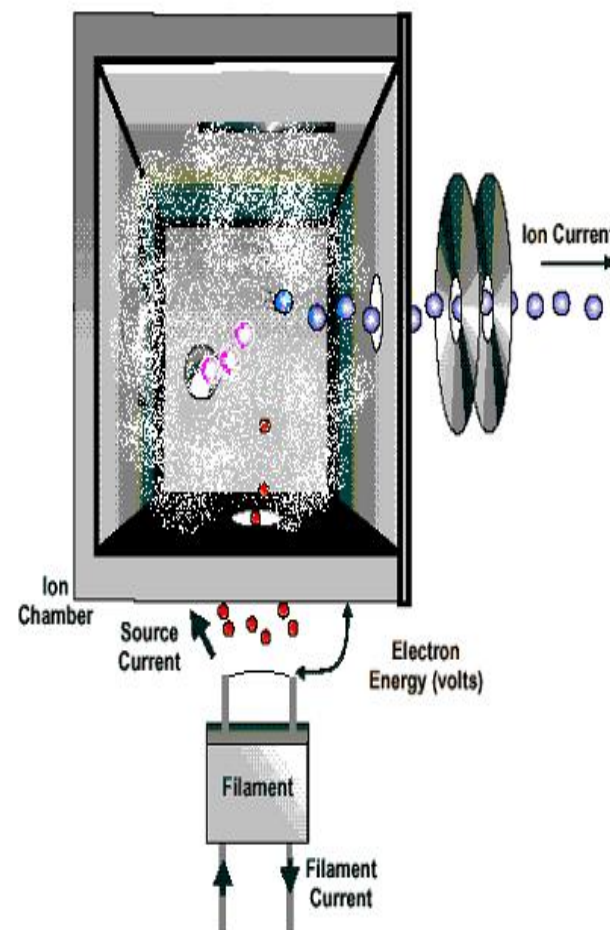




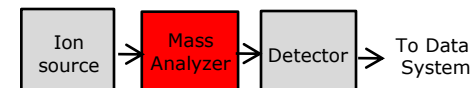
# Chemical Ionization Source (CI)



- In Chemical Ionization (CI) a reagent gas, commonly methane, ammonia or isobutane, fills the ion volume.
- The exit aperture in CI is much smaller to help contain the reagent gas. No repeller is used nor is there a trap for filament current regulation. The filament current is regulated by measuring the input and output current on each leg.
- The filament is a single strand rhenium design versus coiled tungsten for EI. The design and composition allow cooler operating temperatures to help reduce or eliminate fragmentation during CI operation.



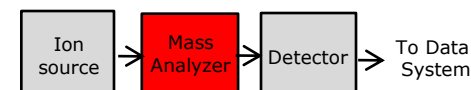
## 2. Analyzer



### Analysis and Separation of sample ions:

- The main function of the mass analyzer is to separate or resolve the ions that were formed in the ionization process (source region) of the mass spectrometer, according to their mass to charge ratios ( $m/z$ ).
- There are many different types of mass analyzers currently available, here is a list of the most common ones:
  - **Quadrupole analyzers**
  - **Time-of-Flight (TOF) analyzers**
  - **Quadrupole ion trap analyzers (3D and 2D)**
- All these analyzers have different features like resolution, mass range and accuracies.
- **Tandem** mass spectrometers (MS/MS) systems are systems with more than one analyzer so that they can be used for different kinds of experiments, such as MS/MS, and are used for structural and sequencing methods.

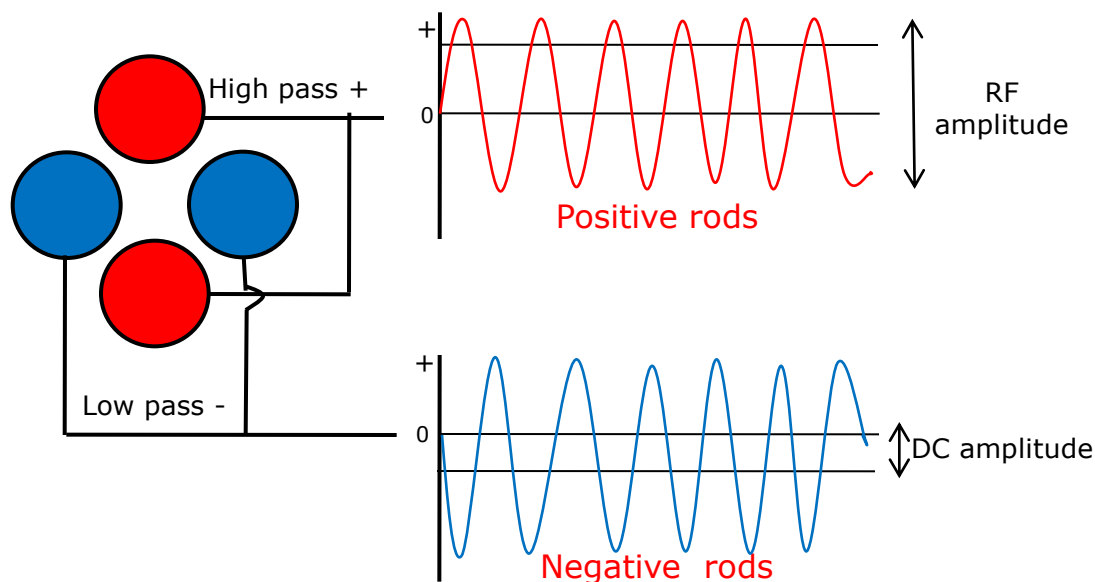
# Quadrupole Analyzer Theory



- This example shows the analyzer for a single mass.
- The potentials on each pair of rods are equal in magnitude but in opposite sign.

