Past, Present and Future of Genomes, Environments and Traits: 140 Characters at a Time

by Dan Vorhaus

The first annual Genomes, Environments, Traits (GET) Conference took place yesterday. The GET Conference was an incredible success, with panels, breakout sessions and presentations from all manner of genomic pioneers and futurists, as well as a tremendous audience, both in person and online. In the next few days I'll share a few thoughts about what we learned at the 2010 GET Conference, as well as what we might expect by the time the 2011 event rolls around. There will also be video from portions of the GET Conference available soon.

In the meantime, if you missed the conference, there was plenty of live Twitter coverage. Everything I tweeted from @genomicslawyer can be found below, and there's much more at the #GET2010 twitter notebook. Thank you to all those who helped cover the conference online, including GET Conference pioneers (Rosalynn Gill, Misha Angrist), moderators (Carl Zimmer, David Dobbs, Dana Waring Bateman), journalists (Edward Winstead, Emily Singer, Kevin Davies, Aaron Rowe), sponsors (Priscilla Oppenheimer), exome sequence winners (Jonathan Eisen) and many, many more.

Now for Genomes, Environments and Traits in 140 character snips:

- And with that #GET2010 draws to a close (except for the cocktails). Thanks to everyone that joined us in person and remotely.
- #GET2010 voting on the winning exome sequencing right now...and the winner is @phylogenomics!
- Conde: showing demo of the @Knome consumer browser. Very slick interface, though it comes w/ hefty price tag #GET2010
- Conde: have come a long way from when they launched (at a price of $350k / sequence). Trying to build Rosetta Stone for genomics #GET2010
- Final piece of #GET2010: Jorge Conde of @Knome is giving away a free exome sequence. Winning idea to be selected by audience via live vote
- Detailed coverage of Ion Torrent winners at #GET2010 from @bioitworld: http://bit.ly/c1SuzZ
- First Ion Torrent winner: John Iafrate, Long Le from Mass Gen. Second winner: Mitchell Sogin from MBL at Woods Hole. #GET2010
- Rothberg: giving away machines for cancer, safe water research. Goal is to democratize sequencing in the same way as computing #GET2010
- Ion Torrent actually giving away a pair of machines at #GET2010. One for cancer sequencing in clinic, one for safe water detection
- Jonathan Rothberg, Ion Torrent: describing the machine he's about to give away. "Watson meets Moore" #GET2010
- Wrapping up a great #GET2010 conference. Awards presentations from Ion Torrent and @Knome. Will have live voting for exome seq coming up
- Enriquez: areas (e.g., Singapore) may not succeed if they are unwilling to tolerate difficult ppl. You need the right climate #GET2010
- Enriquez: moving from reading to copying to understanding to writing life code. And that will be a big deal when we get there #GET2010
- Enriquez: little labs that an build bridges will generate large economies. That's how we move economy, healthcare forward #GET2010
- Enriquez: one difficulty is scientists who continue to focus on research, not the bridges to commerce #GET2010
- Enriquez: describes Harvard as a "desert of an ecosystem," especially in comparison to MIT, Stanford, etc. Why is this? #GET2010
- Enriquez: why are certain places (MIT) so good at building this bridge, while others (Harvard, except HMS) are so lousy? #GET2010
- Enriquez: we need to grow the economy, which means we need to build a bridge to commercialize these technologies #GET2010
- Enriquez: genomics data is becoming so massive that it is beginning to drive large-scale industries (e.g., IBM, Intel development) #GET2010
- Enriquez: big companies - GE, Dupont, etc. - are leveraging this data. This is not all little startups #GET2010
- Enriquez: the growth here is spreading way beyond pharma, the way IT eventually mushroomed outward #GET2010
- Enriquez: if I was going to be investing in 10-15 years, I'd want to be focusing on the brain today. Will be big generator of cos #GET2010
- Enriquez: we now have single labs (eg Church) generating economies equivalent to small countries. This transition is disruptive #GET2010
- Enriquez: going to require exascale computing to manage data on this scale + ability to generate data surpassing ability to store #GET2010
- Enriquez: first zettabyte of data was generated by human species in 2009. Thinks single hospital will deal with that in 5-6 years #GET2010
- Enriquez: moved from human genome project (bounded in size, 3 billion bases) to an unbounded project: G+E+T. Much more complex #GET2010
- Enriquez: points out that the composition of meetings like #GET2010 is changing. Seeing ppl, companies we weren't seeing 2-3 years ago.
- Final Prototypes of the Future speaker is Juan Enriquez of Excel Ventures: "Bridges to Commerce and Other Dirty Words" #GET2010
- Q: have you looked for discrepancies b/w 23andMe, Illumina data? West: happy with error rate of @23andMe #GET2010
- Enriquez: moving from reading to copying to understanding to writing life code. And that will be a big deal when we get there #GET2010
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- West: now turns to sequencing. What data will that provide that genotyping didn’t? Describes process, consent to data #GET2010
- West: used raw data download feature from @23andMe. Huge dataset across family, analysis conducted in Excel #GET2010
- West: decided to use family genotye data to examine compound heterozygosity for DVT. #GET2010 (What qs were you asking at 17?)
