

Time Slot	Edison Room	Woodbridge Room
<p>3:00 – 3:30</p>	<p>IQ™ Technology: A Universal, Homogeneous, Method for High-Throughput Screening of Kinase and Phosphatase Activity</p> <p>Sherri Z. Millis, PhD - Pierce Biotechnology</p> <p>IQ™ Technology is a homogeneous, universal detection platform designed specifically for high-throughput screening of kinase and phosphatase activity. The technology has been tested in 96- to 384- to 1536-well microplate formats and is ideally suited for automated drug discovery screening systems. IQ™ Technology is a direct, non-competitive assay format that does not require antibodies or radioactive reagents to measure phosphorylation state. Kinase or phosphatase activity is quantitated by direct measurement of the phosphorylation state of fluorophore-labeled peptide substrates. Phosphorylation is measured by the change in fluorescence intensity that occurs when a proprietary iron-containing compound binds specifically to phosphoryl groups on dye-labeled peptides. This change in observed fluorescence is proportional to the extent of phosphorylation of the fluorophore-labeled peptide, because the iron-containing compound quenches the fluorescent emission exclusively on the phosphorylated form of the fluorophore-labeled peptide. The technology IQ™ Technology is a sensitive, robust, universal method that can be used with any peptide sequence.</p>	<p>Automated Detection and Classification of Systematic Errors in Array Experiments</p> <p>John Elling, Datect Inc.</p> <p>Large-scale laboratory automation generates arrays of experiments. These arrays are independent experiments that may be spots printed on slides, or genes immobilized on a chip, or may be wells in microtiter plates. Ideally, each experiment is uncorrelated with any other experiment. In the real world, however, experiments may show artifacts that are spatially correlated. For example, these can be "row effects", "column effects" or "edge effects" in plates or chips. Detecting these effects is usually done by manual inspection of a display of the array of results. This manual examination of the data is not only time consuming, but individual scientists use their own judgment in accepting or rejecting data and normalizing data, which can lead to uneven quality in the results. Further, while some of these effects can be detected by manual inspection, others can be quite subtle and evade even visual detection.</p> <p>Datect has developed technology for automatically detecting and reporting systematic spatial correlation errors using periodogram analysis. The analysis yields a single score reflecting the probability of systematic error contained in a plate. The technology also can evaluate any detected correlations against expected correlations in the experiments in order to determine if the special correlations are problematic. Software implementing this technology can be used from Microsoft Excel making it directly applicable to the majority of current informatics systems. These techniques can be used in an automated data validation system and can also be used interactively when scientists are developing new experiments or troubleshooting systematic problems.</p>

