

EMDB

Javascript library for mass spectra analysis

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Not Secure www.chemcalc.org

ChemCalc





Institute of chemical sciences and engineering ISIC

Welcome to ChemCalc

Peptides

Molecular Formula finder

Web service

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Your Molecular Formula

HA1a1000H

List of allowed groups

FWHM : 0.001

Resolution: 7121722

Apply Gaussian: ☐

Submit

Reference version: 2013

FWHM = ΔM
(Peak Full Width at Half-Maximum)

Resolution = $M / \Delta M$

HA1a1000H

MF: C300H502N100O101

MW: 7125.817246

EM: 7121.72194

Unsat.: 100

Element	Count	Percent
C	300	50.566%
H	502	7.101%
N	100	19.656%
O	101	22.677%

Welcome to ChemCalc

If you are using our tools please don't forget to cite us:

ChemCalc: a building block for tomorrow's chemical infrastructure. Patiny, Luc; Borel, Alain
Journal of Chemical Information and Modeling 2013. DOI: 10.1021/ci300563h

Cheat poster: Get HELP on how to use chemcalc !

What would you like to do ?

- Calculate molecular formula, molecular mass / molecular weight, exact mass (monoisotopic mass), elemental analysis and plots the isotopic distribution graph (isotopomers). Just enter a formula in the box on the left. [Check the HELP.](#)
- Find molecular formula from an accurate mass
- Calculate peptide fragmentation
- Integrate the tools in your website

Latest news ...

Tweets by @cheminformatics



Cheminfo

@cheminformatics

Are you teaching structural analysis (mass, IR or NMR) or just would like to make some exercises ? You could try the website we created for our teaching:
cheminfo.org/flavor/structu... (using Google Chrome)

Instructions

In these exercises you should assign each electron in a molecule to a specific orbital. To do this, you should first click on the corresponding molecule in the list below.

YOU SHOULD NOT SELECT OR DISCARD, THEN CLICK ON each line to calculate the spectrum and finally click on the corresponding molecule in the list below.