- West: deep vein thrombosis as ex: diagnosis enables direct treatment, reduces risk. But not straightforward to measure. #GET2010
- Agreed. RT @phylogenomics: Anne West, high school student at #GET2010, is remarkably polished presenting before nobel winners, CEOs, etc
- West: starts by reviewing her family's medical background. history of Alzheimer's, heart disease, cancer, diabetes, etc. #GET2010
- Now up, Anne West (Harker High School) discussing her family’s whole genome sequencing (Illumina) / genotyping (23andMe) #GET2010
- Lincoln: need quality samples to get meaningful results. Low quality tumor samples = low quality results. Garbage in, Garbage Out #GET2010
- First q from @phylogenomics (from Twitter to #GET2010 floor). Unpublished genomes shouldn't count. Lincoln agrees w/ need for public genomes
- Lincoln: challenges: determining what data means (interpretation), determining what data to keep (storage) #GET2010
- Lincoln: learned a lot about DNA sequencing, cranking out data. The bottleneck is finding high-quality samples & interpretation #GET2010
- Lincoln: will be "shocked" if don't end 2010 with thousands of sequenced genomes. Thinks fully loaded cost (data+analysis) is $10K #GET2010
- Lincoln: accumulating lots of data that is not even being seen let alone interpreted Need quality, low-level algorithms to min data #GET2010
- Lincoln: humans don't just have one genome: cancer is a disease of genomic changes. Sequencing of tumor-normal pairs important #GET2010
- Lincoln: now describing differences between exome / WGS sequencing, using Miller family as example #GET2010
- Lincoln: need to look to families, prospective parents, newborns, pre-natal, healthy individuals, clinical cohorts, etc. #GET2010
- Lincoln: this is good, but the numbers need to get much larger. Genomes need to come from variety of groups. #GET2010
- Lincoln: ended 2009 with 100-200 genomes deeply sequenced (not all published); CG did 60 or so alone #GET2010
- Lincoln: this type of story is now becoming much more common. Will continue to do so as WGS expands #GET2010
- Lincoln: sequencing changed the clinical resolution. Avoided liver transplant, changed diet instead. Infant recovered #GET2010
- Lincoln: describing case study of WGS for hypercholesterolemic infant: found putative cause after few days of data analysis #GET2010
- Lincoln: starts with discussion of what GWAS has/has not shown (rare vs. common variant point) #GET2010
- Now up, Steve Lincoln from @CompleteGenomic talking about an infrastructure for the future of human genome sequencing #GET2010
- Q: do you believe in probiotics? Knight: not a believer (at least for brand he studied), but evidence not yet published #GET2010
- Knight: it's a bit like weeding a garden with a bulldozer and hoping what grows back is what you want. #GET2010
- Q: do you recommend using anti-bacterial soap for hand-washing? #GET2010
- Describing #BioWeatherMap, @tgoetz has a great analogy: we are the Earth, the microbes are the weather passing over us #GET2010
- Knight: goal is to expand from dollar bills (churches vs. strip clubs) to other surfaces (crosswalk buttons, schools, etc.) #GET2010
- Knight: #BioWeatherMap can be a keystone example of open-access, citizen driven science. Still needs support #GET2010
- Knight: finishes with a call to action for #BioWeatherMap. Broad-scale sampling across environments, integration w/ PGP data #GET2010
- Knight: conclusions? diff ppl, diff sites harbor diverse microbiota. Prospects for personalized medicine are excellent #GET2010
- Knight: looking at microbiota on dollar bills, comparing those collected from churches vs "adult establishments" #GET2010
- Knight: describing microbiota sampling 20 min after birth. Sharp contrast in communities based on birth type (c-section v natural) #GET2010
- Knight: showing changes in his own phenotype as well based on gut microbes. Lost 60 lbs after trip to Peru, antibiotic regimen #GET2010
- Knight: now describing how microbiomc communities produces different phenotypes in the host (mice obesity) #GET2010
- Knight: sampling microbiome at 27 different body sites. "That's a lot of different places to stick a q-tip" #GET2010
- Knight: research shows that very few microbial "species" are shared. Same results in human gut & human hands. #GET2010
- Knight: describing his open source data integration analysis pipeline (QIIME). Sequencing, barcoding, tree creation #GET2010
- Knight: is there a Wallace-esque biogeography line that separates microbial keyboard on our keyboard? Knight's data says yes #GET2010
- Now up at #GET2010, Rob Knight (Boulder) discussing the BioWeatherMap for microbial communities: mapping what we are all exposed to
- Lipkin: next steps sample prep, Dx & surveillance platforms, sequencing, bioinformatics, serology, gene-env-timing interactions #GET2010
- Lipkin: "it's not the pathogen, per se, but the host-response" / genomics in isolation is not enough #GET2010
- Lipkin touching everything from Poe to cryptography to linguistic hierarchies, all in the name of virus ID. #GET2010
- IL: showing examples of identification of novel disease-causing agents using genomic sequencing #GET2010
- IL: shows a tourism slide just prior to SARS: "Hong Kong: It will Take Your Breath Away" #GET2010
- Bit of misinformation RT @23andMe: @genomicslawyer @phylogenomics @dgmacarthur our SAB is still there, no changes to report
Church: thinks this has already happened, even if we don't notice. ~1800 medically actionable genes, held by 10% of pop'n

