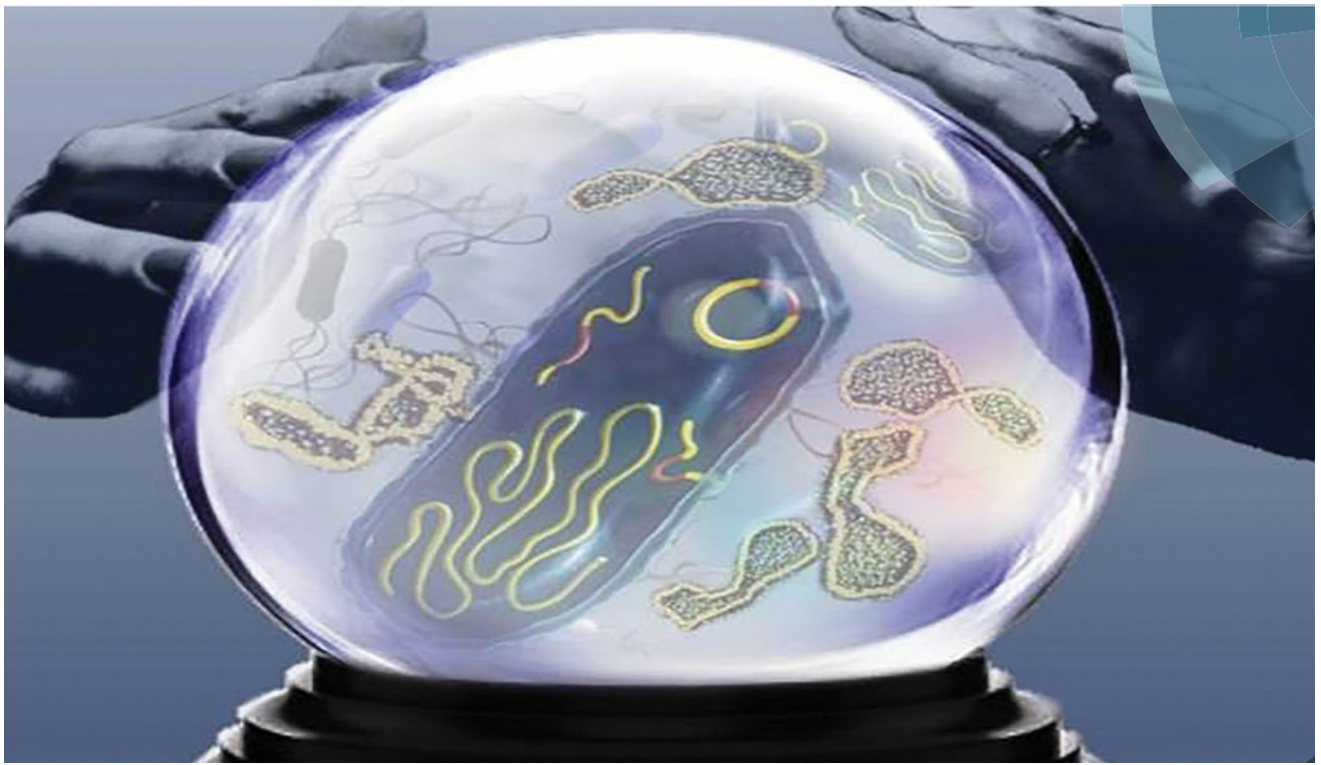
Multi-Omics Data Integration via Machine Learning

Omics Integration and Systems Biology course

Nikolay Oskolkov, Lund University, NBIS SciLifeLab, Sweden



@NikolayOskolkov

https://github.com/NikolayOskolkov

Image adapted from Molecular Omics, Issue 1, 2018

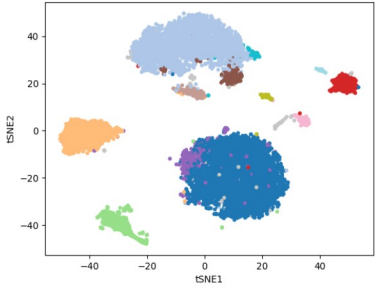
Brief introduction: who am I

2007 PhD in theoretical physics

2011 medical genetics at Lund University

2016 working at NBIS SciLifeLab, Sweden

Single cell



Biomedical data integration

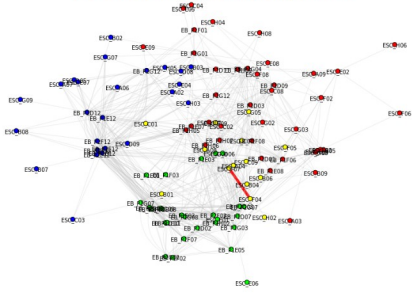
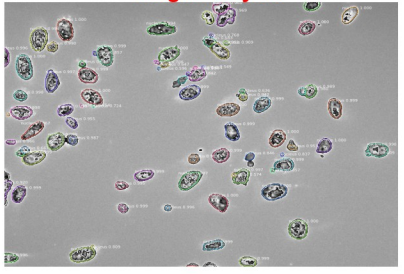
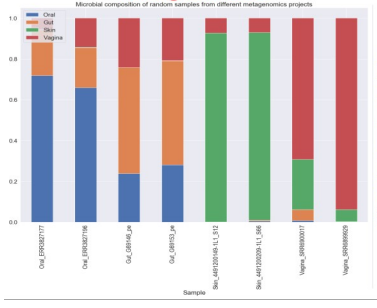