Click on it to display the 13C NMR spectrum

Orbitals	IR	Mass
1	1617.4	
2	1617.4	

Click on it to display the electronic impact spectrum

Orbitals	IR	Mass
1	1617.4	
2	1617.4	

C₁₀

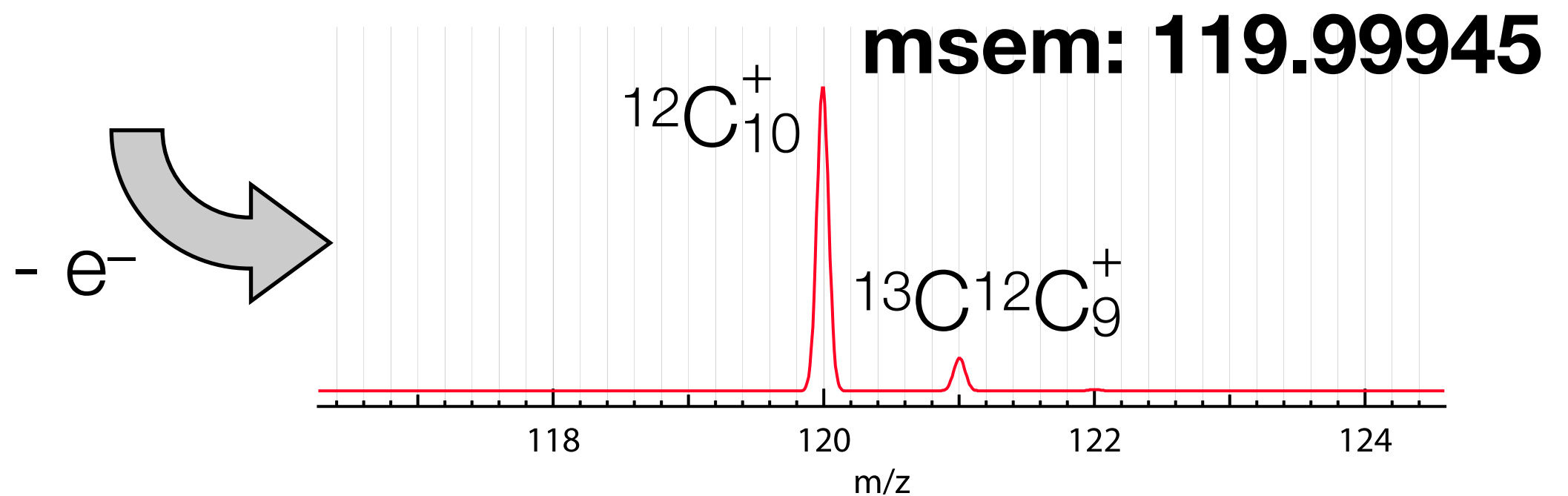
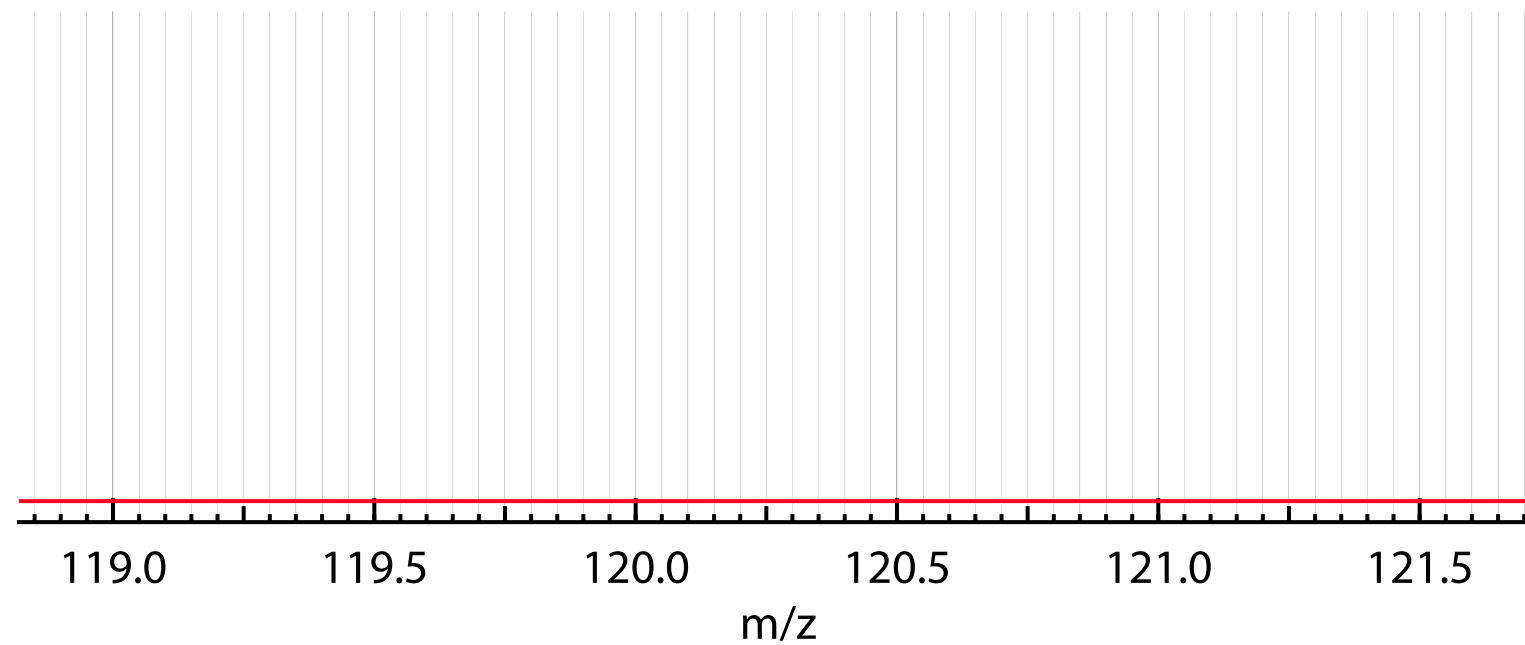
6	C Carbon 12.011	7
14		14

