# BIOE 310: Computational Tools for Biological Data

What this class is all about?

### Instructor

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## **Teaching Assistant:**

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## **Questions and Suggestions:**

maslov@Illinois.edu nambiar4@illinois.edu

Start subject with [BIOE310]

## Homework and Exams

- Homework assignments.
   Due at the beginning of the class on the designated day
- Midterm exam. March either before or after the spring break
- Final exam. Date will be decided by the College of Engineering

#### Grading:

Homework 30%

Midterm 30%

Final 40%

## **Academic Integrity**

- I change the exam problems or modify their parameters regularly
- Do not attempt to blindly reuse the answers from past year exams (or homework)
- People caught doing this for the first time will get
   O points for this problem (benefit of the doubt)
- The second attempt will be reported using the FAIR (Faculty Academic Integrity Report) portal

## Course Website

https://courses.engr.illinois.edu/bioe310

#### Grades will be on

https://my.bioen.illinois.edu/gradebook

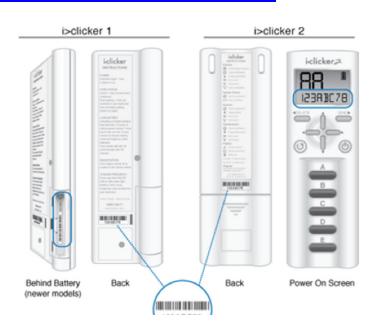
#### **BIOE 310 - Computational Tools for Biological Data**

#### Return to syllabus

#	Date	Topics	Slides	Matlab	Homework	Exams
1	Jan 26					
2	Jan 28					

## Bring your iClickers to my lectures

- Who knows what is an iClicker?
- Show of hands: who has an iClicker?
- I would like you all to have an iClicker and bring it to every class.
   On amazon.com a new iClicker (1<sup>st</sup> generation is OK) costs around \$40. It is also sold at UIUC Bookstore. The used ones are cheaper.
- An alternative solution is using a mobile app: <a href="https://www.iclicker.com/students/apps-and-remotes/apps">https://www.iclicker.com/students/apps-and-remotes/apps</a>
- Your answers <u>WILL NOT</u> be used for grading.
   I need them to see if I lost some of you and what could I rephrase to better explain the material



#### We will use Matlab in class

- Bring your laptops to class
- Poll: who <u>has</u> Matlab?
- Need to have Matlab installed and know the basic user interface (inline commands, plotting)
- We will use Statistics and Machine Learning Toolbox and Bioinformatics Toolboxes
- You can use CITRIX for UIUC students and connect to EWS Windows Lab Software
- .m files and .mat with Matlab commands and data will be on the website after the lecture

## Who has Matlab?

- A. Have on my own laptop
- B. Plan to use CITRIX
- C. I don't have matlab
- D. I don't know yet
- E. I will never use Matlab! Over my dead body

## Get your i-clickers

Possible alternative to purchasing Matlab and toolboxes is to use campus resources.

Engineering Workstations (EWS) have Matlab with statistics and bioinformatics toolboxes installed and can be accessed using CITRIX

See the following link on how to access:

https://answers.uillinois.edu/illinois.engineering/81693

https://go.illinois.edu/citrix

How to transfer data files? See these instructions:

https://answers.uillinois.edu/illinois.engineering/page.php?id=81206

## What will you learn in this course?

- Basics of probability and statistics
  - Basic concepts of probability, Bayes theorem
  - Discrete and continuous probability distributions
  - Multivariate statistics
  - Sampling distributions
  - Parameter estimation
  - Hypothesis testing
  - Regression
- How it is applied to biological data
  - Basics of genomics
  - Systems biology (gene expression, networks)

## The main Probability/Statistics Textbook

Applied Statistics and Probability for Engineers, 5th Edition

D. C. Montgomery and G. C. Runger

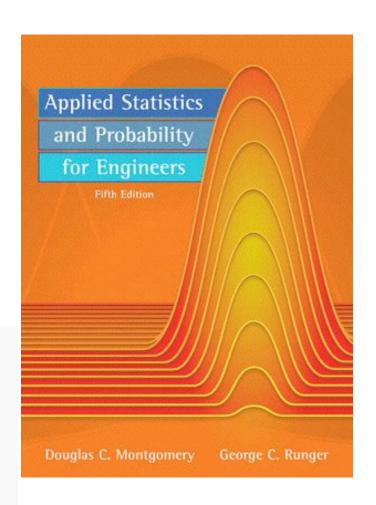
John Wiley & Sons, Inc. (2011)

