How simple can mass-spec files get?

Databases are a speedy, small, and simple solution for MS data storage and access

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Column-based tidy format is simple and intuitive for all MS types

Convert *m/z* and intensity tuples into database columns

Pair with other separation data
- Retention time (liquid chromatography)
- Drift time (ion mobility)
- X/Y coordinate (imaging MS)

Link with MS^n data via scan number

Pair with filename to aggregate multifile
- Optimized *across* files
- Metadata tables saved alongside

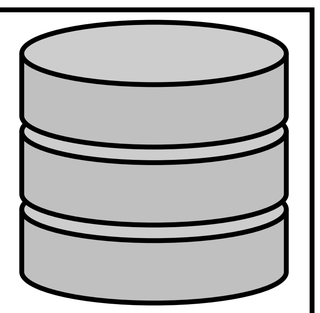
Table: MS1

filename Source file	scan_num Scan number	rt Retention time	mz m/z ratio	int Intensity
Smp_A	1	0.10	60.0452	6618
Smp_A	1	0.10	60.0532	2657
...millions of additional entries...				
Smp_Z	1385	22.35	60.0456	158084
Smp_Z	1385	22.35	60.0531	4673

Table: MS2

filename Source file	scan_num Scan number	prescan Precursor scan	rt Retention time	fragmz Fragment m/z	premz Precursor m/z	int Intensity
Smp_A	2	1	0.12	51.0238	241.0894	36104
Smp_A	2	1	0.12	53.0394	241.0894	243165
...millions of additional entries...						
Smp_Z	1390	1385	22.45	52.0186	185.1932	28371
Smp_Z	1390	1385	22.45	57.0923	185.1932	129604

Ion chromatogram extraction:
```
SELECT * FROM MS1 WHERE mz BETWEEN min AND max
```
Retention time range subset:
```
SELECT * FROM MS1 WHERE rt BETWEEN min AND max
```
Fragment search:
```
SELECT * FROM MS2 WHERE fragmz BETWEEN min AND max
```
Precursor search:
```
SELECT * FROM MS2 WHERE premz BETWEEN min AND max
```



Database
.sqlite
.duckdb
.parquet

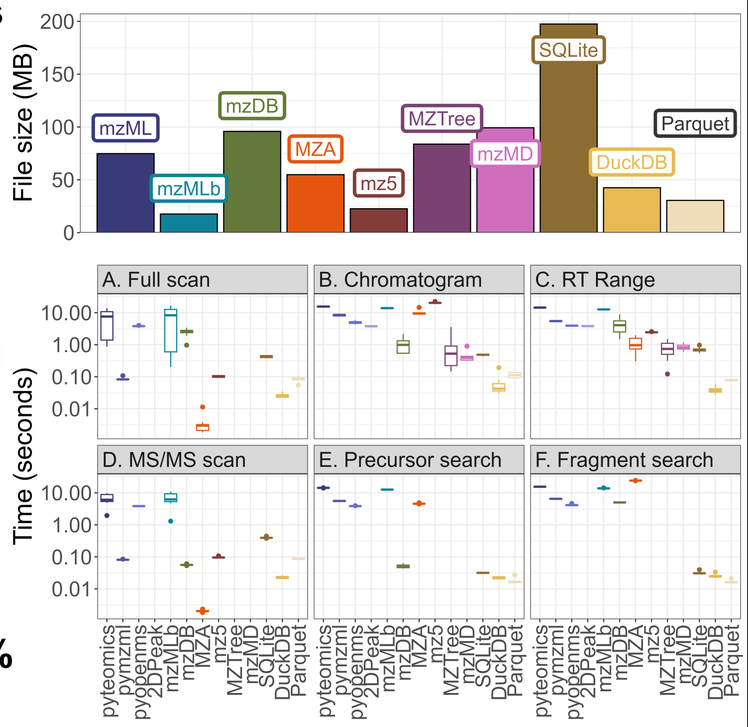
Problem: very large in memory! Solution: simple databases

Databases vs existing MS file options

We compared 13 different mass-spectrometry file types in Python using six metrics
- Single MS^1 scan
- Ion chromatogram
- Consecutive MS^1 scans
- Single MS^2 scan
- Precursor *m/z* search
- Fragment *m/z* search

Databases outperformed on all metrics other than known scan extraction
- Often by 10-100x