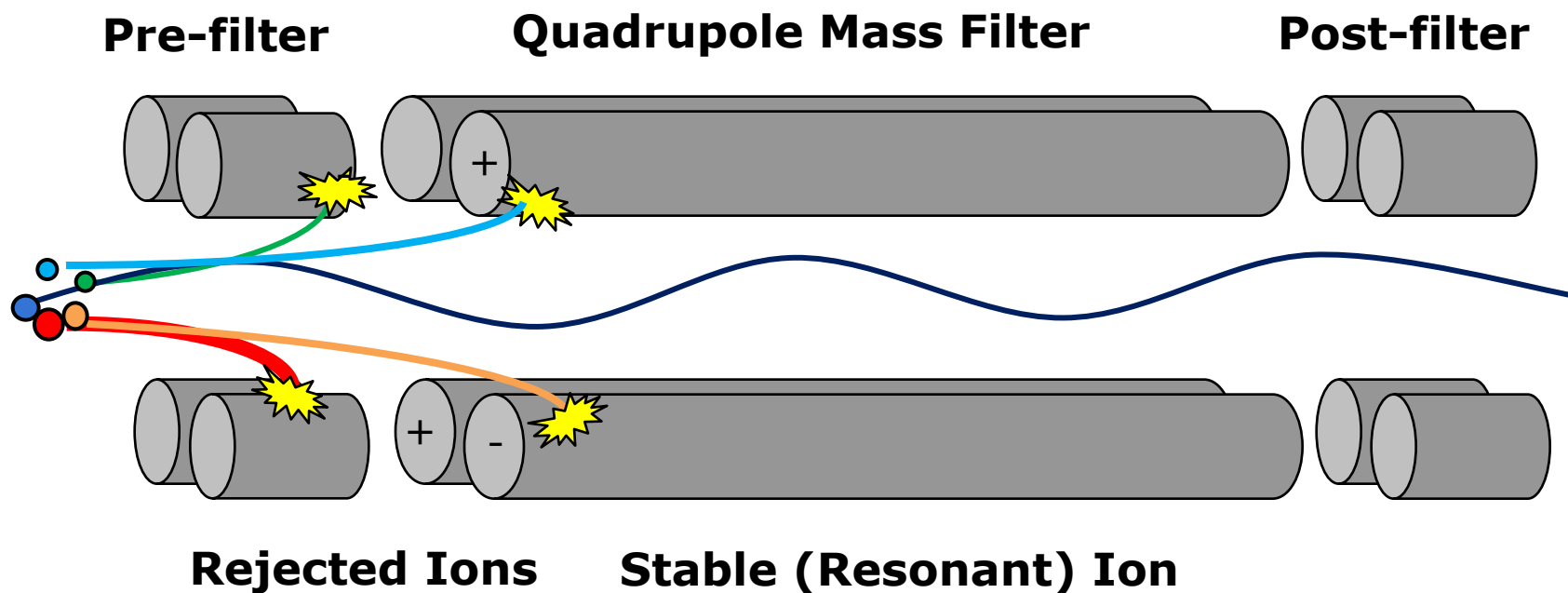
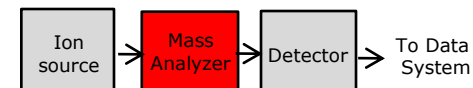
The high wave(pass) rod filters eliminating ions with low  $m/z$ .  
And the low wave(pass) rod filters eliminating ions with a high  $m/z$ .

A combination of a DC (voltage) and RF (frequency) potential is applied and varied  
With time to separate the different ions.

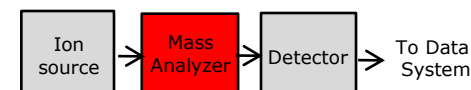


# Quadrupole Analyzer Theory

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# Principle of TOF analyzers



- **In a Time-Of-Flight (TOF) mass spectrometer, ions** formed in an ion source are extracted and accelerated to a high velocity by an electric field into an analyzer consisting of a long straight 'drift tube'. The ions pass along the tube until they reach a detector.
- After the initial acceleration phase, the velocity reached by an ion is inversely proportional to its mass (strictly, inversely proportional to the square root of its  $m/z$  value).
- Since the distance from the ion origin to the detector is fixed, the time taken for an ion to traverse the analyzer in a straight line is inversely proportional to its velocity and hence proportional to its mass. Thus, each  $m/z$  value has its characteristic time-of-flight from the source to the detector.

# Characteristics of TOF analyzers:

- **There is no upper theoretical mass limitation;**

the upper mass limit exceeds 500 kDa.

In practice, there is a mass limitation, in that it becomes increasingly difficult to discriminate between times of arrival at the detector as the  $m/z$  value becomes large.

Another limitation is that very large molecules are difficult to ionize.

