vital challenge is, of course, the creation of mathematical algorithms capable of handling this type of data. Here, we enter the domain of mathematicians and physicists who focus daily on exactly the same mathematical challenges, albeit in entirely unrelated fields. Perhaps the best example is that of aerospace- and defence-related data analysis. For example, hyperspectral data from imaging satellites are large in magnitude, sparse, noisy and multi-dimensional, with weak, well-buried signals [3]. Here, the successful and robust application of pattern-recognition and data-fusion technologies to extract information quickly is not only an everyday occurrence, but sometimes even a matter of life or death.

Swindells and Overington have done an excellent job in defining the mathematical challenges faced in identifying drug targets based upon analysis of sequence and 3D structural information. Their observation that the 'best results' for prioritizing the proteome will probably come from the interplay between experimental and computational methods is, I think, a fundamental insight. The iteration of experiment and computation applies equally well to many aspects of drug discovery research, and particularly to the new and data-prolific tools mentioned above.

The take-home lesson is that the flood of new experimental tools that is producing miraculous amounts of data, imposes an unambiguous requirement for increasingly sophisticated mathematical analysis. For companies that fail to do the math, the numbers might just not add up.

References

1 Swindells, M.B and Overington, J.P. (2002) Prioritizing the proteome: identifying pharmaceutically relevant targets. *Drug Discov. Today* 7, 516–521

2 Maggio, E.T. and Ramnarayan, K. (2001) Recent developments in computational proteomics. *Trends Biotechnol.* 19, 266–272

3 Billingsley, F. *et al.* (2001) Putting a rocket under computing for life sciences. *Sci. Comput. World* 59, 16–20

Edward T. Maggio
Chairman and CEO
Structural Bioinformatics
San Diego, CA, USA

A new era as plate movers get on track

Joanne Clough, joanne.clough@elsevier.com

The second meeting of the *European Laboratory Robotics Interest Group* (ELRIG; http://www.lab-robotics.org/Europe/) was held at the Sanger Centre (http://www.sanger.ac.uk) on 2 May 2002. ELRIG is the European chapter of the Laboratory Robotics Interest Group, which aims to facilitate the free exchange of information between users and providers of laboratory automation. The meeting, subtitled *Plate Movers – Getting the Arm on the Right Track,* was attended by over 400 delegates and included scientist- and vendor-based talk sessions and a 25 vendor exhibition, showcasing everything from bench-top robotics to industrial automation. The inaugural meeting of ELRIG, *Liquid Handling*, was held in November 2001.

New solutions in plate moving

The first session of the day was chaired by John Major (Head of HTS at AstraZeneca's UK Alderley Park site; http://www.astrazeneca.com) and detailed some of the novel technologies for the manipulation of microplates of all types.

Paul Lomax from Perkin Elmer Life Sciences (http://www.perkinelmer.com) compared modular workstations with integrated systems and discussed the benefits of having conveyors, arms or both. The Minitrak™ series was mentioned, which is capable of manipulating 96-, 384- and 1536-well plates. Removable stackers and shuttle mechanisms for plate movements were also described. Advantages of the modular system are that it is high speed and reliable but limitations are that it requires manual scheduling and plate transfer. Integration options include pipetters and grippers of third party devices via the 'diving board' placed on either end of the track.

On a similar track, Simon Sheard (RTS Life Sciences; http://www.rts-group.com/life-science/) described the various options in microplate manipulation. These options include converges, sliders, static robots and track systems. The vision of the future is to be able to pick a single colony or a particular cell of interest. He described the cell culture systems acCellerator™ and AssayPlatform™ and how independent technologies need to be adapted to each particular laboratory, be cost effective, reliable, robust and appropriate to the experiment at hand.

