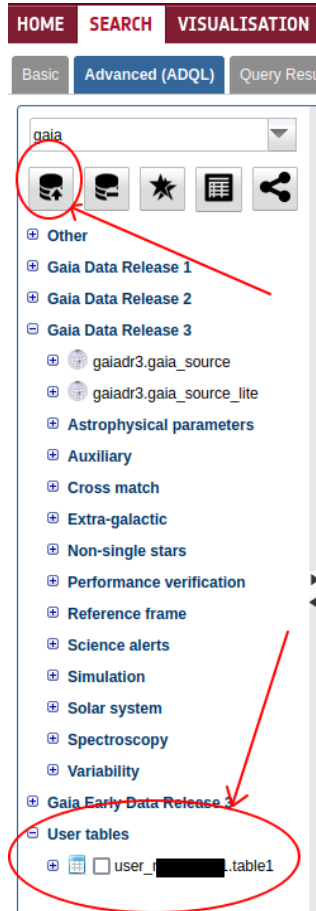


## How to crossmatch you own table within Gaia Archive (and get available spectra)

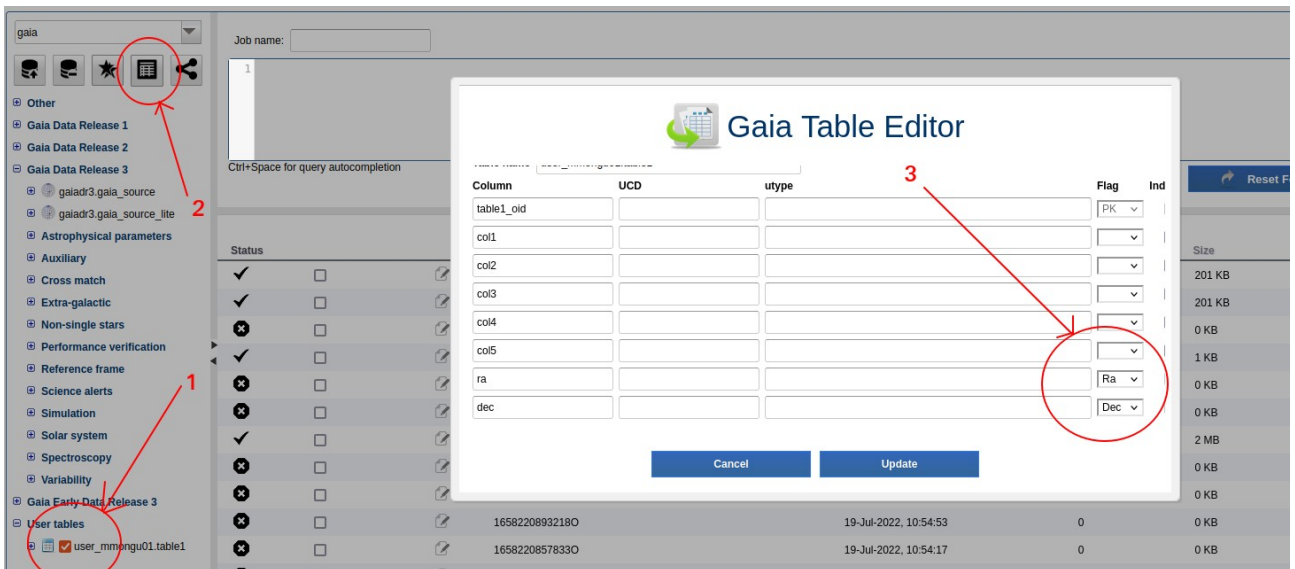
Go to <https://gea.esac.esa.int/archive/> Search – Advance (ADQL)

1.- Upload your catalogue into the Gaia archive (you need to be logged in for that):  
Click on the + button to upload the table. Chose a file name and a file from your computer.



It will show up at the section “User Tables”.  
I called the new table “table1”

