Description of MEA data for Charlesworth et al (2015)

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1 Access to the data

This document describes how you can access the data files associated with the following paper:

> Charlesworth P, Morton A, Eglen SJ, Komiyama NH, Grant SGN (2015) Canalization of genetic and pharmacological perturbations in developing primary neuronal activity patterns. *Neuropharmacology* Available at: http://dx.doi.org/10.1016/j.neuropharm.2015.07.027.

We have used the CARMEN system to share our data. CARMEN is a virtual laboratory to allow neuroscientists to share data and computational services. The data has been uploaded to the CARMEN portal: `https://portal.carmen.org.uk/`

You need a login to access CARMEN. If you wish to simply download our data, you may use the username `g2c1` and password `Hipp5campal` . Once you have logged into the CARMEN system, the data are in the folder "Data -> Shared -> Stephen Eglen -> g2c-1". There are 2819 data files (totalling about 5 Gb), so the system will take a few seconds to view this folder.

The data are also archived at `http://dx.doi.org/10.5281/zenodo.31085`

2 Meta-data

The file `00g2cdata.csv` is a spreadsheet that describes the conditions under which each data file was recorded. The spreadsheet contains the following fields:

1. Timestamp.filename — name of the file.

2. Age — the age of the culture (days in vitro; DIV) at the time of recording.

3. Genotype — either WT for wildtype, or the name of the genetic mutation.

4. Strain — the strain of the mouse. Information is given only for comparing two strains among the wildtype data.

5. Drug — the name of the drug (if any) that was applied to the culture.

3 Format of data files

Each data file is an ASCII text file containing multiple columns, separated by TAB characters. All times are given in seconds. The first three columns describe when the recording started and finished. (Each recording is typically just over 900 seconds.) The remaining columns are the detected spike trains, one column per electrode. The header of the column describes the electrode location. e.g. `ch_12A_unit_0` denotes the electrode at column 1, row 2 in the array. (Electrodes were aligned in a square array, spaced 200 um apart.)

4 Code for analysing data

You can use the package **sjemea** in the R programming language to analyse these data. The package is available at `http://github.com/sje30/sjemea`.