

by Mark Gerstein a few seconds ago

Saved Favorite Mention Tweets from start to 6 Aug. '16 (subset of all)

**Dr. J. Craig Venter**

@JCVenter

[@matthewherper](#) [@statnews](#) [@carlzimmer](#) we will publish our analysis of it/carl z



A YEAR AGO

**Chris Dwan**

@fdmts

[@MarkGerstein](#) [@carlzimmer](#) [@statnews](#) we're gonna be hard pressed to find a molecular mechanism there ... [#hypothesisfree](#) [#bigdata](#)



A YEAR AGO

**Yale University**

@Yale

Yale's [@MarkGerstein](#) among supporting cast in [@carlzimmer](#)'s [#GameofGenomes](#) [bit.ly/29FNTak](#) via [@statnews](#)



2 YEARS AGO

**SWOG Cancer Research**

@SWOG

[#SWOGonc](#)'s [@MarkGerstein](#) from [@YaleCancer](#) helps sequence Carl Zimmer's genome in [@statnews](#) series!!!! [statnews.com/feature/game-o...](#) via [@statnews](#)



2 YEARS AGO

**sushant**

@sushant211

Thanks [@aayushraman](#) It was a team effort by [@MarkGerstein](#) lab and [@carlzimmer](#) was very kind to give us this opportunity.



2 YEARS AGO

PYLENGYNQNHGRKFVQKSIDVACHPGYALPKAQTTVTCMENGSWSPTRCIRVKTCSKSSIDIENGFISESQYTYALKEKAKYQCKLGY
 PKIDVHLVPDRKKDQYKVGVLKFSCPKPGFTIVGPNQSVQCYHFLSPDLPICKEQVQSCGPPPELLNGNVKEKTKEEYGHSEVVEYYCNP
 KCKSSNLIILEEHLKNNKEFDHNSNIRYRCRGKEGWIHTVCINGRWDPEVNCMAQIQLCPLPPQIPNSHNMTTTLNYRDGEKVSVLCQE
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 .11 chr1:196659237:C:T GERP=-9.09;CFH nonsynonymous ENST00000367429.4 3
 ILTGWSWDQTYPECTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTTPTGFTTTLTGGNVFEYGVKAVYTCNEGYQLL
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 PPPIDNGDITSFPLSVYAPASSVEYQCQNLQYLEGNKRITCRNQWSEPPKCLHPCVISREIMENYNIALRWTAKQKLYSRTGESVEFVC
 ILTGWSWDQTYPECTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTTPTGFTTTLTGGNVFEYGVKAVYTCNEGYQLL
 SPDVINGSPISQKIYKENERFQYKCNMGYEYSERGDAVCTESGWRPLPSCEEKSCDNPYIPNGDYSPLRIKHRTGDEITYQCRNGFYPA
 PYLENGYNQNYGRKFVQKSIDVACHPGYALPKAQTTVTCMENGSWSPTRCIRVKTCSKSSIDIENGFISESQYTYALKEKAKYQCKLGY
 PKIDVHLVPDRKKDQYKVGVLKFSCPKPGFTIVGPNQSVQCYHFLSPDLPICKEQVQSCGPPPELLNGNVKEKTKEEYGHSEVVEYYCNP
 KCKSSNLIILEEHLKNNKEFDHNSNIRYRCRGKEGWIHTVCINGRWDPEVNCMAQIQLCPLPPQIPNSHNMTTTLNYRDGEKVSVLCQE
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 .15 chr7:150553605:C:T GERP=-0.636;AOC1 nonsynonymous ENST00000360937.4
 VFSDLNQLKAVHSFLWSKKELRLQPSSTTTMAKNTVFLIEMLLPKKYHVLRLDKGERHPVREARAVIFFGDQEHPNVTEFAVGPLPG
 LHPTGLELLVDHGSTDAGHWAVEQVWYNGKFYGSPEELARKYADGEVDVVLEDPLPGGKGHDSTEEPPLFSSHKPRGDFPSPIHVSGPR
 PETATFLDTFHYDADDPVHYPRALCLFEMPTGVPLRRHFNSNFKGGNFYAGLKGQVLVLRRTSTVYNYDIWDFIFYPNGVMEAKMHA
 KLPKYLLFTSPQENPWGHKRTYRLQIHSMAQVLPQWQEEQAITWARYPLAVTKYRESELCSSSIYHQNDFWHPVVFEEQLHNNENIE

 VFSDLNQLKAVHSFLWSKKELRLQPSSTTTMAKNTVFLIEMLLPKKYHVLRLDKGERHPVREARAVIFFGDQEHPNVTEFAVGPLPG
 LHPTGLELLVDHGSTDAGHWAVEQVWYNGKFYGSPEELARKYADGEVDVVLEDPLPGGKGHDSTEEPPLFSSHKPRGDFPSPIHVSGPR
 PETATFLDTFHYDADDPVHYPRALCLFEMPTGVPLRRHFNSNFKGGNFYAGLKGQVLVLRRTSTVYNYDIWDFIFYPNGVMEAKMHA

In an act of science guinea pigging, @carlzimmer bares his "Zimmerome" bit.ly/29Nrbd2
pic.twitter.com/H39SwQq30j

 STAT @STATNEWS · 2 YEARS AGO

Watch as @carlzimmer is genetically dissected like a frog bit.ly/29JoITS #GameofGenomes
pic.twitter.com/ZsOdaNcTB8

 STAT @STATNEWS · 2 YEARS AGO

ICYMI Game of Genomes: feat @carlzimmer @MarkGerstein @konradjk
statnews.com/feature/game-o... via @statnews #genomics #NGS pic.twitter.com/zXM2rJDVFu

 SUMIT MIDDHA @BIOINFOSM · 2 YEARS AGO



Ethan Weiss
@ethanjweiss

@matthewherper @carlzimmer @statnews Most interesting tidbit was that Gerstein said he would not have had courage to do this himself!