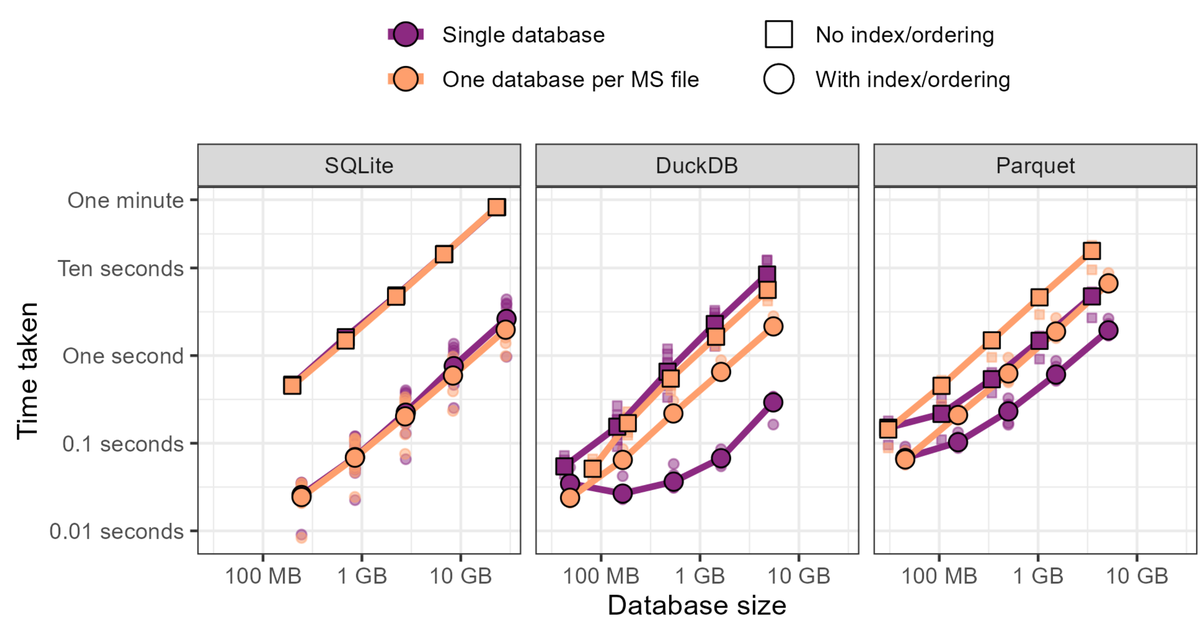
Parquet and DuckDB methods also reduced the on-disk file size ~50%



Optimization: index / order / aggregate

Indexing/ordering databases improved again by 10-100x

Improvements magnified with multiple files in one database



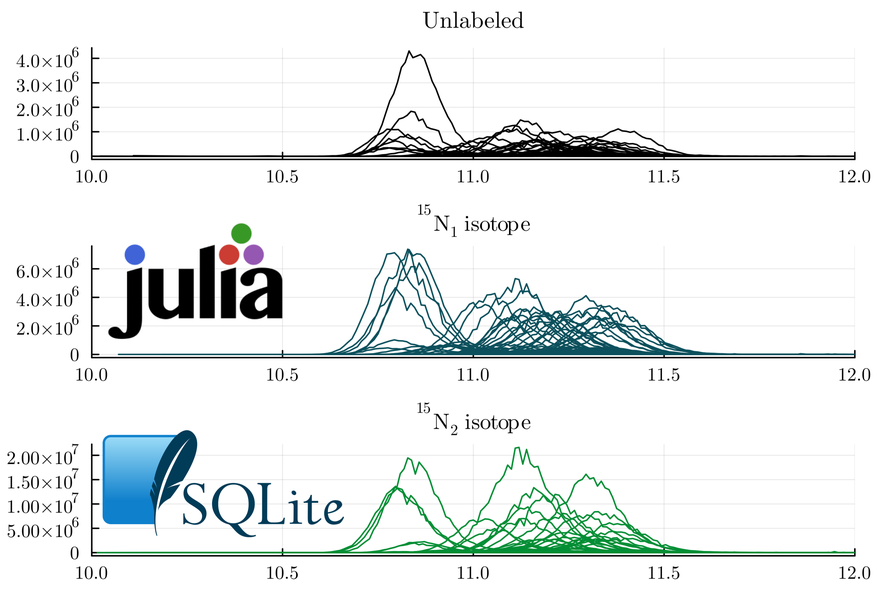
Databases offer language agnostic data access with essentially zero memory overhead

EICs in Julia via SQLite

```
using SQLite, DataFrames, StatsPlots

db = SQLite.DB("chrom_data/chrom_data.sqlite")
targets = [147.0764, 148.0734, 149.0705]
window(m) = (m*(1 - 2/1e6), m*(1 + 2/1e6))
clause = join(["(mz BETWEEN $(mzmin) AND $(mzmax))" for (mzmin, mzmax) in window.(targets)], " OR ")
query = "SELECT * FROM MS1 WHERE ($clause) AND (rt BETWEEN 10 AND 12)"
df = DBInterface.execute(db, query) |> DataFrame
SQLite.close(db)

p1 = @df df[round.(df.mz) .== 147, :] plot(:rt, :int, group=:filename, color="black", title="Unlabeled")
p2 = @df df[round.(df.mz) .== 148, :] plot(:rt, :int, group=:filename, color="#0b505c", title="15Nx1")
p3 = @df df[round.(df.mz) .== 149, :] plot(:rt, :int, group=:filename, color="#028e34", title="15Nx2")
plot(p1, p2, p3, layout = (3,1), dpi=600)
```