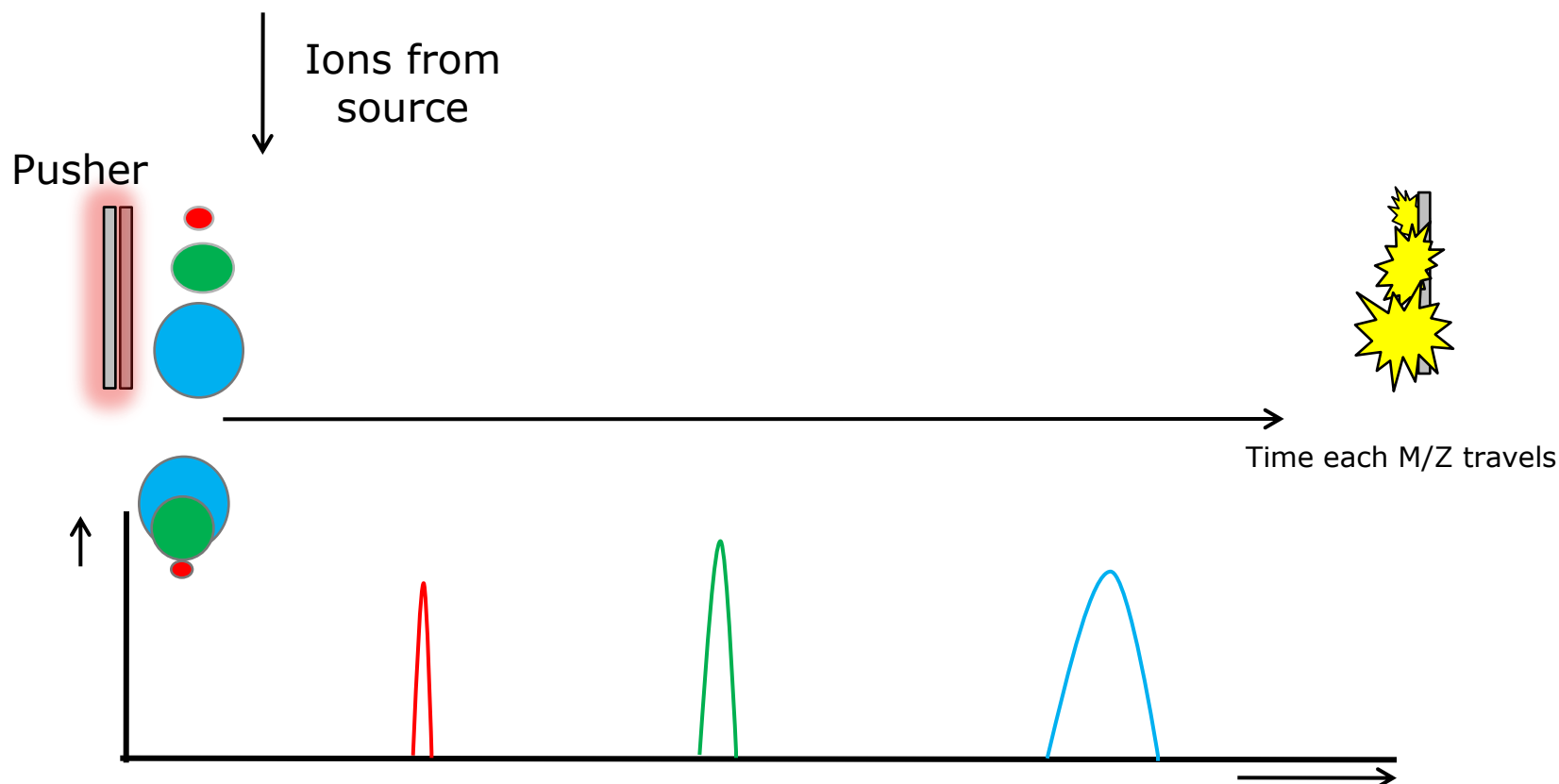
- **Resolution:**

with a TOF instrument, it is possible to obtain 10000 FWHM resolution

- **Mass accuracy:**

better than 5 ppm, using a reference mass; that allows unambiguous formula determination of small organic molecules

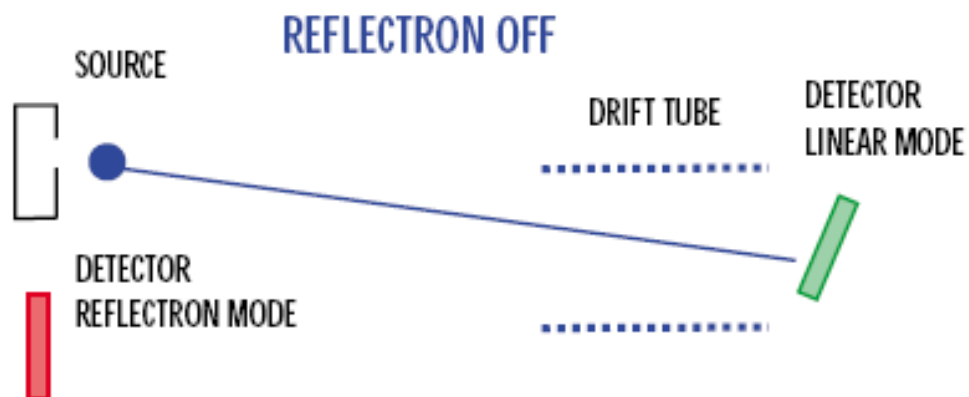
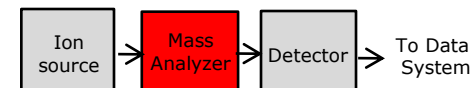




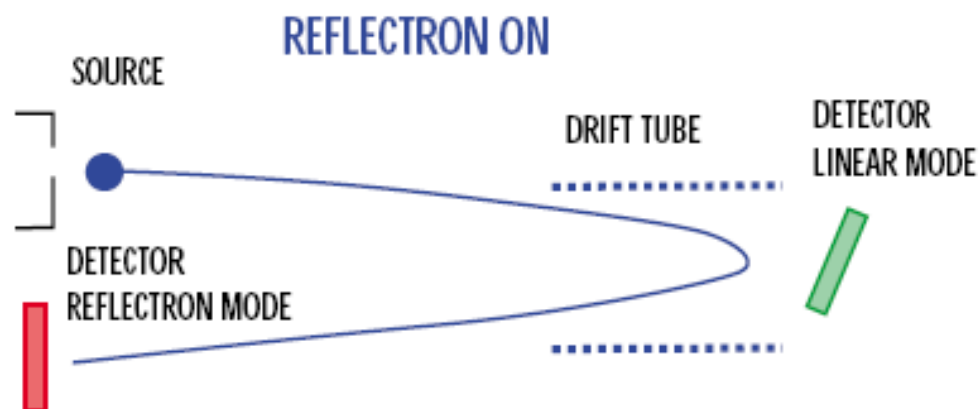
After the initial acceleration phase, the velocity reached by an ion is inversely proportional to its mass (note that all are pushed with the same power)



# Different TOF modes



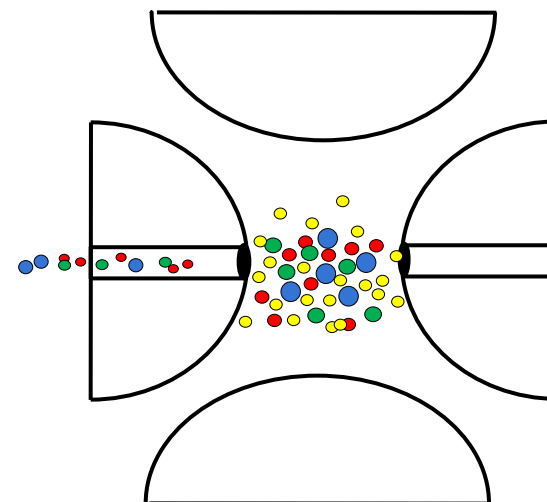
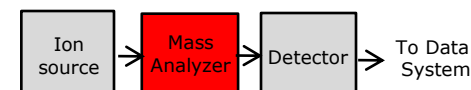
Linear mode