 2 YEARS AGO



Shrikant Mantri
@thinkgenome

About the series: Watching my genome flow into Gerstein's computer made me a little giddy. ...
Scientists hav... bit.ly/29BDpHg

 2 YEARS AGO

Coming 7/11/16 @statnews #GameofGenomes pic.twitter.com/hdoexCkZax

 CARL ZIMMER @CARLZIMMER · 2 YEARS AGO



Grad School at Sinai
@GradSchoolSinai

In case you missed last week's #GBM seminar, here's @MarkGerstein's talk on personal #genomics. bit.ly/1X9qv5d @GradSchoolSinai

 2 YEARS AGO



Grad School at Sinai
@GradSchoolSinai

View @MarkGerstein talk on "Personal #Genomics" @icahn Institute #GBM Seminar on Mon., 6/6, here: bit.ly/1X9qv5d @GradSchoolSinai

 2 YEARS AGO



nature

Genomics, Big Data, and Medicine



Keynote Speaker:

Mark Gerstein, PhD

Albert L Williams Professor
Biomedical Informatics, Molecular Biophysics
and Biochemistry, Yale University

Join Mark Gerstein, PhD for
"Personal Genomics"

Monday, June 6th, 1 - 3 pm
Hess Building, 1470 Madison Ave
Davis Auditorium

Dr. Mark Gerstein's current research is focused on bioinformatics and he is particularly interested in data science and data mining, macromolecular geometry and simulation, and human genome annotation and cancer genomics. He has published considerably in scientific journals, with over 400 publications in total, including prominent venues such as Science, Nature, and Scientific American.

GBM is an annual speaker series presented by the
Icahn Institute for Genomics and Multiscale Biology
Organizers: Judy Cho, Pamela Sklar, Eric Schadt, and Orli Bahcall

Join the conversation at **#GBMseminar**

mt [#bioinformatics](#) [#bioit](#) [@IcahnInstitute](#): 'Today at 1pm: [@MarkGerstein](#), [#Bioin...](#)
[pic.twitter.com/qmvLbCkAOw](#), see more [tweetedtimes.com/search/%23bioi...](#)

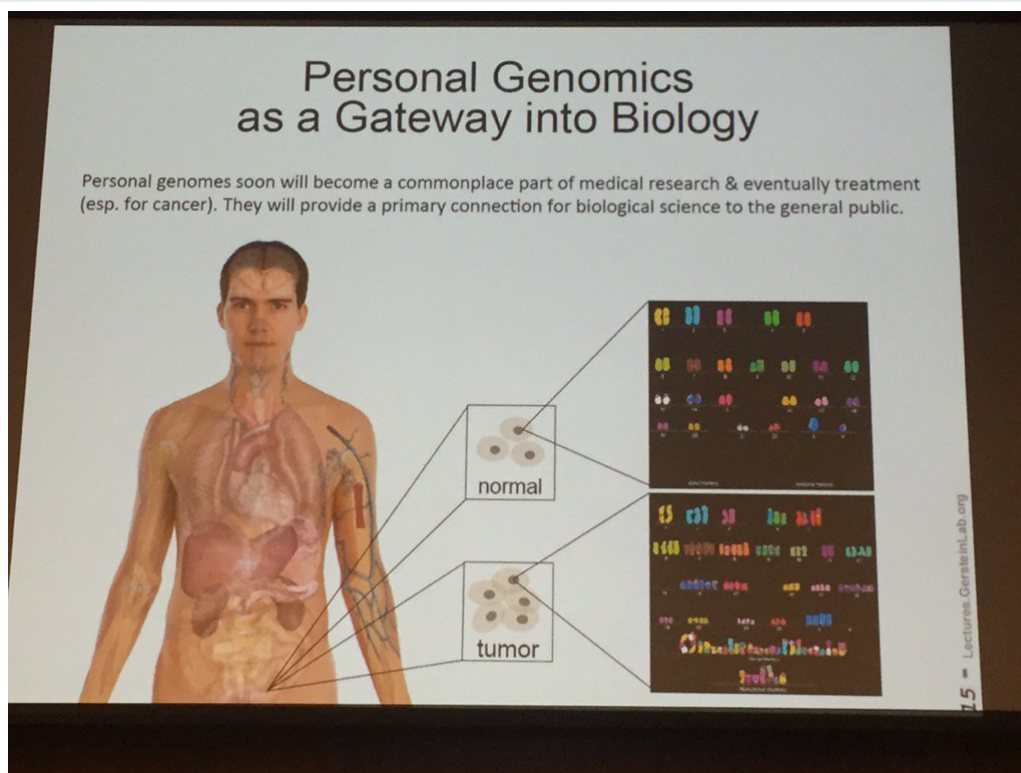
SEQCOMPLETE [@SEQCOMPLETE](#) · 2 YEARS AGO

