Informed consent statement for Oral History Interviews

(This form can be sent in advance and signed or read into the tape at be beginning of the interview.)

The interview will be recorded, and I will use the audio file to make a transcript. The transcript will be shared with you, with an opportunity to correct it. The attached form indicates options for making the final edited transcript available.

My name is Josh McMenemy and I am a student at Duke University. I am in a course on the history of genomics that includes oral history. One goal is to produce a written transcript of interviews with important figures in genomics. Some of the interviews may be archived or made public through a website. The conditions for making the transcripts public (the audio tapes will not be public) are indicated in the accompanying form, and you can choose any of those options, or write in your own conditions.

I selected you as the person I would like to interview. The interview should last 30-45 minutes. Your participation in this interview is strictly voluntary, and you may withdraw at any time. You do not have to answer every question asked. The information that you choose to share publicly will be "on the record" and may be attributed to you, unless use is restricted the conditions you specify on the form.

This interview is being recorded and I may take notes during the interview. The interviews that are posted publicly will be archived as a history resource. If you prefer that the interview be used only for the course and not made public, please indicate this on the form.

One risk of this study is that you may disclose information that later could be requested for legal proceedings. Or you may say something that embarrasses you or offends someone else when they read it on a public website. The benefit of participating in this study is ensuring that your side of the story is properly portrayed in the history of genomics.

Signed: Richard M. Myers Date: October 29, 2014

Person interviewed: __Richard M. Myers__ Student Interviewer __Josh McMenemy__
(Print clearly) (Print clearly)

Use of archived final transcript

Members of the Duke University community, students, faculty and staff at other institutions, or members of the general public may access the digital archives. Typical research uses of interview materials include scholarly or other publications, presentations, exhibits, class projects, or websites. However there may be other uses made as well, since the materials will be available to the general public. Investigative reporters and lawyers engaged in or contemplating litigation have, for example, used the Human Genome Archive.

Your permission to post the edited, written transcript of your interview, and any related documents, to a digital archive is completely voluntary. Unless you consent to their wider use, all materials from your interview will be available only to members of the research team affiliated with this project.

The form below provides you with different options for how, when, and with whom your interview materials will be shared.

(A) X I place **no restrictions** on my interview materials.

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(B) ___My interview materials may be reviewed, used, and quoted by students and researchers affiliated with Duke University; *and in addition* (check all that apply):

___Researchers unaffiliated with the Center for Public Genomics may **read** the interview transcript and any related documents only after obtaining my permission.

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Posting interview materials to public digital archives: In spite of any restrictions listed above, I give permission for my interview materials to be made publicly available on the Internet by deposit in an institutionally affiliated archive:

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___Other: _____ (please specify a date or

Signature: Richard M. Myers Date: October 29, 2014

Phone Interview with Richard Myers
Conducted by Josh McMenemy
A Social and Political History of Genomics
18 December 2012

McMenemy: Hello?

Myers: Is this Josh?

McMenemy: Hey, yeah, this is Josh McMenemy.

Myers: Hey Josh, its Rick Myers.

McMenemy: Thanks again for the opportunity to talk to you, and before we get started did you have any questions regarding the informed consent?

Myers: Sure. No, I signed it and sent it off.

McMenemy: Well my first question is….

Myers: Hold on before we start. Let me just ask you this: one thing I wasn't sure is if this a study or you're doing one for your classes?

McMenemy: Yeah, the class is the Social and Political History of Genomics.

Myers: And you're writing a paper for that?

McMenemy: This is actually for a website archive for students and other people to use for their research, and also to teach us about the interview process.

Myers: I see and what year are you in school?

McMenemy: I'm a freshman.

Myers: Have you studied anything about the science part, not like you've been a scientist, but are you aware about what the genome project did and all that stuff? I am just tying to figure out what level…

McMenemy: Yeah, do you know Dr. Willard by any chance?

Myers: Hunt and I have collaborated for years. I've known him for 25 years.

McMenemy: I was in class with him, too, and it was an overview of all the science, and we touched all the basics from epigenetics to population genetics, so I have a general understanding of everything.