You can also use other editions from 4<sup>th</sup> (2007) to 6<sup>th</sup> (2014)

5<sup>th</sup> edition is available for free

at our library





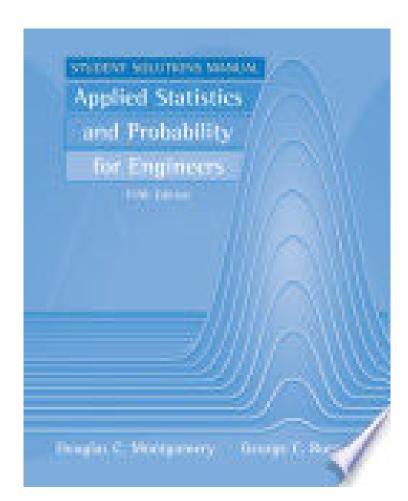
## Problems for our main Probability/Statistics Textbook

Student Solutions Manual Applied
Statistics and Probability for
Engineers, 5th Edition
D. C. Montgomery and G. C. Runger
John Wiley & Sons, Inc. (2010)

You can also use other editions from 4<sup>th</sup> (2007) to 6<sup>th</sup> (2014)

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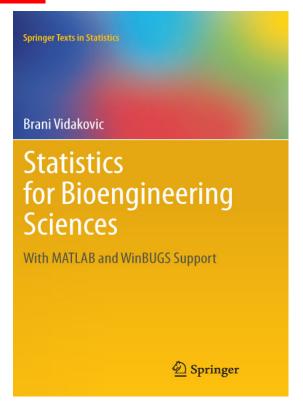
## Probability/Statistics for Bioengineering with Matlab exercises

## Statistics for Bioengineering Sciences with MATLAB and WinBUGS Support

Brani Vidakovic

below

Department of Biomedical Engineering, Georgia Tech (2011) Springer, New York
It is constantly updated with the newest version at the link



Free as a PDF eBook at

http://statbook.gatech.edu/statb4.pdf

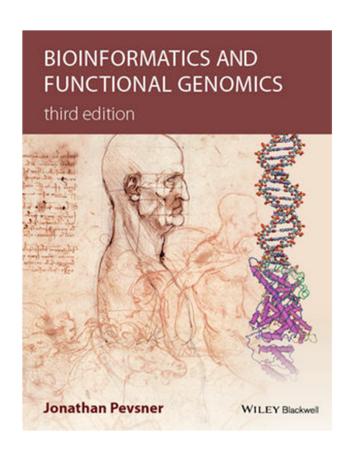
Matlab exercises and datasets are at

http://springer.bme.gatech.edu

## Genomics/Systems Biology Textbook

- J Pevsner
   Bioinformatics and functional genomics
   Wiley-Blackwell,
   2<sup>nd</sup> edition [2009] exists in electronic form
   3<sup>rd</sup> edition [2015] has up-to-date information on NGS: RECOMMENDED
   (about \$60 on amazon)
- 2<sup>nd</sup> edition is available for free in electronic form in our library

