VIDEO INTERVIEW TRANSCRIPT

Rawlings, Chris: transcript of a video interview (04-Aug-2016)

Rawlings, Chris: transcript of a video interview (04-Aug-2016)*

Biography: Professor Chris Rawlings PhD (b. 1954) started his bioinformatics career at the Imperial Cancer Research Fund in 1982 during which time he was the Project Manager for the computing infrastructure needed for the Human Gene Mapping Workshops (10.5 and 11). From 1991 to 1996, he led a group that researched the application of advanced logic languages to genetic mapping and protein structure bioinformatics. In 1996 he moved to SmithKline Beecham, where he was responsible for the bioinformatics platforms supporting human genetics, comparative genomics, and gene expression. From 2000 to 2004, he was the Director of Bioinformatics at Oxagen Ltd, where his group worked on the identification and validation of genes and drug targets from human genetics and genomics technologies. He moved to Rothamsted Research in 2004, where he now leads the Department of Computational and Systems Biology, which comprises over 40 staff and students engaged in research into, and application of, bioinformatics, mathematical modelling, and statistics to problems from the agricultural sciences. His personal research interests are in the development and use of data integration systems for supporting systems biology and for candidate gene discovery from multi-omics datasets. He is a visiting Professor in the Department of Computing at Imperial College London, and was also one of the founding members and former Vice President of the International Society for Computational Biology.

[1].   EARLY INTERESTS IN SCIENCE: PHYSICS & BIOPHYSICS

I think what drove my interest in science was partly the exposure that my mother had given to me when, in her role as a laboratory technician, I'd become familiar with what it was like to work in a laboratory as a career. And while I wasn't particularly interested in what she was doing, I recognized that it was something I might do in my career in the future. I also had a very inspirational physics teacher at school, who inspired me to think about experiments and the role of experiments in science as something that was both a creative and a technical skill, which I enjoyed doing. And that really launched me on to thoughts of a longer term career in the sciences or in medicine. At the time I wasn't really clear which way I would go, so medical school was one of those places I'm glad I didn't get into, unlike most young people, I suspect.

So, I had the opportunity to go on from school, after a period of reflection and recovery after not getting the A level results that I wanted, and found a course in biophysical science at what was then the North East London Polytechnic but is now the University of East London. It appealed to me because it played to my interest in physics and also my interest in biology. I thought if there was anything that was going to suit me it was combining physics and electronics and biology; and I thought that's what I wanted to do. And that's what took me into a place where I could then get enough confidence in the mathematics and the other harder parts of biophysics that I wouldn't have otherwise found a place for. Particularly influential was an opportunity early on in my undergraduate degree to do a week's programming training course in BASIC at the time. That alerted me to a completely new way of working that I really took to, and I enjoyed, and wanted to do more of. So, that was something as an undergraduate that I found and then, when I had an opportunity later, I extended my skills, self-taught, but it became something that would play a big part in my career as it developed.

---

[2]. BECOMING A COMPUTATIONAL SCIENTIST

When I was doing my PhD, which was very much an experimentally based one looking at cell responses to cytotoxic drugs, I developed some programs, some software of my own that would simulate the methodology that I developed in the lab. There wasn't previously any real theoretical basis for or any software that could analyse that data. And so as a side project, while doing my PhD I built some simulation software that enabled me to calibrate the method and to interpret the results in quite a new way. I found that very satisfying, and this was something I was doing completely of my own volition; my supervisor tolerated it rather than supported it. I came out of that feeling very confident about wanting a career that was more theoretical, more computational, and really that I'd done my time at the lab, on the bench, really. But that stood me in really good stead, having been an experimental biologist for a while, even if it was only for 3 years, has helped me a lot as I've gone through my career as a computational scientist, knowing what it means to collect data and how important that is to people.

