TRANSCRIPT – EDGE Webinar – 15 January 2021

SLIDE 1: Ted
Welcome to the Enabling Discovery through GEnomics (EDGE) webinar. The EDGE program is a BIO-wide program and is represented by individuals from all of the divisions within the BIO Directorate. And this year, we are joined by an interagency partner at NIH/NHGRI.

SLIDE 2: Ted
The outline of this webinar today is as follows. We will first cover the program overview, then we will discuss submission requirements and the review criteria. And then we will conclude with plenty of time for for Q & A. Hopefully, we will be able to answer all of your questions about the EDGE program, the solicitation, and in how to create a competitive proposal with this program.

SLIDE 3: Ted
The EDGE Program is a program that has been in existence for five years. And the purpose of this program is to advance the understanding the relationship between genomes to phenomes, specifically aligning with the goal of understanding rules of life and predicting phenotype. In this program, we have two primary goals. The first is we want to support the development of genomic tools that enable research communities, to test hypotheses in emerging model organisms. And secondly, we want to support research in the genotype-to-phenotype space within the context in which those organisms live and function. To accomplish these two goals, we have two tracks within the EDGE program.

You will hear throughout this this webinar, a couple of words, which are that we have emphasized in the new solicitation. These are the context in which organisms live and function, and the generalizability of the results that are drawn from the proposals that are submitted. To this point, we now allow the use of traditional model organisms within the research track, but generalizability of these results must go beyond the focal species.

SLIDE 4: Ted
The new solicitation has two tracks. The Functional Genomic Tools (FGT) track, and there's the Complex Multigenic Traits (CMT) track. The FGT track is focused on the development of tools that are needed to understand genotype-to-phenotype relationship. Projects within the FGT track might include phenotyping methods, innovative approaches for manipulating individual genes or multiple genes simultaneously or approaches to establish the function of single genes or networks of genes. In the CMT track, proposals will focus on hypothesis-driven research rather than development of tools. Applications to the CMT track might be focused on systems level analysis of gene regulatory networks or innovative approaches at linking genes with complex traits within the context in which they live.

SLIDE 5: Ted
For both of these tracks, we place a high priority on projects that are going to cross disciplines in biology and are generalizable beyond single genes, single traits, or single disease-relevant phenotypes. With the addition of NHGRI, this NSF-lead program also considers applications that demonstrate the utility or relevance to human or disease relevant model organisms.

SLIDE 6: Ted
Although the EDGE program's scope has expanded since it was founded five years ago, there are some things that the EDGE program does not support and would be a better fit for other areas of BIO. The primary one is projects that are related to genome scale research or tool development and agriculturally relevant plant species. These projects will likely be best fit in the Plant Genome Research Program (PGRP). Additionally, proposals focused exclusively on bioinformatics tool development may be more relevant for programs in DBI. But I want to highlight this point right in the middle of the slide. Frequently, we can determine if your project is a fit to the EDGE program by sending a brief synopsis (a one-pager) to the bioedge@nsf.gov alias. The EDGE working group can then evaluate these and determine whether or not your project fits within the EDGE program, and which track it might fit best within it.

Now I'd like to turn the webinar over to my colleague Jen Troyer, from National Human Genome Research Institute to tell us about their mission and goals in joining the edge program.

SLIDE 7: Jen
Yeah, hi. So, I am Jennifer Troyer, from the National Human Genome Research Institute, which is part of the National Institutes of Health. I just want to talk to you a little bit about why we are interested in partnering with and joining this particular NSF funding opportunity. As some of you will know from workshops and calls with some of us, we have been talking a lot across agencies about the areas where we have overlapping interests. And really, we're very aware that in genomics, and in understanding how variation in genomes relates to functional differences, and ultimately, trait and phenotypic differences, we all have a lot in common. And so, we want to make sure that both in terms of funding agencies and in terms of the communities we support, we are really exchanging ideas across communities that are asking the same biological questions. We recognize that some of the organisms traditionally supported in different areas have specific evolutionary relationships to others supported by other agencies, where if we put that information together, we get more knowledge out at the end. And finally, we really are interested in strengthening this link between how we do research and what the research community and society needs from this research, in particular.