<p>3:30 – 4:00</p>	<p>A Data Management Architecture for Archiving, Retrieval, Transfer and Report Generation in High Throughput Laboratory Operations</p> <p>John P. He Ifrich, NuGenesis Technologies Corporation</p> <p>Improvements in screening technologies have resulted in throughputs that have increased from 10,000 assays per year to current levels, which can approach more than 100,000 assays per day. The common thread throughout the process is the enormous amounts of data that must be processed, correlated and communicated to provide, knowledge that will lead to the ultimate decision – to proceed on this research path or not.</p> <p>Many existing data system solutions are too rigid to allow automated collection, archiving, retrieval and transfer of disparate instrument readable data (eg. plate readers, LC/MS and NMR) and human readable data (instrument and business reports). A data management platform termed Nugenesis Scientific Data Management System (SDMS) integrates with existing data architectures within the high throughput (HT) lab and provides the data export to other “niche” software tools such as statistics, analytics and visualization packages. This paper will outline the SDMS platform and its direct use in the modern HT lab automation arena.</p>	<p>Autopurification of Nucleic Acids</p> <p>Thomas E. Strader Promega Corporation</p> <p>Automated purification of DNA and RNA is a common technique in molecular biology with downstream applications including PCR, cloning, sequencing, restriction enzyme digestion, transfection, microarray and others. Promega has developed a broad range of products and associated technical expertise to address the specific needs of scientists performing these isolations on automated liquid handlers from a diverse group of starting materials. The family of Wizard® SV96 Systems offers silica-membrane systems optimized for isolation of numerous nucleic acid types including plasmid DNA, DNA fragments, genomic DNA, PCR products, total RNA and messenger RNA. The family of Wizard® MagneSil® products offers paramagnetic particle based systems for isolation of sequencing-grade plasmid DNA, transfection-grade plasmid DNA, PCR products, sequencing products and genomic DNA. In addition, Promega has developed a multi-functional team to meet challenging customer automation needs. This team consists of expert molecular biologists that have been trained on all of the common robotic platforms used in the field of nucleic acid purification in order to assist the researcher with set-up, optimization and operation of their systems. Validated, walk-away methods are continually being developed in cooperation with leading robotics companies. By taking a systemic approach to the integration of chemistry and robotic systems, we believe we can provide superior products and service.</p>
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<p>4:00 – 4:30</p>	<p>Cell Signaling Technology & “Activation-State” Antibodies: Innovative Tools for Therapeutic Discovery.</p> <p>Christopher Bunker, Ph.D., Cell Signaling Technology</p> <p>The growing number of kinase drug targets creates an urgent demand for rapid kinase HTS assay development. A major hurdle in serine/threonine kinase HTS is the identification of in vitro substrates for novel kinases and the availability of robust antibody tools to detect peptide phosphorylation.</p> <p>Cell Signaling Technology, Inc. (CST; Beverly, MA) has developed a Kinase Substrate Screening Kit (#7400) to expedite the identification of optimal peptide substrates and matched phosphorylation-specific antibody detection reagents. The kit consists of 87 biotinylated-peptide substrates of diverse sequences and 87 matched phospho-specific antibodies arrayed in a 96-well plate format. Positive (phospho) and negative (nonphospho) control peptides of identical sequence, and experimental (nonphospho) peptide enable determinations of signal-to-noise for each peptide/antibody pair and kinase activity. All peptides on the array are derived from in vivo phosphorylation sites. Signal-to-noise values range from 10 to well over 1000 by DELFIA® assay.</p> <p>We have validated the #7400 Kinase Substrate Screening Kit as an ideal tool for rapid serine/threonine kinase assay development. We have used Akt1, CKII, and ERK2 validate the utility of the Kinase Substrate Screening Kit. Moreover, the efficiency of optimal substrate identification with the #7400 Kit has been demonstrated repeatedly with novel kinases having no known substrates. Therefore, the Kinase Substrate Screening Kit is of fundamental utility to kinase drug discovery programs.</p>	<p>A New Technology Platform for Drug Discovery</p> <p>Al Akowitz, PhD, Meso Scale Discovery</p> <p>Meso Scale Discovery (MSD) has a new technology platform for drug discovery, high throughput screening and genomics/proteomics research. This platform combines array technologies and electrochemiluminescence detection to achieve rapid, highly sensitive assays in a no-wash format. This poster presents two new instruments that use highly parallel detection (imaging or parallel scanning readout, depending on the instrument) and custom multi-well plates with integrated electrodes to achieve rapid readouts that approach one plate per minute for 96-, 384- or 1536-well plate formats. The instrument platform features high sensitivity (106 molecules), wide dynamic range (6 logs), no-wash assay formats, and the choice between full robotic integration and stand-alone workstation modes. The broad portfolio of MSD™ assays includes assays for: receptor-ligand binding and regulation (EGFR-EGF, GPCRs), enzyme activity (e.g. kinases, ubiquitinylases, proteases, reverse transcriptase), DNA and RNA hybridization, small molecule detection (cAMP, cytokines), and protein-protein interactions.</p>