[3]. NETWORKING THE HUMAN GENE MAPPING WORKSHOPS

So later on, when I moved to the Imperial Cancer Research Fund and was given the opportunity to take part in the human gene mapping conferences, my interest in all matters technical, relating to computing, and actually being a bit of a hobbyist as well, meant that I was pretty familiar when I was asked to provide the computing infrastructure for the mapping workshops, about what was going to be needed. I'd already put the network in for my department so there was an Ethernet within the department at ICRF that nobody else had in the Institute. So when I needed to scale this up I knew the sort of people to talk to, I knew what we were going to have to do, so that really helped a lot, because we were putting in infrastructure in St John's College, Oxford, and subsequently at the Connaught Rooms, where we had to move very quickly and with a lot of outside contractors to deliver that infrastructure on time. I must admit, being an enthusiast and having followed that both through my postdoctoral career and later on was really useful in getting that done. And so that was an important achievement, to provide a complex computing infrastructure over a short period of time, to deliver a one-week jamboree of data entry by scientists in human genetics.

Let me a say a bit more about what we're talking about as computing infrastructure because most people these days will take for granted that their network ports come as a hole in the wall, and they've got WiFi everywhere. This was before, so when we moved into St John's College, there was no infrastructure, there weren't even telephone connections in every room. And we were providing in the region of 30 rooms in a particular accommodation block in St John's with a network connection that they could use to connect back to a server that we had installed in the Oxford University computing service. We had something like three days to install this network infrastructure, and to test that it was working. So it very much felt like I was in charge of a roadie crew that was installing a big enterprise for the sake of three days' work for scientists. I think they had something like three or four days to complete their work. So this was a challenge at St John's College, Oxford, but the following year we had to do the whole thing again. This time we were installing much bigger servers in the Connaught Rooms, which were close to Lincoln's Inn Fields, and close to ICRF, and we were also networking that back to ICRF's computer room. So we had two big Unix servers running Sybase databases; we had arranged with a contractor to string Ethernet throughout the Connaught Rooms, which they hadn't had in place beforehand, and we were providing some work stations in every office for each of the chromosome committees, as well as a PC that was acting as a smart terminal to those work stations. I think we had an extended weekend to install it and a day to take it down again. So yet another rock concert-type operation. The logistics and the planning for that was, I wouldn't say it was meticulous, there was a lot done on the hoof, and if it hadn't been for the skills of a lot of other people that I could call in favours from, it wouldn't have happened.

[4]. SMITHKLINE BEECHAM & OXAGEN: THERAPEUTICS & GENETICS OF HUMAN DISEASE

After I'd been at ICRF for a few years, I went on to work in the pharmaceutical sector. I went to work for

SmithKline Beecham before they merged with Glaxo to become GlaxoSmithKline, and that was a really important time for me to understand how basic science got translated into commercial products in the form of drugs. And I came to realise how complex that process was, and how well-oiled the machine was, but I also came to understand that the scientists at SmithKline Beecham were no different than the scientists working in academia. All this 'us and them' attitude that exists between academic scientists and applied scientists was all a self-constructed vision that, actually, everybody's got the same interests, the same weaknesses, and the same strengths. After SmithKline Beecham I moved to a smaller company, called Oxagen, which was a spinout company and a joint venture between Oxford University and the Wellcome Trust Centre for Human Genetics, where we were looking at the genetics of complex chronic human diseases with the aim of identifying the genetic intervals and the genes involved in chronic disease. Obviously the intention of the company was to be able to pull genes from those intervals, and potentially clone them, and express them, and turn them into therapeutic targets that we could market to the pharmaceutical sector. This was probably the most fun I had in my career, because, for once, I felt very much part of all parts of the way the company worked. I had my role, and it was needed and wanted, and it was clear what my role was, and why it was important. I was involved in a lot of the decision-making within the company, because the way it was run was very much as a team effort. It wasn't driven by an individual personality, which is often the case in academic research. And so that and who the people were just made it work. It took a while to settle in, and it took a while to find my feet, but I was so glad I had that opportunity to work in an SME [small- and medium-sized enterprise] and be that close to all the decision-making and really understand why you're there. Because in the big companies sometimes you do it because you do it, and you can see that somebody else is going to need what you do, but it's not as immediate as it is in a small company where you've got a real chance to influence and a real chance to make a difference.

