Plymouth, 12/06/2016

I: Interviewer (Gregor Halfmann)

R: Respondent (Claire Taylor)

R: So this is what we call a block or a sample. This represents about ten nautical miles and I don’t know, have you seen the workshop before with the cassette where they put in the big roll of silk?

I: Yeah.

R: So actually what happens is, someone is actually doing this today, they are chopping it up into what we call ten nautical mile blocks and allocate it to each analyst. So each analyst gets roughly about ten to twelve of these every week, depending on what other jobs they have got. For instance I get what we call a full load, so I get the full allocation, some people might only get half the load, some people might get three quarters of a load. It depends on what your hours are and what else you have got to do as well. So I don’t know if you can see, the sample is quite green.

I: Yeah.

R: So that relates to what we call the phytoplankton colour index. So when they do the cuts, once a block is cut, each block will get a particular number and that relates to how green it is. And that has probably to do with the amount of plankton that is on the block as well as the amount of chlorophyll.

I: I have a few specific questions about that. As I read, you are using notebooks to write everything down.

R: Yes.

I: When you do the colour assessment do you also have a notebook or how is that practically done?

R: There is what we call pantone colour charts. So there are proper colour charts we look at and that gets recorded on what we call the cutting point sheet and that is done at the point of cut.

I: Okay.

R: And that gets recorded by the cutter. They work on this particular colour chart which we have used for ever and ever and ever, trying to be consistent.

I: So it is a sheet of paper that gets digitised later on?

R: Yes, and we also use a daylight bulb and we use blackout blinds, so we try to keep it consistent. We have got other surveys in the world, our sister surveys, who try to use the same specific daylight bulb. So we are trying to keep it as consistent as we can everywhere. So that is the colour. And do you want me to explain the phytoplankton count or …

I: Yeah, well I know a few things already about it, but yeah …

R: If you want to have a look down. This is a quick snapshot of what we see.

I: Oh, okay.

R: So this one is quite a busy block, it was taken the last month, but we have an autumn and a spring bloom. That is when we find the most productivity.

I: So this is from a bloom.

R: Yes, you can see it’s quite green, it is quite chock-a-block of stuff.

I: So what colour category would that be?

R: I am not a cutter, but I’d say that is probably a three. So that is probably green. They are very pale green, pale green, nil, and green. I don’t do the colour myself, but I think that is probably what they’d call green. … So when it comes sandwiched together we have got the covering silk, which has got these flappy bits on here. That is the covering silk, and that is what we call the filtering silk. So what I do first is basically the phytoplankton count, so I am looking at phytoplankton only which is the plants side of identification. And that has more to do with shape recognition than anything else. So what we do is, when you look down there, you can see they are all made up of little squares. So basically, I start from the top right-hand corner and I go down to the bottom left-hand corner and I am counting ten squares diagonally and I am recording everything that is in that little square that I have randomly put my microscope on. Now especially with phytoplankton you get very small stuff, if there is a [unclear] of the same species in that tiny little square, I will only report it once. So I record the presence of it, not how many are in that particular field. So if we do ten squares that way and ten squares that way the maximum count you can get for the phytoplankton is twenty. So you can’t get any more than that. And with some species it is quite complicated. We can identify certain species, but they then go into a group, where they are called whatever the species … and the total of that count as well. So we try to identify as much as we can and gradually over the years we have been able to identify a bit more and the molecular laboratory comes into it a little bit more. What we think we see, we can get verified now, which we were not used to get before. Our learning has become a lot better.

I: So when you do this, you look at each square one by one and you record everything you see.

R: In that square, yes.

I: Because that is one thing that I was wondering, whether you have like a list of taxonomic entities that you look at …

R: Yes, we do.

I: … And then you go down the list.

R: We haven’t got a checklist as such, but we have got what we call our CPR code [unclear], which is our internal database. We have got a list of species on there. And we have also got what we call our taxon table. It is everything we have ever seen and the date that we have first seen it, so we can backtrack it. But to start with, you look at it and go “oh my god, it’s so much”. We have like 800 entities or things that we see. And this is phytoplankton for example, it goes up to … that is just diatoms, this part is dinophysis and dinoflagellates, they go up to about here. So you can see, that is just phytoplankton.

