How to Use TOF and Q-TOF Mass Spectrometers

October 2011

What do TOF and Q-TOF offer?

TOF

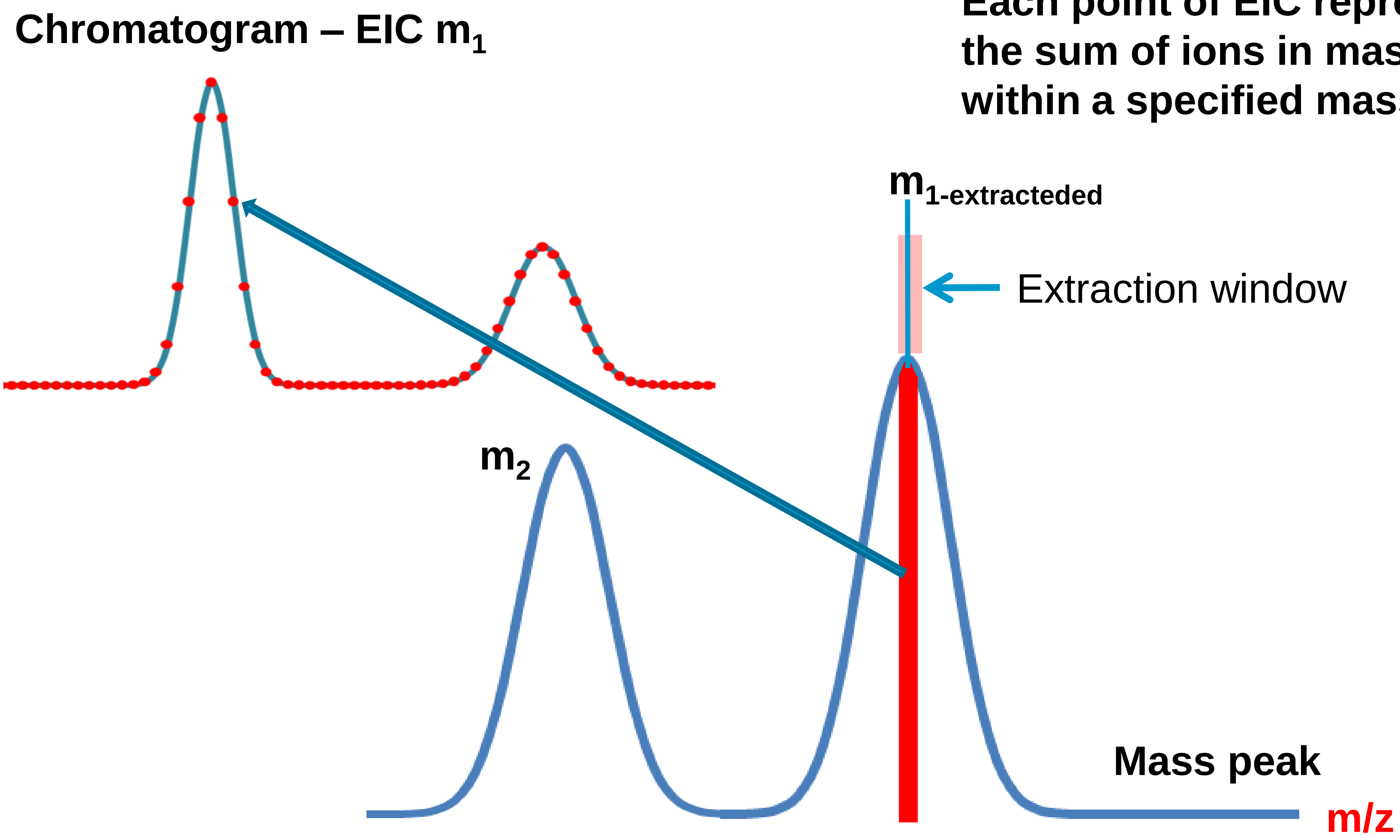
- Fast scanning of full spectrum
- High resolution full scan spectra
- Accurate mass measurements

Q-TOF

- Fast scanning of full spectrum
- High resolution full scan spectra
- Accurate mass measurements
- MS/MS product ion spectra
- Full scan product ion spectra with high resolution and accurate mass

How is accurate mass used?

Extracted ion chromatograms - EIC



Chromatogram – EIC m_1

Each point of EIC represents the sum of ions in mass peak within a specified mass range

$m_{1\text{-extracteded}}$

Extraction window

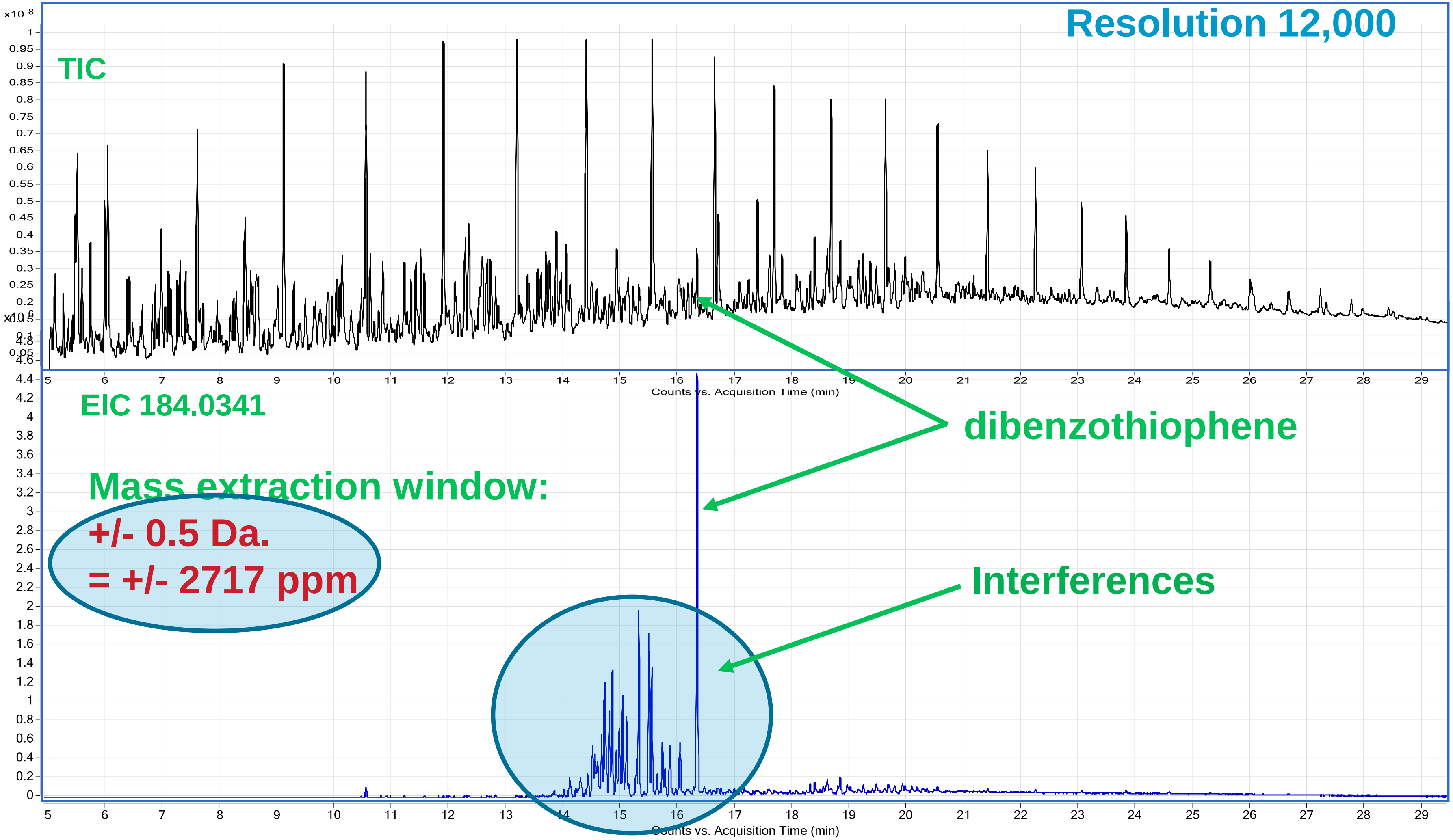
m_2

Mass peak

m/z

Crude oil target analysis – target analysis

Problem: identify and quantify dibenzothiophene



Resolution 12,000

TIC

EIC 184.0341

dibenzothiophene

Mass extraction window:

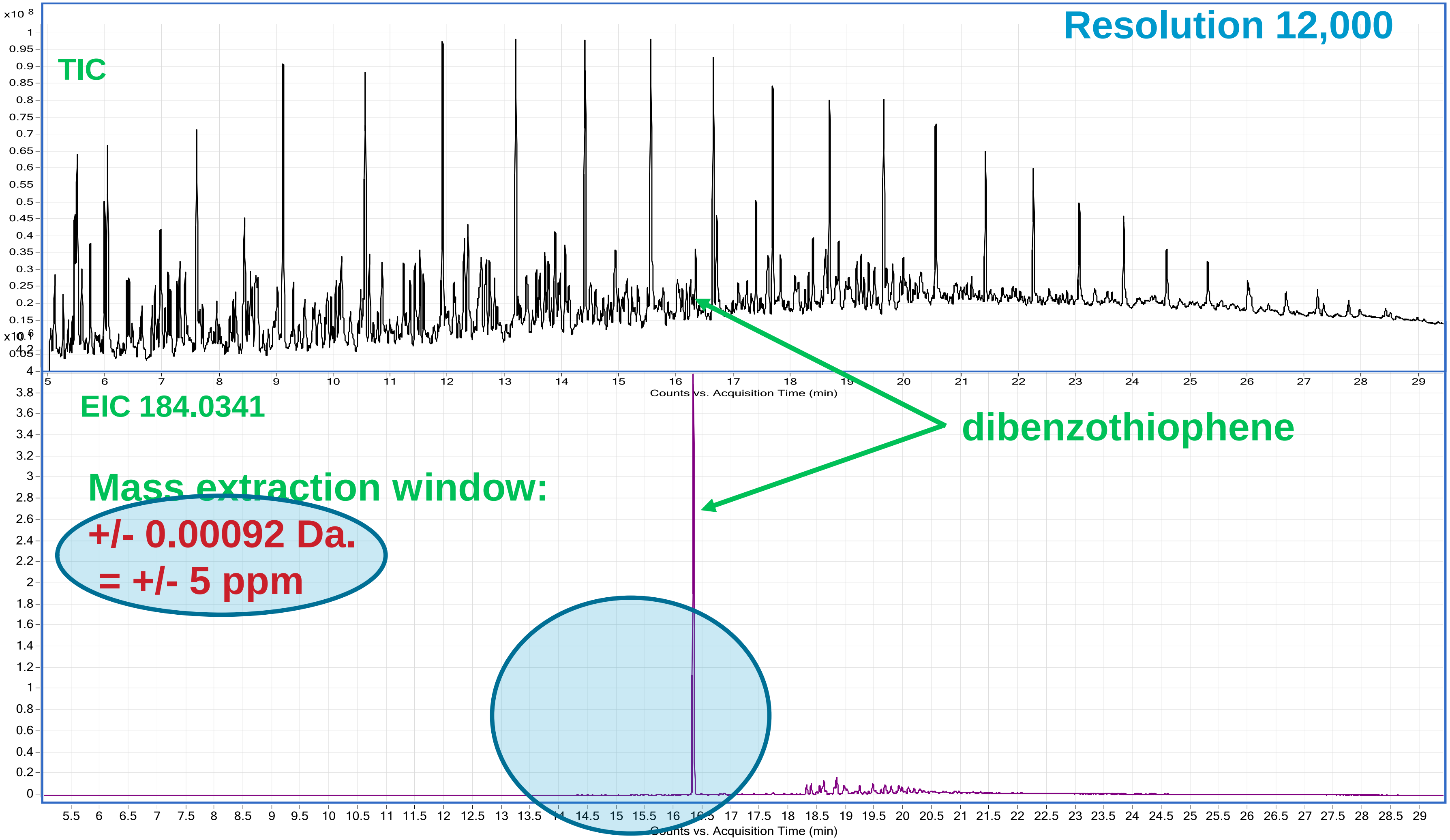
+/- 0.5 Da.

= +/- 2717 ppm

Interferences

Crude oil target analysis – target analysis

Problem: identify and quantify dibenzothiophene



Resolution 12,000

TIC

EIC 184.0341

dibenzothiophene

Mass extraction window:

+/- 0.00092 Da.
= +/- 5 ppm

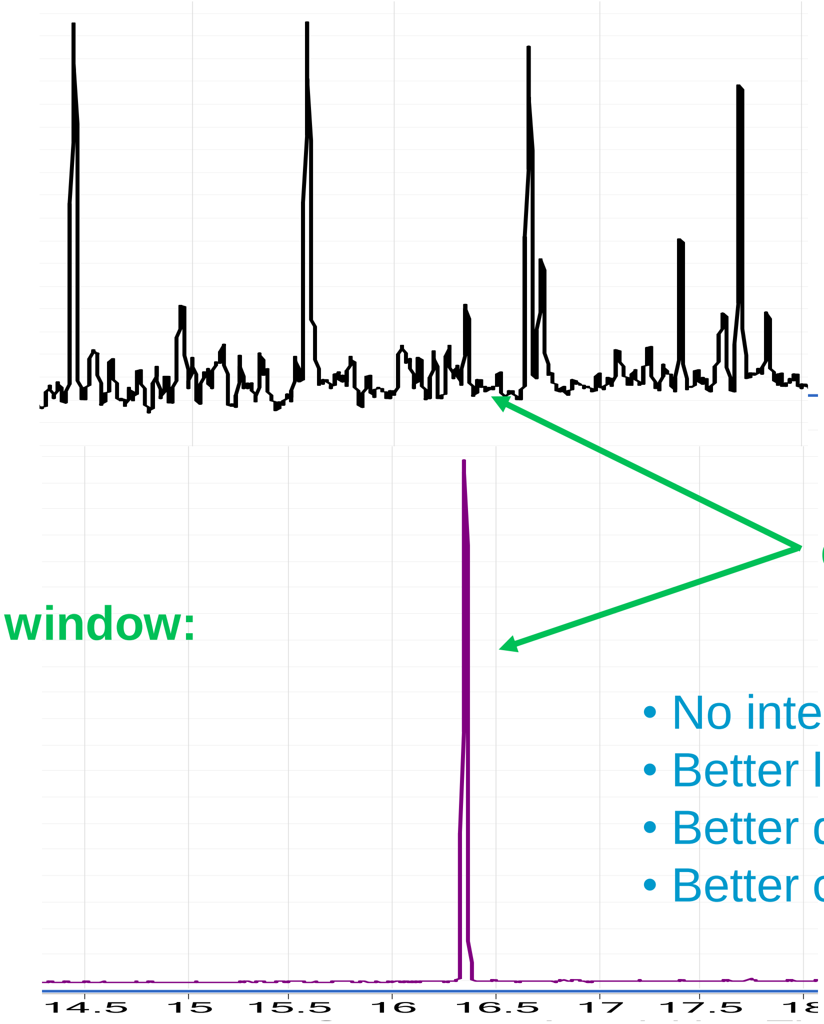
Crude oil target analysis – target analysis