[5]. IMPERIAL CANCER RESEARCH FUND & LAB CULTURE

One of the times I felt that I probably didn't do a particularly good job was when I was coming to the end of my time at the Imperial Cancer Research Fund, where I'd been for 14 years, so it wasn't early in my career there, and I realised that I'd not paid enough attention to the community around me. I'd not done enough of the work within the institute, I'd not been a particularly good scientific citizen within that institution. I had a few key collaborators, but I wasn't well connected, and I'd moved to a different physical building than the majority of the scientists. I'd let myself go out on a limb, and I think that was a mistake, and, I think, it inevitably made it tough for me to continue my career there successfully. I'd not paid enough attention to making the right contacts and to being seen to be part of the community. They changed director and they'd changed scientific direction, which I'd largely ignored as I'd got more and more involved in external science activities and conferences, and collaborations, and that was ultimately the mistake I think I made.

[6]. OPEN SOURCE SOFTWARE & THE OPEN SCIENCE COMMUNITY

When I joined ICRF in 1982, we, the group that I was in under John Fox, we were very much the beneficiaries of a policy of open release of software by the research community in the United States. We were using what are now considered open source software tools even back then. That philosophy of sharing software without regard to intellectual property, and it being something that could be reused and built upon by other scientists, was a culture that came to dominate the bioinformatics community throughout the world. And it's still a very strong commitment to many people that we should be holding no intellectual property, and holding no restrictions on access to our software and the source code that we used to write it, so that you can really build on that and indeed investigate people's methodology. And that's really important, and I think it's still an ongoing project to keep all of the software that we want to keep in the public domain an open source, because there are many pressures in certain areas that this should be protected by intellectual property, and people can build companies out of it. But I think, on the whole, things have become very much more; it's very much easier now to begin by starting from something that somebody else has done and not having to start from scratch and that's a huge benefit to the research community.

I think one of the changes that I've seen through my career is the importance of data as a source of scientific

investigation in its own right. When I began my career the data that was available to me from the collected DNA sequences in the public databases was very small. There were hundreds to thousands of individual sequences. Now we see multiple genomes, there are hundreds to thousands of genomes available. The major development of the high throughput instrumentation and the availability of data openly accessible in public repositories has made a whole new scientific discipline that we can work on. And I think I've seen the development of the open science community evolve, in part in response to the way in which the molecular biology community opened up their access to data through agreements with journals that sequences - all sequences - should be deposited in public databases. And that's a model that has been replicated in other science disciplines, even now, where it isn't yet established as best practice.

[7]. DATA SCIENCE IN THE FUTURE

What I think I'd like to see happen, hopefully before 40 years has elapsed, is that those of us in the area that is now called data science but has been bioinformatics, and might be called something else in the future, have a more obvious structure to our careers, and that the ways in which our success as scientists is measured better reflects what we do in terms of generating products, not just scientific papers. Because for many of us most of our work is around the development of software, the development of websites, the development of tools and methods. And these are much harder for the current methods in academic circles to measure as achievements. It's therefore often difficult for younger scientists to mix this role of tool developer and fundamental scientist in a way that's relevant to the community, and unless we get this right we will always be struggling to recruit the best software engineers into our community.

[END OF TRANSCRIPT]

Further related resources:

1. Jones E M, Tansey E M (eds) (2015) *Human Gene Mapping Workshops c.1973-c.1991.* Wellcome Witnesses to Contemporary Medicine, vol. 54. London: Queen Mary University of London.
2. Tansey E M (intvr); Tansey E M, Beanland S (eds) (2017) *Rawlings, Chris: transcript of an audio interview (04-Aug-2016).* History of Modern Biomedicine Interviews (Digital Collection), item e2017231. London: Queen Mary University of London.