I: But in practice you don’t have a list like that next to you. You just go square by square and …

R: Yeah, I’ll show you my notebook as well.

I: Yeah, that would be great.

R: I went to Australia in October last year and they have a big telechart of list and just tic, tic, tic, tic. We don’t do that. We do [unclear] our inputs.

I: Oh, that’s interesting.

R: So basically, I’m trying to find a busy, busy one. So that’s my phytoplankton count, that’s my traverse count, and that’s my eyecount. We did think about going to direct entry, where we could literally sit there with an ipad or something and do as we go and get rid of these books, but we have not quite let go of these yet. Maybe in the future, but at the moment we still write things down. So we don’t have a checklist as such. It’s fairly [unclear] as I can get it.

I: That’s a very interesting part of all of this …

R: Well, I would have on those, but I don’t have it yet, my microscope number. We have never quite used it yet, but if we think there might be something particular wrong with the microscope and people are missing the same thing all with that microscope we can then say “well, perhaps it’s the microscope rather than human error”.

I: So this means you have seen …

R: Two of nematocysts in the phytoplankton count.

I: In two of twenty fields …

R: Yes. So there is not an awful lot on this one. It looks very green, but it’s actually this one. This one is not so green as that one. It depends on what time of year it is and where it’s from as well, so … That’s what we call the phytoplankton count and then what we do is the traverse count, I don’t know if you …

I: I got one more question about this. Is everybody doing this the same way or is this like your special …

R: No, we all write the same way in our notebooks. We all do exactly the same. The theory is …

I: Okay, so you could also look at other people’s …

R: Yeah, and if for example, we do a quality check on it and if we are going to check something and that person is away, we go to that book. They should have an index in the back, basically, where every route is and every page.

I: That’s interesting.

R: It’s the most boring thing in the world but if you don’t have it, it will be a pain in the bum trying to sit there and go back through books. I mean, this is my book and I’ve been here fourteen years. This is my book 13. Some people have been here double the amount of time. So we do keep all of these as well in one central place. In theory you can go back through and check.

I: Yeah.

R: So traverse … What we then do is we are looking at zooplankton which are the animals, but everything that is fairly small, less than two millimetres, and what we will do is we go in steps. So we’ll go alongside here and stop about there, go up there, so I move it slightly along a bit, so I am not in the same line as the first one. And we step up five times and then come along here onto this side of the silk. That’s the first time we look at this covering silk. Then we go down five times down there. So we are not looking at everything, but we are trying to get an idea of what’s on the block. So we are missing out bits of it. But I don’t know if you have heard of factors at all, we use what we call factors.

I: Yeah, you multiply, right?

R: Yeah, because that is only a sub-sample of the silk. So then everything gets put into the database and gets applied a particular factor, which we used to have to work out years and years ago, but does all [unclear]. And it puts it into a certain grouping. So we can get a category, say four, which is anything from number 5 to 12, and then it’s category five, category six and it goes up to thousands and thousands. So what you can do is put category eight rather than have to count literally everything.

I: So when you write that down, you put the actual category or how many you …

R: No, we put the actual counts. When I first started we didn’t have the database. We had analyst sheets and we had to apply that factor ourselves, but it is subject to human error, too, so it had to be checked again by someone else. Now we enter this actual count into the database and it does all for us, which is quite good. So we have minimised the error that we [unclear] deal with that, could be a bit time-consuming.

I: I think some of these categories cover quite long ranges.

R: Yeah, the higher you go up, the broader the range is.

I: So is it that at some point, you can say “These are so many hundred …”