Church: this is going to penetrate more broadly w/ time. May not be a single tipping point.

Church: think of genome sequence as a cell phone (play and explore) but also as an insurance policy. Risk info you hope not to need

Church: don't need to look 10-20 years ahead. It's what is already available - or was avail 2 years ago - that we should talk about

Krulwich wrapping up the panel with a quote from Barney (and lots of laughter). I think you needed to be here for that one

GC: (response to question) - some data will be compromised, but the more sharing that takes place the better

Audience q: how do we know sequencing is safe? GC: we don't, and shouldn't rush into. Early adopters take some of the body blows

Anne West: considers sequencing/genotyping an investment that pays off over time

Q: what needs to be done to help medical profession catch up to where the technology is? John West: Edu is important but inconceivable that doctors will all become genetic experts. Automated interpretation is needed

Q: what about the third leg? In mice, e.g., we can control environment and genome. What about epigenetics?

John West: methylation is an important, natural extension of the technology. Will be part of rich datasets necessary to advance

Bob Green: science of discovery vs. science of disclosure, linked by science of health outcomes.

Green: not all information is necessary beneficial to human health. Concerned about raiding of the medical commons

Green: we need ways to stratify information, determine what is useful vs. not useful. We can't give everyone DNA sequencing

Q: how will culture change through personal genomes? Will it be like private investigators being replaced by Google searching?

Ryan Phelan, DNA Direct on Genes & Drugs. Topic: translating actionable genomic info into the practice of medicine, today

DW: genetics can become more accessible. Question is what are best strategies to make genetics relevant, accessible? Great idea for RT @andrewhessel, @phylogenomics $100 vs $1 metagenomes would be terrific. Would help with funding too!