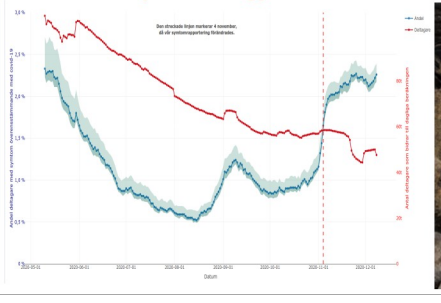
Image analysis



Metagenomics

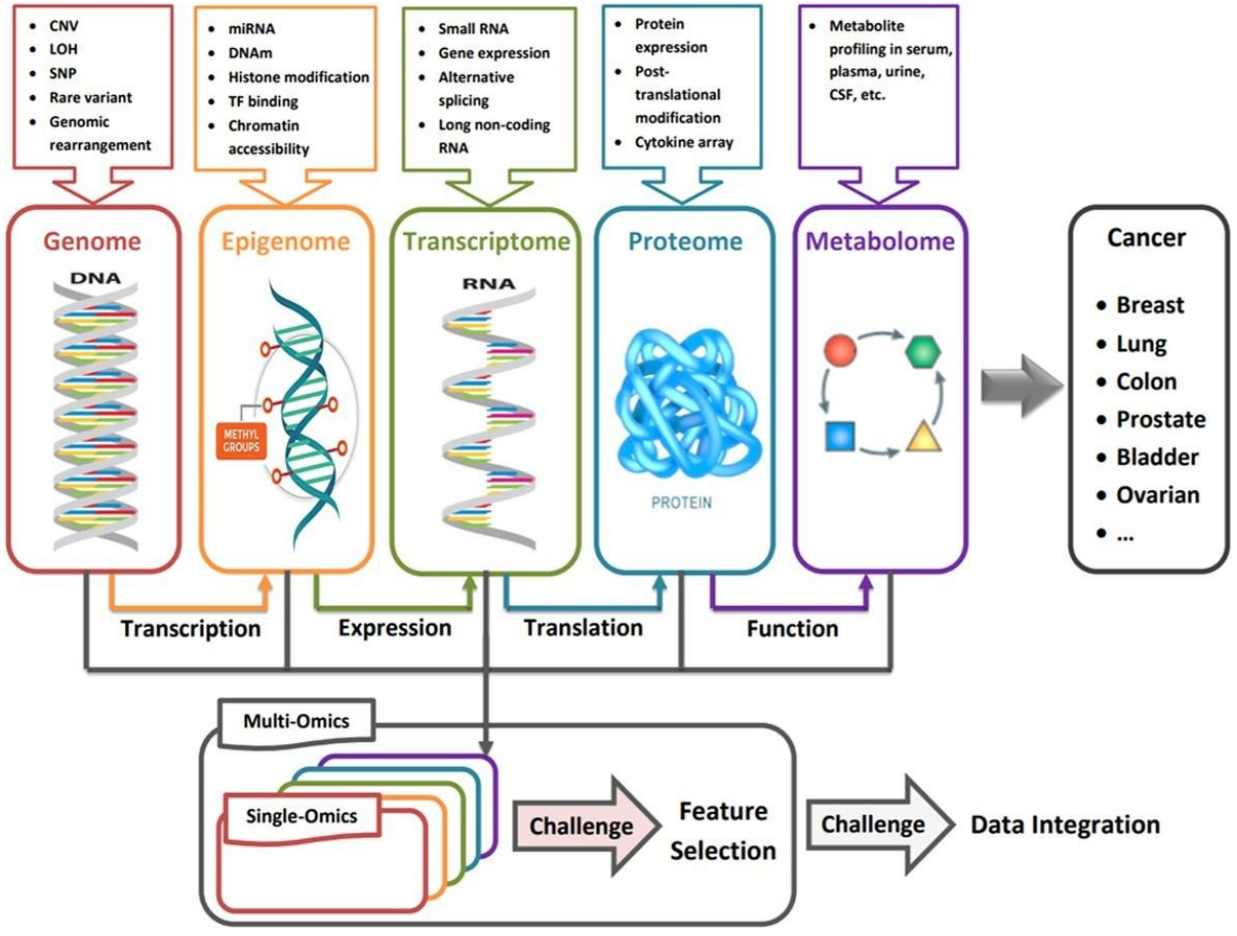


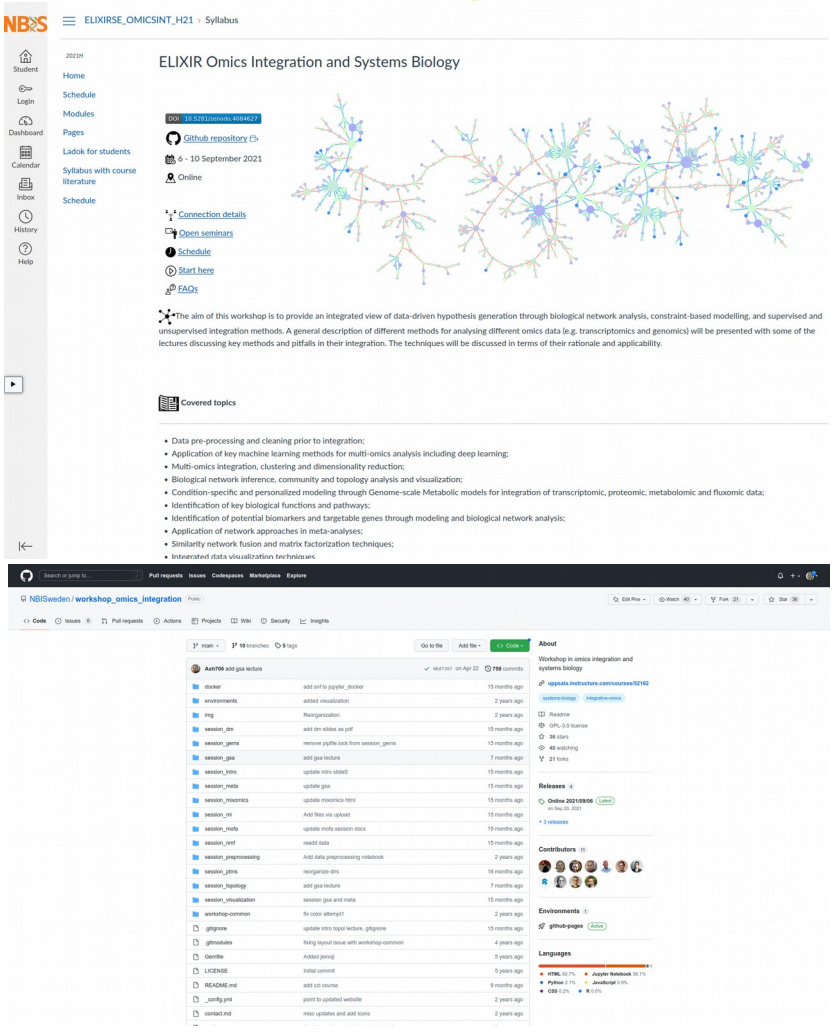
Epidemiology



Ancient microbiome

Multi-Omics Data in Life Sciences





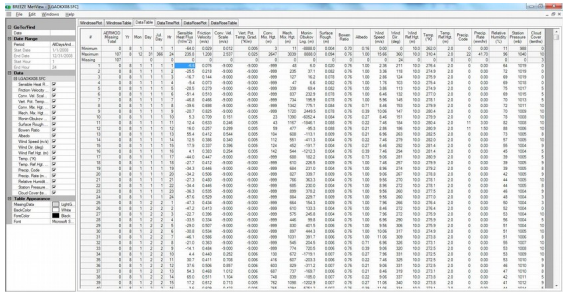
Momeni et al., J Biomed Inform. 2020

https://github.com/NBISweden/workshop_omics_integration

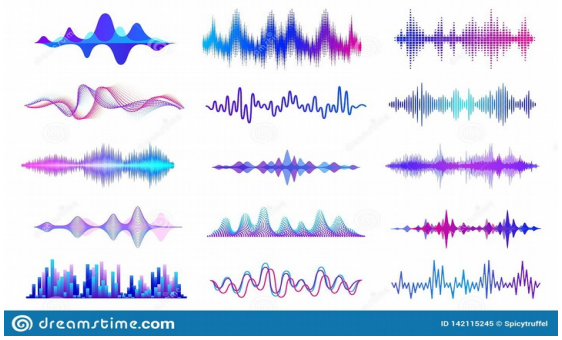
Introduction:
High Dimensional Biological Data

Various types of data around us

Tabular



Sound



Image

Text

Editing Wikipedia articles on

Medicine

Editing Wikipedia can be daunting for newbies, especially if you're contributing to Wikipedia for the first time as a class assignment. This guide is designed to assist students who have been assigned to contribute biomedical-related content to Wikipedia. Here's what other editors will expect you to know.

Be accurate

You're editing a resource millions of people use to make medical decisions, so it's vitally important to be accurate. Wikipedia is used more for medical information than the websites for WebMD, NIH, and the WHO. But with great power comes great responsibility!

Understand the guidelines

Wikipedia editors in the medicine area have developed additional guidelines to ensure that the content on Wikipedia is medically sound. Take extra time to read and understand these guidelines. When you edit an article, ensure your changes meet these special requirements. If not, your work is likely to be undone by other editors as they clean up after you. That takes valuable volunteer time away from creating content. If you're not comfortable working under these guidelines, talk to your instructor about an alternative off-wiki assignment.

Engage with editors

Part of the Wikipedia experience is receiving and responding to feedback from other editors. Do not submit your content on the last day, then leave Wikipedia! Real human volunteers from the Wikipedia community will likely read and respond to it, and it would be polite for you to acknowledge the time they volunteer to polish your work! Everything submitted to Wikipedia is reviewed by multiple, real humans! You may not get a comment, but if you do, please acknowledge it.

Watch out for close paraphrasing

Plagiarizing or close paraphrasing is never okay on Wikipedia and is a violation of your university's academic honor code. It's even worse on Wikipedia, as valuable volunteer time that could be used to create good content is instead used to clean up plagiarized work.

If you plagiarize or too closely paraphrase on Wikipedia, it is extremely likely that you'll be caught by other editors and there will be an online record of your plagiarism tied to your permanent online record.

Note that even educational materials from organizations like the WHO and abstracts of articles in PubMed are under copyright and cannot be copied. Write them in your own words whenever possible. If you aren't clear on what close paraphrasing is, visit your university's writing center.

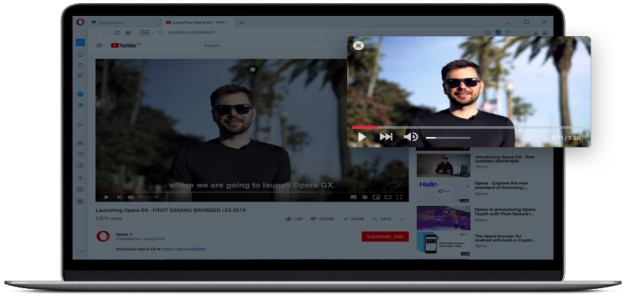
Scared? Don't be!

Everybody on Wikipedia wants to make the best encyclopedia they can. Take the time to understand the rules, and soon you'll be contributing to a valuable resource you use on a daily basis!