mw: 120.11

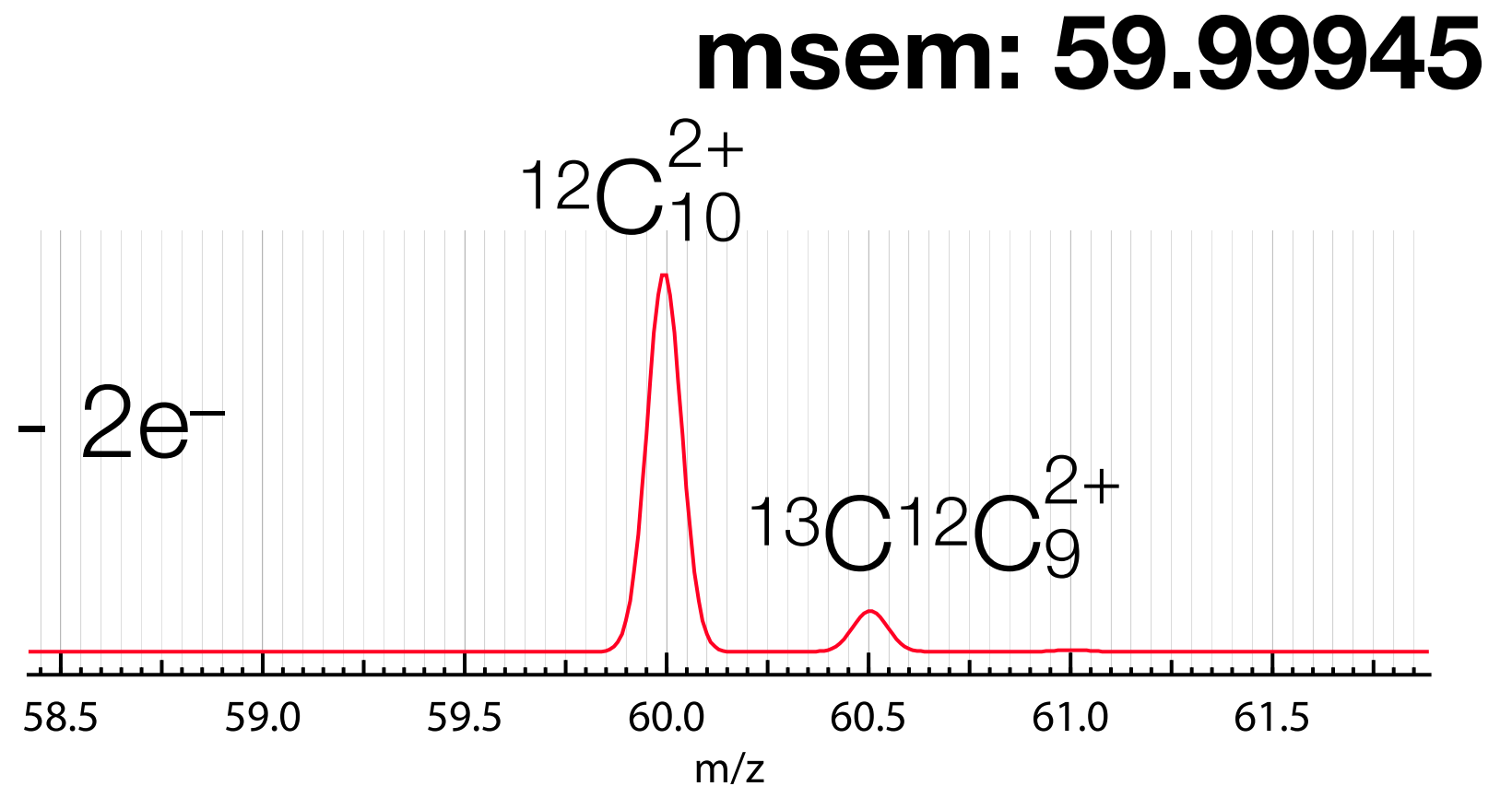
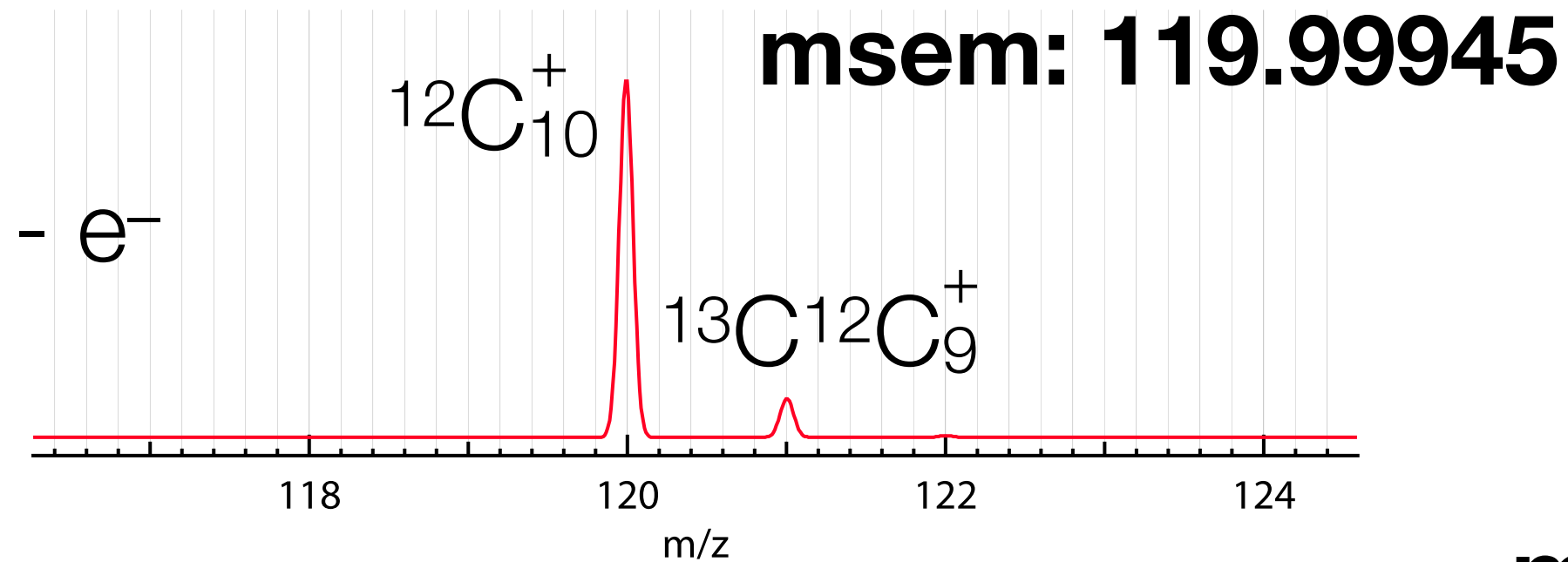
6	C Carbon 12.011	7	N Nitrogen 14.007	8	O Oxygen 15.999
14	Si Silicon 28.086	12	C Carbon-12 12.000	16	S Sulfur 32.065
32	Ge Germanium 72.630	33	As Arsenic 74.922	34	Se Selenium 78.960