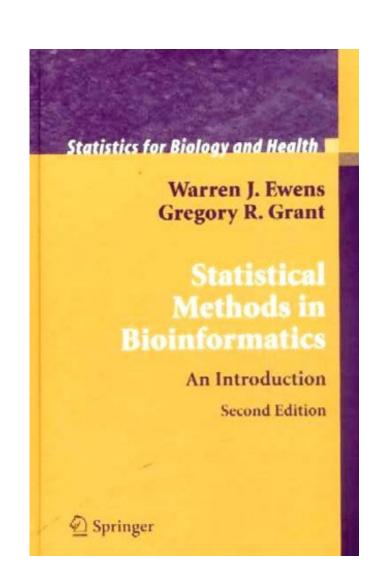


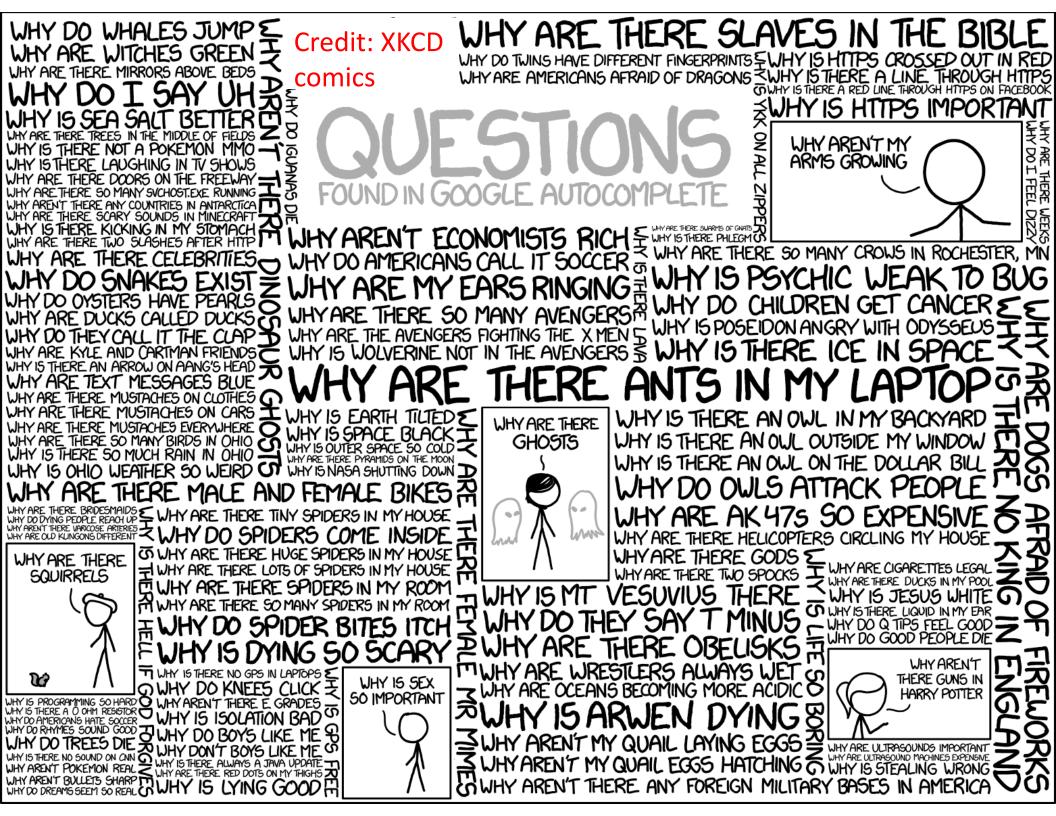


## Another Bioinformatics/Statistics Textbook

- Ewens, WJ and Grant, GR Statistical
   Methods in Bioinformatics: An
   Introduction, 2nd ed, Springer, 2005.
- 2<sup>nd</sup> edition as PDF eBook







This course is about biological data and probability theory and statistics concepts needed for its analysis

## What biological data will be discussed?

#### Will be covered in lectures or Matlab exercises:

- Genomic data: strings of letters ACGT
- Gene Expression data: messenger RNA copy numbers transcribed from genes
- Proteomic data: protein abundances
- <u>Network data</u>: pairs of interacting genes or proteins and protein-protein interaction strengths

#### Will not be covered:

Imaging data such as e.g. fMRI brain scans,
 Brain connectome data, Ecosystem dynamics data

Why do you need probability and statistics to analyze modern biological data?

