Faculty of Science

University of Colombo

Sri Lanka

Annual Research Sessions

17 December 2020

Proceedings
Annual Research Symposium 2020
Faculty of Science, University of Colombo, Sri Lanka

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Faculty of Science
University of Colombo, Sri Lanka

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The Faculty of Science to be a centre of scientific and technological excellence nationally and internationally.

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To develop honest, adaptable productive citizens; with multidisciplinary knowledge, creative thinking and analytical skills with a high degree of civic consciousness. To articulate and promote interaction with public and private sector and society at large, with the view to contributing towards the development of the nation. To institute mechanisms for partnership programs for improving resources and infrastructure facilities.

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I am pleased to extend my warmest congratulations to the Dean, Staff and Students of the Faculty of Science, University of Colombo, on the occasion of the Technical Sessions of its 13th Annual Research Symposium scheduled for the 17th of December 2020.

The Faculty of Science, that reaches its centenary milestone in 2021, is in the forefront of Sri Lanka's Science & Technology research, having made significant contributions towards boosting our university's research profile. The Faculty of Science has demonstrated a high level of commitment in recent years, as is evident by the quality and quantum of its research output and outcomes. Cutting-edge research using advanced technologies and spanning across many disciplines of science has resulted in a multitude of publications in the form of extended abstracts and well cited full publications in high ranking scientific journals, which bear testimony to the high standard of research conducted by the academics and postgraduates of the Faculty. Research has also led to many innovations, international patents and niche areas, with some research having a critical impact on national development.

Notwithstanding the challenges imposed on research this year by the COVID-19 pandemic in Sri Lanka and globally, the academics and postgraduate students have continued to pursue with their research activities. I understand that around 35 abstracts will be presented on a virtual platform which will no doubt allow a wider audience to join in and share knowledge and valuable research insights. The invited lectures by academics would also enrich the technical sessions. I am confident that this year's scientific sessions would prove to be very productive and pave the way for more innovative and advanced research within the Faculty.

I extend my very best wishes for a fruitful deliberation and pledge my best support to the Dean and the Organizing Committee, all academics, presenters and participants. I wish the Annual Sessions of the Faculty of Science every success.

Stay safe and well!

Senior Professor Chandrika N Wijeyaratne

The Annual Research Symposium of the University of Colombo was initiated in the year 2008. During the past 12 years, many academics and postgraduate students of the Faculty of Science have contributed to the symposia by presenting research papers related to the research work carried out by them. This year's Annual Research Symposium of the Faculty of Science of the University of Colombo has been scheduled for December 17, 2020.

The Faculty of Science of the University of Colombo has an excellent postgraduate education system in place with doctoral programmes focusing on 7 subject disciplines (Chemistry, Mathematics, Nuclear Science, Physics, Plant Sciences, Statistics and Zoology & Environment Sciences) and masters programmes offered in approximately 15 disciplines. At any given time, approximately 500 postgraduate students pursue their studies in the Faculty under the guidance of well-qualified academic staff members. The research conducted at the faculty is supported by the Colombo Science and Technology Cell which promotes its commercialization. Due to this, the Faculty of Science is one of the best faculties to pursue higher education related to Science in Sri Lanka, and I am proud to be a part of it.

I would like to take this opportunity to thank all the presenters and their supervisors for contributing to the enhancement of research in the faculty, and for participating in this symposium and sharing their research findings. On behalf of the Faculty of Science, I extend my sincere gratitude to the organizing committee for working under difficult conditions due to the COVID-19 pandemic, to make this event a success.

Senior Professor Upul Sonnadara

INVITED TALKS

The Tiger Beetles of Sri Lanka: Our island biodiversity

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Tiger beetles are predatory insects of order Coleoptera, family Carabidae, subfamily Cicindelinae. 2,822 species are found from many countries of the world with the exception of Antarctica, Tasmania and a few oceanic islands such as Hawaii and Maldives. They are important as biological indicators of environmental health and diversity of other taxa, bio-control agents of pests of agricultural crops and predators of ecological ecosystems.

Six tribes are found in the world of which two tribes are found in Sri Lanka – Cicindelini (ground-dwelling tiger beetles), Collyridini (arboreal tiger beetles). These two tribes are represented by 70 species of which 36 are endemic. Due to the high species number, Sri Lanka is ranked amongst the top 30 countries with the highest number of tiger beetle species. Further, the country is ranked number four amongst the top ten countries with the highest number of endemic tiger beetle species, and number one amongst the top ten countries with the highest number of species per square kilometer.

However, tiger beetles of the island have not been studied for more than a 100 years, and the studies available have not been systematically conducted and are far outdated. Therefore, recent investigations have been conducted by the author and co-workers on the diversity, distribution and habitat types of this biologically diverse, charismatic insect group. The investigations have resulted in disturbing revelations of decline in species numbers, decline and change in distributional ranges and loss of their habitats which is significantly detrimental to habitat specific species such as the tiger beetles.

Nearly twenty years (2002 – to present) of recent investigations have recorded only 23 species of tiger beetles of which 12 species were endemic. Fourteen species were ground-dwelling tiger beetles, while nine were arboreal tiger beetles. The ground-dwelling tiger beetles have short, broad bodies with colourful elytral patterns, while the arboreal tiger beetles have elongate, narrow bodies that are uniformly dark in colour with no elytral patterns. The ground-dwelling tiger beetles were found from open habitats with sparse vegetation such as beaches and coastal areas; water edges of rivers, streams and reservoirs and human-modified habitats such as gardens, lawns and other urban settings. Arboreal tiger beetles occupied vegetated habitats such as forests, woodlands, grasslands and agro-ecosystems. However, endemic tiger beetle species of both tribes mostly occupied locations of the wet zone as is evident for many other animal and plant taxa of Sri Lanka. Endemic species were found on the banks of the Kuru River, Bopath Ella; banks of Maha Oya, Dehi Owita; Sinharaja rainforest; Bodhinagala forest, Ingiriya; Thummodara, Avissawella, Yagirala forest, Kalutara; Kanneliya rainforest, Galle; Makandawa rainforest, Kitulgala; Rambukwella, Kandy and locations in Ratnapura.

Studies revealed that the endemic species are at present limited in distribution and their distributional ranges have significantly declined. For example, the endemic ground-dwelling tiger beetle, *Cicindela* (*Ifasina*) *willeyi* Horn, 1904 is now limited to a single location in Avissawella and 99.5% of its distributional range has declined. Most tiger beetle species have exploited new habitats due to habitat loss and competition by other insect species, which was evident by a mtDNA analysis and haplotype networking study conducted by the author. Recent

studies have revealed that the coastal tiger beetle, *Hypaetha biramosa*, is an efficient biological indicator of environmental health of the beach habitats of Sri Lanka. The arboreal tiger beetle, *Derocrania scitiscabra*, has the potential of being used as a suitable bio-control agent for pests of coconut, tea, betle, pepper, cinnamon and fruit cultivations.

At present, the vast amount of data on tiger beetles collected during the two decades of study have been utilized to develop a machine learning application for the identification of tiger beetles. It is intended that this development will facilitate the identification of other insects as well with future modifications. Insect studies are often hindered by the difficulties in identification. Morphological identification has been weakened by the close similarities evident between species of the same genus, similarities evident between species of different genera, excessive time consumption and lack of skill; while molecular identification has been set back mainly due to cost of equipment and other resources.

Morphometric and habitat data of tiger beetles collected during the 20 years of study and images captured in the field excursions have been utilized to develop two machine learning models – Ensemble Extra Tree Classifier method based on morphometric and habitat data, and the Revised SqueezeNet Tranfer Learning Approach based on image data. The two models can be integrated to develop an approach that is more accurate, efficient and user-friendly.

Insects are the Earth's most diverse organisms, and Sri Lanka's insect fauna represents a large part of its biodiversity. Unfortunately, despite this dominant position they are rarely included in the accounts of biodiversity on the Island. The usual excuse for this negligence is lack of information on Sri Lankan insects due to the inadequacy of taxonomic studies on the group. The recent studies have succeeded in providing information on a very important insect group on the island. Diversity of tiger beetles, their applications as biological indicators and bio-control agents, and utilization of their information in developing a machine learning approach to identify insects has provided a foundation of vast knowledge and data for future studies. However, it is imperative that the necessary resources to study our rich insect fauna are made available sooner while some of the past diversity is still with us.

References

Abeywardhana D.L., Dangalle C.D. and Mallawarachchi Y.W. (2019). Automated identification of Coleoptera, Cicindelinae in Sri Lanka by machine learning. *Proceedings of the Asia-Pacific Conference 2019 Association for Tropical Biology and Conservation*. pp.75.

Dangalle C., Pallewatta N. and Vogler A. (2011). The current occurrence, habitat and historical change in the distribution range of an endemic tiger beetles species *Cicindela* (*Ifasina*) *willeyi* Horn (Coleoptera: Cicindelidae) of Sri Lanka. *Journal of Threatened Taxa* 3(2): 1493-1505.

Dangalle C.D., Pallewatta N. and Vogler A.P. (2012). Habitat specificity of tiger beetle species (Coleoptera, Cicindelidae) of Sri Lanka. *Cicindela* 44(1): 1-32.

Dangalle C.D. (2018). The forgotten tiger: the arboreal tiger beetles of Sri Lanka. *Journal of the National Science Foundation of Sri Lanka* 46(3): 241-252.

Thotagamuwa A., Lokupitiya E., Lokupitiya R.S., Dangalle C.D., Pallewatta N. and Dayananda K.S. (2020). The effects of incident microclimatic and soil parameters on the population sizes of selected tiger beetle species in Sri Lanka. *International Journal of Tropical Insect Science*. 40: 71-79.

Environmental research dealing with climate change and its link to the carbon cycle

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Climate change has become one of the most serious environmental issues of the century. Global temperature has increased over time, and the last decade included the majority of the years with the highest recorded global temperatures. The observed warming on Earth has been attributed to the increased levels of carbon dioxide (CO_2) and other greenhouse gases due to various anthropogenic activities including fossil fuel burning and land use changes. The focus on the issue of climate change has increased during the last few decades due to the irreversible impacts it has caused across the world. Atmospheric CO_2 concentration has increased from 280 ppmv in 1850 to ~410 ppmv in 2019 (NOAA 2020). Therefore, research dealing with human impacts on climate change and perturbations of the carbon cycle has become an important area in environmental research.