em: 120

C_{10} in the spectrometer

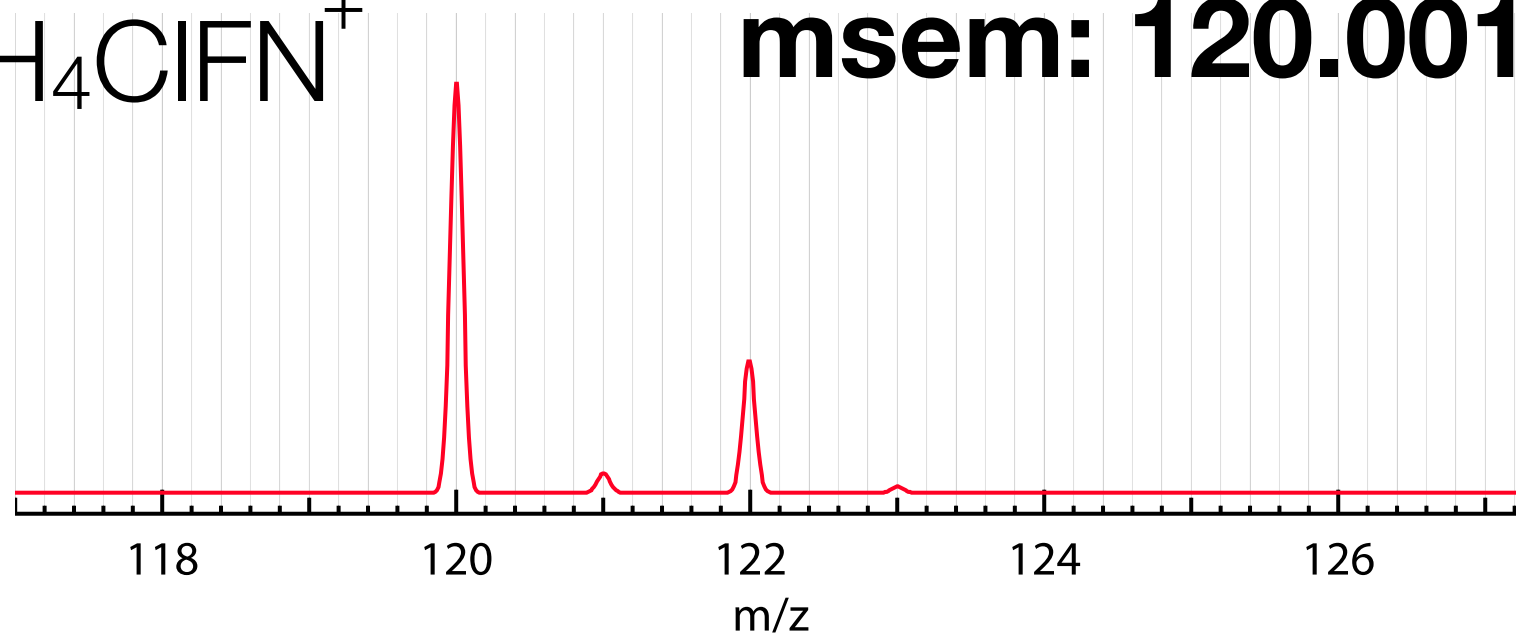


C_{10} and multiple charges

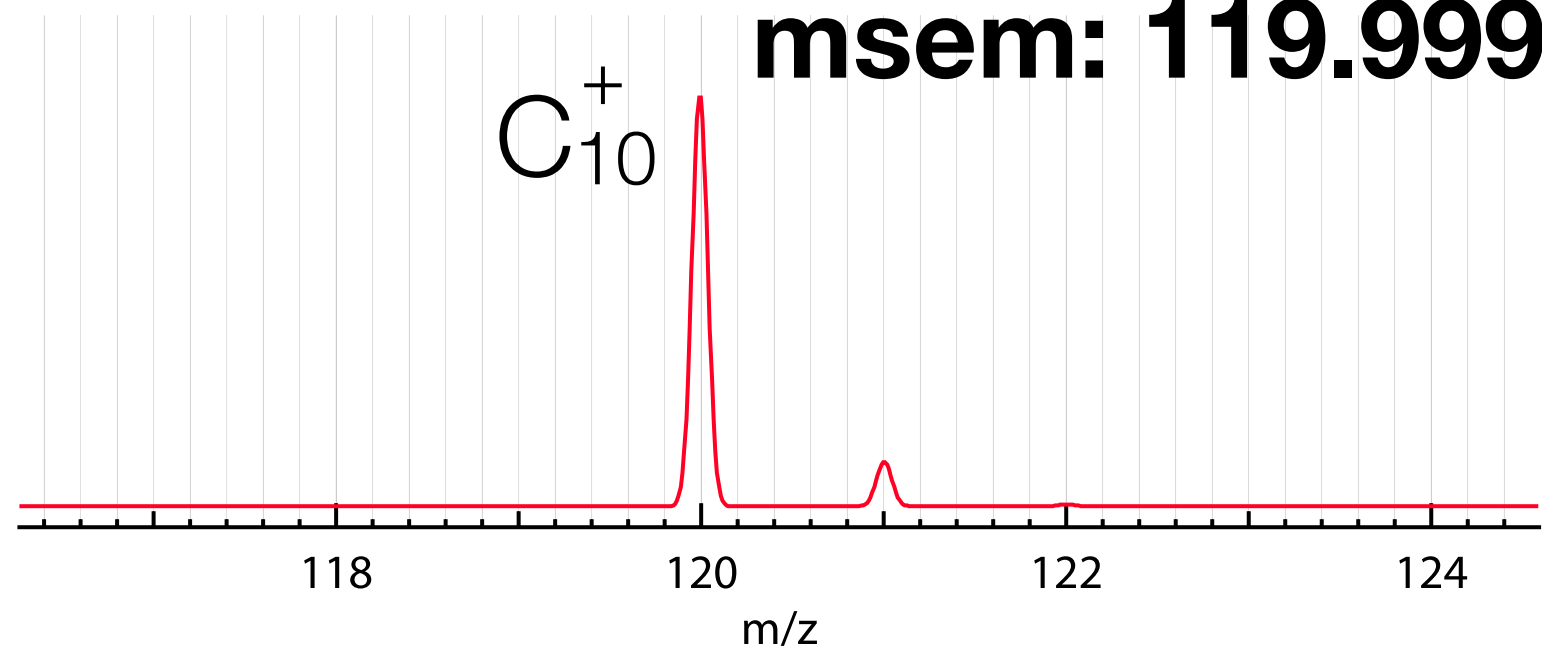