Myers: And what's your major?

McMenemy I'm majoring in Biomedical Engineering and specifically interested in genetics, so like genetic engineering in the future.

Myers: So you're not working in a lab yet? Probably just taking courses and stuff.

McMenemy: Yeah, my goal is to get involved in a lab next semester, now that I have adjusted to life at Duke.

Myers: One of my former post docs started as faculty at a position there about half a year ago, or nine months ago, Tim Reddy. You should probably meet him he is really a good guy.

McMenemy: Okay, how do you spell his last name?

Myers: R E D D Y

McMenemy: Okay, I'll definitely contact him.

Myers: Alright now, let me just tell you I have about half an hour. I don't know how long you need, I could go a little over if I needed too, but I've got another thing I have to do.

McMenemy: Half an hour works, and most of the questions relate to the Human Genome Project, but a lot is on the future implications and the effect on the field.

Myers: Okay. And are you recording, or do I need to talk slowly, or are you trying to write notes?

McMenemy: I am recording, and I'll go back and transcribe.

Myers: Good, so it doesn't matter if I talk a little fast.

McMenemy: No, that's fine.

Myers: Okay, let me go to your question then. So how did it affect the rest of my career?

McMenemy: Yeah.

Myers: Okay, let me give you some background. The human genome project started officially in October 1990, and I had been a faculty member and an assistant professor at…

McMenemy: Okay.

Myers: Do you need me to slow down?

McMenemy: No, that's fine.

Myers: Now if you need to interrupt, tell me because I'll go on and on.

McMenemy: Sounds good.

Myers: All right, so I was an assistant professor at UC San Francisco, UCSF, and I was doing human genetics and collaborating with a more senior, not real senior, fellow who was a MD-PhD named David Cox there studying genetic diseases. We worked on methods for mapping the genome before sequencing was done. So we had the opportunity to apply for one of the first genome center grants that the NIH was funding and we jumped on the opportunity. We won the award. I was still an Assistant Professor, but right around then I got promoted to Associate Professor. The reason this is a big deal, and I don't think these titles matter, but the reason this is a big deal is that when you're first starting out to take on something big like this, it's a little risky and a lot of people warned me that it would be risky. But, David and I, David in particular, decided that I would be the PI, the Principal Investigator, sort of the director of the center and he would be the co-director even though he was more senior. So there was a little bit of worry because the Genome Project was sort of a big, team-oriented approach. A lot of people thought it was going to be just boring, turning the crank, and in fact, it turned out to be far from that. So it was a little bit of a risk, and I think it may be true for some of the other folks who were doing this because it was a new way of doing science at least in biology. It was large scale a lot of things to coordinate and organize, and I have to say it was the best thing I've ever done. I am so glad that I did it. Not only did it not hurt my career, I think it certainly helped it. I continued to do disease research in a smaller laboratory outside the genome center, which connected me to a separate group. That is the way that I've run my career ever since: where we do high throughput production scale generation of data, not just for the initial genome project but for other large scale projects, where the data are then released rapidly to the public. And careerwise we get a lot of it because we learn things from these data and get a lot out of it and frankly the team-oriented sort of community project where everybody gets the data rapidly is extremely rewarding for everybody. It has been for me, and I think for many other people who do this kind of research. It is a little different from the way many other people will do research and so you give up a little bit. Part of thing you give up, a price you pay, if you want to think about it that way, is when you work in a big consortium like that you have to spend a lot of time communicating and coordinating phone calls, video conferences, meetings and things. And sometimes you do big papers together so you kind of forgo being the first author. It is kind of like the physics community where they do high-energy physics. They have like 500 authors in alphabetical order. You get your rewards in another way. So it turned out to be good in my view. I love doing science this way. I love the other way too. It

might be easy for me to say because I was promoted to tenure right before the project started in October and the reason I say that is not because I care about tenure. I frankly think the whole promotion and tenure thing is crazy in academia, and we shouldn't be so hung up about it, but that is what the system requires. There is a concern of how do you get recognized if you're a post doc or young faculty member and you're part of a big group. I tried to all my years at Stanford. I was there for 16 years, and all my years on faculty I tried to help people who are on the review committee and things to understand that these contributions that people make to these big projects are as deeply intellectual and as rewarding and as scientifically driven as anything else…

McMenemy: Yeah, this actually leads into my next question.

