[IW01-1-1]

KSBMB AND BIOCHEMISTRY LAB EDUCATION OF KOREA

Joon Kim[1]

[1]Korea University, Korea

As the academic society with the longest history in Korean biochemistry, the Korean Society for Biochemistry and Molecular Biology(KSBMB) aims to promote the advancement of science and technology as well as the improvement of human health by contributing to the academic development and distribution of biochemistry and molecular biology. The Society was founded as 'The Korean Biochemical Society' in 1948. As the largest academic society currently, with 12 thousand members in the associated biosectors, the Korean Society for Biochemistry and Molecular Biology holds academic conferences more than 5 times a year and issues 3 journals and webzines. For international academic exchange, the Society officially joined the Federation of Asia and Oceania Biochemists and Molecular Biologists (FAOBMB) in 1973 and the International Union of Biochemistry and Molecular Biology (IUBMB) in 1982. The Society invited the 24th IUBMB Conference & the 15th FAOBMB Congress to Seoul and is preparing for a successful hosting of IUBMB in 2018. This conference will provide the momentum to facilitate communication of the most timely and significant advances in research and will contribute to the advancement of biochemistry and molecular biology globally. Most of the college and university students in Life Sciences, medical Sciences, Food Science, Agriculture & Fishery Sciences have to study General Biochemistry courses in Korea. However, comparing to Biochemistry courses, Biochemstry laboratory education in universities are still limited in Korea. In this regards, the more details in the development and education in the field of Biochemistry and Molecular Biology in Korea will be discussed further..

Keyword: Biochemistry, Lab Education, KSBMB

[IW01-1-2]

BIOCHEMISTRY EDUCATION AMONG UNDERGRADUATE STUDENTS IN THE PHILIPPINES

Gracia Fe Yu[1]

[1]University of the Philippines Manila, Philippines

Within the Australian University system there is diversity in how and where Biochemistry is embedded within degree programs. The Department of Biochemistry and Molecular Biology, at Monash University, has been ranked as the premier department in its discipline since the inception of Australian Research Council benchmarking in 1998 and will be used as an exemplar.

Within the Monash University curriculum, biochemistry and molecular biology (BMB) are taught within the Bachelor of Science degree (BSc), the Bachelor of Biomedical Science (BBiomedSc) and health professional programs including Medicine, Nutrition and Radiography. The BSc program offers students a major and minor in Biochemistry and a minor in Molecular Biology with laboratory classes embedded in all BMB units within these programs. In contrast, in the BBiomedSc program BMB is part of the core curriculum, delivered as both independent units and a component of cross-disciplinary units. The biochemistry curriculum in the BMS program has less emphasis on laboratory classes. Laboratory classes are absent from biochemistry curriculum within the health professional programs.

The Learning Outcomes for the Biochemistry major in the BSc include a specific learning outcome for laboratory classes – "Students successfully completing this major will be able to: "demonstrate proficient technical skills in core biochemical laboratory techniques, and explain and interpret the principles and applications of these methods…" But, as science educators, we know that laboratory classes offer so much more. Monash has identified nine employability skills that we endeavor to embed in all our graduates: teamwork, communication, initiative and enterprise, creativity and innovation, problem identification and solution, tools and technologies, intercultural competence and planning and organisation. When viewing these from the perspective of a scientist it is obvious that these are skills our students can develop through participation in well-designed and scaffolded laboratory classes.

Active learning has become a "buzz" word in higher education with an emphasis on promoting higher order thinking skills. Our laboratory classes, in conjunction with developing technical skills provide active learning experiences and align with the higher order thinking levels of Blooms taxonomy – create, evaluate and analyse.

This presentation will discuss examples of how biochemistry laboratory classes, in an Australian university, provide a rich and diverse learning experience.

