00:28:59 Angelica Johnson: Welcome to ELSIconversations! We are glad you will spend the hour with us. We ask that all attendees please abide by the code of conduct, which can be found here: https://elsihub.org/news/code-conduct

00:30:06 Angelica Johnson: This Q&A/networking event will last approximately one hour

Use the "Raise Hand" zoom feature to speak or enter your questions/comments in chat. Remember to lower your hand after you’ve been called on

If you require assistance send a direct message to Dounya Alami-Nassif in this meeting or email info@elsihub.org

00:30:52 Angelica Johnson: Join the ELSI scholar directory: https://elsihub.org/form/submit-scholar

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00:34:04 Angelica Johnson: Moderator: Shoumita Dasgupta, PhD

Biography: https://www.bumc.bu.edu/busm/profile/shoumita-dasgupta

00:34:21 Arupa Ganguly: Someone is not muted giving rise to lot of background

00:35:08 Angelica Johnson: https://jamboard.google.com/d/1XXM387ElPadB1K3LUTR\_a7moDrfL8DR19BKyYofRizg/edit?usp=sharing

Please exit the Full-Screen view on Zoom and minimize the application before pulling up the Jamboard session on your web browser.

00:41:37 Angelica Johnson: Speaker: Julia Gimbernat-Mayol

Biography: https://www.linkedin.com/in/juliagimbernat/?originalSubdomain=uk

00:42:10 Michelle Takemoto: In the Minority Genetic Professionals Network registration form, we have both a multiple choice question, and then a follow up question that allows members to describe their own identity.

00:46:27 Angelica Johnson: Speaker: Carlee Dawson, BA

Biography: https://elsihub.org/directory/carlee-dawson

00:47:59 Sankalpi Carey: I prefer the combination of MC and f/u question - lot more common to have mixed races (ie. South Asian and Caucasian, at a loss when limited to choices)

00:50:33 Angelica Johnson: Speaker: Dee McKnight, PhD

Biography: https://clinicalgenome.org/about/people/staff/mcknight-1665

00:57:28 Elizabeth Fieg: I would love if Invitae could remove 'Caucasian' as an option to select on the test req (Dr. Popejoy happens to have a great paper on this!). It's currently 'White/Caucasian', I think 'White/European' would be much better. I do appreciate that providers can select multiple options for a patient

00:58:49 Shoumita Dasgupta: Yes, Elizabeth, it was a great article which is available here https://www.nature.com/articles/d41586-021-02288-x

01:00:00 LaKisha David: Carlee Dawson mentioned that there is a psychosocial impact for some when asking about ethnicity/ancestry. Could you speak more about this impact?

01:00:23 Bob Cook-Deegan: How do categories from other jurisdictions map to the US categories? How do you manage that? And how do you map your categories to the (sometimes weird) populations labels in gnomAD?

01:00:40 Gabriella Ryan: From Invitae's experience, can you speak to the degree of coverage for genetic testing by payers?

01:01:56 Mildred Cho: For people who collect both multiple choice and open ended data, how do you analyze it?

01:03:12 Rose McGee: +1 for LaKisha David's question

01:03:13 Alice Popejoy: I would love to know from the audience what information is really essential in clinical genetics (if any)?

01:03:56 Mildred Cho: Also, is lab REA data recorded in an electronic health record, and what happens if it is discordant w/EHR data?

01:04:51 Alice Popejoy: RE: Carlee’s findings from our workshop at the WI Genetics Exchange — these examples were reported by (mostly) genetic counselors in the Midwest US.

01:05:08 Gail Henderson: these talks demonstrate the diversity in labels used, which is really important, but doesn't that negate any clinical utility?

01:05:47 Nikita Mehta: I just wanted to add on from the lab perspective, that I think while we REA data is agnostic for variant classification, there may be more nuance here. I want to point out that calculations for whether or not a minor allele frequency of a variant is higher than expected for a disorder is based on incidence estimates that are often specific to one ancestral group (often defined by race or ethnicity in the literature). I also will say that I do find utility in seeing a matched ethnicity between a variant that I suspect is neutral and the population in gnomAD that has the highest frequency (especially if it's the only population).