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<p>4:30 – 5:00</p>	<p>Simultaneous Measurement – Multiplexing - of Multiple Assays using Small Biological Sample Volumes</p> <p>Geoff Alms, Ph.D. Applications Scientist for Upstate USA.</p> <p>To understand the nature of an immune response, it is necessary to profile the presence and levels of soluble cytokines in a biological sample. Cytokine networks are crucial regulators of cell-cell communications involved in hematopoiesis, inflammation, and wound healing. Upstate has developed the Beadlyte™ line of detection kits based upon the Luminex system. Our first line of kits, the Multi-cytokine Detection Kits allow for the simultaneous (multiplex) measurement of up to 22 cytokines from a single 50 ul sample. Beadlyte™ kits are comprised of microsphere based fluorescent sandwich-immunoassays for reading on the Luminex™ multiplex instrument. Beadlyte™ technology is easy to use, flexible with respect to measuring different combinations of cytokines, and requires an order of magnitude less labor than traditional ELISAs. Sensitivities as low as single pg/ml are routinely achieved with low assay variability. Beadlyte™ cytokine kits have been validated for lack of cross-reactivity, and many assays can be performed without any wash steps. Suitable biological samples that have been used in the Beadlyte™ system for immune monitoring include cell culture media, serum, plasma, tears, blood spots, and lavage fluid.</p> <p>Expanding upon the Beadlyte™ line, Upstate has developed several additional applications for this technology. Recent advances include the ability to detect both the total and phosphorylated levels of cell signaling proteins. These capabilities are being rapidly expanded and currently enable the simultaneous detection of 5 proteins. In addition to the cell signaling kits, kinase activity assay kits have been developed that allow for the measurement of the activity and the impact of a compound upon that activity for 3 kinases. The advantages and applications of the Beadlyte™ range of products will be presented.</p>	<p>Advancing Research Through the Integration of Discovery Data</p> <p>Eric Kaldy, IDBS</p> <p>IDBS' ActivityBase software suite is a complete, proven software solution for managing your valuable research data. Our applications help you capture, analyze, and more importantly manage your research data securely and provides for powerful querying and reporting capabilities. Integrate your biological and chemical data across a spectrum of discovery activities — including chemistry, UHTS, HTS, secondary screening, lead optimization, DMPK, early ADME, behavioral and other pharmacology-based assays.</p> <p>This discussion will focus on enhancing productivity with IDBS' latest releases of ActivityBase 5.1 and Decision Support tools. These solutions provide fast and flexible data acquisition and analysis capabilities, improved quality control measures and comprehensive querying and reporting options, enabling scientists to make better decisions efficiently and cost effectively – advancing discovery research.</p>
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<p>5:00 – 5:30</p>	<p>Automating Genomics and Proteomics Applications</p> <p>Zymark Edward M. Alderman, Ph.D.</p> <p>This presentation will focus on the automation of major genomic and proteomic applications. Successful automation requires not only extensive and detailed analysis of the application, and the principal methods to be used, but also consideration of the demanded system throughput and overall system capacity. Examples to be cited include, DNA purification, PCR cleanup, protein crystallization plate setup, and MALDI sample preparation. We will conclude with new system concepts for ELISA, and cell based technologies in support of Imaging and high content biology.</p>	<p>XLfit 3 SDK: Powerful Curve-fitting and Statistical Software Development Package to Create Applications that Suit Your Discovery Data Needs</p> <p>Dennis Curran, IDBS, Inc.</p> <p>Curve fitting is much more than just creating a chart. The results around the fit and the chart indicate its context – how good the fit is. XLfit and the SDK provide investigators access to all of this information.</p> <p>IDBS has developed the XLfit 3 SDK to help you quickly build scientific applications based on your specific user requirements and workflow. Expand the scope of applications by offering an extensive selection of data analysis and calculation objects, including a superior range of fit and statistics models, as well as charts and graphs to visualize, interpret and present any experimental data.</p> <p>This discussion will focus on how to automate and enforce your business and analysis rules for non-linear curve fitting across any of your data sources using an extensive selection of data analysis, calculation and visual objects.</p>
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5:30 – 6:00

