<table>
<thead>
<tr>
<th>DAY</th>
<th>TIME</th>
<th>Grand Ballroom (13F)</th>
<th>Rose Room 1</th>
</tr>
</thead>
<tbody>
<tr>
<td>Oct. 29</td>
<td>8:00 – 9:30</td>
<td>Registration</td>
<td></td>
</tr>
<tr>
<td>Monday</td>
<td>8:50 – 9:00</td>
<td>Welcome from Conference Chair&lt;br&gt;Chair: Professor Jeffrey J. P. Tsai&lt;br&gt;President, Asia University&lt;br&gt;Grand Ballroom</td>
<td></td>
</tr>
<tr>
<td></td>
<td>9:00 – 9:50</td>
<td><strong>Keynote (1)</strong>&lt;br&gt;Professor Scott L. Delp&lt;br&gt;Stanford University, USA&lt;br&gt;Chair: Professor Jean-Claude Latombe&lt;br&gt;Stanford University, USA&lt;br&gt;Grand Ballroom</td>
<td></td>
</tr>
<tr>
<td></td>
<td>9:50-10:40</td>
<td><strong>Keynote (2)</strong>&lt;br&gt;Professor Yusuke Nakamura&lt;br&gt;University of Chicago, USA&lt;br&gt;Chair: Professor Hideo Matsuda&lt;br&gt;(Osaka University, Japan)&lt;br&gt;Grand Ballroom</td>
<td></td>
</tr>
<tr>
<td></td>
<td>10:40-10:55</td>
<td>Coffee Break</td>
<td></td>
</tr>
<tr>
<td></td>
<td>10:55-12:15</td>
<td>S1.1 Biological sequence analysis&lt;br&gt;Chair: Professor Tatsuya Akutsu&lt;br&gt;Kyoto University, Japan&lt;br&gt;Grand Ballroom</td>
<td>S1.2 Biomedical concepts and measurements&lt;br&gt;Chair: Dr. Emma D. Wilson&lt;br&gt;Lancaster University, UK&lt;br&gt;Rose Room 1</td>
</tr>
<tr>
<td></td>
<td>12:15-13:15</td>
<td>Lunch [The Plum Blossom Room (13F) NVIDIA, Taiwan]</td>
<td></td>
</tr>
<tr>
<td></td>
<td>13:15-14:35</td>
<td>S1.3 Sequence alignment and high-performance sequence analysis&lt;br&gt;Chair: Professor Osamu Maruyama&lt;br&gt;Kyushu University, Japan&lt;br&gt;Grand Ballroom</td>
<td>S1.4 Recent advancements in medical engineering&lt;br&gt;Chair: Professor Wen-Cheng Lai&lt;br&gt;National Penghu University of Science and Technology, Taiwan&lt;br&gt;Rose Room 1</td>
</tr>
<tr>
<td></td>
<td>14:35-15:55</td>
<td>S1.5 Biological network inference and analysis I&lt;br&gt;Chair: Professor Jose Nacher Toho&lt;br&gt;University, Japan&lt;br&gt;Grand Ballroom</td>
<td>S1.6 Medical and physiological signal analysis I&lt;br&gt;Chair: Dr. Emma D. Wilson&lt;br&gt;Lancaster University, UK&lt;br&gt;Rose Room 1</td>
</tr>
<tr>
<td></td>
<td>15:55-16:10</td>
<td>Coffee Break</td>
<td></td>
</tr>
<tr>
<td></td>
<td>16:10-17:30</td>
<td>S1.7 Workshop: Cancer bioinformatics and intelligent medicine&lt;br&gt;Chair: Professor Tatsuya Akutsu&lt;br&gt;Kyoto University, Japan&lt;br&gt;Grand Ballroom</td>
<td>S1.8 Biological sensor and data analysis&lt;br&gt;Chair: Professor Golshah Naghdy&lt;br&gt;University of Wollongong, Australia&lt;br&gt;Rose Room 1</td>
</tr>
<tr>
<td></td>
<td>17:30-18:30</td>
<td>Break</td>
<td></td>
</tr>
<tr>
<td></td>
<td>18:30 – 21:00</td>
<td>Reception&lt;br&gt;Chair: Professor Jeffrey J. P. Tsai</td>
<td></td>
</tr>
<tr>
<td>Time</td>
<td>Event</td>
<td></td>
<td></td>
</tr>
<tr>
<td>--------------</td>
<td>-------------------------------------------------------------------------------------------------</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Oct. 30</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>8:00 – 9:30</td>
<td>Registration</td>
<td></td>
<td></td>
</tr>
<tr>
<td>9:00 – 9:50</td>
<td><strong>Keynote (3)</strong>&lt;br&gt;Professor Pui-Yan Kwok&lt;br&gt;Academia Sinica, Taiwan&lt;br&gt;Chair: TBD&lt;br&gt;Grand Ballroom</td>
<td></td>
<td></td>
</tr>
<tr>
<td>9:50-10:40</td>
<td><strong>Keynote (4)</strong>&lt;br&gt;Professor Lydia E. Kavraki&lt;br&gt;Rice University, USA&lt;br&gt;Chair: Professor Tatsuya Akutsu (Kyoto University, Japan)&lt;br&gt;Grand Ballroom</td>
<td></td>
<td></td>
</tr>
<tr>
<td>10:40-10:55</td>
<td>Coffee Break</td>
<td></td>
<td></td>
</tr>
<tr>
<td>10:55-11:55</td>
