

A Decade with the Human Genome Sequence: Charting a Course for Genomic Medicine

Symposium Microblog Transcript

At 2011-02-07 19:46:12, [nihlibrarybioinformatics] said:

We're looking forward to the symposium on Friday.

At 2011-02-11 13:05:58, [benstanfield] said:

Good morning, everyone! If you need any help using the site today, you can let me know by sending me a message that includes @benstanfield, or you can use the hashtag #tech support. But before you can do either of those, you'll need to register with the site by visiting <http://genomics2011.com/main/register>. You can also sign in with an openID account if you have one. Just visit <http://genomics2011.com/main/openid>. You should receive an email asking you to confirm your email address a few seconds after registering. If you don't, it might be hiding in your spam folder.

At 2011-02-11 13:35:08, [lowercase] said:

Are speaker materials available?

At 2011-02-11 13:36:37, [lowercase] said:

video feed is stuck

At 2011-02-11 13:40:31, [larrythompson] said:

We are working on the webcast feed. Should be fixed shortly.

At 2011-02-11 13:48:28, [lowercase] said:

Please let us all know when to expect a working feed so we can go do something else.

At 2011-02-11 13:52:45, [drjonboyg] said:

Short speaker introductions. Good idea.

At 2011-02-11 13:53:24, [drjonboyg] said:

@benstanfield Is there a way to change my avatar in iOS?

At 2011-02-11 13:57:43, [benstanfield] said:

@drjonboyg Unfortunately, I don't think so. However, if you have a gravatar account, you can set that from an iOS device. Click on "account" at the top of the page, then email and make sure your email address is confirmed. Then click on "avatar" and at the bottom of the page, you can click "add" in the gravatar section.

At 2011-02-11 14:00:59, [tf] said:

what do people think of strategic plan?

At 2011-02-11 14:04:00, [ctls4cancer] said:

Perhaps linking it to funding levels would put more teeth in it

At 2011-02-11 14:06:01, [krisw] said:

@ctls4cancer The plan covers the entire field of genomics, not just what NHGRI might fund. However, efforts have already started at NHGRI to determine priorities and develop new initiatives.

At 2011-02-11 14:10:30, [tf] said:

i like the idea of a "grand plan" but would like to see more "arc to clinical" small projects. seems like significant benefits to health care should come far sooner than 2020...

At 2011-02-11 14:10:33, [manoli] said:

The video and audio are out of sync

At 2011-02-11 14:11:39, [manoli] said:

@ctls4cancer During the planning meetings, they very specifically asked us to not include funding constraints in the discussions, which was a challenge

At 2011-02-11 14:15:15, [ctls4cancer] said:

I'm thankful for Francis' big picture view of development

At 2011-02-11 14:17:15, [dnawriter] said:

@lowercase feed should be fine now.

At 2011-02-11 14:17:51, [dnawriter] said:

Also, speaker materials should be up on genome.gov later. Can't say exactly when.

At 2011-02-11 14:18:46, [bsw] said:

how can i view the conference? please help me get on!

At 2011-02-11 14:23:07, [krisw] said:

<http://videocast.nih.gov/>

At 2011-02-11 14:24:11, [bsw] said:

when i FINALLY get the video screen, it is black, and says "live broadcast - paused"; this is not changed by hitting any of the buttons. is there any way to see this conference? or is it not working for anyone? is there a phone number to call, to talk to an actual humanoid?

At 2011-02-11 14:28:10, [benstanfield] said:

@bsw The videocast currently has over 500 viewers, so it's definitely working for some people. We've gotten a variety of reports on the quality of the stream, from excellent, to audio out of sync, to picture refreshing only ever few seconds, but the stream is up and working for most people. The videocast team at NIH has a contact page here: <http://videocast.nih.gov/ContactUs/> with a section on #techsupport. They might be able to help.

At 2011-02-11 14:28:17, [manoli] said:

@bsw It's been working continuously here at MIT

At 2011-02-11 14:28:37, [bsw] said:

please, is there a phone number to call, to talk to a real person, to get help for logging onto this conference

At 2011-02-11 14:30:13, [drjonboyg] said:

My one issue with Moore's law and sequencing: Moore's law applies to transistors on a chip, the basic technology stays the same. Sequencing costs are coming down by moving to totally new platforms and technologies. Still, the end result is the same, I suppose.

At 2011-02-11 14:30:54, [manoli] said:

Cute green/yellow picture of coding vs. non-coding from the 4-yeast paper ;-)

At 2011-02-11 14:31:06, [benstanfield] said:

Videos of all of the talks will be archived and available for viewing after the symposium, so if you're one of the few unable to connect this morning, you'll still have a chance to watch all of the talks.