## Definition of probability theory by Encyclopedia Britannica

a branch of mathematics concerned with the analysis of random phenomena

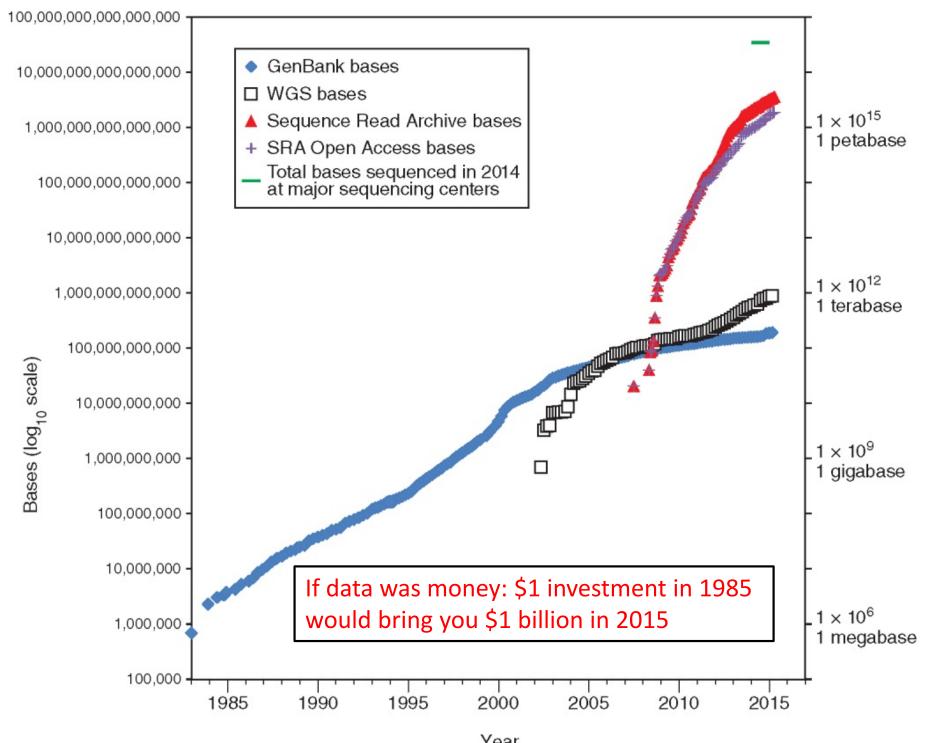
### Definition of statistics by Merriam-Webster

1: a branch of mathematics dealing with the collection, analysis, interpretation, and presentation of masses of numerical data

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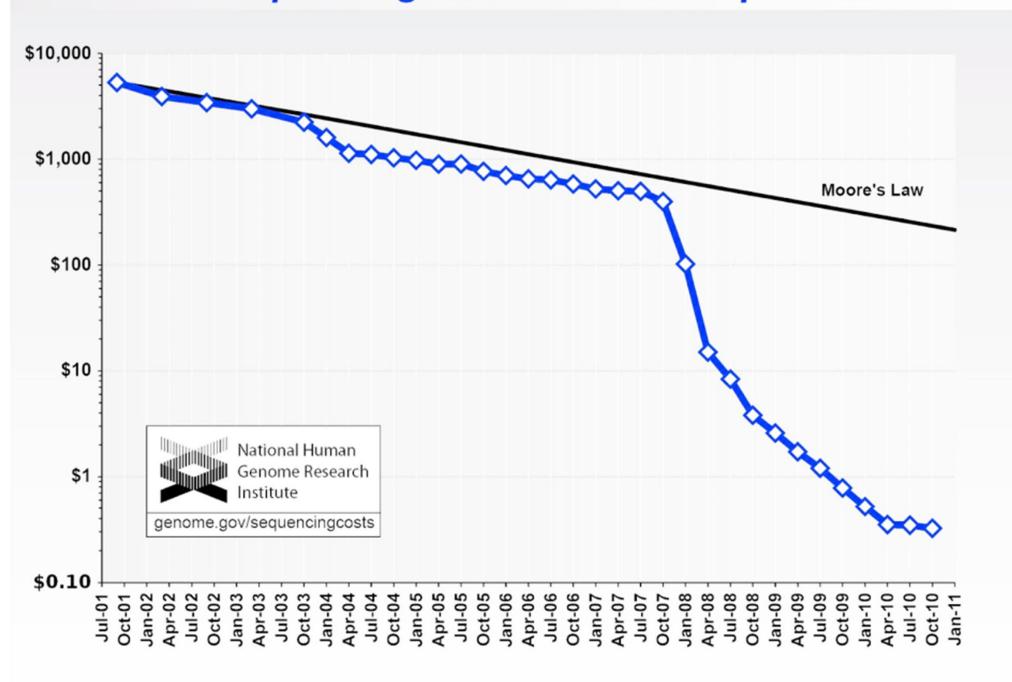
Why do you need probability and statistics to analyze modern biological data?