**Personal Genomics:
Managing Exponential Data Scaling through Prioritizing High-impact Variants**

- Introduction
 - The exponential **scaling** of data generation & processing
 - The **landscape of variants** in personal genomes suggests finding a few key ones
- Evaluating the Impact of Non-coding Variants with Annotation
 - **Annotating non-coding regions** on different scales with MUSIC
 - Prioritizing rare variants with **“sensitive sites”** (human-conserved)
 - Prioritizing in terms of **network connectivity** (eg hubs)
 - Prioritizing using AlleleDB in terms of **allelic elements**
 - Having observed difference in molecular activity in many contexts
- Putting it together in Workflows
 - Using **Larva to do burden testing** on non-coding annotation
 - Need to correct for over-dispersion mutation counts
 - Parameterized according to replication timing
 - Using **FunSeq to integrate evidence** on variants
 - Systematically weighting all the features
 - suggesting non-coding drivers
 - Prioritizing rare germline variants
- Postscript: Analysis of the **Evolution of a Consortium**
 - Differences in “modularity” for members & users
 - Key role for brokers

PersonalGenomics:Managing Exponential DataScaling through Prioritizng High-Impact Variants
[@MarkGerstein](#) #GBMSeminar pic.twitter.com/51niMcmw2s

 ICAHN INSTITUTE @ICAHNINSTITUTE · 2 YEARS AGO



In the future, everyone will have their [#genome](#) [#sequenced](#), particularly if they are sick.
[@MarkGerstein](#) [#GBMseminar](#) pic.twitter.com/5WB13l0Hvf

 ICAHN INSTITUTE @ICAHNINSTITUTE · 2 YEARS AGO



Icahn Institute
 @IcahnInstitute

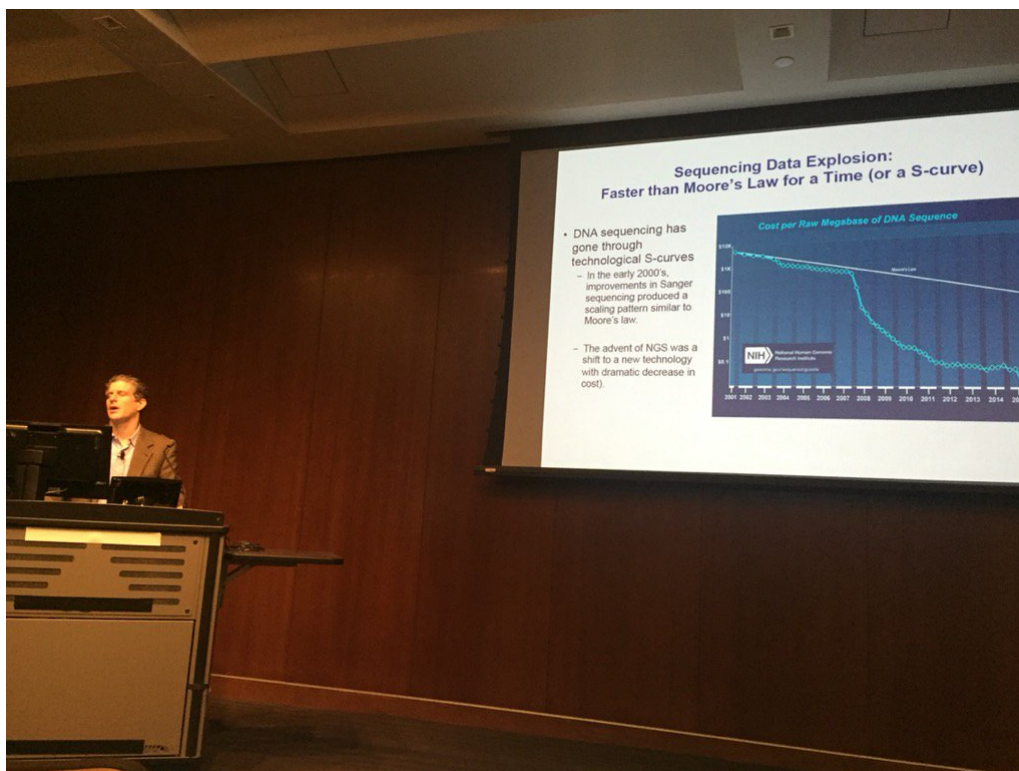
"The big thing happening today is the big amount of private data being collected -> new challenge in terms of access & privacy" [@MarkGerstein](#)

 2 YEARS AGO



See @MarkGerstein's #GBMseminar slides at lectures.gersteinlab.org/summary/Managi...pic.twitter.com/UTRNxYKqMS

 ICAHN INSTITUTE @ICAHNINSTITUTE · 2 YEARS AGO



Excited to welcome @Yale's @MarkGerstein to #GBMseminar for a discussion on Personal #Genomics! pic.twitter.com/8GEFrpfpWR

ICAHN INSTITUTE @ICAHNINSTITUTE · 2 YEARS AGO



Eimear Kenny
@EimearEKenny

Prepping for highly anticipated talk from @MarkGerstein for GBM series @IcahnInstitute @IcahnMountSinai Davis in Hess @ 1pm

2 YEARS AGO



Icahn Institute
@IcahnInstitute

Join us on Monday from 1-3pm for our #GBMseminar to hear @MarkGerstein discuss Personal #Genomics. RSVP for free at events.mountsinaihealth.org/event/GBM_semi...