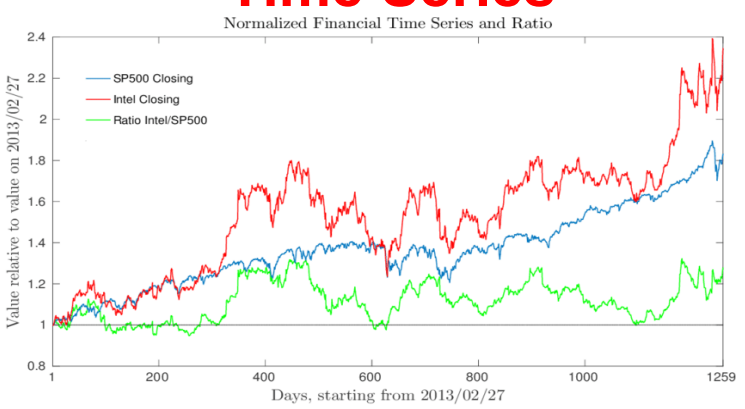
Wiki Edu

DATA

Video



Time Series



Biological Data are High Dimensional

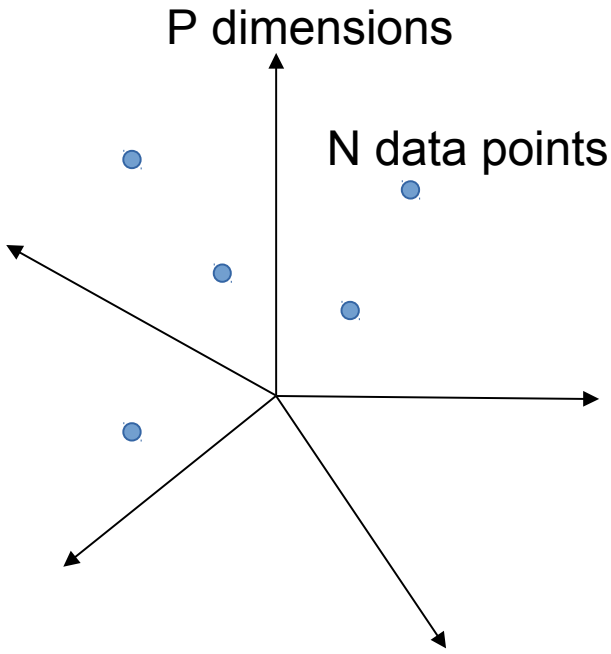
Statistical observations:
e.g. samples, cells etc.

N

P

0	3	1	0	2	3	8	1	1	3
1	1	0	0	7	1	2	2	3	3
1	2	2	0	0	6	7	1	2	2
1	2	3	10	0	4	6	1	0	5
3	2	2	1	4	3	2	1	6	0
7	4	4	5	3	9	6	1	6	1
7	1	1	5	2	8	9	1	3	6
5	0	1	6	2	0	0	0	1	5
1	6	3	3	4	6	2	0	1	1
1	2	2	4	1	1	3	0	8	2

Features: genes, proteins, microbes, metabolites etc.



High Dimensional Data:
P >> N

For a robust statistical analysis, one should properly “sample” the P-dimensional space, hence large sample size is required, N >> P

Types of Statistical Analysis

P is the number of features (genes, proteins, genetic variants etc.)
N is the number of observations (samples, cells, nucleotides etc.)

Biology / Biomedicine

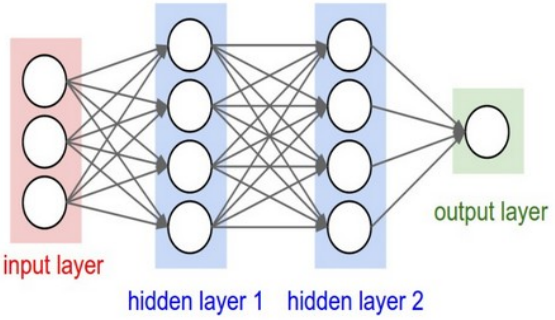
Bayesianism

P >> N

Frequentism

P ~ N

Deep Learning



P << N

Amount of Data

The Curse of Dimensionality

Ex.1

$$Y = \alpha + \beta X$$

$$\beta = (X^T X)^{-1} X^T Y$$

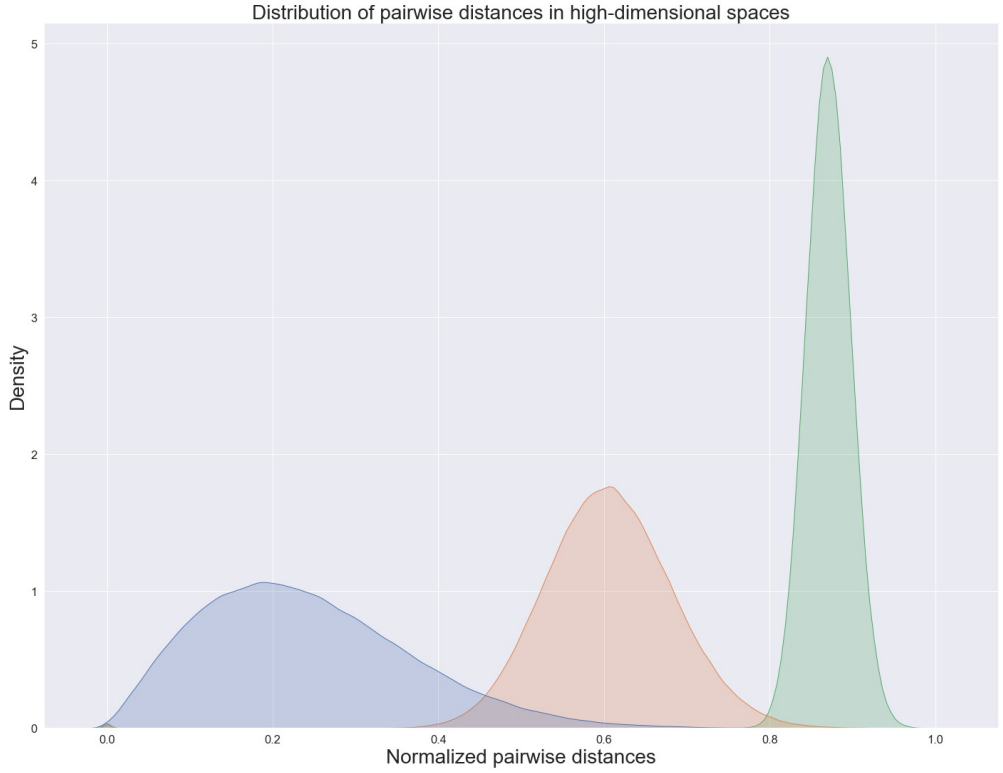
$$(X^T X)^{-1} \sim \frac{1}{\det(X^T X)} \cdots \to \infty, \quad n << p$$

Ex.2 $$E[\hat{\sigma}^2] = \frac{n-p}{n}\sigma^2$$

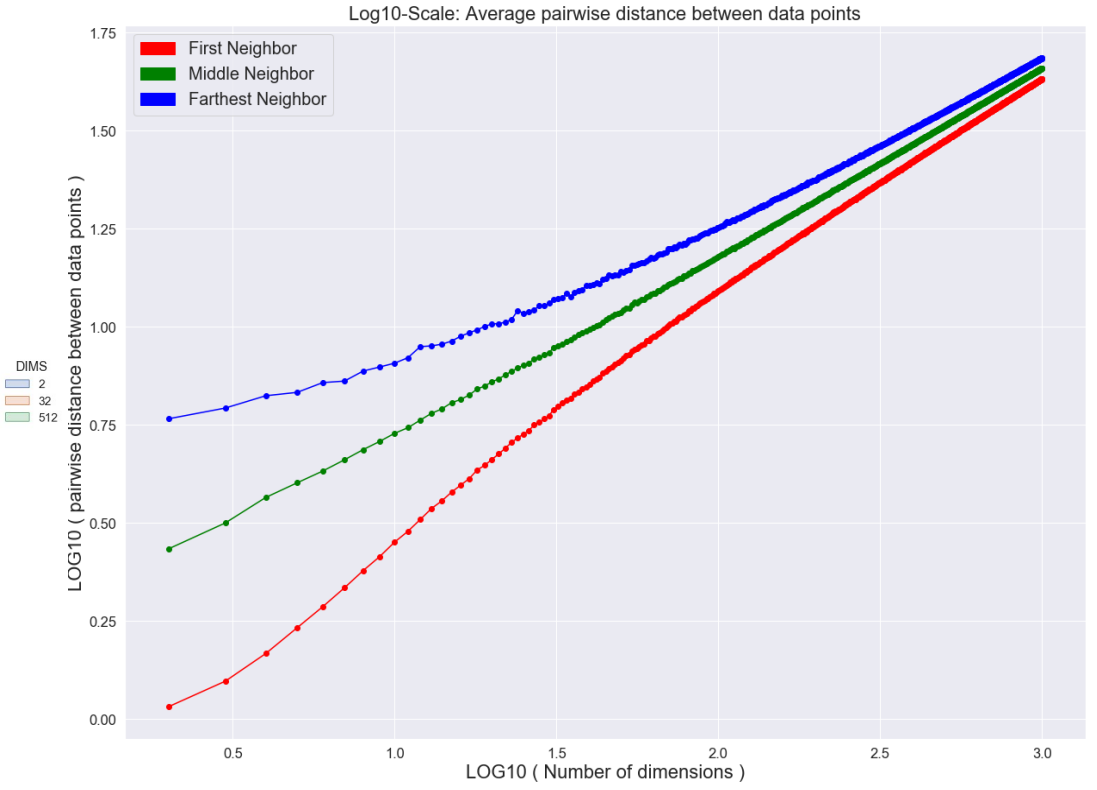
Biased ML variance estimator in HD-space