R: Yeah, what we do with what we call eyecount is, if that block was absolutely plastered with stuff, rather than sitting there and spending three days looking at it, you will take a sub-sample of it, so you can take half of it off, and then we have a look. Say, if you have got calanus, the majority of our eyecount species will be calanus helgolandicus and calanus finmarchicus and on some routes, you can get both of those on there. And to identify between them is tiny little details [unclear] and it can be quite tricky. So we look at twenty of those and decide what they are and then have a quick rough guess of how much we think is on that block and then work out the ratios. So we don’t necessarily have to take every single thing off if it is full of stuff. Sometimes, say, if you have got two hundred calanus on it, [unclear] you are liable to undercount it slightly. But what we do is, we quality check it all again afterwards. So once everybody is finished with the routes, everybody has analysed all their blocks, one of the more senior analysts will go through it and have a look and see if we can see any gaps or if we think they have recorded something that shouldn’t really be there. It might be there, but it should be confirmed by somebody else that they have seen it. So we are trying to pick up any gaps that we think people haven’t seen. If we do sub-sample it, you might as well record in the database that you have sub-sampled it, so that we can see when we go back through “oh yeah, they only picked up twenty”. So we try to be as best we can really. I mean, you can spend hours and hours and hours on a block, but it’s not efficient, so …

I: Is it also a matter of experience that from a quick look you can say that a sample is probably category this or that?

R: Yeah, but it takes a little bit of time. We have got quite an intensive training programme. So to start with, people take about three months before we let them loose on a block and they are only doing blocks of the North Atlantic, they are not doing blocks from anywhere else because that can be completely different with a completely different list of species that you have to learn. It’s quite time-consuming, so when they first start, they are slow and we don’t expect them to be as speedy as everybody else. And sometimes you have to tell them “Don’t count it all, just look at what you should, you know …” You have got a balance of efficiency and accuracy. That is quite hard for people to get to grips with to start with.

I: Okay.

R: So once we have done this step traverse and we have looked at the smaller stuff, we do what we call the eyecount.

I: So, you change the magnification, right?

R: We used to take out the eyepieces and change it, but we don’t any more. We use what you can see here, different field objective sizes and what we count. I don’t know if you want to take a picture of that, it has got some quite useful information. It tells you how big the fields are.

I: So for the phytoplankton and the zooplankton traverse, you use the same setting?

R: Yeah.

I: Okay, I thought it was different.

R: No, it used to be. We used to have really old microscopes with different eyepieces and we used to take one out and take another one in. It is the same microscope and we stay here. It is when we do the eyecount, we go to these. So when we do the eyecount for the zooplankton, basically, we pick off anything that we can see with our eye and anything that is around about two millimetres and over. And then we put it on what we call a Bogorov tray. That is this one here. So those counts are not factorised. They should be everything, apart from when I was talking about sub-sampling, when you see masses of stuff. You have a look at twenty under here and then you make a quick estimate of how much you think is on that block.

I: So these are all above two millimetres actually …

R: Some of them are, yeah, some things you see in the eyecount may be a bit smaller, like fish eggs can be smaller. They can sometimes be like not even [unclear] millimetres, but you are hoping you pick off that [unclear]. Hopefully it comes together, so … If you can see down here, there is a thing with like pigments on it and it has got a large spine and an eye?

I: Yeah.

R: That is a baby crab, that’s a decapod larva.

I: Okay, wow.

R: So as well as black copepods, we also see stages of [unclear] larvae, crabs, [unclear] larvaes … There are lots of animals that have got larvae stages in the plankton as well.

I: I am interested in how you take this stuff off the sample.

R: Do you want me to show you?

I: Yeah.

R: So if I was doing this sample here, what I would do … I got very fine tweezers. These are called cranesbill forceps and they are really bendy. And I basically scrape like that. So I am scraping there, basically, I pull that together. What we also do is check on this side. Sometimes you get little beasts here stuck onto the flap, so you have got to lift them up, too, and pull out everything that you can see stuck. So very crudely … I would do this. And you can hear people scraping all the time. So you are picking up as much as you can. Then I get one of those Bogorov trays, grab it like that, until I’ve got everything off and add water to it and then take it over to that microscope, because there is no construction [unclear] over that, so we don’t need to add formalin to it or anything else. So that is basically what it would look like, plus this side.

I: I’m taking a picture of that. So doesn’t that change any characteristics of the sample, when you …

R: It can do, yeah. When we put it back we try to spread it out a bit rather than leave it in a big clump of mess, but yes, it will do unfortunately.

I: And to the phytoplankton, for example?

