**Instructions**

The BrainGEP package requires the user to download the developing and adult microarray data from the Allen Human Brain Atlas website. The adult AHBA data is found on the webpage shown below:

<http://human.brain-map.org/static/download>

The adult brain samples to be downloaded are named [H0351.2001](http://human.brain-map.org/api/v2/well_known_file_download/178238387), [H0351.2002](http://human.brain-map.org/api/v2/well_known_file_download/178238373), [H0351.1009](http://human.brain-map.org/api/v2/well_known_file_download/178238359), [H0351.1012](http://human.brain-map.org/api/v2/well_known_file_download/178238316), [H0351.1015](http://human.brain-map.org/api/v2/well_known_file_download/178238266), [H0351.1016](http://human.brain-map.org/api/v2/well_known_file_download/178236545)

When the 6 folders containing the adult brain data download, the data for each brain sample will be contained in a folder named with the sample ID. There should be 6 folders as a result, and should be renamed according to their sample IDs: 9861, 10021, 12876, 14380, 15496 and 15697. Save these folders in a desired location and take note of the path (AHB\_path).

The developing AHBA data is found on the webpage below

http://www.brainspan.org/static/download.html

The developing brain samples to be downloaded are

H376.IIIA.02, H376.IIIB.02, H376.IV.02, H376.IV.03.

When the 4 developing brain samples download, each sample will be contained in a folder named with the sample ID. There should be 4 folders as a result and should be renamed according to their sample IDs: 12566, 12690, 12840 and 14751. Save these folders in a desired location and remember the path (DHB\_path)

In the UNIX operating system, the BrainGEP tarball can then be installed using the following command:

R CMD INSTALL BrainGEP\_1.0.4.tar.gz

The user can then go into R and type

require(BrainGEP)

The package is now ready for use. The data initially needs to be processed to get it into a form suitable for our analysis. It also requires the user to specify a path where the processed data is to be saved (save\_path) and then re-loaded (using the Load\_AHBA\_data function) for each subsequent use of the package.

In R, type:

Process\_AHBA\_data(DHB\_path, AHB\_path, save\_path)

**Disclaimer:**

When the analyses in the paper were performed, the adult and developing human brain data were downloaded from the Allen Human Brain Atlas website in March and September 2013 respectively. The probe file for the genes between the adult and developing data sets was identical at the time. A minor update to the adult human brain data took place in September 2013, which resulted in the original 20,782 genes being reduced to 20,737. One of the genes in the reference list (FOXG1) also underwent a change, and is now called FOXG1B. Hence, separate probe files had to be specified for the two data sets and the package was updated accordingly. The overall impact of these slight changes was very minor.