2 YEARS AGO



Brad Hargreaves
@bhargreaves

In which the New Yorker labels me an "affable, nerdy twenty-nine-year-old with a scruffy beard" newyorker.com/magazine/2016/...

2 YEARS AGO



Anthony Mathelier
@AMathelier

@MarkGerstein Really nice work! Using betabinomial is very accurate. But why 0.3 as thr for chipseq? Other tested? 1/2



2 YEARS AGO



Genome Biology
@GenomeBiology

A survey of allele-specific expression in @1000genomes - @MarkGerstein &co @NatureComms bit.ly/1VPCp4h #genomics



2 YEARS AGO



Edward Dove
@EdwardSDove

Temporal Dynamics of Collaborative Networks in Large Scientific Consortia:
sciencedirect.com/science/article... @MarkGerstein et al.



2 YEARS AGO



Journal Picks @ WTGC
@jnl_picks

A uniform survey of allele-specific binding and expression over 1000-Genomes-Project individuals: Nature Commu... bit.ly/1VmglZ1



2 YEARS AGO



Sciencey Things
@ScienceyBot

A uniform survey of allele-specific binding and expression over 1000-Genomes-Project individuals.: A uniform s... 1.usa.gov/1re8kOO



2 YEARS AGO



RNA_seq
@RNA_seq

A uniform survey of allele-specific binding and expression over 1000-Genomes-Project individuals. dlvr.it/L5WKRS



2 YEARS AGO



Yale University
@Yale

Don't forget parents when celebrating a personal genome bit.ly/1Nx53P1 @NatureNews



2 YEARS AGO



NYU Primatology
@nyuprimatology

Amazing new resource @NatureComms of annotated allele-specific binding & expression in 382 human individuals nature.com/ncomms/2016/16...



2 YEARS AGO



Yale University
@Yale

Researchers annotate elements w/ different activity in mother's & father's personal genomes bit.ly/1Nx53P1 @MarkGerstein lab



2 YEARS AGO



Camilla Pang
@millzymai

@MarkGerstein A brill read! I read this paper last week and really enjoyed it! Great that it separates interior/exterior critical residues.



2 YEARS AGO



Wyatt Yue
@Wyatt_Yue

Nice computational tool to identify #allosteric residues to understand disease causing variants. @Structure_CP twitter.com/markgerstein/s...



2 YEARS AGO



Matteo Convertino
@convertino_matt

modsti.cns.iu.edu #ModSTI



2 YEARS AGO



Pavel Prosselkov
@PavelProsselkov

Who Owns Your DNA?: Cell cell.com/cell/fulltext/...



2 YEARS AGO



Geoff Winsor
@glwinsor

The real cost of sequencing: scaling computation to keep pace with data generation
genomebiology.biomedcentral.com/articles/10.11... #genomebiology



2 YEARS AGO



Sumit Middha
@bioinfosm

#Genomics #bioinformatics #PrecisionMedicine twitter.com/markgerstein/s...



2 YEARS AGO



IFB_Bioinformatique
@IFB_Bioinfo

Real cost of #sequencing : scaling #computation to keep pace with data generation by
[@MarkGerstein](https://twitter.com/MarkGerstein) genomebiology.biomedcentral.com/articles/10.11...



2 YEARS AGO



Ioannis Xenarios
@ixenario

[@Piwdb](https://twitter.com/Piwdb) [@MarkGerstein](https://twitter.com/MarkGerstein) always good to read Mark's paper, the general tendency being to shoot data w/o thinking of what to do with it..



2 YEARS AGO



Paul de Bakker
@Piwdb

The real cost of sequencing as argued by [@MarkGerstein](https://twitter.com/MarkGerstein)
genomebiology.biomedcentral.com/articles/10.11...



2 YEARS AGO

**Hedi Hegyi**

@drckitty

@MarkGerstein @ENCODE_NIH Nice figure. Who are the poor souls on the circumference of the wheel?



2 YEARS AGO

**Kevin Faircloth**

@KevinFaircloth1

@MarkGerstein @ENCODE_NIH Awesome! Congratulations Prof. Your paper can easily baseline into #QIS Dynamic interpretations are hard, hence...



2 YEARS AGO

**Heimdall_biotech**

@Heimdall_biotec

"The real cost of sequencing: scaling computation to keep pace with data generation"
genomebiology.biomedcentral.com/articles/10.11... #technologic #feedly



2 YEARS AGO

**Heimdall_biotech**

@Heimdall_biotec

genomebiology.biomedcentral.com/articles/10.11...



2 YEARS AGO

**Enhancer/loops paper**

@loops_enhancers

The real cost of sequencing: scaling computation to keep pace with data generation | Genome Biology | Full Text - go.shr.lc/1RFkYSz



2 YEARS AGO

**Transcriptomes**

@transcriptomes

Large-scale atlas of microarray data reveals the distinct expression landscape of different t...
ncbi.nlm.nih.gov/pubmed/27015116



2 YEARS AGO



Sciencey Things
@ScienceyBot

Large-scale atlas of microarray data reveals the distinct expression landscape of different tissues in Arabido... 1.usa.gov/1pOmRQz

2 YEARS AGO



RNA_seq
@RNA_seq

Large-scale atlas of microarray data reveals the distinct expression landscape of different tissues in Arabidopsis. dlvr.it/KtmRTQ

2 YEARS AGO



Masa-aki Yoshida
@yoshidamasaaki

TCGAでかつつ！ | The real cost of sequencing: scaling computation to keep pace with data generation genomebiology.biomedcentral.com/articles/10.11... #genomebiology

2 YEARS AGO



Jun Sese
@sesejun

Fig 4. にUS51大学のゲノム配列解析に絡んだfaculty position数が出てますね。日本にも51大学くらいありますが、1/5以下じゃないだろうか（数えてません）。 genomebiology.biomedcentral.com/articles/10.11...

