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/c1SzUZ
- 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 Prototype 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
- West: data analysis for family has only just begun, but already seeing medically actionable data, sense of relief w/in family #GET2010
- West: "this brings a sense of reality to what I'm learning in 11th grade AP biology." Also notes need for bioinformatics in school #GET2010
- West: lists as her final next step: "Finish 11th grade" (to a roomful of applause) #GET2010
- West: next steps with this information? Needs some software (other than Excel) to speed up the analysis. Wants to pursue Factor V #GET2010
- No kidding RT @MishaAngrist: this kid is talking about meiotic recombination in her family...she is a genome hacker extraordinaire #GET2010
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 genotype 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: 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 microbiomic communities produces different phenotypes in the host (mice obesity) #GET2010
Knight: sequencing changed the clinical resolution. Avoided liver transplant, changed diet instead. Infant recovered #GET2010
Knight: describing case study of WGS for hypercholesterolemic infant; found putative cause after few days of data analysis #GET2010
Knight: is there a Wallace-esque biogeography line that separates microbial keyboard on our keyboard? Knight's data says yes #GET2010
Knight: return to Darwin. Recall that most life, and most biological evolution, is microbial #GET2010
Knight: microbial abundance raises the question: how human are we? #GET2010
Knight: phenotypes vary, but are highly similar at genetic level. "You are not a beautiful, unique snowflake" #GET2010
Knight: from Dawkins, van Leeuwenhoek to the Human Microbiome Project. We know there as many e.coli in your gut as ppl on earth #GET2010
Now up at #GET2010, Rob Knight (Boulder) discussing the BioWeatherMap for microbial communities.: mapping what we are all exposed to
Knight: next steps/sample prep, Dx & surveillance platforms, sequencing, bioinformatics, serology, gene-env-timing interactions #GET2010
Knight: "it's not the pathogen, per se, but the host-response" / genomics in isolation is not enough #GET2010
Knight: touching everything from Poe to cryptography to linguistic hierarchies, all in the name of virus ID. #GET2010
IL's description of his WHO work re: virus identification sounds like something straight out of Hollywood. #GET2010
IL: now describing research investigating rapid, mysterious decline of bee population #GET2010
IL: important not to focus on a single genetic/viral region; embrace entire microbial universe to understand how they cause disease #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
Q: what will be the discovery/development that will make personal genomic sequencing a societal, medical imperative? #GET2010
Church: thinks this has already happened, even if we don't notice. ~1800 medically actionable genes, held by 10% of pop'n #GET2010

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 #GET2010

Church: don't need to look 10-20 years ahead. It's what is already available - or was available 2 years ago - that we should talk about #GET2010

Krulwich wrapping up the panel with a quote from Barney (and lots of laughter). I think you needed to be here for that one #GET2010

GC: (response to question) - some data will be compromised, but the more sharing that takes place the better #GET2010

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 #GET2010

Q: what needs to be done to help medical profession catch up to where the technology is? #GET2010

JW: interpretation will not scale unless there is automation. Focusing on educating doctors the traditional way will not work #GET2010

Q: about the third leg? In mice, e.g., we can control environment and genome. What about epigenetics? #GET2010
John West: methylation is an important, natural extension of the technology. Will be part of rich datasets necessary to advance #GET2010
West: wishes his MD would take advantage of looking at his genome. It's only become more complicated. #GET2010

Bob Green: science of discovery vs. science of disclosure, linked by science of health outcomes. #GET2010
Green: not all information is necessary/beneficial to human health. Concerned about raiding of the medical commons #GET2010
Green: we need ways to stratify information, determine what is useful vs. not useful. #GET2010

Q: how will culture change through personal genomes? Will it be like private investigators being replaced by Google searching? #GET2010
Church (going back to Bob Green's comment), agrees that there needs to be constant reevaluation of info based on outcomes #GET2010

Q: what about genome sequencing and patent infringement (curious to see what the panel will say) #GET2010
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 #GET2010

Maxey: points out that genotype-phenotype associations require vastly improving our ability to describe, record phenotypes #GET2010

That's it for the morning session from #GET2010. Tweeting will be lighter in the afternoon during the breakout sessions.
• Church/Lucier: sees adoption of EHRs as a separate issue. Sequencing is fundamentally digital, will develop along parallel path.

• Gates handing it over to Kirk Maxey to talk about re-identification with genetic information (in the form of sperm donation) #GET2010

(For background on Maxey’s story, see this Newsweek feature: Maxey: my identification was made much easier by being in the PGP (participant #5); Maxey understood and was in favor of this.

