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CELL SCIENTISTS TO WATCH

# Cell scientist to watch – Guillaume Jacquemet

Guillaume Jacquemet studied biology at the Université de Reims Champagne-Ardenne in France, before joining the lab of Martin Humphries at the University of Manchester in 2008 as part of a Wellcome-funded four-year PhD studentship. There, he studied cell–matrix interactions and the integrin-mediated regulation of small GTPases. In 2014, Guillaume moved to Turku, Finland for his postdoc with Johanna Ivaska to work on the role of filopodia in cell migration and cancer cell invasion. He set up his own research group, the Cell Migration Lab, at Åbo Akademi University, Turku, in 2019, where in addition to investigating the molecular mechanisms of cancer metastasis and cell migration, he also develops deep-learning-based image analysis tools.

Guillaume Jacquemet

**What inspired you to become a scientist?**

I don't have a very special origin story; I liked science courses at school and, when planning to apply to universities, I was told that it would be easier to do research as a medical doctor. I therefore started in medical school but hated it and quit! I did like the molecular cell biology courses though, so that's what I went on to study next. I got to do some placements in research labs quite early on and really enjoyed working at the bench.

**And how did you get interested in studying cell migration?**

I think it had a lot to do with luck and being in the right place at the right time. In France, the labs I was doing internships in were studying cell migration, and once one of the PIs next door sent around information for applying to a Wellcome Trust PhD program in Manchester. I was lucky enough to get selected so I went to do my PhD there; one of the great things about this program was that I had the chance to do rotations in different labs and try out different projects before committing to working on cell–matrix interactions.

**Could you tell us what are the main questions your lab is trying to answer just now?**

We want to understand how cells, and specifically cancer cells, interact with their environments and how this regulates their function. We are especially interested in looking at cells during different steps of the metastatic cascade, and we mostly use microscopy to observe how they interact with other cells and the extracellular matrix as they migrate.

**Your passion for microscopy will be quite obvious to anyone who visits your lab's website**

Yes, and while we use other techniques as well – for example we do quite a bit of mass spectrometry – they somehow don't feel the same. It just doesn't give me the same satisfaction as when using microscopes to observe how cells behave.

**On the image analysis side, there has been a recent revolution with the development of various deep-learning-based tools. How did you get involved with this field in the first place?**

I was really fascinated by some of the early studies that came out; for instance, the original paper using AI to predict what fluorescence images would look like from brightfield images. We didn't really have time to play with this method, but then the really exciting Content Aware Image Restoration (CARE) paper came out about using deep learning to restore and improve microscopy images. I thought this is something we really need to apply to our work, as we do a lot of live microscopy where, because you have to be careful not to kill your sample with too much light, the images never look as good as with fixed samples. We did get a little bit stuck when trying to use this tool, and that's when we started collaborating with different people – and it kind of exploded from there!

**Does this mean that now most of your projects use deep-learning-based tools?**

Yes, it's become very rare for us to have a project that doesn't involve, at one point or another, one of these tools – and the way they work is really a cell biologist's dream! Once you know how to train the tool, all you need to provide is representative data and an example of a result you want to get. So, rather than spending hours trying to optimize different ways of doing the analysis, you let the

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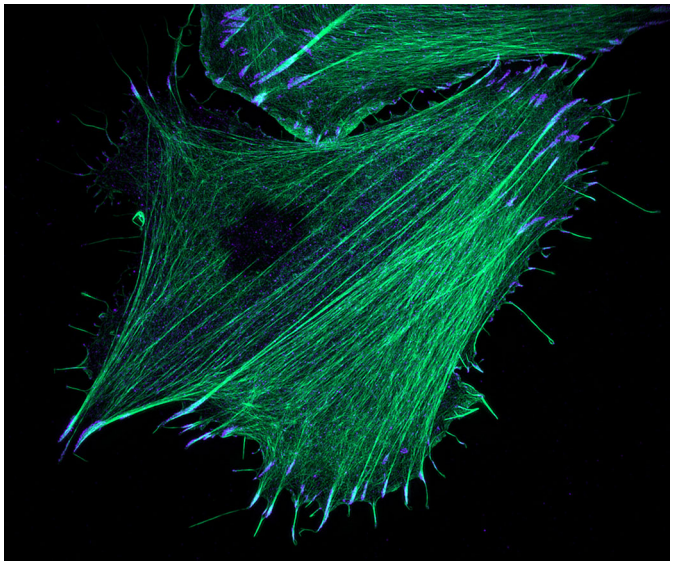

**Cancer cells labeled to visualize their focal adhesions (blue, paxillin) and their actin cytoskeleton (green, F-actin) and imaged using a structured illumination microscope.**

computer sort it out. We use tools such as Noise2Void, CARE, StarDist or cellpose for image segmentation and denoising live microscopy data, and now also have tools for automated tracking of cells in live imaging experiments – this is not only a time-saver, but in the past some of my colleagues actually got repetitive strain injuries from manual tracking because of the many hours of clicking a computer mouse.

**Besides all these advantages, what are the main pitfalls researchers should consider when applying AI-based tools?**

One of the promises of deep learning is to have models provided in a software that will allow you to improve or segment your image with a single click. So, I think the biggest worry is if people start reusing existing models without validating the results carefully – therefore, it's always important to check that the models work for the type of data that you are processing.

**Do you feel that tool development and maintenance is sometimes not appreciated as much as it should be?**

There is more and more appreciation for the importance of tool development, which comes mostly from the community, as well as from journals and editors – I actually think it's become easier to publish a paper about a tool now than it was 5–10 years ago, and such papers are also well recognized. But it's still very challenging to get funding for tool development, at least in Finland, and there certainly isn't any funding available for the maintenance of the tools that you have developed, which is a huge struggle.