Keyword: Biochemistry education

[IW01-1-3]

BIOCHEMISTRY LABORATORY EDUCATION IN AUSTRALIA

Janet Macaulay[1]

[1]Monash University, Australia

Within the Australian University system there is diversity in how and where Biochemistry is embedded within degree programs. The Department of Biochemistry and Molecular Biology, at Monash University, has been ranked as the premier department in its discipline since the inception of Australian Research Council benchmarking in 1998 and will be used as an exemplar. Within the Monash University curriculum, biochemistry and molecular biology (BMB) are taught within the Bachelor of Science degree (BSc), the Bachelor of Biomedical Science (BBiomedSc) and health professional programs including Medicine, Nutrition and Radiography. The BSc program offers students a major and minor in Biochemistry and a minor in Molecular Biology with laboratory classes embedded in all BMB units within these programs. In contrast, in the BBiomedSc program BMB is part of the core curriculum, delivered as both independent units and a component of cross-disciplinary units. The biochemistry curriculum in the BMS program has less emphasis on laboratory classes. Laboratory classes are absent from biochemistry curriculum within the health professional programs. The Learning Outcomes for the Biochemistry major in the BSc include a specific learning outcome for laboratory classes – "Students successfully completing this major will be able to: "demonstrate proficient technical skills in core biochemical laboratory techniques, and explain and interpret the principles and applications of these methods…" But, as science educators, we know that laboratory classes offer so much more. Monash has identified nine employability skills that we endeavor to embed in all our graduates: teamwork, communication, initiative and enterprise, creativity and innovation, problem identification and solution, tools and technologies, intercultural competence and planning and organisation. When viewing these from the perspective of a scientist it is obvious that these are skills our students can develop through participation in well-designed and scaffolded laboratory classes. Active learning has become a "buzz" word in higher education with an emphasis on promoting higher order thinking skills. Our laboratory classes, in conjunction with developing technical skills provide active learning experiences and align with the higher order thinking levels of Blooms taxonomy – create, evaluate and analyse. This presentation will discuss examples of how biochemistry laboratory classes, in an Australian university, provide a rich and diverse learning experience.

Keyword: Laboratory classes, Curriculum, Higher order, Learning outcomes, 5. Australia

[IW02-1-1]

PROTEIN STRUCTURE PREDICTION AND REFINEMENT

Chaok Seok[1]

[1]Seoul National University, Korea

The three-dimensional structure of a protein is intimately related with its physiological function and provides important clues for regulating the function. Protein structure can be predicted accurately from its sequence by template-based modeling when the sequence identity is sufficiently high (e.g. >30%). A general procedure of template-based protein structure prediction will be explained in terms of domain parsing, template recognition, sequence alignment, model building, and refinement. Top-ranked methods in recent CASP (Critical Assessment of techniques for protein Structure Prediction) competitions will also be introduced. The issue of model refinement will be treated in more detail. Even at a high sequence identity, the predicted side chain structure may be less accurate than the backbone structure, whereas at a lower sequence identity, the predicted structure may have significant errors in both side chain and backbone structures. Although ab initio protein structure prediction from sequence is notoriously difficult, ab initio refinement starting from a reasonable initial structure is expected to be less difficult. Methods for refining loop structures and for refining overall structures will be introduced in this context. The refinement methods can be applied to modeling interfacial loops and overall conformational changes involved in protein-protein interactions. A method for predicting structural flexibility of G-protein-coupled receptors accompanied by ligand binding will also be presented.

Keyword: protein structure prediction, protein structure refinement, structure modeling, CASP, GPCR

[IW02-1-2]

NETWORK-BASED ANALYSIS OF OMICS DATA

Sun Kim[1]

[1]Seoul National University, Korea

Now sequencing technologies are routinely used to measure genome sequences and expression level of transcripts in a whole cell, which is known as omics data. Thus, it is very important to investigate condition-specific biological mechanisms underlying different phenotypes using the huge amount of omics data. However, DNA and RNA interact in a very complex way and our understanding on the interaction is limited. Fortunately, network-based analysis of omics data has been powerful enough to analyze multi-omics data. In this tutorial, I will present recent advances in network-based bioinformatics analysis in five categories: network propagation, network sub-module detection, biological pathway analysis, analysis of omics data from knockout experiments, and analysis of time-series omics data. Network propagation has been successful in detecting cancer driver genes at both DNA and RNA levels and also for systems biology. Techniques for network sub-module detection can detect genes that are condition-specific to certain phenotypes and has begun to change the definition of differentially expressed genes (DEG) at the gene interaction level. Biological pathway analysis can use gene expression quantity information directly, rather than simply mapping DEGs to biological pathways, thus can show activation status of certain pathways. Omics data from knockout studies now can be effectively analyzed using various biological networks. In addition, omics data from time-series experiments can be analyzed while considering both time and phenotype dimensions.