Problem: identify and quantify dibenzothiophene

TIC

EIC 184.0341

Mass extraction window:
+/- 5 ppm



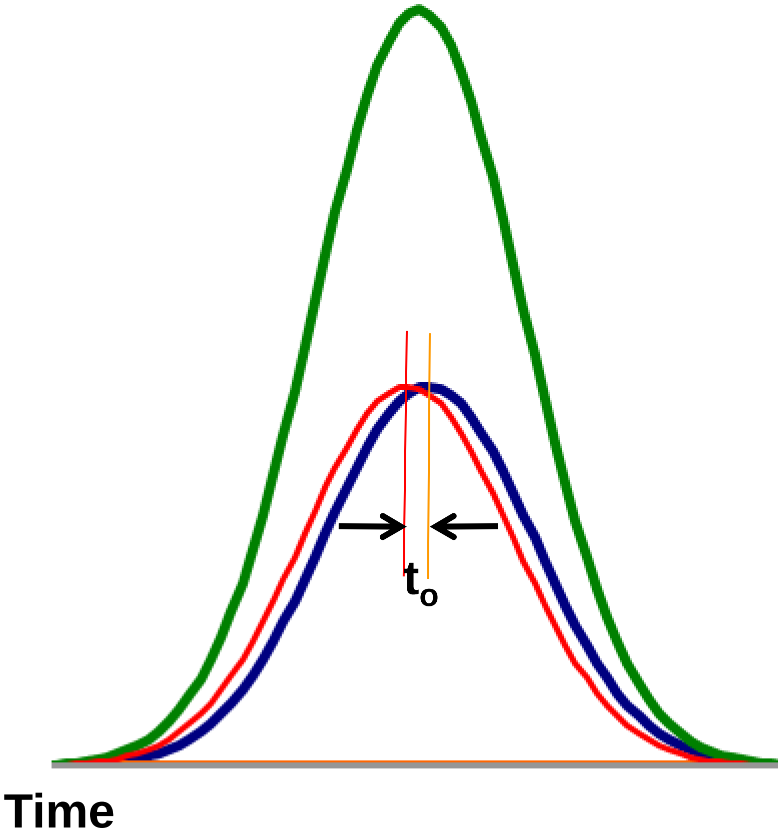
Resolution 12,000

dibenzothiophene

- No interferences
- Better low level peak integration
- Better quantitation
- Better confirmation

Fast scanning of full spectrum

“*Speed*” enhances deconvolution



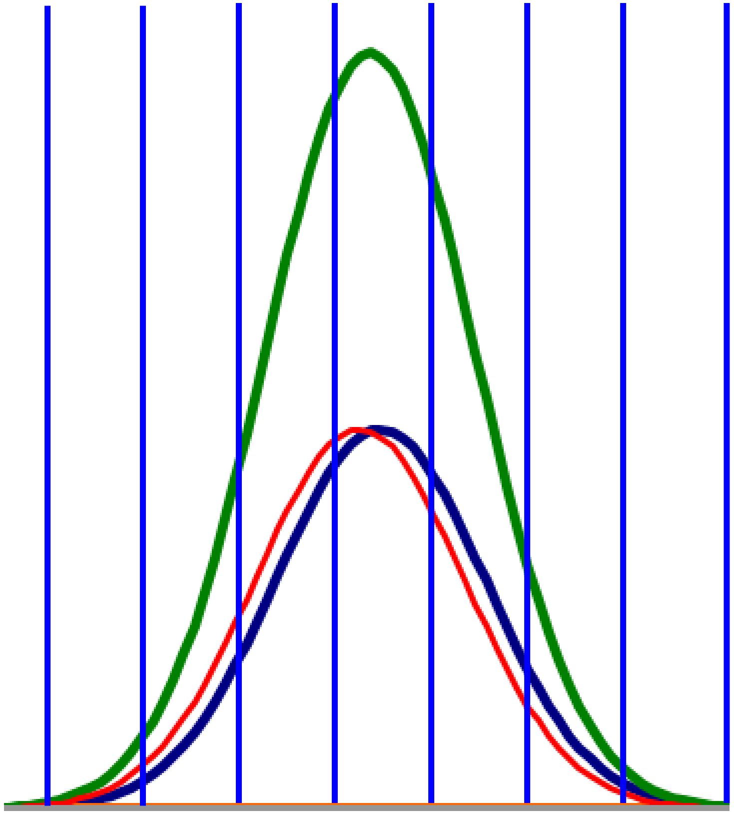
Deconvolution Requires:

- Retention time difference $t_o > (1/10)\ W_{1/2}$
- At least one mass that is different for each component
- Peak sampled $< t_o/2$

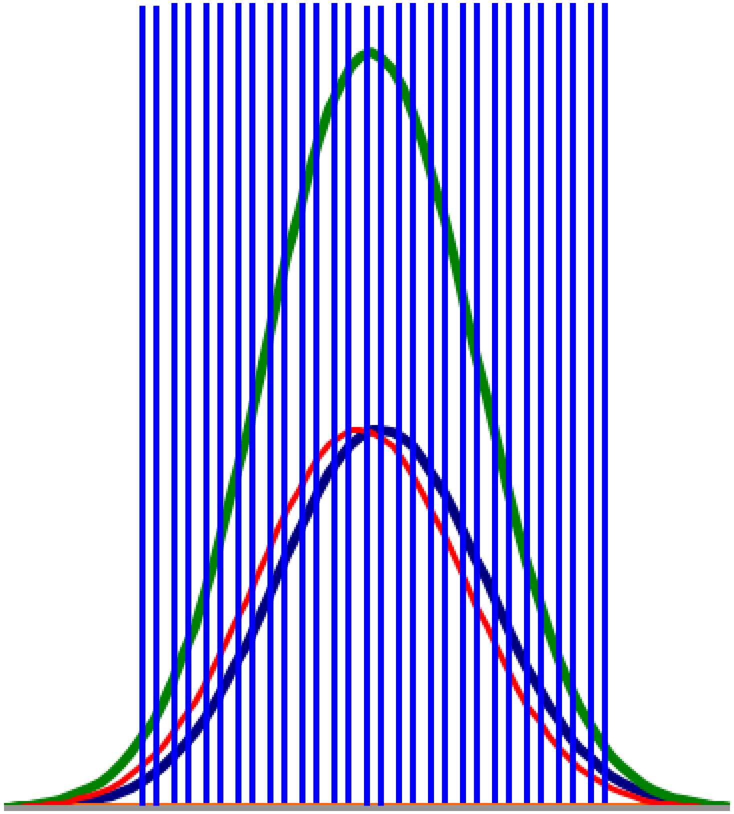
Example:

- $W_{1/2} = 1$ second
- $t_o > 0.1$ second
- Peak sampled < 0.05 second = 20 spectra/second

