

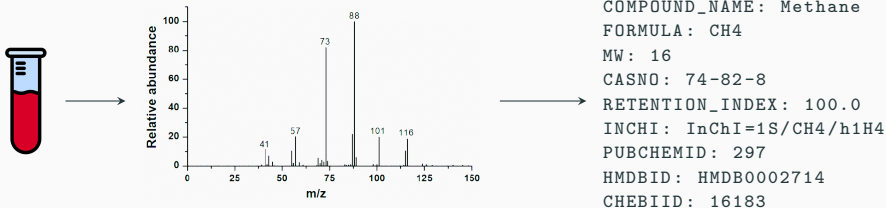
MSMetaEnhancer: A Galaxy Tool for Mass Spectra Metadata Annotation

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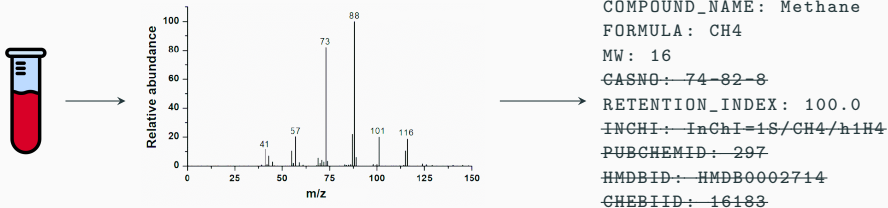
Mass spectrometry

- identify unknown compounds in a sample
- spectrum associated with metadata containing identifiers



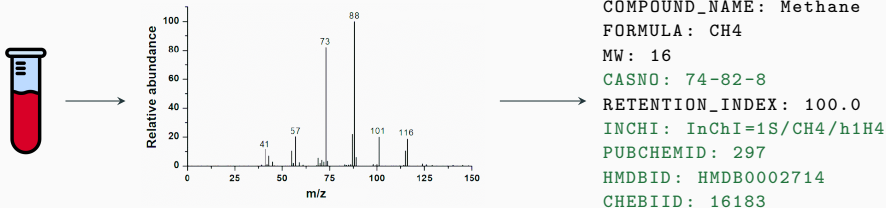
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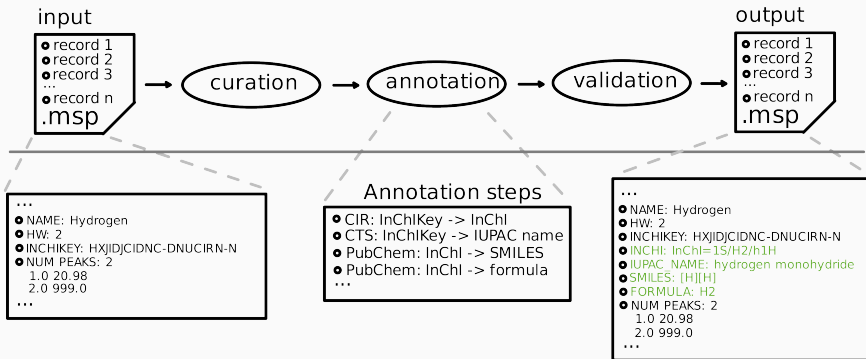


Mass spectrometry

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MSMetaEnhancer – overview



- customisable annotation process (semi-automatic)
 - conversion: `service: source` → `target`
 - defined vs. arbitrary order
- support for web services (via API) and compute engines (CIR, CTS, IDSM, PubChem, BridgeDB, ...)
- supported identifiers (InChI, InChIKey, SMILES, IUPAC chemical name, CAS number, many database-specific IDs, ...)
- iterative annotation with asynchronous approach (service limitations)
- additional curation (input data) and validation (obtained data) steps

Galaxy wrapper

- select single conversion in repeat mode

Ordered conversions

1: Ordered conversions 

Available conversions

PubChem: compound_name -> inchi 

2: Ordered conversions 

Available conversions

IDSM: inchi -> inchikey 

3: Ordered conversions 

Available conversions

CTS: compound_name -> inchikey 

 Insert Ordered conversions

- select multiple conversions

Other conversions

Select/Unselect all

RDKit: smiles -> mw

BridgeDB: pubchemid -> chemspiderid

BridgeDB: pubchemid -> hmdbid

MSMetaEnhancer



<https://github.com/RECETOX/MSMetaEnhancer>



<https://toolshed.g2.bx.psu.edu/view/recetox/msmetaenhancer>



<http://bioconda.github.io/recipes/msmetaenhancer>

Demo – Wednesday @ 10:20 AM

Thank you for your attention!