Reason 1:
Biology now has Lots of Data



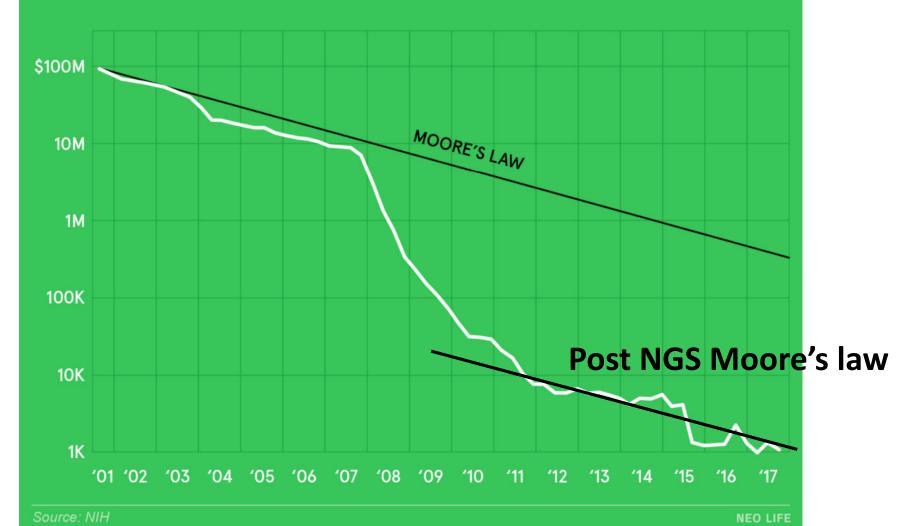
J. Pevsner, Bioinformatics and Functional Genomics, 3<sup>rd</sup> edition, Wiley-Blackwell (2015)

#### Cost per Megabase of DNA Sequence



#### **Cost per Genome Sequenced**

The cost of sequencing a human genome compared with the reductions that would be expected at the rate Moore's law predicts for computer chips. Over the past decade, next-generation sequencing and cloud computing drove the figure down. The average bumped higher in recent years because of brief slowdowns in production.



## Who will have bigger data by 2025?

Data Phase	Astronom	ı <u>y</u>	Twitter	
Acquisition	25 zetta-b	ytes/year	0.5–15 billion tweets/year	
Storage	1 EB/year		1–17 PB/year	
Peta=1	.015	Exa=10 <sup>18</sup>	Zetta=10 <sup>21</sup>	
YouTube	<u> </u>		Genomics	
500–900 million hours/year			1 zetta-bases/year	
1–2 EB/y	ear		2–40 EB/year	

Z. Stephens, S. Lee, F. Faghri, R. Campbell, C. Zhai, M. Efron, R. Iyer, M. Schatz, S. Sinha, and G. Robinson (2015) PLoS Biol 13: e1002195.

Base pairs	Unit	Abbreviation	Example
1	1 base pair	1 bp	A, C, G, $T = 2$ bits = 0.25 bytes
1000	1 kilobase pair	1 kb	
1,000,000	1 megabase pair	1 Mb	
10°	1 gigabase pair	1 Gb	š
1012	1 terabase pair	1 Tb	
1015	1 petabase pair	1 Pb	

Size	Abbreviation	No. bytes	Examples	
Bytes	_	1	1 byte is typically 8 bits, used to encode a single character of text	
Kilobytes	1 kb	10 <sup>3</sup>	Size of a text file with up to 1000 characters  Size of a text file with 1 million characters  Bacterial genome  War & Peace Y	
Megabytes	1 MB	106	Size of a text file with 1 million characters $\mathscr{L} = "War 2 Peace"$	
Gigabytes	1 GB	10°	600 GB: size of GenBank (uncompressed flat files) ftp://ftp.ncbi.nih.gov/genbank/gbrel.txt (WebLink 2.84)	
Terabytes	1 TB	1012	385 TB: United States Library of Congress web archive (http://www.loc.gov/webarchiving/faq.html) (WebLink 2.85)	
			464 TB: Data generated by the 1000 Genomes Project (http://www.1000genomes.org/faq/how-much-disk-space-used-1000-genomes-project) (WebLink 2.86)	
Petabytes	1 PB	1015	1 PB: size of dataset available from The Cancer Genome Atlas (TCGA)	
			5 PB: size of SRA data available for download from NCBI	
			15 PB: amount of data produced <u>each</u> year at the physics facility CERN (near Geneva) (http://home.web.cern.ch/about/computing) (WebLink 2.87)	
Exabytes	1 EB	1018	2.5 exabytes of data are produced worldwide (Lampitt, 2014)	