High data rate = better deconvolution



Slow data rate will not pick each peak apex



Fast data rate will allow deconvolution of closely eluting peaks

High resolution, mass accuracy and scan speed

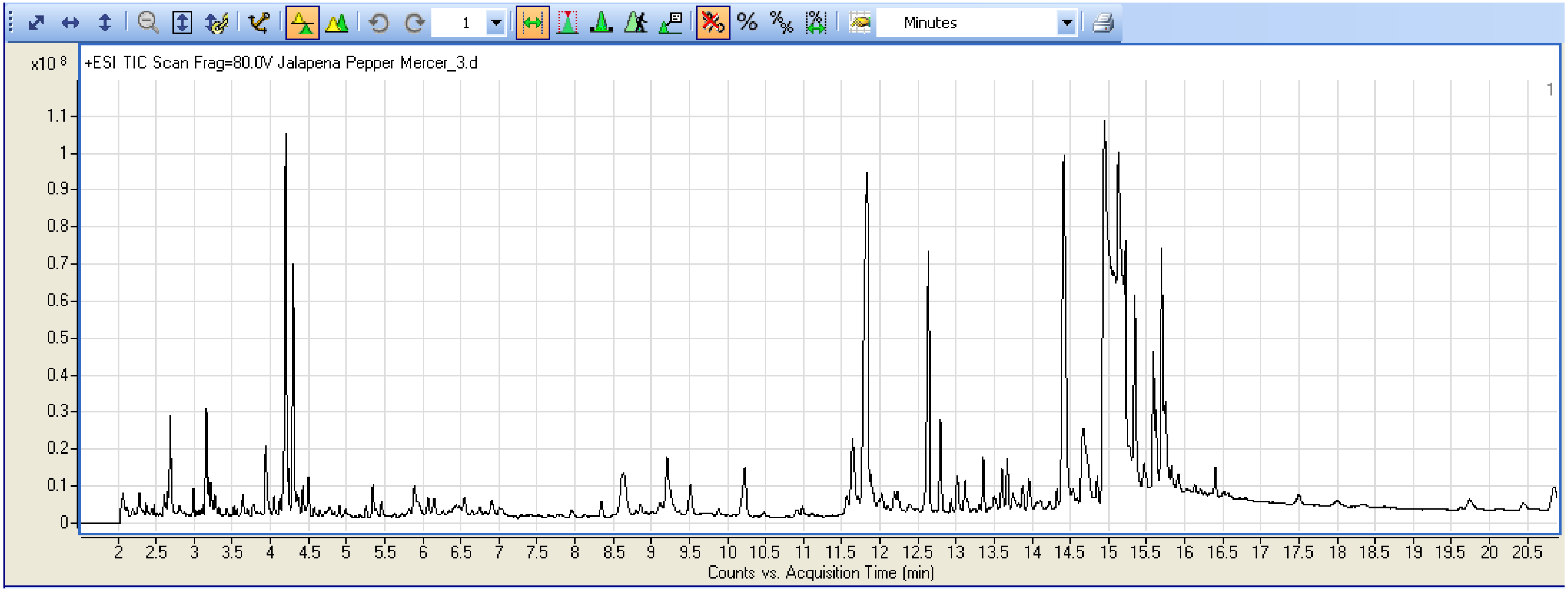
Using factional masses for deconvolution

TOF and Q-TOF

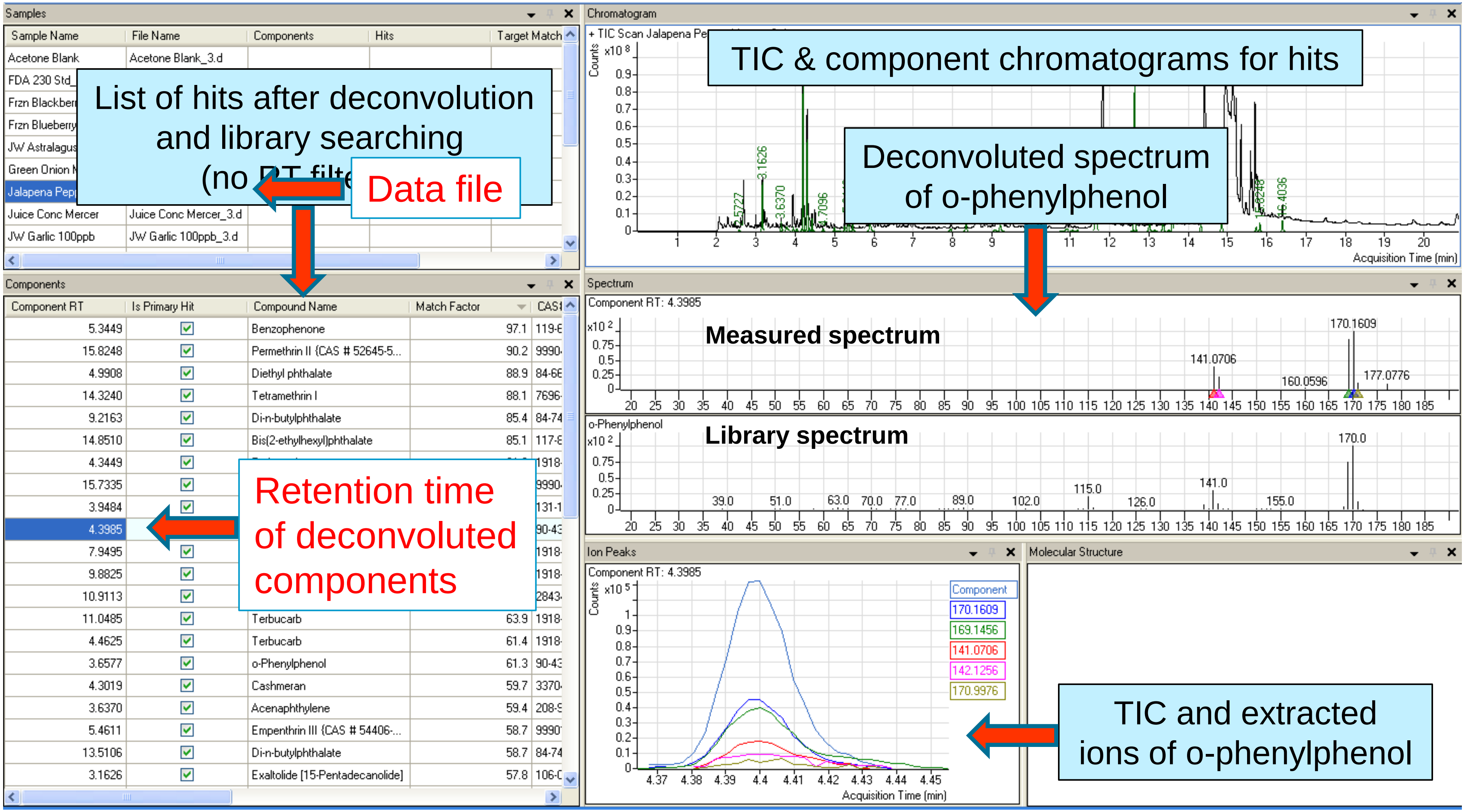
- Fast scan rates >50 spectra/second facilitate deconvolution of peaks with small retention time differences
- Using high mass accuracy spectra with fractional masses rather than integer masses provides:
  - more masses that are distinct between the two co-eluting compounds
  - better deconvolution particularly at low levels
  - better sensitivity

