Screen Shots of survey (https://www.surveymonkey.com/s/L8XYNCH)

Making Sense of the Sequence: Advances in Population Sciences

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Introduction

The National Cancer Institute (NCI) is planning a meeting titled "Making Sense of the Sequence: Advances in Population Sciences." The meeting is tentatively scheduled to occur May 15 - 16, 2013; however, we are still awaiting official approval from the National Institutes of Health (NIH).

On behalf of the meeting planning committee, we invite your responses to the five questions in the following survey. All responses will be anonymous. The combined responses will be used to help shape the meeting agenda and to guide working groups that will be convened prior to the meeting. We want to be sure that the meeting topics are timely and relevant.

The aim of the meeting is to advance the use of sequencing technologies in epidemiologic studies of cancer, and to enhance the integration of cancer genomics and somatic sequencing with population-based germline sequencing studies. The meeting will include speaker presentations, discussion sessions, and working group reports. The collaborations stemming from this meeting will lead to improvements of our understanding of the genetic architecture of cancer, and the biology and mechanisms underlying this complex disease.

The meeting will bring together experts in the field to discuss key emerging themes, including:

1) establishment of best practices for applying germline and somatic sequencing in population based studies;
2) integration of recent advances in cancer genomics, such as The Cancer Genome Atlas (TCGA), with sequencing studies in epidemiology;
3) identification of opportunities, challenges and resource needs for facilitating the interpretation and application of next generation sequencing in large-scale studies.

We would appreciate your response to this survey by (survey will be open two weeks) even if you will not be able to attend the meeting.

Please don't hesitate to contact us if you have any questions about this survey, or this meeting.

Thank you,

Tiffany Green, M.H.S., M.P.H., e-mail: greentif@mail.nih.gov
Carolyn Hutter, Ph.D., e-mail: huttercm@mail.nih.gov
Leah Mechanic, Ph.D., M.P.H., e-mail: mechanil@mail.nih.gov

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Please answer Questions #1-5 below.

1. Other than time and money, what would you categorize as the most significant obstacles to applying existing next generation sequencing technologies in epidemiologic studies of cancer?

2. What would you categorize as the primary barriers or resource needs to facilitate the interpretation and application of next generation sequencing in large-scale studies of cancer risk?

3. What would you categorize as key unanswered questions that can be answered through integration of germline and somatic data in a population sciences setting?

4. Given the meeting goals, what are topic areas you would like to see included in the meeting agenda?

5. Given the meeting's stated goals, what are other specific issues or questions you would like working groups to address?

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Thank You

The meeting planning committee would like to thank you for taking the time to respond to these questions.

Please contact us if you have any questions about this survey, or the upcoming meeting.

Tiffany Green, M.H.S., M.P.H., e-mail: greentif@mail.nih.gov
Carolyn Hutter, Ph.D., e-mail: huttercm@mail.nih.gov
Leah Mechanic, Ph.D., M.P.H., e-mail: mechanil@mail.nih.gov

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