J. Pevsner, Bioinformatics and Functional Genomics, 3<sup>rd</sup> edition, Wiley-Blackwell (2015)

## What makes genomic data so big?

- There are ~9 millions species each with its own genome
- Each of us humans (7.5 billions and counting) has unique DNA: we want to compare them all to each other
- Each cell has just 1 genome (DNA) but multitude of transcriptomes (RNA levels) and proteomes (protein levels)
- Cancer cells acquire mutations in their genomes: need to track multiple lineages in a tumor vs time to understand cancer
- DNA was proposed as a long-term storage medium of information

Farfetched? Storage standards evolve fast but DNA standard remained unchanged for 4 billion years

Note: Nature article started the comparison with a hard drive and flash memory skipping the floppy disk







**NATURE | NEWS FEATURE** 







#### How DNA could store all the world's data

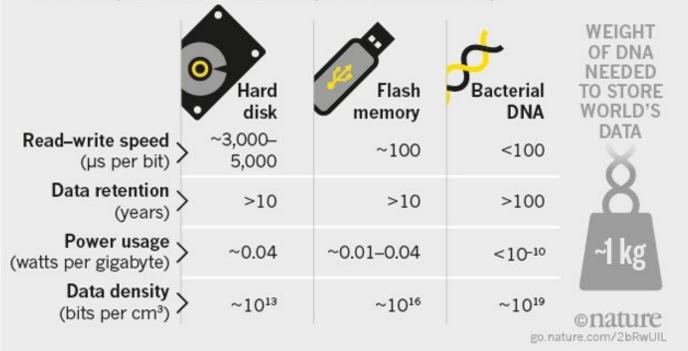
Modern archiving technology may hold an answer to that pro-

#### **Andy Extance**

31 August 2016

#### STORAGE LIMITS

Estimates based on bacterial genetics suggest that digital DNA could one day rival or exceed today's storage technology.

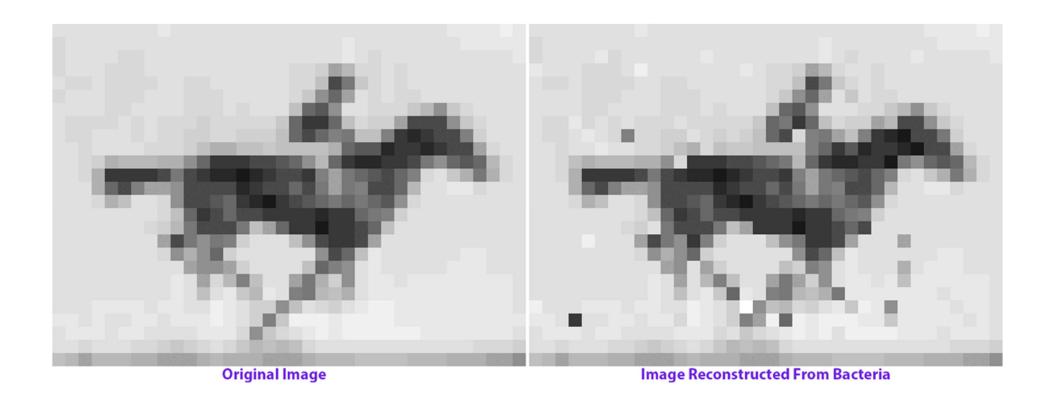


 Prof Olgica Milenkovic from Electrical and Computer Engineering UIUC is a local expert on this topic

 Profs. George Church and Sri Kosuri (Harvard Medical School) explains a potential use of DNA as storage medium in 2012

https://www.youtube.com/watch?v=IJAdqAVjQqY

## Fast-forward from 2012 to 2017



Shipman SL, Nivala J, Macklis JD, Church GM. CRISPR—Cas encoding of a digital movie into the genomes of a population of living bacteria. Nature. 2017;547: 345–349. doi:10.1038/nature23017

Why do you need probability and statistics to analyze modern biological data?