Deconvolution – identify unknown residues

Jalapeno Pepper Extract – GC/TOF Analysis



Unknowns analysis – one page for everything



List of hits after deconvolution and library searching (no RT filte

Data file

Retention time of deconvoluted components

TIC & component chromatograms for hits

Deconvoluted spectrum of o-phenylphenol

Measured spectrum

Library spectrum

TIC and extracted ions of o-phenylphenol

Samples

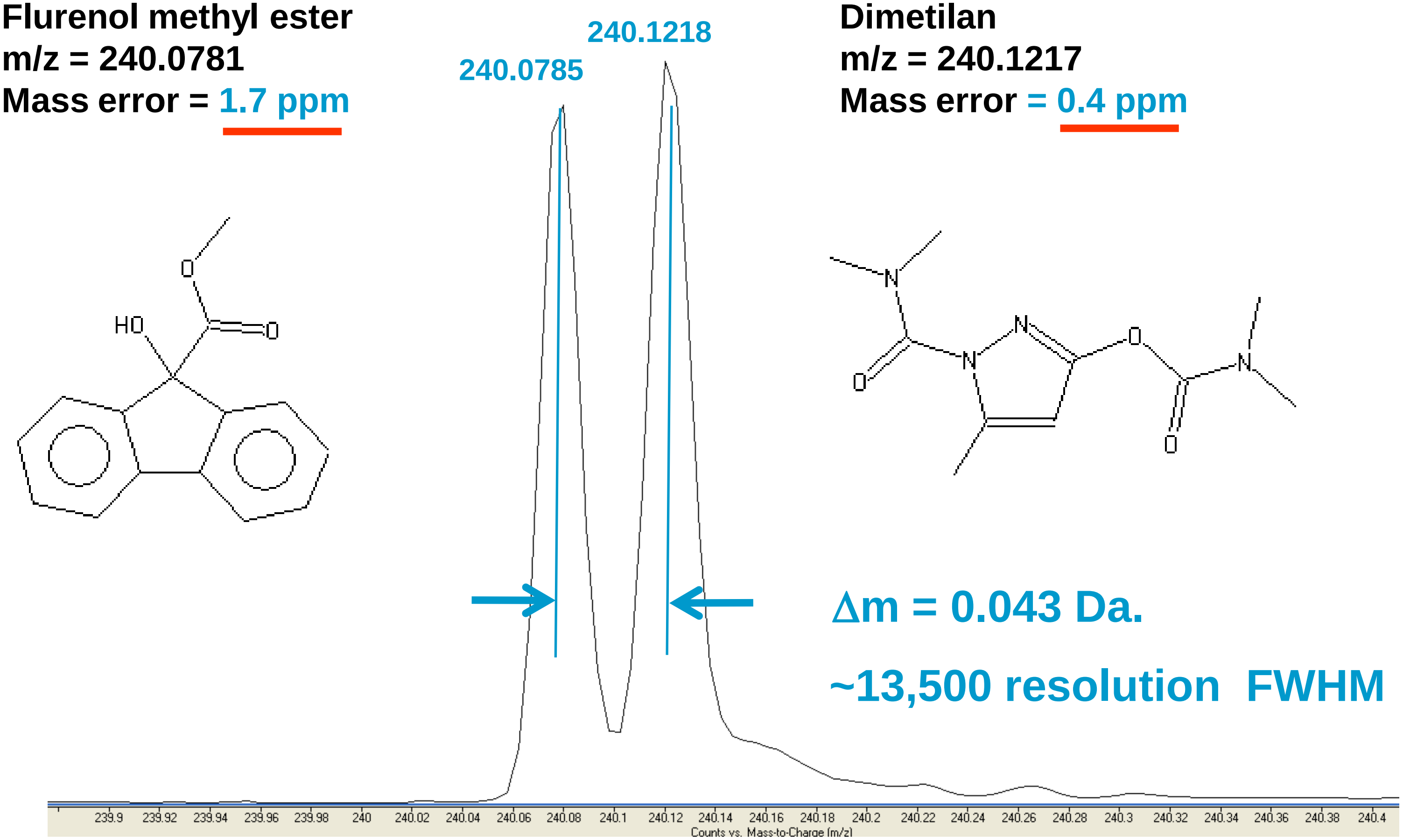
Sample Name	File Name	Components	Hits	Target Match
Acetone Blank	Acetone Blank_3.d			
FDA 230 Std_				
Frzn Blackberr				
Frzn Blueberry				
JW Astralagus				
Green Onion M				
Jalapena Pepp				
Juice Conc Mercer	Juice Conc Mercer_3.d			
JW Garlic 100ppb	JW Garlic 100ppb_3.d			

Components

Component RT	Is Primary Hit	Compound Name	Match Factor	CAS
5.3449	☑	Benzophenone	97.1	119-6
15.8248	☑	Permethrin II {CAS # 52645-5...	90.2	9990
4.9908	☑	Diethyl phthalate	88.9	84-66
14.3240	☑	Tetramethrin I	88.1	7696
9.2163	☑	Di-n-butylphthalate	85.4	84-74
14.8510	☑	Bis(2-ethylhexyl)phthalate	85.1	117-8
4.3449	☑			1918
15.7335	☑			9990
3.9484	☑			131-1
4.3985				90-43
7.9495	☑			1918
9.8825	☑			1918
10.9113	☑			2843
11.0485	☑	Terbucarb	63.9	1918
4.4625	☑	Terbucarb	61.4	1918
3.6577	☑	o-Phenylphenol	61.3	90-43
4.3019	☑	Cashmeran	59.7	3370
3.6370	☑	Acenaphthylene	59.4	208-9
5.4611	☑	Empenthrin III {CAS # 54406-...	58.7	9990
13.5106	☑	Di-n-butylphthalate	58.7	84-74
3.1626	☑	Exaltolide [15-Pentadecanolide]	57.8	106-0

How much resolution is enough?

Relative abundance of co-eluting compounds affects the result



Flurenol methyl ester
m/z = 240.0781
Mass error = 1.7 ppm

Dimetilan
m/z = 240.1217
Mass error = 0.4 ppm

240.0785

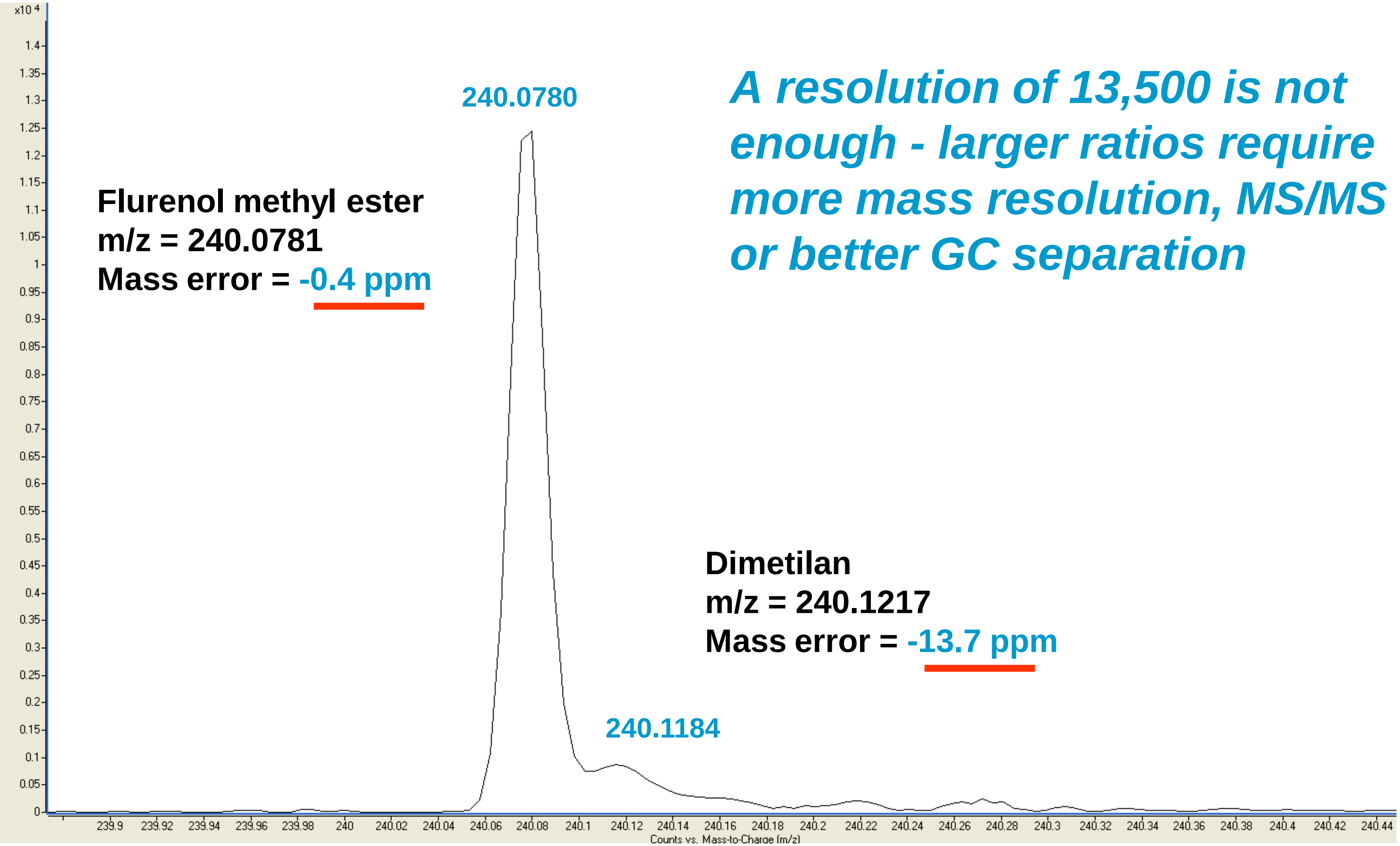
240.1218

Δm = 0.043 Da.