Monoisotopic mass

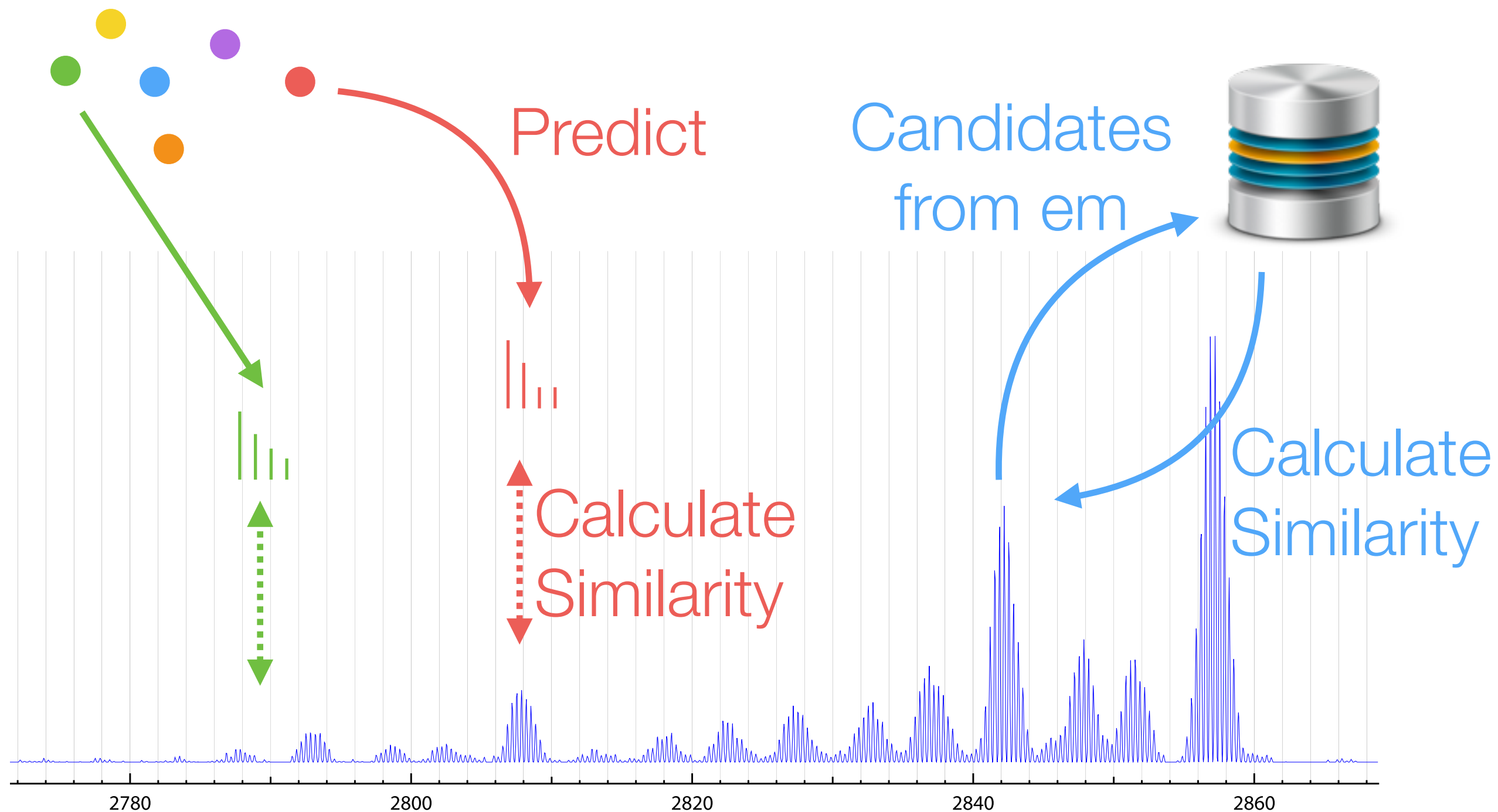
$\text{C}_4\text{H}_4\text{ClFN}^+$ **msem: 120.00108**