Dana Waring, Personal Genetics Education Project on Education. Preparing next generation for intro of genetics into daily life

Jason Bobe (PGP) on DlY Genomics. If you like DTC genomics, you'll love DIY. If you hate DTC, you'll hate DIY even more

PR: topics for discussion: ID recessive risk alleles, prenatal diagnosis, newborn screening, PGx, etc.

Philip Reilly, Third Rock Ventures on Disease. Remember: 1/6 of world's ppl does not have access to clean water. How do we improve?

GI: going to be describing #BioWeatherMap, microbiomic sequencing of dollar bills

Gerard Irzyk, Roche/454 on Desktop Sequencing & Analysis. Looking for feedback on how to make sequencing available to more ppl

JT: investigating how genetics gives a better picture of the consumer, and how it will lead to novel consumer products

JT: why consumer genetics? Cos like P&G are inherently involved in manipulating biology at individual level

( Won't be able to live-tweet the breakout sessions; 10 happening simultaneously. Incentive to come in person to get a sense of the above

Getting started w/ the afternoon at #GET2010. Breakout session "pitches" are beginning, starting with Jay Tusman, P&G on Consumer Products.

That's it for the morning session from #GET2010. Twitter will be lighter in the afternoon during the breakout sessions.

Maxey: points out that genotype-phenotype associations require vastly improving our ability to describe, record phenotypes

West: doesn't think it's a bad thing if people have patents and want to charge for it. If I could get a medical benefit I'd pay

Church: discusses Myriad: whoever wins the court battle, the larger battle is being won by technology obviating (certain) patents

Q: about genome sequencing and patent infringement (curious to see what the panel will say)

Church: (going back to Bob Green's comment), agrees that there needs to be constant reevaluation of bio info based on outcomes

Q: how will culture change through personal genomes? Will it be like private investigators being replaced by Google searching?

Green: we need ways to stratify information, determine what is useful vs. not useful. We can't give everyone DNA sequencing

Green: not all information is necessary beneficial to human health. Concerned about raiding of the medical commons

Bob Green: science of discovery vs. science of disclosure, linked by science of health outcomes

West: wishes his MD would take advantage of looking at his genome. It's only become more complicated.

John West: methylation is an important, natural extension of the technology. Will be part of rich datasets necessary to advance

Q: what about the third leg? In mice, e.g., we can control environment and genome. What about epigenetics?

JW: interpretation will not scale unless there is automation. Focusing on educating doctors the traditional way will not work

John West: Edu is important but inconceivable that doctors will all become genetic experts. Automated interpretation is needed

Lucier: this is a huge concern. Sponsoring MD certification program (Topol), MD training fellowships. Will do more...

Q: what needs to be done to help medical profession catch up to where the technology is?