**There is now also more emphasis on following 'open' practices in research, and the bioimaging community has many advocates, including yourself. Could you tell us what open science means to you?**

I guess there are different levels of being open. Of course, one aspect is to make everything available, so it's important that things are Open Access and open source. But to me, it's even more important to make tools usable, so if there isn't enough documentation, or if the code is very messy and hard to read or reuse, then there is less value in it for me. Currently, I feel there is more focus on Open Access than on usability, but we do always put a lot of effort into both aspects – for example, in our recent TrackMate 7 paper we had over 120 pages of documentation.

**What benefit does Twitter have for scientists and what role, if any, has it played for you in starting collaborations?**

Twitter can be extremely useful for scientists to connect with people who share similar interests, and for me, it has been especially beneficial because I work at a small university in a small city, so it's harder to find experts in my specialized area to discuss science with. And indeed, we've set up several collaborations thanks to Twitter; for example, the TrackMate 7 project started with me posting some of our imaging data on Twitter to show how we were combining two tools for tracking. Jean-Yves [Tinevez], who I've never worked with before, thought this was very cool and wrote to me, so we started collaborating. Similarly, I've worked with Ricardo [Henriques] on different projects but only knew him from Twitter – we actually met in person for the first time at the recent ELMI conference.

**"Twitter can be extremely useful for scientists to connect with people who share similar interests, and for me, it has been especially beneficial because I work at a small university in a small city […]"**

**You were one of the main organizers of ELMI – what was that experience like?**

Very exciting, but also very challenging! I was largely in charge of the program, which also meant coordinating with the scientific advisory board. It was great to be able to invite so many people who are interested in developing microscopy tools. I also contacted a lot of microscopy-related companies, and discussing with them what sort of things they are interested in, and what they expect from the meeting, was really enlightening. During the meeting itself, I was mostly running around with the other organizers trying to fix all the small issues that came up, so I only really managed to enjoy the conference when my part was done – it's a bit like organizing a big wedding where a lot of things go wrong in the background.

**Based on the science presented at ELMI, where do you think the bioimage analysis and microscopy fields are heading, and what are some future challenges?**

I think on the software side, it's more and more clear that interoperability, meaning that the tools that are being developed can 'talk' to each other, will be key for streamlining different analysis pipelines.

In terms of hardware, I feel that there is a massive fragmentation happening; a number of different smaller techniques have been recently developed that are kind of outshoots of larger ones. Also, every system is becoming hyper-specialized. Many new microscopes are picked up by companies and are being commercialized, which does help with the dissemination, but their high costs together with decreasing funding for infrastructure means that only some of them make it into core facilities – it's impossible for a facility to buy 20 different instruments, so they have to make difficult choices about which ones to buy and maintain. This is why I hope that more modular solutions will start to emerge, where we can easily fit different modules on the same instruments and swap or repair them when needed – and I think 3D printing will offer some solutions here. We will also need better coordination and

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sharing of instruments between institutes, and initiatives such as EuroBioimaging are doing a great service in this aspect.

**Let's go back to the time when you set up your lab; were there any challenges you faced that you perhaps didn't expect?**
For me, the biggest challenge was recruitment, and it took quite some time to get my first lab members. I think it's in general difficult for new PIs to attract students, because they often want to go to more famous or established labs. I started the lab in 2019, with the first students joining around January 2020, so the COVID pandemic slowed things down considerably.

**What do you think is important to consider for researchers who are seeking independence?**
Bearing in mind that in academia no two career tracks are the same, I think there are a lot of advantages of having a group at a smaller university over going to a very high-profile place, where it is much harder to stand out, and where you might feel like just being noise in the background. To get more stable and permanent positions later, you will have to be noticed by your colleagues and the administration, and be put forward as someone who is important for the profile of the university or institution – this is difficult to do in places where there are already a lot of very visible researchers.

**Do you have any advice on how young researchers can get the most out of meetings in the early stages of their career?**
My answer to this is breakfast! It's useful to go to smaller conferences where participants stay on site, and then breakfast is the best time to network. Attendees, and especially more senior researchers, often gather in smaller crowds or meet up with people they want to talk to after the sessions or at lunch, making it harder to connect with them. However, people generally don't plan their breakfasts or when they want to wake up, so it's much easier to grab a coffee and sit next to someone you really want to talk to.

**What is the best science-related advice you ever received?**
One of them is that if you want to succeed in science, you cannot do it alone – you'll need support from below, from people that work with you, and from your peers or mentors. It's therefore also very important to be kind, which will get you more noticed than just being smart, as unfortunately in science not everyone is kind or understanding. Another piece of advice I found important is that authorships are cheap. It doesn't cost you anything to add someone who has contributed to a paper – even if in a small way – as a co-author, but it might benefit your future collaborations with them. Maybe next time they will help you build something bigger!

**"It doesn't cost you anything to add someone who has contributed to a paper – even if in a small way – as a co-author, but it might benefit your future collaborations with them."**

**Finally, could you tell us something about yourself that people wouldn't know by looking at your CV?**
I have two young children, so my hobbies and activities are mostly centered around them. One of the great things about living in Finland is that my house is a 10-minute drive from work, but it's also between a forest and a lake. So, we spend quite a lot of time on the beach – going swimming in the lake in summer or ice skating in the winter. Something else people might not know is that I'm a big fan and user of Audible, so when spending long hours at the microscope or doing data analysis I listen to loads of audiobooks.

Guillaume Jacquemet was interviewed by Máté Pálfy, Features & Reviews Editor at Journal of Cell Science. This piece has been edited and condensed with approval from the interviewee.