

## **Counting regions for tissuecyte**

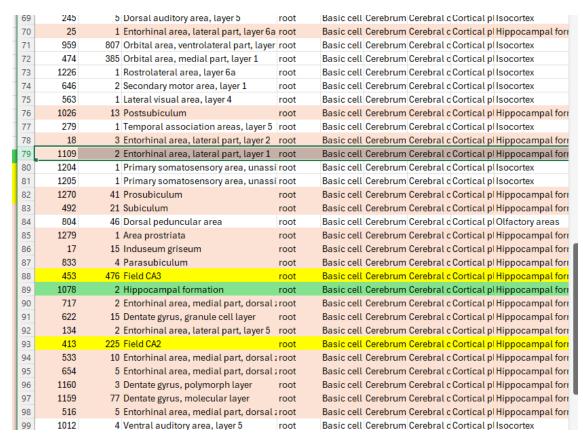


## **Description**

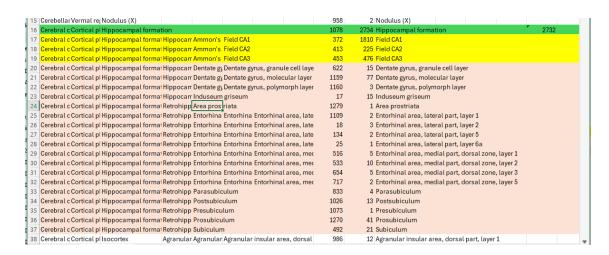
- ▼ newer discussion on 240827, use B0039,240826\_Gui\_registration\_second\_test result as an example.
  - we need to figure out how counting code output files can be converted to 300 summary regions output
  - First question:
    - what does region number refer to for cell\_counts.csv file? Is it referring to parcellation\_index or id in the
      - 1\_adult\_mouse\_brain\_graph\_mapping\_all\_reigons file?
    - for example for region = 1080 in cell\_counts.csv file, I found 1080 exist as both parcellation\_index and id which refers to different brain regions.

	Α	В		С
1	region	count		
2	926		1	
3	1053		1	
4	641		1	
5	1080		4	
6	958		2	
-	740		4	

- I have figured out based on CA1. I believe region number refers to parcellation\_index. And the current cell\_region\_count.csv is correct.
- So the cell\_count.csv = this file store all detected signals and their location (parcellation\_index).
- Then based on 1\_adult\_mouse\_brain\_graph\_mapping\_all\_reigons file, it can know the all detected signal which brain regions they belong to. This create the cell-region\_count.csv. But this file only have counts for all finest regions. It does not sum fine regions to higher level. For example: all yellow and orange are the finest regions (eg: CA1,CA2,CA3, parasubiculum etc.), but green is the higher level region (hippocampal formation = 2). (This means annotation file has hippocampal parcellation index and 2 cells falls in this index.)



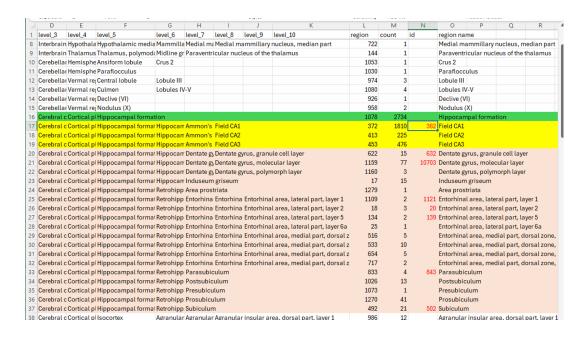
 region\_count.csv is the <u>spatially</u> organized version of cell\_region\_count.csv. At the same time, it added lower level regions counts to higher order. For eg: Green = yellow + orange +2 (the 2 cell detected just in hippocampal formation) =2732+2 =2734.



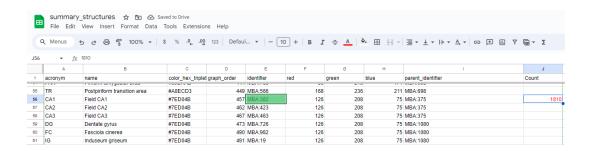
• Now we want convert region\_count.csv to 300 summary regions file.

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- for all the regions in region\_count.csv, based on their region number/parcellation\_index, find their id number from 1\_adult\_mouse\_brain\_graph\_mapping\_all\_reigons file.
- eg: red numbers are the ids that i found manually



for some regions, like CA1, id =382, it can also be found in 300
 summary\_structures.csv. Put the count number (1810) for id (382) in 300 summary\_structures.csv.

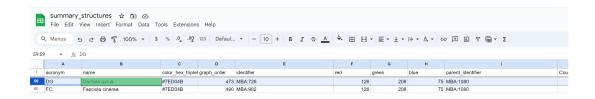


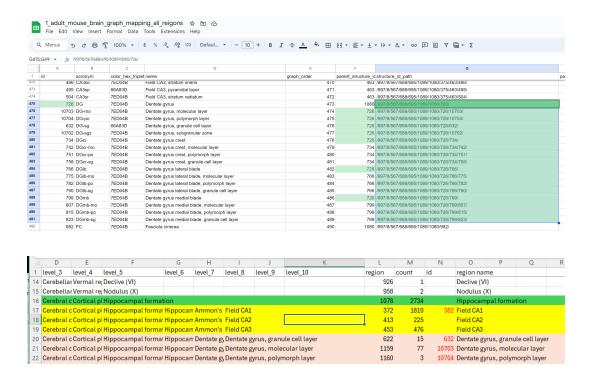
for some other regions, like dentate gyrus, granule cell layer, region number/parcellation\_index =622, id=632. It can not be found in 300 summary\_structures.csv, because this region level is smaller than the 300 regions we want. We need to figure out for this region (dentate gyrus, granule cell layer, region number/parcellation\_index =622, id=632) is the lower level region of which regions inside 300

**summary\_structures.csv.** Or in another way, we need to know for the 300 summary\_structures, what are the subregions they have. Once we know that info, we can know id=632 belongs to which 300 summary regions.

