@MarkGerstein's tweetbook of favourites

Created by Mark Gerstein

(Includes tweets from 07/12/2015 till 05/25/2019)

@MarkGerstein
Mark Gerstein
#Bioinformatics Professor, interested in #DataScience, with Photography, Triathlons History as hobbies
Yale

@MarkGerstein's tweetbook of favourites
Contains 428 tweets tweeted between 07/12/2015 and 05/25/2019.
Created on 26/05/2019 by http://tweetbook.in.

2015

July

12th July, 2015

14:00 @dikwizdumb: @markgerstein t question isn't y can't they, t question is why should they? what do potential&current employees as well as company get4It? □

2017

November

28'th November, 2017

23:58 @JoanieLemercier: https://t.co/7lLcdGLfHi

December

18'th December, 2017

16:59 @NatureCareers: Check out our latest podcast for some top tips on meaningful #mentoring and #cybersecurity for holiday travellers… https://t.co/zB1NdDZQNl

21'st December, 2017

03:10 @FNavarroBioInfo: 2017 in 14 pics (from Nature) @markgerstein https://t.co/VRco0XudKd (Credit: NASA/SDO) https://t.co/4eazhH5m0q

30'th December, 2017

17:47 @MrEwanMorrison: "The most famous actress the world has ever known" - Sarah Bernhardt (1844-1923) was also a skilled sculptress. Her… https://t.co/1PZ025TMXv

2018

January

4'th January, 2018

15:11 @gcosma1: Gentle Introduction to the Bias-Variance Trade-Off in Machine Learning https://t.co/yK99FPqX7o

11'th January, 2018

17:58 @sushant211: @MarkGerstein https://t.co/yVMcmN7qNu

13'th January, 2018

18:07 @gamzeandgursoy: @MarkGerstein @ozgunharmanci https://t.co/dluMxIE8pN

14'th January, 2018

01:57 @MarkGerstein: What to expect in '18: science in the new year https://t.co/5UGv6YfMJL Insights from cancer & ancient #genomes. Cur… https://t.co/B4mLoIj6HH

21'st January, 2018

13:54 @StevenSalzberg1: The flu season is bad, and now we're shutting down the CDC. Great. https://t.co/Hm3aCYMTtl

25'th January, 2018

18:12 @gamzeandgursoy: 3D printing with light! @MarkGerstein https://t.co/Lqdp8o48Pd

29'th January, 2018

01:07 @ClarksysCorner: Universal Alternative Splicing of Noncoding Exons - https://t.co/iX3V59e2XP "a fundamental distinction between pro… https://t.co/Myno5rqnnK

February

1'st February, 2018

17:45 @YaleMed: The new Yale Center for Biomedical Data Science will be the focus of the @YaleMed Dean's workshop on Feb. 7.… https://t.co/m23lnvkuFd

4'th February, 2018

03:19 @conormyhrvold: .@Glassdoor profiled in the New Yorker: Improving Workplace #Culture, One Review at a Time https://t.co/JQrvKSgWi9 #tech #corporateculture

16:54 @mashable: This ridiculous bike invention wants to keep you dry https://t.co/0uN3aSb73O

7'th February, 2018

18:02 @YINSedge: The inauguration of the Yale Center for Biomedical #DataScience @Yale #CBDS7Feb #collaboration https://t.co/XU7DHOQwuj

18:09 @KrishnaswamyLab: Excited about the start of the new biomedical data science center here at Yale! #CBDS7Feb https://t.co/uAqycntBCU

18:17 @allenlh: Great sight: Dean @RuthMontgomery1 kicking off new Yale Center for Biomedical Data Science standing room only!… https://t.co/apVrqw6S7v

18:21 @YINSedge: Amazing progress with #scaling and integration with genotype-phenotype relationships. Exponential scaling changes g… https://t.co/zWJcIJDfDZ

18:28 @VinCannataro: Mark Gerstein @MarkGerstein starting off #CBDS7Feb comparing genomics to photography. Used to be available to a few… https://t.co/8bqIDCN16d

18:28 @YalePCCSM: At #CBDS7Feb introduction @MarkGerstein mentions that Caroline the Center was Dr. Carolyn Slayman's Vision - We all… https://t.co/kOKqHbJ0Vi

18:30 @allenlh: Honoring Dean Carolyn Slayman: her "fingerprints are all over" new @YaleMed Center for Biomedical Data Science… https://t.co/IpvFR9kQRU

18:38 @YalePCCSM: Hongyu Zhao : @YaleMed is a great place with superb scientists - the Center for Biomedical Data Science will serve… https://t.co/26HsnqpOzJ

18:39 @sushant211: Monika Jadi talking about modeling of neurophysiological data #CBDS7Feb

18:43 @YINSedge: Computational modeling of neurophysiological #data from new faculty Monika Jadi (psychiatry and neuroscience)… https://t.co/k9RSxL2xJV

18:44 @sushant211: MJ: rate code pattern or time coding to represent information. How visual system encode this information? #CBDS7Feb

18:56 @YINSedge: The moment when @hmkyale walked into the auditorium at EXACTLY the moment he's summoned to the podium. Audience bur… https://t.co/CaEPAkT4Rs

18:58 @sushant211: HK: aggregation of data, analytics and application needs to come together to provide end to end solution in health care. #CBDS7Feb

19:02 @allenlh: "In vivo, to in vitro, to in silico" @hmkyale notes we must get smarter with every interaction, use expert automati… https://t.co/H68lsWepMh

19:03 @zekavatm: @YaleMed Inauguration for Biomedical Data Science Center. Looking forward to learning and contributing to this comm… https://t.co/hluNH3CwmJ

19:07 @l_peer: Making the point that science, including data science, should be judged by its positive impact on people's lives @hmkyale #cbds7feb

19:09 @FNavarroBioInfo: Medicine has been moving from "In vivo, to in vitro, to silico" @hmkyale #CBDS7Feb

19:13 @sushant211: Murat Gunel: different era of genetics. Discovery of gene for Mendelian disease, GWAS fo common disease, role of de… https://t.co/3RTRgnYBrE

19:15 @YINSedge: Now on deck, Murat Günel discussing feasibility of identifying genetic variants. In the near future, data from geno… https://t.co/1Xl8RetvBB

19:28 @sushant211: SK: how to look into very high dimensional data. Also issue of sparsity and non linearity. #CBDS7Feb

19:38 @YINSedge: Understanding the shape of biological #DataScience @KrishnaswamyLab where they have the best names for tools… https://t.co/jVKq3Pu42x

19:40 @KaminskiMed: Wow! #CBDS7Feb https://t.co/JdKdu7tZ7z

19:43 @yaledatascience: Professor Daniel Spielman presents at the Inauguration of the @Yale Center for Biomedical #DataScience #CBDS7Feb an… https://t.co/ni8B53gqbX

19:51 @YINSedge: Dan Spielman (@YINSedge co-director) reports that new faculty Yihong Wu can infer the uninferrable. Stellar present… https://t.co/VLpxWxf11Q

19:56 @FNavarroBioInfo: DataHack@Yale - April 2018: https://t.co/9lc7PITMNA Department of statistics and data science #CBDS7Feb

20:18 @YINSedge: Finally, Andre Levchenko whose work is extremely complex in systems biology. #CBDS7Feb https://t.co/d42HWpP7rC

20:23 @BigDataBatman: Session on Batman center @YaleMed #CBDS7Feb Will it be a success where greatest need: clinical medicine? https://t.co/57jHQsqejK

20:33 @sushant211: Shirley Liu: hidden immunology signals from Tumor RNAseq #CBDS7Feb

20:44 @sushant211: SL: what kind of patient will respond to immunotherapy? Looked at TCGA rnaseq data to estimate tumor purity, merged… https://t.co/zEGiKxB3Yr

20:53 @sushant211: SL: Hot and Cold tumor based on immune invasion profile. Tested each gene interaction with T cell levels to influen… https://t.co/JcYmWudm1T

21:06 @hipcProject: @SesmaLab @RuthMontgomery1 @ImmPortDB @ImmuneSpace Congratulations to all. #datascience #datasharing #CBDS7FEB

21:09 @DaiweiTang: Shirley Liu: Leveraging RNA-Seq data from TCGA for infiltrating Immune cells(TIMER) and TCR profiling (TRUST) ▯ … https://t.co/XL6FmVHgiK

22:14 @yaleHFdoc: #CBDS7Feb @yalediscovers @MarkGerstein @hmkyale @YODAProject @YalePCCSM Important talk on real world big data appli… https://t.co/xu0WcSXJnj

8'th February, 2018

00:30 @kirandkeshav: Great #CBDS7Feb event @RuthMontgomery1 @YaleCRC

23'rd February, 2018

17:16 @artologica: Oh cool, the show I'm in at @MP4A got a nice review in the @washingtonpost https://t.co/P6X15quLOM #sciart

25'th February, 2018

13:11 @mashable: These continue to terrify us https://t.co/Lwy80jLE3y

26'th February, 2018

12:53 @StevenSalzberg1: Thinking about having some coffee today? Be warned (if you're in California)... https://t.co/eodmVIf8yG

March

4'th March, 2018

14:21 @StevenSalzberg1: Roger Bannister, the first human to break the 4-minute mile, dies at 88. The video of his historic race, narrated b… https://t.co/3rQr77Z4rf