R: Yeah, you might find that you have scraped up … and some of the more armoured and heavy dinoflagellates or phytoplankton you can see … So if I scrape this off, I might find something in that step that I might not have seen before when I did the other steps. So I would do what we call “plus it”. So I have not recorded an actual number, but I know it’s on the block. I’ve seen it, but I’ve not seen it in the stage that I should have seen it in. So that’s what we call “plus”. Also, if species are damaged, we might sometimes plus them. If we think we probably know what they are, although they are missing, say, fifty percent of their body or they are missing their head, we don’t record it as a one, we record it as a plus. So that is the eyecount. So what we do then is basically record everything that we see under there and that is not put into factors or applied to factors. It is just actual counts. And then we will record that in our notebook and then we would go up to what we call our CPR console and enter that into our database, but we don’t finalise it at that stage. What we then do is get another analyst, we have our buddy-buddy system, where we will sit down together and we’ll go through it again. So it is liable to errors, because there is so much to record and certain things you put out totals, too, so it takes a little bit of time to get your eye in on it. And sometimes there is no logic in how you record it, it is just the way we have always done it. So we keep the continuity going of how we have recorded that before. So we do dual entry and then we do our finalising. So that route gets finalised, but after that it gets quality controlled, I don’t know if you have heard about check blocks.

I: Yeah, I have heard of that.

R: So basically, the three of us will go through the actual route looking for gaps, looking for maybe if analysts … we can pick up a particular weakness in an area and we might have a look at that a bit more thoroughly. Or we’ll identify things that we don’t think are in that area. So any regional things we would say “hang on a minute”, but that only comes with time. So once you have been here for a time, you start to get a feel for what you should see in each area. But saying that, it does change, so …

I: So you manually check all the data?

R: Yes, and we’ll check all the colour matches up to … what I said about these cutting point sheets. I’ll show you how we mark the colour, you might take a picture of those. So we are busy cross-comparing everything … So these are what the cutters work to and these are created, so … this comes back from the ship. This is what we call a log form. That basically means … That’s the name of the route, it was the 650th tow of the SA route. That is not the date, it is the second tow done in June of 2016. That’s the cassette number that we used in there, the actual machine, and the propeller, because each got its own number. So what propeller was used, where the silk started, and where the silk ended. Then basically, they will put on all the times [unclear] and the ships and we check that as well. We put it into our console, our database, and it maps it for us. So we check, because sometimes if there is an error and it looks like it’s going over land. So we then have to go back to the ship and say “I don’t think that’s right”. So we have got that one. And that card comes back from the workshop team, they put all their data basically on there. We don’t tend to use this really, but we keep everything together. So everything that attains to this route is held together. So then we get created three sheets. This is basically when it was put into the water and when it was pulled out of the water and the times in GMT and the dates. So we get those. And we get what is called the silk end reading. This is called the tow record information sheet. So what we use when we cut it is this silk end point and it is always one less than the silk end reading. It ends at 68.6 and the silk end reading is 69.6. This is what we use when we cut it.

I: So what exactly is the number 69 or 68?

R: That’s where the silk ends, we think. You know it goes continuously around and that’s when it stops and gets pulled out of the water.

I: So it has like running numbers on …

R: Yeah, you can see it is sort of blank a bit and then there is a colour and you can see where it starts and where it ends the colour just stops. So we have little bits at the end and start, too. So this is what the cutters use. They work out … On the silk there are numbers, I’ll show you the numbers. So you can see here it is 20 and 21. So we can work out ... Section 1 to the first sample should be between 1 and 2.8, so up to about 3, and then so on and so forth. So these are analyst numbers. Everybody has got an analyst number. And when they join they have a new analyst number. We don’t use old people’s numbers. We are up to about 115 now, or so, to our newest analyst. So these are basically what each person has been assigned. And that’s the colour, the PCI. So that shows that our cutter cut it on the end of June. Between blocks 1 to 24 it was very pale green and from 25 right down to the end it was pale green. So that’s how we record it, that’s the colour index. And then a third sheet, we don’t particularly use these, but it breaks down these into each sample, so we can see when things are in the night and when they are in the day. There are certain species that are night-time … It is called diel migration when they move up the column at night time. So in the night time you can get completely different species than in the daytime. So when we are doing the checks in check-blocking we go along and see what people have recorded and sometimes you can see when it changes from night to day and you think “okay, that’s why they have not recorded that”.