More on the Curse of Dimensionality

Distances in High Dimensions



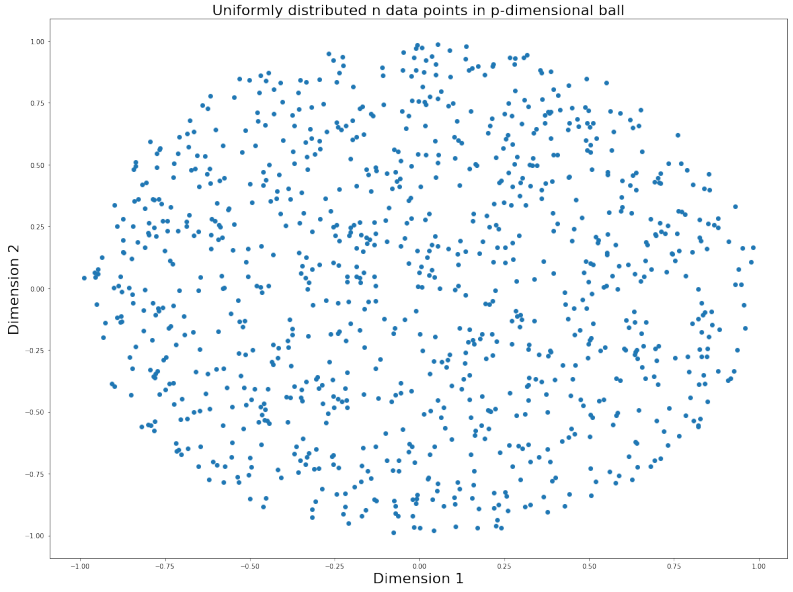
Data points become far from each other and equidistant in high dimensions

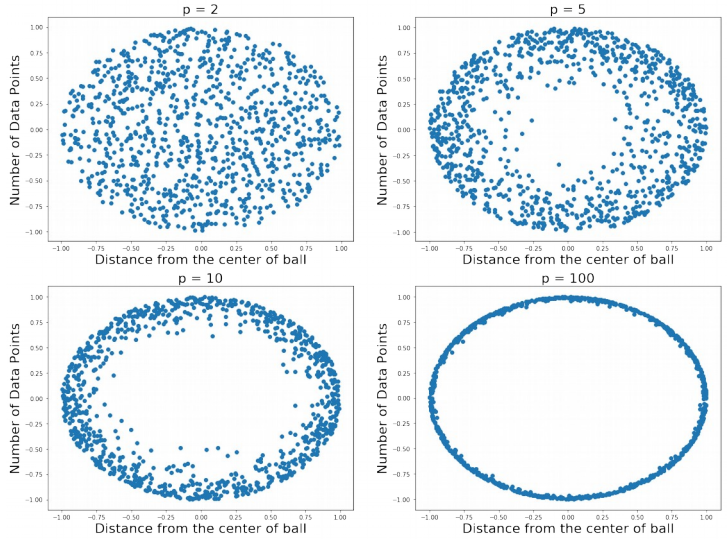


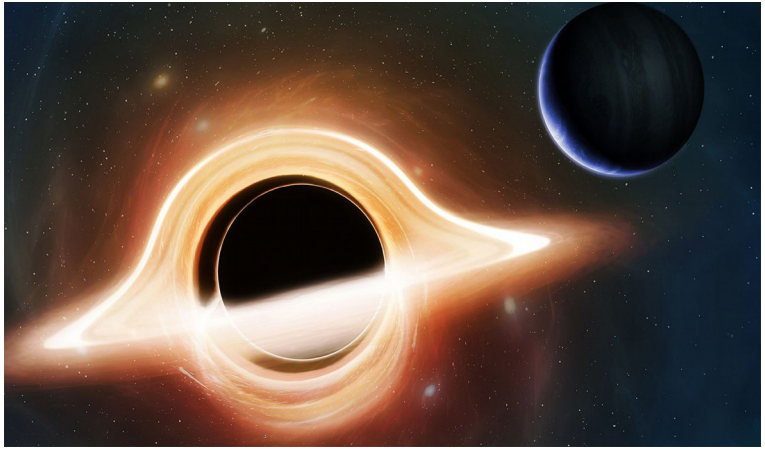
The differences between closest and farthest data point neighbours disappears in high-dimensional spaces: can't run cluster analysis

In high-dimensional space we can not separate cases and controls any more

High-dimensional data make black holes







High-dimensional data can be viewed as having a **“hole in the middle”**, hence the concept of mean / centroid loses its validity, hence we can’t use Gaussian distribution

Literature on the Curse of Dimensionality

POINTS OF SIGNIFICANCE

The curse(s) of dimensionality

There is such a thing as too much of a good thing.

Naomi Altman and Martin Krzywinski

We generally think that more information is better than less. However, in the 'big data' era, the sheer number of variables that can be collected from a single sample can be problematic. This embarrassment of riches is called the 'curse of dimensionality'[1] (CoD) and manifests itself in a variety of ways. This month, we discuss four important problems of dimensionality as it applies to data sparsity[1,2], multicollinearity[3], multiple testing[4] and overfitting[5]. These effects are amplified by poor data quality, which may increase with the number of variables.

Throughout, we use n to indicate the sample size from the population of interest and p to indicate the number of observed variables, some of which may have missing values for some samples. For example, we may have $n = 1{,}000$ subjects and $p = 200{,}000$ single-nucleotide polymorphisms (SNPs).

First, as the dimensionality p increases, the 'volume' that the samples may occupy grows rapidly. We can think of each of the n

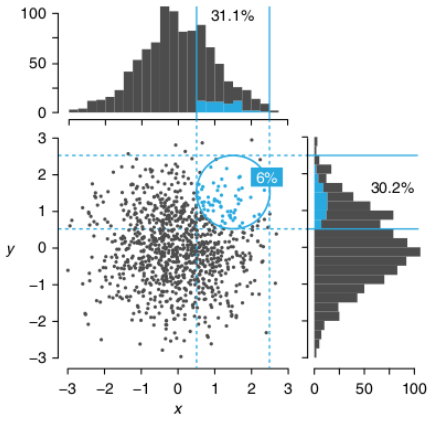


Fig. 1 | Data tend to be sparse in higher dimensions. Among 1,000 (x, y) points in which both x and y are normally distributed with a mean of 0 and s.d. $\sigma = 1$, only 6% fall within σ of $(x, y) = (1.5, 1.5)$ (blue circle). However, when the data are projected into a lower dimension—shown by histograms—about 30% of the points (all bins within blue solid lines) are within σ of 1.5. Blue

A and 100 to have the minor allele a. If we tabulate on two SNPs, A and B, we will expect only ten samples to exhibit both minor alleles with genotype ab. With SNPs A, B and C, we expect only one sample to have genotype abc, and with four or more SNPs, we expect empty cells in our table. We need a much larger sample size to observe samples with all the possible genotypes. As p increases, we may quickly find that there are no samples with similar values of a predictor.

Even with just five SNPs, our ability to predict and classify the samples is impeded because of the small number of subjects that have similar genotypes. In situations where there are many gene variants, this effect is exacerbated, and it may be very difficult to find affected subjects with similar genotypes and hence to predict or classify on the basis of genetic similarity.

If we treat the distance between points (e.g., Euclidian distance) as a measure of similarity, then we interpret greater distance as greater dissimilarity. As p increases, this

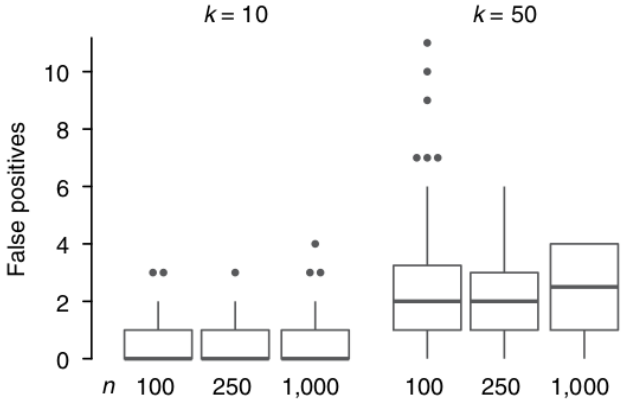


Fig. 3 | The number of false positives increases with each additional predictor. The box plots show the number of false positive regression-fit P values (tested at $\alpha = 0.05$) of 100 simulated multiple regression fits on various numbers of samples ($n = 100$, 250 and 1,000) in the presence of one true predictor and $k = 10$ and 50 extraneous uncorrelated predictors. Box plots show means (black center lines), 25th and 75th percentiles (box edges), and minimum and maximum values (whiskers). Outliers (dots) are jittered.