15:30 @bobehayes: These are the best books for learning modern #statistics—and they're all free https://t.co/hbwtruNaaT #datascience… https://t.co/jDu3kQkeVT

5'th March, 2018

18:47 @DShaywitz: Heck of a piece by @sarahkliff on the shitshow of healthcare interoperability leading to continued reliance on fax… https://t.co/v6i15jxR7P

18:57 @bit_player: Patterns in hailstone deposition. Presumably, when a falling hailstone hits a bare patch, it bounces; but when it l… https://t.co/QUE2oOE3Gc

9'th March, 2018

09:59 @PaulFlicek: 25 years ago today, this press release announced the creation of @emblebi. I'm thrilled to be part of this great or… https://t.co/q0acgq4rP6

14'th March, 2018

16:08 @ozgunharmanci: We are organizing a session on biological data privacy at Pacific Symposium on Biocomputing on Jan 3-7, 2019, takin… https://t.co/JLDKUGMvyw

15'th March, 2018

20:45 @andrewsu: The more I hear about this program, the more I think it is a GREAT opportunity for recent/upcoming PhD grads intere… https://t.co/5gqWqsXMoz

22'nd March, 2018

01:46 @SBAmin: Via @jacksonlab FusorSV - a tool to assess performance and merge SV calls from an ensemble SV callers… https://t.co/z021HBRQKP

23'rd March, 2018

04:13 @zevkronenberg: @MarkGerstein @PaulFlicek @FNavarroBioInfo @CristinaSDSisu Nice paper, congrats @IanFiddes

05:26 @sarveshnikumbh: Interesting - "[..]how a single nucleotide mutation transformed a specific SINE element into an active CTCF binding… https://t.co/aP8VECZ7Ic

19:10 @robinhanson: It still amazes me that academic fields, connected by co-citation, are arranged in a ring. Is there a missing "dark… https://t.co/cYXNd8J9Hi

April

8'th April, 2018

21:15 @YINSedge: Honorable mention goes to Team 11 from @Yale (undergrads Chi Tong, Elaine Hou, and Ngan Vu) working on… https://t.co/q6jylTez60

21'st April, 2018

13:02 @moorejh: The 2015 #deeplearning review in Nature by Geoffrey Hinton [PDF] https://t.co/PCapGNkRCM #machinelearning… https://t.co/S7dlK7c4Dt

25'th April, 2018

16:32 @YINSedge: Full house and standing 20 deep, @adamauton of @23andMe delights with industry seminar on a rainy day in New Haven… https://t.co/Diq0MFK9PH

17:17 @carlzimmer: Students from @MarkGerstein's class puts my my genome into their pipeline to look for Neanderthal DNA… https://t.co/EtROS0OAkg

26'th April, 2018

01:58 @Mengting_Gu: Cooked@Yale □ @MarkGerstein https://t.co/3fDlFC3wBy

28'th April, 2018

17:31 @Ahighervision: UP CLOSE: Ahead of STEM report, Yale takes stock https://t.co/Mcjv41Hfk6

30'th April, 2018

15:16 @mike_schatz: Very excited to announce "Accurate detection of complex structural variations using single-molecule sequencing"… https://t.co/ttpCh5iRMg

May

4th May, 2018

10:41 @JFBrock: We need a Mathematics of AI - AI researchers allege that machine learning is alchemy https://t.co/w2GpeqXCAf

9th May, 2018

14:48 @averydavisbell: Can't be reminded enough how much we are missing by doing GWAS mostly in Europeans (ST giving great examples) #BoG18

14:50 @MarkGerstein: @averydavisbell 81% of GWASes have been done in people of European descent #BoG18

14:51 @FNavarroBioInfo: For more on skin color variation in Africans with .@SarahTishkoff : Check TwiEvo podcast: https://t.co/f9fhljp1zZ #BoG18

14:54 @averydavisbell: ST pigmentation work is great example of followimg GWAS to function, and how using the populations with diversity o… https://t.co/NnlG90EYNU

15:04 @ninadoak: Sarah Tishkoff talks about skin pigmentation loci in African population. #BoG18 https://t.co/WslUH5FmWY

15:09 @kzkedzierska: So excited about first talk from @UniofOxford where I'll be starting my PhD this fall. Patrick Alberts is talking a… https://t.co/GW0midtzBp

15:16 @konradjk: PA: what fraction of _your genome_ is shared with _another genome_ back in time? Using allele aging approach genome… https://t.co/pDoXkHibcU

15:19 @vivekbhr: Patrick albers shows a video of an individual genome ancestry going back up to million years.! #BoG18 #Genomics #Bioinformatics

15:20 @averydavisbell: PA soon to release an atlas of allele age for over 16 million alleles! #BoG18

10'th May, 2018

00:14 @averydavisbell: Piero Carninci on RADICL-seq: method to map as many RNA-chromatin interactions as possible. What's going on with no… https://t.co/8tMwdTbZt4

00:22 @JavierHerrero7: Piero Carninci - Modalities of interactions. RNA-chromatin interactions seem to form a triple helix #BoG18

00:33 @_sbay: Griffiths quotes Lewis Wolpert: "It is not birth, marriage, or death, but gastrulation which is truly the most impo… https://t.co/sLD0ZUUWfA

00:34 @JavierHerrero7: Jonathan A. Griffiths — quotes Lewis Wolpert: "It is not birth, marriage or death but it is gastrulation which is t… https://t.co/O1v2BiaXg0

00:40 @MarkGerstein: JG: tSNE of mouse gastrulation atlas. Shows nice clusters & paths of early cell types #BoG18

01:22 @ilyakorsunsky: Enhancers don't always have consensus binding sites. Suboptimal binding actually required for restricted expression… https://t.co/qp0ncW9XEz

01:23 @averydavisbell: EF hypothesis: enhancers are suboptimal to ensure tissue specificity. Makes great sense with data, shows that enhan… https://t.co/VdMjoA09vF

01:51 @MarkGerstein: JY cites Clock-dependent chromatin topology modulates circadian transcription & behavior https://t.co/Zjc4o0cah0 Ch… https://t.co/VKaZyfjOeC

01:59 @averydavisbell: Minal Caliskan is penultimate speaker tonight - fine mapping in the liver. Last speaker will be Parisa Razaz on fun… https://t.co/7TSVzXt4mP

02:08 @MarkGerstein: MC cites Fine-mapping cellular QTLs with RASQUAL & ATAC-seq https://t.co/Fdatccl5YA In relation to finding hQTLs in her liver dataset #BoG18

16'th May, 2018

18:27 @carlzimmer: Our insect-eating ancestors 200-million years ago made enzymes to digest their exoskeletons. We humans carry broken… https://t.co/2ahZEI2B3q

17'th May, 2018

15:30 @gamzeandgursoy: @MarkGerstein @hoondy https://t.co/O86C4KRIth

20'th May, 2018

17:02 @Mengting_Gu: How about replacing #Macbook with #HuaweiMatebookXPro @HuaweiDeviceUSA https://t.co/Vgorileiif

21'st May, 2018

01:31 @michael_nielsen: Incredible chart. Take mortality statistics & subtract infectious disease. You see: (a) in the twentieth century we… https://t.co/dVIpGgSsBy

23'rd May, 2018

18:34 @georgemias: Great review @MarkGerstein! #Network Analysis as a Grand Unifier in Biomedical #DataScience @AnnualReviews… https://t.co/OL4FsyQnCp

26'th May, 2018

04:24 @ahmadcbukhari: Semantic Web in the Age of Big Data: A Perspective Will we drown in a data tsunami or enter a knowledge utopia?https://t.co/t0jjbAl9F4

30'th May, 2018

20:00 @sushant211: @MarkGerstein https://t.co/8GMRyxG8cU

June

1'st June, 2018

21:27 @gamzeandgursoy: @KateBradfordSci @JohnsHopkins Gerstein lab (@MarkGerstein) is always looking for motivated PhDs. https://t.co/Bl3X9ixU2Y

2'nd June, 2018

13:52 @JcvasqV: Shout out to @ranjitbindra and Bindra Lab's work on IDH mutations and synthetic lethality with PARP inhibitors… https://t.co/zqKUHwQsbu

7'th June, 2018

12:06 @moorejh: Great to see you @MarkGerstein! #yale https://t.co/TYaeEmwq1K

12'th June, 2018

15:34 @gamzeandgursoy: Our new preprint is online https://t.co/RTd2bOZuxv. Sensitive information leakage from functional genomics data: qu… https://t.co/OYILduMGT7

17'th June, 2018

03:13 @jwbelmon: "What he sees as the fundamental mystery about the origins of modern capitalism is not why it took so long to be es… https://t.co/w7WMNAEyAF

19'th June, 2018

17:41 @michaelhoffman: Sensitive information leakage from functional genomics data: Theoretical quantifications & practical file formats f… https://t.co/PyslXYyOwp

25'th June, 2018

07:41 @BrunelResearch: We look forward to the keynote speech of Prof @MarkGerstein from @Yale at today's event focusing on the revolution… https://t.co/eufLGGCdr8

14:30 @diegogaleano05: Great talk today at Brunel, keynote speaker Prof. @MarkGerstein on Variants in Personal Genomes #gemnet #brunel… https://t.co/OafvA4pXjP