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Q: what will be the discovery / development that will make personal genome sequencing a societal, medical imperative?
• Church/Lucier: sees adoption of EHRs as a separate issue. Sequencing is fundamentally digital, will develop along parallel path
GET2010
• Q from @carlzimmer: is healthcare ready for personal genomes? Can you drop that data into a patient’s traditional medical record?
GET2010
• Lucier: understanding genomes is fundamental to science, & a viable biz. There are many applications beyond what we’ve discussed
GET2010
• Kruulwich: sees personal genomes as a slog - through public acceptance, privacy issues, science, etc. Why is this perception wrong?
GET2010
• West: preventative medicine fundamentally lowers costs, improves outcomes. GET2010
• Q: are we going to just be generating needless medical workups, tests, etc. Will we overburden doctors? #GET2010
• John West: don’t sequence to find out about diseases we already knew we have. Learning new information that is actionable #GET2010
• Wests: MD didn’t find anything, but now they can monitor over time and detect - and treat - at early stage. Ex of why to sequence
GET2010
• Wests: talking about “exfoliation glaucoma”. No reason to suspect risk of this, but learned it from genotyping. Went to see MD #GET2010
• Changing the panel one last time: back on stage: George Church, Anne and John West, Greg Lucier #GET2010
• Gill: enthusiasm (& investment) created technologies, progress we could have never imagined. So there is reason for excitement
GET2010
• Dyson: discussing @23andMe SAB, and how attitudes changed (opened) about what data could be returned #GET2010
• Dyson: scientific progress proceeds one funeral/investigator at a time. Getting the public engaged speeds this #GET2010
• Lupski: science is hard; anybody who doesn’t think that is fooling themselves. Will take time to separate signal from noise #GET2010
• Q for panel: “is there a disconnect between enthusiasm at #GET2010 and how complicated/hard this is?” #GET2010
• Kim: has also sequenced wife and two kids as well. Interested in whether kids share the same genetics risks he does #GET2010
• Kim: based on genotype, phenotype data (temporary vision loss) he is taking preemptive steps to try to address risks #GET2010
• Seong Jim-Kim now talking about learning of his own risk for macular degeneration, usefulness of his own sequence #GET2010
• Lupski as Columbo for genetics. Moving from SNPs to gene panels, and soon will simply do whole-genome once #GET2010
• Lupski: we’ve learned an incredible amount over the past years. It’s not all in the base pairs. We need sequencing #GET2010
• Lupski: now discussing his exp (and that of his family) w/ Charcot-Marie-Tooth disease #GET2010
• Lupski: as MDs, we should not be paternalistic & control what info ppl can have access to. Should instead tell them what it means
GET2010
• Flatley: we have abstracted those in a way that creates actionable information; we need to do the same for whole-genome sequences
GET2010
• Flatley: remember that genetic tests are done every day; in most cases neither MD nor patient understands underlying technology
GET2010
• Lupski: but complications, fear, should not stop us from learning (and he is most interested in medically actionable variants) #GET2010
• Lupski: it is hard. We don’t understand function of 90-95% of human genes. That is humbling #GET2010
• Angrist: if we focus solely on individual understanding/value we lose sight of the value this contributes to science #GET2010
• Q: are the stories our genes tell us simply too hard for (some) individuals to understand? #GET2010
• Gill: emphasizing that understanding neither starts nor stops at the genome. You have to focus on environmental components as well
GET2010
• Dyson: we are helping people understand their own genetics. If they can understand the Red Sox, they can understand @23andMe
GET2010
• Dyson: it will take a long time to understand personal genomes. So there is value in starting now #GET2010
• Dyson: thinks MDs are good when you need them. But shouldn’t be required for ppl to look at their own data. #GET2010
• Flatley: philosophically agree that no MD should be necessary, but thinks involving one is most robust regulatory / safety approach
GET2010
• Gill: chal: Sciona ran into was access to capital, not regulatory hurdles. But we need is greater clarity in what is allowed #GET2010
• Panelists, including Gill and Dyson now being asked about regulatory enforcement / hurdles. Are they worried about this? #GET2010
• Flatley: still trying to get the iPad app right internally. Plenty of underlying issues, but this is where we see the future #GET2010
• Flatley: have ported application from iPhone to iPad. Allows sharing of genome with MD, pharmacist, family, etc. App still internal
GET2010
• Kruulwich asking Flatley about his prototype Illumina iPhone app. Is instantaneous analysis the future? #GET2010
• Transition now from the burdens of genomic sequencing to the benefits - for individuals, as well as the cos, investors #GET2010
• Stepping down: Maxey and Gates. Coming back up: Flatley, Gill, Jim Lupski, @MishaAngrist, @edyson, Seong Jim-Kim #GET2010
• Maxey: not all donors want to be found; but that’s a minority. Most find it a great experience to reconnect w/ donor-conceived kids
GET2010
• Maxey: no reason/value for denying ppl access to their genetic information, including sperm donor children seeking to locate him
GET2010
• Maxey: my identification was made much easier by being in the PGP (participant #5); Maxey understood and was in favor of this
GET2010
• Maxey: donated sperm numerous times in the 80; years later he was located by his children. It was a “wonderful day” #GET2010
• (For background on Maxey’s story, see this Newsweek feature: http://bit.ly/4Dh5aO #GET2010)
• Gates handing it over to Kirk Maxey to talk about re-identification with genetic information (in the form of sperm donation) #GET2010
Angrist: daughters are aware of the PGP (recommends "Here Comes Science" by They Might Be Giants for explaining DNA to kids)

Angrist: biggest concern was daughters were finding out they were at risk from the internet; wanted them to find out from parents

Angrist: helps that daughters will only receive probabilistic knowledge (mother's genome not public)

Angrist: if genomic science has taught us anything, it is that this information is not powerfully predictive

Anne West talking about the Facebook generation's privacy preferences

AW: thinks what is acceptable to talk about publicly changes with generations, although it's not as if there are no distinctions

AW: first genotyped by @23andMe, which led to Illumina sequencing. Prompted by father's embolism. Treatable, but need to know.