SLIDE 8: Jen
I'll talk about the NHGRI a little bit because some of you may not be familiar with us. So, as with all of the National Institutes of Health, our focus is on human health and disease. However, we are one of what we call the “disease agnostic” institutes, in that we're really there to support genomics. Now, there's a lot of genomics in disease research that is supported across the NIH. We're a rather small Institute, we get only a small percentage of the total funding of NIH, so our mission really is in this area of developing resources, approaches and technologies that accelerate genomics research much more broadly across the NIH. And so, [we support research] in this area of resources, approaches and technologies, where we are looking at basic biology, the structure of genomes, the biology of genomes, and how genomes relate to function and biology of disease. And then we also have a branch that is specifically focused on using genomics to advance the science of medicine, improve the effectiveness of health care, and there are [also] several cross-cutting areas that we fund in ethical, legal, and social implications, bioinformatics, a lot of technology development, research, training and career development in genomics. Our focus is always, and so here's this term again, on generalizable methods and knowledge about genomics in relation to phenotype. And so, we feel like EDGE is a very appropriate call for this kind of work. And we will be considering [proposals] after review (we'll talk about the process later; Floh will) but after review [we will consider] applications that have some utility and relevance to human health. This does not mean you have to be researching in humans or traditional model organisms just that there's relevance, and again, that there are methods or novel applications that are generalizable.

SLIDE 9: Floh
Hi, I'm Floh Thiels. I'm also program director at the NSF in the same division as Ted in Division of integrative organismal systems. I will take a few moments to talk about the submission requirements. If you happen to follow along with the solicitation, the submission requirements are described in Section V of the solicitation. We are not going through each aspect of the solicitation and therefore recommend highly that you read the solicitation. We are using this webinar to point out some elements of the solicitation we consider to be particularly important for you to pay attention to, and because they may be a little bit different from aspects of other proposals you typically submit. First of all, there is a deadline with this solicitation, and the deadline is the 16th of March, 5pm your local time. This is a hard deadline. Another piece of information to keep in mind is that there are two tracks: the Functional Genomic Tools track and the Complex Multigenic Traits track, and we would like you to indicate the track in the title of your submission. So, your project title should have a prefix of either FGT or CMT. Another aspect of the proposals that may be unfamiliar to you is that the Project Description, which is the body of the proposal, has to have specific named subsections. Of the two required subsections, one has to be titled “Intellectual Merit”. This subsection covers the science, that is, the meat of the proposal, and it is the part you are used to writing when submitting a research proposal. And then there is another subsection that is required for all proposals submitted to the NSF. This subsection is called “Broader Impacts”, and I’ll mention a few words about broader impacts, because this element probably is a little bit less familiar to

some of you. There are four general domains of broader impacts: One is training the next generation. You may be engaged in training the next generation above and beyond what is your job description. The second domain is engagement in activities that increase the diversity of the scientific workforce. The third is activities through which you try to bring the science to the general public, basically, public science education. And the fourth domain concerns the societal impact of the proposed science and how it benefits society. So, the broader impact section is the section in which you describe what the broader impact is of the work that you do, including in the context of training, educating the public, diversifying the workforce, and the benefit to society. If if you submit to the Functional Genomic Tools track, you also have to include a third named subsubsection, which describes the impact of what you are doing on the research community. Basically, spell out what is the bottleneck that you will overcome with the tools or technology you are proposing, and how overcoming that bottleneck will catalyze science in the target research community.