<td>S2.1 Cancer bioinformatics&lt;br&gt;Chair: Professor Y-h Taguchi&lt;br&gt;(Chou University, Japan)&lt;br&gt;Grand Ballroom</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>S2.2 Medical image and signal analysis I&lt;br&gt;Chair: Professor Kenshi Saho&lt;br&gt;Toyama Prefectural University, Japan&lt;br&gt;Rose Room 1</td>
<td></td>
<td></td>
</tr>
<tr>
<td>11:55-13:00</td>
<td>Lunch [The Plum Blossom Room (13F)]</td>
<td></td>
<td></td>
</tr>
<tr>
<td>13:00-13:50</td>
<td><strong>Keynote (5)</strong>&lt;br&gt;Professor Antonios G. Mikos&lt;br&gt;Rice University, USA&lt;br&gt;Chair: TBD&lt;br&gt;Grand Ballroom</td>
<td></td>
<td></td>
</tr>
<tr>
<td>13:50-15:50</td>
<td>S2.3 Tutorial:&lt;br&gt;Professor Nikolaos G Bourbakis&lt;br&gt;Grand Ballroom&lt;br&gt;S2.4 Medical signal, sequence detection, DNA barcode&lt;br&gt;Chair: Professor Hiroshi Hagiwara&lt;br&gt;Ritsumeikan University, Japan&lt;br&gt;Rose Room 1</td>
<td></td>
<td></td>
</tr>
<tr>
<td>15:50-16:05</td>
<td>Coffee Break</td>
<td></td>
<td></td>
</tr>
<tr>
<td>16:05-17:25</td>
<td>S2.5 Cancer and medical bioinformatics&lt;br&gt;Chair: Professor Hsueh-Ting Chu&lt;br&gt;(Asia University, Taiwan)&lt;br&gt;Grand Ballroom</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>S2.6 Medical image and signal analysis II&lt;br&gt;Chair: TBD&lt;br&gt;Rose Room 1</td>
<td></td>
<td></td>
</tr>
<tr>
<td>17:25 – 18:30</td>
<td>Break</td>
<td></td>
<td></td>
</tr>
<tr>
<td>18:30 – 21:00</td>
<td>Banquet&lt;br&gt;<strong>Keynote (6)</strong>&lt;br&gt;Professor Jan-Gowth Chang&lt;br&gt;(China Medical University, Taiwan)&lt;br&gt;Chair: Professor Jeffrey J. P. Tsai&lt;br&gt;President, Asia University, Taiwan&lt;br&gt;Grand Ballroom</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Oct. 31</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>8:00 – 9:00</td>
<td>Registration</td>
<td></td>
<td></td>
</tr>
<tr>
<td>9:00 – 9:50</td>
<td><strong>Keynote (7)</strong>&lt;br&gt;Professor Wen-Hsiung Li</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Time</td>
<td>Session</td>
<td>Location</td>
<td></td>
</tr>
<tr>
<td>-----------------</td>
<td>----------------------------------------------</td>
<td>------------------------------------</td>
<td></td>
</tr>
<tr>
<td>9:50-10:50</td>
<td>S3.1 Special paper session</td>
<td>Grand Ballroom</td>
<td></td>
</tr>
<tr>
<td></td>
<td>- Biomedical Big Data</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Chair: Professor Jan-Gowth Chang</td>
<td>Grand Ballroom</td>
<td></td>
</tr>
<tr>
<td></td>
<td>(China Medical University, Taiwan)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>9:50-10:50</td>
<td>S3.2 Biological text mining and biomedical</td>
<td>Rose Room 1</td>
<td></td>
</tr>
<tr>
<td></td>
<td>informatics</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Chair: Dr. Khai Nguyen</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>National Institute of Informatics, Japan</td>
<td></td>
<td></td>
</tr>
<tr>
<td>10:50-11:05</td>
<td>Coffee Break</td>
<td></td>
<td></td>
</tr>
<tr>
<td>11:05-12:05</td>
<td>S3.3: Biological network inference and</td>
<td>Grand Ballroom</td>
<td></td>
</tr>
<tr>
<td></td>
<td>analysis II</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Chair: Professor Wen-Ling Chan</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>(Asia University, Taiwan)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>11:05-12:05</td>
<td>S3.4 Computational Modeling and sensor in</td>
<td>Rose Room 1</td>
<td></td>
</tr>
<tr>
<td></td>
<td>biomedical engineering</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Chair: Professor Michael Yong Zhao</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Nazarbayev University, Kazakhstan</td>
<td></td>
<td></td>
</tr>
<tr>
<td>12:05 – 13:00</td>
<td>Lunch [The Plum Blossom Room (13F)]</td>
<td>(Close)</td>
<td></td>
</tr>
</tbody>
</table>