Correcting for multiple testing does not solve the problem of too many false-positive hits

Altman N, Krzywinski M. The curse(s) of dimensionality. Nat Methods. 2018 Jun;15(6):399-400. doi: 10.1038/s41592-018-0019-x. PMID: 29855577.

Typical Dimensions of Omics Data

$\begin{pmatrix} 0 & 1 & 0 & 1 \\ 1 & 0 & 1 & 1 \\ 1 & 1 & 0 & 1 \\ 1 & 0 & 1 & 1 \end{pmatrix}$ Metabolomics
N ≈ P

$\begin{pmatrix} 0 & 1 & 0 & 1 \\ 1 & 0 & 1 & 1 \\ 1 & 1 & 0 & 1 \\ 1 & 0 & 1 & 1 \end{pmatrix}$ Proteomics
N ≈ P

$\begin{pmatrix} 0 & 1 & 0 & 1 \\ 1 & 0 & 1 & 1 \\ 1 & 1 & 0 & 1 \\ 1 & 0 & 1 & 1 \end{pmatrix}$ Metagenomics
N ≈ P

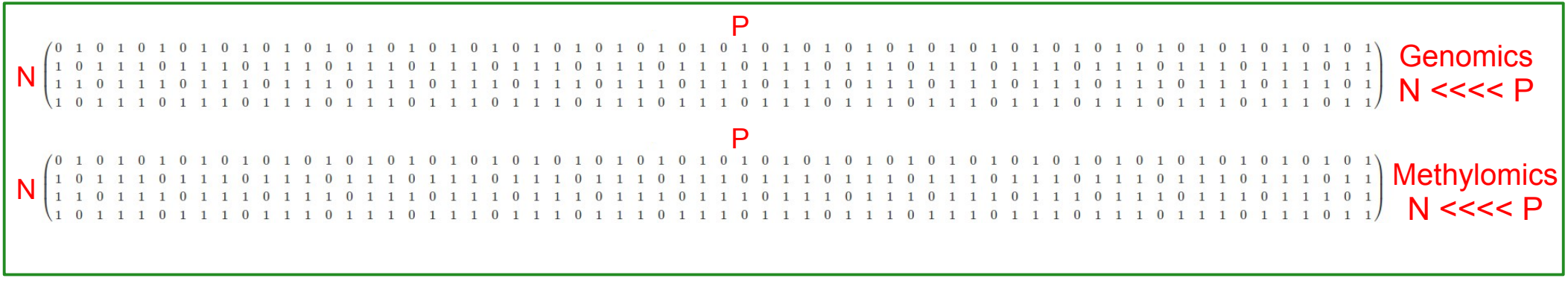
← **manageable**

P

N $\begin{pmatrix} 0 & 1 & 0 & 1 & 0 & 1 & 0 & 1 & 0 & 1 & 0 & 1 & 0 & 1 & 0 & 1 \\ 1 & 0 & 1 & 1 & 1 & 0 & 1 & 1 & 1 & 0 & 1 & 1 & 1 & 0 & 1 & 1 \\ 1 & 1 & 0 & 1 & 1 & 1 & 0 & 1 & 1 & 1 & 0 & 1 & 1 & 1 & 0 & 1 \\ 1 & 0 & 1 & 1 & 1 & 0 & 1 & 1 & 1 & 0 & 1 & 1 & 1 & 0 & 1 & 1 \end{pmatrix}$

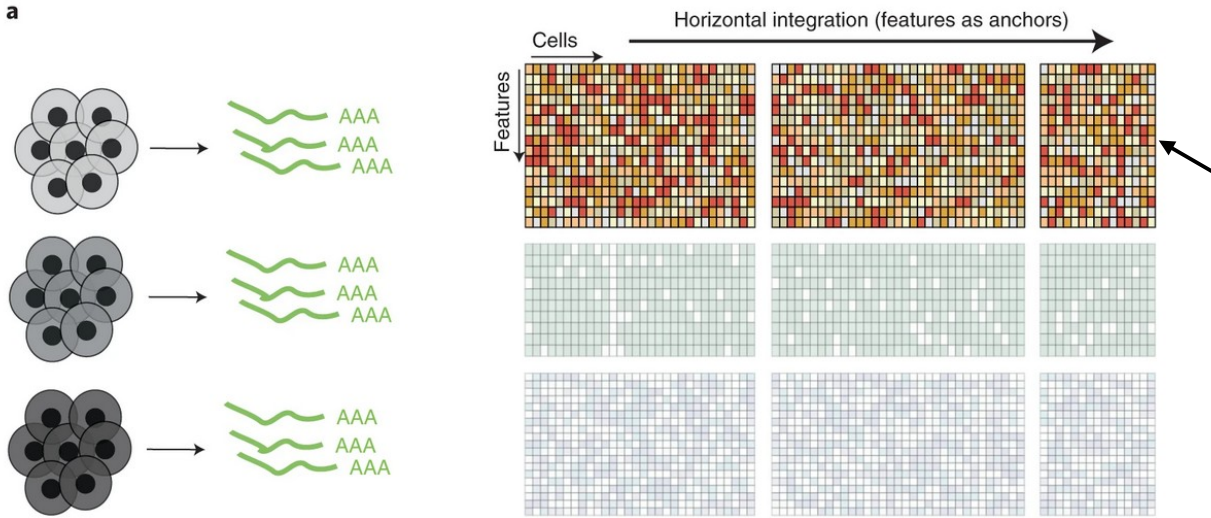
Transcriptomics
N << P
(Single cell: N <= P)

challenging

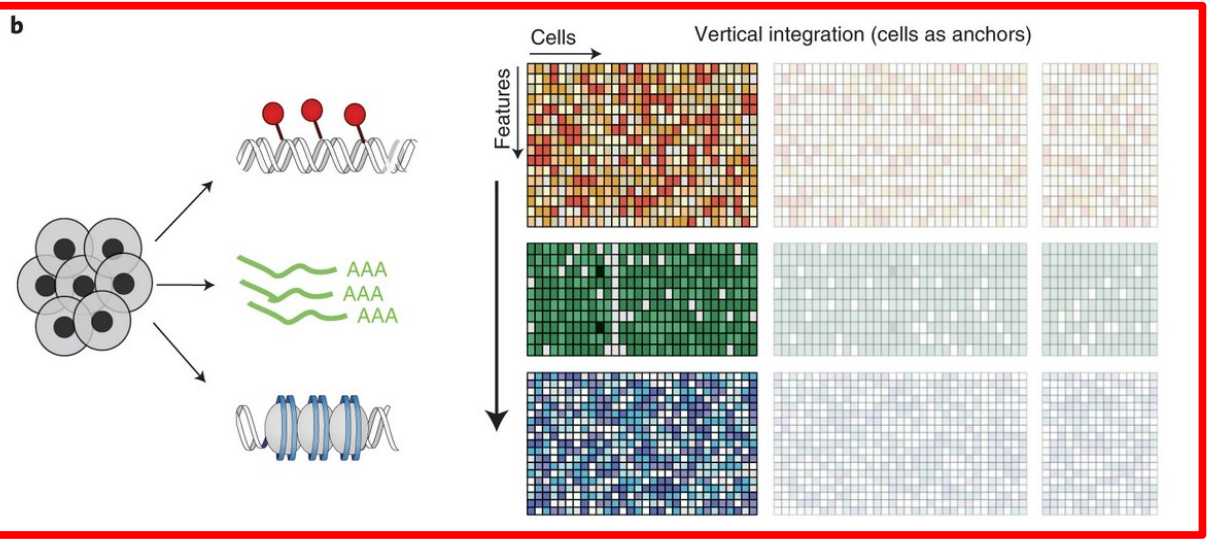


Multi-Omics Data Integration

Integration Across Features vs. Samples



Similar to batch correction problem



Here I will focus on integration across features

Argelaguet et al., 2021

Integrating Omics Across Features

Statistical observations:
e.g. samples, cells etc.

Features: genes, proteins, microbes, metabolites etc.