Integrated Tube- and Plate-Based Sample Management System for Maximum Flexibility and Discovery Process Control

W. Steven Fillers, Ph.D.; TekCel, Inc.

Abstract: A modular approach to sample management allows staged implementation and progressive expansion of the libraries within existing laboratory space. A completely integrated, inert atmosphere system for the storage and processing of a variety of microplate and microtube formats is currently available as an integrated series of individual modules. The storage units operate at -20°C and all modules maintain a nitrogen or an argon atmosphere. Storage types include 96- and 384-well standard height and half-height deep well microplates as well as 0.7 and 1.4 ml microtubes. Liquid handling for reformatting and replication into microplates plus high capacity cherry picking can also be performed within the inert environmental envelope to maximize compound integrity. The microplate storage units are designed to attach and detach from the system and may be easily shipped to remote locations. Implementing such a system significantly reduces process time from hours to minutes while minimizing exposure to agents that compromise sample integrity.

6:00 – 6:30

The Parallab™ Workstation Technology a fully automated, integrated workstation for high-throughput nanoliter volume reactions

Chris Abbott
Brooks-PRI Automation, Inc.

The quest to sequence the human genome and move into the post-genomics era has led to many technological advances primarily focused on reducing cost, increasing processing speed and improving the throughput of obtaining DNA sequencing data. The most notable improvements have been in the development of capillary electrophoresis (“CE”) systems. These systems have lower operating costs as they are more highly automated and are able to detect smaller and smaller amounts of highly sensitive fluorescent dyes. To date, liquid handling systems used to prepare reactions for CE have not kept pace with the ever-shrinking amount of reagents required for analysis. A system capable of processing no more than what is needed to obtain quality sequence data will present a significant cost savings to all users.

The Life Sciences Group at Brooks-PRI Automation, Inc. has developed, the Parallab™ Workstation. At the core of this technology is the Nano-Pipetter, which processes 96 reactions in parallel using standard chemistries. Using only nanoliters of reagents, the Parallab Workstation can aspirate, mix, thermal cycle, purify and dispense samples completely ready for analysis. Unlike conventional automated pipetting systems, the Nano-Pipetter is cleaned and reused, eliminating additional consumables and consumable costs. In the Parallab Workstation, a typical sequencing reaction is 500nl in total, using 1/42nd the volume of a standard fluorescent reaction mix. This high-throughput workstation also uses a proprietary high-speed thermal cycler and is capable of simultaneously processing multiple Nano-Pipettors to achieve ultra high-throughput unattended operation. The Parallab Workstation is a unique combination of low cost, high-throughput and miniaturized sample processing that is not attainable on any other platform. The simplicity and low costs afforded by the technology will make DNA sequencing available for many more applications and laboratories.

Automated Sample Preparation/Concentration of Biological Samples prior to Analysis via MALDI-TOF Mass Spectroscopy

Kirby Reed, Gilson, Inc.

Matrix-assisted laser desorption ionization time-of-flight mass spectrometry (MALDI-TOF) is used to obtain fast and accurate determinations of molecular mass. MALDI-TOFMS is a popular qualitative tool based on its high sensitivity, rapid analysis time, and extensive mass range. Non-volatile and thermally labile molecules such as protein and peptides can also be analyzed via MALDI-TOFMS. The applications of MALDI-TOFMS for proteins and peptides in biological fluids is urgently required by researchers in the expanding area of proteomics. Being able to couple a sample preparation procedure prior to MALDI spotting of such biological samples would improve the analysis of the analyte by decreasing the background, signal suppression and improve resolution of the MS signal. The use of pipette tips that contain a bed of chromatographic media in the tips or a similar phase coated on the inside walls of the tips will allow the sample cleanup and concentration of the analytes, essentially mimicking a solid phase extraction column prior to MALDI-TOFMS. The sample can be prepared in as little as a few microliters and spotted directly onto a MALDI plate for analysis.

A diverse array of biomolecules covering an extensive molecular weight range and present in biological fluids will be evaluated under the sample preparation procedures and analyzed via MALDI-TOFMS. Results will be presented in regards to the analysis of the proteins and peptides, recovery and the practical limitations associated with automating the sample preparation procedure and MALDI spotting.