At 2011-02-11 14:31:07, [bsw] said:

@manoli - please - how did you get on? i get only a black screen saying paused

At 2011-02-11 14:32:09, [manoli] said:

@bsw If you click on this, it will open in a separate realplayer window
<http://videocast.nih.gov/ram/nhgri021111.ram>

At 2011-02-11 14:33:20, [drjonboyg] said:

@bsw Have you tried a different browser? Or restarting your browser?

At 2011-02-11 14:33:29, [bsw] said:

@benstanfield can you please tell me how to see something other than a black screen with no sound, saying pause

At 2011-02-11 14:35:38, [bsw] said:

@drjonboyg both Safari and Firefox give the same black screen, saying paused

At 2011-02-11 14:37:40, [krisw] said:

@bsw Try contacting the NIH Help Desk: <http://videocast.nih.gov/ContactUs/Default.aspx?bhcp=1>

At 2011-02-11 14:43:25, [benstanfield] said:

@larrythompson Webcast feed just markedly improved for me. Looks like things are getting better.

At 2011-02-11 14:51:18, [manoli] said:

Eric Lander making a very strong case for disease studies

At 2011-02-11 14:52:49, [manoli] said:

First explain the biology, then understand the heritability. Drugs can have strong effect despite small heritability. Parallel pathways change the denominator

At 2011-02-11 14:53:52, [dnawriter] said:

I could listen to Lander speak all day. He's like a really good PBS special.

At 2011-02-11 14:56:25, [alice] said:

Make sure to check out Eric Lander's article in this week's issue of Nature

At 2011-02-11 14:57:44, [manoli] said:

@alice <http://www.nature.com/nature/journal/v470/n7333/full/nature09792.html>

At 2011-02-11 15:05:14, [dnawriter] said:

fly genomics. cool.

At 2011-02-11 15:06:01, [manoli] said:

Very good question on analysis by Deana, answered by cost of sample preparation, storage, but computational biology aspect should be emphasized more

At 2011-02-11 15:06:40, [manoli] said:

Sean Eddy on comparative genomics and the Rosetta Stone

At 2011-02-11 15:07:56, [manoli] said:

"source code" to the wonderful creatures ;-)

At 2011-02-11 15:08:08, [tf] said:

why do speakers not thank/acknowledge funding sources... or did I miss?

At 2011-02-11 15:09:24, [manoli] said:

Eddy: celera coffee mug = viking enemy skull

At 2011-02-11 15:14:23, [wyattsgirl] said:

#NHGRI: Eddy- pattern of conservation is also informative.

At 2011-02-11 15:14:32, [krisw] said:

@tf I think the talks that have occurred so far weren't about specific work that the speakers have done under particular funding.

At 2011-02-11 15:15:10, [bsw] said:

@krisw thanks so much! that page gave phone numbers, one of which was answered by a live person, who got me to another person, who said the lines were over-subscribed, so were showing only black to us "extras". and they finally put on ore capacity. so i got on now. yay!!

At 2011-02-11 15:17:06, [krisw] said:

Genome scientists = computer hackers

At 2011-02-11 15:17:06, [manoli] said:

Decoding typed characters based on audio pattern of spacings. Neat idea, worth demonstrating

At 2011-02-11 15:18:00, [manoli] said:

Lagging strand more prone to deamination of C -> depletion on lagging strand

At 2011-02-11 15:18:42, [manoli] said:

Mutational biases have already been used for gene finding (FEAST)

At 2011-02-11 15:18:46, [drjonboyg] said:

RT @manoli Very good question on analysis by Deana, answered by cost of sample preparation, storage, but computational biology aspect should be emphasized more

At 2011-02-11 15:22:21, [manoli] said:

Surprising that no new structural classes were found (and a tid bit disappointing... could we have found them all??)

At 2011-02-11 15:26:23, [dnawriter] said:

Blast tool most important tool in comp biology...

At 2011-02-11 15:28:15, [manoli] said:

By the way, here's cracking typing by listening to keyboard:

http://www.cs.berkeley.edu/~tygar/papers/Keyboard_Acoustic_Emanations_Revisited/tiss.preprint.pdf

At 2011-02-11 15:33:10, [david] said:

The symposium video is now available in Flash, which should help with the sync problems, etc.

At 2011-02-11 15:33:25, [david] said:

Here's the Flash URL: <http://videocast.nih.gov/live-lb.asp?live=9981>

At 2011-02-11 15:37:16, [nihlibrarybioinformatics] said:

Nice graphic from Eddy of BLAST as an approximation to a profile HMM

At 2011-02-11 15:46:49, [themichaelbk] said:

@dnawriter Yes, same here. He's a rare example of someone who is simultaneously brilliant, enthusiastic and impassioned about his topic of expertise but can also make it accessible to the lay person. I thoroughly enjoyed listening to him speak.