Academia Sinica, Taiwan
Chair: Professor Chi-Ren Shyu
University of Missouri, USA
Grand Ballroom
S1.1: Biological sequence analysis
DegSampler:Collapsed Gibbs sampler for detecting E3 binding sites*
Osamu Maruyama and Fumiko Matsuzaki
Constructing the Relationship Tree of All Viruses via Whole Genomic Sequences
Jing-Doo Wang and Yi-Chun Wang
Stratification of Human Gut Microbiome and Building a SVM-Based Classifier
His-Chung Kung, Jeffrey J. P. Tsai, Rong-Ming Chen and Rouh-Mei Hu
iLMS, computational identification of lysine-malonylation sites by combining multiple sequence features
Md. Mehedi Hasan and Hiroyuki Kurata
Protein Secondary Structural Class Prediction Using Effective Feature Modeling and Machine Learning Techniques
Sanjay Bankapur and Nagamma Patil

S1.2: Biomedical concepts, measurements and image analysis
Model Predictive and Proportional Integral Control of Blood Clotting Speed Using Warfarin When Data Are Missing*
Emma D. Wilson, Quentin Clairon, Robin Henderson and C. James Taylor
Stochastic Non-minimal State Space Control with Application to Automated Drug Delivery*
Emma D. Wilson, Quentin Clairon and C. James Taylor
Adjacent Network for Semantic Segmentation of Liver CT Scans*
Indriani Puspitasari Astono, James S. Welsh and Stephan Chalup
Texture biomarkers of Alzheimer’s disease and disease progression in the mouse retina*
Ana Nunes, António Ambrósio, Miguel Castelo-Branco and Rui Bernardes

S1.3: Sequence alignment and high-performance sequence analysis
Detection of Errors in Multi-Genome Alignments Using Machine Learning Approaches*
Jaspal Singh, Ramchalam Kinattinkara Ramakrishnan and Mathieu Blanchette
A High-Performance Sequence Analysis Engine for Shotgun Metagenomics through GPU Acceleration*
Ying-Feng Hsu, Morito Matsuoka, Nicolas Jung, Yuki Matsumoto, Daisuke Motooka and Shota Nakamura
RLALIGN: A Reinforcement Learning Approach for Multiple Sequence Alignment
Ramchalam Kinattinkara Ramakrishnan, Jaspal Singh and Mathieu Blanchette
An Efficient GPU-based de Bruijn Graph Construction Algorithm for Micro-Assembly
Shanshan Ren, Nauman Ahmed, Koen Bertels and Zaid Al-Ars