<p>6:30 – 7:00</p>	<p>Improving Luciferase Genes for Use as Genetic Reporters</p> <p>Erika Hawkins, MSc Promega Corporation</p> <p>Ideally, genetic reporters respond to give a sensitive, exact and specific reflection of changes in transcription rates. Promega has created new synthetic reporter genes encoding firefly and Renilla luciferases that better exemplify this ideal. The new genes have been modified to reduce the intracellular stability of the reporter molecule to better couple the genetic response to the measurable output – changes in the expression of the reporter molecules occur more quickly, and the magnitude of the change is more extreme. Three-fold changes have been measured in model systems 2 hours after induction of the new genes, whereas the changes in cells containing the old genes were generally insignificant at this same time. These new genes are synthetically constructed to optimize mammalian codon usage, typically increasing expression levels by 10- to 100-fold in mammalian cells; and they have been modified to minimize consensus sequences for transcription factor binding, splice sites, etc., reducing background expression and anomalous expression within cells. Promega’s new firefly and Renilla luciferase genes maximize expression and link it more precisely with changes in transcription rates,</p>	<p>ORIGEN® Technology: A highly sensitive electrochemiluminescence detection technology providing an effective format for a variety of assay applications</p> <p>Irene C. Griff, Ph.D. IGEN International, Inc.</p> <p>There are many choices for detection technologies in research, each of which has attributes that provide performance for a limited number of applications. However, these platforms may not be applied broadly without sacrificing performance and quality of results. IGEN's ORIGEN Technology is capable of detecting a wide range of biological compounds, including proteins, small molecules, and microorganisms because of its revolutionary process that uses labels designed to emit light when electrochemically stimulated. This seminar will focus on key applications for signal transduction in drug discovery and the ease of automation of these homogeneous assay formats. Assay formats include membrane-bound receptor-ligand interactions and receptor autophosphorylation assays.</p>
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<p>7:00 – 7:30</p>	<p>Automation of a High Throughput Assay for Determination of Plasma Protein Drug Binding</p> <p>Tim Blankenship – Advanced Life Science Specialist – Millipore Corp.</p> <p>Determining the amount of drug binding to serum proteins is important in both the discovery and clinical phases of drug development. The extent to which a molecule is bound to proteins in blood will likely determine the amount of drug that is available to diffuse into target tissues. The level of plasma protein binding (PPB) of a drug is critical to predicting its pharmacokinetic profile and determining appropriate oral dosing.</p> <p>The most certain way to determine whether and to what extent a drug candidate will be bound by serum proteins is to test the compound directly in a protein-binding assay using human serum or plasma. Researchers commonly use centrifugal devices that incorporate ultrafiltration membranes capable of separating free from (protein) bound drug. One such method utilizes the new Millipore MultiScreen™ Ultracel®-PPB plate. Protocols developed for this 96-well plate generate up to 96 samples for LC/Mass Spec or radiometric analysis in less than 2 hours. PPB measurements may also require determining mass balance (total drug recovery) since the potential loss of drug due to metabolism, sample preparation, and non specific binding (NSB) can lead to misinterpretation of data. Here we demonstrate full automation of the plasma protein binding assay utilizing a Genesis® Freedom™ Workstation. The automated process includes the dilution of drug compounds in plasma (or serum), transfer of samples into the MultiScreen Ultracel PPB plate, centrifugation, and filtrate volume determination (necessary for determining mass balance) by chromophore dilution.</p>	<p>Secondary Screening In The Drug Discovery Process: Biacore's Contribution To Smarter And Faster Lead Selection</p> <p>Jaymie DeWitt, Biacore, Inc.</p> <p>Informed decision making, using the highest quality information, is fundamental to optimizing efficiency and effectiveness in today's highly competitive drug discovery world. Biacore is the world leader in the detection and monitoring of biomolecular binding using its surface plasmon resonance (SPR) technology and, recently, its new cell-based technology has added a new dimension of information-rich data for the secondary screening laboratory.