01:06:12 Kate Garber: Related to the gnomAD question - remember that testing labs are not trying to match the tested individual’s REA data to the subpopulations in gnomAD, as Dr. McKnight said. Rather, the gnomAD data are split into different supopulations to make it more powerful. If all the data were lumped together, you would average out variant frequencies, rather than being able to see high local frequencies in certain ancestral groups. The highest subpopulation frequency is what we use in variant interpretation and it is used regardless of the tested individual's REA data.

01:06:36 Anna Lewis: Question for Dee on the polygenic scores differential performance: will you put individuals into genetically inferred continental ancestry categories and give them the risk associated to that category, or do you have a way to avoid putting people into a large category at all?

01:06:41 Charu Kaiwar: Dee' slide on how labs are using this data is important. My take away message from that is the information is not being used for any clinical decision making process, except for risk assessment., which can be done in the clinic, if the lab provides data that is available for the various populations? So why is it on laboratories to collect this data?

01:07:10 Alice Popejoy: Adding to Mildred’s question — If there were an informatics tool that clinical labs could use to map free-text/open-ended responses as well as multiple choice categories onto a single data structure that could be leveraged for analyses, would there be interest and feasibility in using such a tool?

01:07:21 Gail Henderson: that's helpful -- but of course we are worried about all the implications described in this session

01:07:59 Laura Duque Lasio (She/Her): For Dr. McKnight — I really appreciated you saying that information in requisition forms as much as we'd like to say its "self-reported" we do not know that. its whatever the person filling out the requisition found (either from genetics notes or just demographic info from the chart)

01:08:52 Mildred Cho: +1 @Gail, also implications/utility for researchers

01:09:03 Gail Henderson: absolutely

01:09:43 LaKisha David: What is the process to change the forms?

01:10:35 Alice Popejoy: @LaKisha that is the topic of our next session on 05/20 🙂

01:11:09 Alice Popejoy: Here is the link to register: https://us06web.zoom.us/meeting/register/tZ0rdu6gqzouHNXLuLXGo-tYsYtJHNL8KHis

01:11:21 Michelle Takemoto: @Mildred, since our data collection is not for clinical purposes, we haven't done much analysis of the "other" and free text answers. We offer those options so that our members have the opportunity to share more about their identities. It's been interesting seeing how many people don't fill out the open ended option, or provide very minimal information. I suspect that in the US context people are not accustomed to being offered that option and don't know how to answer. The majority of our members are under 30, or even 25, and anecdotally, many are wrestling with their own identities. Our data is not gathered in a clinical context, but can inform the ways people answer these questions in clinic

01:14:05 Alice Popejoy: @Michelle It’s interesting that you’re not finding many people who use the free-text option. Have you tried flipping the multiple-choice and open-ended questions, so the open-ended question appears first? I’ve piloted this and found that the order of these questions (and how they’re worded) influences whether people enter free-text info. Also, those who identify as ‘white’ tend to use the free-text option less often, so that may explain part of your observation.

01:15:16 Joanna Bulkley: For a PRS, self-reported REA could have an impact, but not through genetics. Due instead to variation of lived experience related to REA.

01:17:28 Michelle Takemoto: @Alice, this discussion has me rethinking the order of those questions! The vast majority of our members are non-white, quite a few are of mixed geographical and cultural identities. We do also give the opportunity for multiple entries in the MC question. (Apologies for being off camera, before 7a here in Honolulu!)

01:19:30 Mildred Cho: https://www.aap.org/en/news-room/news-releases/aap/2022/american-academy-of-pediatrics-calls-for-elimination-of-race-based-medicine/

01:19:45 Dave Kaufman: Alice given that changing the order changes the answers is there an objective sense about which order is 'better', given the plusses and minuses of both data types?

01:20:22 Alice Popejoy: @Michelle Thank you for sharing! And no worries — we all have logistical constraints (myself included, today). If it’s helpful, I can share the way these questions have been asked on the ClinGen survey as well as a pilot study I’ve been running to collect open-ended descriptions of “race”, “ethnicity” and “ancestry” over the last 4-5 years.

01:21:34 Mary Relling: In pharmacogenetics, one can't interpret the main genetic tests without knowing "race," because 2 genes are adequate in "whites" but a 3rd gene must be added for "blacks" in order to avoid giving a bad recommendation on warfarin dosing. (But I believe this is the only example in Pgx).