I: I was interested in that actually. Is there any kind of data processing afterwards to account for that night or day effect, or …

R: You will have to ask David for when he extracts the data, he will probably show you, I would imagine, what’s on there, because that’s quite important as well. I don’t see when it comes out the other side, but David will be the person to ask about that. So yeah that is quite important. So that’s the three sheets that we use. And when we have actually check-blocked it, we then do what we call finalise it. Although we call finalising on a [unclear], we have a final finalising button. So that means everything on this is checked again, and everything on this is checked, everything on this is checked again. And then you hit a finalising button and it becomes available. It disappears off our system and it is basically made available to any researchers or students that want our data. So it has all been quality-checked as far as we can and then we let it go. So that is basically the analyst programme in a nutshell. I don’t know have you heard of our archive?

I: The sample archive?

R: Yeah.

I: Yeah, I have been there actually.

R: Yeah, so we got samples back there going from 1958, but we are running out of room there now, so we need to try and find somewhere else, which is fun. We just store our stuff in, eh …

I: I have one more question about the quality control. You said that you check all the data with somebody else. But I think there is also a software in place that is doing like a check …

R: We check the actual samples ourselves. Years ago, there used to be something that used to flag up certain questions that were problems, but we don’t do that any more. We just go from analyst experience. That’s with the data anyway. I don’t know when the data comes out on the other side, I think David checks it all first to make sure that it is [unclear] and we think it’s correct before we release it. But no, we don’t. We used to have prompts but that was before we had this new package which came in in about 2008. Before then, there probably was something, because I remember it seeing when I first started. But no, it just goes on your experience really. But there are three of us, so if I think “hmm, I’m not sure”, I go and ask one of the others and ask “would you pick up on this, would you?” Because it is all a bit subjective, but we are trying to do the best that we can with what we have got, so …

I: So how long would it take you to analyse a sample like this, roughly?

R: Roughly about anything from three quarters of an hour to an hour on that one, because I know that is not too bad and I know it is from the KC route which is in the North Sea. So you are quite familiar with those. If we get to look at one over Newfoundland, what we call the EB routes, especially at night time, you can get some really diverse stuff on there. And you can get one particular species which you haven’t seen for ages. But you can get lots of different species, so the diversity is better, but the biomass isn’t there, whereas on these you tend to, especially on the Z routes which are again over Newfoundland, but they are a bit further North, it is just the same species and you can get masses of it. But yeah, it can be a bit more tricky and there is another one called BD, [unclear] that can be a bit trickier and more challenging. Then we have got the Pacific’s, which is a completely different ballgame again, completely different species and also, because we started that one after the Exxon Valdez oil spill, that’s where it started from, and they need to know different stages of organisms as well. So for copepods, not just adults. They have different moulting stages, they have stage 1, stage 2, stage 3, stage 4, stage 5, and then they go to adults. So they want to know particular stages. So not only do you have to know what species they are, you have to know what stage they are. So you have to count how many segments they have got on their bodies and that works out how old they are, basically. So that can be really time-consuming. But analysts don’t tend to do those until after they have been here about three years. So they are confident and they have got their speed up on North Atlantic’s stuff, but they have got to re-learn the Pacific’s stuff. And we have also been doing tows in Bass Strait and the Southern Ocean, from Falklands to South Georgia, so that’s a whole new learning process again, because they are completely different species. Some of them are the same and bigger than what we see, but they do also have their own species, so … That cannot happen until they have been here for about five years. So that is what we call the specialist analyst team. So yeah, it can be quite tricky, to start with it’s quite “oh my god”, but we’ve got everybody here. We are always looking at each other’s samples all the time. It’s not that a day goes past where you are not going to go and look at someone else’s stuff, and then you write down that you got helped by somebody else as well and who they were. And we also got loads and loads of books, the internet has got some really got stuff on, too. Sometimes we get stuff checked, as I said, by our molecular analyst. So if we see some particular eggs or some sort of blobs or stuff that we are not quite sure about, they can run it through a PCR and then have a look and decide what it is. So we have got that as well if we need it. We also have got a flow cam as well, I don’t know if you’ve heard it.

I: Flow cam?