</p> <p>This presentation will overview these newest developments for providing information-rich data for small molecule characterization. Biacore S51 offers the unique ability to generate high quality, real-time comprehensive kinetic characterization data on potential lead compounds – with the ability to provide K_D, k_a, k_d, R_{50} all from one experiment. Further, the combination of Biacore S51 kinetic characterization of small molecule target interactions with compound structural information makes kinetics based QSAR a reality. By providing clear insights into how structural changes affect not just activity, but also association and dissociation rates, a quantitative structural and functional activity relationship can be determined.</p> <p>Also to be discussed is the newly launched Procel™. High quality cell-based secondary screening and pharmacological profiling are vital to improving the selection process and Procel™ has been specifically developed to provide potency, efficacy data and in-depth understanding of compound mechanism of action- essential to smarter and faster lead selection. The system can rapidly characterize potential new drug leads based on their effect on these targets in live cells, which enables scientists to predict how lead compounds might behave in vivo with a greater degree of confidence.</p>
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<p>7:30 – 8:00</p>	<p>Structure Based Drug Discovery using Advanced Computational Methods</p> <p>Jeff Hudson, Structural Bioinformatics</p> <p>While there have been tremendous advances in throughput. HTS is still a very costly and low yield step in the drug discovery process. While focused libraries cut down on the huge sample numbers, the risk of missing a potential drug candidate increases. SBI has developed a computational, structure-based approach to screening that still allows for the screening of large libraries and produces focus lists of “hits” with built-in specificity for YOUR targets. The process is both efficient and cost effective. This talk will describe this service and give real examples.</p>	<p>GeminiChemistry:- automating Rapid Analog Synthesis in solution using a Tecan Genesis Robot.</p> <p>John Brohan. Traders Micro Montreal; tel 514 995-3749 jbrohan@videotron.ca</p> <p>Rejean Fortin Medic inal Chemistry Merck Frosst, Montreal</p> <p>The GeminiChemistry Software using a Tecan Genesis Liquid Handler tackles some of the problems of automating Organic Synthesis in 96 vial racks (VarioMag).</p> <p>During a reaction, several sequential operations or steps have to be done in the right order. One might have to Cool the reaction block(s) to -70 C, Reflux, Stir, Add reagents slowly under argon, Wait for several hours, Transfer, Take a sample, or perhaps Quench the reaction with excess of acid or base. All these possible combinations of steps are difficult to write in the native language of a liquid handler especially when reaction conditions are always changing.</p> <p>The Addition, Transfer and Dilution are simple operations driven from an Excel spreadsheet coming from Library Management Software, in our case: ChemTRACK.</p> <p>The chemist has to design the operations and the reaction conditions. He expresses them through the convenient GUI of GeminiChemistry Software, which in turn executes the reaction on the Tecan robot.</p> <p>The scope and limitation of this novel software will be presented.</p>
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8:00 – 8:30

The Discovery Data Explosion: A Lab to Enterprise Data Storage, Retrieval and Transfer Solution for Drug Discovery through Manufacturing in the Biopharmaceutical Industry

John P. Helfrich
NuGenesis Technologies Corporation

Managing and tracking data through the discovery, optimization, development, clinical and manufacturing processes requires a compilation of many different types of inter-departmental analytical, biological, and document report outputs. Data collaboration from the discovery to manufacturing arena across the entire enterprise, is critical to making crucial go/no go decisions regarding lead candidate development at all stages of the discovery to manufacturing process.

This talk will focus on the principles and application of good data management that will allow scientists, management and regulatory personnel to seamlessly leverage data as an asset, protect valuable intellectual property, transfer knowledge and ensure the accurate and easy creation of compliant regulatory-ready documents throughout the drug development process. Specifically, the process of utilizing embedded hyperlinks for data “drilling” from the assembled management approved document reports down to archived raw and meta data files for High Throughput Screening, LC/MS, Gel Electrophoresis imaging, NMR and other spectroscopic instruments will be outlined.