N

P_1

0	3	1	0	2	3	8	1	1	3
1	1	0	0	7	1	2	2	3	3
1	2	2	0	0	6	7	1	2	2
1	2	3	10	0	4	6	1	0	5
3	2	2	1	4	3	2	1	6	0
7	4	4	5	3	9	6	1	6	1
7	1	1	5	2	8	9	1	3	6
5	0	1	6	2	0	0	0	1	5
1	6	3	3	4	6	2	0	1	1
1	2	2	4	1	1	3	0	8	2

Omic1: RNAseq

N

P_2

0	3	1	0	2	3	8	1	1	3
1	1	0	0	7	1	2	2	3	3
1	2	2	0	0	6	7	1	2	2
1	2	3	10	0	4	6	1	0	5
3	2	2	1	4	3	2	1	6	0
7	4	4	5	3	9	6	1	6	1
7	1	1	5	2	8	9	1	3	6
5	0	1	6	2	0	0	0	1	5
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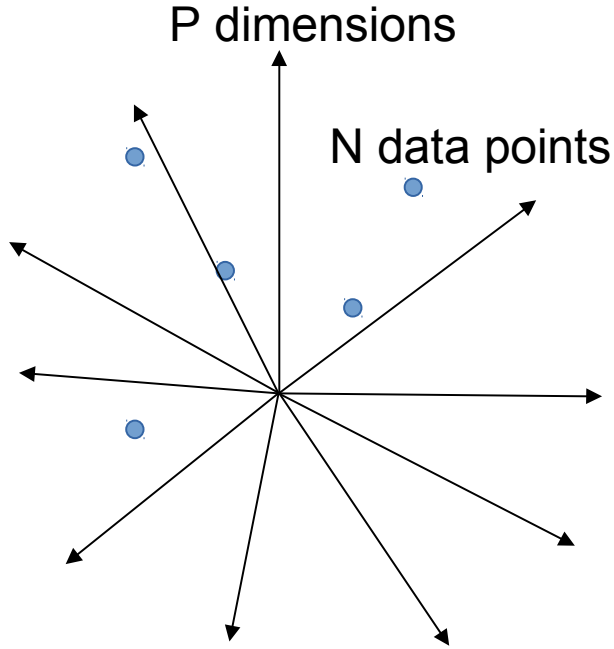
1	2	2	4	1	1	3	0	8	2

Omic2: BSseq



$P_1 + P_2 >> N$ integration across features leads to even more high-dimensional data

Big Data in Single Cell Genomics

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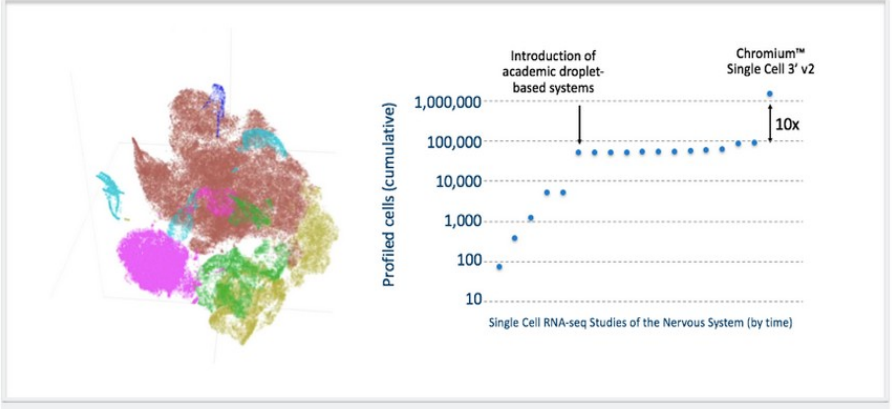


Our 1.3 million single cell dataset is ready to download

0 KUDOS

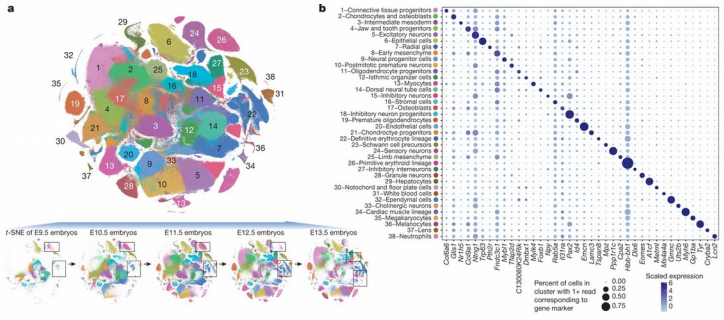
POSTED BY: grace-10x, on Feb 21, 2017 at 2:28 PM

At ASHG last year, we announced our 1.3 Million Brain Cell Dataset, which is, to date, the largest dataset published in the single cell RNA-sequencing (scRNA-seq) field. Using the Chromium™ Single Cell 3' Solution (v2 Chemistry), we were able to sequence and profile 1,308,421 individual cells from embryonic mice brains. Read more in our application note Transcriptional Profiling of 1.3 Million Brain Cells with the Chromium™ Single Cell 3' Solution.

MENU nature

Fig. 2: Identifying the major cell types of mouse organogenesis.

From: The single-cell transcriptional landscape of mammalian organogenesis



a, t-SNE visualization of 2,026,641 mouse embryo cells (after removing a putative doublet cluster), coloured by cluster identity (ID) from Louvain clustering (in **b**), and annotated on the basis of marker genes. The same t-SNE is plotted below, showing only cells from each stage (cell numbers from left to right: n = 151,000 for E9.5; 370,279 for E10.5; 602,784 for E11.5; 468,088 for E12.5; 434,490 for E13.5). Primitive erythroid (transient) and definitive erythroid (expanding) clusters are boxed. **b**, Dot plot showing expression of one selected marker gene per cell type. The size of the dot encodes the percentage of cells within a cell type in

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Single Cell Analysis

5,500,000 cells will be indexed into BioTuring Single-cell Data Repository this September

by biomembers • August 30, 2019

Human Cell Atlas, single-cell data

We are glad to announce that we will upsize the current single-cell database in BioTuring Single-cell Browser to 5,500,000 cells this September. With this release, we will double the current number of publications indexed in BioTuring Single-cell Browser, and cross the number of cells hosted on available public single-cell data repositories like Human Cell Atlas (HCA) and Broad Institute's Single-cell Portal.

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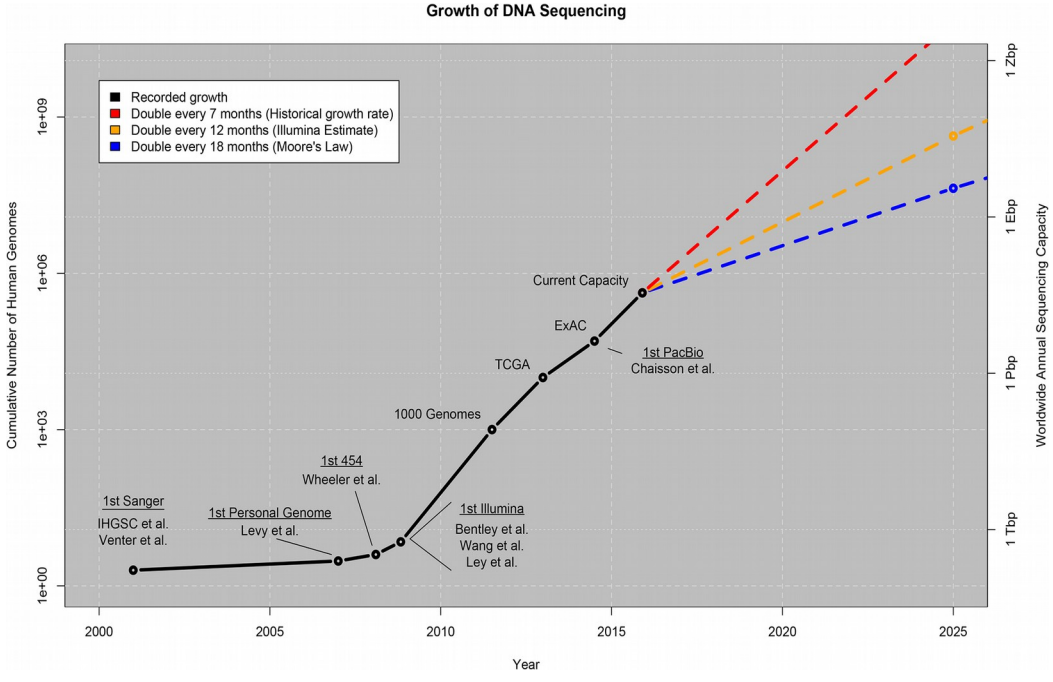
RECENT POSTS

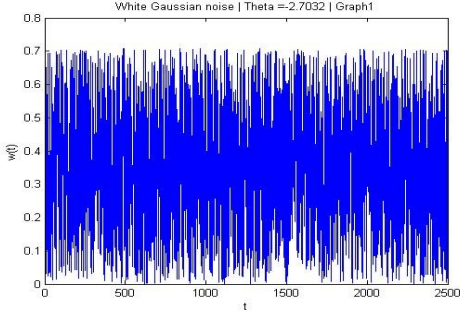
A new tool to interactively visualize single-cell objects (Seurat, Scanpy, SingleCellExperiments, ...)
September 26, 2019

5,500,000 cells will be indexed into BioTuring Single-cell Data Repository this September
August 30, 2019

Big in Size or Sample Size?