Myers: Okay.

McMenemy: A lot of the non-hypothesis driven large scale projects such as ENCODE, the 1000 Genomes Project, and HapMap are now a common occurrence. Do you think the current balance between smaller hypothesis-driven and these large-scale projects is ideal, or do you foresee this needing to change?

Myers: I think it's perfect. Very few of the people, well, it may be true that some of the people in the large projects only are thinking about the production aspects, but almost everybody and certainly those of us who are trained to do hypotheses-driven science from the beginning are doing it because we want to learn from it. If we didn't have that, genomics, and the high throughput methods, we wouldn't be able to design them as such the other way. But again it depends on the individual scientist. Not everyone approaches the way we do it at my laboratory. For instance, the people who are part of ENCODE at my laboratory, the post docs, the graduate students, the technicians and senior scientists, too, who are a little bit more production driven, but all of them are driven by something… they want to learn from it. Then they go sort of separate from ENCODE or 1000 Genomes and try to learn whatever biology they can from it. I have to say hypothesis-driven versus not is a little bit of an artificial construct even though I use it too. Not getting onto you.

McMenemy: Yeah, it's no problem.

Myers: But we talk like that a lot and it actually is kind of meshed together, but yes you might cast a really wide net. So here is an example: we do a lot of stuff where we are trying to work on diseases as well as ENCODE, so we do a lot of stuff where we study clinical trials and one of them is breast cancer. Let's say there are a bunch of women with breast cancer and they are trying to figure out how to improve a new drug because cancer is not just one disease, it's a heterogeneous disease.
So if you treat with the new drug in a clinical trial and lets say a third of the women respond well to the drug and actually get much better and two thirds don't. So we do genomics a non-hypothesis ... I'm not really sure if it is even non-hypothesis…

McMenemy: Because it's testing an association?

Myers: Yeah, we sequence all the RNA let's say or maybe the exome or DNA methylation studies, which look whole-genome, and then see what is different between the responders and the non-responders. Now that's a huge experiment. You could say it's a fishing expedition casting a wide net but every time we've done this we have found a bunch of genes that distinguish responders from non-responders. This is extremely valuable, even if we don't understand it. But now we can home in on those genes and biomarkers. Also some of those markers might be great targets for drugs because maybe the responder has a new gene that no one has ever thought about. So now you follow that up with a detailed study of that gene or a set of genes, it's never just one gene but several genes, rather than the whole genome. The second one is now hypothesis-driven, but in fact I would argue that my original experiment was hypothesis-driven in that I have a hypothesis that there is some genetic difference or expression difference between responders and non-responders. So it's not quite as dry as a lot of the old fashioned biologists, as I was trained, who do hypothesis-driven research. By the way, old fashioned meaning they use the old method, not that they are old-fashioned.

McMenemy: Yeah, I understand.

Myers: So that's the way I think about it, and if you think about it this way, it is a good balance. If you don't think about this, you could run into problems.

McMenemy: So what's your specific advice for young scientists getting involved in these larger projects?

Myers: Absolutely. So first if you're going to get involved in genomics and large scale genetics you need to be as quantitative as possible. I unfortunately was not trained as deeply in this. All these young folks run circles around me in terms of statistical and computational methods.

McMenemy: So bioinformatics?

Myers: Yes, bioinformatics, whatever you want to call it. They do a huge scale of data analysis and data handling, so you need to be able to do that. But if you do only that, or you only learn how to run sequencing machines, or only prepare the samples, and you don't deeply understand the biology, then you're going to only be asking the questions other people ask. You want to ask the questions yourself, too. So to do this you really need to deeply understand biology, the way Hunt Willard was teaching you for instance, where you actually know how chromosomes work, you know how genes work, you know something about gene expression, you know something about the organ systems that you're studying, if you're studying breast cancer, you better know everything that's been done on that, as well as how the physiology works. So that's a tall order, but in fact the young folks who are doing this who figure out those sets of skills and get it from the beginning are going to be way more

successful than those who are so single-minded. There is nothing wrong with being purely bioinformatics, for instance, but you really need to understand the biology instead of just doing the stuff other people to tell you that you need to do.