Reflection  
mode

# Ion Trap analyzers (3D traps)

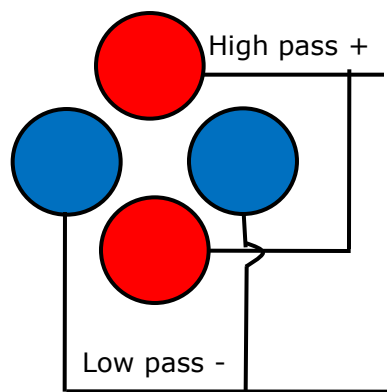
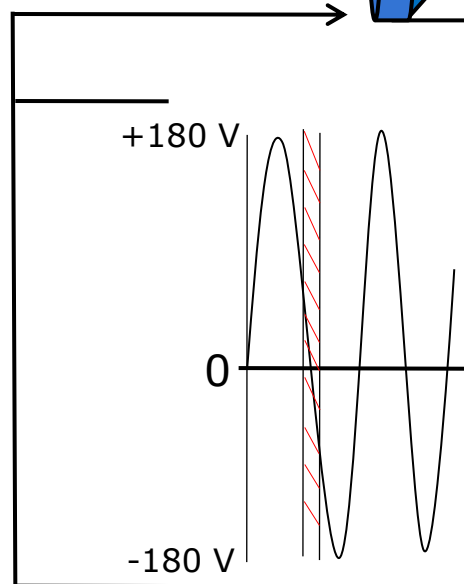
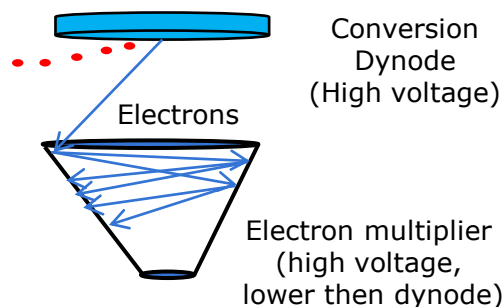
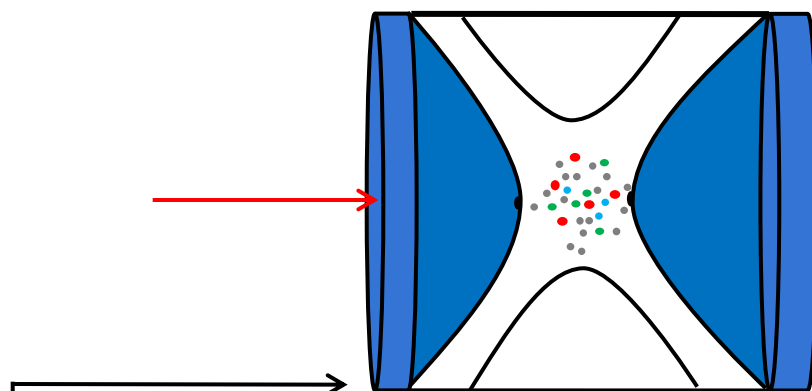
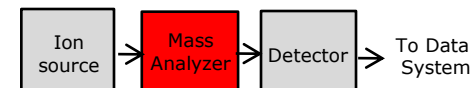
- The principle of the 3D trap is to store ions in a device consisting of a ring electrode and two end cap electrodes.
- The ions are stabilized in the trap by applying a RF voltage on the ring electrode. For maximum efficiency, the ions must be focused near the centre where the trapping fields are the least distorted.
- This is achieved by introducing a dampening gas(99.998% helium) that collisionally cools injected ions, damping down their oscillations until they stabilize.



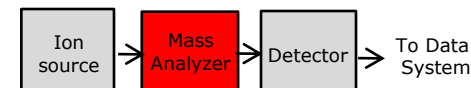
# 3D Ion Traps

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- Ionization and mass analysis is taking place all at the same place
- Due to the RF there is only a small moment that ions can be trapped.

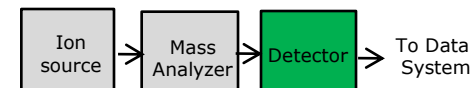


A Mass spectrometer analyzes ions by sorting and counting ions.

*Simplified (with the coin example)*

- Like pocket change(coins) —————> ■ Mixture of molecules
- Are like dimes, nickels, quarters, dollars —————> ■ Molecules with different weights and sizes
- Is like sorting your change —————> ■ Separation by mass by value

# 3. Detectors



There are three main detector types :

- **Electron multiplier**
- **Photomultiplier**
- **Microchannel plate**

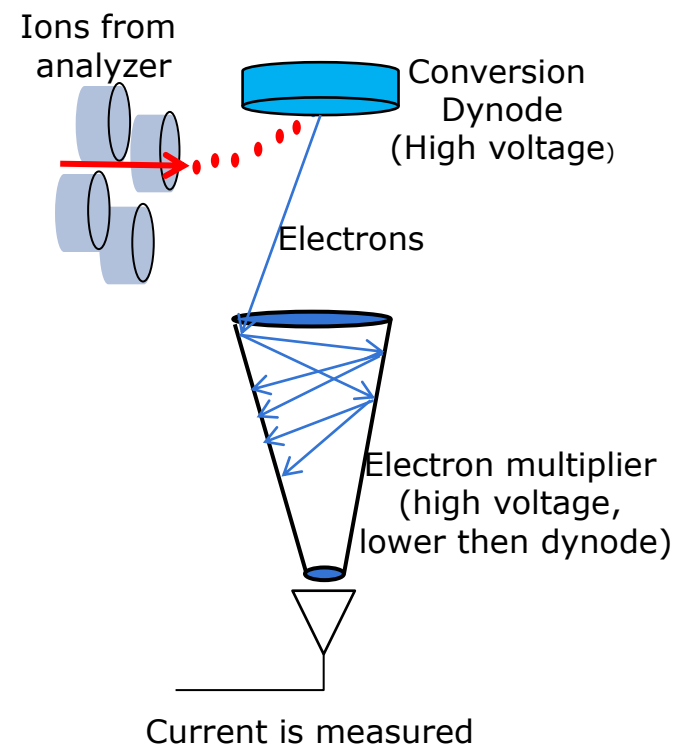
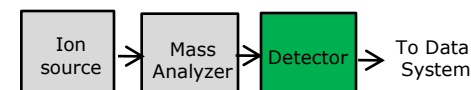
## ■ **Fundamentally:**

- These detectors multiply the incoming signal in order to produce a strong enough signal that the data system can use to convert into a readable format.

# 3. Detectors

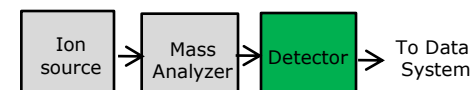
## ■ Electron multiplier:

- The electron multiplier, uses a conversion dynode to convert either positive or negative ions into electrons. Using a cascade effect, the electrons are amplified to produce a current.
- Electron multipliers (some times called channeltrons) are widely used in quadrupole and ion trap instruments.