S1.4: Recent advancement in medical engineering
Low Cost Micro-Droplet Formation Chip with a Hand-Operated Suction Syringe*
Gamal Abdel Nasser, Ahmed M.R. Fath El-Bab, Hisham Mohamed and Ahmed Abouelsoud
A parametric 3D-printed body-powered hand prosthesis based on the four-bar linkage mechanism*
Marlene Bustamante, Rodrigo Vega-Centeno, Midori Sánchez and Renato Mio
Design of a Portable Radial Piston Pneumatic Compressor for Wearable Robot System
Ryeonho Kang, Ho Seon Choi and Yoon Su Baek
Study on the Channel Characteristics of Auxiliary Medical Devices Based on MDAPSK Technology
Xueping Li, Yuan Yang and Ningmei Yu
SAR ADC with DAC and SC Low-Pass Filter for Positron Emission Tomography Application
Wen Cheng Lai

S1.5: Biological network inference and analysis I
Inference of Genetic Networks Using Random Forests: Use of Different Weights for Time-series and Static Gene Expression Data*
Shuhei Kimura, Masato Tokuhisa and Mariko Okada-Hatakeyama
An Intensive Search for Higher-order Gene-gene Interactions by Improving Deep Learning Model*
Suneetha Uppu and Aneesh Krishna
Interpretable Prediction of Vascular Diseases from Electronic Health Records via Deep Attention Networks*
Seunghyun Park, You Jin Kim, Jeong Whun Kim, Jin Joo Park, Borim Ryu and Jung-Woo Ha

Pathway Analysis of Marker Genes for Leukemia Cancer Using Enhanced Genetic Algorithm-Neural Network (enGANN)
Hau Cherng Wong, Christine Siew Ken Lee and Dong Ling Tong

SIPMA: a systematic identification of protein–protein interactions in *Zea mays* using autocorrelation features in a machine-learning framework

S1.6: Medical and physiological signal analysis I
Biomedical Data Acquisition and Processing to Recognize Emotions for Affective Learning*
Armin Gruenewald, David Kroenert, Jonas Poehler, Rainer Brueck, Frédéric Li, Kathrin Schnieber, Artur Piet, Julian Littau, Marcin Grzegorzek, Henrik Kampling and Bjørn Niehaves

KnowPain: Automated System for Detecting Pain in Neonates from Videos*
Rajkumar Theagarajan, Bhanu Bir, Danilyn Angeles and Federico Pala

Brain Structural and Functional Representation Based on the Local Global Graph Methodology
Spyridon Manganas, Nikolaos Bourbakis and Konstantinos Michalopoulos

Comparison of Region of Interest Segmentation Methods for Video-based Heart Rate Measurements
Peixi Li, Yannick Benezeth, Keisuke Nakamura, Randy Gomez, Chao Li and Fan Yang

S1.7: Workshop: Cancer bioinformatics and intelligent medicine
Deep Learning with Evolutionary and Genomic Profiles for Identifying Cancer Subtypes
Chun-Yu Lin, Peiying Ruan, Ruiming Li, Jinn-Moon Yang, Simon See and Tatsuya Akutsu

Convolutional Neural Network Approach to Lung Cancer Classification Integrating Protein Interaction Network and Gene Expression Profiles
Teppei Matsubara, Tomoshiro Ochiai, Morihiro Hayashida, Tatsuya Akutsu and Jose Nacher

Identification of the PCA28 gene signature as a predictor in prostate cancer
Jung-Yu Lee, Si-Yu Lin, Yi-Hsuan Chuang, Sing-Han Huang, Yu-Yao Tseng, Chun-Yu Lin, Hung-Jung Wang and Jinn-Moon Yang

Detection of Fusion Genes from Human Breast Cancer Cell-line RNA-Seq Data Using Shifted Short Read Clustering
Yoshiaki Sota, Shigeto Seno, Hironori Shigeta, Naoki Osato, Masafumi Shimoda, Shinzaburo Noguchi and Hideo Matsuda