~13,500 resolution FWHM

How much resolution is enough?

Abundance Ratio - flurenol methyl ester:Dimetilan = 10:1



Flurenol methyl ester
m/z = 240.0781
Mass error = -0.4 ppm

A resolution of 13,500 is not enough - larger ratios require more mass resolution, MS/MS or better GC separation

Dimetilan
m/z = 240.1217
Mass error = -13.7 ppm

What occurs when the measured mass shifts

- Large shifts in measured mass reduces value for confirmation – necessitates larger extraction windows

- Large shifts in measured mass changes EIC as peak elutes because the ratio of analyte to matrix changes and therefore the mass shift changes

What to do when you run out of resolution?

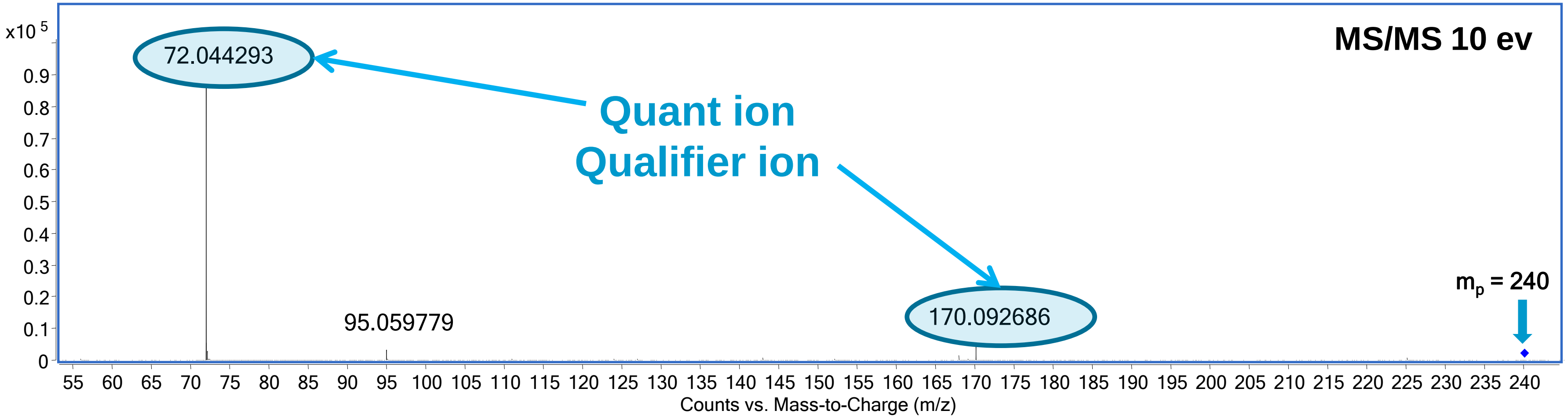
Use MS/MS

- MS/MS product ions are generally well separated in mass
- Therefore - product ion masses do not shift due to lack of resolution
- Why use Q-TOF rather than triple quadrupole?
  - Sometimes qualifier ions have low abundance
  - Accurate mass measurement of quantitation ion offers more confirmatory information than using a low abundance qualifier ion

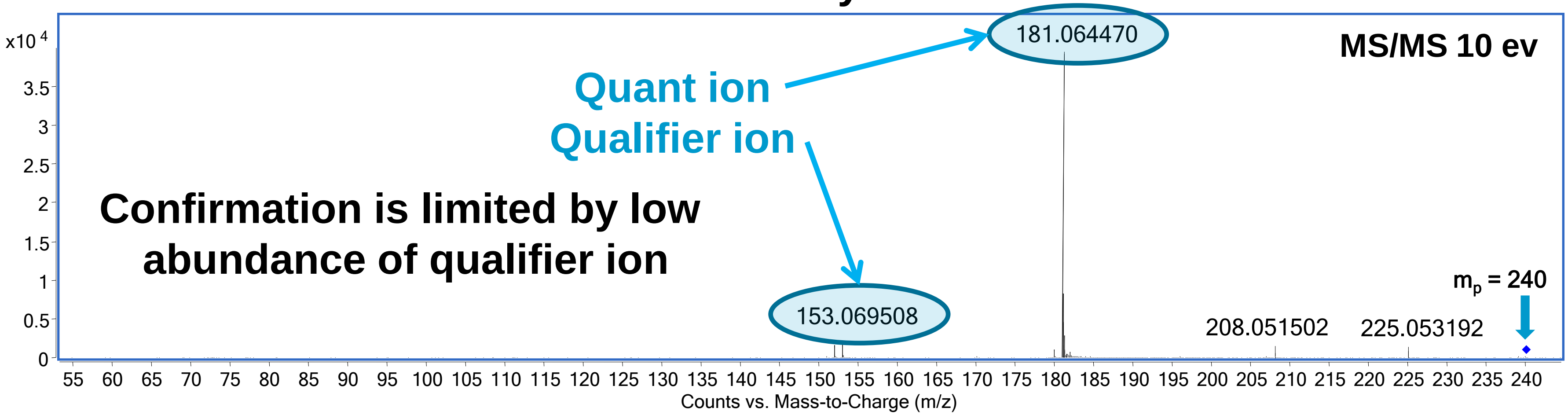
What to do when you run out of resolution?

Use MS/MS

Dimetilan



Flurenol methyl ester

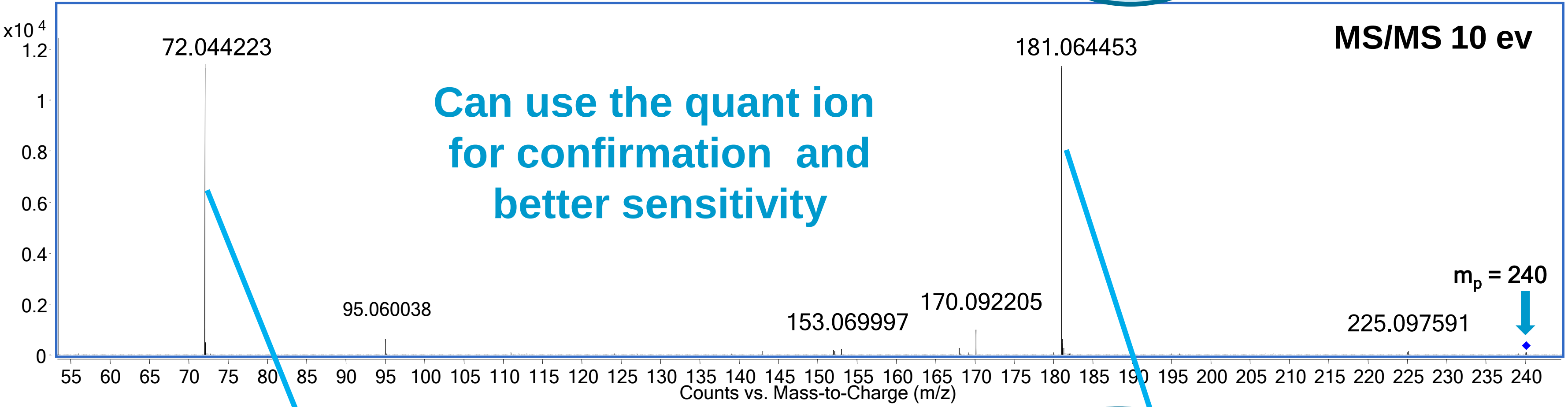


Confirmation is limited by low abundance of qualifier ion

What to do when you run out of resolution?

