AN EXCLUSIVE FACILITY TOUR OF SEVERANCE HOSPITAL
21st August 2017, 2:00pm-4:00pm (More details on page 4)

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#GEPMBD17
Global Engage is proud to present the Precision Medicine and Big Data Congress Asia 2017 which will be held on the 22nd and 23rd August, 2017 in Seoul, South Korea. This congress is part of our Drug Discovery series which includes Human Microbiome, Synthetic Biology, qPCR/dPCR, Digital Pathology & Biologics among others.

This year’s congress will feature innovative topics and cutting edge techniques and technologies from presenters from around the world. Clinicians and medical experts are calling for more personal attention and treatments by medical practitioners after finding a large number of patients failed by “one-size-fits-all” treatments leading to ineffective cures, preventions and adverse side-effects. The congress presents an insightful overview to the myriad factors of precision medicine. The availability of big data on individual genetic variations, combined with the improved ability to measure environmental factors and other new technologies have led to the era of precision medicine.

Designed for drug and DX developers, payers, healthcare providers, academics to technology solution providers and research centers, this congress aims to covers the most important developments in the advancement of precision medicine.

EXPERT SPEAKERS Include:

DAVID I SMITH, PH.D.
Professor and Consultant, Chairman of the Technology Assessment Group, Mayo Clinic Center for Individualized Medicine, US

VINCENZO TENEGGI
Senior Medical Director D3 (Drug Discovery and Development), A*Star, Singapore

TAO HUANG
Director of Bioinformatics Core Institute of Health Science, Chinese Academy of Sciences, China

SHANRONG ZHAO
Director - Computational Biology and Bioinformatics Pfizer Worldwide Research & Development, US

PHILIPPE PINTON
Country Head Medical Division Takeda Pharmaceuticals, South Korea
PRECISION MEDICINE

Precision Medicine: Accelerating Biomedical Discoveries and Enabling Accurate Diagnosis and Treatment
- Precision Dosing: Right Drug to the Right Patient at the Right Time
- Gene Therapies
- Clinical Application of Discoveries
- The Economics of Precision Medicine
- Precision Diagnosis for Precision Medicine
- Computational Pathology
- Precision Microbiota Application in Clinical Therapy and Diagnosis
- Precision Medicine and its Journey to Patients and Physicians
- Use of Molecular Assays for Patient Selection

COMPANION DIAGNOSTIC & BIOMARKERS

Companion Diagnostic & Biomarkers
- Regulatory Updates
- Biomarker Development
- Targeted Therapies
- Co-Developing Diagnostic and Therapeutics
- Clinical Diagnostics, NGS & Genomic Markers and Genetic Testing

GENOMICS AND SEQUENCING

Genomics and Sequencing
- Collection of the First Million Genomes
- DNA Sequencing
  - Biobank in Advancing Precision Medicine and Contributing to Research and Improved Healthcare
  - Use of Clinical Genome and Exome Sequencing in Patients with Potential Genetical Disease
- Accelerating and Improving Cancer through Drug Target and Biomarkers
- Tracking Genomic Cancer Evolution for Precision Medicine
- Construction of Gene Panels

HEALTHCARE BIG DATA & TECHNOLOGY

Healthcare (Big) Data and Technology in Delivering Precision Medicine
- Artificial Intelligence for Cancer Treatments
- Online Monitoring and Healthcare Management
- Personalised Healthcare
- Health Technology Assessments
- Sharing of Software and Genomic Datasets to Evaluate and Improve Accuracy of Genome Sequencing

TRANSLATION

All presentations will be in English, Korean audio translation will be available onsite
AN EXCLUSIVE FACILITY TOUR OF SEVERANCE HOSPITAL
21st August 2017, 2:00pm-4:00pm

Severance Hospital is one of the oldest and biggest university hospitals in South Korea. The facility tour covers the main building of Severance Hospital, Clinical Trials Center and Cancer Center.

Join this tour for an additional USD50! Transportation from Grand Hilton Seoul to Severance Hospital will be provided.

*Available for the first 20 registrations for the Precision Medicine and Big Data Asia Congress.
MAKING A POSTER PRESENTATION

Poster presentation sessions will take place in breaks and alongside the other breakout sessions of the conference. Your presentation will be displayed in a dedicated area, with the other accepted posters from industry and academic presenters. We also issue a poster eBook to all attendees with your full abstract in and can share your poster as a PDF after the meeting if you desire (optional). Whether looking for funding, employment opportunities or simply wanting to share your work with a like-minded and focused group, these are an excellent way to join the heart of this congress.