R: Yeah, it’s a recognition machine and we can programme it to have a look at different species. We have just bought that recently just to have a look at some stuff. And we also have got instruments on our machines as well, like temperature and salinity data and all that. We have got that as well. So what we also do is, we all wrap it up the same way.

I: Yeah, I am interested in that, too. But first, what are these lines actually, the horizontal, blue lines.

R: Oh that’s when they first mark it up, when it comes from the workshop, they do all this and I think it’s, I’m not sure, it must have something to do with the speed of the machine, I think, how the lines go. We got [unclear]. I’ll ask my colleague, he might know a bit more about that. So when I am finished with this one, as I said, I spread it out as much as I can …

I: Oh, so it actually went like this through the mechanism, right?

R: Yeah, yes.

I: Oh okay, I first though it would move like this, but now it makes sense because on the outside it’s white.

R: Yeah, I think it has something to do with the speed of the ship. It’s quite technical, actually. You look at it and “oh yeah …”, but … So what I’ll do is I spray it with a bit of formalin to preserve it. And then I’ll put the top back on and then we’ll fold it in a certain way. So we go from right to left, put it into the middle, put the label back on. I should have some gloves on … So on there, it tells you the sample and the analyst. I am number 94. So that was on the 47th KC tow, block 11, and I am number 94. So everybody should do the same. And basically we fold it back up, and then we put it like this. So on that route we have only analysed just the odds, on some routes, smaller routes, we analyse every block. There is a Plymouth to Roscoff route for example that we analyse every block on. On most of them we just do the odds, so then we have got the even if we need it for any further investigations or if there is any new technology that is coming up, we also got another block [unclear] as well. We have got a route box, it is this one. So you can see that 47KC is my one and that means there are 36 total samples, not just the odds in that 47KC. So we write that on there as well. A box like this can hold around 250 or so samples. We can’t squash it all in either, so that will go in here, but it goes in chronological order as well. So you can see at the end, there is [unclear], the one I got out earlier. I have done block 11, but people in between haven’t done theirs yet, so if you see on the earlier ones, they go backwards to … 33. That’s done wrong, that should be 35. No, 33, 30. So it goes backwards 29, 28, 27, bla, bla, bla … all the way back. What we’ll then do is, it seems that all we do is checking, it feels like it. Once the whole route has been finished with and the box is full, we’ll then go through and make sure it’s in the right order, because [unclear] the amount of people that don’t always put the right ones in the right order. Sometimes they are quite sticky, so they can get stuck to other samples and sometimes they will turn up in a completely different box, so it’s the last check of that before it goes to the archive. And one of my colleagues creates a survey, every couple of months she’ll go through and make sure that some of the boxes are in good condition still or if they need topping up the formalin. So we constantly try to keep it up to date because you never quite know when you will meet it again. So yeah, that’s it in a nutshell, I think. Are there any more questions you wanted to ask. I sort of bombarded you with stuff.

I: No, it’s been great. But I am still puzzled that you use the same magnification for these things …

R: We have got different eyepieces here, different magnifications. So I’ll tend to use this one for traverse and that one for phytoplankton, but we don’t change these, which is what we used to do.

I: Ah, I see.

R: I don’t know if that’s where you got confused.

I: Yeah, so for phytoplankton you look with greater magnification, I guess.

R: Yeah, you need to get it quite [unclear] because some of it is so so small. It’s like [unclear]. And you do find sometimes … We have an inverted microscope in the corner there. If we are doing a particular … Some of us do we call it BEQUALM test, it is like an inter-[unclear] test, so each person in each laboratory does the test to make sure we are all doing the same thing correctly, and to make sure that we are not learning all wrong from one person. So we use that one, which is more detailed than these. But we try to keep ours all the same for consistent methodology, that’s why we don’t use one of those each. It is quite technical and there is quite a lot to it.

I: Yeah, but it is very interesting, the steps of manually doing stuff …

R: Yeah, I mean you could probably replace us with machines, I guess, but you’ve got to have someone to input the machine and there are so many taxa to do and we go down to quite a low level, so you would lose that if you did that. So yeah, it is interesting. It’s hard, but … If you talk about being in marine biology, you think everything you do is look at sharks, but “what’s plankton?” Until you show them and they are like “oh my god, yeah”. It’s [unclear], but we enjoy it.

(end of recording)