SLIDE 10: Floh
One of the submission elements is called supplementary documents, and here we want to highlight a few of those supplementary documents. Regardless of which type of proposal you submit, if you submit from more than one institution, in the NIH language, if it is a multi-PI type of proposal, then you have to have a Project Management Plan. We would like to know how you are tackling the problem of coordinating across the institution and across the different investigators. If you are submitting to the Functional Genomic Tools track, you also need to describe how you will disseminate the technologies you are developing among the community and how you will educate the research community to use your tools or technology. Furthermore, if you use human subjects, we need to know something about the human subjects protection, and if you use vertebrate animals, then we would like to know something about the procedures related to the vertebrate animals. Regarding the vertebrate animal section, please see: https://olaw.nih.gov/guidance/vertebrate-animal-section.htm. Finally, all NSF proposals require a Data Management Plan. Something equivalent also is required for NIH proposals. We ask you to describe how you manage the data, how you store it, how you preserve it. You can find out more about the various submission requirements for this solicitation not only in the solicitation document itself, NSF 21-564, but also in a document called the Proposal and Award Policies and Procedures Guide 20-1.

SLIDE 11: Floh
I'm continuing with submission requirements. We allow Letters of Collaboration where collaborators are individuals that are not co-PIs but individuals who contribute something to the project and their contribution is described in the Project Description. However, they are not co-PIs or, in the NIH sense, co-Investigators, in that they do not submit a budget. The letters from these collaborators need to follow a particular format that is quite different from the NIH format. The prescribed format is described in the Proposal and Award Policies and Procedures Guide. The NSF does not allow Letters of Support. So, if you typically submit to the NIH, the kind of Letters of Support you submit for fellow scientists must not be submitted to this solicitation. Now, I'll talk briefly about budget and project duration. Regarding budgets, the maximum you can request for direct costs is 2 million dollars. So, if your proposal is a multi-institution project, the direct costs combined across all participating institutions shall not exceed the maximum of 2 million. Of course, that does not mean that you have to request 2 million. The request should be commensurate with the science you propose. There also is an upper limit for the project duration, and that limit is 4 years. As is the case with the budget, the duration should be commensurate with what you are proposing. It is perfectly fine to submit a proposal for a two-year project and a matching budget.

SLIDE 12: Floh
We now are switching to review criteria. It probably is of interest to you to know what questions reviewers ask about your proposal, that is, what the instructions are that reviewers receive, and what they likely will pay attention to. Well, they will be asked to evaluate all components of your proposal, including both the intellectual merit and the broader impacts. Thus, they will evaluate the potential of the work to advance knowledge and the scientific field, and they will evaluate the potential of the broader impact activities to benefit society. Overall, the review criteria are very similar to the NIH review criteria. There are five questions or criteria along which both the intellectual merit and, separately, the broader impacts will be evaluated. These questions are: What is the significance and the potential impact? Is it original and novel? Is it potentially transformative? Is the approach rational and well thought-out? Are mechanisms in

place to assess the success of the approach? Are the individuals qualified to carry out the proposed work? And finally, is the local infrastructure for the project to succeed in place, basically, are the facilities adequate for the proposed work?

SLIDE 13: Floh
In addition to the NSF standard review criteria, there are several solicitation-specific review criteria, meaning questions we will ask the reviewers to consider that are specific to this program. So, if your proposal was submitted to the Functional Genomic Tools track, then the reviewers will be asked to also comment on the potential catalytic impact for the organisms targeted in your proposal, and whether the tools you are proposing have the potential to have catalytic impact. They also will be asked to evaluate the dissemination and education plan. The plan for tool dissemination to and education of the community is an important aspect of Functional Genomic Tools track proposals. In the case of proposals submitted to the Complex Mutagenic Traits track, the reviewers will be asked to evaluate whether the proposed work gets at the question you propose to tackle and the question of causality with respect to genomes and phenomes, and whether you are really asking questions that target complex multigenic traits, and not traits driven by one gene. They also will be asked to evaluate whether the research you propose will advance the ability to predict, that is, the ability to go from genotype to phenotype in a predictive fashion. And then, as alluded to already several times, reviewers will be asked to evaluate the generalizability of the conclusions beyond the particular target organism of your proposal.