Keyword: Network propagation, Network sub-module, Pathway analysis, Knockout, Time-series

[IW02-1-3]

IDEEP LEARNING FOR BIOINFORMATICS AND HEALTH INFORMATICS

Sungroh Yoon[1]

[1]Seoul National University, Korea

In this era of big data, transformation of biomedical big data into valuable knowledge has been one of the most important problems in bioinformatics. Meanwhile, deep learning has advanced rapidly since the early 2000s, and now demonstrates state-of-the-art performance in various fields. Accordingly, the application of deep learning in bioinformatics to gain insight from data is emphasized both in academia and industry. This tutorial will review deep learning in the bioinformatics and presents examples of current research. To provide a useful and comprehensive perspective, the presenter will categorize related research both by bioinformatics domain (i.e., omics, biomedical imaging, biomedical signal processing) and deep learning architecture (i.e., deep neural networks, convolutional neural networks, recurrent neural networks, emergent architectures) and present brief descriptions of each study. Additionally, there will be discussion on theoretical and practical issues of deep learning in bioinformatics and suggestions for future research directions. This tutorial will provide valuable insight and serve as a starting point for researchers to apply deep learning approaches in their bioinformatics studies.

keyword: bioinformatics, deep learning, artificial intelligence

[IW02-1-4]

BIOINFORMATICS FOR MICROBIOME STUDIES

Byung-Yong Kim[1]

[1]ChunLab, Inc., Korea

Human body is a habitat for a large number of microorganisms, called microbiome. Microbiome has been recognized as a key factor in understanding human health and diseases. Bacteria is a major component of most of human body including gut. The study of human microbiome has been accelerated by the invention of next generation sequencing and bioinformatics. Application of the concept and techniques used in microbial ecology to microbiome allows us to understand the role and effects of microbiome, especially gut microbiome to human health and diseases. NGS technology has stimulated the development of complicated bioinformatics tools to analyze the enormous amounts of data generated. Researchers therefore need a clear understanding of the key concepts required for the design, execution and interpretation of NGS experiments on microbiomes. In this presentation, the principles of human microbiome and current related bioinformatic methodology will be explained. In particular, two main approaches for analyzing the microbiome, namely, 16S ribosomal RNA (rRNA) gene amplicons and shotgun metagenomics, will be presented with analyses of libraries designed to highlight their strengths and weaknesses.

Keyword: microbiome, NGS, bioinformatics, metagenomics

[FA01-1-1]

ROLE OF DNA STRUCTURAL VARIABILITY IN PROMOTER FUNCTION

Venkata RajeshYella[1], Devesh Bhimasaria[2], Debostuti Ghoshdastidar[1], Aseem Ansari[2] and Manju Bansal[1]

[1]Indian Institute of Science, Bangalore, India, [2]University of Wisconsin-Madison, USA