2 YEARS AGO



Jun Sese
@sesejun

計算機の速度と配列解析の歴史。//The real cost of sequencing: scaling computation to keep pace with data generation genomebiology.biomedcentral.com/articles/10.11...

2 YEARS AGO



David Shaywitz
@DShaywitz

@MarkGerstein @GenomeBiology @dnanexus yes, right after the singularity

2 YEARS AGO



 2 YEARS AGO

DAVID SHAYWITZ @DSHAYWITZ · 2 YEARS AGO



 WEIGEL LAB @PLANTEVOLUTION · 2 YEARS AGO

**Lilia Boucinha**

@em_c77

The real cost of sequencing: scaling computation to keep pace with data generation
genomebiology.biomedcentral.com/articles/10.11... #genomebiology



2 YEARS AGO

**Cameron Thrash**

@jcamthrash

The real cost of sequencing: scaling computation to keep pace with data generation
genomebiology.biomedcentral.com/articles/10.11...



2 YEARS AGO

**Tim Knutsen**

@timknut

"The real cost of sequencing: scaling computation to keep pace with data generation"
genomebiology.biomedcentral.com/articles/10.11... #genetics #feedly



2 YEARS AGO

**Pathobiome**

@gr_pathobiome

The real cost of sequencing: scaling computation to keep pace with data generation
genomebiology.biomedcentral.com/articles/10.11...



2 YEARS AGO

**JMBelloso**

@chemabelloso

The real cost of sequencing: scaling computation to keep pace with data generation
buff.ly/1XQJ9fa



2 YEARS AGO

**Hedi Hegyi**

@drckitty

@MarkGerstein Yeah. Thanks God there is no Nobel for them (sorry Werner :-)) How many of your former people are now in that category?



2 YEARS AGO



EuADS
@EuADSorg

The real cost of sequencing: scaling computation to keep pace with data generation - Genome Biology nzzl.us/RR91dAV

2 YEARS AGO



Genetics at BioMed
@OAGenetics

The REAL cost of sequencing: scaling computation to keep pace with data generation genomebiology.biomedcentral.com/articles/10.11...

2 YEARS AGO



Jo Rhodes
@JohannaRhodes

The real cost of sequencing: scaling computation to keep pace with data generation genomebiology.biomedcentral.com/articles/10.11...

2 YEARS AGO



Shin Kawano (エセレシキさん)
@orenottwitter

The real cost of sequencing: scaling computation to keep pace with data generation genomebiology.biomedcentral.com/articles/10.11... #genomebiology

2 YEARS AGO



Elisabeth Bik
@MicrobiomDigest

The real cost of sequencing: scaling computation to keep pace with data generation - Paul Muir genomebiology.biomedcentral.com/articles/10.11...

2 YEARS AGO



Fabrice Leclerc
@rnomics

Top #tweeted story in #bioscience: The real cost of sequencing: scaling computa... genomebiology.biomedcentral.com/articles/10.11..., see more tweetedtimes.com/v/1341?s=tnp

2 YEARS AGO



Scott Givan
@sgivan

The real cost of sequencing: scaling computation 2 keep pace w/ data generation [ht.ly/ZTB24](https://t.co/ZTB24) via @GenomeBiology #bioinformatics



2 YEARS AGO



Kadir C Akdemir
@kcakdemir

The real cost of sequencing: scaling computation to keep pace with data generation genomebiology.biomedcentral.com/articles/10.11... #genomebiology



2 YEARS AGO



Verena E. Kutschera
@vekutschera

The real cost of sequencing: scaling computation to keep pace with data generation [ow.ly/ZTuYi](https://t.co/ZTuYi)



2 YEARS AGO



Ann Meyer
@meyer_ann

Interesting article on bioinformatics' data generation and scaling computation to keep pace [goo.gl/9CQZGQ](https://t.co/9CQZGQ) #genomebiology