John West: first point: why are we talking about risks of genome sequencing when @edyson is talking about being shot into space?

JW: talking about the risks of sequencing, but what about the risks of NOT sequencing; not having access to actionable information

JW: in our family, the information is medically actionable today

Anne West: not planning to publish her own data, possibly at 21, probably not until later. Her brother also keeping data private

Gates: tracing relatives through genetics

Gates: high point of Faces of America was showing unexpected relatedness to the guests. Putting faces, timelines to haplotype grps

Break over. Now on stage, Skip Gates (PGP#12) and Kirk Maxey (PGP#15) talking about tracing relatives through genetics

Quake: the cost is $0, George is right. Thinks not just sequencing, but also interpretation will go to $0 as well.

Flatley: if the price drops to $0, as Church says, then we have a problem

Flatley: thinks the market is "incredibly elastic": concerns about commoditization, but volume will expand rapidly

Dyson: one reason Chinese market is growing is that they are not as worried about the ethical / privacy issues

Flatley: we need 100s, 1000s of genomes in a single place. We're still ramping up to that. Needs to sequence first.

Dyson: China is becoming the dominant market. China will have access? Goal is to make it integrated part of healthcare (eg every child born is seq). Still 10 years away

Gates: has had to raise $21M for his various genealogy secrets. Now describing how he landed Oprah

Flatley, Quake, Dyson and Seong-Jim Kim discussing price of sequencing

Flatley: we are very very very careful to call this a "medical service" since that is regulated

Flatley: @23andMe will be offering a whole genome sequencing service "some day," but ancillary services will remain critical

Flatley: more than pure sequencing (eg what @23andMe is doing) is important to consumers; saw a "huge response" to DNA Day $99 sale

Flatley: if the story that is shared isn't one that you want to hear (e.g., Havasupai Indian) example?

Flatley: thinks it is tough to get informed consent. Considers himself reasonably informed, but took him a long time.

Q: is this a peculiarly American set of values? Would the same story resonate in France or in China?

Dyson: China is becoming the dominant market.

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Watson back on stage to talk about collaboration between Cold Spring Harbor & China

Dyson: more than pure sequencing (eg what @23andMe is doing) is important to consumers; saw a "huge response" to DNA Day $99 sale

Dyson (in response to question of whether $99 is good enough, why pay $48K): in 2-3 years we won't do SNPs. "Why bother?"

Flatley, Quake, Dyson and Seong-Jim Kim discussing price of sequencing

Flatley: @23andMe is offering a whole genome sequencing service "some day," but ancillary services will remain critical

JW: talking about the risks of sequencing, but what about the risks of NOT sequencing; not having access to actionable information

John West: he's not sick, but he's still at risk (embolism as an example).

John West: first point: why are we talking about risks of genome sequencing when @edyson is talking about being shot into space?

