

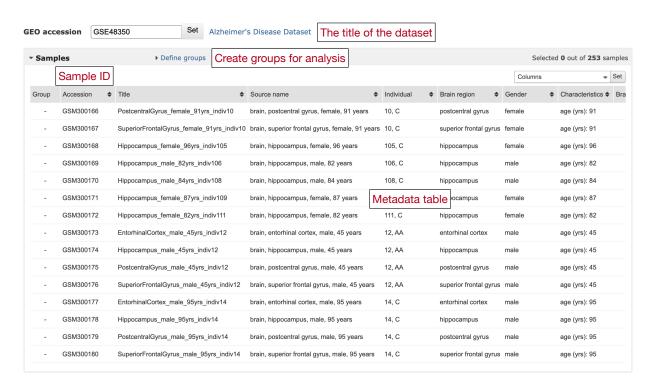
### Tutorial: Differential expression analysis using GEO2R

Database URL: https://www.ncbi.nlm.nih.gov/geo

Example dataset: GSE48350 (https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE48350)

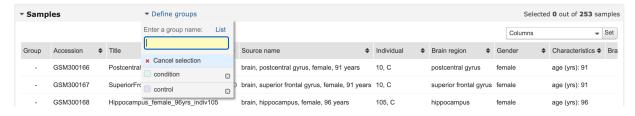
The URL for analysis will be: <a href="https://www.ncbi.nlm.nih.gov/geo/geo2r/?acc=GSE48350">https://www.ncbi.nlm.nih.gov/geo/geo2r/?acc=GSE48350</a>

#### The interface:



#### Step 1: Create groups for the analysis

Let's create two groups: "condition" and "control"

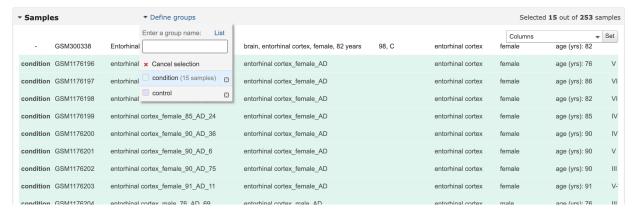


## Step 2: Select samples for each group

In this tutorial, let's only consider samples from the Entorhinal Cortex region.



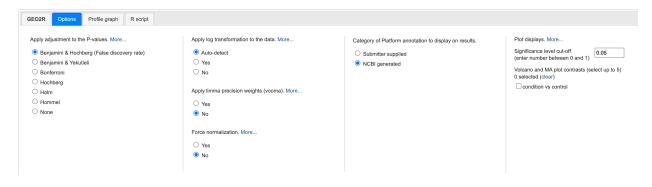
Find the sample with the suffix "AD" and add them to the "condition" group. To select multiple samples next to each other, select the first sample, hold the shift button, and select the last sample. After the samples are selected, click on the group "condition" to add all selected samples to this group.



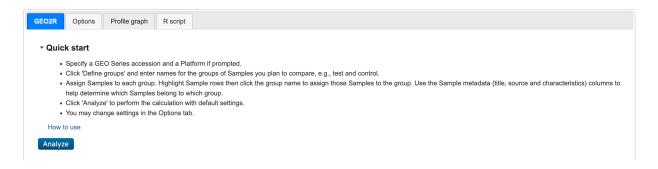
Next, select the remaining samples of this brain region for the "control" group.



# Step 3: Select options:



### Step 4: Start the analysis:



Click the analyze button. This process can take from 3-10 minutes depending on how many samples are selected.

Step 4: Download the results