Maxey: no reason/value for denying ppl access to their genetic information, including sperm donor children seeking to locate him #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

Stepping down: Maxey and Gates. Coming back up: Flatley, Gill, Jim Lupski, @MishaAngrist, @edyson, Seong Jim-Kim #GET2010

Transition now from the burdens of genomic sequencing to the benefits - for individuals, as well as the cos, investors #GET2010

Krulwich asking Flatley about his prototype Illumina iPhone app. Is instantaneous analysis the future? #GET2010

Flatley: have ported application from iPhone to iPad. Allows sharing of genome with MD, pharmacist, family, etc. App still internal

Panelists, including Gill and Dyson now being asked about regulatory enforcement / hurdles. Are they worried about this? #GET2010

Gill: received cease & desist letters from CA, NY and MD. Thought regulations didn’t apply; regulators didn’t. Uncertainty is tough #GET2010

Dyson: @23andMe has a slightly different story, but the same basic issues exist. Give information, not advice #GET2010

Dyson: @23andMe also received letters from states, and adapted to comply. States like MDs as gatekeepers. #GET2010

Dyson: “Can’t talk to god yourself; you need a priest. But we are heretical, just like Gutenberg” #GET2010

Flatley: philosophically agree that no MD should be necessary, but thinks involving one is most robust regulatory / safety approach #GET2010

Flatley: my MD refused to write a prescription for full genome sequence (required by $ILMN) b/c he knew nothing about it #GET2010

Lupski: says @23andMe just disbanded their scientific advisory board? (Did I hear that correctly?) #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

Gill: emphasizing that understanding neither starts nor stops at the genome. You have to focus on environmental components as well #GET2010

Gill: 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

Flatley: challenging 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

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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

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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/4Dh5a0 #GET2010)

Gates handing it over to Kirk Maxey to talk about re-identification with genetic information (in the form of sperm donation) #GET2010
Gates: there are cultural diffs, but everyone shares the impulse to understand one's ancestors. Just need to tie in genetics #GET2010
Gates: the world values genealogy (aside: Mormons are "the Borg of genealogy - eat up all the records we can find") #GET2010
Q: is this a peculiarly American set of values? Would the same story resonate in France or in China? #GET2010
Gates: this allows us to see ourselves as a genetic bouillabaisse, which is what we are. A new measure of identity #GET2010
Gates: was pre-tested for BRCA1/2 common mutations. Once those came back clean, his greatest fear was removed #GET2010
Angrist: daughters are aware of the PGP (recommends "Here Comes Science" by They Might Be Giants for explaining DNA to kids) #GET2010
Angrist: biggest concern was daughters were finding out they were at risk from the internet; wanted them to find out from parents #GET2010
Angrist: tries not to think about the fact that, in time, new knowledge will crop up. Daughters will learn plenty from the internet #GET2010
Angrist: if genomic science has taught us anything, it is that this information is not powerfully predictive #GET2010
Anne West talking about the Facebook generation's privacy preferences #GET2010
AW thinks her generation is much more open, public #GET2010
AW: thinks what is acceptable to talk about publicly changes with generations, although it's not as if there are no distinctions #GET2010
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? #GET2010
JW: talking about the risks of sequencing, but what about the risks of NOT sequencing; not having access to actionable information #GET2010
John West: not's he's not sick, but he's still at risk (embolism as an example). #GET2010
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Gates: comparing genealogy to photography. Both are representations. We need to learn how to read a genome way we read a photograph #GET2010
Flatley who will have access? Goal is to make it integrated part of healthcare (eg every child born is seq). Still 10 years away #GET2010
Flatley: we need 100s, 1000s of genomes in a single place. We're still ramping up to that. Need to sequence first. #GET2010
Dyson: China is becoming the dominant market. Flatley: we have one customer who will be end of year have capacity of entire US
Dyson: one reason Chinese market is growing is that they are not as worried about the ethical / privacy issues #GET2010
Flatley: thinks the market is "incredibly elastic"; concerns about commoditization, but volume will expand rapidly #GET2010
Quake: the cost is $0, George is right. Thinks not just sequencing, but also interpretation will go to $0 as well. #GET2010
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Flatley: if the price drops to $0, as Church says, then we have a problem #GET2010
Flatley: thinks the market is "incredibly elastic"; concerns about commoditization, but volume will expand rapidly #GET2010
Dyson: one reason Chinese market is growing is that they are not as worried about the ethical / privacy issues #GET2010
Watson back on stage to talk about collaboration between Cold Spring Harbor & China #GET2010 Still believes US is better at technology #GET2010
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 sequence 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 @edysong 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
Rosalyn Gill: "knowledge is power...I want to know all of the information, and the same for my family."
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%"
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, Rosalyn 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 Lucifer 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
JW: limiting factor at this point is intelligence of scientists, not $. Encourage ppl to put genomes online ("send them a pie...") #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 diff opinions re: nasty traits #GET2010
JW: 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 Krulwich 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: personal genome -> traits, with stops in between: epigenome, microbiome, immune-ome, etc. #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/ strings: 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