C_{10}^+ **msem: 119.99945**



Two possible workflow



Required tools

- Molecular formulas + ionizations
 - monoisotopic mass
 - isotopic distribution
- Monoisotopic mass + ionizations
 - possible molecular formulas
- Isotopic distribution similarity

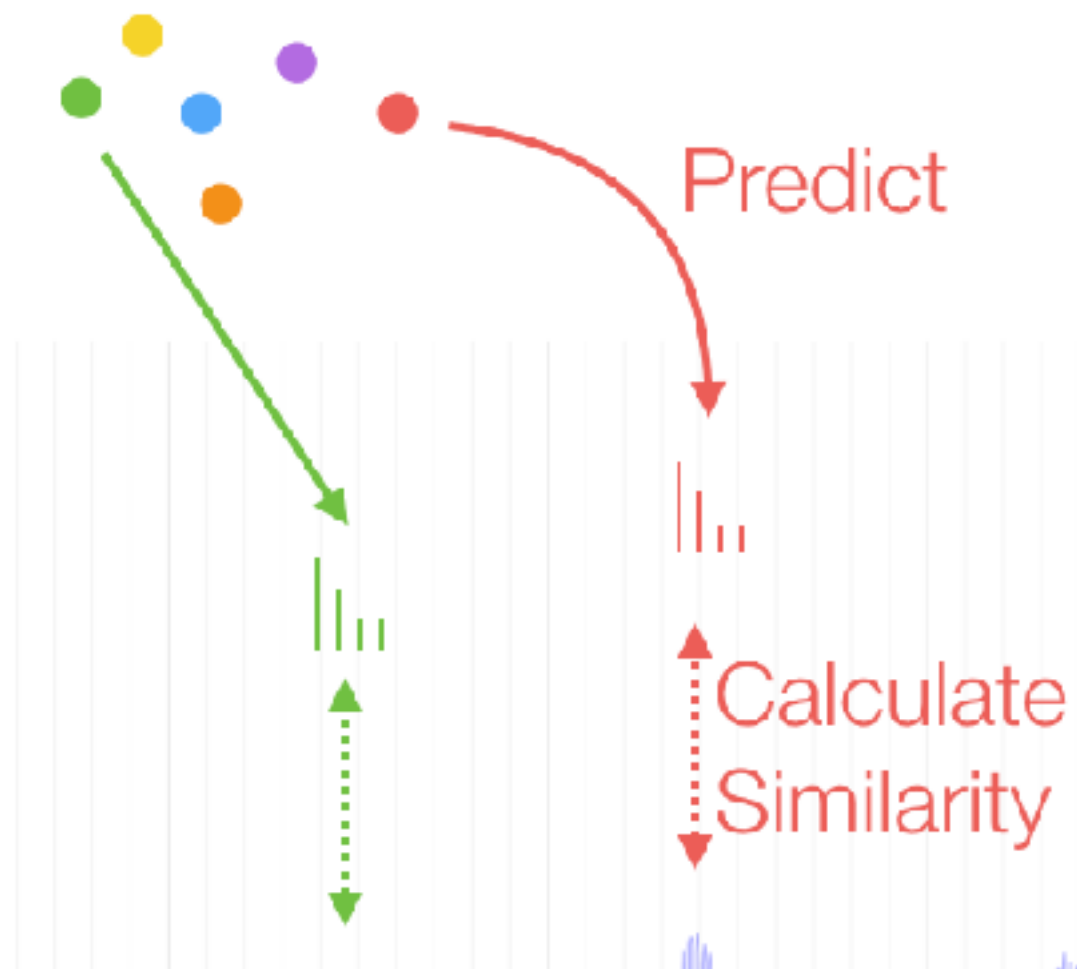
EMDB ?

Exact mass database

<https://www.npmjs.com/package/emdb>

- open-source MIT library
- javascript
- 3 important classes:
 - EMDB.Util.MF
 - EMDB.Util.IsotopicDistribution
 - EMDB

Information for a MF



```
const EMDB = require('emdb');
```

```
let mf = new EMDB.Util.MF('Et3N');
```

```
console.log( mf.getInfo() );
```

OUTPUT

```
{  
  mass: 101.19022990269394,  
  monoisotopicMass: 101.12044948788001,  
  charge: 0,  
  mf: 'C6H15N',  
  atoms: { C: 6, H: 15, N: 1 },  
  unsaturation: 0  
}
```

```
const EMDB = require('emdb');
```

```
let dist = new EMDB.Util.IsotopicDistribution('Et3N', {  
  ionizations: 'H+,Na+'  
});
```

```
console.log( dist.getParts() );
```

OUTPUT

```
[  
  {  
    mf: 'C6H15N',  
    mass: 101.19022990269394,  
    monoisotopicMass: 101.12044948788001,  
    charge: 0,  
    ionization: { mf: 'H+', em: 1.00782503223, charge: 1 },  
    ms: { ionization: 'H+', em: 102.12772594020095, charge: 1 }  
  },  
  {  
    mf: 'C6H15N',  
    mass: 101.19022990269394,  
    monoisotopicMass: 101.12044948788001,  
    charge: 0,  
    ionization: { mf: 'Na+', em: 22.989769282, charge: 1 },  
    ms: { ionization: 'Na+', em: 124.10967018997094, charge: 1 }  
  }  
]
```

```
const EMDB = require('emdb');
```

```
let dist = new EMDB.Util.IsotopicDistribution('Et3N', {  
  ionizations: 'H+,Na+'  
});
```