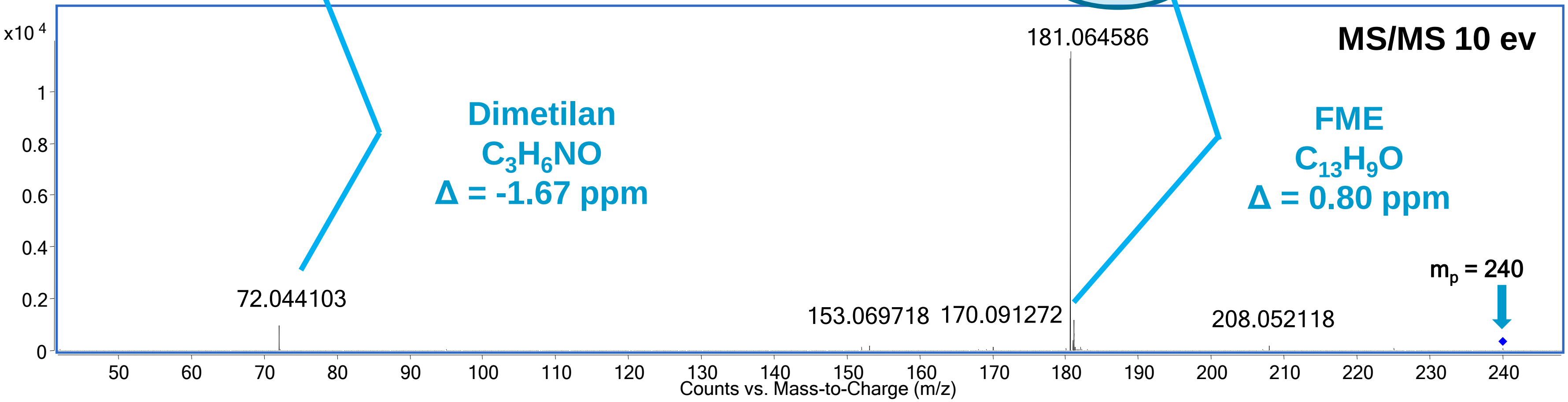
Use MS/MS

Flurenol methyl ester + Dimetilan 1:1



Can use the quant ion for confirmation and better sensitivity

Flurenol methyl ester +Dimetilan 10:1

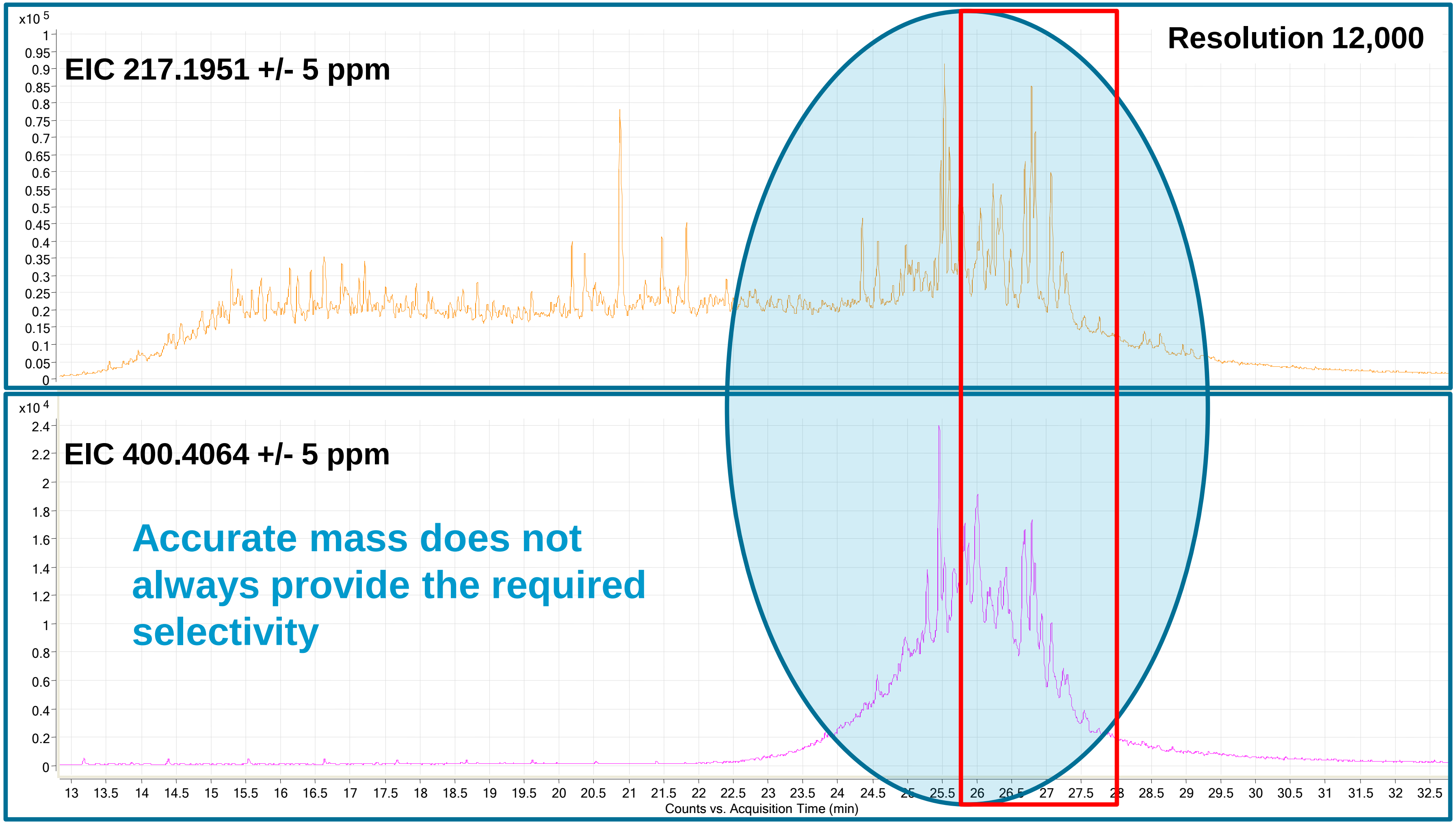


Dimetilan
C_3H_6NO
Δ = -1.67 ppm

FME
$C_{13}H_9O$
Δ = 0.80 ppm

Crude oil: steranes – MS

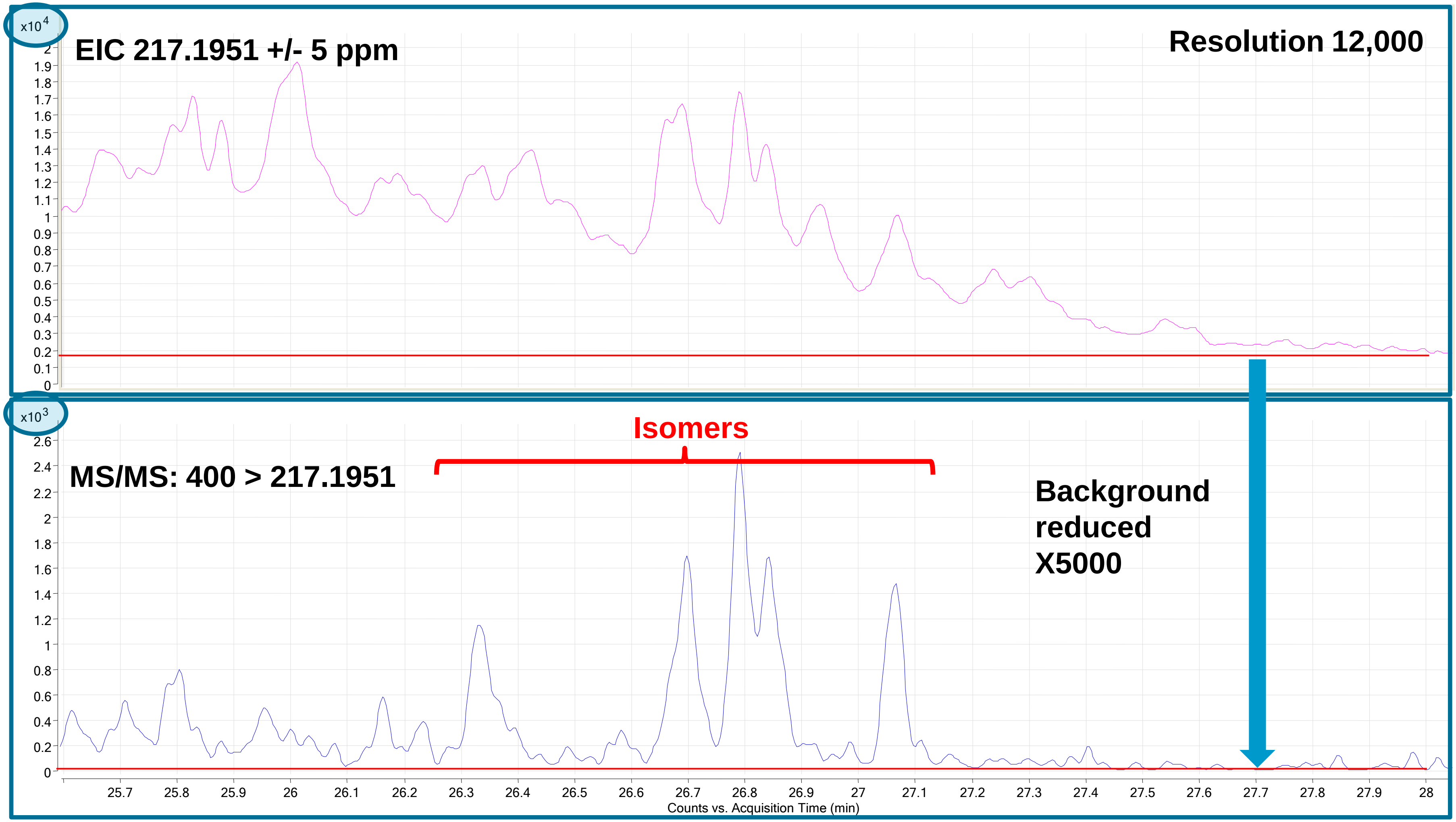
Problem: identify and quantify isomers



Accurate mass does not always provide the required selectivity

Crude oil: steranes – MS/MS

Problem: identify and quantify isomers



EIC 217.1951 +/- 5 ppm

Resolution 12,000

Isomers

MS/MS: 400 > 217.1951

Background reduced X5000

MS/MS accurate mass EIC

10 pg sample – resolution 13,000