In order to present a poster at the congress you need to be registered as a delegate. Please note that there is limited space available and poster space is assigned on a first come first served basis (subject to checks and successful registration). We charge an admin fee of $50 to industry delegates to present, that goes towards the shared cost of providing the poster presentation area and display boards, guides etc. This fee is waived for those representing academic institutions and not for profit organisations.
CONFIRMED SPEAKERS

DAVID I SMITH, PH.D.
Professor and Consultant, Chairman of the Technology Assessment Group, Mayo Clinic Center for Individualized Medicine, US

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SHANRONG ZHAO
Director - Computational Biology and Bioinformatics Pfizer Worldwide Research & Development, US

TAO HUANG
Director of Bioinformatics Core Institute of Health Science, Chinese Academy of Sciences, China

KETAN PATEL
Health Informatics Director - Advanced Analytics Centre AstraZeneca, UK

TONG GUO
Head of Biostatistics, South Africa and Asia Quintiles, China

SUSAN HAZELS MITMESSER
Senior Director – Nutrition & Scientific Nature’s Bounty, US

MICHAEL WINTHER
Associate Director of Business Development Genome Institute of Singapore, Singapore

DONGKIU KIM
Secretary General Global Centers of Excellence in Clinical Trials (SCI-Consortium), South Korea

WOONG-YANG PARK
Director Samsung Genome Institute, South Korea

LAWRENCE WEE
Chief Data Scientist Zuellig Pharma, Singapore

DAVID W. HEIN
Professor and Chair of Department of Pharmacology and Toxicology University of Louisville, US

BRIAN ABEL
Head of Immunogenomics Core, Deputy Director, Immunomonitoring Platform, Singapore Immunology Network, A*STAR, Singapore

MICHAEL NOVA
Chief Innovations Officer, Pathway Genomics, US

YANNICK SIMONI
Senior Research Fellow Evan Newell, Singapore Immunology Network, A*STAR, Singapore

MATHIAS GOESCHL
Vice President, Digital Content Molecular Health, Germany

ENRICO RUBAGOTTI
Bioinformatician

MICHAEL HERMAN
Head of Business Development Biopharma OncoDNA, Belgium

YOOSEP CHONG
Research Professor, The Catholic University of Korea, Korea

VENKATESH TADINADA
President & CEO, Solivar Inc, US
Advances in DNA sequencing over the past 15 years have been remarkable. While it used to cost hundreds of millions of dollars to completely sequence one human genome, the current cost is less than $1,000 and this will approach $100 in just the next few years. The most powerful tool to characterize cancer genomes is whole genome sequencing (WGS), but this is just the cost of sequencing. Assembling that sequence together and making sense out of it costs considerably more. In addition, the cost of storing that information can be even more expensive. The Mayo Clinic has been exploring the use of an alternative strategy, which is called mate-pair next generation sequencing (MP-Seq). This technique produces a library of fragments that used to be kilobases apart and is the ideal substrate for paired end next generation sequencing. With this technique one can obtain genome-wide information about genomic rearrangements with only 5 Gigabases of DNA sequencing. A clinical test based upon this technique is now available at the Mayo Clinic and it is an ideal tool for characterizing genomic rearrangements that have occurred within a cancer genome. My laboratory has been employing this technique to characterize cancers that are caused by human papillomavirus. We demonstrate that with MP-Seq that we can characterize where HPV has integrated in these cancers and simultaneously characterize other genome rearrangements including insertions, deletions, and chromosomal translocations. Furthermore this technique identifies novel junctions hence can identify cancer-specific alterations which are ideal for monitoring a cancers response to therapy through the use of the liquid biopsy. I will discuss how MP-Seq is rapidly becoming a powerful clinical tool for cancer patients.
DAY 1 | TUESDAY 22ND AUGUST 2017

12:00-12:30

MICHAEL WINther
Associate Director, Senior Project Manager
Genome Institute of Singapore, Singapore

Precision Medicine through Pharmacogenomics
Pharmacogenomics is the study of genetic variations in individuals on drug safety and efficacy. This science has developed over the past two decades into a body of knowledge that is ready to be implemented with a beneficial impact on public health. This presentation will review barriers to implementation and how they might be overcome. Pharmacogenomics will be the first wave of precision medicine to impact the general population.

TONG GUO
Head of Biostatistics, South Africa and Asia
Quintiles, China

Big Data on Site Identification and Patient Recruitment

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samuel@global-engage.com or +603 2117 5195

12:30-13:00

SOLUTION PROVIDER PRESENTATION

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12:30-13:00

SOLUTION PROVIDER PRESENTATION

12:00-12:30

ENRICO RUBAGOTTI
Bioinformatician
Awaiting Topic

13:00-14:00

Networking Lunch

Room: TBC

14:00-14:30

DONGKYU KIM
Secretary General, Global Centers of Excellence in Clinical Trials (SCI-Consortium), South Korea

Utilisation of EHR Data for Optimisation of Clinical Trial Design

The aim of this talk is to present a practical application in clinical trial protocol development, especially in the area of target disease subpopulations, eligibility criteria and other interventional study designs. Clinical Data Retrieval System (CDRS) was built and implemented in 2007 for the first time in Korea, which enables queries of clinical data from de-identified healthcare activities of about 6.3 million patients who have visited Severance Hospital and Gangnam Severance Hospital for the last 10 years.