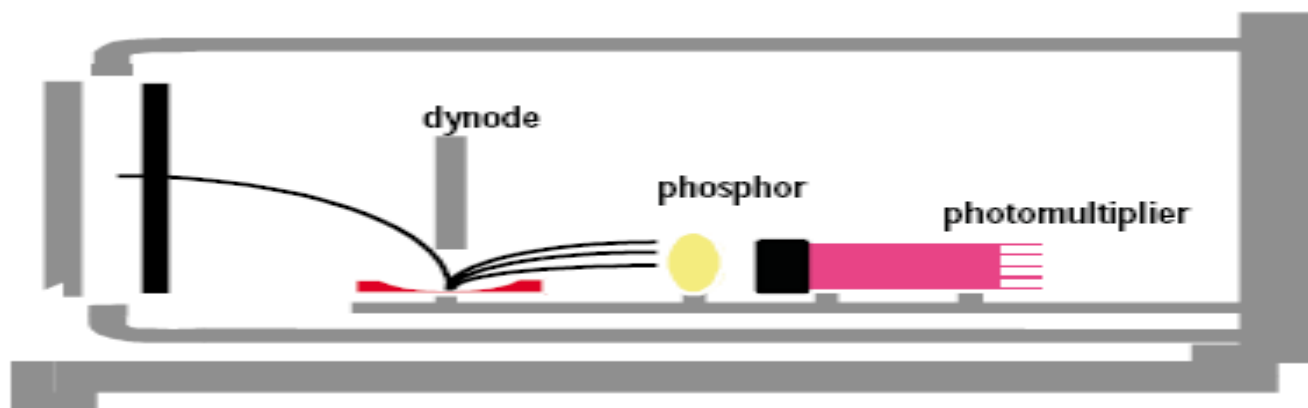


# 3. Detectors



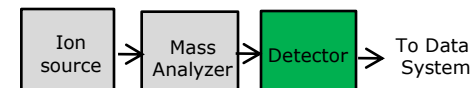
## ■ Photomultiplier

- Ions exiting the analyzer region are converted to electrons by a conversion dynode.
- These electrons excite the phosphor emitting photons in the process.
- Photons then hit a photocathode at the front of the photomultiplier producing electrons.
- The new electrons generate a signal that is amplified by the photomultiplier.

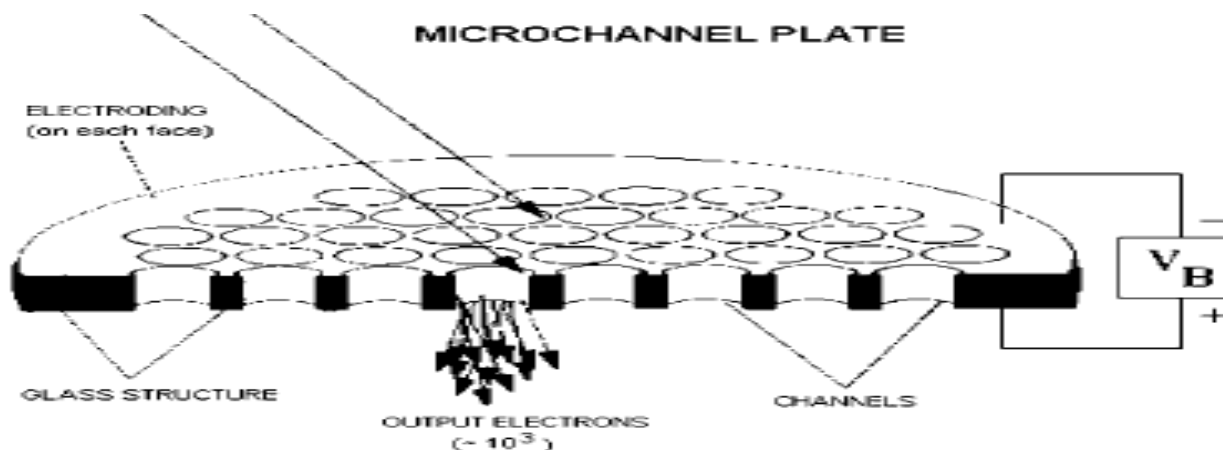


# 3. Detectors

## ■ Microchannel plate



- Microchannel plate detectors are mostly used by TOF mass spectrometers because of their time response capability.
- Most microchannel plate detectors have a response time of  $< 1$  ns.
- The large detection area of mcp's give the mass spectrometer a large acceptance range.
- Only a few channels out of thousands are effected by the detection of a single ion, as a result mcp's can detect many ions at the same time.



From <http://hea-www.harvard.edu/HRC/mcp/mcp.html>

## Data output, storage and retrieval

- **SDMS (scientific data management software) systems addressing the workflow and storage to reduce the data mining process**
- The **first question** in any data scenario must address;  
**What does the customer intend to do with the data they collect?**
- High-resolution, mass-accurate data can generate about 1GB/h. After 180 days of operation, five mass spectrometers, each producing 24 of data per day, will present you with a need to store, retrieve, sort, and otherwise make sense of 21.6 terabytes (TB).

To ensure that the ions travel freely from the ionization region to the detector we need sufficient vacuum.

There are three main pump systems that are being used with Mass spectrometers:

- Turbo-molecular pumps (high vacuum pumps)
- Oil-diffusion pumps (high vacuum pumps)
- Rotary-Vane pumps (fore-vacuum pumps)

Other pumps are:

- Dry scroll pumps (gaining in popularity)
- Ion pumps (very high vacuum)

# Fundamentals Important Performance Factors

## **Resolution:**

How Well Separated Are Peaks from Each Other?

**Resolving power** (or the ability of a mass spec to separate two masses) often called 'res' for short

Low res = unit mass = 1

Higher or moderate res = 1000 to 10,000

High res 10,000+

(up to millions with FTICR or Magnetic sector systems)

## **Sensitivity:**

How Small an Amount Can be Analyzed?