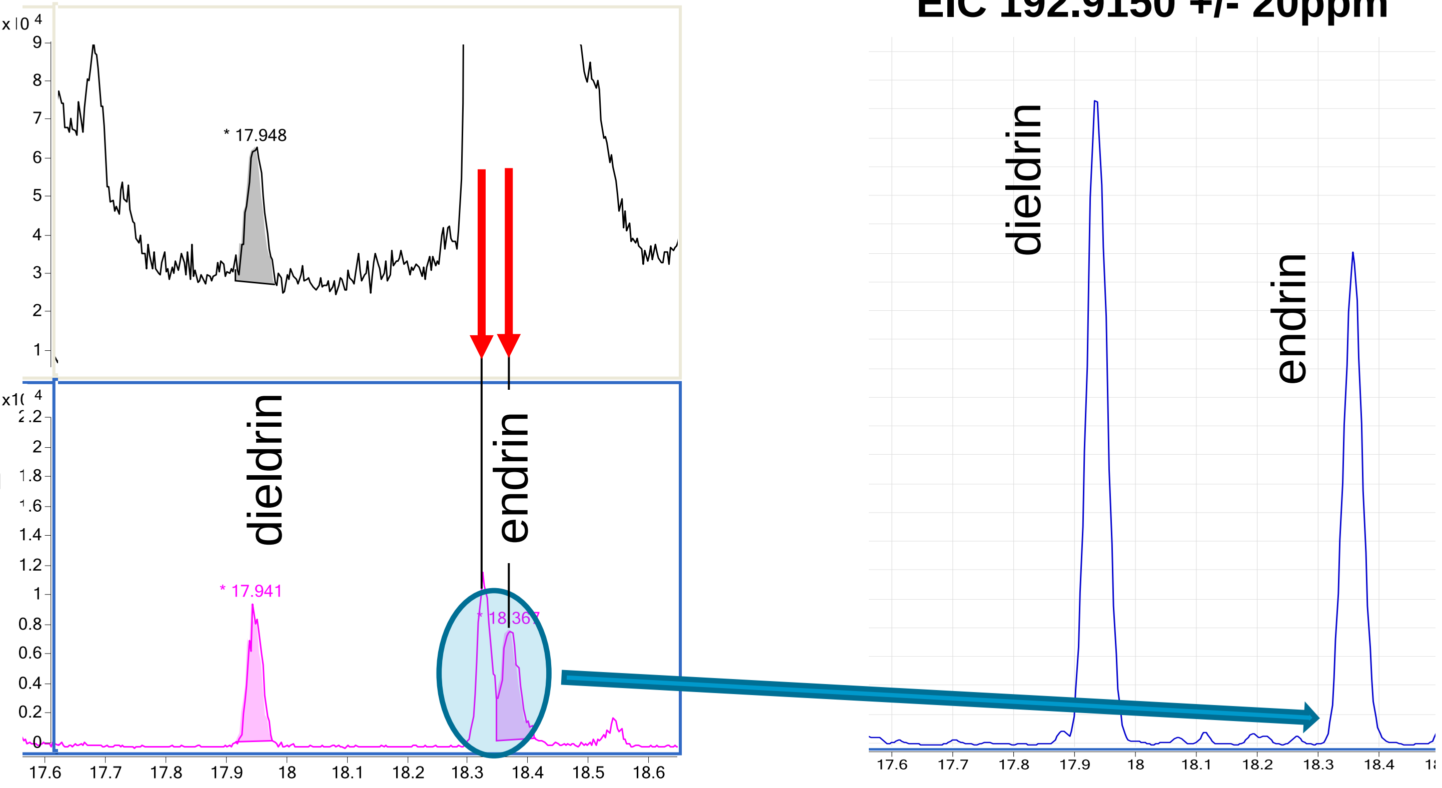
Full scan MS
High resolution/accurate mass

MS/MS 263>192.9150
High resolution/accurate mass

EIC 192.9150 +/- 20ppm

EIC
262.8564 ±0.5 Da.

EIC
262.8564 ±20 ppm



Resolution and accurate mass are insufficient – MS/MS solves the problem

Summary

- The resolution and mass accuracy available from a TOF instrument can solve many analytical problems
- For some analyte and matrix combinations there is not enough mass resolution to confirm and quantify over the required analyte/matrix concentration range
- Q-TOF MS/MS provides constant measured product ion mass values over a larger analyte concentration range than TOF alone when there is not enough resolution

Thank you for your attention