Reason 2: Life is random and messy

## Show video "Cell organelles"

- Made at the Walter and Eliza Hall Institute of Medical Research at Victoria, Australia
- Animated by award-winning artist Dr. Drew Berry
- Go to <a href="https://www.wehi.edu.au/wehi-tv">https://www.wehi.edu.au/wehi-tv</a> for other videos

## Life is messy, random, and noisy

Yet it is beautifully complex and has many parts (see statistics)

## Why life is so random?

- Biomolecules are very small (nano- to micro-meters) → Brownian noise
- # molecules/cell is often small 

   Large cell-to-cell variations
- Genomic data comes from biological evolution
  - the Mother of all random processes
- Genomic data involves (random) samples
  - We have genomes of some (not all) organisms
  - We have tissue samples of some (not all) cancer patients

## Why life is so complex?

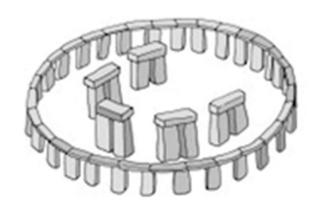
Primer on complex system

## Complex systems have many interacting parts

- All parts are different from each other
  - 10s thousands (10<sup>4</sup>) types of proteins in an organism
  - 100 thousands (10<sup>5</sup>) organizations (AS) in the Internet
  - 1 billion (10<sup>9</sup>) people on Facebook
  - 10 billion (10<sup>10</sup>) web pages in the WWW
  - 100 billion (10<sup>11</sup>) neurons in a human brain
  - NOT 10<sup>23</sup> electrons or quarks studied by physics: they are all the same and boring!
- Yet they share the same basic design
  - All proteins are strings of the same 20 amino acids
  - All WWW pages use HTML, JavaScript, etc.
  - All neurons generate and receive electric spikes

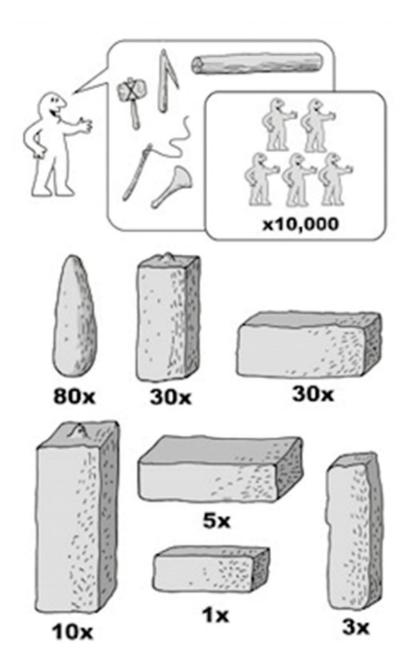
## Example: a complex system with many parts