2 YEARS AGO

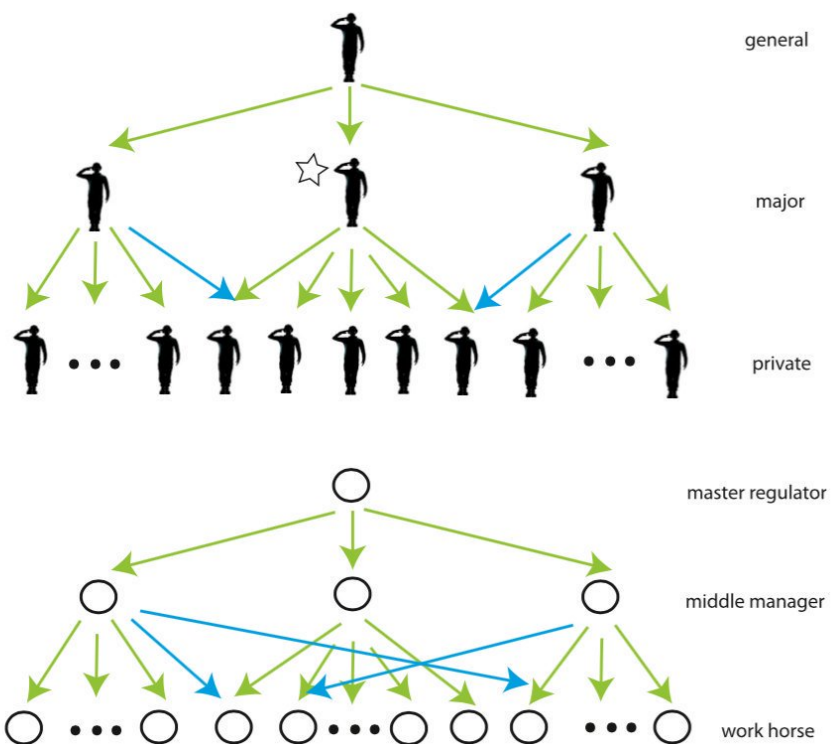


Fabrice Leclerc
@rnomics

Top #tweeted story in #bioinformatics: The real cost of sequencing: scaling com... genomebiology.biomedcentral.com/articles/10.11..., see more [tweetedtimes.com/v/1343?s=tnp](https://t.co/1343?s=tnp)

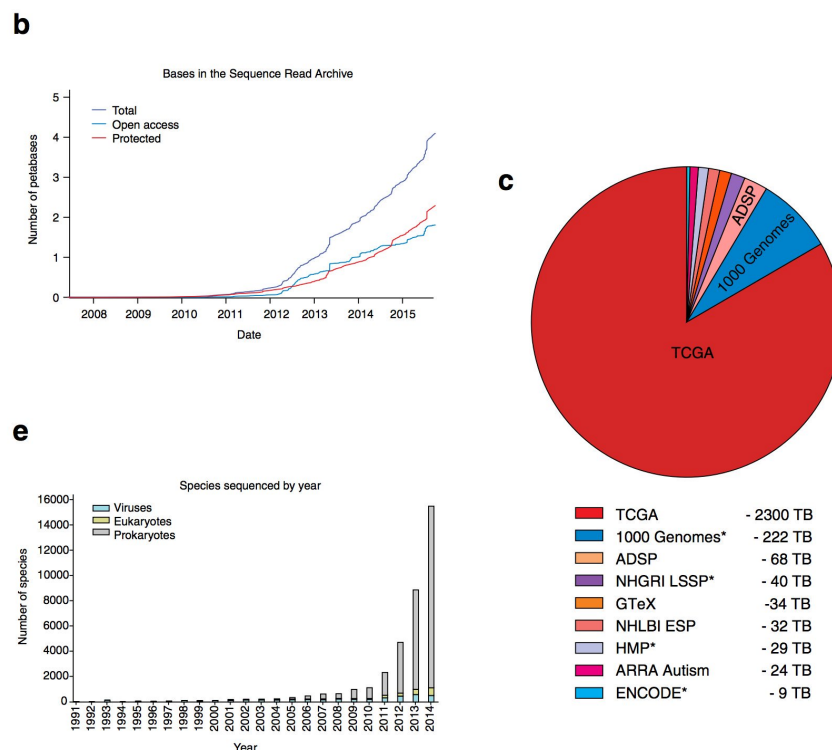


2 YEARS AGO



Great paper about networks comparison, biological vs human networks [@CellSystemsCP](https://twitter.com/CellSystemsCP)
bit.ly/1RjbSJ5 pic.twitter.com/W8dLP1T1r1

 CAROLINE BERGER @BERGERCAROLINE5 · 2 YEARS AGO



Where next for analysis+storage of sequencing data? From [@MarkGerstein](#) & [@GenomeBiology](#)
genomebiology.biomedcentral.com/articles/10.11... pic.twitter.com/55bwQlkAkW

SEVEN BRIDGES GENOMICS [@SBGENOMICS](#) · 2 YEARS AGO



Nicolas Robine
[@notSoJunkDNA](#)

"The real cost of sequencing: scaling computation to keep pace with data generation", by
[@MarkGerstein](#) et al genomebiology.biomedcentral.com/articles/10.11...

2 YEARS AGO



Genome Biology
[@GenomeBiology](#)

Where does all my money go? [@MarkGerstein](#) &co on the real cost of [#sequencing](#)
bit.ly/21InDKC [#genomics](#)

2 YEARS AGO



ECBA
[@ECBA_EU](#)

The real cost of sequencing: scaling computation to keep pace with data generation...
fb.me/4Kf9cq1Cr

2 YEARS AGO



Anita Schürch
@AnitaSchurch

The real cost of sequencing: scaling computation to keep pace with data generation
genomebiology.biomedcentral.com/articles/10.11... #genomebiology

 2 YEARS AGO



Mike Inouye
@minouye271

Matchmaking b/n hairballs: Nice networks perspective from @MarkGerstein in
[@CellSystemsCP cell.com/cell-systems/f...](http://@CellSystemsCP.cell.com/cell-systems/f...)

 2 YEARS AGO



Janet
@Janis3_14159

Cross-Disciplinary Network Comparison: Matchmaking between Hairballs
sciencedirect.com/science/articl...