26'th June, 2018

10:45 @DD_FaFa_: The Quartz guide to artificial intelligence: What is it, why is it important, and should we be afraid? https://t.co/9GEGFXfTxw

12:52 @SGorokhova: New preprint from @MarkGerstein on the ways to protect subject's privacy when sharing functional genomics data https://t.co/uBwP5U7pQq

16:17 @sushant211: @ozgunharmanci @MarkGerstein https://t.co/ZSpJXxaUWM

30'th June, 2018

11:09 @segal_eran: Genes linked to many brain structural features! Expect many papers soon linking genes to imaging features https://t.co/Vr9QgG196C

15:56 @flightradar24: Yesterday was the busiest day of the year in the skies so far and our busiest day ever. 202,157 flights tracked! Th… https://t.co/3znW9BA6ed

July

1'st July, 2018

02:56 @alwaysabluesky: https://t.co/lQxMVyqpQR thanks to @Amazon and #AI #DataScience #MachineLearning #DeepLearning #innovation like… https://t.co/gSMUrDxWgO

2'nd July, 2018

16:25 @cbrueffer: The #bioconda paper is finally out in @naturemethods! Congrats to everyone involved, especially @bjoerngruening, Ry… https://t.co/0QjBnTkxgS

6'th July, 2018

03:25 @FNavarroBioInfo: .@MarkGerstein I mentioned this earlier today. "Comparing Image Recognition APIs" "cowboy with horse painting" tha… https://t.co/EbhHkcCE0O

9'th July, 2018

18:43 @DOEKBase: Excited to announce that the #KBase paper has been published in @NatureBiotech!!! https://t.co/tzwUGLn7g9… https://t.co/iApQXAB2CD

10'th July, 2018

20:56 @kirandkeshav: □ @YaleCRC □ □ @MarkGerstein □ https://t.co/bdGz0R55vP

11'th July, 2018

09:20 @ricard_sole: What is the structure of the universe of language/communication networks? Our paper "The morphospace of language ne… https://t.co/z2VCgcuCaL

23:06 @JohnNosta: Very interesting! So what would the average age of a start up founder who fails be? #innovation #digitalhealth https://t.co/7bpjf4xrsb

23'rd July, 2018

22:20 @YueLabSGC: Great talk by @MarkGerstein #ACAtoronto Look forward to trying out the aptly named prediction tools STRESS, FRUSTRA… https://t.co/yFttymtDFz

25'th July, 2018

01:26 @moorejh: Here is Brook's 2001 Nature paper on "The relationship between matter and life" https://t.co/JidIdoD8Ne. #alife2018 #artificialintelligence

26'th July, 2018

12:17 @FNavarroBioInfo: People can actually hack into Illumina GAII (DNA sequencer) and modify it for other purposes. “The GAII is basic… https://t.co/LhqzT3ONn0

22:45 @jmschreiber91: For fun, I made an animation showing Avocado learning to impute an epigenomic experiment. It's trained on 1,013 epi… https://t.co/vEBmcaGBVp

28'th July, 2018

04:13 @CatchTheBaby: Can you see the big "8" between the diamonds? https://t.co/25VvPLv0do

August

7'th August, 2018

13:43 @EricTopol: Patient-derived xenografts—mouse "avatars"—for #cancer were touted to be the way to optimize #cancer treatment. But… https://t.co/5876ZnzOBA

13'th August, 2018

21:34 @gamzeandgursoy: Congrats @ozgunharmanci and @MarkGerstein for featuring in Editors' Highlights @NatureComms https://t.co/dp68sKeIBo

24'th August, 2018

11:27 @MarkARubin1: Allele-specific epigenome maps reveal sequence-dependent stochastic switching at regulatory loci @MarkGerstein… https://t.co/nhke16Y0Ns

25'th August, 2018

14:00 @CellCellPress: Book Review of “Who We Are and How We Got There” By David Reich: “Ancient DNA is a triumph for genomics, demonstrat… https://t.co/tA8mCBEj52

September

1'st September, 2018

18:43 @LauraSRobinson: I'm starting to suspect I'm married to a psychopath https://t.co/JBaBzEi3Il

10'th September, 2018

21:10 @yaledatascience: #DataScience project pitches today! Opportunities for applying DS techniques to curing cancer, using GPS to track a… https://t.co/IoDNikeopx

19'th September, 2018

00:14 @shantaolee: "Another Ph.D. pseudogenized from this lab!" After five years at Yale with a wonderful advisor @MarkGerstein, I jus… https://t.co/odmtTkpV0i

21'st September, 2018

09:44 @andrewejaffe: @MarkGerstein @mjpchaisson @mike_schatz @bioinfo_mark @sebatlab @mason_lab @notSoJunkDNA its just confusing b/c dbS… https://t.co/JrDo2INNTR

15:12 @gpandeylab: @MarkGerstein giving an exciting talk on transcriptome mining at the @SinaiGenetics @IcahnInstitute seminar series. https://t.co/6B7JXEwRHM

17:22 @mjpchaisson: @andrewejaffe @MarkGerstein @mike_schatz @bioinfo_mark @sebatlab @mason_lab @notSoJunkDNA I'm sure most positions w… https://t.co/WEr6uzhup3

17:52 @YaleData: A brief history of data science https://t.co/kasVp3o8l7

18:02 @ZeynepHG: awesome talk by @MarkGerstein today at @IcahnInstitute on transcriptome mining & data privacy & population genetics… https://t.co/auUyVkFzEK

October

15'th October, 2018

17:43 @gamzeandgursoy: I'm so happy and proud to announce that Team GersteinLab (@MarkGerstein) won the #iDASH 2018 #genomeprivacy challenge track 1

21'st October, 2018

01:54 @johnobeto: I wholly agree. https://t.co/VAkCNgKYF3

22'nd October, 2018

15:04 @Yale: Op-ed by @markgerstein: The data debris we leave on our devices & why we should be able to properly clean them… https://t.co/OX5kccQPS8

23'rd October, 2018

13:33 @WillMeyerson: 3 times as many genomic variants are concurrently listed in a somatic mutation database and a germline mutation dat… https://t.co/TZrO8XMkii

26'th October, 2018

12:55 @erin_rod_phd: Happy #Halloween! Enjoy FrankenPumpkin! A flat bottom flask with a face, drawn by #GWU undergrad, J. Tanen. Chlorop… https://t.co/6DTt0wq5fl

November

9'th November, 2018

16:11 @EricTopol: 2 excellent pieces on @harari_yuval's work and his dystopian (and I think far-fetched) views… https://t.co/UWjiTnG4vn

10'th November, 2018

16:56 @CitizenHealthio: @EricTopol @harari_yuval @NellieBowles @Doctor_V @sciencemagazine @dovgreenbaum @MarkGerstein Just got done digesti… https://t.co/Uj0fmVNreb

December

3'rd December, 2018

00:09 @statesdj: Google's AlphaFold said to dramatically improve performance in protein structure prediction, but I find it hard to… https://t.co/S5rmZ9tw3w

6'th December, 2018

11:54 @suganthibala: @dgmacarthur @paulpharoah Good to hear that you have moved away from the 5% threshold. You probably remember that w… https://t.co/nmriUqXgiK

13:15 @dgmacarthur: @suganthibala @paulpharoah @MarkGerstein Oh no, I totally didn't remember that you also implemented this in ALoFT -… https://t.co/khkDJ9zYIU

16:00 @simongerman600: The 1949-1990 division of Berlin in East & West Berlin is still visible today in the Tram network. Source:… https://t.co/TzzkUa9Qey

7'th December, 2018

01:00 @suganthibala: @dgmacarthur @paulpharoah @MarkGerstein Yes indeed. Does LOFTEE plugin work well with HG38?

9'th December, 2018

17:36 @ZelminaL: #Deeplearning for #Immunotherapy #Biomarkers #rsgdream18 https://t.co/DxTVPZMEDy

17:47 @lzamparo: Shirley Liu's keynote at #rsgdream18 was amazing. Tools for getting a tone of extra mileage out of just bulk tunor RNA

30'th December, 2018

12:12 @Rainmaker1973: Photographer Amos Nachoum captures amazing moments of the life in the oceans, like this leopard seal on the brink o… https://t.co/46dSzy2oEf

2019

January

17'th January, 2019

01:33 @shantaolee: WGS is unbiased & more powerful in detecting coding variants (plus noncoding of course) and, counterintuitively, ac… https://t.co/MRkdpDt4tu

18'th January, 2019

16:03 @SheerPriya: Waiting for the start of the #SteitzSymposium @yale to celebrate the work and life of Tom Steitz https://t.co/WRVS4AfgV6

21:25 @calkan_cs: @shantaolee @MarkGerstein "... describe whole-genome sequencing as lacking bioinformatics tools" ▯ ♂️

22:33 @mbaudis: @shantaolee @MarkGerstein Paywalled. Not #openaccess, #openscience

19'th January, 2019

19:19 @pauline_pytka: Probability is a mathematical concept NOT a scientific truth! Wrongly applied in too many situation for self inte… https://t.co/vb2zBUWXLG

20'th January, 2019

01:22 @Mengting_Gu: I enjoyed reading the piece! @MarkGerstein https://t.co/rSlLiYCgMb

22'nd January, 2019

13:05 @mike_schatz: Opinion by @StevenSalzberg1 arguing for open sharing of genetic data for those that would like to share: Let People… https://t.co/esHhEk9KZI

13:30 @gamzeandgursoy: @MarkGerstein https://t.co/snO2h5sZth

23'rd January, 2019

14:38 @KidneyCancerDoc: @Williamson_SR @lalpritu @JournalCancer @virajmaster Very low rate of somatic alterations. The population incidenc… https://t.co/hUXszPLuy3

24'th January, 2019

06:49 @Aubrey_tweetuje: @MarkGerstein @boschbot @gamzeandgursoy There is third word, though. Herbata.