SLIDE 14: Jen
Yeah, so um, as Floh mentioned, and I'll be very brief, but I'm happy to answer follow-up questions either here or offline. But really the NSF review criteria and the NIH review criteria, in terms of how proposals are evaluated by reviewers, are very similar in terms of what they're looking for; we just have different language. And so there will be an NIH scientific review officer present at these reviews. And the reviewers will also be asked to address specifically scores in the NIH language for these criteria. And so first of all, there's the quality of the project management plan for multiple organizations working together and multi PIs working together to make sure that you have a good plan for that. And then specific review criteria. And these are also on our website, are the **overall impact score**, **significance**, which is how much does this move the field forward? How much do we learn if this if this is successful? The **investigators:** how qualified is the team to do the work they're proposing? **Innovation:** How novel is this? How new is the approach? How innovative is it? And then how practical is it? The **approach** is really: have you described well how what you are going to do is going to give you the answers that you say it's going to. Then the **environment** are the things that are necessary to get this work done. And then a few additional things that reviewers are asked to comment on again, if applicable, are the **protection of human subjects**. So, if you have human subjects, are you conducting that research ethically and appropriately? And similarly, **vertebrate animals**, so if at any point, during this process, you have live animals, how are you treating them? How many, what are the conditions under which you are doing this research, and is it justified to use those animals in this way? Similarly, biohazards and budgets, periods of support, are those appropriate for the work? Our reviewers are asked to comment on this. And that's all I've got for you.

SLIDE 15: Floh and Jen
Some of you may wonder, and, in fact, we have received some questions on how is the process actually is going to work? So, briefly, here is the process at a glance. You will submit the proposal to the NSF following the instructions as provided in solicitation NSF 21 546. The proposal review will be managed by the NSF but in consultation with NHGRI, something that hopefully transpired from what Jen just went over. Then, the NSF and NHGRI will work together to identify meritorious proposals that they think are appropriate to recommend for support. If it is a proposal that the NSF would like to support, then we will handle and continue the process as we usually do when a proposal is submitted to the NSF. That is, we will follow standard NSF procedures. If the proposal is one that the NIH would like to support, then you will be contacted and invited to submit the proposal as a R01 proposal to the NIH, as you would when you normally submit a R01 proposal to CSR. Jen, do you wish to add something to that step?

Yeah. J just to be very clear, it will not be re-reviewed, it will not go back out to a review panel. The scores will already have been given. However, it will be taken to our NHGRI Council prior to funding for our second level of review, as are all NIH applications.

And just a reminder, there is a deadline. We are stressing this point because in the past few years, the solicitations of the EDGE program did not have a deadline. The deadline is 16th of March, 5pm local time.

SLIDE 16: QUESTIONS & ANSWERS
Please see the email address where you can contact all of us. And, as mentioned earlier, send us a brief summary of your project if you are not sure whether or not your ideas are a good fit for the program and which of the tracks would be the appropriate one.

The first question is: "Will the slides be shared later?" Yes, they will; the slides as well as a transcript of this webinar will be posted on a website to which you will have access through the EDGE program page shown here on the slide. And we hope that that information is available in a couple of weeks from now.

The next question, which Steve will answer, is: "Does EDGE support genome-scale research for agriculturally relevant animals?" My name is Steve Ellis. I'm a program officer in the Division of Biological Infrastructure, a member of the EDGE working group and I used to do my research in Dairy Science and lactation physiology. So, I do appreciate the question very much and I will let you know that NSF is really species agnostic. The answer to the question is "yes," we can support this kind of research with agriculturally relevant animal species, but the whole point is to make sure that whatever system you select for your studies and investigations, you should explain and justify the strengths of that experimental system that make it the appropriate one to ask your research questions. If you think about it in terms of Krogh's Principle, you should be matching the experimental system to your question. Or, if you already have picked your system, then make sure you use the right questions for it. But broadly speaking, we have no species bias against any agricultural animals or anything else.