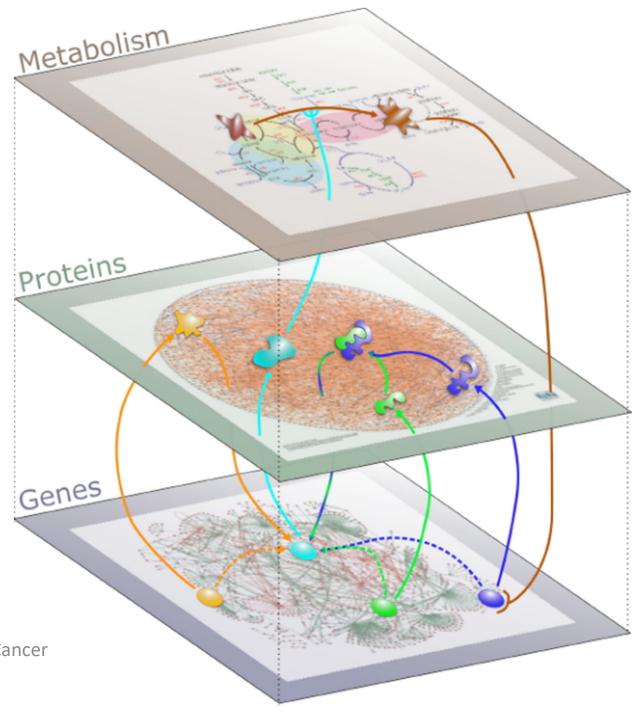


## Parts interact $\rightarrow$ they need to be assembled to work

**x30** 30x

Justin Pollard, http://www.designboom.com

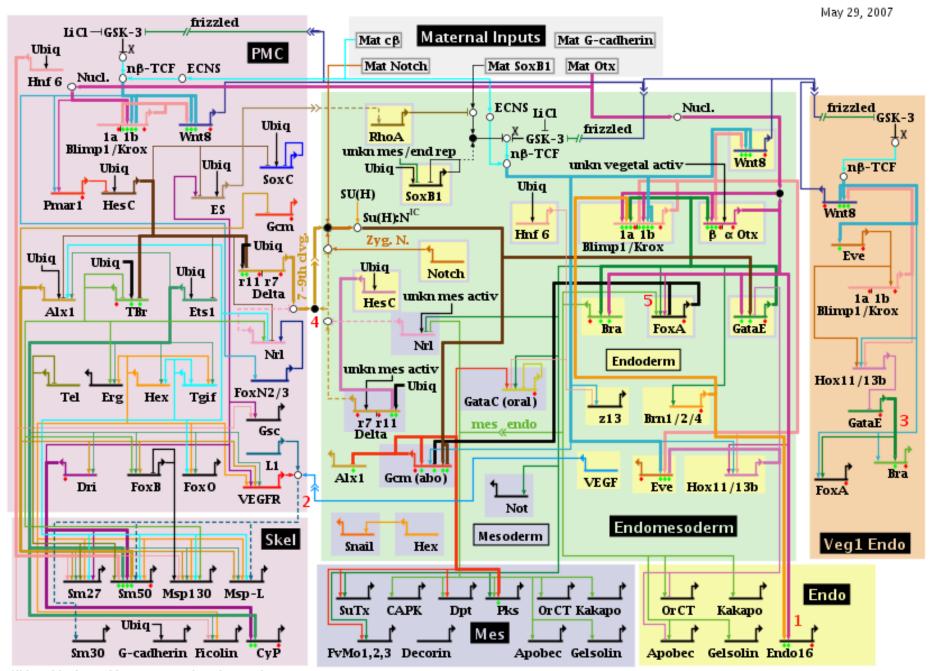
Intra-cellular Networks operate on multiple levels



Slides by Amitabh Sharma, PhD

Northeastern University & Dana Farber Cancer Institute

#### Sea urchin embryonic development (from endomesoderm up to 30 hours) by Davidson's lab

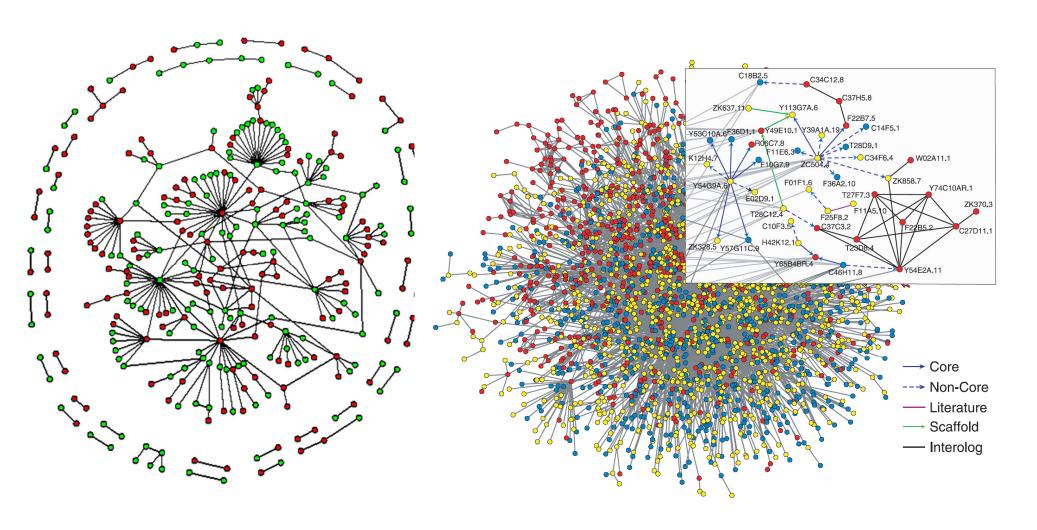


Ubiq=ubiquitous; Mat = maternal; activ = activator; rep = repressor; unkn = unknown; Nucl. = nuclearization;  $\chi = \beta$ -catenin source;  $n\beta$ -TCF = nuclearized b- $\beta$ -catenin-Tcf1; ES = early signal; ECNS = early cytoplasmic nuclearization system; Zyg. N. = zygotic Notch

Copyright © 2001-2007 Hamid Bolouri and Eric Davidson

## Protein-Protein binding IntAct Database (Dec 2015)

Interactions: 577,297 Proteins: 89,716



Baker's yeast *S. cerevisiae* (only nuclear proteins shown) From S. Maslov, K. Sneppen, Science 2002

Worm *C. elegans* From S. Lee et al , Science 2004

#### Metabolic pathway chart by ExPASy: 5702 reactions as of December 2015