The talk will outline some of our recent studies wherein structural variability or flexibility in DNA is found to be strongly correlated with its function. Recent experimental and in silico analyses of promoters indicate that while there is considerable variation in their base composition and sequence, leading to presence of some non-B-DNA structural motifs, some DNA structural properties also show significant conservation. We have analyzed various structural features, such as stability, bendability (using both DNase1 sensitivity and nucleosome positioning preference models), intrinsic curvature and groove width, in promoter regions of both prokaryotic and eUnited Kingdomaryotic genomes1 and compared these with coding regions. Published experimental data from genome wide transcriptome analysis, correlates well with DNA structural features and their variability in different classes of promoters2,3. . We have also performed high-throughput in vitro and in silico analyses to understand the influence of flanking sequences outside the cognate sites in binding of three most prevalent TF families (Zinc finger, homeodomain, and bZIP) in vertebrates. In vitro binding affinities of each TF for all possible DNA sequences (entire sequence space) were correlated with a wide range of DNA structural parameters. It is found that local structural features of flanking sequences are instrumental in determining the binding affinity of TFs. DNA structural models employed in our study can provide detailed mechanistic insights into DNA-protein recognition, which will help refine computational tools for more accurate binding site search prediction and modelling of TF binding. 1. Kanhere, A. and Bansal, M. (2005) A novel method for prokaryotic promoter prediction based on DNA stability. BMC Bioinformatics 6, 1, doi:10.1186/1471-2105-6-1. 2. Bansal, M., Kumar, A. and Yella, V.R. (2014) Role of DNA sequence based structural features of promoters in transcription initiation and gene expression. Current Opinion in Structural Biology, 25, 77-85. 3. Yella, V.R., Kumar, A. and Bansal, M. (2018) Identification of putative promoters in 48 eUnited Kingdomaryotic genomes on the basis of DNA free energy, Scientific Reports, 8:4520.

Keyword: Promoters, Free Energy, Bendability, Genome analysis, Gene Expression

[FA01-1-2]

SYSTEMS BIOLOGY APPROACH TO INVESTIGATE EPIGENETIC LANDSCAPE OF NUCLEOSOME AND TRANSCRIPTION FACTORS

Varodom Charoensawan[1]

[1]Mahidol Univeristy, Thailand

Transcription in eUnited Kingdomaryotes is tightly regulated by the interplay between transcription factors (TFs) and nucleosomal histones. The vast majority of eUnited Kingdomaryotic genomes are occluded by histone octamers (i.e. nucleosomes), which restrict the accessibility TFs, RNA pol II, and other proteins to bind to DNA. To elucidate how different TFs in a genome interact with nucleosomes, we have computationally analyze DNA binding preferences of over two thirds of TFs in budding yeast Saccharomyces cerevisiae. We were able to characterize two major classes of yeast TFs: histone-correlated (HC); and histone-anti-correlated (HA) groups. The HC TFs have their intrinsic DNA-binding sequence preference overlapping with that of nucleosomal histones, which means they would compete to bind to similar DNA sequences in theory. These are the majority of yeast TFs and most of them function as activators, and induce nucleosome disruption upon transcriptional activation. In contrast, the HA TFs are predominantly repressors, which can bind to nucleosome-free regions, possibly with less effort as nucleosome replacement is not required. We further elucidate the dynamic interplay between TFs and nucleosomes in response to environmental cues, by focusing on their global DNA-binding profiles subjected to temperature changes. The plant TF Heat Shock Factor 1 (HSF1), and the histone variant H2A.Z, both play a major role in mediating transcription in response to temperature changes, one of the most important external stimuli, especially in extreme environments due to climate changes. We investigate this long-standing question using a model plant Arabidopsis thaliana (wild-type and hybrids). Plants have to adapt to fluctuating temperatures both diurnally and seasonally, and thus serve as a useful model for this particular genome-environment interaction question. We have shown that the warm ambient temperature transcriptome is dependent upon the HSFA1 clade of Arabidopsis HSFs, which cause a rapid and dynamic eviction of H2A.Z-nucleosomes at target genes. We propose that the antagonistic effects of H2A.Z and HSF1 provide a mechanism to activate gene expression rapidly and precisely in response to temperature, while preventing leaky transcription in the absence of an activation signal.

Keyword: Systems Biology, Gene expression regulation, Transcriptomics, Epigenomics, Bioinformatics

[FA01-1-3]

MULTI-TARGETED INHIBITION OF AN ESSENTIAL BACTERIAL ENZYME

Tatiana P. Soares da Costa[1], Chamodi K. Ghardi[1], Rebecca Christoff[1], J. MarkSutton[2] and Matthew A. Perugini[1]

[1]La Trobe University, Porton Down, Salisbury, Australia, [2]Wiltshire SP4 0JG, United Kingdom