The next question, which Steve will answer as well, is: "Why are bioinformatics tools not considered part of the Functional Genomic Tools component?" In part, it's because we have a standalone program that can support activities like that, I will paste into the chat button, a link to the DBI Innovation Program, where we have a program track specifically for bioinformatics tools development [see: https://www.nsf.gov/funding/pgm_summ.jsp?pims_id=505459&org=DBI&from=home]. The tools can address a broader community, not just those that are underserved by current resources. The EDGE program was designed to enable a broad and diverse group of experimental systems. The bioinformatics tools tend to translate across kingdoms of life. So, we have a standalone program that regularly has panels, and can review all the tools. We have the Innovation program for new tools and new ideas and new algorithms, and the Capacity program for expanding and distributing the established bioinformatics tool resources.

The next question, which Ted volunteered to answer, is: "NSF and NIH have different indirect cost limits to FFRDCs. Which one should apply to this application? The most restrictive?" This is an NSF-lead program. So, you should apply as though you are applying to NSF. If your project is one that is recommended for an award and this award will be picked up by NHGRI, we will have a discussion about how to resubmit the proposal to NIH as an R01. Jen, do you have anything that you'd like to add to that?

Yeah, I was going say so this might be a good time to address one of the other questions, which is, is there an easy way to reformat an NSF proposal to NIH format? Or is there a lot of rewriting involved? And so I, you know, I wouldn't call any grant submission "easy" to any agency. What we don't want you to do is rewrite the scientific content of the proposal. So yes, there is reformatting of budget requests, and perhaps some recalculating of your indirects and things like that, that will need to happen to have it fit on to the NIH forms, but the body of the application should remain the same, the amount of money that you're requesting and direct costs should remain the same, because that is what was reviewed. I hope that helps.

The next question is: "Are international co-PI is receiving a portion of the budget allowable? That is, I think NIH will send funds overseas, but NSF will not (correct me if I'm wrong) - with NIH involved, which agency's budget rules will apply in this case?" As Ted just mentioned, EDGE is an NSF-led activity, and NSF does not send money directly overseas, colloquially spoken. However, subawards can be to

organizations in foreign nations. There has to be a very compelling rationale why the subaward has to go to foreign organization, that is why the contribution from that organization cannot be achieved within the U.S., such as when the appropriate expertise is not available in the U.S. And there are restrictions on what can be included in the budget of a foreign subaward. Typically, the budgets [of foreign subawards] are smaller.

The next question is: "Can these grants be led by PIs at National Labs?" Researchers from national labs cannot serve as PIs. However, some National Lab researchers also have appointments at universities or institution that are eligible to apply. Also, subawards can be made to National Labs, but there has to be very strong argument why the expertise provided by the National Lab is critical and not readily available elsewhere. As mentioned earlier, the Proposal and Award Policies and Procedures Guide (PAPPG) is an incredibly useful resource, and we encourage you to look up exactly that question. You can find more details on this matter in the PAPPG document.

The next question is: "I am a little bit confused about the review process. Will it be reviewed by a combined NSF/NIH panel? It seems like it will be sent to NIH after NSF reviews? How will funding decisions be split" We will certainly take recommendations for reviewers from the NIH. This is a partnership activity. However, the review process is managed by the NSF. And decisions will be made jointly afterwards and reflect the interests of each of the two agencies.

