

Genomics & Data Science



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#3 - Simulation

Prediction based on physical principles (eg Exact Determination of Rocket Trajectory) Emphasis on: Supercomputers

#4 - Data Science

Data gathering and storing Data analysis including data mining, modeling, visualizing

Creative use of data exhaust and protection of privacy

Emphasis: networks, "federated" DBs

Science Paradigms

- Thousand years ago: science was empirical describing natural phenomena
 - Last few hundred years: **theoretical** branch using models, generalizations Last few decades:

a computational branch

simulating complex phenomena

• Today:

data exploration (eScience)

- unify theory, experiment, and simulation
 - Data captured by instruments
 - Or generated by simulator
- Processed by software
- Information/Knowledge stored in computer
- Scientist analyzes database / files using data management and statistics









FOURTH

PARADIGM

Gray died in '07. Book about his ideas came out in '09.....

What is Data Science? An overall, bland definition...

- Data Science encompasses the study of the entire lifecycle of data
 - Understanding of how data are gathered & the issues that arise in its collection
 - Knowledge of what data sources are available
 & how they may be synthesized to solve problems
 - The storage, access, annotation, management, & transformation of data
- Data Science encompasses many aspects of <u>data analysis</u>
 - Statistical inference, machine learning, & the design of algorithms and computing systems that enable data mining
 - Connecting this mining where possible with **physical modeling**
 - The presentation and visualization of data analysis
 - The use of data analysis to make practical decisions & policy
- Secondary aspects of data, not its intended use eg the <u>data exhaust</u>
 - The appropriate protection of **privacy**
 - Creative **secondary uses** of data eg for Science of science
 - The elimination of inappropriate bias in the entire process

- Ads, media, product placement, supply optimization,
- Integral to success of GOOG, FB, AMZN, WMT...





Data Science in the "Big Tech": a buzz-word for successful Ads



Data Scientist: The Sexiest Job of the 21st Century

by Thomas H. Davenport and D.J. Patil



Artwork: Tamar Cohen, Andrew J Buboltz, 2011, silk screen on a page from a high

When Jonathan Goldman arrived for work in June 2006 at LinkedIn, the business ne up. The company had just under 8 million accounts, and the number was growing qu friends and colleagues to join. But users weren't seeking out connections with the per rate executives had expected. Something was apparently missing in the social expe

Data **Science in Traditional Science**

High energy physics -Large Hadron Collider



Astronomy -Sloan Digital Sky survey



- Pre-dated commercial mining
- Instrument generated
- Large data sets often created by large teams not to answer one Q but to be mined broadly
- Often coupled to a physical/biological model
- Interplay w/ experiments



DNA

- Scientific data often coupled to a physical/biological model
- Lauffenburger's Sys. Biol. 4Ms: Measurement, Mining, Modeling & Manipulation (Ideker et al.'06. Annals of Biomed. Eng.)
- Weather forecasting as an exemplar
 - Physical models & simulation useful but not sufficient ("butterfly" effect)
 - Success via coupling to large-scale sensor data collection

Coupling of Scientific Data to Models & Experiments



Genomics & Data Science

- **Background** on data science & the biomed. sub-domain
 - Placing genomics in this context -- 3V & 4M frameworks
 - Types of data & integration betw. types + Moore's law scaling
- Main practical heath applications
 - Designing drugs, customizing treatments....
 - Focused example on identifying drug targets for neuropsych. diseases
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Drivers of Biomedical Data Science

- Integration across data types
- Scaling of individual data types



The Scaling of Genomic Data

Science:

Powered by exponential increases in data & computing

(Moore's Law)

[NHGRI website + Waldrop ('15) Nature]

Cost per Raw Megabase of DNA Sequence



Kryder's Law and S-curves underlying exponential growth

 Exponential increase seen in Kryder's law is a superposition of S-curves for different technologies



[Muir et al. ('15) GenomeBiol.]

Time

Sequencing cost reductions have resulted in an explosion of data

[Muir et al. ('15) GenomeBiol. Navarro et al. GenomeBiol. ('19, in press)]

 The type of sequence data deposited has changed as well.





From '00 to ~' 20, cost of DNA sequencing expt. shifts from the actual seq. to sample collection & analysis



[Sboner et al. ('11), Muir et al. ('15) Genome Biology]



Alignment algorithms scaling to keep pace with data generation



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How will the Data Scaling Continue? The Past, Present & Future Ecosystem of Large-scale Biomolecular Data



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Major Bioinformatics Applications

I. Designing Drugs from Structural Targets

- Understanding how structures bind other molecules
- Designing inhibitors using docking, structure modeling





II. Finding Homologs

- Model structures based on currently available structures
 - Find experimentally tractable gene targets

III. Customizing treatment in oncology

- Identifying key disease causing mutations
- Cancer immunotherapies targeting neo-antigens





IV. Personal Genome Characterization

- Identify mutations in personal genomes (SNPs, SVs, &c)
- Integrate with digital phenotyping (eg wearables)

(From top to bottom: figures adapted from Olsen Group Docking Page at Scripps, Sci. Am., Druker BJ. Blood 2008, Institute for Systems Biology)