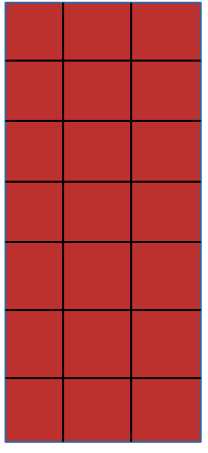
Stephens et al., (2015). Big Data: Astronomical or Genomical? PLoS Biology 13(7)



A file with **White Noise** can also take a lot of disk space

Genomics / WGS: **Little Data**

$N_1 \sim 10^3$

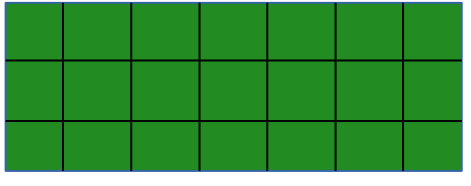


$P_1 \sim 10^6$

$N_1 * P_1 = N_2 * P_2 = 10^9$

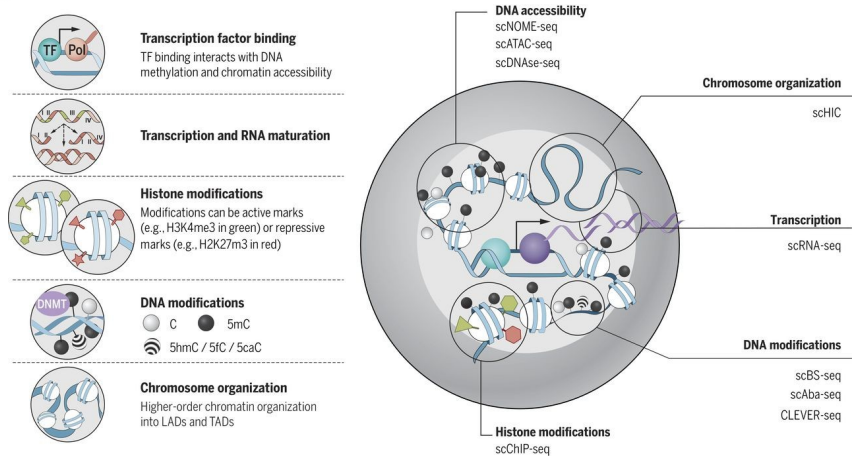
scRNAseq: **Big Data**

$N_2 \sim 10^6$

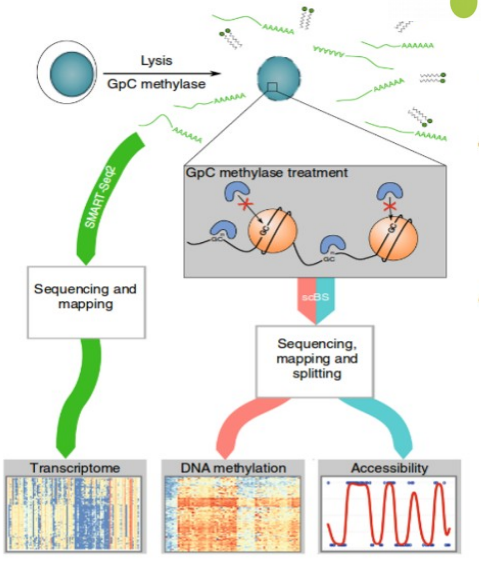


$P_2 \sim 10^3$

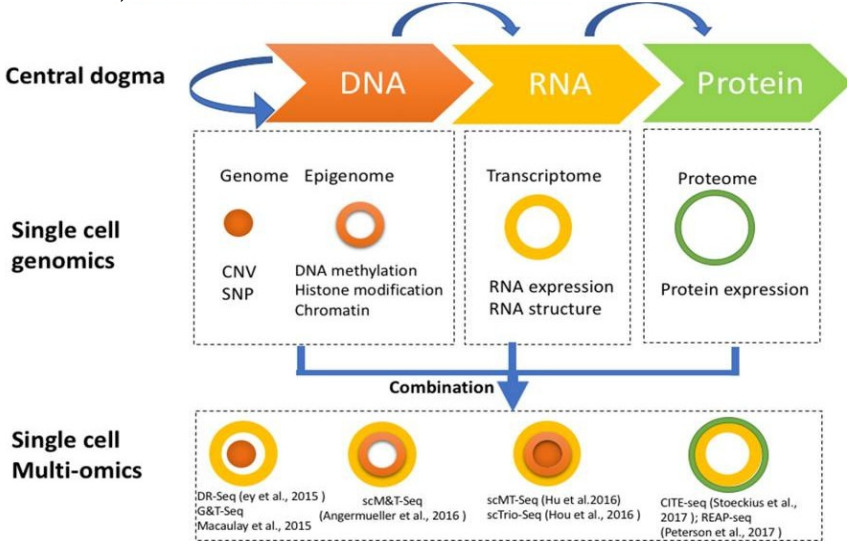
Multi-Omics in Single Cell Genomics



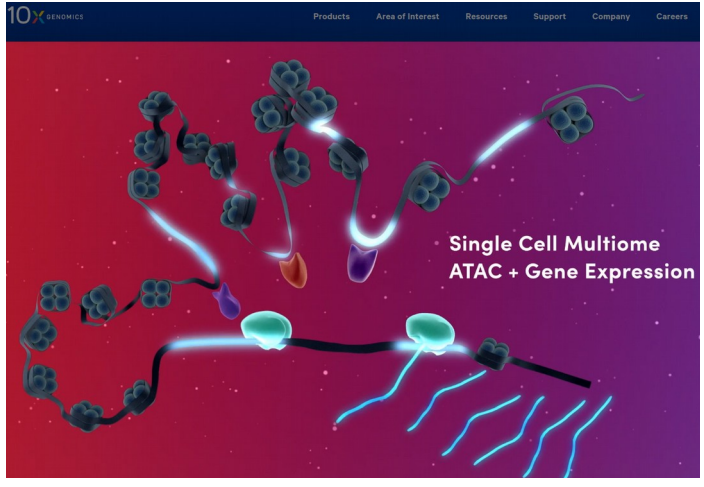
Kelsey et al., 2017, Science 358, 69-75



Clark et al., 2018, Nature Communications 9, 781



Hu et al., 2018, Frontier in Cell and Developmental Biology 6, 1-13



How to define and evaluate multi-Omics data integration?