The next question, which Jen will answer, is: "My proposal is solely plant oriented and I don't see any relationship between my project and the objective of NIH. Do I still have to consider NIH criteria in addition to those from the NSF?" Yeah, so the answer to this is that actually, so there are additional criteria that reviewers are asked to consider. You are writing for the reviewers. But if you don't have human subjects, if you don't have vertebrate animals, you do not have to consider those and the standard review criteria of NIH are very similar to those of NSF, just we'd have specific language and they each get a specific score. So, this is all going to happen. After you submit it, the review is going to take it and look at all those criteria. But you should just be writing the best proposal you can for this funding opportunity, given the science that you're doing, you should not be writing it specifically for one agency or the other, just write it for the call.

So I'll add there was a related question by another panelist; "For clarification, is the entire plant kingdom out of scope for this program?" It is definitely not out of scope. We do absolutely expect encourage and will welcome plant related proposals as well. I should have been more complete in my prior answer about the agriculturally relevant animal species. We do have another core program, the Plant Genome Research Program (PGRP) that is set up to support projects that involve agriculturally relevant plant species and some others. But the EDGE program can support development of systems or complex multigene trait analyses in some less enabled plant species. So, in that sense, consideration of proposals focused in plants are definitely welcomed.

Yeah, and I would want to point out that, and this is a good place to answer the question: "Is there a place where we specify if the proposal has been written to fit the NHGRI scope?" And there was also a question: "If the project is entirely health related, would NSF consider it, that is, would this program be an appropriate place to submit to?" I think that NIH has a lot of good funding opportunities for specifically health related research. And so, contact us if you're not quite sure about your proposal, but what you want to ask is, does your science fit this call, and if it does, submit it with all the relevant information, and NHGRI will decide if we are interested in funding meritorious applications? You don't have to be deciding that upfront. So, don't write it specifically for our scope, right for the scope of our calls. Write for the scope of this funding opportunity.

The next question, which Jen will answer as well, is: "Is there an 'easy' way to reformat an NSF proposal to NIH format or is it a lot of free writing involved?" Yeah, so I hope I will say it again, "easy" might be overstating it. What we want is minimal rewriting when you do resubmit, only to change the format not to change the content. So, you will be required to put in all the information that is needed for NIH application and funding and when we invite you to apply, we will make sure you have all the information you need of what should and shouldn't change. But I will also note that when you are invited to do that rewriting your

proposal is on its way to Counsel. So, we've decided we will only contact you to rewrite for NIH [if we are recommending it] if we are going to be making a recommendation. So, it's probably worth the effort in the rewrite that you need to do

The next question, which Ted will answer, is: "Do all proposals in this call need to be related to NIH or can they be broader scientific research?" I feel like that's been answered. I mean, this is focused on the generalizability points that we bring up. And so I feel like Jen addressed that.

The next question is: "What is the difference between Letters of Collaboration and Letters of Support?" Letters of collaboration in NSF format are letters that literally consist of one sentence affirming that you will be participating in and offer your expertise to support the project, should it be selected for funding. As the PI, if you solicit such a Letter of Collaboration from a collaborator, be sure to mention the collaboration in the project description. So, submitting a Letter of Collaboration from an individual whose contribution to the project is not described in the Project Description does not make sense. Letters of Support, that is, letters that are more like letters of recommendation, the NSF does not allow to be included, as specified in the solicitation.

The next question, which Ted will answer, is: "I have a question about fit for EDGE versus a regular NSF program? For instance, NSF IOS versus PSS which stands for physiological structural systems. Should I send a one pager BIO in creed just through the bio edge alias that we mentioned earlier, or also to the program officer, in this case PSS program?" I've been typing into most of these just that. Please send us one-pagers. And I just flagged that question so that it would get read out loud to send us one-pagers if you have questions about fit. If you've typed something about that into the chat that relates to specific projects, I've been putting that in so I'd say to Andrew asking the question, please send us a one-pager, and we will be happy to talk to you about fit. Yeah, and the other thing that I would just add, I know that this is true on the NSF side and on the NIH, if you send us that on- pager and we think that it's more appropriate for another program, we can put you in touch with those program directors as well.

