Annals of Biomedical Science and Engineering

Volume - 6, Issue - 1

Research Article **Published Date:- 2022-12-31**

Feasibility study of magnetic sensing for detecting single-neuron action potentials

Understanding the magnitude of the local magnetic fields generated by neurons is critical to assessing the feasibility of novel magnetic field sensors to record in vivo neuronal activities at cellular resolution. However, the strength of the magnetic fields induced by individual neurons and neuronal networks has not been systematically studied. This step is critical for evaluating and benchmarking the ability of different magnetic field sensors to record neuronal activities with far better spatial and temporal resolution. Herein, FEM exemplary models and open-source computational libraries are used to calculate the magnetic fields generated by individual neurons and neuronal networks at micrometer distances. Our theoretical results show that the magnetic field generated by a single-neuron action potential can be detected by ultra-high sensitivity sub-pT magnetic field sensors, which opens the door to future in vivo decoding of neuronal activities through custom neural networks. We anticipate that the identification of single-neuron signals with high-sensitivity magnetic devices will allow the interface of nanoscale devices to interpret biological signals supported by machine-learning techniques capable of monitoring and predicting the localized activities underlying brain computations.

Research Article **Published Date:- 2022-09-24**

Determination of foot-and-mouth disease serotypes from naturally infected cattle by solid phase competitive ELISA (SPCE) techniques

Objective: Foot and mouth disease (FMD) is a highly infectious and economically important disease affecting cloven-hoofed domestic and wild animals. Early diagnosis and serotyping of the agent are very important to effectively design and implement the control approach. This study was conducted on serum samples collected from Amhara, Tigray, Oromia and Addis Ababa between October 2018 to February 2020. The animals were kept under a semi-intensive to an extensive system of rearing. Serum samples with low OD values (positive) using competition NSP-ELISA were subjected to serotyping ELISA.
Results: In the present study, three serotypes were identified from 186 NSP ELISA positive sera of which 156 serotype O, 40 serotypes A and 28 serotype SAT2. In this analysis, multiple serotype infection was observed which is why the number of serotypes was beyond the samples analyzed. Among 23 samples from Addis Ababa 10, 3 and 5 were O, A and SAT2 serotypes respectively, while in samples from the Oromia region 12 were O and 3 were SAT2 serotypes. From the Amhara region, 99 samples analyzed were found to be serotype O and SAT2 in 7 of the serum samples. From the Tigray region, 30 samples were seen to have Serotype O infection, whereas 13 of them were SAT2. The proportion of serotypes identified based on the production system practices was also found that semi-intensive production takes the largest share in all three serotypes followed by extensive production. Generally, early determination of the serotype from past infection helps to aware of the epidemiology as well as the infection immunity of the herd/individual animals.

Research Article **Published Date:- 2022-07-04**

Enhancing functional expression of L-glycerophosphate oxidase in Escherichia coli by controlling the expression rate

---

Heterologous expression of proteins often pursues high expression levels, but it can easily result in misfolding and loss of biological function. L-?-glycerophosphate oxidase (GlpO) is a flavin adenine dinucleotide (FAD)-dependent oxidase which is widely used in the clinical determination of triglycerides. We found that the total enzymatic activity of GlpO expressed in Escherichia coli (E. coli) was extremely low, probably due to the absence of FAD cofactors and the misfolding of GlpO at a high synthesis rate. Therefore, decreasing the expression rate was used to improve the activity of GlpO. The specific activity of GlpO expressed on the pUC19 vector with lac promotor was approximately 30 times higher than that expressed on the pET28a vector with T7 promotor, but the expression levels of GlpO on the two vectors were completely opposite. It indicated that the specific activity of GlpO was increased as the expression level decreased. However, too low expression greatly influences the total amount and activity of the functional enzyme. In order to resolve this problem, two new plasmids, GlpO-CG4 and GlpO-CG6, were constructed by inserting 4 or 6 nucleotides, respectively, between the ribosome binding site (RBS) and the start code (ATG) on pET28a. Compared with the expression on the GlpO-pET vector, the expression rates of GlpO on the GlpO-CG4 and GlpO-CG6 were dramatically decreased. The total activity of GlpO expressed on GlpO-CG6 was 11 times and 1.5 times higher than that expressed on the GlpO-pET and GlpO-pUC, respectively. Results suggest that the activity of GlpO can be improved by decreasing the expression rate.

Research Article **Published Date:- 2022-01-20**

[Applications of convolutional neural networks in chest X-ray analyses for the detection of COVID-19]

Throughout global efforts to defend against the spread of COVID-19 from late 2019 up until now, one of the most crucial factors that has helped combat the pandemic is the development of various screening methods to detect the presence of COVID-19 as conveniently and accurately as possible. One of such methods is the utilization of chest X-Rays (CXRs) to detect anomalies that are concurrent with a patient infected with COVID-19. While yielding results much faster than the traditional RT-PCR test, CXRs tend to be less accurate. Realizing this issue, in our research, we investigated the applications of computer vision in order to better detect COVID-19 from CXRs. Coupled with an extensive image database of CXRs of healthy patients, patients with non-COVID-19 induced pneumonia, and patients positive with COVID-19, convolutional neural networks (CNNs) prove to possess the ability to easily and accurately identify whether or not a patient is infected with COVID-19 in a matter of seconds. Borrowing and adjusting the architectures of three well-tested CNNs: VGG-16, ResNet50, and MobileNetV2, we performed transfer learning and trained three of our own models, then compared and contrasted their differing precisions, accuracies, and efficiencies in correctly labeling patients with and without COVID-19. In the end, all of our models were able to accurately categorize at least 94% of the CXRs, with some performing better than the others; these differences in performance were largely due to the contrasting architectures each of our models borrowed from the three respective CNNs.