01:21:35 Michelle Takemoto: @Alice, thank you, We would love to see that.

01:21:38 Anna Lewis: Whenever we emphasize genetic ancestry, we emphasize the significance of biological differences between groups. Which history tells us is a dangerous path.

01:22:37 Elizabeth Fieg: Geographical ancestry is also complex because borders change (#abolishborders)

01:22:51 Charu Kaiwar: Thanks for the discussion everyone, have a great day.

01:22:57 Alice Popejoy: @Dave I’m not sure there is an objectively “better” way to collect this information; it just depends on the goal of the investigation. For my methods development work, I care more about how people would describe their REA (and sex and gender, by the way) when given an open-ended option to self-identify. We follow up with the MC question to see how they typically identify on forms in the US. So, in that sense — the order preference of my work is based on the US context in which people are accustomed to checking a box (or boxes). In other countries, the categories wouldn’t make sense.

01:23:45 Milton Datta: From a practical clinical aspect, in the US healthcare systems are not using race in the EMR. For genetic testing in clinical decision making we use the gene agnostic approach like Invitae. If there is a patient interest with respect to race/ethnicity we use a personalized shared decision making approach led by our genetic counselors. Often social determinants of health are more important than race/ethnicity. We are well aware that having genetic testing results are biased towards high economic status.

01:23:48 Anna Lewis: (A group of us reiterated these and some other points here: https://www.science.org/stoken/author-tokens/ST-437/full)

01:23:56 Shoumita Dasgupta: Getting genetic ancestry right for science and society https://www.science.org/stoken/author-tokens/ST-437/full

01:24:03 Shoumita Dasgupta: From Anna Lewis and team

01:24:25 Elizabeth Fieg: IF we are to continue collecting REA data, is there value in labs doing/offering a chip assay to calculate genetic ancestry to at least have somewhat of a consistent, objective measurement?

01:25:09 Nikita Mehta: Perhaps if our comparison in variant interpretation is to these pre-defined continental groups, even taking out the REA question wouldn't really solve the problem.

01:25:42 Alice Popejoy: It sounds like there are large differences among participants here (~90 people) in beliefs and practices about the clinical utility of REA for variant interpretation. While some are saying it is necessary, others don’t use it. Fascinating!

01:26:25 Michelle Takemoto: I appreciate the way that Diana described that Invitae is using the data on ancestry, not using it to make clinical decisions. I do still think that having some "genetic ancestry" data is important, no matter how flawed. It is important in terms of the discovery of founder mutations as she described. Things like that may affect medical management for specific communities.

01:26:28 Alice Popejoy: For our continued work toward the development of guidelines for REA in clinical genetics, we certainly have our work cut out for us. And we need all hands on deck! Thanks so much to everyone who participated today, and we hope to see you on our next ELSIconversation!

01:26:47 Nikita Mehta: I will clarify that I don't think it's necessary. I can certainly do without it. I loosely think that it might help us with resolving VUS in non-European groups, but I don't know how likely that is. It may not be worth getting the data compared to the harms it causes.

01:27:25 Angelica Johnson: We invite you to register for our next ADWG ELSIconversations session - Revisions to Demographic Representations on Clinical Lab Requisition Forms

https://us06web.zoom.us/meeting/register/tZ0rdu6gqzouHNXLuLXGo-tYsYtJHNL8KHis

We would appreciate your feedback. Please fill out our survey to discuss your experience and to make suggestions for topics and speakers:

https://cumc.co1.qualtrics.com/jfe/form/SV\_9SjVJonotBAQJBY

01:27:29 Alice Popejoy: I would love to find out moving forward what information we would collect in a perfect world — what is it that we REALLY need? Because the current categories aren’t working.

01:27:38 Gail Henderson: Following up on the Pediatrics guidelines, Nancy Cox gave a talk at the NHGRI symposium recently about disparities produced by testing for different 'race' groups

01:27:42 Michelle Takemoto: Perhaps responses from open ended questions can be put into a word cloud?

01:28:03 Alice Popejoy: @Michelle let’s follow up offline! Happy to show you what we’ve been working on.

01:28:22 Gail Henderson: thank you!

01:28:24 Jennifer Geurts: excellent work everyone!