 2 YEARS AGO



George Mias
@georgemias

Going beyond geek chic sfchronicle.com/opinion/openfo... via @sfchronicle @MarkGerstein

 2 YEARS AGO



timelivenews
@timelivenews

Going beyond geek chic — CeBIT google.com/url?rct=j&sa=t...

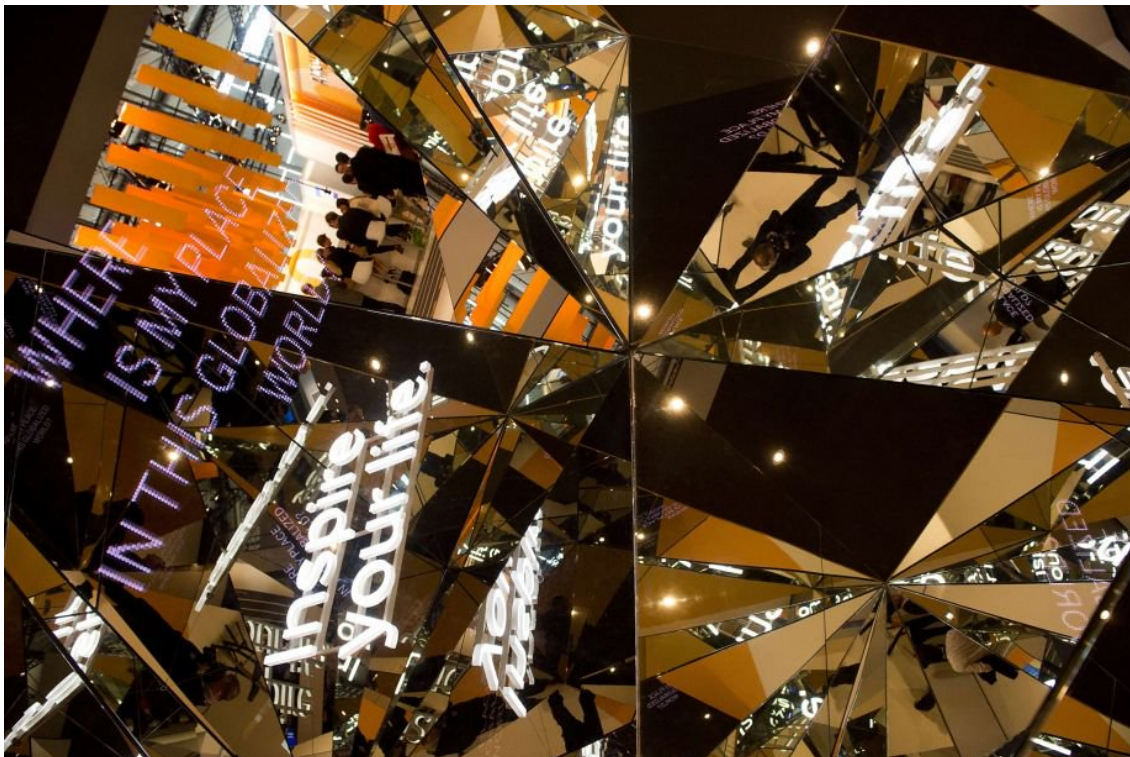
 2 YEARS AGO



Yale University
@Yale

Going beyond geek chic — by @MarkGerstein et al. bit.ly/1nDvdZp

 2 YEARS AGO



Opinion: Going beyond #geekchic — #CeBIT. sfchronicle.com/opinion/openfo...
pic.twitter.com/QPp9gvD1xl

 SAN FRANCISCO CHRONICLE @SFCHRONICLE · 2 YEARS AGO



Lois Kazakoff
 @lkazakoff

Going beyond geek chic — CeBIT sfchronicle.com/opinion/openfo... via @sfchronicle

 2 YEARS AGO



Evil Geek Magazine™
 @evilgeek

Going beyond geek chic — CeBIT - San Francisco Chronicle bit.ly/1UjMJ1M

 2 YEARS AGO



Charles Williams
 @ComputerOneStop

Going beyond geek chic — CeBIT: Kaleidoscopic mirrors reflect slogans and fair visitors at the stand of German... bit.ly/1TyB5Bh

 2 YEARS AGO



Lien Bazar

@LienBazar

Going beyond geek chic — CeBIT: ... last season's shoes to fashion week, failing to keep up with the latest de... bit.ly/1TyuuXA

 2 YEARS AGO



New File Formats

@newfmts

Going beyond geek chic — CeBIT - San Francisco Chronicle: Going beyond geek chic — CeBITSan Francisco Chroni... bit.ly/1UjAhyY

 2 YEARS AGO



#Code2Cure

@code2cure

Learn about BreakSeq2: a fast and accurate junction-mapping approach for detecting structural variants bit.ly/1WSw2tc

 2 YEARS AGO

Phenotype ID	HIV status	Phenotype 1	Phenotype 2	...	Phenotype q
PID-1	HIV+	0.1	-2.7	...	90.3
PID-2	HIV-	0.5	8.6	...	63.5
⋮	⋮	⋮	⋮	⋮	⋮
PID-n	HIV-	-0.2	5.4	...	50.3

Genotype ID	Variant 1	Variant 2	...	Variant q
GID-1	0	1	...	1
GID-2	2	1	...	0
⋮	⋮	⋮	⋮	⋮
GID-m	1	2	...	1