26'th January, 2019

02:21 @wntyuli: Great read.... https://t.co/LQIBJjYJWp

27'th January, 2019

09:07 @Meitar_IDC: Great Job, as always by Gerstein Lab @MarkGerstein https://t.co/oVpUpYtOc7

30'th January, 2019

21:11 @exRNA: Join us for the next #ERCCseminar, Thursday Feb 7th at 1pm ET / 10 am PT. Joel Rozowsky from @MarkGerstein lab… https://t.co/ZY0ULzQhbl

February

1'st February, 2019

21:04 @likalo_llc: Who knows your coffee machine might be spying on you □ □ □ Have a great weekend! #productivity #starup #docsie… https://t.co/HbXkoRyXPA

4'th February, 2019

03:51 @anne_churchland: Big news from @biorxivpreprint ! Can't wait to see it. https://t.co/lfLmyWN0O8

04:26 @cathcoste: Life expectancy in Britain has fallen so much that a million years of life could disappear by 2058 — why? https://t.co/kByEHbzqPo

6'th February, 2019

12:58 @suganthibala: @deannachurch @JeffreyMKidd Agree! Also, the human-centric thinking (evolutionary perspective lost). We wrote a per… https://t.co/6NJkuBp1j2

16:09 @michaelhoffman: EK: Noncoding elements in the cancer genome. Review with @MarkGerstein @NatureRevGenet #19w5128… https://t.co/fzQHYDNFEw

16:14 @michaelhoffman: EK: FunSeq: Functional Impact of Sequence Variants: identifying non-coding mutations with functional impact. with… https://t.co/tHpFysgsEQ

20'th February, 2019

19:12 @JShendure: Thrilled to share our 2 million cell atlas of mouse organogenesis A single experiment with sci-RNA-seq3 E9.5 to E1… https://t.co/dZ8yz6gDSt

21:35 @coletrapnell: Our atlas of gene expression during mouse organogenesis is out today (https://t.co/5lYKZDDVVW) ! Joint work with… https://t.co/nW6Gbv41Ub

24'th February, 2019

16:57 @SBAmin: That's going to be a good comeback for Nokia; teaming up with @TheLightCo https://t.co/AqQZ1BamZa @MarkGerstein you may like this.

28'th February, 2019

20:00 @ftmaestre: If you have not read yet this @nature letter about small vs. large scientific teams https://t.co/cP8g60wjeT you sho… https://t.co/KuEH2rbRke

March

2'nd March, 2019

11:04 @animalculum: Untangling the Formation of DNA Loops https://t.co/7wNXo5PdrR New discoveries on ancient loops in DNA offer clues… https://t.co/k3IbNc6EnO

8'th March, 2019

22:43 @Mengting_Gu: After five wonderful years with my great advisor @MarkGerstein and people in the Gerstein lab, I successfully defen… https://t.co/FvP8d96r1T

13'th March, 2019

01:16 @Mengting_Gu: Does it suggest anything if people are more impressed by my graduation cake than my thesis ▫ https://t.co/MeApc87Kmv

14'th March, 2019

14:26 @YaleRNA: Interested in identifying protein-#RNA interactions? Join us next Thursday in Brady Auditorium for a workshop on… https://t.co/uEXQ4fXEJf

16'th March, 2019

02:42 @sushant211: Many congratulations to @patmcgillivray for matching to @JohnsHopkinsDOM. @MarkGerstein https://t.co/NCVMQmvuJN

18'th March, 2019

13:31 @asbonerw: Nice Q&A with @MarkGerstein on the benefits of WGS compared to WES. Time to move to WGS and generate the basis for… https://t.co/ihfMg1Zfx4

28'th March, 2019

18:00 @skydog811: The 1st Yale Workshop on AI, Ethics, and Society https://t.co/vOBwfHW6YJ

29'th March, 2019

03:09 @MarkGerstein: Posting my talk tomorrow at MCBIOS '19 in Alabama https://t.co/4YGGe0ZAhA Using...functional genomics to suggest po… https://t.co/9URqQG4tvD

03:10 @bnlasse: #MCBIOS19 keynote talk by @MarkGerstein here: https://t.co/6oQ8PQS5ZS

15:57 @SteveQinEmory: Looking forward to @MarkGerstein ‘s keynote talk at #MCBIOS19 . https://t.co/GtHN2RWufb

16:04 @bnlasse: @MarkGerstein keynote now at #mcbios19 on #brain #genomics (see slides linked above--thanks for sharing Mark!)

16:12 @d_kihara: Keynote by @MarkGerstein on PsychENCODE at #MCBIOS19 #mcbios https://t.co/KDdlHPzVcv

16:52 @jakechen1: @MarkGerstein from Yale is giving a fascinating keynote at #MCBIOS19 about psychENCODE project, leading to hopes fo… https://t.co/2q6SRSS4sP

18:02 @ZonePhysics: 10 million years ago, turtles could eat you with a single bite. https://t.co/qLtKjJ4vaU

22:58 @rjdoerksen: @MarkGerstein Great talk!

30'th March, 2019

16:47 @mashable: This augmented reality room is so trippy https://t.co/dDMi8Esicq

18:20 @bnlasse: #MCBIOS19 keynotes were favorite. Thanks speakers! (cc @MarkGerstein) https://t.co/VsTGcvGdW1

31'st March, 2019

17:48 @SiobhanvGordon: Rembrandt in the Blood: An Obsessive Aristocrat, Rediscovered Paintings and an Art-World Feud https://t.co/DRnyBwOPjT

April

2'nd April, 2019

04:22 @NisheethVishnoi: Excited to co-organize the 1st @Yale workshop on AI, Ethics, and Society with @profelisacelis @jackbalkin and Zolta… https://t.co/RGm8zXKssK

04:22 @NisheethVishnoi: Participants include those from @YaleLawSch @YaleEconomics @YaleSOM @yaledatascience @yaleseas @ProfJeffBrock… https://t.co/BduTl2d41z

13:48 @l_peer: RDA keynote by @stoyanoj (streaming now https://t.co/dTlEUOhOKF) relevant to @YaleLawSch symposium on Friday on AI,… https://t.co/X9MfbuLhYq

19:46 @yaleseas: From medicine to philosophy and law, the implications of artificial intelligence will be discussed Friday, April 5… https://t.co/xMjhpEhEWA

3'rd April, 2019

17:16 @profelisacelis: Excited for the 1st Yale Workshop on AI Ethics and Society, which is happening THIS FRIDAY! Looking forward to grea… https://t.co/csOIT3VIeA

19:36 @JenLucPiquant: Scientists Need More Cat DNA, and Lil Bub is Here to Help. Unusual DNA helped make Lil Bub a cat celebrity. Now tha… https://t.co/hoeV1E6avt

4'th April, 2019

15:19 @NIH_CommonFund: Our Extracellular RNA Communication program (co-led by @ncats_nih_gov, @theNCI, @nih_NHLBI, & @NIDAnews) is moving… https://t.co/CS7YweNqhK

15:25 @CellCellPress: The new issue of Cell is out! Featuring the Extracellular #RNA Communication Consortium (https://t.co/FBeywo0rjZ),… https://t.co/a6ORyodygQ

15:29 @CellCellPress: NIH Extracellular RNA Communication Consortium: An #extracellular #RNA atlas from 5 #human #biofluids reveals 6 RNA… https://t.co/WQBLD5Jbe9

18:02 @amilosav: The first map of a new type of intercellular communication in humans is now available at https://t.co/5VHHbSIYig… https://t.co/HGAZWORxQ2

18:34 @NIH_CommonFund: News from @BCMHouston featuring one of our #ExRNA Communication program's papers published today in @CellCellPress. https://t.co/ZE32BySEo0

18:59 @Yale: A catalogue of profiles from the @MarkGerstein lab shows how RNA helps cells communicate https://t.co/7dRMxFFF0k… https://t.co/fgV4I9zcEm

19:53 @YaleSOM: Mark Gerstein (@markgerstein) will give a Convening Yale talk on "Genomics & Data Science" on April 23. Register:… https://t.co/Aj2eSS1tkb

20:07 @NCIPhySci: The Extracellular RNA Communication program is moving extracellular RNA biology forward by making #exRNA protocols,… https://t.co/r4IRDOItEq

20:28 @Jarecot: RT Extracellular RNA Communication Consortium: A systematic comparison of 10 extracellular #RNA #isolation #methods… https://t.co/KFGNgtqWZr

21:34 @CellPressNews: Extracellular, extraordinary! Read insights from the Extracellular RNA Communication Consortium, now published in C… https://t.co/gdIJblC7vr

5th April, 2019

04:26 @daniel_abadi: This auto-reject site (https://t.co/dFgtRmVo3c) highlights the charade the peer-review process has become in modern… https://t.co/kVbWhrSFAU