S1.8: Biological sensor, device and data analysis
Recovering a Chemotopic Feature Space from a Group of Fruit Fly Antenna Chemosensors*
Martin Strauch, Latha Mukunda, Alja Lüdke, C. Giovanni Galizia and Dorit Merhof

Mechanical Testing Methods for Body-Powered Upper-Limb Prostheses*
Renato Mio, Midori Sánchez and Quino Valverde

Investigating Electrode Sites for Intention Detection During Robot Based Hand Movement Using EEG-BCI System
Maryam Butt, Golshah Naghd, Fazel Naghd, Geoffrey Murray and Haiping Du

Remote Assessment of Gait Deterioration Due to Memory Impairment in Elderly Adults Using Micro-Doppler Radar
Kenshi Saho, Kazuki Uemura and Michito Matsumoto
Estimating GRF (Ground Reaction Force) and Calibrating CoP (Center of Pressure) of an Insole Measured by an Low-Cost Sensor with Neural Network
Ho Seon Choi, Myounghoon Shim, Chang Hee Lee and Yoon Su Baek

**S2.1: Cancer bioinformatics**

MVPNets: Multi-Viewing Path Deep Learning Neural Networks for Magnification Invariant Diagnosis in Breast Cancer*
Padmaja Jonnalagedda, Daniel Schmolze and Bir Bhanu

Tensor Decomposition-based Unsupervised Feature Extraction for Integrated Analysis of TCGA Data on MicroRNA Expression and Promoter Methylation of Genes in Ovarian Cancer*
Y-H. Taguchi and Ka-Lok Ng

Cancer Screening Using Biomimetic Pattern Recognition with Hyper-Dimensional Structures
Leonila Lagunes and Charles H. Lee

**S2.2: Medical image and signal analysis I**

Automated Evaluation of Hand Motor Function Recovery by Using Finger Pressure Sensing Device for Home Rehabilitation*
Yuta Furudate, Nanami Onuki, Kaori Chiba, Yuji Ishida and Sadayoshi Mikami

Nonlinear CMOS Image Sensor with SOC Integrated Local Contrast Stretch for Bio-microfluidic Imaging
Nan Lyu, Likang Xu, Ningmei Yu and Hejiu Zhang

Software Defined Radio-Based Testbed for Wireless Body Area Network
Zhiyu Chen, Junchao Wang, Kaining Han and Zeljko Zilic

**S2.3 Tutorial: Assistive Research Biotechnologies for People in Need**
Professor Nikolaos G Bourbakis

**S2.4: Medical signal, sequence detection, DNA barcode**

Decision Theory-Based DNA Barcoding Through Quick Response Code Representation*
Cheng-Hong Yang, Kuo-Chuan Wu, Hsueh-Wei Chang and Li-Yeh Chuang

Species Identification using Partial DNA Sequence: A Machine Learning Approach
Tasnim Kabir, Abida Sanjana Shemonti and Atif Hasan Rahman

Comparative Analysis of System-Level Acceleration Techniques in Bioinformatics: A Case Study of Accelerating the Smith-Waterman Algorithm for BWA-MEM
Ernst Houtgast, Vlad-Mihai Sima, Koen Bertels and Zaid Al-Ars

Psycho-physiological Changes Depend on Differences in the Presentation Ratio of Non-target Stimuli
Hiroaki Yoshikawa and Hiroshi Hagiwara

Quantitative Frailty Assessment Using Activity of Daily Living (ADL)
Yasmeen Naz Panhwar, Fazel Naghdy, David Stirling, Golshah Naghdy and Janette Potter

Novel Parameters for ECG Signal Analysis Irrespective of Patient's Age, Sex and Heart Rate
Salah Hamdi, Asma Ben Abdallah and Mohamed Hedi Bedoui

Improved Multifactor Dimensionality Reduction for Epistasis Detection
Li-Yeh Chuang, Cheng-Hong Yang and Yu-Da Lin

**Signaling System 7: Limitations and Resolutions**
Poornima Patel and Subrata Acharya

**S2.5: Cancer and medical bioinformatics**

Identification of Several Core Overexpressed MicroRNAs that Could Predict Survival in Patients with Ovarian Cancer*
Eskezeia Y. Dessie, Ezra B. Wijaya, Chien-Hung Huang, David Agustriawan, Jeffrey J.P Tsai and Ka-Lok Ng

