

The Protocol for Database Design

The source for raw data:

Source: <https://portal.brain-map.org/atlasses-and-data/rnaseq/>

The Process:

Gene Expression data for mouse cortex and hippocampus by Cluster, median were downloaded obtained from the above website. The dataset for the MySQL database was created after normalization using the expression of Gapdh as 100. Latest GeneID, synonyms and descriptions for each corresponding gene symbols were downloaded (<ftp://ftp.ncbi.nih.gov/gene/>) and added to each gene symbol of the ABA trimmed means output.

The cell population was sorted into inhibitory (expression of Slc32a1), excitatory (expression of Slc17a7 and Nrn1) and other cell types. The expression values could be obtained by search under geneID, gene symbol, synonyms or gene description.

The final table was saved as a csv file and uploaded to the MySQL database online which served as the source for searching the expression data using either GeneID, symbol, synonyms or name (description) as the search input. The normalized dataset is also accessible by clicking on the dataset tab on the header.

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