CDRS has accumulated a huge amount of health care data such as disease characteristics (e.g., diagnosis, staging), patient subpopulation (e.g., co-morbidity and complication), treatment (e.g., medicine, procedure, surgery), and clinical results (e.g., laboratory result and pathology report), thus allowing to retrieve key elements information in developing clinical protocols. EHR-driven profiling of target disease characteristics can be well correlated to successful mitigation of potential risks associated with incomplete information of clinical progression, patient eligibility, procedure compliance, etc. Along with DB-driven information, Yonsei University Health System (YUHS) initiated a multi-disciplinary consultation by strategic advisory leadership team (SALT), which is composed of clinicians and basic scientists at the University Hospital. Its goal is to mainly focus on discussion of patient-centered unmet needs and clinical development plan for a target drug by working together with industrial partners at the early stage of drug development.

Taken together, the integrated clinical development supportive system of professional consultation with healthcare data information will provide tailored solutions to the identified obstacle and inefficiency inherent in the conventional system of clinical protocol design.
N-acetyltransferase 2 (NAT2) is the primary enzyme involved in the metabolism of the anti-tuberculosis drug INH and is subject to genetic polymorphism in human populations resulting in rapid, intermediate, and slow acetylator phenotypes. Cryopreserved human hepatocytes obtained from rapid, intermediate, and slow acetylators were used to investigate the role of NAT2 polymorphism on the N-acetylation of INH both in vitro and in situ.
SOLUTION PROVIDER PRESENTATION:
MICHAËL HERMAN
Head of Business Development Biopharma, OncoDNA, Belgium
NGS & IHC Based Patient Enrollment and Sourcing using Solid and Liquid Biopsies Profiling Combined with Precision Medicine Knowledge Database
Daily, OncoDNA draws the complete molecular profile of cancer patients, combining DNA and molecular pathology in the analysis of a solid and of a liquid biopsy. Most of the treatment options are FDA or EMA approved drugs, but often, the best or the only option for those patients are compounds which are still under clinical investigation. Biopharma sponsors are more and more facing the challenge of finding patients who may be eligible for open trials. As the European cancer precision medicine leader, and beside helping patients and oncologists, OncoDNA is also helping biopharma companies through their drug development process. We serve as a central lab for molecular characterization or we do improve compound theranostic knowledge through our cancer precision medicine expertise, but we also have initiated this unique and innovative approach to improve patient recruitment. This presentation will be an illustration of how OncoDNA is putting together its cancer precision medicine expertise, the oncologist and the biopharma to give patients the access to the best cancer care.

PANEL DISCUSSION:
Benefits and Challenges of a Precision Medicine Knowledge Sharing Network
Overcoming massive logistical barriers to achieve results and revolutionizing the accessibility of information for precision medicine. The intersection of Big Data and Precision Medicine sits at the heart of this panel discussion. This session will look beyond the promise of big data as organisations start to see results from using enhanced data analytics and data sharing.

SHANRONG ZHAO
Director – Computational Biology and Bioinformatics, Pfizer Worldwide Research & Development, US
Isoform Quantification in RNA Sequencing: Challenges and Applications in Personal Medicine
Due to alternative splicing, over 90% of human genes have multiple transcript isoforms. Isoforms of the same gene can play distinct or even opposite biological rules. For instance, gene TP53 has an important role in oncology and different cancer types show different expression profiles of its transcript isoforms. However, the expression isoforms are tissue and disease specific. Therefore, it is beneficial to quantify RNA-Seq experiments at the transcript level, rather than at the gene level. Recently, a number of tools have been developed for RNA-seq isoform quantification, including RSEM, Cufflinks, eXpress, Tigar2, Kallisto, Salmon and Sailfish. We performed a systematic evaluation on those methods using both simulated and experimental datasets, and furthermore investigated the impact of gene/isoform structures on the accuracy of isoform quantification. Our research has a broad implication on precision medicine

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Closing Remarks / End of Day One

17:30

Networking Drinks Reception

17:45-18:45

Room: TBC

17:00-17:30

TAO HUANG
Director of Bioinformatics Core Institute of Health Science, Chinese Academy of Sciences, China