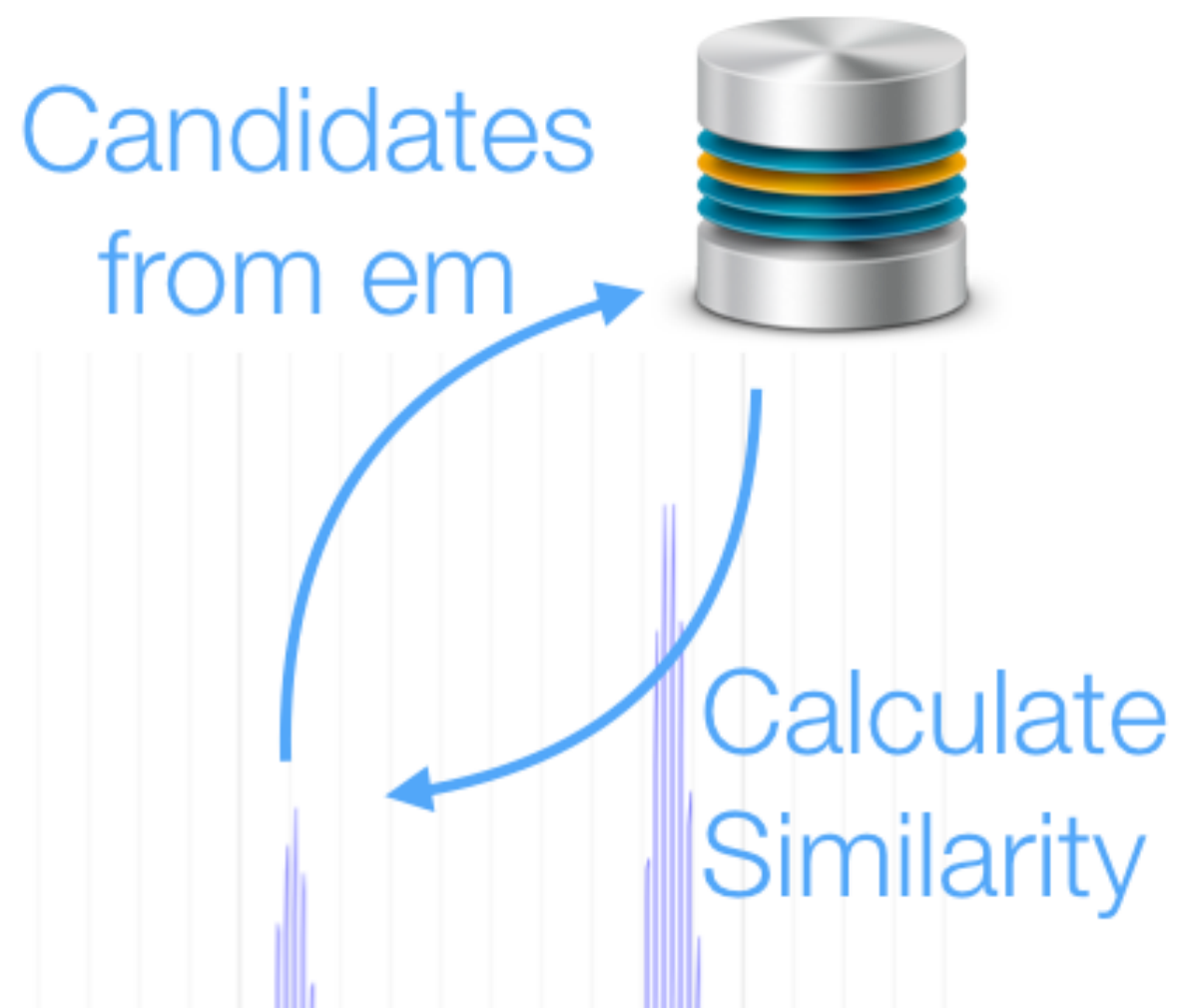
```
console.log( dist.getDistribution() );
```

OUTPUT

```
[  
  { x: 102.12772594020095, y: 0.9324705776936805 },  
  { x: 103.1308239513846, y: 0.06552738010342345 },  
  { x: 104.13387461619692, y: 0.00196884208125381 },  
  { x: 105.13686740231948, y: 0.0000328661707952177 },  
  { x: 106.13974366256402, y: 3.2893209212721756e-7 },  
  { x: 124.10967018997094, y: 0.9324705776936805 },  
  { x: 125.1127682011546, y: 0.06552738010342345 },  
  { x: 126.11581886596692, y: 0.00196884208125381 },  
  { x: 127.11881165208948, y: 0.0000328661707952177 },  
  { x: 128.121687912334, y: 3.2893209212721756e-7 }  
]
```