At 2011-02-11 15:50:32, [dgmacarthur] said:

Ouch! Jennifer Wagner from Duke has a scathing critique of the NHGRI strategic plan, which she describes as an "EPIC FAIL": <http://bit.ly/fFoitG>

At 2011-02-11 16:08:10, [tf] said:

i don't see these talks (so far) as adding up to the title.

At 2011-02-11 16:12:55, [dnawriter] said:

@tf Most of the talks right now are about the last decade of research, but I think we'll see more about the future of genomics in upcoming talks.

At 2011-02-11 16:23:48, [nihlibrarybioinformatics] said:

Yes, Eddy's talk is the kind that inspires one to go back and read more of his papers.

At 2011-02-11 16:28:31, [nihlibrarybioinformatics] said:

Maybe we will be using some super fast version of HMMER more often than BLAST one day.

At 2011-02-11 16:32:31, [marivas] said:

fascinating findings on kindreds

At 2011-02-11 16:36:11, [wyattsgirl] said:

@dgmacarthur her view is clearly not one that looks at the entire strategic plan but one component... not sure that narrow analysis is fair to call the entire plan an epic fail

At 2011-02-11 16:49:11, [nihlibrarybioinformatics] said:

Regarding the kindreds, is Lifton's diagram of nine generations around a rectangle a common representation?

At 2011-02-11 16:55:52, [marivas] said:

it is an unusual kindred diagram...

At 2011-02-11 18:22:40, [dnawriter] said:

It's cool to hear a real patient's perspective. Good for you Rick Del Sontro

At 2011-02-11 18:31:33, [alice] said:

The panel has already alluded to some important current issues in genomics- return of results and confidentiality

At 2011-02-11 19:07:23, [genmol] said:

I see with very much concern, that a computer algorithm will interpret genetic results instead of a highly trained professional. Sometimes, not even these professionals can answer those questions, and most of the times those results are patient specific, thus very difficult to address. I do not believe that a web-based software would be able to give a real-life accurate interpretation of those results.

At 2011-02-11 19:10:14, [manoli] said:

Brad Bernstein on surveying human epigenomes

At 2011-02-11 19:22:07, [manoli] said:

Very nice intro to recent findings in epigenomics

At 2011-02-11 19:26:16, [manoli] said:

Clustering cell types using principle components of H3K4me1/me3/K3K36/H3K27me3

At 2011-02-11 19:28:34, [manoli] said:

ENCODE project 9 cell types x 9 marks

At 2011-02-11 19:45:21, [nihlibrarybioinformatics] said:

Bernstein's proposal to use epivenomic to triage variants found in GWAS studies seems very powerful. It could be useful in

At 2011-02-11 19:46:08, [nihlibrarybioinformatics] said:

It could be useful in many sequencing studies.

At 2011-02-11 19:47:50, [manoli] said:

@nihlibrarybioinformatics A public track with the chromatin state annotation for all nine cell types will soon be available on the UCSC browser

At 2011-02-11 19:52:46, [nihlibrarybioinformatics] said:

@manoli We look forward to telling our users about it.

At 2011-02-11 20:05:20, [tf] said:

While all these presentations have been brilliant, I continue to feel that today should be much more about going forward -- NIH, give me a better/brighter picture of real progress towards genomic medicine and a shift of investment/effort from mostly pure science to mostly translation to health care. When/how will we see genomics move the meters of mortality rates and health care costs? What can/should health care professionals and market players do to accelerate the advance? And can/how these investments spur economic development, new businesses, and non-government jobs?

At 2011-02-11 21:16:40, [beckerjes] said:

AGREED! More open publishing!

At 2011-02-11 21:23:58, [drjonboyg] said:

I don't know what Amy Harmon is talking about. NIH research has to be published as open access, or the papers have to be deposited in NLM's open access database by law (signed in 2007 no less):

http://www.sciencecodex.com/public_access_mandate_made_law

At 2011-02-11 21:33:02, [beckerjes] said:

@drjonboyg @drjonboyg There is a *lot* of research--not just in the genetics/genomics fields--that is stuck behind a pay-wall (almost anything published by Elsevier comes to mind...). I'm aware of the public access laws (and of Congress's attempts to repeal them) for NIH-funded research, but there is a lot more to be done. She has a very good point and I do not think it should be dismissed.

At 2011-02-11 21:38:26, [drjonboyg] said:

@beckerjes I have been as big an advocate for open access as anyone I know, all the way back to grad school in the 1990s. But it's just not factually correct to call NIH out for not using open access when there is a legal mandate to do exactly the opposite.

At 2011-02-11 21:45:46, [beckerjes] said:

@drjonboyg Not all research is funded by the NIH; not everyone is covered by the open access laws. My comment is more general, covering all of scientific research in general. I agree that the NIH is actually very good about this.