## **Accuracy:**

How can we compare precision among instruments - millimass units (mmu), measurement error (ppm)

# Fundamentals Resolution and Mass Accuracy

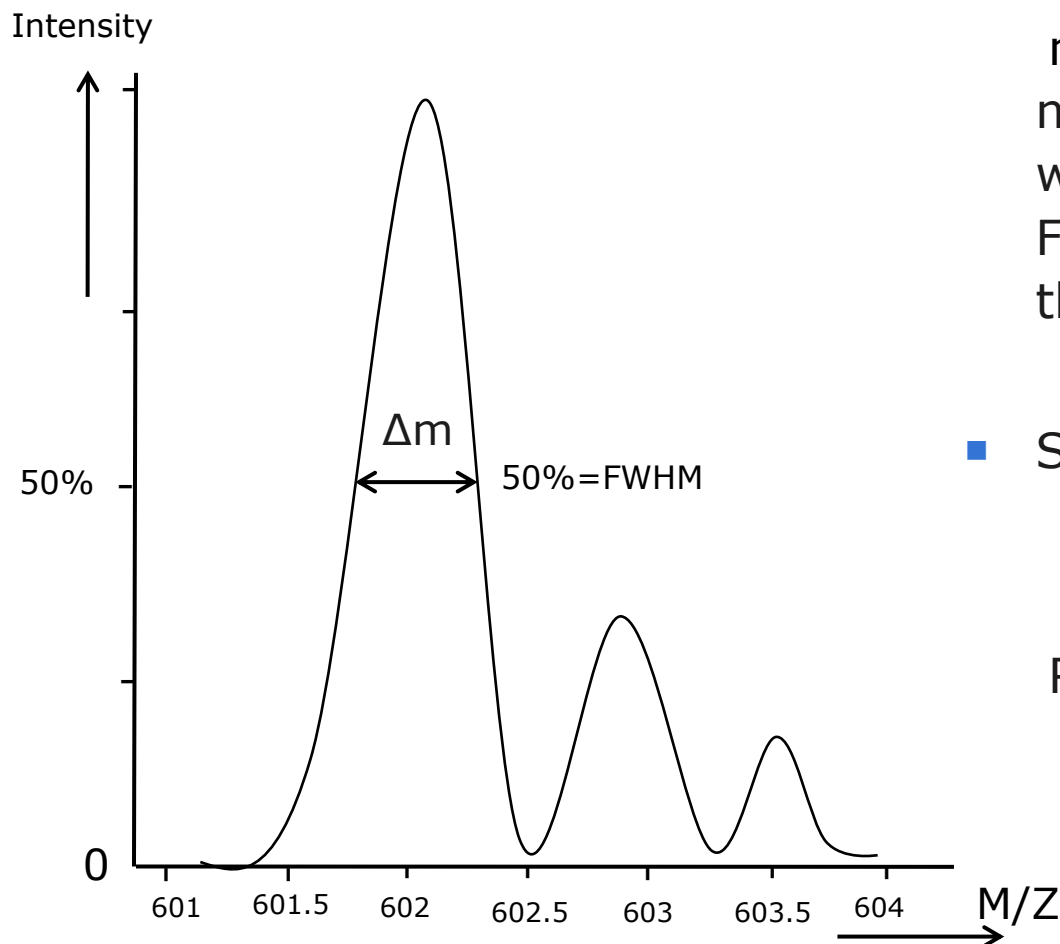
- High mass resolution is generally considered a significant criterion for achieving good mass accuracy.
- High resolution is used to eliminate chemical interferences and is not otherwise required for achieving good mass accuracy.
- Accurate mass measurements can be achieved in the 5 ppm range even at low resolution if interferences are not present. However, a sufficient amount of data points must be collected.
- Without high mass spectral resolution, the ability to discern the presence of an interference is greatly reduced.



# Fundamentals

## Defining Resolution (FWHM)

### Full Width Half Maximum (FWHM)



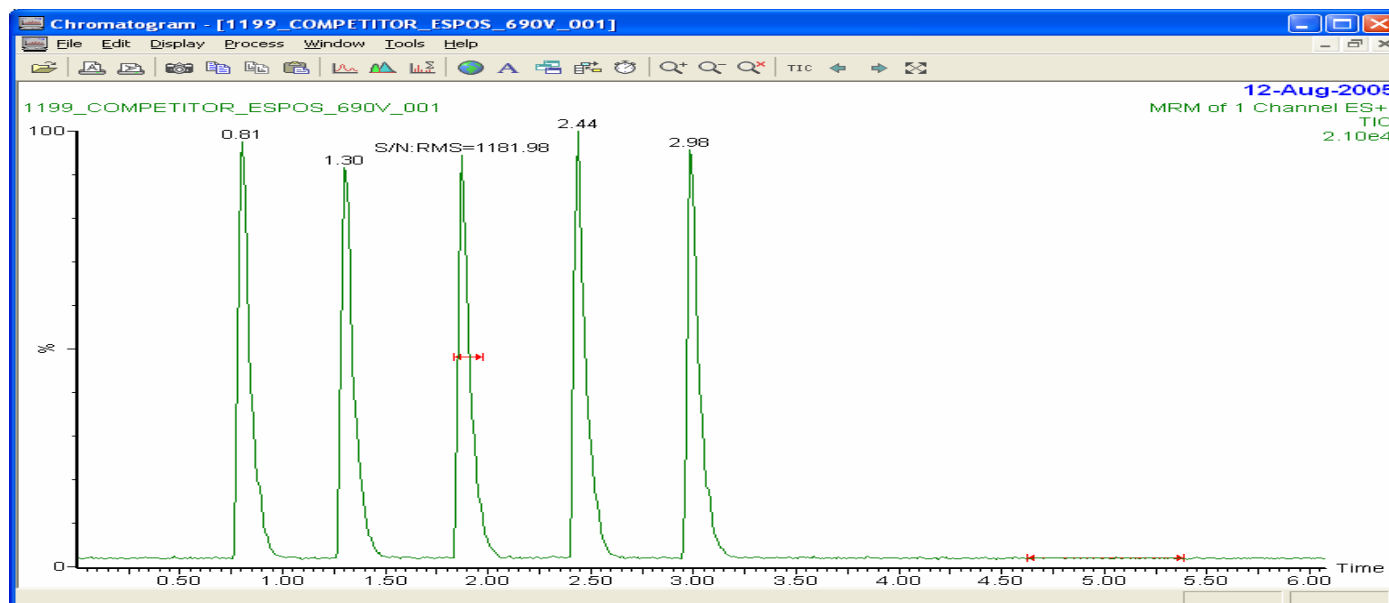
- The resolution is calculated by  $m / \Delta m$ , where  $m$  is the exact mass (centroid) and  $\Delta m$  is the width of the peak at (FWHM = Full width at half mass) 50% of the peak height and full width.

