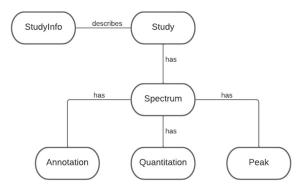
Name: Drashti Mehta, SID: 801262877

Lab 11

We continue working on our Metabolomics Database. As a reminder, this is the conceptual schema of the database.



This time, we'll focus on the **Annotation** data. Files "spectra.tsv" (note the extension) contains annotations for some of the spectra in each study. Not all spectra have corresponding annotations!

In addition to these files, we'll use the PubChem (https://pubchem.ncbi.nlm.nih.gov/) to retrieve extra data for each compound (molecular weight and SMILES). On the PubChem website, you can type any molecule name and see what information is available for it.

Task 1

Download the script "read_annotations.py" from Canvas, and execute it for each file "spectra.tsv" as follows:

> python3 read_annotations.py FILENAME.tsv

This script will read all annotations from the file, and then use REST API to search compound names in PubChem and retrieve their molecular weight and SMILES if available. The script will create file "spectra.pubchem.csv" with all the information needed for the database.

If interested, you can take a look at the line 13 in the script, which contains the URL pattern to retrieve the data from PubChem.

WARNING: there is 1 second delay between each URL request. Don't remove it! Usually, websites don't like receiving too many requests from the same IP address (which is similar to the DDOS attack), so it's a good practice to have a short delay between requests.

Task 2

Create a new table **annotations** in your database "metabolomics.db" from Lab 9. This table should contain columns: signal, name, monoisotopic_mass, matching_score, formula, cas, molecular_weight, and smiles. Import the annotation data from all four studies.

Name: Drashti Mehta, SID: 801262877

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	signal	name	monoisoto	matching_s	formula	cas
1	#1 73.0000@5.7190 MS1+	d-Mannose, 2,3,4,5,6-pentakis-O-(trimethylsilyl)-, o-methyloxyme, (1Z)-	569.288	944	C22H55NO6Si5	12
2	#2 73.0000@5.8930 MS1+	D-Xylopyranose, 4TMS derivative	438.211	911	C17H42O5Si4	5
3	#3 73.0000@5.7554 MS1+	d-Mannose, 2,3,4,5,6-pentakis-O-(trimethylsilyl)-, o-methyloxyme, (1Z)-	569.288	933	C22H55NO6Si5	12
4	#4 73.0000@5.8068 MS1+	L-Tyrosine, 3TMS derivative	397.192	915	C18H35NO3Si3	5
5	#5 73.0000@2.8264 MS1+	Lactic Acid, 2TMS derivative	234.111	964	C9H22O3Si2	1
6	#7 73.0000@5.6847 MS1+	d-Galactose, 2,3,4,5,6-pentakis-O-(trimethylsilyl)-, o-methyloxyme, (1Z)-	569.288	883	C22H55NO6Si5	12
7	#8 73.0000@5.7510 MS1+	d-Galactose, 2,3,4,5,6-pentakis-O-(trimethylsilyl)-, o-methyloxyme, (1Z)-	569.288	929	C22H55NO6Si5	12
8	#10 73.0000@3.1849 MS1+	Oxalic acid, 2TMS derivative	234.074	946	C8H18O4Si2	1
9	#14 73.0000@6.1836 MS1+	9H-Purine, 9-(trimethylsilyl)-2,6,8-tris[(trimethylsilyl)oxy]-	456.186	845	C17H36N4O3Si4	95
10	#15 73.0000@6.1670 MS1+	Myo-Inositol, 6TMS derivative	612.301	955	C24H60O6Si6	
11	#16 73.0000@3.3871 MS1+	Urea, 3TMS derivative	276.151	871	C10H28N2OSi3	6
12	#18 116.0000@3.0341 MS1+	L-Alanine, 2TMS derivative	233.127	942	C9H23NO2Si2	2
13	#19 73.0000@3.5346 MS1+	L-Norvaline, 2TMS derivative	261.158	914	C11H27NO2Si2	
14	#20 73.0000@3.3031 MS1+	3-Hydroxybutyric acid, 2TMS derivative	248.126	931	C10H24O3Si2	5
15	#21 73.0000@3.8926 MS1+	Glycine, 3TMS derivative	291.151	920	C11H29NO2Si3	
16	#24 73.0000@4.6323 MS1+	L-5-Oxoproline, , 2TMS derivative	273.122	838	C11H23NO3Si2	3
17	#25 73.0000@6.9322 MS1+	Edetic Acid, 4TMS derivative	580.249	881	C22H48N2O8Si4	