Machine Learning and Graph Theory in Health Sciences
To make medicine predictive and preventive, we need to develop targeted interventions and stop disease before it even starts; for each patient, the individual variations should be considered and the treatment should be personally tailored. With the emergence and growing impact of multi-omics study, new methods and tools are needed to deal with the high-dimensional data. It is important to identify the relevant information from complex omics data ("data mining") and understanding how biological systems work as an integration of components at different levels ("systems biology"). The integrative analysis of multiple big data, such as genomics, epigenomics, metabolomics, EMR history, lab tests, imaging, social factors, environment, lifestyle choices, with the latest development in computer science, such as deep learning and graph theories, will accelerate Precision Medicine.
BRIAN ABEL  
Head of Immunogenomics Core, Deputy Director, Immunomonitoring Platform Singapore Immunology Network, A*STAR, Singapore  
**Slgn’s Clinical Immunomonitoring Platform for the Deep Assessment of Immune Responses in Pre-Clinical Models, Cohort Studies & Clinical Trials**  
The Clinical Immunomonitoring Platform at the Singapore Immunology Network (Slgn) is dedicated to defining immunomarkers & immunological endpoints with clinically relevant impact via high-throughput acquisition of immunological data from pre-clinical models, cohort studies and clinical trials. It has a very successful track record of supporting academia, clinical collaborators, and industry partners in studies spanning diverse fields such as immunology, cancer immunotherapy, aging biology and stem cell research. The Platform leverages on the scientific expertise of Slgn’s Principal Investigators supported by a suite of capabilities including the following facilities: Flow Cytometry, FACS, Luminex, CyTOF, Immunogenomics & Bioinformatics. The Platform may be involved from the initial stage of study design to sample processing, biobanking, assay running & ultimately, downstream analysis. The Platform has a well-defined workflow & project management infrastructure, which is capable of engaging all phases of research from early biomarker discovery, novel target identification, technology development, and all the way through to the assessment of Phase IV vaccine clinical trials. Examples of current clinical trials & studies conducted by the Platform that will be briefly discussed include (i) The assessment of responsiveness to flu vaccination in the elderly, (ii) The longitudinal assessment of dengue natural infection vs. dengue vaccination and (iii) The assessment of tumor antigen-specific CTLs in syngeneic tumor models.

YANNICK SIMONI  
Senior Research Fellow, Evan Newell, Singapore Immunology Network, A*STAR, Singapore  
**Profiling Neoantigen-Specific CD8 T Cells in Human Cancer**  
The clinical relevance of CD8+ T cells in the control of human cancers is now beyond doubt. It is well established that CD8+ T cells can recognize cancer cells and that therapeutic manipulation of these cells can induce tumor regression (e.g. via anti-PD-1 treatment). In this context, the identification of mutated expressed self-tumor antigens (i.e., neoantigens) are currently under intense investigation for the development of therapeutic cancer vaccines. However, the identification of neoantigen-specific CD8+ T cells is difficult since rare cell populations in size-limited patient samples need to be detected. Here we used next-generation sequencing and combined mass cytometry together with a multiplex tetramer staining approach to screen for CD8+ T cell antigen specificity in lung and colorectal tumor resection samples. Our results show that neoantigen-specific CD8+ T cells infiltrated human tumors and exhibited an exhausted profile. Furthermore we also detected a large fraction of CD8+ T cells that were specific for cancer unrelated antigens, such as EBV, HCMV or flu viruses. These observations highlight that not all tumor infiltrating CD8+ T cells specifically recognize tumor antigens. Based on these findings, we compared the phenotypes of neoantigen-specific and cancer unrelated CD8+ T cells in human tumors. Although many markers were shared between both T-cell populations (i.e. PD-1, CD103, TIGIT), we found that some markers were specifically expressed by neoantigen-specific CD8 T cells. Our results suggest that this profile of tumors-specific cells could be a powerful biomarker to identify responder patients for checkpoint blockade immunotherapy. Moreover we demonstrate value for our neoantigen-specific CD8 T cells screening approach for the benefitting designing therapeutic cancer vaccines.

MICHAEL NOVA  
Chief Innovations Officer, Pathway Genomics, US  
**Artificial Intelligence and Big Data for the Consumer**  
- How Machine Learning and AI are revolutionizing Precision Medicine  
- Analyzing large data sets using data mining and Machine Learning  
- Mobile consumer and physician point-of-care application for Precision Medicine  
- How precision omics/genomics technologies linked to AI can change patient behavior

16:00  
Closing Remarks / End of Conference
Grand Hilton Seoul,
353 Yeonhui-Ro,
Seodaemun-Gu, Seoul
120-710, South Korea

The Grand Hilton Seoul is located 15 minutes from downtown Seoul. Enjoy easy access to the city center, Itaewon and Hongik University subway station with our complimentary shuttle service. Our modern Convention Center, which can hold up to 2,500 guests, is ideal for any event. Pick any of our stylish restaurants and indulge in the gourmet cuisine, perfect for any occasion.