Climate change related research could aim at both adaptation (i.e. action to reduce the impacts of climate change) and mitigation (i.e. action to reduce the sources or greenhouse gas emissions associated with climate change). Sri Lanka has been an island vulnerable to a variety of impacts of climate change, including impacts from increased frequency of extreme weather events such as droughts and floods, and sea level rise, etc. Such impacts can negatively affect the absorption of atmospheric CO_2 by various ecosystems. Therefore, research focusing on the climate change impacts, including those on the carbon cycle, and the associated adaptation and mitigation aspects, has become a timely need.

The research led by the author at the Department of Zoology and Environment Sciences has focused on a variety of environmental concerns/issues including air pollution, climate change and its link with the global carbon cycle. Specific research areas include the analyses of observed climatic trends and their impacts on various ecosystems, potential adaptation measures, evaluation of the existing carbon stocks and stock changes in specific terrestrial and coastal/marine ecosystems to identify their role in mitigation of climate change and atmospheric CO_2, measurements and modeling of the greenhouse gas emissions, etc. These research studies have incorporated multidisciplinary approaches and analyses involving measurements, modeling, GIS, and remote sensing, etc. and have been funded through both local and foreign grants, published in indexed journals, and presented at various scientific meetings. In conducting the research, the author has collaborated with both local and foreign scientists and research institutes.

Statistical methods for detecting disease outbreaks

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The World Health Organization defines a disease outbreak as the occurrence of disease cases in excess of normal expectancy (https://www.who.int/). An infection, transmitted from one human to another, animals to humans, from the environment or other sources, can result in a disease outbreak. It is worth to take precautionary actions before a disease becomes widespread rather than handling large numbers of patients within a short period of time. Public health authorities of a country/government needs to identify the exact outbreak location in advance in order to take necessary steps to control the spread of a disease.

Health Indicator Surveillance, Symptom based Surveillance and Internet based Bio-surveillance are some of the methods used for disease surveillance (Buckeridge, 2007). However, these surveillance systems are time consuming and cost ineffective. With the development of rapid data collection tools, shareable database platforms and modern data analytical tools, computerized disease surveillance systems have today become very popular. These systems are cost effective and has the ability to detect a diseases outbreak location very quickly. Data related to emergency department visits, pharmacy sales, hospital hotline calls, ambulance dispatches has to be effectively analysed to detect disease outbreak areas. Statistical methods play a prominent role in analysing such data.

In Syndromic surveillance medical data are analysed to detect or forecast disease outbreaks (https://en.wikipedia.org/wiki/Public_health_surveillance). A variety of statistical methods are applied in past studies to detect disease outbreaks. A widely used statistical method to detect a shift in the number incidences (infected cases or deaths) by epidemiologists is the CUSUM charts with the assumption of Poisson distribution. However, this method has limitations due to the size, the structure of the at-risk population and the baseline rate which may not be constant during the period of surveillance. An improvement to the CUSUM procedure, based on the normal approximation to a Poisson process was proposed to overcome these limitations (Rossi, Lampugnani & Marchi, 1999).

Forecasting the number of patients/deaths using time series approaches, such as ARIMA models, which is also a popular statistical method applied in disease surveillance. Studies done by Reis and Mandl (2003) and Burkom, Murphy and Shmueli (2007) are a few examples for such applications.

The aforesaid statistical methods take only the time dimension into account when detecting a disease outbreak. However, in general, we say that there is a disease outbreak if a significant number of incidents is evident in a comparatively small area within a short period of time.

Kleinman, Lazarus and Platt (2004) pointed out that the ignorance of spatial variation is a weakness of some widely used statistical methods in detecting a disease outbreak. They applied an approach incorporating generalized linear mixed models to detect incident clusters of a disease in small areas. In addition to generalized linear mixed models, multiple linear

regression, Poisson regression and logistic regression have been also used to detect disease outbreaks (Wieland, Brownstein, Berge, & Mandl, 2007).

Scan Statistic is a density-based clustering technique which is used to detect clusters in a series of randomly positioned points (Tilakaratne & Liyanage-Hansen, 2018). This is the most popular statistical method used in detecting disease outbreaks. Spatial Scan Statistics (Kulldorff & Nagarwalla,1995) is the first version of scan statistic that was applied for detecting spatial clusters of a disease. Ignorance of the time dimension is a major drawback of this method. Then space-time scan statistic (Kuldroff, 2001) which accounts for both space and time dimensions in detecting disease outbreaks was introduced. Thereafter, several versions of space-time scan statistics were developed from time to time and those versions are currently very popular. However, all these scan statistics assumes Poisson distribution to identify significant disease clusters and this assumption has limitations as the occurrences of an infectious disease are not independent of each other. Other statistical methods which were mentioned beforehand, are also associated with distributional assumptions. Failure of distributional assumptions will lead to false alarms or non-detection of disease outbreaks. Hence, it is worth to consider distributional free statistical methods to detect disease outbreaks.

Mann Whitney scan statistic (Cucala, 2016) allows the detection of clusters in continuous data indexed by time or by space, without using any distributional assumptions. However, inability of taking into account both space and time simultaneously prevents the application of this method in detecting disease outbreaks. Under the author's guidance, Hettige (2019) developed the Space-time Mann Whitney scan statistic by extending the Mann Whitney scan statistic which was applied successfully to detect disease outbreaks using a simulated data set. High computational time taken for calculating space-time Euclidian distances between individual data points is a drawback in this statistic.

Future research directions must focus on the reduction of the computation time of the Space-time Mann Whitney test. Application of an improved clustering algorithm to identify disease clusters is one option. Instead of ARIMA models, the spatial-temporal aspect can also be incorporated by applying the Spatio-temporal Autoregressive models to forecast the number of infected persons.

References
Buckeridge, D. L. (2007), Outbreak detection through automated surveillance: a review of the determinants of detection, Journal of biomedical informatics, 40(4) 370-379.

Burkom, H. S., Murphy, S. P., & Shmueli, G. (2007), Automated Time Series Forecasting for Biosurveillance, Statistics in Medicine, 26 (2) 10.1002/sim.2835.

Cucala, L. (2016) A Mann–Whitney scan statistic for continuous data, Communications in Statistics - Theory and Methods, 45(2), 321-329, DOI: 10.1080/03610926.2013.806667.

Hettige K, H. (2019). Application of widely used Spatio Temporal Scan Statistics to detect disease outbreak areas: A case study (Unpublished BSc thesis), Department of Statistics, University of Colombo.

Kleinman, K., Lazarus, R. & Plat, R. (2004). A generalized linear mixed models approach for detecting incident clusters of disease in small areas, with an application to biological terrorism, American Journal of Epidemiology, 159(3) 217–224.

Kulldorff, M. & Nagarwalla, N. (1995) Spatial Disease Clusters: Detection and Inference. Statistics in Medicine, 14, 799-810.

Kulldroff, M. (2001). Prospective time periodic geographical disease surveillance using a scan statistic, Journal of the Royal Statistical Society: Series A (Statistics in Society), 164(1), 61-72.

Reis, B. Y. & Mandl K. D. (2003). Time Series Modeling for Syndromic Surveillance, BMC Medical Informatics and Decision Making, 3(2). https://doi.org/10.1186/1472-6947-3-2

Rossi, G., Lampugnani, L. & Marchi, M. (1999). An approximate CUSUM procedure for surveillance of health events, Statistics in Medicine, 18(16) 2111-2122.

Tilakaratne, C. D., & Liyanage-Hansen, L. (2018). A Review of Strengths and Weaknesses of SpatioTemporal Data Analysis Techniques, International Conference on Machine Learning and Data Engineering, Sydney, Australia.

Wieland, S. C., Brownstein, J. S., Berger, B. & Mandl, K. D. (2007). Density-equalizing Euclidean minimum spanning trees for the detection of all disease cluster shapes, Proceedings of the National Academy of Sciences of the United States of America, 104 (22) 9404-9409; DOI: 10.1073/pnas.0609457104

ABSTRACTS

Variation in amino acid composition of rice (*Oryza sativa* L.) as affected by the cooking technique

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The study was aimed at investigating the impact caused by the cooking method and the rice type on the amino acid (AA) levels in cooked rice. Four rice types (fully milled raw, non-milled raw, fully milled parboiled and non-milled parboiled) that were cooked using five different methods with rice cooker (RC) and gas cooker (GC) were analyzed for the AA composition using liquid chromatographic techniques. Rinsing prior to cooking accounted for elevation of nutritional gamma amino butyric acid (GABA) levels in raw rice. However, rinsing did not have any significant ($p<0.01$) impact on the total amino acid (TAA) levels in all rice types while causing inconsistent variations in free amino acid (FAA) levels. Irrespective of the rice type, both total and FAA levels decreased upon cooking. The fully milled raw rice showed the overall highest loss in total FAAs. However, except for the cooking with draining method, fully milled raw rice reported relatively the lowest percentage loss in TAA levels upon cooking. Under identical water to rice ratio (2:1), raw rice types cooked using the GC and RC demonstrated comparable TAA levels. However, for parboiled rice types, rice cooked with RC retained significantly higher TAA levels compared to the rice cooked using the GC. Cooking rice in excess water with draining and cooking with soaking accounted for the overall highest losses in total and FAAs in all raw rice types. During cooking with the draining method, parboiled rice retained higher TAA levels compared to the raw rice types. Study indicates that the change of AA levels in different rice types upon cooking significantly varied with the cooking technique used. Hence, findings highlight the importance of selecting cooking practices that would ensure the optimum AA retention in cooked rice.

Validation of a reversed-phase high performance liquid chromatographic method for the determination of stevioside and rebaudioside A in food and beverages

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Currently there is a trend of using non-caloric high-intense sweeteners, as substitutes for sugars in food, carbonated and non-carbonated beverages to acquire the required sweet taste. Steviol or steviol glycosides that has stevioside followed by rebaudioside A, as major components is used as one of non-caloric natural sweeteners with a sweetening potential of 250-300 times more than that of sucrose. The aim of the present study is to develop and validate a HPLC method to determine the most abundant steviol glycosides in Sri Lankan food and beverages. The analytes were separated by C18 column (250 mm x 4.5 mm, 5 µm) at 35 °C with an eluent composed of 20 mM phosphate buffer and acetonitrile in a ratio of 65:35 (v/v). Detection was carried out with the diode array detector at the wavelength of 210 nm. Validation of the method performed in terms of limit of detection (LOD), limit of quantification (LOQ), linearity, working range, precision and accuracy according to the Eurachem guidelines using USP reference standard. LOD values for stevioside and rebaudioside A, were 2.6 mg/kg and 3.9 mg/kg while the LOQ values were 3.1 mg/kg and 4.6 mg/kg respectively. Working range of stevioside and rebaudioside A were 2 mg/kg to 500 mg/kg and 5 mg/kg to 500 mg/kg respectively with a linearity of ≥0.9999. Accuracy for stevioside was between 86.8%-102.4% while for rebaudioside A, it was between 80.7%-118.7% for spiked levels from 25 mg/kg to 300 mg/kg. The precision for both stevioside and for rebaudioside A, were lower than 3.5% when expressed as relative standard deviation. In conclusion, the developed analytical procedure is sensitive, simple, and accurate to determine the levels of stevioside and rebaudioside A, in carbonated and non-carbonated beverages and sugar free biscuits.