The next question is "Is this program just for basic science departments and universities and biased against medical schools?" The answer is No. It depends on the science that is proposed, and there is no bias against proposals from medical schools. There is a related comment from the audience stating that "The historical record of previous EDGE awards all went to basic science departments and Not any medical school departments, yes?" If that is the case, then it is coincidence and not the result of a specific plan. It is the proposed science that is relevant, and not the type of institution or the department within the institution.

The next question, which Ted will answer, is: "Are the budgets comparable for proposals considered by NIH versus NSF?" Yeah, so the budget, the budget details are outlined in the solicitation. The budgets are comparable to previously funded projects out of edge and at some level NIH as well. Additionally, as was stated earlier, they should be in comparable with the scope of the project that is being proposed.

The next question, which Jen will answer, is: "Can the project focus on cancer?" So, this is another one where I would say write a one pager. And it really depends on what the goal of the project is. What your scientific scope is. So, we're not we're not saying no, but we're not saying yes, at this point, either. It depends on what you're proposing.

The next question, which Ted will answer, is: "Even though I'm not at a primarily undergraduate institution, my lab is undergraduate driven. That is, the person has no Ph D. students. Do you feel a program such as EDGE would be relevant to us, if all other aspects are equal?" Yes, the program would be relevant to you. We fund projects that have/that are run primarily by PIs with undergrads all the time at NSF. And it's just demonstrating that you can pull off the project with the staff that you have included in your lab.

The next question, which Diane will answer, is: "I would like to clarify the question regarding other culturally relevant species. Is there an EDGE type format for PGRP? Would PGRP fund methods to

develop functional genomic assays in high throughput without a hypothesis (i.e., for maize, soybean, or tomato)?" So, I'm Diane Jofuku Okamuro and I am a program officer in the Division of Integrative Organismal Systems, PGRP Cluster. Yes, PGRP actually has a tools technology and resource development track, **TRTech-PGR.** This track supports the development of functional genomics resources for plant species that have agricultural relevance - it is up to you, the PI, to make the case that providing these tools will give us new insight into processes that will relate to the bioeconomy.

The next question, which Ford will answer, is: "If bioinformatics is critical to the approach to be successful, and it is hard to envision when this would not be true, is it considered a plus to the overall mission or should this aspect not be elaborated in the proposal?" So I'll introduce myself briefly, I'm a program officer in the Division of Environmental Biology. Like with any other part of the research plan, you should include enough of the detail, so that it's clear to a reviewer what you're trying to do, and whether or not you're going to be able to achieve it. I wouldn't over-emphasize or de-emphasize an approach or method in an effort to be strategic. Keep the solicitation-specific criteria in mind, and make sure you're addressing them adequately. And if particular bioinformatics methods are critical for you to achieve your aims, you should be able to make a compelling case for using them.

The next question, which Ted will answer, is: "Besides the partnership of the NIH and the fact that they have some additional related criteria of interest to them, and the existence of two tracks, how has the mission and review criteria of edge changed relative to previous years? For instance, are the characteristics of a successful proposal from three to four years ago the same kinds of things EDGE is currently seeking to support?" The program has changed significantly from three or four years ago, when it was only focused on the development of genomic tools in emerging model systems. In the last year the CMT track was added to the solicitation, and this year the solicitation has changed very little except for the addition of NIH/NHGRI. Proposals funded over the last three to four years in EDGE will look like the functional genomic tools track and not the CMT track as this is only the second year for this track. But relative to proposals that came in last year, the solicitation has not changed much. Changes to the solicitation are a greater emphasis placed on generalizable results throughout the solicitation, and in the CMT track we now allow the use of traditional model systems with strong emphasis on the word generalizable.

The next question, which Ford will answer, is: "Can a foreigner working as a full-time research scientist at a US university submit the application as a PI?" If your university can be awarded an NSF grant, then your university must give you permission to serve as a PI on a grant. You should talk to someone at your Sponsored Programs Office about obtaining PI status at your institution. Your nationality is irrelevant to whether you can serve as PI.