Major Application V: Finding molecular mechanisms & drug targets for diseases we know little about (Neuropsychiatric Diseases)

Disease	Heritability*	Molecular Mechanisms			
Schizophrenia	81%	C4A			
Bipolar disorder	70%	-			
Alzheimer's disease	58 - 79%	Apolipoprotein E (APOE), Tau			
Hypertension	30%	Renin–angiotensin–aldosterone			
Heart disease	34-53%	Atherosclerosis, VCAM-1			
Stroke	32%	Reactive oxygen species (ROS), Ischemia			
Type-2 diabetes	26%	Insulin resistance			
Breast Cancer	25-56%	BRCA, PTEN			



Many psychiatric conditions are highly heritable

Schizophrenia: up to 80%

But we don't understand basic molecular mechanisms underpinning this association

(in contrast to many other diseases such as cancer & heart disease)

Thus, interested in developing predictive models of psychiatric traits which:

Use observations at intermediate (molecular levels) levels to inform latent structure.

Use the predictive features of these "molecular endo phenotypes" to begin to suggest actors involved in mechanism

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Automing gene expression development, and disease a 1202

Science Montainer

Schizophrenia: up to 80% But we don't understand basic molecular mechanisms underpinning this association (in contrast to man Thus, interested in deve Use observations interested in deve Use observations addressing this, involving Use the predictive suggest actors invitient in an antipart of the suggest actors invitient in the suggest actors in the suggest actors invited in the suggest actors in the suggest act



Developing a gene regulatory network for the human brain



Developing a gene regulatory network for the human brain



Deep Structured Phenotype Network (DSPN)

- Embed Gene Regulatory Network in deep neural network
- Allows transcriptome (+other) imputation & trait prediction



y: phenotypes

- X: intermediate phenotypes (e.g. expression, enhancers)
- h: hidden units (e.g., circuits)
- Z: genotypes (e.g., SNPs)

Deep Boltzmann Machine Energy model:

 $p(\mathbf{x}, \mathbf{y}, \mathbf{h} | \mathbf{z}) \propto \exp(-E(\mathbf{x}, \mathbf{y}, \mathbf{h} | \mathbf{z}))$

Deep Structured Phenotype Network (DSPN)

 Allows prioritization of genes / modules through network interpretation (using path tracing)



y: phenotypes

- x: intermediate phenotypes (e.g. expression, enhancers)
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27 = Lectures.GersteinLab.org

Mid-level of the hierarchy has many high-connectivity bottlenecks





Governmental hierachies exhibit even more pronounced mid-level bottlenecks



Level in hierarchy

Connectivity v. Constraint: in biological networks, less mutations tolerated at hubs & bottlenecks



Genes & proteins that have a more central position in the network tend to evolve more slowly and are more likely to be essential. This phenomenon is observed in **many organisms & different kinds of networks** – e.g. Protein-Protein Interaction Networks (human, yeast, E coli, worm, fly), miRNA networks, regulatory networks, &c

30 = Lectures.GersteinLab.org

Kim et a. PNAS 2007

==Centrality=>

Biological Networks tend to have more "democratic" hierarchies, easing bottlenecks, than many social ones



Middle Managers Interact the Most in Efficient Corporate Settings

- Floyd, S. W. et al (1992) Middle management involvement in strategy and its association with strategic type Strategic Management Journal 13, 153-167.
- Woodward, J. (1982) Industrial Organization: Theory and Practice (Oxford University Press, Oxford).
- Floyd, S. W. et al (1993)
 Dinosaurs or Dynamos? Recognizing Middle Management's Strategic Role The Academy of Management Executive 8, 47-57.
- Floyd, S. W. et al (1997)
 Middle management's strategic influence and organizational performance

Journal of Management Studies 34, 465-485.



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Transcriptional regulatory network vs Linux call graph

			<i>E. coli</i> transcriptional regulatory network	Linux call graph	
	Basic properties of systems	NodesGenes (TFs & targets)Functions (subroutines)		Functions (subroutines)	
		Edges	Transcriptional regulation	Function calls	
		External constraints	Natural environment	Hardware architecture, customer requirements	
		Origin of evolutionary changes	Random mutation & natural selection	Designers' fine tuning	
		kswapd			A subnetwork in the Linux
_bitmap_empty		balance_pgdat	set_cpus_allowed	1	call graph from CodeViz
[0]	shrink_slab	ond_reschedput_swap_token) shrink_zone zone_wa	termark_ok refrigerator	
PNAS		cond_resched th	rottle_vm_writeout shrink_inactive_li	ist shrink_active_list recalc_si	gpending _spin_lock_irq
n et al.,		congestion_wait	get_dirty_limits	recalc_sign	ending_tsk
tinish_wait	prepare_to_wait	io_schedule_timeout bdi_writeou	ut_fraction Clip_bdi_dirty_limit (task_dirty_limit determine_dirtya	able_memory

Dominated by "out hubs" - crp



35 - Lectures.