19:14 @profelisacelis: Now for an interesting discussion on how we at Yale can further the hugely important questions at the intersection… https://t.co/YkvF0rvKZa

20:59 @ozgunharmanci: New Paper: Congrats @rozowsky @MarkGerstein https://t.co/l6wrlPP8Sq #exRNACC #exRNA

7'th April, 2019

15:03 @JMRothberg: Omit needless words https://t.co/DmwBmzXMkX

8'th April, 2019

10:34 @ewanbirney: A little twitter moan about the semi recurrent meme that "GWAS is just correlation". People point out the interesti… https://t.co/EVdT4NsQex

16:02 @high_fly2026: Stony evidence of the hellfire that drove dinosaurs to extinction - Economist - Science https://t.co/urLWzz6n5r

15'th April, 2019

16:01 @7homaslin: Scott Kelly Spent a Year Taking Photos in Space. They're Beautiful. via @nytimes Left: A frozen lake in the Himalay… https://t.co/YRcyCKE2GT

16'th April, 2019

15:15 @mjpchaisson: This was a huge effort that we are all proud to have out! https://t.co/uyJw8luQhe . There are so many contributors… https://t.co/1GmfsUEINl

20:32 @mjpchaisson: 6/n ... (continuing after catching breath) thank you @s_mccarroll, Goo Jun, Li Ding, Chong Lek Koh, Bing Ren,… https://t.co/P20SZLL1ns

17'th April, 2019

17:16 @YaleNeuro: @YaleMed researchers led by @YaleNeuro @KavliAtYale Professor Nenad Sestan report in @Nature on restoration of brai… https://t.co/Kr5bE7deD0

17:41 @KavliAtYale: Researchers in the lab of @KavliAtYale Investigator, Nenad Sestan, report on specialized #technology that restores… https://t.co/nDGqW7kJSk

23:52 @JShendure: IN DEAD PIGS https://t.co/1QVUH3rNFd

18'th April, 2019

04:03 @JohnRMoffitt: Dispite my strong belief that all problems can be solved with Duct Tape, I was surprised to see them repairing a pa… https://t.co/Tvanuna77e

11:30 @YaleRNA: Dr. Nenad Sestan, faculty member of @YaleRNA, publishes in @nature on a new system to restore molecular and cellula… https://t.co/qHccREGVnt

22'nd April, 2019

22:07 @carlzimmer: @alanburdick Today @MarkGerstein's students got through chromosomes 1-5. At this pace, we'll be done with my genome in 2023.

23'rd April, 2019

15:02 @YaleSOM: Today: A look at biomedical data science in a lecture with @Yale #bioinformatics prof. @MarkGerstein.… https://t.co/kMa1POs7Uu

25'th April, 2019

02:19 @EricTopol: i don't know about you, but I was pretty blown away by what she did! No need for #AI. Just her human I.

26'th April, 2019

14:05 @michaelhoffman: Does the answer change if correct tones are missing or present?

28'th April, 2019

17:42 @michaelhoffman: @GermHunterMD @ORCID_Org allows you to specify a Twitter username but so few have it set up or displayed publicly t… https://t.co/UfRXeDEiN3

19:22 @michaelhoffman: @egonwillighagen @wikidata I feel like I should add this information to my biosketch https://t.co/wIIbl5ATyE

May

1'st May, 2019

18:47 @patmcgillivray: I greatly enjoyed speaking at the Yale Rare Disease Seminar organized by @theFourier2k @sanderpajusalu about our wo… https://t.co/yEFo1oEkYV

4'th May, 2019

22:55 @nomad421: I guess I'm lucky that I found my room! #RECOMB2019 https://t.co/mCBJvUaEbu

23:13 @MarkGerstein: Posting my "highlights talk" tomorrow in Washington, DC at #RECOMB2019 (#RECOMB19) https://t.co/P1iON8Ld8E Focuses… https://t.co/wnoBipsKKZ

23:14 @nomad421: @MarkGerstein Looking forward to your talk!

5'th May, 2019

01:33 @evan_cofer: @MarkGerstein Looks like it will be a good talk. Can't wait!

11:55 @manoliskellis: Excited to chair the #RegulatoryGenomics session at #RECOMB2019 tonight, with: FOCS @tomAhait… https://t.co/jtWXeeiJRN

13:05 @gibsonkeylie: Excited to see all of you at @recomb2019 today at the main conference! Come see @Alfons_Valencia open up the confer… https://t.co/LMUzmeW7cd

13:26 @dcdanko: Will we use 'digital twins' to predict patient outcomes before giving medical interventions? If Prof. Valencia a… https://t.co/YTZvhOJXhj

13:27 @gibsonkeylie: @Alfons_Valencia speaking about correlations with comorbidities and gene expression studied with publicly available… https://t.co/bsVlOgLmvN

13:28 @MarkGerstein: At #Recomb2019, @Alfons_Valencia (working in the most beautiful supercomputing facility in the world!) describes h… https://t.co/rx0O8O8b5o

13:32 @ldoroud: Some diseases are anti-correlated. People with schizophrenia have lower chance of getting lung cancer. Networks can… https://t.co/qMvT7Yktmb

13:34 @MarkGerstein: @ldoroud Inverse comorbidity for schizophrenia & lung cancer particularly surprising since SCZ individuals smoke mo… https://t.co/QCbzX8bZOw

13:40 @ldoroud: An example of disease relationships... In a GWAS study, anti correlations of asthma/allergies and pancreatic cancer… https://t.co/FX5R9l8ET5

13:40 @johannhawe: @Alfons_Valencia kicking off the main conference #RECOMB2019 with his key-note on digital twins, stratified comorbi… https://t.co/0348mMCR09

13:50 @RachidOunit: #recomb2019 just started with @Alfons_Valencia as 1st keynote speaker: Understanding #comorbidity using models base… https://t.co/v1UYuVxJLe

14:05 @ldoroud: Mark Gerstein @MarkGerstein : A lot of the psychiatric conditions are highly heritable and thus genomics can help u… https://t.co/ubvirhePwS

14:08 @ldoroud: How to use a deep learning model to use genotypes and gene regulatory networks to predict phenotypes #recomb2019… https://t.co/vvUX906u5z

14:12 @ldoroud: Using deep learning models you can sometimes get a slight improvement over PRS — what happens if we try to impute t… https://t.co/ozfkxG2xNy

14:16 @Alfons_Valencia: Very much of an amazing talk by @MarkGerstein on the neuropsychiatric disorders -psychencode.org consortium paper.… https://t.co/9dlA5uTjk7

14:16 @dcdanko: Wish you had more datatypes for your subjects? Deep Structured Phenotype Networks impute missing transcriptomic da… https://t.co/rMQQbxykLt

14:19 @hajirasouliha: Next is SNP heritability estimation by Ali from the infamous @UCLA crew! #recomb2019 https://t.co/0a595VP9o5

14:19 @johannhawe: Great talk by @MarkGerstein about generating interpretable deep learning models (DSPNs) by embedding gene regularly… https://t.co/KzswzuD6jL

14:26 @ldoroud: Ali Pazoki talking about heritability, how to calculate it and what are important parameters. For instance chromoso… https://t.co/woCX0U5lHT

14:31 @ldoroud: Using Hutchinson's estimator, we can use matrix-vector multiplications instead of matrix-matrix multiplications for… https://t.co/j6L1iXMue4

14:33 @dcdanko: Modular linear models will help us reach the long tail of SNP heritability in sublinear time. Great talk by Dr. Al… https://t.co/kXRUwaoQRK

14:39 @ldoroud: It's sad to see only ~500 attendees at #recomb2019 when similar #ML conferences attract thousands ...

14:43 @samsungilkim: Very lucid talk on "Interpretable deep learning modeling embedding gene regulatory network" by @MarkGoldstein… https://t.co/OwKYsYInVF

15:27 @hajirasouliha: Good to see the genome sequencing cost slide for the 87th time at a talk (yes I do keep track) #recomb2019 https://t.co/aavrCmCe3K

15:32 @ldoroud: Alan Kuhnle is talking about r-index and how it solves the challenges with suffix arrays and FM index specially for… https://t.co/7BII2KWHhC

15:40 @ldoroud: Using prefix-free parsing to compress repetitive strings (so smaller suffix array construction, etc) — anyone knows… https://t.co/CaiVzb91HF

15:42 @DCGenomics: Using Salmonella Genomes from GenomeTrakr as a benchmark a new mapper (bigbwt) #RECOMB2019 https://t.co/BzKxDkEgIo

15:43 @gibsonkeylie: #til that the human genome reference is mostly comprised of a single individual from mixed ancestry. #RECOMB2019 @recomb2019

15:43 @iScience_CP: Reference genome largely represents a SINGLE genome. Diversity representation? L #recomb2019

15:50 @ldoroud: Roughly 10% of the data from sequences are not being represented in the reference genomes and thus are ignored. Are… https://t.co/QxjQNSvpcK

15:55 @gibsonkeylie: 296.5 Mb non-human genome reference insertion sequences were found from 910 humans of African descent. The longest… https://t.co/sqPBzOwuvt

15:55 @traingene: Finally made it to #recomb2019, and fortunately arrived just in time for a highlight talk I was really looking forw… https://t.co/cxL4uF12NM