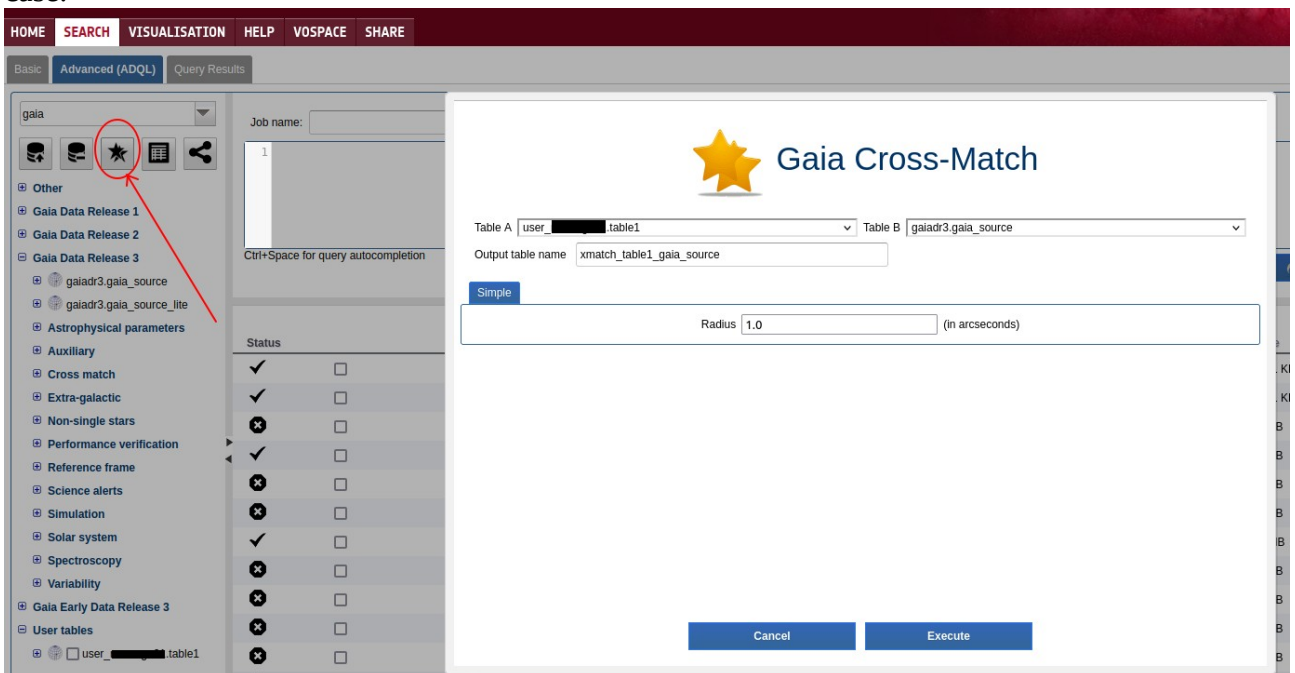
2.- Tell the archive what are the RA-DEC columns:  
Select the table (1), and click on the table button at the top (edit table, 2).  
Indicate through the Flag options, which are the ra-dec columns (3):



### 3.- Crossmatch your table with the Gaia table:

Click on the double star.

Select your table (user\_xxxx.table1) and the Gaia table of your choice (gaiadr3.gaia\_source) in that case.



A new table called user.xmatch\_table1\_table2 (i.e. user\_xxxx.xmatch\_table1\_gaia\_source in this case) will show up in your user table section. This table contains two columns, first, the id of the first table, and in the second the id from the second table they crossmatch with.

### 4.- Obtain all required columns from the two tables.

Now you can use the crossmatch table to join the two tables. You can do that with the following query:

```
SELECT b.*, a.* FROM gaiadr3.gaiia_source AS a, user_xxxx.table1 AS b,
user_xxxx.xmatch_table1_gaiia_source AS c WHERE (c.gaiia_source_source_id =
a.source_id AND c.table1_table1_oid = b.tablersg_oid)
```

That uses the three tables, and the id columns from each of them. Here all columns are selected from the two input tables through the \*, but you can list the output columns you want. If the query worked, you will see the output of the job in the list below, next to a V (otherwise, an X will appear). From there you can e.g. download the output table (1), see the first 2000 columns (2), or see the datalink tables (3).

The screenshot shows a query execution interface. At the top, there is a text input field for the job name and a 'Query examples' link. Below this is a text area containing the SQL query: `SELECT b.*, a.* FROM gaiadr3.gaiia_source AS a, user_xxxx.table1 AS b, user_xxxx.xmatch_table1_gaiia_source AS c WHERE (c.gaiia_source_source_id = a.source_id AND c.table1_table1_oid = b.tablersg_oid)`. Below the query area are buttons for 'Reset Form' and 'Submit Query'. At the bottom, there is a table with columns: Status, Job, Creation date, Num. rows, Size, and three numbered icons (1, 2, 3). The table contains one row with a checkmark in the Status column, job ID 16642250666390, creation date 26-Sep-2022, 22:44:26, 413 rows, and 201 KB size.

## 5.- Download spectra

By clicking at the datalink (3), you can see what data are available. In that case 99 RVS spectra or 388 sampled spectra in DR3. You can choose to download one file for each source tarballed in to a tar file (individual), or a single fits file with each source in a different extension (combined). Get in touch if you want help to read this with python. Otherwise, topcat should read it too.

You can choose the output format (I always go for fits). You can download all available data (MSC + XP + RVS + ...) by clicking at "Save all data" or only the RVS by clicking at the icon next to it.

The screenshot shows the 'Gaia Job DataLink' interface. It includes a logo, a title, and a link to 'Archive Help'. The job ID is 16639278109380. There is a dropdown for 'IDs Column' set to 'designation' and a 'Show Data' button. Below this are dropdowns for 'Data release' (Gaia DR3) and 'Data structure' (INDIVIDUAL). A list of data products is shown with icons: MCMC MSC (410), XP mean sampled spectra (388), XP mean continuous spectra (388), Epoch photometry (356), RVS mean spectra (99), and MCMC GSP-Phot (17). The 'RVS mean spectra (99)' entry is circled in green, and a red arrow points to its icon. At the bottom, there is a 'Download format' dropdown set to 'VOTable' and a 'Save All Data' button. A 'Close' button is at the very bottom.

Hope that helps!