The cell wall of Gram-negative bacteria consists of peptidoglycan chains linked together by oligopeptidic sequences comprised of the amino acids L-Ala, D-Ala, D-Glu and meso-diaminopimelate (DAP). Meso-DAP is synthesised via the DAP pathway that also yields the basic amino acid, L-Lys. Gene knock-out studies show that enzymes functioning in the DAP pathway are essential to bacteria, including dihydrodipicolinate synthase (DHDPS). DHDPS is an allosteric enzyme that catalyses the first-committed and rate-limiting step in DAP biosynthesis. It forms a homo-tetrameric structure that gives rise to at least two 'druggable' sites, namely (a) the active site and (b) the allosteric site, which binds lysine to mediate a feedback inhibition response. Given its essentiality to bacteria and absence in humans, DHDPS represents a valid but as yet unchartered target for antimicrobial development. Recently, we have developed two classes of small molecule inhibitors that target the DHDPS active site and allosteric site using a contemporary multi-disciplinary workflow spanning biophysics, biochemistry, medicinal chemistry, microbiology and structural biology. Inhibition studies in combination with biophysical techniques have demonstrated that these compounds are broad-spectrum inhibitors of bacterial DHDPS in vitro, representing the most potent DHDPS inhibitors discovered to date. Using viability and time-kill assays, these inhibitors have been shown to be bactericidal against both drug-sensitive and drug-resistant strains of Gram-negative bacteria (MIC = 8 – 64 μg/ml), including Acinetobacter baumannii, Pseudomonas aeruginosa and Escherichia coli, but are non-toxic to cultured human cells at >1028 μg/ml. Importantly, these compounds have been shown to synergise with FDA-approved classes of antibiotics, including β-lactams, fluoroquinolones, rifampicin and aminoglycosides. This study illustrates the potential for DHDPS inhibitors to be developed into a new class of antimicrobials with excellent potential to be combined with current antibiotics to yield innovative multi-targeted formulations to minimise the emergence of resistance.

[SS10-1-1]

GENDERED INNOVATIONS : APPLICATIONS IN BIOMEDICAL RESEARCH

Hee Young Paik[1]

[1]Korea Federation of Women's Science and Technology Associations (KOFWST), Korea

'Gendered Innovations' integrate sex and gender analysis into all phases of basic and applied research to stimulate new knowledge and to develop technologies appropriate for all human population. Although sex and gender considerations are important for excellence in research and product developments in all range of science and technology, they are particularly significant in biomedical field. All elements of biomedical research should consider sex and gender and analyze how they interact with each other. From January 2016, NIH requires grant applications of preclinical studies involving vertebrate animals and humans to account for sex as a biological variable (SABV). This is a big expansion of the global efforts, such as Horizon 2020 of European Union, to implement sex and gender analysis in STEM research. The Center for Gendered Innovations in Science and Technology Research (GISTeR) has been working to stimulate sex and gender integration in Korea. During the past two years, a research project has been carried out and it includes policy development and case studies team. Researchers of the case study research team apply sex and gender analysis in their own research topics of four areas - basic science, health and nutrition, engineering, city planning and environment. Activities and examples of research topics and achievements, especially in biomedical area will be presented.

Keyword: gender analysis, sex analysis, biomedical research, policy development

[SS10-1-2]

SEX DIFFERENCES OF FEEDING BEHAVIOR IN RESPONSE TO STRESS IN RAT

Yong Sung Kim[1], Han-Seung Ryu[1], Suck Chei Choi[1], Eul Sig Choi[1], Min Seob Kim[1] and Moon Young Lee[1]

[1]*Digestive Disease Research Institute, Wonkwang University, Korea*

Exposure to stress may alter feeding behavior and stress hormone such as ACTH and corticosterone. The aim of this study was to investigate the difference of feeding behavior and gastric emptying according to the type of stressor, sex and type of food in rat.

Both sex of Wistar rats were used. All rats underwent foot shock stress (FSS) for 5 minutes one day before experiment and overnight fasting. "FSS" was used as physical stress and "watching other rat exposed to FSS" was used as psychological stress. In each type of stress, rats were randomly divided into three groups as (1) regular chow food supply without stress group (control), (2) regular chow food supply with stress group (Chow), and (3) regular chow and sweet food supply concomitantly with stress group (Sweet) in male and female, respectively. After stress session, food consumption, onset time to food intake, food preference, serum ACTH and corticostereone were measured in all rats.