AW: first genotyped by @23andMe, which led to Illumina sequencing. Prompted by father's embolism. Treatable, but need to know.
● Angrist: his concern was BRCA status, given family history and his two daughters. Long family discussion before joining PGP #GET2010
● RK: What about "the Cassandra problem": learning something about future development of children that perhaps should not be known? #GET2010
● Now coming on stage at #GET2010, @MishaAngrist, John West and Anne West #GET2010 to talk about sequencing and families
● Flatley: makes a point that genomic sequencing is like credit cards online: uncomfortable at first, but pros outweigh the cons #GET2010
● Flatley: worrying about theoretical bad sequencing is understandable, but need to tip the balance so costs outweigh the cons #GET2010
● Dyson: disease is clearly important. But seemingly frivolous things (eg genealogy) are important to the growth of the field #GET2010
● Lucier: focus of why people should get sequenced is to solve disease. Not to dismiss consumer aspects, but priority to disease #GET2010
● RT @tgoetz: Fwiw I'm on @npr's here&now today w @edysongena talking DNA & health. Natl showtimes here: http://bit.ly/bJ445q #GET2010
● RK: what about identifying which parent supplies certain alleles/traits? Has this created any interest among marriage counselors? #GET2010
● GC: we encourage family enthusiasm and discussion around participation in the PGP #GET2010
● RK: what about if you have a twin and they disagree? GC: PGP policy is that identical twins cannot join unless both join #GET2010
● TW: became concerned once she became a mother. Thinks her daughter should make the decision for herself. GC went ahead, TW did not #GET2010
● TW: their family treats sequencing as a matter of personal choice. Describing her own reservations about publishing her own seq #GET2010
● Ting Wu (George Church's wife) talking about how genomic sequencing has been discussed in their family. #GET2010
● RG: raising awareness of the value of DNA as information is important. "guess what, it didn't kill me to find out about my DNA" #GET2010
● RG: my family is very intellectually curious. Not concerned about publishing genome. If it helps raise awareness, that's worthwhile #GET2010
● Rosalynn Gill: "knowledge is power...I want to know all of the information, and the same for my family." #GET2010
● ED: Not worried sharing her genome. "I'm 58, I'm not dead yet. Will die of something, but total risk of dying cannot exceed 100%" #GET2010
● ED: thinks the legal restriction against insurers using genomes (GINA) is a problem, because it prevents lowering treatment costs #GET2010
● ED: training to be a Russian cosmonaut. Had to have her health insurance notarized, but they had no interest in seeing her genome #GET2010
● Esther Dyson: PGP#3 and early adopter of @23andMe. Invited her whole family, never occurred to her that they wouldn't be interested #GET2010
● Now coming up on stage: Esther Dyson, Rosalynn Gill, George Church & Ting Wu #GET2010
● JF: biggest argument against sequencing was implications for children. But it is a personal choice (Flatley's wife not interested) #GET2010
● JF: similarly unconcerned about privacy issues. For me, sequencing was really not a question. #GET2010
● GL: thinks the privacy issues will simply be handled. Wants to lead by example for personal genomics #GET2010
● GL: for his family, because of his biz, this has become a very familiar conversation. Sequencing the family is "next logical step" #GET2010
● JF & GL: both discussed with their families, and not with their boards of directors #GET2010 Lucier going to sequence his whole family nxt
● Q: should an executive of a multi-billion dollar company publish their genome? #GET2010 Flatley's is up, Lucier's is coming up soon
● Watson stepping down. Now on stage at #GET2010: Jay Flatley and Greg Lucier to talk about biz of genomics #GET2010
● JW: limiting factor at this point is intelligence of scientists, not $. Encourage ppl to put genomes online ("send them a piece...") #GET2010
● JW: the ethical objections to genomic sequencing are just "crap" - a minor blip on the radar screen #GET2010
● JW: "I am very happy that we can do it. Don't have to talk about $. Just whether humans are bright enough to get its act together." #GET2010
● Q for Watson: are you amazed that we are now at a point that we can do intimate investigations of an individual's inheritance? #GET2010
● JW: thinks PGD will be very important in the future (e.g., for bi-polar disease) People will have different opinions re: nasty traits #GET2010
● Q: is lowering the price of genomic sequencing enough? JW: it should be. Immoral not to pursue it #GET2010