McMenemy: That makes sense. Since we are about halfway through, I am just going to a transition in the questions focus.

Myers: Sure, no problem.

McMenemy: One of the main images that comes to mind, even if it may not be totally correct, when reflecting on the Human Genome Project is the race between the public and private. What impact do you think this had on public-private relationships in the field?

Myers: Well, first of all, I was there in the room when this all started in the middle of this. We are talking about Craig Venter here of course…

McMenemy: Yea

Myers: Craig was part of the public effort then and decided to go off and do it on his own. There was a huge, huge amount of publicity and brouhaha about this, the press just loved it. In truth, it was sort of a fight, and of course, I was on the other side of Craig because we believed making this freely available for people was important. But mind you I am not anti-company. I am a founder of two biotech companies, for instance. I have been involved in the business. I think this is great, but I think the way that he approached that was historically misrepresented in the press because it was so overblown. But in fact Craig argued to congress that they didn't need to bother paying the public effort. Celera got a rough draft of the genome then stopped or didn't continue to work on it, unlike the public effort, which didn't have the aid of his data like he did to our data. They did do a decent job considering the time, but they had some real guns in there to do the computational part of it and all that. So in the end that was a little distasteful, and Craig was quite bitter at all of us. That is just the way Craig does things. But the truth is it caused some harm because it painted this not very accurate picture, and you can read all the historic books on this because there is quite a few. I got so tired of this that I threw up my arms midway through and said, I don't care what he does I just want to finish our business. I have to tell you that Craig would like to think that as having a huge impact on the world, and he had some impact, but the truth is this goes way beyond any one individual person – him, Francis Collins, John Sulston, Eric Lander, anybody. This is a project that was formed for the free release of data and the historic first human genome. Now I'd be surprised if we don't have many thousands of genomes done because it is so valuable to have them. Economically the impact it has on business is huge.

McMenemy: I've read the Common Thread…

Myers: Yeah, but read the Battelle Report. It came out about a year a half ago. Battelle is a consulting group. If you remind me, I'll send you this as well as a paper that Maynard Olson wrote in the 90's or in the early 2000s after the Venter stuff happened. But the Battelle Report talks about the economic impact of the human genome project.

McMenemy: I'll definitely read it.

Myers: Yeah, you should it's huge, like a 141 fold for every public dollar spent.

McMenemy: Wow.

Myers: And that happened because it is publicly available, and people mine it and get something out it, or patent something out of it and maybe start their own company based on it. The idea behind the Human Genome Project was a big casting of the wide net for free for everybody. Then use our patent system and our entrepreneur business system to do something with it. By the way, its not only businesses that are doing this, probably far more people in academia are using it, too.

McMenemy: HudsonAlpha is in a unique position where it is non-profit academic style, but also aids many small biotech companies.

Myers: Well, they are in the same building with us. That is the reason it is a little unique and it encourages that. But mind you, universities encourage this, too, just the companies are off campus, like Duke University. Stanford is also very entrepreneurial. UCSF is as well, but until recently didn't have the physical connection to them. Well, as our institute the companies are in the same spot, so we interact a lot. They are separated financially, though, because we are non-profit. So it's a unique model. It's an unusual model.

McMenemy: Interesting, I look forward to how that works out. On another topic, you have been to almost every Cold Spring Harbor Laboratory Genome Meeting, and I was wondering what the major atmosphere changes are since those initial meetings discussing the Human Genome Project.