Task 3 (15pts)

Now we need to link the tables **annotations** and **spectra**. To link the two tables, you need to add a foreign-key column into one of the tables. Think which one, and what values this foreign-key column should contain.

Report the SQL statement to update the foreign key values.

Alter table annotations add foreign key (signal) REFERENCES Spectrum (name)

Task 4 (20pts)

Finally, let's make sure that the link between **annotations** and **spectra** works. In order to do that, try to calculate the number of annotated spectra in each study.

As I mentioned earlier, some of the spectra in the table **spectra** will have corresponding annotations in the table **annotations**, and other spectra will have no annotations at all. You need to count the number of spectra with annotations for each study.

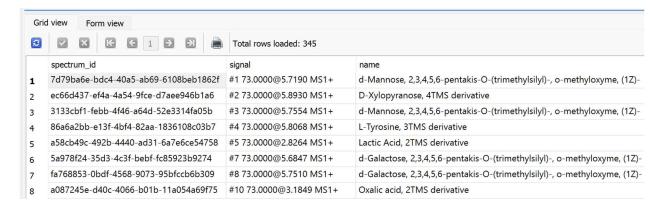
Report the following:

A. SQL query to calculate the number of annotated spectra in each study.

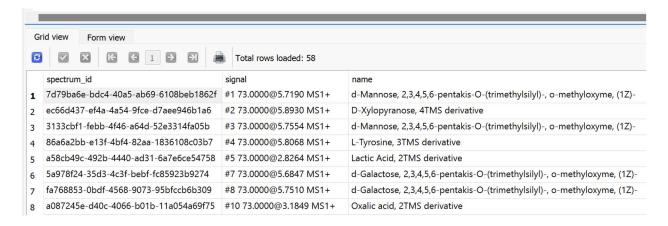
Ans:

1. select Spectrum.spectrum_id, annotations.signal, annotations.name from Spectrum join annotations on Spectrum.name = annotations.signal

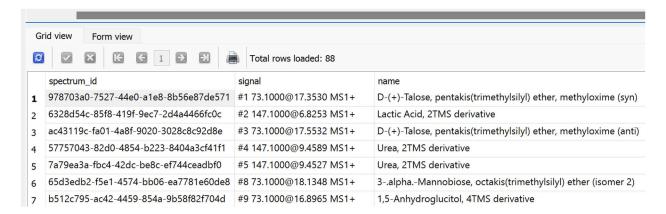
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- B. The number of annotated spectra in each of the four studies.
- select Spectrum.spectrum_id, annotations.signal, annotations.name from Spectrum join annotations on Spectrum.name = annotations.signal where Spectrum.study_id = "ST001270"

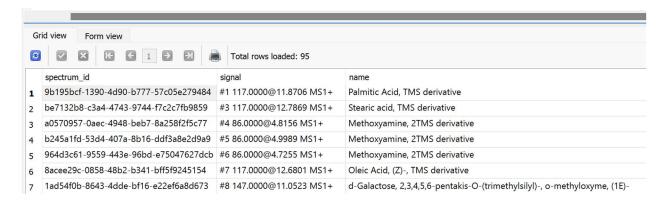


 select Spectrum.spectrum_id, annotations.signal, annotations.name from Spectrum join annotations on Spectrum.name = annotations.signal where Spectrum.study_id = "ST001369"



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3. select Spectrum.spectrum_id, annotations.signal, annotations.name from Spectrum join annotations on Spectrum.name = annotations.signal where Spectrum.study_id = "ST001399"



4. select Spectrum.spectrum_id, annotations.signal, annotations.name from Spectrum join annotations on Spectrum.name = annotations.signal where Spectrum.study_id = "ST001613"