Dominated by "in hubs" - printf

[Yan et al., PNAS (2010), in press]

Connectivity v. Constraint: differences betw. biological & technological networks

More Connectivity, More Constraint : A Variation in call graph measured from number of theme borne out in many evolutionary edits to Linux source studies of biological network E Vonsynonymous to Synonymous SNP Ratio 25 r= -0.1, P=4x10⁻⁴ of Mutati evision frequency of function (normalized) 20 0 15 0 10 ate 5 Ŷ +0.29, P=3x10⁻⁹⁷ 10⁴ 10^{7} 10` 100 10 Betweenness Centrality Degree centrality ==Centrality=> Kim et a. PNAS 2007 Yan KK et al. PNAS 2010

Perspectives on Random Change v Intelligent Design

- Central points = hubs & bottlenecks
- If changes random, best not to put them in central pts.
- If changes made rationally, can put them into central pts.
 - Moreover, good to do this, as these more often used
 i.e more efficient
 - Why there's so much GWB construction



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Data Exhaust

- Creative use of data is key to data science!
- Data exhaust = exploitable byproducts of big data collection and analysis





Exhaust Mining Application: Using Science to Study Science (SOS)

- ENCODE member
- non-member
- ENCODE member broker
- non-member broker
 - ___ co-authorship



- Mining output of science (Scientific Publications) to understand how science works as a social enterprise
- Co-authorship network of members of the human genome annotation group (ENCODE) & users of this groups data



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Genomics has similar "Big Data" Dilemma as in the Rest of Society

- We confront privacy risks every day we access the internet (e.g., social media, e-commerce).
- Sharing & "peer-production" is central to success of many new ventures, with analogous risks to genomics
 - **EG web search**: Large-scale mining essential





Genetic Exceptionalism :

The Genome is very fundamental data, potentially very revealing about one's identity & characteristics **Personal Genomic info. essentially meaningless currently but will it be in 20 yrs? 50 yrs?**

but will it be in 20 yrs? bu yrs? Genomic sequence very revealing about one's children. Is true consent possible?

Once put on the web it can't be taken back **Ethically challenged** history of genetics

> Ownership of the data & what consent means (Hela) Could your genetic data give rise to a product line?

[Seringhaus & Gerstein ('09), *Hart. Courant* (Jun 5); Greenbaum & Gerstein ('11), *NY Times* (6 Oct), D Greenbaum & M Gerstein ('08). Am J. Bioethics; D Greenbaum & M Gerstein, Hartford Courant, 10 Jul. '08; SF Chronicle, 2 Nov. '08; Greenbaum et al. *PLOS CB* ('11); Greenbaum & Gerstein ('13), The Scientist; Photos from NY Times, it.wisc.edu]



The Dilemma

- The individual (harmed?) v the collective (benefits)
 - But do sick patients care about their privacy?
- How to balance risks v rewards

 Quantification

The Other Side of the Coin: Why we should share

- Sharing helps speed research
 - Large-scale mining of this information is important for medical research
 - Statistical power
 - Privacy is cumbersome, particularly for big data



[[]Economist, 15 Aug '15]

[Yale Law Roundtable ('10). Comp. in Sci. & Eng. 12:8; D Greenbaum & M Gerstein ('09). Am. J. Bioethics; D Greenbaum & M Gerstein ('10). SF Chronicle, May 2, Page E-4; Greenbaum et al. *PLOS CB* ('11)]

Current Social & Technical Solutions: The quandary where are now

- Closed Data Approach
 - Consents
 - "Protected" distribution via dbGAP
 - Local computes on secure computer
- Issues with Closed Data
 - Non-uniformity of consents & paperwork
 - Different, confusing int'l norms
 - Computer security is burdensome
 - Many schemes get "hacked" .
 - Tricky aspects of high-dimensional data (ease of creating quasi-identifiers)

Open Data

- Genomic "test pilots" (ala PGP)?
 - Sports stars & celebrities?
- Some public data & data donation is helpful but is this a realistic solution for an unbiased sample of ~1M



Linking Attack Scenario



Linking Attack Scenario



Linking Attacks: Case of Netflix Prize

Many users are shared

· The grades of same users are correlated

A user grades one movie around the same date in two databases

Anonymized Netflix Prize Training Dataset made available to contestants

Linking Attacks: Case of Netflix Prize

	N E T	FLIX		Na	mes available for mar	Db hy users!	
User (ID)	Movie (ID)	Date of Grade	Grade [1,2,3,4,5]	User (ID)	Movie (ID)	Date of Grade	Grade [0-10]
NTFLX-0	NTFLX-19	10/12/2008	1	IMDB-0	IMDB-173	4/20/2009	5
NTFLX-1	NTFLX-116	4/23/2009	3	IMDB-1	IMDB-18	10/18/2008	0
NTFLX-2	NTFLX-92	5/27/2010	2	IMDB-2	IMDB-341	5/27/2010	-
NTFLX-1	NTFLX-666	6/6/2016	5				

- Many users are shared
- The grades of same users are correlated
- A user grades one movie around the same date in two databases
- IMDB users are public
- NetFLIX and IMdB moves are public

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