1359-6446/02/$ – see front matter PII: S1359-6446(02)02419-4

CRS BioDiscovery (http://www.crsrobotics.com) are hoping to flip the plate automation paradigm by using distributed motion, as presented by Steve Johnson. A new system, termed High Speed Distributive Motion, combines a conveyor that moves plates between instruments with small 'flipping-motion arms'. The linear conveyor is fast, of simple design, and the bidirectional motion enables multiple plates to be moved to and from devices simultaneously. Using this approach, HTS systems are easily scalable, providing high flexibility, and the handling of individual plates means that no modifications to the instruments are required. To increase the complexity of the system, the track length is simply increased and more flip-movers added, so the plate mover is no longer the rate-limiting step in such systems

Tim Ward, from Beckman Coulter (http://www.beckman.com) gave a brief history of microplate automation through Beckman's own history and automation products, and talked about their strategy of plate moving automation equipment and why their products tend towards automated workstations, which give more flexibility, productivity and reliability.

Technology in practice

Chaired by Terry Wood (the Pfizer Liquid Sample Bank Manager; http://www.pfizer.com), this session brought together presentations from users of lab automation in practice. Tony West of the Sanger Centre spoke about the automation scale-up and high-throughput DNA handling at Sanger, which generates >5 million raw bases of sequence per day, requiring ~7.2 million sequences to be processed per month. The Sanger Centre has a new high-throughput sequencing pathway enabling the vast amount of bases to be sequenced. The 'plate versus robot', 'workstation versus integrated platform' and 'arm versus track system' conundrums, were likened to 'the chicken and the egg' scenario. The choice between arm and track systems depends on the type and format of the plates being used. The track format is preferred as it is a parallel process and is faster, as the arm can only access one plate at a time. However, plate storage retrieval systems still need to be arm based.

Bill Janzen of Amphora (http://www.amphora.com) spoke on the subject of chemical genomics via microfluidics; the large-scale analysis of small molecules to study the function of gene products. Microfluidics increases the precision, accuracy and reproducibility of an assay, and decreases compound consumption. Current assay technologies, such as those by Caliper (http://www.calipertech.com), include fluorogenic assays, like those for proteases, the CYP450s and phosphatases, where 1–2 μg gives rise to one million data points. He described the volume reductions associated with conducting chip-based assays; either on-chip or off-chip mobility shift assays, which use a few nanolitres of reagent, although the majority of the assay is still performed in plates of 25 μl assay volumes so the reduction in reagent is so far theoretical. However, plateless screening is not yet realistic as we still require plates to store our compound collections and until these can be stored in 'chip-based' nanolitre formats, plates are still a vital component of the process.

Current practices and automation choices

Do we really need large-scale automation in HTS? Andreas Sewing (Pfizer) gave a critical evaluation of current practices. Automation includes primary HTS, accelerated intelligent drug discovery, IC_{50} values and secondary screening for cytotoxicity. The benefits of full automation are speed, quality and reproducibility of the output. However, full automation can create problems as well as solving them. New skilled operators are required, it is inflexible and large dead volumes are generated, as well as a high capital investment being required. Therefore, we have the choice between speed, cost saving and quality. Benefits of miniaturization are a decrease in reagent costs and assay volumes, whereas the complexity of assay development and costs increase. He concluded by saying that systems must be more user-friendly and practical for scientists to run assays such as protein–protein interactions and receptor binding.

There are multiple choices in automation, whether it be Cartesian, cylindrical, articulated or tracked. Should this affect the user requirement specification (URS)? This was the question posed by Colin Bath from AstraZeneca. Using semi-automated workstations, it took one week in the past simply to dilute and replicate samples and to label plates. The standard URS is minimum man-handling, exemplified by the 'walk away' system, which enables minimal operating requirements after loading of the plates and reagents. The Asset™ system (co-developed with The Automation Partnership; http://www.automation-partnership.com), enables 100,000 compounds to be screened, and has reduced the screening campaign from 6 months to 5 weeks. It also has high precision and quality, a controlled environment, versatility and can handle 96-, 384- and 1536-well plates.

The future of automated plate movers

This meeting brought together vendors and users of laboratory automation alike, with presentations on the future of plate movers and the current robotics on the market and in the laboratory. The future for plate movers is certainly interesting and many different opinions on HTS and recent developments were discussed.

Acknowledgements

I would like to thank the organizing team of the ELRIG for their assistance with this article.