Effect of long term consumption of porridges made with *M. charantia* on glycemic and lipidemic parameters of diabetic Wistar rats and cytotoxicity assay

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Many diabetics use *M. charantia* and claim that it has a glucose lowering effect. The present study was conducted to evaluate the long-term effect of consumption of *M. charantia* porridges made with different parts of the plant; fruit (FR), leaves (LF), seeds (SS) on diabetic Wistar rats. The glycemic and lipidemic parameters of diabetic rats and the potential cytotoxicity of aqueous and methanolic extracts of *M. charantia* were also studied using brine shrimp assay. Normal control (NC) and diabetic control rats were fed with the standard rat diet while porridges made with FR, LF, SS and coconut milk porridge (CM) were included into diets of diabetic rats. The study was continued for three months. Fasting blood glucose was measured at the end of each month. After three months, HbA1c, fasting blood glucose (FBG), Creative Protein, total cholesterol (TC), and high-density lipoprotein (HDL) levels were monitored. Significantly higher feed and water intake was observed among diabetic groups when compared to NC ($p < 0.05$). All animals in FR (mean $= 40 \pm 19$ g) and NC (mean $= 115 \pm 9$ g) groups gained weight in contrast to the other groups. Between the diabetic groups, FR group had the lowest mean value for fasting blood glucose (FBG) and increment percentage of FBG (44.38%) and HbA1c (5.8 ± 2.1). Increment percentage of FBG and HbA1c of FR group was not significantly different ($p > 0.05$) to the NC (35.16%; 4.7 ± 0.7). Lowest TC level among the diabetic groups (119 ± 20.6 mg/dL) and highest HDL values (33 ± 6.3 mg/dL) were also monitored in FR group. The study proved that FR porridge reduced the loss of weight, elicited hypoglycemic and hypolipidemic properties in diabetes induced Wistar rats. Methanolic extracts had a higher cytotoxic potential (LD_{50} values of water extract was 1000 ppm and 400 ppm where methanolic extract was 80 ppm and 10 ppm respectively after 24 h and 48 h) due to constituents, saponins and phenolics.

Screening of *Monascus* spp. on water-soluble adipogenesis inhibitory activity

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Monascus-fermented rice, which is known as red mold rice has been used as Chinese herbal medicine for treating hyperlipidemia for many years. Monacolin K and citrinin, showing adipogenesis inhibitory activity, are water-insoluble secondary metabolites of *Monascus* spp. However, less attention has been paid regarding water-soluble adipogenesis inhibitors from *Monascus* spp. Thus, the current study was conducted to screen *Monascus* fungi for their water-soluble adipogenesis inhibitors. A total of 25 strains of *Monascus* fungi were used in screening for water-soluble adipogenesis inhibitors. *Monascus* strains were maintained on potato dextrose agar (PDA) medium at 30 °C for 7 and 10 days, and the spores of these strains were collected and stored separately at 4 °C until further use. Each strain was cultivated on steamed rice (RMR) and barley (RMB) separately at 30 °C and 35 °C for 7 and 14 days, and their respective water extracts were prepared. Cell viability was determined by MTT assay, and the accumulation of triglycerides in adipocytes was examined by oil red O staining using mouse 3T3-L1 cells. Results of MTT assay confirmed that all tested samples do not affect the viability of 3T3-L1 cells, and this confirmed that the reduction of lipid accumulation is not due to any cell death, but due to a secondary metabolite/s produced during the production of RMR or RMB. Moreover, TLC results revealed that water-soluble fractions of both RMR and RMB are free from lovastatin and citrinin. According to the obtained results, it can be concluded that the water extracts of RMR showed a higher adipogenesis inhibitory activity than that of RMB. Further, since it showed a significantly low lipid accumulation percentage (61.86% ± 3.6) *M. pilosus* NBRC4507 grown at 30 °C for 14 days was selected as the best strain and the cultivation condition respectively, in production of RMR with higher adipogenesis inhibitory activity.

Keywords: Adipogenesis inhibitors, Genus *Monascus*, lipid accumulation inhibition, red mold rice, water-soluble
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Determination of antibacterial activity of *Xylaria feejeensis* endophytic fungi from *Geophila repens*

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Geophila repens is a perennial herb with medicinal properties in the Rubiaceae plant family. Interestingly, the plant is reported to exhibit antifungal, antioxidant, antibacterial, and anticholinesterase activity. Different parts of the plant are used to treat different diseases such as diarrhea, soreness, earache, cough, and intestinal ailments. Previous studies have shown the antioxidant and antibacterial effects of this plant, however, these effects in relation to its inhabitant endophytes are poorly explored. The objective of this study was to isolate endophytic fungi from this plant and to study antibacterial properties of them. The *G. repens* plant was obtained from the Ayurveda Research Institute, Navinna, and was authenticated by National herbarium, Peradeniya. In order to isolate endophytic fungi of the plant, surface sterilized stem segments were cultured on PDA media for 10-15 days at room temperature. Several fungi were isolated and morphologically identified. Out of many, one fungus was DNA sequenced using universal primers ITS1 and ITS4 and identified as *Xylaria feejeensis*. Ethyl acetate (EtOAc) and methanol (MeOH) extracts of *X. feejeensis* were prepared and both extracts were tested for its antibacterial activity. The antibacterial activity was conducted against two Gram-positive (*S. aureus-ATCC 25928*, *Bacillus cereus –ATCC 11778*) and two Gram-negative (*P. aeruginos–ATCC 9027, E.coli-ATCC 35218*) bacteria by disk diffusion method. Gentamycin was used as the positive control and the solvent itself was used as the negative control. Only the EtOAc extracts of *X. feejeensis* showed significant antibacterial activity against both Gram positive bacteria *S. aureus* (10.3 ± 0.6 mm for 300 µg/disk) and *B. cereus* (12 ± 0.1 mm for 600 µg/disk). Minimum inhibitory concentration (MIC) of EtOAc extract of *X. feejeensis* for *S. aureus* is 50 µg/disk (6.8 ± 0.3 mm) and *B. cereus* 100 µg/disk (7.2 ± 0.2 mm). Further, these results revealed that the presence of compounds with antibacterial activity in the isolated fungal extract. The investigations of endophytic fungi with effective antibacterial activity demonstrate the potential for producing novel drug leads.

Investigation of antimicrobial properties of *Axinella donnani* and *Xestospongia sp*.

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Sponges (phylum Porifera) are sessile marine filter feeders that have developed efficient defense mechanisms against their enemies which include viruses, bacteria, or eukaryotic organisms. Sponges are a good source of nucleosides, terpenes, sterols, cyclic peptides, alkaloids, fatty acids, peroxides and amino acid derivatives. These types of extracted bioactive substances have shown excellent anticancer, antibacterial, antifungal, antiviral, antiprotozoal, anthelmintic, anti-inflammatory, immunosuppressive, neuro suppressive and antifouling activities. However, very few studies have been conducted on Sri Lankan sponge fauna to investigate such properties. Hence, the main objective of this study was to investigate the antimicrobial activity of selected sponge samples from Pigeon Island, Trincomalee, Sri Lanka. Methanol (MeOH) and 1:1 dichloromethane:methanol (DCM:MeOH) extracts of *Axinella donnani* and *Xestospongia sp.* were tested for antimicrobial activity via disk diffusion assay against Gram positive bacteria: *Bacillus subtilis, Staphylococcus aureus*; Gram negative bacteria: *Pseudomonas aeruginosa, Escherichia coli* and two fungi, *Penicillium notatum, Curvularia lunata*. Antibacterial assay of the present research revealed that only methanol extracts of *Axinella donnani* sponge has antibacterial activity against Gram negative bacteria; *P. aeruginosa* showing 10.3 ± 0.1 mm inhibition zone. However, other three extracts did not show any antibacterial activity against the tested Gram positive and Gram negative bacteria. The methanol extract of *A. donnani* was subjected to Minimum Inhibitory Concentration (MIC) assay and the results showed the MIC value of 300 µg per disk for *P. aeruginosa*. Also, antifungal assay with MeOH and DCM:MeOH extracts did not show any activity against the both fungal species tested in the study. Further studies are ongoing to isolate antimicrobial compounds from *A. donnani* sponge.

Determination of the stability of cysteine-rich peptides isolated from the deep-sea marine sponge *Stryphnus fortis* in human serum

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Cysteine-rich peptides are potential candidates for a broad spectrum of applications due to their highly stable disulfide frameworks. A handful of cysteine-rich peptides have been isolated from marine sponges so far. Investigation of the stability in body fluids would be important to utilize these peptides specially in *in-vivo* applications such as development of drug leads and drug delivery agents. Initially, the aqueous (60% Methanol in water) extract of the deep-sea marine sponge *Stryphnus fortis* (Demospongiae, Tetractinellida, Ancorinidae) was fractionated using Fast Protein Liquid Chromatography. The fractions consisting of peptide like masses were further purified using Reversed Phase – High Performance Liquid Chromatography to isolate three peptides, peptide A, B and C, having three intramolecular disulfide linkages between six cysteine residues. The stability of these peptides in human serum was evaluated up to 24 h including the time intervals 0, 3, 6 and 8 hrs. The percentage of peptides remaining in serum at each time interval was quantified using Liquid Chromatography coupled to Ultraviolet detector at 215 nm. Approximately 85% of the peptides remained without degradation for up to 24 h, which signifies an extreme stability of peptide A and C in human serum. In contrast, a drastic decrease of peptide B was observed from 90% to 20% within 6 h to 24 h. Asteropsin A to G from the sponge genus *Asteropus* are the only known linear knot peptides from sponges that showed extreme stability in both human plasma and gastrointestinal fluids due to its highly stable disulfide framework. Further studies are required to understand the deviation of peptide B as well as to determine the cytotoxicity and oral bioavailability of peptides A and C to broaden their potential applications in a therapeutic setting. Discovery of cysteine-rich peptides is important to unravel their ecological role and to establish their potential applications in pharmaceutical and biotechnological fields.