15:57 @RachidOunit: A significant amount of human genomic information is lost/missed because of references sequences that are incomplet… https://t.co/Bruubc4cxe

15:59 @ldoroud: Rachel Sherman @rshermanjhu: It seems like reference genomes do not have systematic bias for any particular populat… https://t.co/RTSg8P2cQx

16:02 @MarkGerstein: At #Recomb2019, @RShermanJHU ends with the note that the “pan-genome is still open” - ie there’s seemingly a linea… https://t.co/RfdID2rZAw

16:02 @gibsonkeylie: It will be good to keep in mind that there’s a lot that we’re missing and there’s probably a lot that we’re going t… https://t.co/UW66SN46gg

16:04 @johannhawe: Hunting for the missing reference - @rshermanjhu from @StevenSalzberg1's lab talking about her work on why unaligne… https://t.co/j5amqGg4bO

16:09 @MarkGerstein: @gibsonkeylie @rshermanjhu In the #Recomb2019 Q&A, @RShermanJHU argues that the linear increase suggests that graph… https://t.co/tcSK7599Yc

16:09 @hajirasouliha: The pan-genome is still open. We need more methods / sequenced genomes to assemble novel sequences. #recomb2019 https://t.co/r0e4BynS2f

16:12 @nomad421: Amazing talk by @rshermanjhu at #RECOMB2019 on her work on on assembly of a pan-genome, finding a large amount of s… https://t.co/5dN62bplhm

16:47 @StevenSalzberg1: @MarkGerstein @gibsonkeylie @rshermanjhu Couldn't agree more. Talk to @BenLangmead if you want to hear more on how… https://t.co/jc5wUCea5q

17:46 @bvhalldorsson: @MarkGerstein @hajirasouliha @rshermanjhu A linear increase with number of sampled genomes seems more consistent wi… https://t.co/R0EuGB5y2F

17:57 @rshermanjhu: @bvhalldorsson @MarkGerstein @hajirasouliha We are quite confident these are not falsely identified variants. That… https://t.co/LEetJ4rk4v

19:09 @MarkGerstein: At #Recomb2019, Sason presents multinomial mixture model for determining cancer mutational signatures. Does better… https://t.co/cc1Weo0uFy

19:53 @iScience_CP: The advantages of FOCS: enhancer and gene activity patterns infers an extensive enhancer—promoter map #Recomb2019 https://t.co/om8fprFeEe

20:25 @iScience_CP: #Recomb2019 variability in methylation: known knowns, unknowns unknowns, and in-betweens https://t.co/MxZMoLPpw0

6th May, 2019

17:34 @gibsonkeylie: Please remember this when attendeding conferences in person or via twitter! Being kind is the most important thing. https://t.co/Twn5D1NXxu

8'th May, 2019

13:31 @skathire: #BoG19 should do a pool on how many Manhattan plots will be shown at Biology of Genomes 2019 @cshlmeetings □

13:32 @CharlestonCWKC: HC: Take each SNP, deconvolute the effect based on average of 6 fields x 2 eyes into each of the layers/field/eye,… https://t.co/vD59OvfzAM

13:34 @carninci: Hannah Currant, on UK Biobank, 500K individuals, 96M variants: focus on retinal phenotype. Retina inspected for phy… https://t.co/3k36d6T6vj

13:40 @ewanbirney: HC: Clusters SNPs in a 24-dimensional space from the OCT data, and fall out into 3 quite separate clusters. One of… https://t.co/i8wuUGHVzy

14:00 @fellgernon: Now we have Nicole Rockweiler @nonfiniteloop from @washugenetics on work with the @GTExPortal Consortium #BoG19 foc… https://t.co/8OkXdW4rtX

14:00 @CharlestonCWKC: NR: postzygotic mutations can explain phenotypic variation (on top of germline variation, environment, epigenome).… https://t.co/eyagwuoUNa

14:01 @NeBanovich: I just generally enjoy talks about postzygotic mutations/mosaicism #bog19

14:02 @NeBanovich: Nicole Rockweiler is "repurposing" GTEx data to study postzygotic variation #bog19

14:02 @CharlestonCWKC: NR: Can we detect? When and where did post-zyg mutations occur? Use GTex data (~960 normal donors, ~17 tissues per… https://t.co/S2UfS33hUH

14:04 @NeBanovich: NR: Developed method to identify postzygotic mutations from bulk RNA-seq data. Showing results validating known bio… https://t.co/K0KE1qMm1s

14:05 @brimittleman: .@nonfiniteloop discussing the importance of postzygotic mutations on phenotype with some great figures to demonstr… https://t.co/BT4NfLQavD

14:06 @hagentilgner: Nicole Rockweiler: 7% of somatic mutations found in multiple tissues. #BoG19

14:08 @MarkGerstein: At #BoG19, @noninfiniteloop finds more postzygotic mutations in the GTEx sun-exposed skin samples, particularly for… https://t.co/QaRurRV2Gn

14:09 @CharlestonCWKC: NR: Postzygotic mutations accumulate with age for some tissue: e.g. whole bloos, sun-exposed skin, esophagus, lymph… https://t.co/sgTE9T7s3D

14:12 @CharlestonCWKC: NR: Estimate ~80% of mutations occurring before Gastrulation, rest are downstream on the developmental tree (ectode… https://t.co/l9H99TQNBM

14:13 @carninci: Rockweiler/3. Mutations are tissue specific (example: C->T in skin). Brain less mutations. Age/timing? Shared mutat… https://t.co/HNOciq02QF

14:19 @skathire: Really beautiful talk by @nonfiniteloop on post-zygotic mutations in GTeX What looks to be first survey of somatic… https://t.co/lYHFILDNmD

14:20 @ewanbirney: We're giving Nicola Rockweiler a bit of tough set of questions. She's handling them well, going back to data. My ow… https://t.co/vRgPlM2KPJ

14:20 @preetiaahir: Algorithm to detect postzygotic mutations from RNA-Seq. @nonfiniteloop tells us early cell divisions are more mutag… https://t.co/JPLkPcZS6A

14:20 @MarkGerstein: At #BoG19, @noninfiniteloop’s talk triggers many Qs but not any associated with cancer or associated mutational processes. Wonder why?

14:42 @CharlestonCWKC: Barbara Engelhardt (@BeEngelhardt): discovering and distinguishing as many cell types as possible. #BoG19

14:46 @ewanbirney: BE: experimental design (and Bayesian). (editorial - love it) - this old a problem. Alexander Corbet in early 20th… https://t.co/eqib6IDXAq

14:49 @ewanbirney: Great phrase "Idea: Frame sequential design as a contextual multi-armed bandit". I am all for a contextual multi-armed bandit! #bog19

14:50 @CharlestonCWKC: BE: Given finite budget, and what have already been see based on # cell type from each organ, how to maximize the p… https://t.co/ue8kQJzyq8

14:50 @brimittleman: Sampling butterfly species as an analogy for discovering cell types from @BeEngelhardt. She uses this to outline a… https://t.co/Z4dhytxfuA

14:52 @becky_furlong: I think the UK MPs should have used a contextual multi-armed bandit process for indicative votes on Brexit, althoug… https://t.co/dRGjYuHVAg

14:57 @aaronquinlan: Really fun talk from @BeEngelhardt on a Bayesian approach for optimizing experimental design to maximize cell type… https://t.co/FdFwsPIPo0

14:58 @fellgernon: BE @BeEngelhardt & @datumbeet developed GT-TS and used it with simulated mouse cell atlas data New results (not on… https://t.co/MBVvt52X1a

15:04 @carninci: When the session organizer/co-chair speaks overtime, what is the message for trainees? #bog19

15:05 @CharlestonCWKC: Michael Schatz: 100 Genomes in 100 Days: the structural variant landscape of tomato genome. #BoG19

15:06 @StevenSalzberg1: @mike_schatz talking now about sequencing 100 tomato genomes in 100 days. Very cool project. I hope this will lead… https://t.co/HmH85dAn0K

15:08 @CharlestonCWKC: MS: reference genome published in May 2012. Heinz sample, 12 chromosomes, 950 Mb genome, used for GWAS in tomato. S… https://t.co/hRohiRaWg7

15:10 @MarkGerstein: At #BoG19, @Mike_Schatz points out that in tomato, SVs are known to be drivers of quantitative variation

15:13 @brimittleman: Looks like structural variation are driving phenotypic variation rather than snps in tomato. Could this be due to a… https://t.co/eg1Cxg6gig

15:14 @CharlestonCWKC: MS: greedily identify the most diverse species from short-read data to identify candidates for long-read sequencing… https://t.co/l2E6gYmZ6G

15:17 @fellgernon: Mike @mike_schatz gave a shoutout to this nice review done by others (Rang et al, 2018) https://t.co/TV1cYHmswL Fi… https://t.co/oTk9iqpOnz

15:18 @StevenSalzberg1: Love it that the genome scaffolders used by @mike_schatz for the tomato genome are called SALSA2 and RaGOO. Coincidence? #BoG19

15:20 @SarahJGeisler: @mike_schatz provides a delicious example of how technology advances, looking at you PromethION, catapulted their e… https://t.co/wgeON5SXe0

15:22 @ewanbirney: Quick COI note here: for the followers who don't know, I'm a long term consultant to @nanopore, so have a Conflict… https://t.co/WsfRPV9OgA