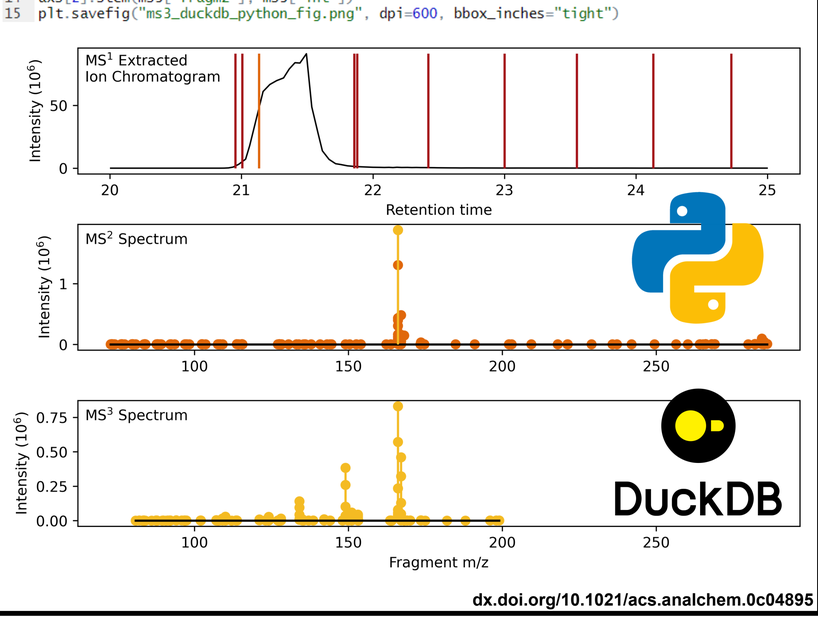


MS^3 in Python via DuckDB

```
import duckdb, matplotlib.pyplot as plt, pandas as pd

con = duckdb.connect("ms3_data/ms3_data.duckdb")
ms1 = con.execute("SELECT * FROM MS1 WHERE mz BETWEEN 282.1186 AND 282.1208").fetchdf()
ms2 = con.execute("SELECT * FROM MS2 WHERE premz BETWEEN 282.1186 AND 282.1208").fetchdf()
ms3 = con.execute("""SELECT * FROM MS3 WHERE prepremz BETWEEN 282.1186 AND 282.1208 AND
                  premz BETWEEN 166.0718 AND 166.0731""").fetchdf()
con.close()

fig, axs = plt.subplots(3, 1, figsize=(6, 4))
axs[0].plot(ms1['rt'], ms1['int'])
axs[0].vlines(ms2['rt'], ymin=0, ymax=ms1['int'].max())
axs[1].stem(ms2['fragmz'], ms2['int'])
axs[2].stem(ms3['fragmz'], ms3['int'])
plt.savefig("ms3_duckdb_python_fig.png", dpi=600, bbox_inches="tight")
```

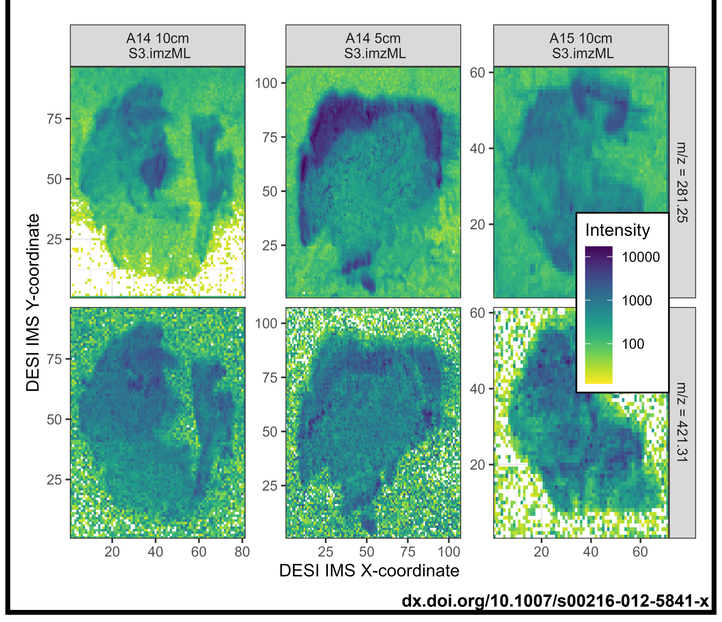


dx.doi.org/10.1021/acs.analchem.0c04895

Imaging in R via Parquet

Seamless interface via `dplyr`

```
library(tidyverse)
library(RaMS)
arrow::open_dataset("imzml_data/pqds") %>%
  filter(mz%between%pmppm(421.3111, 10) | mz%between%pmppm(281.2484, 10)) %>%
  mutate(mz=paste("m/z =", round(mz, 2))) %>%
  collect() %>%
  ggplot(aes(x, y, fill=int)) + geom_raster() + facet_grid(mz~filename)
```



dx.doi.org/10.1007/s00216-012-5841-x

Simpler is often smaller *and* speedier