

Interview

The Wellcome Trust Sanger Institute is a non-profit genome research institute funded by one of the largest charities supporting biomedical research. The institute uses a broad range of technology and platforms to support genomic research applications such as large-scale sequencing, informatics, and analysis of genetic variation. Whether designing spotted arrays, offering bioinformatic analyses and experimental design advice, or conducting experiments from sample extraction to final analysis on commercial platforms, the Microarray Facility is involved in all aspects of Sanger's array-based research except genotyping, which happens within the core Genotyping Facility. Dr. Cordelia Langford, Head of Microarray Facility, took a break from her busy schedule to answer a few of our questions.

i: What are the main responsibilities of your core facility?

CL: In the past, by far the majority of our work involved developing and optimizing custom spotted arrays. But as external technology has evolved, the Microarray Facility has also become involved in supporting commercial platforms and offers this as a service to our collaborating researchers. While it has proven to be a very popular working model, we have a lot of pressure from collaborators to provide data as quickly as possible. The data also have to be reliable and reproducible. Almost everyone has budget constraints, so the technology has to be affordable as well.

i: You agreed to beta test Illumina® Gene Expression BeadChips. Can you describe your experience?

CL: One of the original experiments we performed using Illumina BeadChips was a self versus self hybridization experiment. We took one RNA sample, labeled it in separate labeling reactions and hybridized the samples onto consecutive arrays

both within and between chips. With the analysis software we looked at the dot plots (correlations between two arrays). With the BeadChips—I can still remember seeing one of these plots come up—they were just bang on the diagonal. We were really shocked at how tight the data were. We saw really high correlation.

i: Is there any new work going on in your lab you are particularly excited about?

CL: In collaboration with Cambridge University and the National Health Service Blood and Transplant unit, we've just finished the first phase of a major study: the Hematology Expression Atlas. This study was carried out as part of the Bloodomics project supported by the European Union 6th Framework Program. It involves the generation of "Transcription Atlas" gene expression profiles for all end-stage blood cells in humans. We are very excited about the findings and aim to make the data publicly available following publication. This project will have a major impact, and we did it using Illumina BeadChips.



Dr. Cordelia Langford, Head of MicroArray Facility, Wellcome Trust Sanger Institute

ADDITIONAL INFORMATION
To learn more about Illumina's Gene Expression portfolio, visit our website at www.illumina.com.

We are committed to providing you with the content you want as a member of the Illumina community. Please email us with comments and suggestions for topics at icomunity@illumina.com.

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