- So in this case  $m = 602$   
 $\Delta m = 0.6$

$$\text{Resolution} = \frac{602}{0.6} = 1003$$

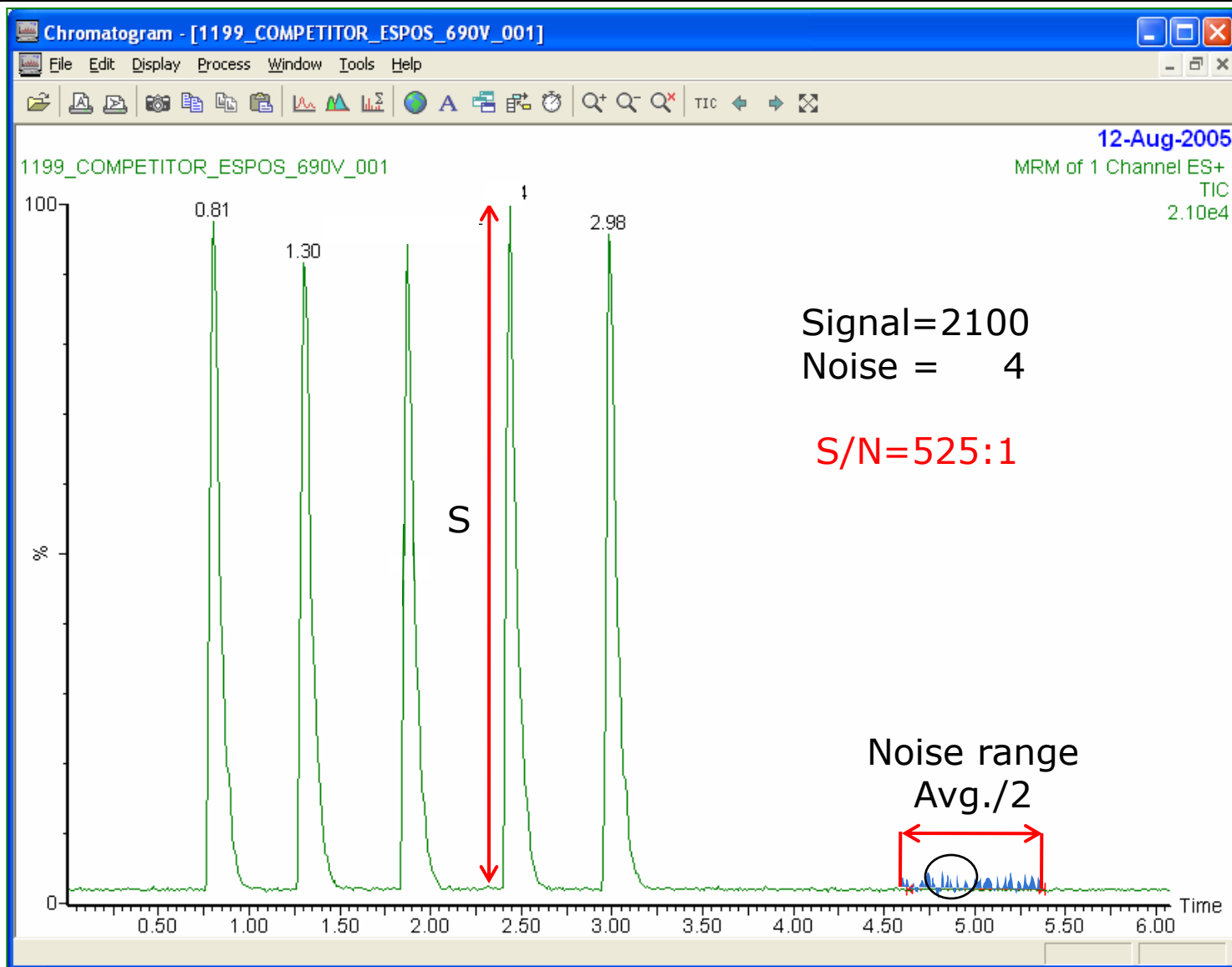
# Fundamentals Sensitivity

- Sensitivity can be measured by the total intensity of a peak and the average noise in a range close to that chromatographic peak.
- This is called the Signal to Noise ratio S/N



# Fundamentals Sensitivity

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# Fundamentals Accuracy Terminology

## **Nominal** (or unit mass)

Sulphamethazine [C<sub>12</sub>H<sub>14</sub>N<sub>4</sub>O<sub>2</sub>S]

**Nominal = 278**

**Average mass** is calculated using all the isotopes of each element and their natural abundance.

Sulphamethazine [C<sub>12</sub>H<sub>14</sub>N<sub>4</sub>O<sub>2</sub>S]

**avg. mass = 278.3313**

**Calculated exact mass** (monoisotopic) is determined by summing the masses of the individual isotopes for a given ion.

Sulphamethazine [C<sub>12</sub>H<sub>14</sub>N<sub>4</sub>O<sub>2</sub>S]

**exact mass = 278.0837**

**Accurate mass** (really “measured accurate mass”) is what we do with our instruments. It is the measure of an m/z reported to (typically) four decimal places.

Sulphamethazine [C<sub>12</sub>H<sub>14</sub>N<sub>4</sub>O<sub>2</sub>S]

**accurate mass = 278.0837**

# Fundamentals

## Mass Measurement Accuracy

- The accuracy of the measurement is quoted as the **difference** (error) between the **measured** (Accurate)**mass** and the **calculated** (Monoisotopic)**mass**
- The accuracy is measured in
  - milliDaltons (1mDa = 0.001 mass units)
  - ppm = parts per million =  $\Delta m/m \times 10^6$
- The Theoretical Error Calculation:
  - $Dm = m_{\text{theoretical}} - m_{\text{measured}}$
  - ppm Error =  $Dm / m_{\text{theoretical}} \times 10^6$

# Fundamentals

## Mass Measurement Accuracy

### Example:

Nominal or "True" mass = 400.0000

Measured mass = 400.0020

Difference = 0.0020

$$\text{ppm error} = \frac{0.002}{400} \times 10^6 = 5\text{ppm}$$

So in this case for a mass of 400 with a mass difference of 0.002  
the accuracy is **5 ppm**



# Fundamentals

## The periodic table

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1 H																	2 He																		
3 Li	4 Be																	5 B	6 C	7 N	8 O	9 F	10 Ne												
11 Na	12 Mg																	13 Al	14 Si	15 P	16 S	17 Cl	18 Ar												
19 K	20 Ca	21 Sc	22 Ti	23 V	24 Cr	25 Mn	26 Fe	27 Co	28 Ni	29 Cu	30 Zn							31 Ga	32 Ge	33 As	34 Se	35 Br	36 Kr												
37 Rb	38 Sr	39 Y	40 Zr	41 Nb	42 Mo	43 Tc	44 Ru	45 Rh	46 Pd	47 Ag	48 Cd							49 In	50 Sn	51 Sb	52 Te	53 I	54 Xe												
55 Cs	56 Ba	57 La	72 Hf	73 Ta	74 W	75 Re	76 Os	77 Ir	78 Pt	79 Au	80 Hg							81 Tl	82 Pb	83 Bi	84 Po	85 At	86 Rn												
87 Fr	88 Ra	89 Ac	104 Rf	105 Db	106 Sg	107 Bh	108 Hs	109 Mt	110 Ds	111 Rg																									
																						58 Ce	59 Pr	60 Nd	61 Pm	62 Sm	63 Eu	64 Gd	65 Tb	66 Dy	67 Ho	68 Er	69 Tm	70 Yb	71 Lu
																						90 Th	91 Pa	92 U	93 Np	94 Pu	95 Am	96 Cm	97 Bk	98 Cf	99 Es	100 Fm	101 Md	102 No	103 Lr