● JW: the argument for sequencing is the same as for motherhood: why wouldn't you just do it? #GET2010
● JW: we should sequence 100,000 genomes. Cost will be nothing, interpretation will be everything. Goal is to find pathways #GET2010
● RK: does sequencing complicate parenthood? JW: why should it? It's an absurd sentence. It's just genetics #GET2010
● What did he learn? JW: lactose intolerance, cytochrome P450 (which changed my beta-blocker medication). That was very useful #GET2010
● JW: "I didn't think about sequencing because I have other things to think about" #GET2010
● JW: lack of concern reflects his age. At 20 he would have worried. At 80, what is there to worry about? #GET2010
● JW: at this stage of my life, I tend to say yes. Willing to be sequenced (other than APOE) (and we know how that worked out) #GET2010
● Jim Watson now up on stage #GET2010, sandwiched between CZ and RK. Why did Watson decide to be sequenced? "JW: I don't remember"
● Now up at #GET2010: Robert Kruelwich and @carlzimmer leading the genomics pioneers session. No idea what to expect...
● GC: PGP is not a monopoly, not the sole model. It is intended to inspire creativity, help us move forward #GET2010
● GC: some subset of us must share genomes + environment + traits in order to really understand, test deep connections #GET2010
● immune-ome does not escape a #badomics award RT @phylogenomics: @genomicslawyer not approved not approved #GET2010
● GC: we should sequence 100,000 genomes. Cost will be nothing, interpretation will be everything. Goal is to find pathways #GET2010
● GC: what else can you examine? "immune-ome" (@phylogenomics approved?) using 454/Roche sequencing. Looking at vaccination response #GET2010
● GC: what else can you do with PGP / open communities? Collaborating w/ IMRI researchers to examine PGP population #GET2010
● GC: what about epigenetics? PGP collects tissue, creates IPS lines to reprogram to any tissue. Showing published data #GET2010
● GC: "which traits to focus on?" Many ways to conceptualize. Not everything must be life-threatening to be important #GET2010
- GC: oldest PGP volunteer is PGP #11 - Skip Gates, Sr. Demonstrating allele identification, interpretation tool #GET2010
- GC: if we act as a community, we can improve genomic interpretation. http://evidence.personalgenomes.org #GET2010
- GC: "how many complete genomes are there?" (Putting aside the missing 7%), probably around 17 #GET2010
- GC: now discussing specifics of PGP. For more visit personalgenomes.org #GET2010
- GC: even if you can encrypt data, controlling access to the material itself is difficult #GET2010
- GC: on re-identification: we can promise privacy, but that would be disingenuous. And what about cell lines? #GET2010
- GC: "Who to sequence?" Need to embrace non-experts. Families are the best non-experts to embrace. Amazing what you can from family #GET2010
- GC: "Why public GET datasets?" Remove barriers to research & serendipity. We want to encourage imagination. #GET2010
- GC: "What if there is no cure? Do we not want to know?" GC wants to know. Inspired by Odone, Fox, Rienhoff, Heywood, Melton, etc. #GET2010
- GC: Genetests: 1770 genes: highly predictive & medically actionable. Why don't they show up in DTC tests? #GET2010
- GC: "Are rare diseases so rare?" Add them up and 10% of us have a rare disease, and more are carriers #GET2010
- GC: "Should we cure genetic diversity?" Tricky question comes with trade-offs. Depends on the gene in question. #GET2010
- GC: "what if the gov't started testing babies for intelligence genes?" This already happens: PKU #GET2010
- GC: #GET2010 more than just cheerleading. Imagine the unintended consequences of personal genomes - positive & negative
- GC: $0 genome comes w/string: ex: data sharing. What are other ways that the cost will be covered? Inspect your genome's label #GET2010
- GC: the endpoint is the $0 genome. Cost somebody something, but costs the individual nothing. #GET2010
- GC: "who is my choice for the seq technology winner?" Answer: "yes" (Puts up a list of 20 companies) #GET2010
- GC: over 200M base pairs still missing - that's a huge gap. #GET2010
- GC: "mission accomplished...except 7%" We haven't finished a single human genome yet. E.g, 20M base pairs missing on chromosome 1 #GET2010
- GC: history of DNA Day from 1953 to 2010. Focus on DNA structure, HGP and GINA. Interesting to see GINA elevated to that level #GET2010
- GC: beginning with a Q&A of himself. First question: when is the next personal genomes meeting? #GET2010
- And we're off at #GET2010. George Church delivering intro keynote. Starts with a slide of nudibranchs...
- #GET2010 getting ready to begin. Agenda here: http://bit.ly/anBDd6 Morning will be free-flowing convo w/ genomic pioneers