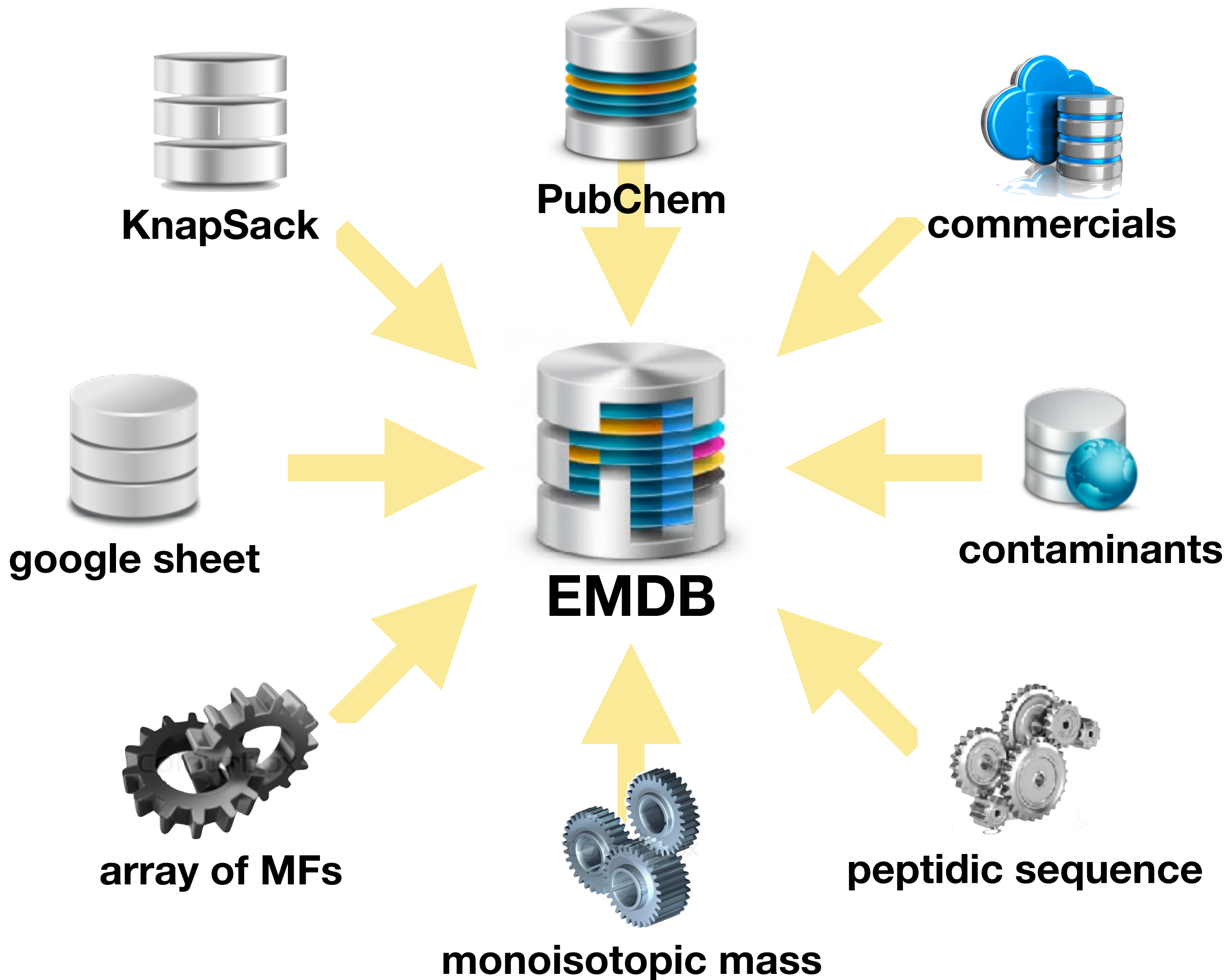
Demo

MF from monoisotopic mass



Database of monoisotopic mass

1. Create an in-memory database
2. (Search)
3. Show results



PubChem webservice

- Improved copy of PubChem
 - <https://github.com/cheminfo/docker-pubchem>
 - correct calculation MF (isotopes, charges, monoisotopic mass)
 - docker-compose project
- 96515520 molecules
- C H N O F Cl S: 452836 unique MFs

Monoisotopic Mass

```
emdb.fromMonoisotopicMass(300, {  
    precision: 10,  
    ranges: 'C0-50 H0-50 Cl0-50 O0-50 N0-50 Br0-50',  
    ionizations: '(H+)2, K+',  
    unsaturation: {  
        min: 0,  
        max: 10,  
        integer: true,  
        nonInteger: false  
    }  
});
```

- test over 5000000 MFs / s

From array

```
fromArray([  
    '(CH2CH2O)0-9 H0-9 N0-9 O0-9',  
    'F, Br, Cl, I, '  
], {  
    ionizations: 'H+, Na+, K+, (H+)2',  
    filter: {  
        minMSEM: 100,  
        maxMSEM: 105  
    }  
});
```

- mw
- em
- msem
- charge
- unsaturation

Contaminants database

- Based on a google spreadsheet
- Over 1000 possibles contaminants
- Can be filtered depending the technique

[Link](#)

Demo

Conclusions



Conclusions

- Very flexible library for mass calculations
- Allows to solve complex mass problems
- Open-source in javascript