15:25 @CharlestonCWKC: Ruthie Johnson (@ruthie_johnson): dissecting genetic architecture of complex traits through local polygenicity usin… https://t.co/f8yGDGAnhH

15:25 @NatalieTelis: Tomato genome talk made everyone hungry. SO, Since we all want to have lunch, moving on to @ruthie_johnson looking… https://t.co/c2oBeXo7qo

15:26 @EBartom: Really nice talk by @mike_schatz showing the power of long reads for detecting structural variation with PromethION… https://t.co/McvWr7xfsx

15:28 @PLOSBiology: Loads of methodological advances here at #BoG19 - remember that @PLOSBiology now considers Methods & Resources pape… https://t.co/NHwNYnz1pK

15:28 @CharlestonCWKC: RJ: Causal effect size distribution parameterized by effect size (beta) and number of causal SNPs (k) (Zhang et al.… https://t.co/npTL7RNAuc

15:29 @NeBanovich: @ruthie_johnson Describing BEAVR (Bayesian EstimAtion of Variants in Regions) which estimates local polygenicity fr… https://t.co/5Ymso7Auhn

15:31 @ChrisOmics: My girl @ruthie_johnson talking about her new method BEAVR estimating proportions of causal SNPs in a region at… https://t.co/NmUDBW8AZq

15:34 @CharlestonCWKC: RJ: Applied to GWAS summary statistics, estimate height to have ~14000 causal SNPs genome-wide, explaining h2 ~0.6.… https://t.co/8kSA3HafrA

15:37 @MarkGerstein: At #BoG19, @Ruthie_Johnson shows that heritability is highly correlated with the number of causal SNPs. Deviations… https://t.co/a3P1H10GkH

15:38 @sorrywm: .@ruthie_johnson's BEAVR method chows down on the tough wood of estimating how many causal SNPs in a region contrib… https://t.co/FRMZl9bMtr

15:38 @aesrth: On our way to the morning session! @CHSL has a beautiful campus! #BoG19 #GenomesSparkJoy @genomeresearch https://t.co/Ve5YEFUN4a

15:42 @ZeynepHG: @MarkGerstein @ruthie_johnson How else would it be?

15:42 @CharlestonCWKC: RJ: show examples where certain regions of genome show excess of heritability explained for certain traits. Aggrega… https://t.co/CJ3mqtFSs0

15:44 @NeBanovich: Yi Qiao discussing scBayes to study subclonal chromatin accessibility in tumors #bog19

15:44 @bpasaniuc: Great job from @ruthie_johnson presenting the regional polygenic estimation work at the #BoG19 ! https://t.co/WTwsxEDLdQ

15:52 @fellgernon: YQ (@MarthGabor lab) describes their solution: scBayes for computing the posterior probability that given the scRNA… https://t.co/vBZzs8vD9x

15:57 @SarahJGeisler: Yi Qian is closing out the session with scBayes as a method for combining tumor subclone-specific single cell data… https://t.co/wMPp6Tkvwt

16:01 @jkalleberg2: Second day at #Bog19 has begun! @cshlmeetings #genomessparkjoy https://t.co/1wUdba3ynC

16:01 @sorrywm: Interesting finding from Yi Qiao's talk: "mis-classified" sub-clones from breast cancer longitudinal dataset using… https://t.co/Q8j0T3w0dm

17:36 @ajprice20: Lost in translation #BoG19 #GenomesSparkJoy https://t.co/xiKZq1OpPc

18:26 @trentmpc: Functional and computational genomics sessions are complete at #BoG19! Feeling inspired by the impressive rising re… https://t.co/WNwg0uKge3

19:15 @ajprice20: #BoG19 #GenomesSparkJoy this place is magic https://t.co/7oA3uY11c1

20:05 @laxvid: #GenomesSparkJoy the other campus https://t.co/Egn1mGvAaz

21:08 @genomeresearch: Adenovirus Gazebo @cshlmeetings #BoG19 #genomessparkjoy https://t.co/o2dOFNs2j4

21:09 @DrSNilson: #GenomesSparkJoy #BOG19 https://t.co/jUsF91w8kM

21:10 @DrSNilson: #GenomesSparkJoy #BoG19 https://t.co/e5jSz3FGHQ

21:26 @msuvakov: #GenomesSparkJoy #BoG19 https://t.co/h42312o1ag

21:31 @msuvakov: #GenomesSparkJoy #BoG19 https://t.co/uHBAZBDfJ5

22:08 @theJARMlab: #genomessparkjoy #bog19 https://t.co/jr41iTMpTJ

22:38 @theJARMlab: #GenomesSparkJoy #BoG19 https://t.co/qHqJkEWWYd

22:44 @MichaelLouisPl1: Is Conference Room Air Making You Dumber? - The New York Times https://t.co/A1lEOrxT5E

22:55 @laxvid: #GenomesSparkJoy https://t.co/y1cjr6uy7K

23:05 @genomeresearch: The first winner of the #GenomesSparkJoy photo contest has been announced on our instagram page!! #BoG19 --> https://t.co/R0c6zez8mx

23:12 @JonLerga: Making DNA at the mecca of genetics #GenomesSparkjoy #CSHL https://t.co/KSMH73hn7C

23:33 @CharlestonCWKC: Sek Kathiresan (@skathire): PRS and Risk Prediction for MI #BoG19

23:40 @CharlestonCWKC: SK: polygenic score in 300k individuals was a nice bell curve. The score has r = 0.02 with the ACC/AHA risk score.… https://t.co/Qj5V0Yubm4

23:40 @ewanbirney: Sek takes us through the construction of polygenic risk score - from MI GWAS, selected best score from 20 with firs… https://t.co/iMlGxgzAKy

23:43 @carninci: Kathhiresan, on the myocardial infarction heritable components (less than 55 years old). Example monogenic: hyperch… https://t.co/HgKOPBK4CT

23:44 @fellgernon: In Khera et al @skathire used data from the @uk_biobank and found that high polygenic risk score individuals had in… https://t.co/gfV4xYV9yf

23:46 @CharlestonCWKC: SK: Raw PRS not doing very well in non-European ancestry population if applied, but ancestry-adjusted PS would brin… https://t.co/7AgqDldKqH

23:46 @fellgernon: Then @skathire went beyond the @uk_biobank and looked at other ethnic groups: lead to a glass half full story since… https://t.co/D4ZiSVrmd4

23:51 @CharlestonCWKC: SK: extend PRS to diseases beyond MI: atrial fibrillation, diabetes, IBD, breast cancer. Anywhere between 2-6% of p… https://t.co/YfagSzaq2e

23:56 @SarahJGeisler: in the first talk of the evening session at #BoG19 @skathire is describing polygenic risk scores with an outlook of… https://t.co/iDQFoyxqRP

23:59 @fellgernon: Took me a bit to find the actual figure I wanted to tweet initially (it was under "box 1" instead of figures) This… https://t.co/6jfKHiwiuq

9'th May, 2019

00:02 @fellgernon: Next Kasper Lang @kasper_lage on protein networks and their relation to genetic risk variants He gave a shoutout t… https://t.co/rXaz2zmGbB

00:09 @fellgernon: Kasper @kasper_lage found some genes with risk for schizophrenia for which they can generate some good protein-leve… https://t.co/ssM0jwnSxD

00:13 @carninci: Kasper Lage on the proteomics networks in schizophrenia. CACNA1C most enriched protein, together with a series of s… https://t.co/Pz3roukKuI

00:15 @fellgernon: Kasper @kasper_lage is showing the "social Manhattan plot" which shows how the genome-wide significant risk genes i… https://t.co/YAYq2C7NMW

00:15 @MarkGerstein: At #BoG19, @Kasper_Lage shows a nice visualization of both the Manhattan plot from GWAS & protein-protein interacti… https://t.co/3PF1AdRLA4

00:18 @JavierHerrero7: Based on the cool code from @_lazappi_, here are some tweeting stats for #BoG19 so far: https://t.co/wYpwRbutkX

00:19 @SarahJGeisler: In a herculean @kasper_lage is integrating #genetics with #proteomics in neurons to find protein interaction networ… https://t.co/R4djCAGtYp

00:20 @JavierHerrero7: Halit Ongen — Putative non-coding cis-regulatory drivers in chronic lymphocytic leukaemia and skin cancer #BoG19

00:22 @ewanbirney: Next up Halit Ogen from University of Geneva on non-coding regulatory elements in cancer. Beyond TERT there is a re… https://t.co/McRjnkwuOI

00:25 @brimittleman: H.Ongen wants to identify non-coding somatic drivers for cancer. Method: identifying cis regulatory domains from fu… https://t.co/CHhNpVkoHV

00:27 @fellgernon: Olivier Delaneau lead a project with @halt81 (SysGenetiX project SGX) I think that it's https://t.co/35GpYoeNA5 b… https://t.co/VvG4dVwwU2

00:30 @aesrth: Sunset @CSHL #BoG19 #GenomesSparkJoy @genomeresearch https://t.co/Oc62ri0Ft2

00:31 @JavierHerrero7: Halit Ongen — Mutational signatures in significant vs non-significant CRDs, shows some big differences supporting i… https://t.co/FbM5m0LsYi

00:33 @KVittingSeerup: You can find more info in their 2018 biorxive paper here: https://t.co/9EnhvUL3bU #bog19

