

Topic 2: Unsupervised Deep Learning meets Bioinformatics and Neural Engineering

We have been working on the application of Computational Intelligence (CI) in invitro neuronal network behaviour patterns that can be used to cluster drugs for brain deceases and in applications in Metagenomics. In lab experiments involving multiple drugs applied to live brain tissues, vast amount of data can be generated using Multiple Electrode Array (MEA) technology.

We use an extended version of Self Organizing Map (SOM), which is one of the widely used Unsupervised Neural Networks. It has the ability to map high dimensional characteristics or data from multiple drugs into a two dimensional feature map, which is expected to be topology preserving allowing users to visually identify clusters. Our extended methods including Growing Self Organizing Maps (GSOM) further allow the map size to be determined by the algorithm, which relies upon a user set parameter called "Spread Factor" (SF). Using GPU compatible implementation of GSOM, we can vary SF and obtain multiple GSOMs from a small number of compact clusters to a large number of sparse clusters.

Key journal papers reflecting my own work relevant to Topic 2:

A two-tiered unsupervised clustering approach for drug repositioning through heterogeneous data integration, P. N. Hameed, K. Verspoor, S. Kusljic and S.K Halgamuge, BMC Bioinformatics, 2018

Use of adaptive network burst detection methods for multielectrode array data and the generation of artificial spike patterns for method evaluation, GDC Mendis, E Morrisroe, S Petrou, SK Halgamuge, Journal of neural engineering 13 (2), 026009, 2016, Citations: 6

ViQuaS: an improved reconstruction pipeline for viral quasispecies spectra generated by next-generation sequencing, D Jayasundara, I Saeed, S Maheswararajah, BC Chang, SL Tang, Bioinformatics, btu754, 2014, Citations: 23

Inferring copy number and genotype in tumour exome data, KC Amarasinghe, J Li, SM Hunter, GL Ryland, PA Cowin, IG Campbell, ...S.K. Halgamuge, BMC genomics 15 (1), 732, 2014, Citations: 46

CONTRA: copy number analysis for targeted resequencing, J Li, R Lupat, KC Amarasinghe, ER Thompson, MA Doyle, GL Ryland, ...SK Halgamuge... Bioinformatics 28 (10), 1307-1313, 2012, Citations: 174

Unsupervised discovery of microbial population structure within metagenomes using nucleotide base composition, I Saeed, SL Tang, SK Halgamuge, Nucleic acids research 40 (5), 2011, Citations: 51