Phenotype 1	←→	Variant 1
Phenotype 2	←→	Variant 2
...		
Phenotype q	←→	Variant q

Phenotype ID	HIV status	Variant 1	Variant 2	...	Variant q
PID-1	HIV+	1	0	...	2
PID-2	HIV-	2	2	...	1
⋮	⋮	⋮	⋮	⋮	⋮
PID-n	HIV-	0	1	...	1

Genotype ID	Phenotype ID	HIV status	Variant 1	Variant 2	...	Variant q
GID-1	PID-8	HIV+	0/0	1/1	...	1/1
GID-2	PID-3	HIV-	2/2	1/1	...	0/0
GID-3			1/0	1/0	...	0/2
GID-4	PID-1	HIV+	2/2	0/0	...	1/1
GID-5			0/1	1/1	...	2/1
⋮	⋮	⋮	⋮	⋮	⋮	⋮

1 Genotype data set (stolen/hacked/queried)

2 Phenotype-genotype correlation data set

3 Genotype prediction

4 Genotype comparison and matching

Quantifying private info leakage from #phenotype-#genotype data rdcu.be/gaWn @MarkGerstein @naturemethods pic.twitter.com/oTvQlhnKqo

 GEORGE MIAS @GEORGEMIAS · 2 YEARS AGO

**Orli Bahcall**

@obahcall

Quantification of private information leakage from phenotype-genotype data [@MarkGerstein](#)
[@naturemethods](#) [rdcu.be/f8tp](#)

2 YEARS AGO

**Nicolas Robine**

@notSoJunkDNA

Quantification of private information leakage from phenotype-genotype data: linking attacks by
[@MarkGerstein](#) [nature.com/nmeth/journal/...](#)

2 YEARS AGO

**Alfonso Valencia**

@Alfons_Valencia

'Identifying individuals using phenotypes' ... a needed caution note by [@MarkGerstein](#) lab
[nature.com/nmeth/journal/...](#) [@nature](#) via [@anavinuela](#)

2 YEARS AGO

**nextgenseek**

@nextgenseek

Quantification of private information leakage from pheno-genotype data: linking attacks.
Harmanci & [@MarkGerstein](#) [nature.com/nmeth/journal/...](#)

2 YEARS AGO

**Nature Methods**

@naturemethods

AOP: What's the risk of being identified by independent data on phenotype & genotype? (\$) [bit.ly/1PMs6Fl](#)

2 YEARS AGO

**Yale University**

@Yale

As genomic information grows, so do privacy risks — as shown by work in [@MarkGerstein](#) lab
[bit.ly/1nIormo](#)

2 YEARS AGO

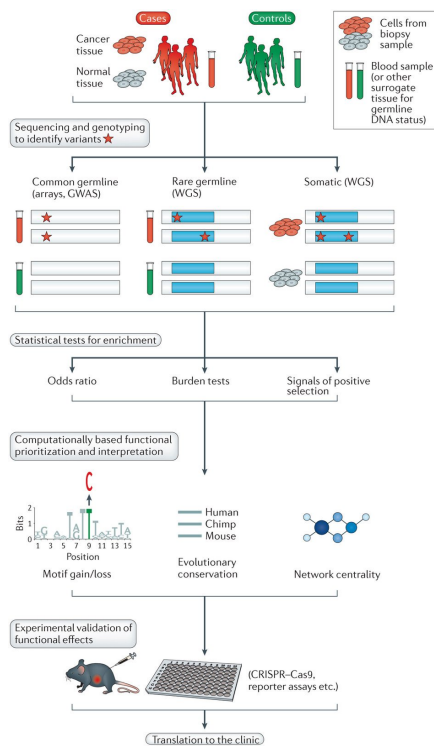


Margarida Ruas
@guidaruas

@MarkGerstein review of The Deeper Genome by @JohnParrington cell.com/cell/abstract/...



2 YEARS AGO



Nature Reviews | Genetics

Great read! #genomics ...non-coding sequence variants in #cancer rdcu.be/fVbn @ekta_khurana @MarkGerstein pic.twitter.com/vKCQ0LdzYn



SUMIT MIDDHA @BIOINFOSM · 2 YEARS AGO



Alfonso Valencia
@Alfons_Valencia

Interesting review "Role of non-coding sequence variants in cancer go.nature.com/Ouytfp " @MarkGerstein lab. via @cwcyau @Piwdb



2 YEARS AGO



Michael Hoffman
@michaelhoffman

Role of non-coding sequence variants in cancer by @ekta_khurana @MarkGerstein in @NatureRevGenet nature.com/nrg/journal/va... (\$)



2 YEARS AGO

**Ekta Khurana**

@ekta_khurana

Our review on the role of noncoding variants in cancer is now online
nature.com/nrg/journal/va... w/ @MarkARubin1 @MarkGerstein



2 YEARS AGO

**Genome Biology**

@GenomeBiology

.@MarkGerstein &co review the role of non-coding variants in #cancer @NatureRevGenet
bit.ly/1Pd092n #genomics



2 YEARS AGO

**Nicolas Robine**

@notSoJunkDNA

Role of non-coding sequence variants in cancer by @ekta_khurana @MarkARubin1
@MarkGerstein et al. nature.com/nrg/journal/va...



2 YEARS AGO

**Sumit Middha**

@bioinfosm

#bioinformatics #Genomics LARVA: analysis of recurrent variants in noncoding annotations
nar.oxfordjournals.org/content/43/17/... @MarkGerstein @ekta_khurana



2 YEARS AGO