The next question, which Patrick will answer, is: "How many proposals will be funded in the first EDGE cycle [under the current solicitation]?" Yeah, like Ford. I'll use this question as an opportunity to introduce myself. I am Patrick Abbot, I'm rotating program officer and iOS in the behavioral systems cluster as well as the edge working group. And in terms of numbers, of course, it depends on how many proposals we receive. And one thing I will say both as a program officer as a PI that funding rates have been encouraging in recent years. And so, I would say, please submit in that kind of optimism and hope that I would have as a PI in the current environment. So, it really depends on how many proposals we receive, but I would definitely reach out if you have a question about suitability, send a one pager. And then if you get a positive response, and encouragement from the EDGE working group, or from one of us, please do submit.

The next question, which Steve will answer, is "There's a possibility that a proposal would integrate and target two suggested tracks, what is your advice for such proposal?" Thank you. The very short answer to this question would be to remind you that we have two tracks for a reason. We think that there is a requirement for sufficient detail and supporting rationale in either track to occupy the full space available to you in the Project Description and other parts of the proposal. If you start to blend categories, for example, if you need to develop a tool that is high risk or hasn't been done, and then you need that tool to answer your complex multigenic trait question and your hypotheses, you really submit a proposal with

interdependent aims. Reviewers tend not to like such proposals because of increased risk and suspect feasibility of your project if you submit it that way. It might take a few years to really develop the technique anyway. So, you might be better off starting with a more focused proposal that addresses the necessary elements for developing a tool and then come back with more preliminary data and a proven method. This is not a one-time only program. We expect to be here for several years. So, please come back or focus around testable hypotheses for your complex multigenic traits. But what you want to avoid is submitting a proposal that has inherent flaws and feasibility problems. My other colleagues may wish to comment on that as well.

Ted: I agree with that. Hybridizing the tracks is not generally a good idea because it tends to generate interdependent aims.

The next question is: "Can someone comment on the amount of preliminary data required for a competitive proposal? Since the lab has been in COVID lockdown for almost a year, little data has been collected for the anticipated proposal." As you probably know, preliminary data is a very useful weapon, for lack of a better term, to address concerns from reviewers. Preliminary data demonstrate the technical feasibility, and typically also the conceptual feasibility. Also, you can use them to demonstrate how you will move from the data to the conceptual question that prompted the work in the first place. It is hard to envision how a proposal without any preliminary data will be compelling. We appreciate that, given the situation for the past 12 months, preliminary data may be less extensive as all PIs would have liked, and so you are competing against other individuals who have been in the same challenging situation. It is not the case that because of COVID, preliminary data are no longer required. And you will be reviewed by reviewers who have been in the same situation.

The next question, which Ted will answer, is: "Is there a template/required format for the one pager project description?" There's not. What we need is enough detail to evaluate what it is that you are proposing to do in the in the project and in the broader impacts. There is not a template but we just need enough detail so that we can evaluate the fit to edge or the fit to other programs that we might be guiding you towards.

The next question, which Anthony will answer, is: "Would developing a high-quality reference genome as an initial step be considered to fall under Track 1, or could that be incorporated as an aim in Track 2?" I should introduce myself first. I'm Anthony Garza and I'm a program director in the Division of Molecular and Cellular Biosciences. Based on what you wrote, it seems that the project would fit in Track One. It would be helpful to have a page describing the project detail, though. I would say in general projects should fit in either track one or track two. And don't craft projects that aim to fit in both tracks.

This concludes the EDGE webinar. If you have questions, please keep in mind that you contact the EDGE program directors at the alias bioedge@nsf.gov, and you can send us a one-pager, so we can give feedback on program fit and pointers with respect to the two tracks. Thank you for joining the webinar.