Modified GC temperature program method for analysis of fatty acid profiles in ready-to-eat composite diets in Sri Lanka using correction factors

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The official methods (AOCS Ce1j-07 and Ce1h- 05), describe the methods for analyses of fatty acids in specific fat sources and consists of several steps including GC temperature program to resolve all fatty acids and the use of either theoretical correction factor (TCF) or empirical correction factors (ECF) for flame ionization detector response of each fatty acid. Determination of fatty acids in ready-to-eat diets using these GC temperature programs have not consistently resolved the chromatographic peaks due to complexity of the matrix and due to chromatographic conditions. This study aims to develop a temperature programme specific to laboratory GC conditions to resolve the long chain fatty acids in ready-to-eat diets. The laboratory optimized new programme (initial temperature of 90 °C increased to 140 °C with 5 °C min^{-1} and then to 175 °C with 0.5 °C min^{-1} rate in turn increased to 220 °C at 20 °C min^{-1} and held for 20 min) has separated all 44 fatty acids in the reference standard mixture (GLC 714, Nu-check prep, USA) with improved resolution and sensitivity, including co-eluted polyunsaturated fatty acid pairs (C20:3n3, C20:4n6), (C20:4n6, C23:0), (C20:5n3, C24:0) and (C24:1, C22:4) compared to AOCS conditions. Two types of diets, fried rice and rice and curry (n=18), were randomly sampled from the Colombo municipal area and analyzed for fatty acid composition using ECF and TCF separately, in the modified GC temperature program. The NIST certified secondary reference material was used as a quality control sample. The test data of fatty acids composition were revealed, that use of laboratory specific ECFs for determine some of the saturated and monounsaturated fatty acids (between C4:0 to C18:0) including C16:0, C17:0, are more accurate and reliable and also the modified temperature program is able to analyse both saturated and higher chain polyunsaturated fatty acids with better accuracy and sensitivity in the food matrix of ready-to- eat diets.

Keywords: Empirical correction factors, fatty acids, GC temperature program, theoretical correction factors
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Dye removing ability of metal oxide nanoparticles synthesized with plant extracts

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Release of untreated effluents from various industries into water bodies is one of the main concerns of environmental pollution. Among many pollutants released into waterways, dyes are one of the major contributors of water contamination. Hence, it is necessary to find more environmentally convenient methods to remove these dyes from waste effluents. In this research, the potential of metal oxide nanoparticles synthesized with plant extracts to remove dyes in water media was investigated. Copper oxide nanoparticles were synthesized from dried Kahata (*Careya arborea)* leaf extract using the co-precipitation method and characterized using UV-vis spectroscopy, Fourier-transform infrared spectroscopy, scanning electron microscopy, and X-ray powder diffraction. The synthesized nanoparticles were tested for removing Rhodamine B (RB), a basic dye and Acid Orange 7 (AO7), an acidic azo dye under different conditions including pH, light source, irradiation time, temperature and the amount of nanoparticles. Highest dye removal was observed with both dyes at acidic pH ($\leq$ 4), under sunlight when treated for 1 h. Further, an increase in dye removal was observed at elevated temperatures (~80 °C). Dye removal capacities were found to be 68% for RB (10 mg L^{-1} initial dye concentration, 50 mg/mL of nanoparticles) and 70% for AO7 (50 mg L^{-1} initial dye concentration, 20 mg/mL of nanoparticles) when treated for 1 h at pH 4 and ambient temperature under sunlight. Similar removal capacities were observed after simple ethanol wash, up to 2 and 3 cycles for AO7 and RB, respectively. Dye removal capacities for chemical synthesized nanoparticles without plant extracts were ~20% and ~50% for RB and AO7, respectively. Dye removing mechanism was studied using adsorption isotherms and both Langmuir and Freundlich isotherms showed best fits to data indicating possibility of variable adsorption sites due to different functional groups on nanoparticle surface. This study showed an improved dye removal ability of green synthesized CuO nanoparticles compared to chemically synthesized CuO nanoparticles. This could be attributed to the incorporation of various functional groups from plant extract onto the surface of the nanoparticles in green method.

In-silico study of binding interaction of a xanthone of *Hypericum mysorense* with aldose reductase

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In present, emphasis on plant research has vastly increased worldwide and a large body of evidence has been collected to show the immense potential of medicinal plants used in various traditional systems. *Hypericum mysorense*, is one such plant, a shrub with yellow flowers commonly found in central highlands of Sri Lanka. The timber of this plant has been reported to contain the xanthone, 3-hydroxy-2-methoxy xanthone, which has shown promising binding interactions with Aldose Reductase (AR), as a result inhibiting its action. AR is known to play a vital role in the secondary complications of diabetes, and therefore its inhibition proves to be an important drug target for the treatment of diabetes. For the *in-silico* studies, Tolrestat was used as reference. Docking and Binding energy calculations were performed using AutoDock Vina, and the active site of AR was defined using data from literature studies. Receptor and ligand complexes were subjected to Molecular Dynamic (MD) simulations using AMBER with GPU acceleration, where the dynamic behaviour of protein-ligand complex at different timescales was determined. MD simulations is applied in order to explore conformations of the protein receptor, optimize the structures of the final complexes, and calculate accurate energies. RMSD plots of the protein-ligand complexes within a 100 ns long trajectory were compared and it was prominent that 3-hydroxy-2-methoxy xanthone was well bound and stable within the active site of AR as compared to Tolrestat. This was further validated using the interaction diagrams of the ligands within the active site pocket. Followed by the MD studies, the absorption, distribution, metabolism, and excretion (ADME) properties, pharmacokinetic properties and the druglike nature of 3-hydroxy-2-methoxy xanthone was studied. 3-hydroxy-2-methoxy xanthone showed favourable physiochemical properties for oral bio availability with a very high gastrointestinal absorption and blood brain barrier permeation using the SwissADME web server.

Analysis of volatile constituents of *Gyrinops walla* Gaertn. found in the Sinharaja Forest Reserve

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Gyrinops walla Gaertn. (Family- *Thymelaeaceae*) is an evergreen tree which grows in the wet zone of Sri Lanka. It is locally known as "Walla patta" and is also known as "Sri Lankan agarwood" or "Sri Lankan agaru" in the international market. Further, it is the only endemic species found in Sri Lanka, which produces an agar-wood type resin. Due to its unique fragrance and high retention of fragrance, it is mainly used in perfumery industry as well as cosmetics, incenses, ingredient in traditional medicine and aroma therapy. Two heart wood samples representing *G. walla* Gaertn. trees located in the Sinharaja forest (Trees located closed to Deniyaya entrance and close to Kudawa entrance) were subjected to hydro-distillation, resulting in essential oil yields of 0.2 ± 0.05 % and 0.3 ± 0.05 % (w/w), respectively. Using GC–MS analysis, a total of 57 (85.4% of the total volatiles) and 48 (84.7% of the total volatiles) volatile compounds were identified respectively. The two oil samples showed quite different volatile profile, however most of the major compounds are common, which is characterized by the dominance of β-patchoulene, naphthalene derivative, prezizaene, allo-khusiol, aromadendrene oxide-(2), (E)-isovalencenal, aristol-1(10)-en-9-ol, spiro[4.5]dec-8-en-7-ol, 4,8-dimethyl-1-(1-methylethyl), khusiol, 5-isopropylidene-6-methyldeca-3,6,9-trien-2-one, longiverbenone, khusimol and (-)-isolongifolol. Desired compounds, such as (-)-isolongifolol (15.1 - 20.9%), khusimol (5.6 - 6.2%), allo-khusiol (14.4 - 18.5%) khusiol (1.0 - 1.1%) and longiverbenone (3.4 - 3.8%), suggesting that the essential oils could be commercialized as fragrant materials of high value. Further, the study implies that, stem essential oil of *G. walla* Gaertn. has very unique chemical profile which deviates from the other type of agarwood chemical profile including *Aquilaria crassna* and *Aquilaria malaccensis*. Therefore, GC-MS finger print can be implemented as an international recognized test for identification of *G. walla* Gaertn. from other agarwood bearing stems of *Aquilaria crassna* and *Aquilaria malaccensis*.

Multifunctional HAP nanocomposites for antimicrobial activity

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Contamination of water bodies by chemical and biological pollutants has resulted in shortage of clean and safe drinking water all over the world. Hydroxyapatite based nanocomposites have been identified as promising materials which can be used in water purification as adsorbents due to their versatile adsorption properties. In addition, these materials have a great potential to act as antimicrobial agents. In this work different HAP based nanocomposites which were identified as promising adsorbents in our previous and ongoing work were considered to evaluate and compare their antimicrobial properties. Nanocomposites of HAP were prepared with four biopolymers, (chitosan (CTS), carboxymethylcellulose (CMC), alginate (ALG) and gelatin (GEL)), montmorillonite (MMT) as a nano clay and titanium dioxide (TiO_2) as a nontoxic metal oxide and they were named as HAP-CTS, HAP-CMC, HAP-ALG, HAP-GEL, HAP-MMT and HAP-TiO_2 respectively. All the synthesized materials were characterized using Fourier-Transformed Infrared Spectroscopy (FTIR), Scanning Electron microscopy (SEM) and X-ray Diffractometry (XRD). Antimicrobial activity of these composites were compared using *E.coli* as a gram negative bacteria and *S. aureus* as a gram positive bacteria by measuring the optical density (OD) at 600 nm in the presence of the bacterial samples with 20 mg of each composite in 50 ml of fresh LB broth, for 10 h in 30 minutes time intervals. According to results, antimicrobial properties were amply exhibited by all nanocomposites compared to the control. Of all composites, HAP-TiO_2 showed the highest activity and its activity for *E. coli* and *S. aureus* were 58.9% and 71.1% respectively. Therefore, HAP-TiO_2 was identified as the best HAP based nanocomposites to remove both *E. coli* and *S. aureus* from water.

Synthesis of MMT-La-Alginate composite for water purification

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In this study, MMT-La-Alginate (MMT-La-ALG) composite was synthesized, characterized, and analyzed for its fluoride adsorption capacity and antibacterial properties. The composite was synthesized using MMT, lanthanum nitrate, and sodium alginate, and characterized using SEM-EDX, TGA, and FT-IR. Investigation of the morphology of the composite using SEM-EDX mapping showed the uniform distribution of Lanthanum (III) throughout the surface of composite. The TGA analysis of the composite showed the presence of a 1:0.6 (w/w) ratio of alginate and inorganic materials (MMT and lanthanum based materials) in the composite. Also the blue shift appeared at the region 1644 cm^{-1} (stretching vibrations of O-C-O) of FT-IR spectrum of MMT-La-ALG evidence the formation of La alginate complexes. The prepared MMT-La-ALG composite was used for the removal of fluoride ions from drinking water. The adsorption isothermal profile of the fluoride was well fitted with the Langmuir adsorption isothermal model and it indicates that the adsorption process at equilibrium is on a homogeneous surface and binding sites of MMT-La-ALG for fluoride ions are energetically equivalent. In this study, it was found that the equilibrium fluoride adsorption capacity on the composite was 40 mg/g. Furthermore, kinetic studies carried out showed that the fluoride adsorption on to MMT-La-ALG follows pseudo-second-order kinetics. Further, the antibacterial performance of MMT-La-ALG against *E. coli* and *S. aureus* was also studied by monitoring the bacterial inactivation. Results showed significant anti-bacterial property of MMT-La-ALG, indicating its potential in applying water disinfection protocols. Consequently, it can be concluded that the prepared MMT-La-ALG is a versatile adsorbent and therefore promising material to be used in water purifications.

