

Learning Activated Microarray Dataset

Description:

Each spreadsheet contains the complete, analyzed, microarray data described Haberman et al, 2008 (see complete reference under "Publication"; a full description of subjects, behavior and microarray analysis is given in this manuscript). Briefly, this study examined gene expression differences in three hippocampal subfields (CA1, CA3 and the dentate gyrus) of young adult male Long Evans rats after exposure to a spatial learning condition (LA) relative to a control condition (CTL) in Morris watermaze task. In both conditions, the escape platform was visible but only the LA task condition contained spatial cues informative for the platform location. Hippocampal subfields were dissected either one or 48 hours after task completion, immediately after a probe trial given to assess spatial memory. The performance of rats in the LA condition indicated a spatial bias to the platform location while the CTL rats showed no such bias, despite equal time spent in the water and equivalent escape latencies. RNA was extracted from each hippocampal subfield and assayed on Affymetrix 230A microarrays such that each subfield of each rat was run on a single chip. Raw microarray intensities are normalized with gcRMA and analyzed using Significance analysis in Microarray (SAM). In all cases differential expression was determined between the LA condition v the CTL condition. To determine if a probeset was considered "present" an empirically derived low expression cut-off measure was used such that any average probeset intensity exceeding this cut-off was given a value of 'true' and considered expressed in the subfield.

Microarrays:

LA Y 1H CA1: CA1 subfield data- 1 hour from the end of training

LA Y 1H CA3: CA3 subfield data- 1 hour from the end of training

LA Y 1H DG: Dentate gyrus subfield data- 1 hour from the end of training

LA Y 48H CA1: CA1 subfield data- 48 hours from the end of training

LA Y 48H CA3: CA1 subfield data- 48 hours from the end of training

Abbreviation/category explanation:

AffyIDs - Affymetrix probeset ID

GeneSymbols – Entrez gene symbol*

GeneNames – Entrez gene name*

GeneRefSeqs – Genbank reference sequence ID*

MeanIntGCRMA – mean \log_2 probeset intensity across all subjects

GCRMAlocutIndx – T = probeset considered "present"; F = probeset considered "absent"

SAM@fold - relative change in LA vs CTL subjects; values>1 indicates increased expression in LA relative to CTL; values<1 indicate decreased values in LA relative to CTL

SAM@d – SAM d-statistic value

SAM@p.value - SAM p-value

SAM@q.value - SAM q-value; proxy for false detection rate

LA Yn 1H CA3C-1: indicate data for individual control subjects; Log₂ transformation of gcRMA raw intensity: LA (refers to learning activated microarray experiment); Yn (young adult rats); 1H (1 hour time point); CA3 (hippocampal subfield); C-1 (control subject #1)

LA Yn 1H CA3LA-1: indicate data for individual learning activated subjects; Log₂ transformation of gcRMA raw intensity: LA (refers to learning activated microarray experiment); Yn (young adult rats); 1H (1 hour time point); CA3 (hippocampal subfield); LA-1 (Learning activated subject #1)

* Annotations are not updated since the original publication. Updated probeset annotations can be found on the Affymetrix website.

Publication:

Publication of a reanalysis of the data obtained from this website is permitted pending appropriate citation of the data source and the following manuscript:

Haberman RP, Lee HJ, Colantuoni C, Koh MT, Gallagher M (2008) Rapid encoding of new information alters the profile of plasticity-related mRNA transcripts in the hippocampal CA3 region. Proc Natl Acad Sci U S A 105: 10601-10606.