Myers: That's a good question. I have been to all but one, I think. I don't know why I missed one. Trying to remember – no, it wasn't when my son was born. These meetings are in May, and they are really good meetings and have been since the beginning. They have evolved so much. At the beginning, there was only talk about the technology and about gene mapping. I mean, it really didn't have much to the futurists. It's been interesting, the meeting, in my view, the recent meetings have been really exciting because there has been so much in next generation sequencing, but before that there was a little bit of lull where it wasn't quite as interesting because it seemed so similar to the previous year. I think there are cycles that fields go through, and the field of genomics has always been soaring since it got started,

but like in any field you get lulls. Often it's technology jumps, you know, a new technology comes along, new ideas come from it, and a lot of these are talked about at meetings and published right around that time. Then it takes a little while, like a year or two to start using it. So the nature of the meeting has changed quite a bit but I still think it is, well it's not the only one, but one our critical meetings.

McMenemy: Where do you think these meetings are heading in the future?

Myers: That's where will the field go in the future. I think we are going to see a lot more medical applications because it really is going to start being applied in that way. And I think we are dealing a lot with the issues of how we interpret the information, if you sequence a whole genome or exome and how you apply it that's right here and now. I think you'll see a lot of that. One of the things that ENCODE does but it's really a lot of other researchers do but we are probably going to see a whole lot more functional analysis of the genome. Meaning okay, we think this regulatory element is important. How do we do high throughput genetics on that. I mean, how do we knock them out or do this or that so that we can actually really be able to predict if you make a base pair change in this base, it's going to cause this phenotype or at least cause a molecular phenotype change. I think that this is the direction we are going in. Futuristically well, another one Josh, that you have heard about as well is that clearly this technology is moving so rapidly that we get surprised at these meetings about new ways of doing things. We are working towards the $1,000 genome where you can sequence a whole genome for a $1,000 and even get some analysis from it. We are not there yet, although we are not too far away from it. But what if somebody comes up with a $40 genome? I don't know – they might. What if somebody comes up with a new way of computation because right now, one of our rate limiting steps is the amount of electrons that have to move to both compute and store and disseminate all of this information, because it is huge.

McMenemy: Especially when you integrate epigenetics, too, I'd imagine.

Myers: Yes, all the functional stuff too. All of this is a huge amount of data, and in fact, biology if it hadn't, hasn't already, will certainty surpass all other fields in the use of computation in terms of the total amount of CPU time and storage. We are already probably there, but even more when it is going to be applied to everyone in the clinic. I think what I don't want to lose in the Cold Spring Harbor Genome Meeting, and in our academic as well as commercial entities, is the fact that we still have lots to learn and discover so we really need research that needs to be basic as well as applied. If we ever make the mistake: that we say, all right it is done, so we can stop here, apply it. The field will get stale, it will never move forward. Again, let me go back to just the sequencing cost alone. What if we said, well we are happy with a $1,000 genome that's part of their medical records etc. we are happy with that and just do it that way. Then we are precluding the opportunity to make that a 100 times cheaper because that is likely to happen.

McMenemy: And that money could then be used for other applications.

Myers: Right, and then the other is that you know about the biomarkers like what we are discovering in the cancer drug trials. I mean that goes for any disease any drug treatment any environmental impact. If we don't study the basic biology of those things we discover as biomarkers, then we won't do anything new with it. So you might hear this from my colleagues, your colleagues they are not just mine, doing research, that we don't understand everything – that these tools have to be used to understand basic problems, as well as deeply applied ones.

McMenemy: Okay, now that ENCODE, HapMap and the Microbiome project are ending or will be ending in the next years, what do you foresee as the next large projects?

Myers: First off, ENCODE just did start another round of funding, so we got another four years, and our lab is actually a part of it, fortunately. I think you're going to see this associated with each disease or certainly the National Cancer Institute along with the Genome Institute are doing big things in cancer genomics. So future directions: one of them is not just finding biomarkers and measuring them in biopsies, but let's see if we can find them in cells or DNA that is floating around in the blood. People are starting to do this a little, but it is not there yet. So that you could actually do a noninvasive test for ovarian cancer, kidney cancer, prostate cancer and several of the others, many of them which you don't get symptoms until it is very late and it's already spread. So early detection would be a huge thing, not just in cancer, but in all diseases. I think the pharmaceutical-genetic side of this meaning which drug works best for this particular individual or set of individuals.