Comparative analysis of *Kajjali* (1:1) in Ayurveda *Rasashastra* with synthesized β-HgS

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The black colour compound prepared manually by grinding purified mercury and purified sulphur is known as *kajjali* in Ayurveda *rasashastra*. This insoluble inorganic compound is known as β-HgS in chemistry. Although *kajjali* has been evaluated as a nano-range compound, there is no comparative research evidences with synthesized β-HgS. Therefore this research was carried out to elucidate the structural, chemical patterns of *kajjali* (1:1) with β-HgS. For this purpose, purified mercury and purified sulphur (1:1) were manually ground in a ceramic motor to obtain *kajjali* (1:1). β-HgS was synthesized using a controlled precipitation process by injecting Na_2S and NaOH into the $Hg(NO_3)_2$ solution. The prepared samples were analysed using Scanning Electron Microscopy (SEM), Energy Dispersive x-ray Spectroscopy (EDS), X-ray diffraction (XRD), Fourier Transform Infrared Spectrometry (FTIR), Raman spectroscopy, X-ray Fluorescence (XRF) spectroscopy, particle size analysis (PSA) and CHN elemental analysis. According to SEM images (10.0kV, x50.0k) of the samples highlighted the agglomerated nano-spheres in the *kajjali* while in nano-spheres coupled with nano-flakes in the β-HgS. The EDS data show mercury (47.5%) and sulphur (31.5%) in *kajjali* and mercury (80.5%) and sulphur (11.5%) in β-HgS. XRD peaks agree with meta-cinnabar in both samples and low intense peaks remained reference to free sulphur in *kajjali*. FTIR spectra of *kajjali* explains the changes in functional groups while purification in Ayurveda and Raman spectra of β-HgS shows the amorphous nature. XRF results reveal higher sulphur percentages in both samples and it is with good agreement with support of sulphur in chelation. PSA show the particles within the 58.77 nm–1718 nm in *kajjali* and 58.77 nm–712.40 nm in β-HgS. CHN analysis shows changes in carbon, hydrogen and nitrogen levels in both samples with their procedures. Although samples show the similarities, still *kajjali* expresses more applicability as a medicine according to FTIR and EDS data.

Improving the moisture management properties of cotton fabrics with chitin nanofibers

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Effective moisture management of fabric will depend mainly on its ability to transport moisture away from the inner side of the fabric to the outer surface where more spreading and evaporation occurs. This will significantly enhance the drying rate while providing a cool and dry feeling to the wearer. Cotton has poor moisture management properties compared to other types of fabrics, primarily driven by low wicking rate and high moisture absorption capacity. Cotton has been subjected to partial carboxymethylation (pCM) through the reaction with monochloroacetic acid in the alkali medium to increase overall wicking property. Fabrics were treated with 2 M NaOH and 1 M monochloroacetic acid at 80 °C for 30 min. The reaction occurs in an alkaline setting where nucleophilic substitution between sodium cellulose and monochloroacetate takes place. FT-IR band emerging around 1734 cm^{-1}, which was attributed to carboxylic acid groups confirmed the reaction. Chitinnanofibers (CNFs) were prepared by fibrillation of crab shell chitin using ultrasound technique and used as a side selective surface modifier through a special apparatus. The objective of this treatment is to increase the moisture absorbance capacity in one side of the fabric to facilitate moisture across the fabric structure. This surface modification was confirmed by SEM and AFM analysis. Modified fabrics showed improved wicking and spreading ability and higher water-binding capacity compared to untreated cotton fabrics. The pCM reaction shown to increase the wicking rate (at 10 min) by 27.4%. It was also seen that with the CNFs treatment of pCM cotton fabric, the moisture pickup ratio significantly reduced from 26.1 ± 3.8 % in cotton to 8 ± 1.7 % in pCM with 0.75 g/l CNFs (0.75CNF) treatment. However, the drying rate of fabrics modified with CNFs was found to be lower than that of untreated cotton fabrics as remained water ratio of the cotton fabrics were maintained at ~58% while 0.75CNF system showed only 67%. This property can be improved by using different strategies in future research.

Application of thermally derived merino wool carbon quantum dots for the detection Hg^{2+} in aqueous medium

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A facile, simple and low-cost approach for synthesizing highly fluorescent carbon quantum dots (CQDs) is reported. Wool consists of amino acids linked together by peptide linkages is abundant in C, N, H, O and S. Due to the presence of N containing chemical compounds can be used to synthesize CQD with relatively high quantum yield. Carbon quantum dots (CQDs), as an emerging type of fluorescent nanomaterial, have drawn the attention in recent years due to their unique properties, such as low-cost, easy synthesis, good water dispersibility, stable fluorescence, low toxicity and biocompatibility. Herein, we report a novel and simple approach for synthesizing highly fluorescent CQDs by a one-step thermal treatment of merino wool fibers. The as-prepared CQDs with a quantum yield (QY) of 30 % showed excitation-dependent emission behavior, excellent photo stability and high stability in high salt conditions. We have studied the application of CQDs as nanosensors for metal ions. The CQDs can be utilized to detect Hg^{2+} with good selectivity and sensitivity via Hg^{2+} induced fluorescence quenching mechanism. TEM and AFM analysis showed the prepared CQD are in the size range of 7-9 nm. The derived CQDs are rich in nitrogen and oxygen with hydroxyl, carboxyl and amine groups.

A simple reciprocal service cost allocation model and a generalization - for manufacturing firms

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A simple reciprocal service cost allocation model is a prime requirement of all manufacturing firms as cost accountants find it difficult to understand most existing models. This research is aimed at addressing this limitation. Initially, an easily understandable reciprocal service cost allocation model using a system of linear difference equations is introduced. This is a new model, and is solved using the theory of linear difference equations. Then this model is converted into the existing linear algebra model, which is solved using general matrix theory. It is assumed throughout that all service departments serve at least one production department, which is a meaningful assumption for real life problems. Any set of allocation ratios chosen for the service departments satisfying this general assumption will lead to a matrix of the form $\begin{pmatrix} 0 & B \\ 0 & A \end{pmatrix}$, where the matrix $A = (\mu_{ij})_{n \times n}$ represents the proportions of the reciprocal cost allocation between service departments, where n is the number of service departments and μ_{ij} denotes the proportion of service department j's overheads assigned to service department i, at each allocation. The matrix $B = (\eta_{ij})_{m \times n}$ represents the proportions of service costs allocated to the production departments, where m is the number of production departments and η_{ij} denotes the proportion of service department j's overheads assigned to production department i, at each allocation. A special property of A is that it is a non-negative square matrix with all column sums less than one. This property is used to establish unique solutions for both models. Two simple problems are solved using these models and a sensitivity analysis is done for the entries of A in one problem. Finally, complete solving techniques using both models are explained for reciprocal allocation problems with dual cost allocation ratios, one for variable cost and another for fixed cost, for the service departments' costs. This technique can be easily extended to any number of cost classifications within the service departments. Furthermore, for each model, an R-programming script is written, which provides readily usable formats for users.

Framework for optimal pulse sequence design for balanced steady state free precession in magnetic resonance fingerprinting (MRF)

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Magnetic resonance fingerprinting is an emerging technique that allows for a non-invasive quantification of multiple tissue properties by using a set of acquisition pulses. To accurately classify the tissue properties, the measured signal evolutions arising from nuclear magnetisation should be as separable from one another as possible. As the signal evolutions are a function of both tissue properties as well as pulse excitation parameters, the magnetisation signals generated are varied by physically changing the pulse excitation parameters in a Magnetic Resonance Imaging machine. In MRF, the pulse sequence parameters are traditionally chosen at random, leading to the risk that some of the magnetisation signals may not be separable. Therefore, in this study, a simulation framework to optimise the level of separability of magnetisation signals from different tissues using a balanced steady state free precession [BSSFP] sequence is demonstrated. A Bloch equations simulator for a BSSFP sequence was built to simulate the magnetisation of tissues. The input variables of a BSSFP sequence are flip angle, time to repeat the pulse and number of images. An optimising mechanism was built by combining a genetic algorithm and a distance correlation function which indicates the level of separability of the magnetisation signals. The combined system was run a number of iterations until convergence was achieved. Given the parallel nature of the Bloch equations and the distance correlation function, to improve the speed of execution, the system was coded to utilise a Graphical Processing Unit [GPU]. It was observed that, not only was the system able to increase the separability of magnetisation signals as the generations of the genetic algorithm progressed, but that the number of images required could also be maintained as low as thirty.

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Experimental verification of range estimation for a dark-field entomological passive LIDAR

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Application of dark-field passive LIDAR in entomological studies has been an emerging technology which is capable of identifying insects and detecting their activities in situ. With the use of simplistic instrumentation, passive LIDAR is capable of producing results comparable to more sophisticated technologies such as RADAR and Active LIDAR, although range resolving in passive LIDAR is a challenging task. Moreover, it has a minimal impact on the targeted flora and fauna, and no associated health hazards. One promising method of range estimation is to use a passive LIDAR range equation developed based on ray tracing. The objective of this study is to experimentally evaluate the passive LIDAR range equation (under its linear mode). The intensity variation of the probe volume was recorded by using a quadrant photodetector (QPD) attached to the image plane of a Newtonian telescope (f=1200 mm, $\emptyset_{tel}$ = 20 cm). The system was calibrated by observing the time domain parameters of the intensity variations of adjacent QPD segments corresponding to a pendulum oscillation. These were conducted at different locations along the probe volume with 10 m increments. System parameters were adjusted to comply with the passive LIDAR range equation's linear mode. This was done by matching the width of the QPD image on the dark terminator with the diameter of the telescope aperture. It was observed that the range can be estimated with an accuracy of $\pm$ 3.29 m for a maximum range of 80 m. The observations were aligned with previously published simulated insect signal-based retracing. It was also noted that the deviations in range estimation accuracy is due to the finite thickness of the pendulum and it can be minimized by using a thinner pendulum. This method can be applied to resolve the range information on daytime insects.

