Case Study Aberdeen University

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[TL] Background information. Provide a brief background of the department and the research areas you focus on.

[CP] Working for the Proteomics core facility currently based at the Rowett Institute but operating under Aberdeen University. We provide protein analytical services to academics and companies, mostly in the local area but also worldwide. We offer a wide range of services to try and accommodate any needs, these can vary from simple protein identifications to large scale gel/mass spec experiments. Currently we are mainly offering services in: Gel electrophoresis (1D, 2D, DIGE), In-depth proteome analysis (Q-Exactive LC-MS), molecular histology (MALDI-imaging), protein identification/quantification, mapping of protein modifications and rapid microbial identification (MALDI Biotyper). Previously we were also conducting our own research, mainly into urinary tract infections. That has settled down since our boss has retired but we still have a PhD student and are equipped to carry out small projects for honours/masters students. We deal with a wide variety of samples. recently we have worked with plant, animal, microbial and viral samples. We do a lot with Zoology down the road which deals mainly with fish samples (recently we completed a big study into fish mucus). We are about to start a big study into sarcoma samples from paraffin embedded tissue sections.

[TL] What is your typical 2D experimental design?

[CP] We do lots of 1D gels, 2D gels and Western blots right now. We have a DIGE imager and have done lots of DIGE projects in the past but this seems to be too expensive for most people so they just stick to the regular 2D gels.

[TL] How has SpotMap helped you to overcome challeenges you have previously experienced with your analyses?

[CP] We have had real difficulty matching reactions on blots to the corresponding areas on the gels. With our previous technology it genuinely wasn't possible so adding the SpotMap software to our facility has helped greatly. Because a big reaction on blots doesn't necessarily mean a big amount of protein on the gel it's sometimes hard to match patterns by eye. In the past we have had to rely on matching patterns by eye and end up cutting out the wrong area of the gel. Once we had the images put through the SpotMap software it corresponded to areas that personally I would have never matched (which ended up being the correct areas).

[TL] What are the benefits to you of using SpotMap?

[CP] I like the layout and it's very user friendly. The best part is I can depend on the results and (hopefully!) not have to worry about if I'm cutting out the correct area of the gel for our subsequent protein identification. The different windows that show you the transitions between images is very useful, as is the image editing.

[TL] How has SameSpots helped you to overcome challenges you have previously faced with you analysis?

[CP] SameSpots has greatly helped our analysis and productivity. Recently we have had huge projects with sometimes over 100 gels for 1 set of analysis. Without the software it would be near impossible to accurately compare the gels. It is sometimes useful to have the dried gels and lay them on top of each other to get an idea of patterns and any major differences but to rely on that solely would be insane (and would probably drive the person doing the analysis by hand insane too!). We have also tried your competitors software that we've inherited from the Rowett when we joined our facilities. I thought it was overall an inferior product compared to SameSpots. I personally found it [the competitor] much harder to use and navigate.

[TL] What are the benefits to you of using SameSpots?

[CP] I like the statistics layout in the new version. Seems a lot more obvious than before (e.g. the PCA) and it's a lot easier to transfer the graphs, images, etc. into a separate document. I like overall how the SameSpots works. I particularly like the overview with the 4 different windows in alignment screen to give you an idea of the overall analysis and the transitions between the overlapping gels in the different colours. I also find the 3D image of the spot very useful and gives you a better understanding of how it looks / if it's an actual spot.

[TL] Any other comments?

[CP] Since we have moved to our new building we seem to be doing lots more blots (which is where SpotMap will come in useful). The big gel experiments we've had in the past with 100+ gels are getting less and people seem to be moving more over to our mass spec side of things. We still have enough work to keep us busy but it's mostly small projects. TotalLab as a company have been good in my dealings with them so far. We had an issue with using SameSpots where the software would freeze if you tried to open anything or create a new experiment (which turned out to be an issue on our end with the University's internet security). I got prompt responses and they were very helpful all the way throughout.