McMenemy: So personalized medicine?

Myers: I don't like to use that term. Everybody does and I do too… I'm not sure if it's the right term for it because its not that every person has a specific drug that they need, its that every disease has half a dozen or two dozen different subtypes, meaning they are caused by different things, so you need to figure out what category each disease is in to figure out the best regimen of treatment. So I think we are starting to see that already and that needs to be done in a big, big way. I think we still need animal models for things because when you just learn everything it's hard to get at tissues. Another big thing, which ENCODE is trying to do and so are many other groups, whether it's a big consortium or not, is trying to figure out how to do these genomic measurements like RNA, DNA methylation, and other epigenetic things, and even sequencing the genomes, but doing all of those on tinier and tinier amounts of cellular material, meaning even single cells. I think that is a direction as well. One of the new directions that is sort of related to functionalizing the genome is, again I am going to use a worn out term, synthetic biology: the idea that you use DNA synthesis and other ways of manipulating genomes and building genomes to study function. This is really important. Maybe we will see that in terms of making

products as well. But I see it being especially valuable in basic research problems and in answering questions that we still need to answer.

McMenemy: Going back to the single cell, do you see a big growing in microfluidic device?

Myers: Well, part of the way to deal with single cell stuff is that you have to deal with stuff on such a small volume that you have to have microfluidic devices. There are some really clever things out there that people have already developed for handling PCR for instance and various other manipulations on tiny amounts of material that are not in a test tube, not even in a micro-titer plate. We are now talking about sub nanoliter reaction sizes, and I see that as being both exciting and challenging, and a lot of people are working on this. I wouldn't say there is a solution to anything yet, and there won't be a single solution there will be lots of different ways.

McMenemy: Yeah, I was curious because I had read some of Steve Quake's recent publications.

Myers: Yeah, Steve is one of the leaders in this, but there are lots of people working on this stuff, and when you have a challenge for people, it's amazing how clever people come up with ideas on how to do it. I mean some of the sequencing methods you would have never dreamed of, and maybe dreamed of, but thought this would never be possible. Today's technology of single-cell seemed so remote even a few years ago, and now here we go.

McMenemy: I realize we are running short on time. Do you have time for another question?

Myers: Yeah, I don't want to short-change you.

McMenemy: One of HudsonAlpha's stated missions is to help train the next generation of scientists and entrepreneurs. What approaches are you taking to accomplish this challenge, especially with how rapidly the field is developing?

Myers: Well, so first of all, I've been doing this long before I came here, and people in our field should take seriously that we need to train the next generation. I think some might think of graduate students or post docs as labor, but in fact they are the ones who will start taking over from those who are getting old like me, well not old but older, and so it is critical. There has always been the question, even before I started graduate school in 1977, of if there will be jobs for me. The US has always been the leader, the very strong leader, in research in all fields and particularly in the life sciences, and I think we still do very, very well, but we will lose that edge if we don't continue to think about the next generation and how to support them. It's not just more money. It's mechanisms that support them. The whole team science approach that was not even an approach one would think about when I was in graduate school, and yet we move more and more in that direction. The bigger most