Exploration of the lightning climatology over the University of Colombo and its surrounding area

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A study of spatiotemporal variation of lighting activities over a particular area is a critical investigation to explore lightning risks and to propose and implement appropriate safety guidelines for the community. Lightning climatology over the University of Colombo (6.9000^0 N, 79.8588^0 E) and its surrounding region covering an area of 20 km × 20 km was studied using lightning flash data obtained from the Lightning Imaging Sensor (LIS) onboard NASA's Tropical Rainfall Measuring Mission (TRMM) satellite. Lightning satellite data for the period 1998 to 2014 were gridded in an area of 5 km × 5 km, to analyze the lightning flash density over the study area and a raster lightning flash density map was designed using ArcGIS 10.1 software. The maximum lightning flash density was 20.0 flashes km^{-2} $year^{-1}$ recorded at 3.52 km and 10.58 km away from the university premises. Moreover, the overhead annual lightning flash density over the university area was 10.0 flashes km^{-2} $year^{-1}$. Furthermore, the maximum number of lightning flashes (49%) had occurred in the first inter-monsoon season with an overhead flash density of 6.0 flashes km^{-2} $year^{-1}$ over the university premises in the months of March and April for the period of 1998-2014. On the other hand, a lesser number of lightning flashes of 7% had been recorded over the study area during the southwest monsoon season. The maximum number of lightning hits had occurred in April and the second highest number during November. It is suggested that the university should avoid outdoor activities in the period of the first inter-monsoon season to avoid high lightning hazard risks. It would be better if the university can schedule their work during the southwest monsoon season predominantly in May, June, July, August and September as a lesser number of lightning activities are shown during this season. The diurnal variation shows that 59% of the total lightning flashes occurred in the afternoon hours (12.00 to 18.00 LT) over the university premises. Consequently, afternoon outdoor activities impose higher risks to students' safety, especially during April and November which are the two highly active months for lightning. Results based on satellite data were compared with the thunder data available for the respective period.

Impact of the electrical voltage transient nature of the auxiliary power system on the DC-DC converters in hybrid, PHEV and BEV automobiles

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Numerous design challenges have been encountered due to electrical transients in the circuits and subsystems available in automobiles. These challenges became prominent, especially during the transition from traditional fuel-based automobiles to Hybrids, PHEVs (Plug-in hybrid electric vehicles) and BEVs (Battery EV). Traditional auxiliary operations such as air conditioning and heating directly from the HV battery, while keeping the galvanic isolation of high-voltage (HV) and low-voltage (auxiliary) regions in the automotive supply system, are examples of the associated design challenges encountered. Moreover, EM coupling and transient vulnerability issues affect the sensitivity of deliberate sophisticated solid-state control circuits like DC-DC converters. Furthermore, the transient nature of the loads beyond the acceptable power quality standards will impart severe stresses on the auxiliary system. In battery-supported automobiles, the DC-DC converter with an onboard 200-800 V high voltage battery generates and caters 12 V_{DC} (or 48 V_{DC}) to power up auxiliary elements such as headlights, other lights, wipers, winkers, etc. Thus, measurements and analysis have been carried out to identify the risk levels of such transients for vehicular control, in preference to the DC-DC converters which connect the HV battery and auxiliary side. The aforementioned transient measurements were carried out covering a fleet of late-model hybrid and PHEV automobiles using a Tektronix P6015A High Voltage Probe and a PicoScope 3206A Oscilloscope with 200 MHz resolution. There were 354 transients observed in this study and amplitudes of the voltage transients were recorded up to 45.20 V. The rise time of the transients were recorded within the range of 0.3 – 50 μs and respective burst durations were up to 0.5 ms. The recorded transient amplitudes exceed the rated 13.8 V output value of the commercially available DC-DC converters. These findings will be an eye-opener to the current market of electric vehicles. Thus, it is suggested that manufacturers should improve the respective withstand capabilities against the transients generated in electromechanical segments in EVs.

Multifaceted importance of native dairy microorganisms

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Lactic Acid Bacteria (LAB) and yeasts are extensively employed in food production, preservation and numerous other industrial processes. In the absence of industrial microbial culture production in Sri Lanka, industries solely depend on imported freeze dried cultures. Hence, the objective of the study was to isolate, characterize and identify beneficial LAB and yeasts from Sri Lankan dairies. For the exploitation of beneficial strains, raw bovine milk and curd prepared with indigenous starters were collected from three different climatic zones of the country as per the SLSI: 1404:2010. From over 1045 and 780 different colonies grown on selective media for LAB and yeast respectively, 300 LABs and 246 yeasts were identified from physiochemical tests. Out of these 105 LABs and 56 yeasts possessed strong probiotic properties and 46 LABs and 46 yeasts were safe for live consumption. These isolates were genotypically identified by PCR amplification with universal primers of 16S rRNA gene of LAB (27F and 1495R) and 18S rRNA gene of yeast (ITS1 and ITS4). The pool of beneficial dairy species identified were: *L. plantarum* (n=26), *L. fermentum* (n=12), *L. pentosus* (n=5), *E. faecalis* (n=2) and *L. rhamnosus* (n=1). Advantageous yeasts were *Pichia kudriavzevii* (n=9), *Kluyveromyces marxianus* (n=7), *Clavispora lusitaniae* (n=5), *Diutina rugosa* (n=3), *Candida orthopsilosis* (n=4), *Lachancea thermotolerans* (n=3), *Candida parapsilosis* (n=2), *Debaryomyces hansenii* (n=1), *Wickerhamiella pararugosa* (n=2) and *Yarrowia lipolytica* (n=1) *Pichia* sp. (n=1) *Candida* sp. (n=1), *Candida rugosa* (n=1) *Candida aaseri* (n=2) *Candida tropicalis* (n=1), *Candida versatilis* (n=1) and *Diutina mesorugosa* (n=1). Sequences of the isolates were deposited in GenBank® of the National Centre for Biotechnology Information (NCBI). LAB and yeast isolates with antimicrobial, antioxidative and cholesterol lowering properties could be used as candidates for health food formulation. The LABs capable of utilizing complex carbohydrates and having amylolytic properties could blend with prebiotics to make synbiotic foods. A majority grew, fermented and survived in milk. These milk technological properties were favourable for fermented dairy food development. Number of LABs exhibited potentials to be used in exopolysaccharide (EPS), lactic and acetic acid, virgin coconut oil and bacteriocin production. Yeasts that grew at high osmotic pressures can be ideal candidates in bioremediation and single cell protein (SCP) production. Beneficial isolates obtained from the present study has laid foundation for the establishment of a dairy culture collection within ITI.

Effectiveness of *Aspergillus japonicus* in improving soil phosphate availability in cinnamon plantations

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Use of phosphate solubilizing microorganisms is an inexpensive strategy that can confer solubility of insoluble phosphates (P). *Aspergillus japonicus,* an effective native phosphate solubilizer identified by whole genome sequencing in a previous study was used to investigate the effectiveness of improving soil P in cinnamon (*Cinnamomum verum* Presl syn. *Cinnamomum zeylanicum* Blume) cultivations. A field experiment was conducted at Ekarella Estae, Opanayake, Sri Lanka. Randomized Complete Block Design (RCBD) with nine treatments and three blocks was employed. A total of 27 plots were accommodated with six plants/plot. The treatments were: Inoculum (I)+Carrier material (CM) [T1]; I+CM+Eppawala rock phosphate (ERP) Recommendation [T2]; I+CM+50% of ERP Recommendation [T3]; CM [T4]; CM+ERP Recommendation [T5]; CM+50% of ERP Recommendation [T6]; No ERP [T7]; ERP Recommendation [T8] and 50% of ERP Recommendation [T9]. Muriate of potash and urea were added to all the treatments. Pits (30 cm x 30 cm x 30 cm) were filled with compost and a mixture of ERP and 50 g of inoculum (spore density- 6.5×10^8 g^{-1}) was applied. Then, four-month old seedlings were planted, four per pit. After six months, NPK fertilizers were applied as per the recommendations of the Department of Export Agriculture followed by a second inoculum application (50 g) after 2 months of NPK application. Soil sampling was done quarterly for a year and analyzed for available P by Bray method. The data were statistically analyzed by using SAS package. A significant difference was noted ($p < 0.05$) between the three blocks at first and second sampling but not in the third and fourth samplings. Even though not significantly different ($p > 0.05$), all inoculated treatments showed higher mean available P contents throughout the sampling period compared to the recommendation. At first sampling T3, T1 and T2 treatments had soil available P contents of 12.17±2.96, 11.44±3.94 and 8.28±3.45 mg Kg^{-1} soil, respectively while the recommendation (T8) showed only 5.82±1.19 mg Kg^{-1} soil. At second sampling the T3, T2 and T1 had 9.04±1.57, 8.52±0.84 and 7.85±0.64 mg Kg^{-1} soil while T8 showed only 7.56±0.92 mg Kg^{-1} soil. This trend was evident with third and fourth samplings. Interestingly, inoculum alone gave a higher soil P content than ERP alone treatment. Accordingly, it is evident that application of *A. japonicus* can improve the soil available P status of cinnamon plantations.

Some records of Ascomycete macrofungal species from selected areas of dry zone of Sri Lanka

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Fungi that produce fruit bodies large enough to be observed by the naked eye are identified as macrofungi and these are distributed among the two sub Divisions of Ascomycota and Basidiomycota. While majority of Ascomycetes are smaller in size, a minor portion can be considered as macrofungi due to their prominently visible fruiting bodies. Although few old published fungal collections are available on macrofungi, recent studies are lacking in Sri Lanka. Further, habitat destruction and climate change endanger the species diversity of organisms and hence recording the biological wealth and their habitats would pave the way for formulating conservation strategies. The Ascomycete diversity which was observed during a study carried out in the Dry zone of Sri Lanka, with the objective of identifying and recording the diversity of macrofungi species is reported here. Opportunistic and random sampling was carried out and an area of 50 – 100 m radius into the forests/National parks (Dambulla, Sigiriya, Minneriya, Kaudulla and Wasgamuwa) from either side of the walking path was used for sampling. Morphological characteristics (shape, colour, hymenial surface) of the fruiting bodies and anatomical characteristics (hyphal system, presence/absence and measurements of sterile structures and ascospores) were analyzed. Identification was confirmed by sequencing the Internal Transcribed Spacer (ITS) region in the nuclear ribosomal repeat unit, using the primers ITS1 and ITS4. All recorded Ascomycetes belonged to Family Xylariaceae and were found on decaying logs. The collection consisted of *Daldinia eschscholtzii, Hypoxylon polyporoideum, Hypoxylon* sp., *Xylaria feejeensis, X. papulis, X. polymorpha, X. regalis* and *X. schweinitzii.* As per the literature, the collection is of medicinal importance with evidences of anticancer, antimicrobial, antibacterial and antioxidant activities and economical importance with secondary metabolites of *Daldinia eschscholtzii* proved to be nematicidal. Further, *X. regalis*, is reported to have the potential to be used as a bio-bleaching agent of pulp in the paper industry.