- Every element found in nature has unique masses
- Elements are combined to produce compounds with distinct masses and physical properties
- Compounds can be detected by mass spectrometry and thus their masses measured

# Fundamentals

## Nominal mass measurements

- **C** (carbon) has a nominal mass of **12**
  - **H** (hydrogen) has a nominal mass of **1**
  - **O** (oxygen) has a nominal mass of **16**
  - **N** (nitrogen) has a nominal mass of **14**
- Quadrupole and Ion trap instruments are Nominal mass systems
    - This means that they are unable to distinguish between the elemental combinations of atoms which have the same nominal mass

**CO** , **N<sub>2</sub>** and **C<sub>2</sub>H<sub>4</sub>** all have a nominal mass of **28**

# Fundamentals

## Exact mass measurement

- When we look at the same compounds we see that for example Oxygen is not 16 as a nominal measurement may tell us but an exact mass of  $m/z$  15.9949
- Only exact mass measurement instruments like ToF's, FT- ICR, Magnetic sector and Orbitrap's are able to distinguish between elemental combinations
  - C (carbon) has a exact mass of **12.0000**
  - H (hydrogen) has a exact mass of **1.0078**
  - O (oxygen) has a exact mass of **15.9949**
  - N (nitrogen) has a exact mass of **14.0031**

*The real masses of Atoms are not whole numbers (except Carbon "12")*

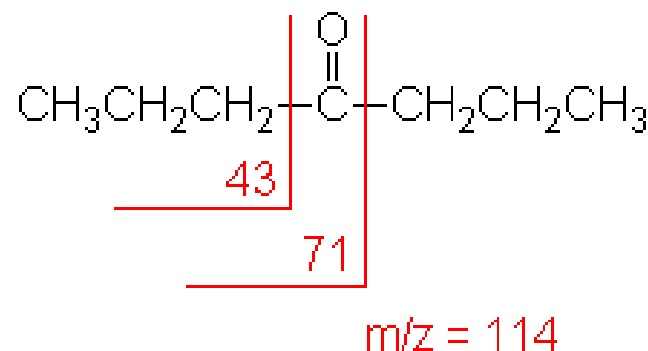
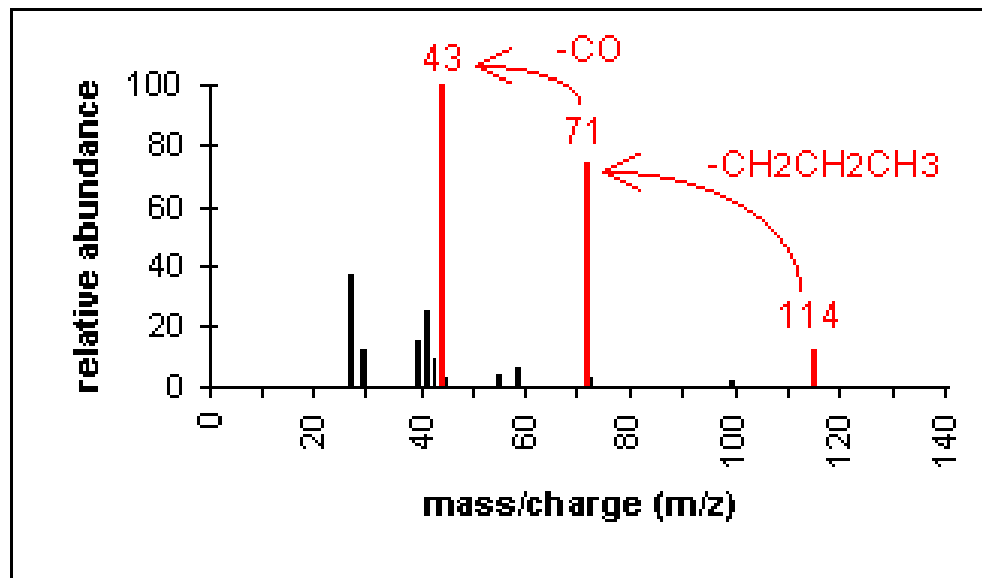
# Fundamentals

## They are no longer all mass 28!

- **CO** = 27.9949 (toxic substance)
  - **N<sub>2</sub>** = 28.0061 (80% of our atmosphere)
  - **C<sub>2</sub>H<sub>4</sub>** = 28.0313 (Flammable substance)
- 
- These elemental combinations CO , N<sub>2</sub> and C<sub>2</sub>H<sub>4</sub> all have a nominal mass of **28** but different exact mass!
  - A nominal mass measurement cannot distinguish these!
  - You need exact mass when you have to be sure!

# Fundamentals Chemical Fingerprints

- Mass spectrometers change neutral molecules into charged “ions”
- We can then measure the mass of these ions
- Fragmentation of these ions gives spectra that can be used as “*Chemical Fingerprints*”



- Mass Spectra are “chemical fingerprints”
- They can be used to identify molecules just like people’s fingerprints can - we use databases or libraries of spectra
- Also, there are rules that relate a molecule’s fingerprint to its structure
  - This is the equivalent of being able to tell a person’s hair colour, height, age, sex, place of birth etc from a fingerprint





# Fundamentals

There are only two things you can do with a mass spectrometer.....

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1. Identify molecules

2. Quantify molecules

# Fundamentals

## But.....One thing is missing!

- Mass Spectrometers are very **bad** at analysing mixtures
  - Imagine 10 pesticides in a mixture
  - All of these get ionised at the same time the spectrum produced is a mixture from all the molecules
    - Almost impossible to identify the components
    - Hard to Quantify
  - All this made harder if the 10 components are in blood, urine, food extract which have can 1000's of other components
- **Bad News** – almost all real world samples are mixtures



# Fundamentals

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That's why MS combined with chromatography is  
such a **powerful tool**.