00:34 @MarkGerstein: At #BoG19, Ongen describes a method to find CRD (cis-regulatory domains) that may be enriched for non-coding cancer… https://t.co/TfJ0rlG42y

00:47 @SarahJGeisler: @halt81 presents efforts diving into non-coding cis-regulatory drivers of under selection in tumorigenesis at #BOG19

00:54 @msuvakov: #BoG19 abstract book word cloud #GenomesSparkJoy https://t.co/NFlIj5hajG

01:15 @CharlestonCWKC: CW: immunotherapy now one of pillar of cancer care (along with surgery, radio and chemotherapy). But only 30% patie… https://t.co/OUfUi39rOt

01:23 @JavierHerrero7: Catherine Wu — Looking for neoantigens as a target for immunotherapy and vaccines. Proof-of-concept vaccines using… https://t.co/B3JM6V0zTw

01:30 @NeBanovich: Really great talk from Catherine Wu. It's very exciting to see the neoantigen -> personalized vaccine pipeline work… https://t.co/rw18xgande

01:42 @CharlestonCWKC: PD: 10,000 GWAS traits x 14M SNPs matrix, with cell value = effect size (+ se). Joint analysis has 3 challenges int… https://t.co/mIZAUZaQJK

01:43 @skathire: #BoG19 @genemodeller describes resource that @Genomicsplc has built □ □ Impressive. https://t.co/e77tFrZuZn

01:44 @JavierHerrero7: .@genemodeller — Co-analysis of 1000’s of GWAS to find common signals => increases power, improve fine mapping, pro… https://t.co/HP7ShnkQE0

01:44 @CharlestonCWKC: PD: Bayesian approach to cluster signal plots - those with no association, those with similar pattern suggest same… https://t.co/gvjCPcYosz

01:45 @fellgernon: Peter @genemodeller listed 3 key advantages of their approach: - borrow information across traits - improve fine m… https://t.co/NJwcnSi6Gx

01:46 @MarkGerstein: At #BoG19, @genemodeller starts off by describing a huge matrix of 14M SNPs X 10K phenotype & trait measurements. W… https://t.co/OofRxo2I55

01:48 @CharlestonCWKC: PD: Ex 1 C1orf106, originally assoc with Crohn's disease, ulcerative colitis, IBD. Improve stability of epithelial… https://t.co/gr0zStAfGK

01:57 @CharlestonCWKC: PD: For heart disease, stratify by individuals with high, intermediate, or low AHA risk scores, PRS can further dif… https://t.co/wkmM1SItHT

01:58 @brimittleman: .@genemodeller also discussing polygenic risk scores for complex traits and calls for increasing diversity in sampl… https://t.co/VBsMm3r12b

01:59 @MarkGerstein: At #BoG19, @genemodeller uses PRSes for coronary risk to further stratify high- & low-risk individuals (based on tr… https://t.co/Ook1ReKBUc

02:04 @CharlestonCWKC: Ashley Sanders: surveying structural variation landscapes in single cells reveals complex genomic rearrangement process #BoG19

02:06 @fellgernon: Next, Ashley Sanders (Jan Korbel's lab @emblebi) (final tweetable talk today) is showing us why methods that measur… https://t.co/s1WJlkqyZY

02:23 @EliseScience: Day two of #BoG19 had me weeping tears of joy and willowing in great science #badatpuns #itried #GenomesSparkJoy https://t.co/yz4MeWnF0L

02:30 @AnupriyaDalmia: #bog19 #GenomesSparkjoy https://t.co/th4NF2PCjo

02:33 @EBartom: #genomessparkjoy #bog19 https://t.co/IDT4FTQZvh

04:40 @fellgernon: Making of Amanda Joy @ajprice20’s #GenomesSparkJoy modeling entry ▯ at #BoG19 PS check her poster and preprint inv… https://t.co/4odufumdL2

05:09 @MarkGerstein: @ZeynepHG @ruthie_johnson I guess the way I wrote it sounds too obvious - but the key is the emphasis on causal SNPs.

11:48 @obahcall: Hello from your friendly Nature editors #BoG19! Here with ▯@beckyfurlong ▯@NatureComms & @VDominguesNEE ▯ ▯… https://t.co/qkgnvrRCXD

11:50 @JavierHerrero7: After a long day of talks, @cshlmeetings goes to sleep. #GenomesSparkJoy #BoG19 https://t.co/HwsqzbnX2f

12:31 @yuvalsim: These horseshoe crabs sure had fun yesterday at #bog19. Their #GenomesSparkJoy. https://t.co/uNgtt2Gegr

13:56 @aesrth: @CSHL #BoG19 #GenomesSparkJoy @genomeresearch https://t.co/0TYn2qfo6k

13:58 @aesrth: Flowers in bloooooom! @CSHL #BoG19 #GenomesSparkJoy @genomeresearch https://t.co/c40R7a8OHH

14:21 @saumya_bio: McClintock lab #genomessparkjoy @genomeresearch #BoG19 #MyScienceHero https://t.co/izxWwLFKjF

15:28 @MarinaLaplana: For science! Wine & cheese party @CSHL @cshlmeetings #GenomesSparkJoy #BoG19 https://t.co/MqUvN0ygDF

19:18 @ewanbirney: Peak east coast techno-hipster cryptocurrency Americana cannabis genome #bog19 https://t.co/x4hOYHdeGe

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00:19 @NatureEcoEvo: Wynn Meyer: Using convergent evolution to annotate yeast genome #BoG19

00:35 @EugenomeUK: Why do I like @CarlosEcolEvol's image of ant queens running around with little crowns on??? #bog19

00:49 @AnnaCuomo92: Science shore is nice when it's done on the beach. 'Tis the sea-son for #BoG19 #genomessparkjoy https://t.co/h6dxAdjl7X

03:55 @lucapinello: @CSHL is a magic place #BoG19 #GenomesSparkJoy https://t.co/9wH3j4ig2h

16:40 @IEEEembs: Are you a student/postdoc and hungry for a chat with world-class Biomedical Engineering Leaders? Then, join us at "... https://t.co/nTgNcz42hi

17:26 @skathire: A nice piece by @FayCortez on our evolving understanding of penetrance (what fraction of patients with a given muta... https://t.co/ZFOMhzjW7e

17:28 @manoliskellis: The quantified selfie #BoG19 #GenomesSparkJoy #PersonalGenomics #PearsonalGenome #Snyderome https://t.co/PgJdTrfd4K

17:50 @mindyshi: Finally a quick sketch before poster session begins! Here we go @ryan_e_mills #GenomesSparkJoy #BoG19 https://t.co/ND4YXXB56r

18:21 @AllisonInDC: A look down the superhighway of life #GenomesSparkJoy https://t.co/JPpc7Ul18g

20:59 @msuvakov: Can someone sequence this? #hasdna #BoG19 #GenomesSparkjoy https://t.co/YN02mFu2s4

11'th May, 2019

02:50 @MarkGerstein: For #BoG19's #GenomesSparkJoy picture compilation, I've been busy snapping shots of the great sculptures @CSHL. My… https://t.co/vTXHWdEDQd

14:00 @CharlestonCWKC: Bogdan Pasaniuc (@bpasaniuc): accurate estimation of SNP heritability from biobank data regardless of genetic architecture. #BoG19

14:03 @fellgernon: Now Bogdan Pasaniuc @bpasaniuc on comparing SNP heritability against heritability: we need to keep in mind the SNPs… https://t.co/I47Nf1kzuH

14:08 @CharlestonCWKC: BP: assumptions of the model => causal vector size ("polygenicity", # of non-zero effect), normality (generally rob… https://t.co/rTn3InvdJK

14:14 @MarkGerstein: At #BoG19, @BPasaniuc gives a nice overview of SNP heritability in previous literature. How it is enriched in vario… https://t.co/N7apg9tWGK

14:15 @fellgernon: Bogdan @bpasaniuc showed a set of excellent slides on how the different SNP-heritability methods work Now he is sh… https://t.co/6H1qWeQvTL

14:16 @sorrywm: .@bpasaniuc formalizes a Generalized Random Effects model for estimating SNP-heritability where each SNP can do its… https://t.co/iWWH8IPhDh

14:16 @SarahJGeisler: @bpasaniuc talks about dropping our assumptions in achieving accurate SNP-heritability at #BoG19

14:18 @obahcall: #BoG19 @bpasaniuc estimation of SNP-heritability from biobank-scale data using UKB, directly and accurately, irresp… https://t.co/S3WENbeRP5

14:51 @ewanbirney: This is happening in trillions of places in your body right now, providing you with energy. Biology is ... amazing… https://t.co/v2jLcHg0TG

12'th May, 2019

17:29 @crashius: He pioneered technology that fueled the Human Genome Project. Now his greatest challenge is curing his own son https://t.co/pIjGh9nR9y

24'th May, 2019

17:59 @FNavarroBioInfo: Our new preprint on deconvolving pervasive from autonomous transcription when estimating LINE-1 expression in RNA-s… https://t.co/9MIfi4F6zx

25'th May, 2019

14:49 @mike_schatz: Congratulations to @BenLangmead for his promotion to Associate Prof with tenure! Very well deserved!!! @JHUCompSci https://t.co/3lCPYvWoxX

@MarkGerstein's tweetbook of favourites

Created by

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