Key words: Ascomycetes, dry zone, macrofungal diversity, *Xylaria*
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A study on factors associated with nutrient use in paddy production in the districts of Anuradhapura, Polonnaruwa and Ampara in Sri Lanka

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Paddy is the main crop cultivated in the districts of Ampara, Anuradhapura and Polonnaruwa using major irrigation systems. A profitable production requires efficient use of fertilizer. Hence, application of a proper nutrient amount to the paddy plant is essential. Though several studies have been conducted to identify the factors associated with paddy production, nutrient use in paddy cultivation is not well understood. This study was carried out to identify the factors associated with nutrient consumption in the three districts. Data were obtained from a survey conducted by the Hector Kobbekaduwa Agrarian Research and Training Institute in 2015. Variables that are associated with the response variables were identified using correlation analysis, and then multiple linear regression (MLR) analysis was carried out. MLR models revealed that the district, farmer's satisfaction on availability of paddy lands and knowledge in fertilizer application were significantly associated with all four responses, namely, nitrogen, phosphate, potash and total nutrient consumption. In addition, nitrogen consumption was significantly associated with farmer's satisfaction on availability of highlands and hired labour man-days; phosphate consumption with farmer's age, potash consumption and hired labour man-days; potash consumption with agricultural experience in years, receive of extension services by agricultural officials, phosphate consumption, yield and price gained per 1 kg of paddy; and total nutrient consumption with agricultural loans obtained, fertilizer cost and the yield. Residual analyses were performed for each MLR and no assumptions were violated. Based on the results, farmers must be encouraged to perform soil tests to identify the best fertilizer recommendation instead of using a recommendation to the district. Expansion of extension services through agricultural officers is a must in implementing this procedure. It is advised to encourage organic fertilizer production, and thereby reduce importation of chemical fertilizers. It is also suggested to conduct similar surveys often, to update the information for policy decisions.

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Assessment of current status of ICT among households in Colombo district, Sri Lanka

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ICT has become an inseparable component in the development of individuals and countries. This study focuses on Colombo district due to its importance to Sri Lanka, and investigates ICT device availability and its usage among Colombo district households. The study uses an extract of the countrywide assessment of ICT access and usage by households and individuals, on current status in Sri Lanka conducted by ICTA. The available data of 426 households were used for the research. Descriptive statistics, odds ratios, cross-tabulation and logistic regression were used for the analysis. The study revealed that a large proportion of the population in Colombo still do not use ICT devices/facilities such as mobile phones and mobile/wireless broadband. The reason for their non-usage is that they do not consider the facility as essential. It was also revealed that most of the households use ICT devices/facilities only if they own it and not from anywhere outside. Mobile phones have been identified as the most used device for education, work and gaming. ICT usage is observed to decline with age. Males' ICT usage is found to be higher than females' usage. Those employed have 2.331 times the odds of using a smartphone compared to the unemployed. The odds of using Facebook is 58 times higher for smartphone users than for non-users. Internet and smartphone usage were also observed to increase with higher education. The average smart phone equipment cost is close to Rs. 30,000. Furthermore, 81% of the households have gone through a virus attack. The study concluded on the note that there is still plenty of room for ICT-based development in Colombo. The usage of ICT devices/facilities is still to be encouraged among females, the unemployed, individuals with lower education levels and the older population in the district.

A case study on final inspection result in garment products

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Quality can be expressed as one of the key factors of business sustainability in the apparel industry. There are several quality controlling mechanisms to ensure product quality. Final inspections, which is the final step of the quality controlling process at supplier level, has to be carried out according to customer guidelines. Obtaining a final inspection pass rate of 100% is vital for suppliers. However, for the selected supplier of the study, it is currently maintained at 96%. The focus of the research is to ensure that the pass rate of inspections achieves its full rate. The main objective is to identify the critical factors related to their final inspection result. As the initial step, customer wise inspection systems and different quality processes in garment manufacturing were reviewed. Then a secondary database was created containing 1857 inspections recorded over six months. The collected data includes internal data from an online database and manual records. Initially, there were thirteen different variables, among which, some values were defect ratios measured from different quality control points such as In line, End line, etc. Other important nominal categorical variables such as Customer, Production plant, etc., were also included. Based on descriptive analysis, chi square and simple logistic regression test results, eight independent variables were selected for the final model. Since the dependent variable is binary with rare events, the model was built in logistic regression using a complementary log link function. As per the model outcome, five variables (Customer, Region, Inspection type, End line defect rate, In line defect rate) were identified as significant. The confusion matrix, deviance statistics and residual plots validate model accuracy and adequacy. Considering factor coefficients, the supplier can create customized quality control limits at production. The significant factors should be maintained properly to ensure that the final inspection pass rate is at its maximum level.

Comparison of association rule mining performances: market basket analysis of a mini-supermarket

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Market Basket Analysis discovers consumer purchasing patterns by identifying important and interesting association rules among the products bought in a shopping basket. This field of study is not only useful in the decision-making process, but also to increase the sales and profit of an organization. Association rule mining is one of the prime data mining techniques. Among the algorithms studied under association rule mining, 'Apriori', 'ECLAT' and 'FP-Growth' are key algorithms applied in diversified fields. Although an enormous number of studies have been conducted in association rule mining in market basket analysis, it is still a budding area in Sri Lanka, especially in the field of retailing of small and medium enterprises. The research is based on grocery transaction data obtained from a local mini-supermarket during a four-month time period, to discover important information and interesting relationships to aid decision making to enhance performance and to gain a competitive advantage. The goals of the study are: to identify frequently consumed items and to generate association rules to understand the purchasing patterns of the customer to make recommendations for cross-selling and up-selling of products using the dataset; to use three algorithms of association rule mining and compare their performance using different datasets with varying characteristics of inputs which reflect the small and medium retail industry. The findings listed the most frequently purchased items and brands along with the items that were bought together most of the time, leading to many recommendations and planning strategies. In addition to these findings, the performance evaluation of the association rule mining algorithm findings showed that the 'Apriori' performs best in terms of execution time, even with a higher number of candidate generation at low minimum support values, compared to the other two algorithms 'ECLAT' and 'FP-Growth'.

Keywords: Apriori algorithm, association rule mining, ECLAT algorithm, FP-growth algorithm, small and medium enterprises
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Factors associated with child nutritional status in the Karachchi DSD in the Kilinochchi district: A case study

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Malnutrition is a global health problem that is particularly common in children in the developing world. This has been a stagnant problem over the last several decades in Sri Lanka as well, especially in the North and East. The primary focus of this research is to identify factors associated with child malnutrition in the Karachchi Divisional Secretariat Division (DSD) in the Kilinochchi district. This study used secondary data of a baseline study conducted by World Vision Lanka in 2018 and considered a sample size of 277 households with children under five years of age in the Karachchi DSD. The nutritional status of the children was considered as the response variable which is classified as nourished and malnourished. In addition, twenty variables describing demographics, information on the parents, dietary habits etc., were considered as explanatory variables in this study. Both descriptive and inferential statistics were used to analyze the data. Since the response variable is dichotomous, binary logistic regression was used to identify the factors significantly associated with the nutritional status of the children. The descriptive analyses show that the overall prevalence of stunting is 21.66%, wasting is 12.64% and underweight is 17.69%. The logistic model reveals that the nutritional status of the children under five years of age in the Karachchi DSD is significantly associated with four of the twenty explanatory variables which were tested to explore the relationship. The four explanatory variables explicitly are birth weight, mothers' education level, dietary diversity of the children and the number of family members. The nutritional status of the children increases with the increase in birth weight, mothers' education level and dietary diversity of the children, and in contrast, the nutritional status of the children reduces with the increase in the number of family members in the household.

A study on mobile phone preference of graduates of University of Kelaniya, Sri Lanka

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Nowadays, a mobile phone is not just a communication device, but also a device that performs multiple tasks. As a result of changing needs and the preferences of customers, the mobile phone market is highly competitive and dynamic. This study explores factors associated with mobile phone preferences of graduates of the Faculty of Science, University of Kelaniya, Sri Lanka. An online survey was conducted and data were collected through a questionnaire. To identify the factors associated with mobile phone preferences, factor analysis was carried out and seven factors were identified; namely, basic features, camera features, performance and updated technology features, durability with safety standards, marketing strategy, pricing strategy and brand. The same procedure can be extended to find the factors associated with the mobile phone preferences of the graduates in Sri Lanka. Furthermore, a Latent Class model was fitted for the attributes of each factor revealed, and it showed that a majority of the respondents are highly interested in special offers and methods of payment. Performance and updated technology related features also influenced the graduates of University of Kelaniya when selecting a mobile phone. Awareness of the fact that consumers are looking for value for the amount paid, with durable and branded phones, is important for mobile phone vendors in enhancing the sales of mobile phones.

Selecting the most suitable classification algorithm for tiger beetle identification using morphometric data and habitat data

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Habitat heterogeneity is a main factor in ecology which affects species diversity. Therefore, habitat details can be used as factors that influence species identification. Tiger beetles are highly habitat specific species. Different species of tiger beetles that have morphometric variation can be found restricted to different habitat types in temperate and tropical areas of the world. Therefore, habitat and morphometric data of tiger beetle species were used to develop a predictive model for the identification of tiger beetle species. Data gathered on ground-dwelling tiger beetle species collected from 45 locations by Dangalle (2002-2015), and 150 locations by Thotagamuwa (2014 -2017) were used to construct the dataset required for the study. Then data pre-processing was done to convert nominal data to numerical data, detach records with missing data and correct imbalanced data. Data resampling was also done. Further, an evaluation was performed for feature selection to determine the most important attributes for species identification predictions. Finally, a dataset containing 468 records (individuals of species) having 13 attributes of 14 species was constructed and 351 records were selected for the training set while 117 records were selected for the test set. This dataset was fed to several multiclass algorithms belonging to both single (KNN, Naïve-Bayes, SVM) and ensemble classifiers (Gradient Tree Boosting, Extra Tree Classifier and Random Forest). The performance of each algorithm was evaluated by calculating accuracy values for each model and the results revealed that ensemble classifiers yield a higher accuracy than that of single classifiers. Hence it was proven that ensemble models have a positive effect on the overall quality of predictions, in terms of accuracy, generalizability and lower misclassification costs and are more stable than single classifiers. Further, when considering the different types of ensemble classification algorithms, bagging (averaging) ensemble classification algorithm performed better than boosting methods. When considering the two bagging ensemble classification algorithms - Ensemble Extra Tree Classifier and Random Forest algorithm, both revealed almost the same overall accuracy (85%) with less than 0.12% difference. Therefore, both ensemble classification algorithms are effective for species prediction using habitat and morphometric data. However, when considering the computational time with performance, Ensemble Extra Trees Classifier can be considered as the most suitable algorithm for the scenario.