- we need to first go over each row inside 300 summary regions.csv, based on the id number, check the column structure\_id\_path in
  1\_adult\_mouse\_brain\_graph\_mapping\_all\_reigons.csv.
- as long as the structure\_id\_path has the id number, it means those rows belong to that id.
- for eg, see pics below: row 59 in summary\_structures.csv, id =726.
   The column structure\_id\_path in

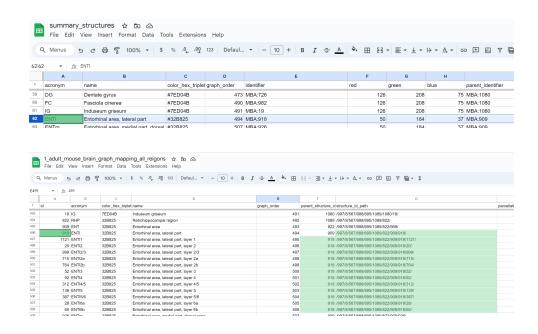
  1\_adult\_mouse\_brain\_graph\_mapping\_all\_reigons.csv that has 726 contains row 475-491. All ids ( row 475-491.) covered by these rows belongs to the DG/dentate gyrus/id=726. Therefore, all the counts for these ids ( row 475-491) should be counted towards DG/dentate gyrus/id=726.
- if we use B0039 as an example: the 300 summary\_structures.csv
  output file for B0039, DG should have counts = (632/15 + 10703/77 +10704/3) = 95 cells. [the numbers has a format of id/counts]



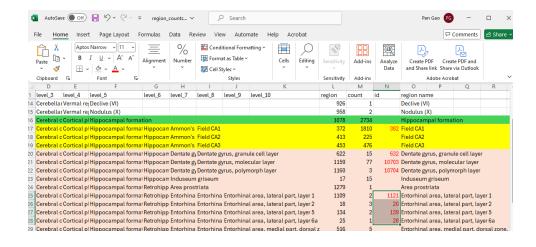


## More example:

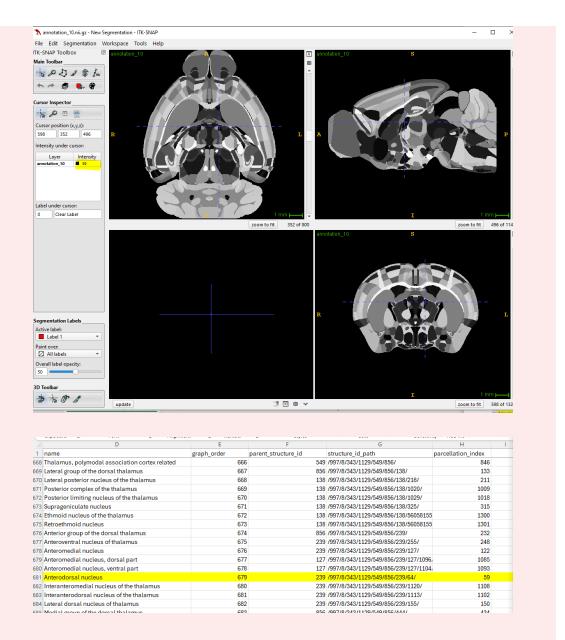
if we use B0039 as an example: the 300 summary\_structures.csv output file for B0039, ENTI = Entorhinal area = id 918, lateral part should have counts = (1121/2 + 20/3 +139/2 + 28/1) id/counts format = 8 cells.



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- ▼ The steps to find counting number for summarized regions file location G:\Brain\_Stitch\Brain regions and summary regions
  - 1. First create a new column at the end of all regions file and summary structure files and call it counting number column.
  - Use <u>all regions file</u> to find the detected cell number for all regions by using parcellation index number. Put the detected cell number to the **counting** number column for <u>All regions file</u>. Do that for all regions in side All regions file.



- use the parcellation\_index and the id and parent\_structure\_id and structure\_id\_path to place correct cell numbers for all regions/all rows.
- 3. Then look at <u>summary structure files</u>, go to first row and identify the <u>identifier number/id</u> (MBA:xxx) for that row. Then use the id to find the correct rows in **All regions file** by checking the **id** column.

(For example for row 119 in <u>summary structure files</u>, Anterovenral nucleus of thalamus, the identifier number =255. Go to <u>All regions file</u> and the id column with 255, which will locate you to row 677. Take the counting

number for that row and place and paste it in **summary structure files**, **counting number column**)

- 4. Repeat this step for all rows in **summary structure files.**
- 5. Output the both the summary structure files and all regions file.

1\_adult\_mouse\_brain\_graph\_mapping.csv

<u>summary\_structures.csv</u>