Quantitative Analysis of ECI2 Expression from RNA-seq for Breast Cancer Gene Signatures
Ming-Yi Yen, Hsueh-Ting Chu, Yu-Ching Chen and Jeffrey J. P. Tsai
Identification of Potential Long Non-coding RNA Biomarkers for Breast Cancer Patients with Somatic BRCA1 Mutations from RNA-Seq Datasets
Jia-Hua Cai, Yu-Ching Chen, Hsueh-Ting Chu and Jeffrey J. P. Tsai
The Potential Dual-target Inhibitors for HER2/HSP90 Proteins from Traditional Chinese Medicine
Jhih-Ying Chen, Chia-Min Chen, Pei-Chun Chang and Jeffrey J.P. Tsai

S2.6: Medical image and signal analysis II
Detection of *H. pylori* Induced Gastric Inflammation by Diffuse Reflectance Analysis*
Alexandre Krebs, Vanía Camilo, Eliette Touati, Yannick Benezeth, Valérie Michel, Grégory Jouvion, Fan Yang, Dominique Lamarque and Franck Marzani
Implementation of an Ultrasound Platform for Proposed Photoacoustic Image Reconstruction Algorithm*
Enkhbat Batbayar, Enkhaatar Tumenjargal, Chulgyu Song and Woongchul Ham
Three-Dimensional Segmentation of Mouse Embryonic Stem Cell Nuclei for Quantitative Analysis of Differentiation Activity Using Time-lapse Fluorescence Microscopy Images*
Yuan-Hsiang Chang, Hideo Yokota, Kuniya Abe and Ming-Dar Tsai
Using NIRS to detect brain oxyHb changes during short-term memory tasks
Takuya Sasabe and Hiroshi Hagiwara
Corticospinal Tract (CST) reconstruction based on fiber orientation distributions (FODs) tractography*
Youshan Zhang

S3.1: Special paper session - Biomedical Big Data
Mutation Analysis of Second Primary Tumors in the Head and Neck Cancer by Next Generation Sequencing
Ting-Yuan Liu, Chien-Chin Lee, Hsi-Yuan Huang and Jan-Growth Chang
The Amiloride Derivatives Regulate the Alternative Splicing of Apoptotic Gene Transcripts
Chien-Chih Lee, Wen-Hsin Chang, Ting-Yuan Liu, Yu-Chia Chen, Guan-Yu Chen, Yang-Chang Wu and Jan-Growth Chang
The Role of mRNA Transporter in Human Cancer
Yu-Chia Chen, Chien-Chih Chiu, Han-Lin Chou and Jan-Growth Chang

S3.2: Biological text mining and biomedical informatics
EP-CapsNet: Extending Capsule Network with Inception Module for Electrophoresis Binary Classification*
Elizabeth Tobing, Murtaza Ashraf, Keejun Han and Mun Yong Yi
Semantic Relation Extraction for Herb-drug Interactions from the Biomedical Literature Using an Unsupervised Learning Approach
Khang Trinh, Duy Pham and Ly Le
Learning Effective Distributed Representation of Complex Biomedical Concepts
Khai Nguyen and Ryutaro Ichise
Regression-based Documents Reranking for Precision Medicine
Juncheng Ding, Wei Jin and Haihua Chen

S3.3: Biological network inference and analysis II
A Systems Biology Approach to Model Gene-Gene Interaction for Childhood Sarcomas
Dong Ling Tong and Christine Siew Ken Lee
Prediction of Plant-Disease Relations Based on Unani Formulas by Network Analysis
Shaikh Farhad Hossain, Sony Hartono Wijaya, Ming Huang, Irmanida Batubara, Shigehiko Kanaya and Md. Altaf-Ul-Amin
Computational Modeling of the Early Development of Embryonic Leaves in Maize
Charles C.N. Wang, Pei-Chun Chang, Phillip C.Y. Sheu and Jeffrey J.P. Tsai

S3.4 Computational Modeling and sensor in biomedical engineering
Finite Element Modelling for the Detection of Breast Tumor