Baseline analysis of stress levels of the Indian flying fox (*Pteropus giganteus*) in Sri Lanka

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Flying foxes (Pteropid bats) are known for disease transmission of viral diseases to other animals and to humans for decades. One suspected factor for the viral shedding in bats is physiological stress. Although flying fox colonies are found island wide, no study has been carried out to assess and interpret the stress hormone levels of bats in Sri Lanka. Glucocorticoids (cortisol and corticosterone) are known stress hormones which change in terms of physiological stress. Therefore, we assessed physiological stress levels of tested flying foxes using urinary cortisol measurements. Urine was collected non-invasively from two different roosts in two climatic zones; Viharamaha Devi Park Colombo – wet zone (6°54'44.4"N 79°51'45.0"E) (n=432) and Thaleimannar – arid zone (9°05'31.5"N 79°43'38.5"E) (n= 402) in Sri Lanka for a 6-month period from November 2018 – April 2019. Collected samples were inactivated using a standard inactivation protocol (RKI in-house SOP) under BSL 3 laboratory conditions at the RKI, before assessing cortisol levels. Urine creatinine was measured, and these creatinine values were used to normalize the cortisol concentration. Cortisol concentration ranged between 10.90 – 2912.17 ng/ml with average of 195.15 ng/ml in Thaleimannar roosting site and ranged between 4.89 – 2451.74 ng/ml with average of 173.85 ng/ml in Colombo roosting site. Overall urinary cortisol concentration of *Pteropus giganteus* ranges from 4.89 – 2912.17 ng/ml in Sri Lanka with average of 199.68 ng/ml. Results showed that cortisol concentration in urine tend to vary each month in both locations. This could be due to the environmental factors such as temperature, rainfall, and availability of food in the particular time period. It could also be due to physiological changes caused by mating and pregnancy. With these initial data, the study is continuing to include intermediate and dry climatic zones to get a clear understanding of the fluctuations of physiological stress in flying foxes in Sri Lanka.

Analysing features importance for identification of tiger beetles using machine learning

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Performance of machine learning models mainly rely on the quality of the input data fed into the model. Therefore, using all of the features/attributes in a dataset as input data may have a negative effect rather than a positive effect on the resulting model causing increase of training time and to model over-fitting. The present study was conducted to identify the most suitable features that can be used in a machine learning model developed to identify ground-dwelling tiger beetle species. As input data, habitat and morphometric data of tiger beetles collected from 2002 – 2017 from various locations of Sri Lanka were used. The data set comprised of 468 records with 12 features of 14 species. Each specimen collected was considered as a single record of the dataset, and climatic zone, GPS co-ordinates of location, habitat type, elevation, air temperature, solar radiation, relative humidity, wind speed, soil moisture, soil salinity, soil pH and body length of the specimen were considered as features. The dataset was pre-processed and fed into various algorithms: KNN, SVM, Naïve Bayes, Ensemble Extra Trees Classifier. From above, Ensemble Extra Trees Classifier yielded a test accuracy of 85.35% and was selected as the most suitable algorithm. Therefore, Ensemble Extra Trees Classifier was selected to evaluate the hierarchical importance of the features of the current dataset. The study revealed that body length, habitat type and elevation of the locations were the three most informative features in the dataset which supported species identification. However, using a fewer number of attributes which provide higher feature importance values reduced classification accuracy. The main reason for above scenario was that features except body length were more or less similar and had slight variation while body length had high variation that results in overfitting of the machine learning model. In order to prevent overfitting and increase validation accuracy combining all the features is necessary.

A preliminary virological surveillance of field-caught adult *Aedes aegypti* (L.) and *Aedes albopictus* (Skuse) mosquitoes in selected sites in the District of Colombo and Gampaha of Sri Lanka

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Aedes aegypti (L.) is widely recognized as the principal dengue vector. *Aedes albopictus* (Skuse) has also reported to mediate dengue outbreak situations in some countries. In Sri Lanka, *Ae. albopictus* predominates over *Ae. aegypti* in some areas of high dengue prevalence. As such, current study was aimed to conduct a virological surveillance of field caught *Ae. aegypti* and *Ae. albopictus* mosquitoes in two dengue endemic areas in Sri Lanka to assess their relative roles in dengue transmission. Adult mosquitos were collected weekly for 2-5 weeks from the Districts of Colombo (urban) and Gampaha (suburban) using Improved Prokopack Aspirator during 8.00–11.00 am and were identified, sexed and counted. The number of adult mosquitoes per house for each species was calculated and the statistical significance was determined by the Student's *t* test. RNA was extracted using pooled heads and thoraxes of 1-5 female *Aedes* mosquitoes and the presence of dengue virus was tested with nested reverse transcriptase PCR. A total of 4154 mosquitoes belonging to four species; *Culex quinquefasciatus* (3151; 75.9%)*, Anophelus culcifaices* (204; 4.9%), *Ae. aegypti* (487;11.7%)*, Ae. albopictus* (312;7.5%) was collected from 19 sampling sites in the two districts. In the District of Colombo, there were more ($p< 0.05$) *Ae. aegypti* per house (male: 1.8, female: 1.36) compared to *Ae. albopictus* (male: 0.21, female: 0.23). In contrast, District of Gampaha had more *Ae. albopictus* per house (male: 0.9, female: 0.67) compared to *Ae. aegypti* (male: 0.32, female: 0.16). In both districts, the number of males were significantly higher than the females for the dominating *Aedes* species ($P<0.05$) in the district. None of the adult female *Aedes* mosquitoes collected were positive for dengue virus. Our results confirm the distorted sex ratio characteristic of Culicine mosquitoes and the preference of *Ae. aegypti* for more urban habitats compared to *Ae albopictus*. The absence of dengue infection among the captured mosquitos, irrespective of the reported dengue incidences in the studied areas, might point at the ability of an infected *Aedes* mosquito to transmit the virus to many healthy individuals. Our results suggest that dengue epidemics are possible even with extremely low mosquito infection rates. However, further analysis is necessary to confirm this observation.

Immunoepidemiology of *Plasmodium vivax* MSP-1 and AMA-1 in two previous high malaria endemic districts in Sri Lanka under the prevention of re-establishment phase

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Sri Lanka was certified malaria free by the WHO in 2016. The presence of the malaria vector in the island, and imported malaria cases pose major risks during the current Prevention of Re-establishment (POR) phase in Sri Lanka. As serological parameters may indicate malaria transmission dynamics, assessment of antimalarial antibody prevalence/titers in populations will be indicative of the status of current infections and hence of malaria transmission. Yet, malaria immunoepidemiology studies in countries successful in eliminating malaria are nonexistent. We aimed to determine the prevalence of antibodies to *Plasmodium vivax* vaccine candidate antigens, PvMSP1-19 and PvAMA1, in residents of two previous high malaria endemic districts, Hambantota and Kilinochchi; Nuwaraeliya served as the control/malaria-free district. Indirect ELISAs assayed antibody responses against two recombinant proteins, PvMSP1-19 and PvAMA1, on serum samples collected with informed consent from study participants. In a total of 3129 individuals (Hambanthota-1231, Kilinochchi-1398, and Nuwaraeliya-500) recruited for the study, Anti-MSP1-19 antibody prevalence was 2.0%, 5.0% and 1.0% while anti-AMA1 antibody prevalence was 5.0%, 14.0% and 2.0% in Hambanthota, Kilinochchi and Nuwaraeliya districts, respectively. Compared to the controls, antibody magnitudes to both PvMSP1-19 and PvAMA1 were significantly higher in Kilinochchi ($p<0.005$ and $p=0.022$, respectively) than in Hambantota ($p=0.001$ and $p<0.005$). Previous exposure to malaria was significantly associated with antibody responses against both PvMSP1-19 and PvAMA1 among all three districts ($p<0.05$). In comparison, based on previous records the prevalence of antimalarial antibodies to MSP1-19 and AMA1 in the Hambantota district during 1998–2003 were 59% and 54%, respectively. In conclusion, though significant seroprevalence to *P. vivax* antigens, MSP1-19 and AMA1, was evident in residents of previous high malaria endemic areas in comparison to a previous malaria non-endemic area under a POR setting, compared to malaria pre-elimination data, these have declined to low levels which may suggest the absence of current malaria transmission.

Molecular identification of rufous horseshoe bat, *Rhinolophus rouxii* from the Wellawaya Wavulgalge cave in Sri Lanka

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The rufous horseshoe bat, *Rhinolophus rouxii* (family Rhinolophidae) has a wide distribution and has been recorded from China, India, Myanmar, Nepal, Vietnam, and Sri Lanka. It is a medium sized bat (11-13g), and shows enormous cryptic diversity. Recent research has shown that *R. rouxii* contains many morphologically diverse, species complex and fur color as well as the echolocation call frequency varies in different populations. We have used molecular techniques for establishing the accurate identity of *R. rouxii*, recorded in one of the largest cave populations in Sri Lanka. Bats were caught using a hand net and saliva samples (n=21) were collected non-invasively from each bat using a sterile oral swab. Nucleic acids were extracted from oral swab samples following the QIAmp Viral RNA Mini kit (extract both DNA and RNA) protocol. Mitochondrial cytochrome b gene was amplified using cytochrome b, RrFP and RrRP primers. PCR products were visualized using gel electrophoresis. Purified PCR products were sequenced using Sanger sequencing. Sequence analyses were carried out using the GeneiousPrime application. FASTA sequences of each bat obtained from sequencing were trimmed and assembled to form the consensus sequences. Aligned sequences were compared with sequences in the database at National Center for Biotechnology Information Support Center (NCBI). Cytochrome b gene sequences of *Rhinolophus rouxii* bats were downloaded from NCBI database and aligned with the consensus sequences using the Geneious alignment tool. The phylogenetic tree was constructed using the Neighbor-Joining method. This study identified the *Rhinolophus* species recorded in Wellawaya cave as *Rhinolophus rouxii* with an average identity of 98.40%. Phylogenetic analysis showed it is closely related to the same species identified in Karnataka district in India. This study reports the first molecular confirmation carried out on *Rhinolophus rouxii* in Sri Lanka. This will provide the basis for a genetic database for Sri Lankan bats.