Onset time to food intake was significantly shortened when sweet food was concomitantly supplied in both male and female without stress. In male rats, both psychological and physical stress decreased the food consumption regardless of type of food supply. In female rats, however, only physical stress decreased the food consumption when only regular food was supplied. The gastric emptying rate significantly increased under the physical stress regardless of gender, type of stress or time of food supply. However, when food was given after the stress, the gastric emptying rate significantly increased in male group only in the psychological stress regardless of type of food. Even though the total food consumption was decreased under the physical stress in female rats and the psychological and physical stress in male rats, corticosterone was significantly reduced in Sweet group under the physical stress in female rats and physical and psychological stress in male rats.

These results suggest that sex as well as type of stressor is a crucial factor affecting on feeding behavior and gastric emptying in response to stress in rat and sweet food might have an ameliorated effect to relieve stress.

Keyword: Sex difference, foot shock stress, psychological and physical stress, sweet food, ACTH

[SS10-1-3]

GUIDELINE TO INTEGRATE SEX/GENDER AS A BIOLOGICAL VARIABLE IN BIOMEDICAL RESEARCH PAPERS

Youngmi Kim Pak[1], SUnited Kingdom Kyeong Lee[2], Hee Young Paik[3], Eui-Ju Yeo[4] and Heisook Lee[3]

[1]Kyung Hee University School of Medicine, Korea, [2]The Catholic University of Korea, Korea, [3]Korea Federation of Women's Science and Technology Associations (KOFWST), Korea [4]Gachon University, Korea

In recent years there have been many scientific evidences that sex and gender as well as the two interactions can affect not only molecular cellular processes and clinical medical characteristics but also health and disease. On November 11, 2017, an article 'sex matters in experiments on party drug-in mice' appeared in Nature news which suggests that even the sex of researchers has to be considered or reported in the future. Our presentation will introduce a few examples in biomedical research why both sex and gender should be investigated as biological variables for healthier world for both men and women as well as for better knowledge. We then suggest, as a guideline how to integrate the gender dimension in the entire research process from research idea, formulation of research problems, research design, data collection and analysis, answering the research questions, theoretical interpretation of the results, comparison with earlier research and to conclusions depending on sex and gender.

Keyword: gender analysis, sex analysis, biomedical research, guideline

[SS10-1-4]

CELL DB : CELLS WITH DEFINED SEX

Mi-Na Park[1], Ji Hyun Park[2], Hee Young Paik[3], and Suk Kyeong Lee[4]

[1]Seoul National University, Korea, [2]Mokpo National University, Korea, [3]Korea Federation of Women's Science and Technology Associations (KOFWST), Korea, [4]The Catholic University of Korea, Korea

Recently, funding agencies and scientific journals are starting to require the integration of sex in basic and preclinical as well as in clinical studies. However, the change is very slow. To investigate how major cell banks that supply cells worldwide describe the sex of their cells, we analyzed the homepages of three representative cell banks: American Type Culture Collection, European Collection of Cell Cultures, and Japanese Collection of Research Bioresources. We found that approximately 15.5% of human cell lines were sold without sex identification. Animal cell lines lacked sex identification more often than human cell lines. Majority of primary cells and stem cells were sold with undefined sex. Among the primary cells and stem cells with sex identification, male cells outnumbered female cells. Most of all, some cell line banks do not provide sex-based search engines for researchers. To facilitate sex-based cell search, we have established GISTeR Cell DB (http://gister.re.kr). The DB is valuable as it provides information for 6,247 commercially available cells categorized according to their species, sex, cell category, disease state, tissue origin, cell type, and vendor. Cells suitable for research interest can be easily searchable by multiply clicking choices under each cell character menu. The need to integrate sex/gender as biological variables in basic, preclinical, and clinical studies should no longer be overlooked in unbiased and reproducible research. The GISTeR Cell DB can help researchers to quickly pinpoint the cells having characteristics they want and to balance sex of cells in their experiments.