important thing is to help our politicians, and our leaders, and the public understand that this is an incredible investment that the country and humanity, and I don't want to be jingoistically patriotic about it although I do care about the US. We've done great at this, and I want us to continue to do great at it, but part of that is assessing and making sure that we make opportunities for them. There are lots of opportunities for them, but it's getting harder and harder because essentially funding levels have declined or flattened. Staying flat basically means declined because you're not growing. I think sometimes we need a little different models for doing this. The Genome Project helped me think about it, and I think a lot of people think about doing this a little differently. You don't have to be a faculty member to help lead or play a serious role in this since having other kinds of positions that we're calling senior scientist. The computational people, the pharmaceutical people, the biotech industry people and the agricultural industry people and in other places where there are broader things for people to do. Now the other way that I have participated in for a long time and were especially doing this at HudsonAlpha, and I did this at Stanford, I learned early on what we call education outreach, which is telling people about science who are not scientists or who are not going to be scientists. That means and it's something that I feel like we owe the public. We do it, but a lot of people don't. I frankly learned this from Bruce Albert, a real guru, who was one of my mentors and senior people who advocated how important this was even back in the 1980s… so we do a huge amount of this at HudsonAlpha, and I did this at Standard and UCSF, as I mentioned, where we do all sorts of things. Internships for high school and college students, for instance. We are not necessarily trying to turn them into scientists, but to come up with a scientifically literate public. So we do a huge amount of outreach to the adults here, and we teach courses, and we do a whole program, if you're interested in looking it up, it's our education group led by Neil Lamb, who is a former faculty member at Emory. But that's part of it. The other part of is training students and post docs in your laboratory. I think teaching them about the social implications and how important it is to think about the impact of your research is really, really important. All this ties together, and part of it is making sure that we try to be leaders in this country, which means to invest in this. It is not pork this far from money wasted. I mean if you think about the many, many advancements that have been made because the US has done this in the past, a good example is when I was a kid if a child was diagnosed with childhood cancer leukemia or anything like that, their chances of making it through were very low, probably only like ten percent and now it's 85 percent. Now you tell me that we haven't made advances in science, that is remarkable. Now that 85% come about because of basic research as well as biomedical research and pharmaceutical applied research and everything all of those things, but it would not have happened if we had not made the investment in it. That's really important. Anything else.

McMenemy: Depends on your time?

Myers: Well Josh, let's go one more. If you have a lot more, I can arrange another one. Go ahead and ask me another one and see how it goes.

McMenemy: Are there any specific training techniques that are different for this generation?

Myers: Yeah, I mean first of all any time you do anything in large amounts of data, you have quality controls and things like that. You learn to analyze data at a preliminary state so you don't waste a lot of money. But the truth is I did purely hypothetical exploratory research in college and beyond.

McMenemy: Which do you find more interesting?

Myers: I love them both. I will not choose because I believe they are both so powerful. I've had the luxury to combine them because I was trained in the more basic way, and I have learned a lot of this other way more recently.

McMenemy: Yeah, I've noticed you've done a wide range of research from large population genetic studies to specific transcription research.

Myers: I have a short attention span, but nevertheless, I think both are really relevant. One of the things I try to teach the young folks who are purely genomic who come through is to understand some of the other biochemical approaches other people do and vise versa. It's a mission for me to get those two areas together whenever I can. Some of my collaborations are like that and it's wonderful to have someone who deeply, deeply thinks about mechanisms biological stuff and never thought about genomic stuff at all. Then they collaborate with us and get all this other kind of new information that they have never got before. Yet if it were purely genomics it wouldn't be as interesting. So it is really this nice interplay between the two, and it's a false dichotomy to separate them. A lot of people initially choose one or the other, but they don't think about the other side at all, but a lot of people do what I'm talking about as well, and I think that is part of the future, too.

McMenemy: So you're saying it's important not to specialize too much?

Myers: Well, no. Focusing in on a problem is important. Where you do the specialization has some real merit, but if you never understand what the other folks do, you might miss out on something. Not that everyone has to be so broad. I am a little self-critical here. There are things I'd like to focus on more and do more mixing and matching. So I think we have this spectrum of how we do this, and we need to keep that whole spectrum, but it's important for people at the extremes of those spectrums to understand what the others do. And that is a part of what I spend my time doing.

McMenemy: Okay, is there anything you would like to add before we conclude?

Myers: No, I think what you're doing sounds like an interesting project. I hope you're getting a lot of this. It's an exciting field, and I hope you talk to a bunch of people on

stuff, but good luck. And listen, if there is anything you need me to look at that you write that would help, I would be happy to.

McMenemy: Okay, thanks, I got a ton of useful information. I will definitely make sure to contact the people you gave me, too.

Myers: Alrighty, well have a good one.

McMenemy: You too, thanks again for your time.

Myers: Sure. Take care bye.

McMenemy: You too.