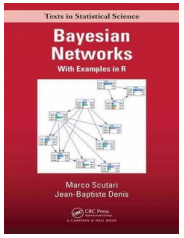
What I mean by Omics Integration

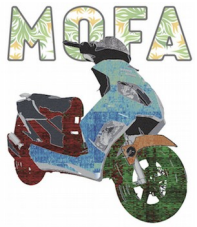
OnPLS

JIVE

DISCO

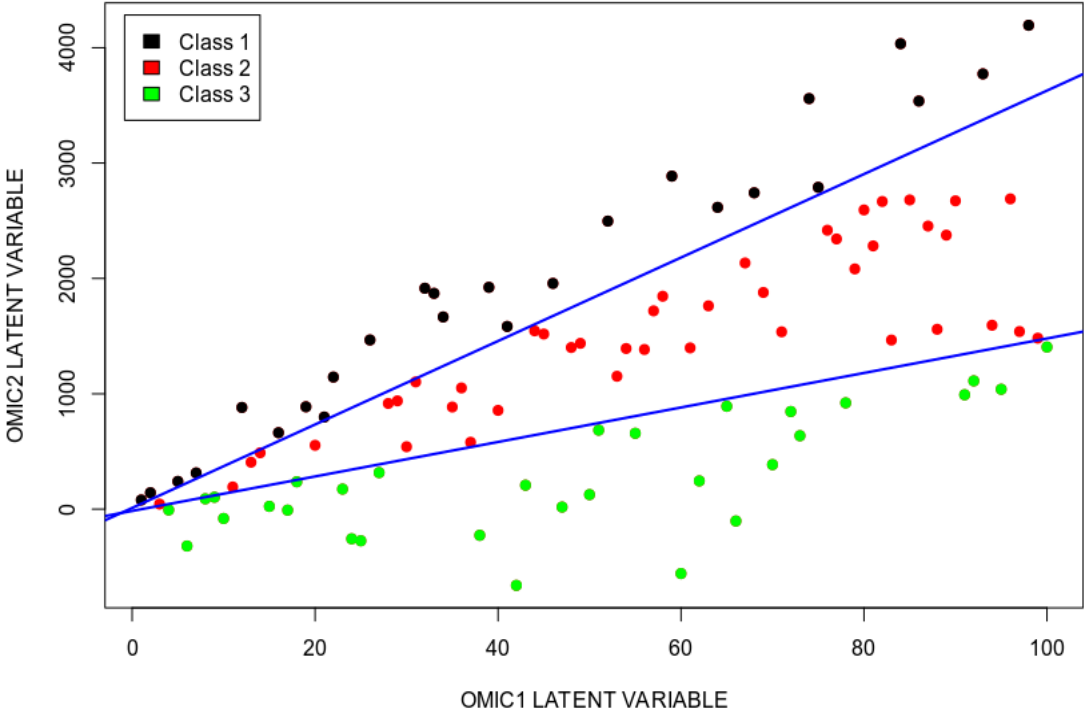
mixOmics

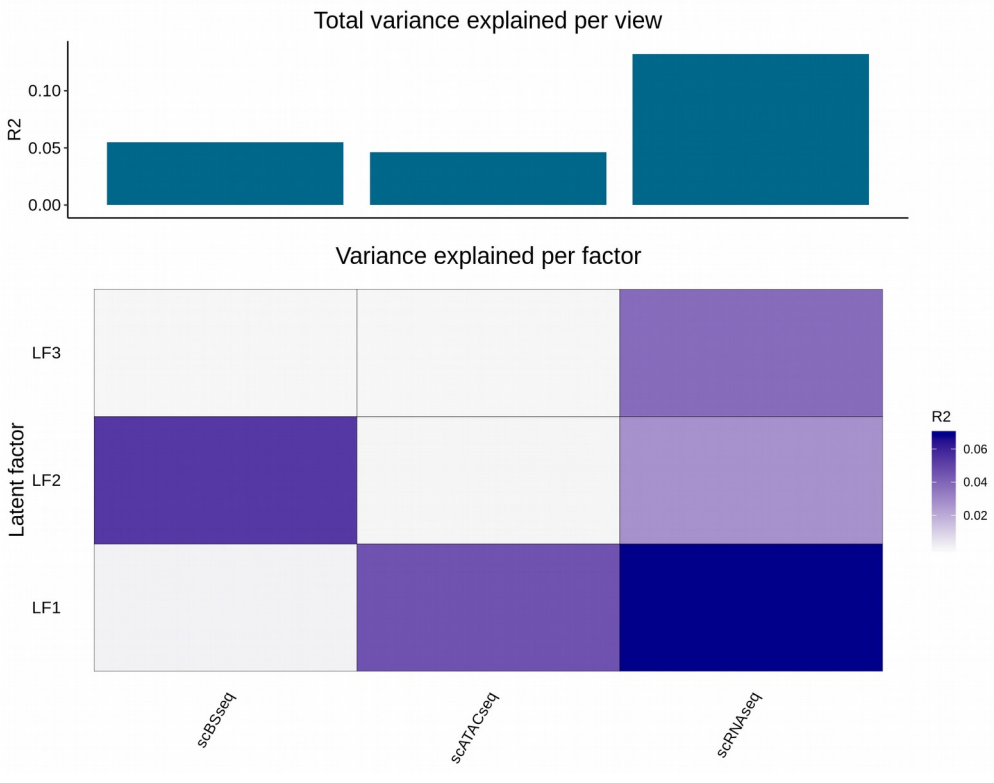




Clustering of Clusters

Idea Behind Omics Integration:
See Patterns Hidden in Individual Omics

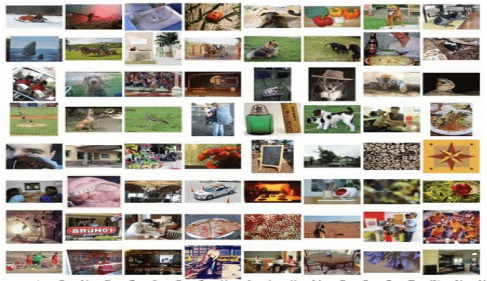




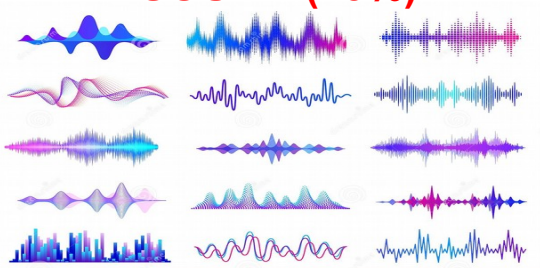
How I Evaluate Omics Integration

TEXT (78%)

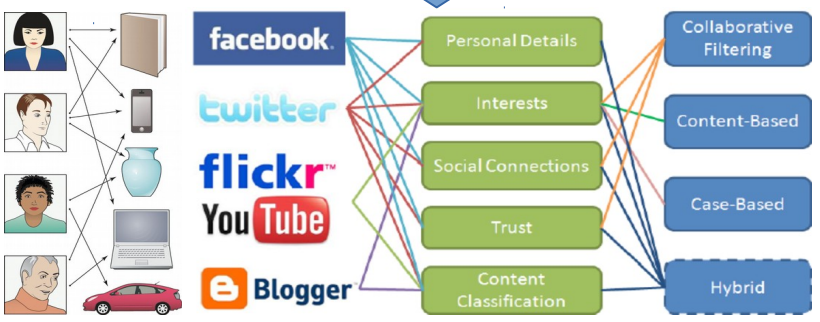
IMAGE (83%)



SOUND (75%)



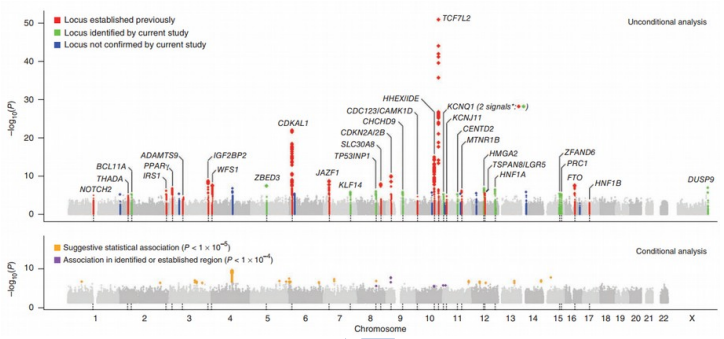
Predict Facebook user interests



Data Integration Accuracy: 96%

Prediction as a Criterion of Success

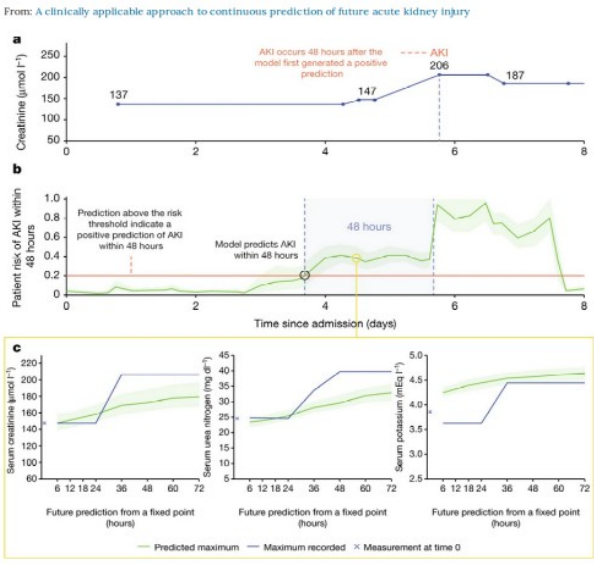
Statistics searches for candidates



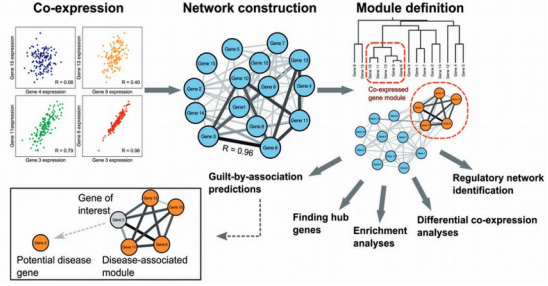
Consequence

B. Maher, Nature 456, 18-21 (2008)

Machine Learning optimizes prediction

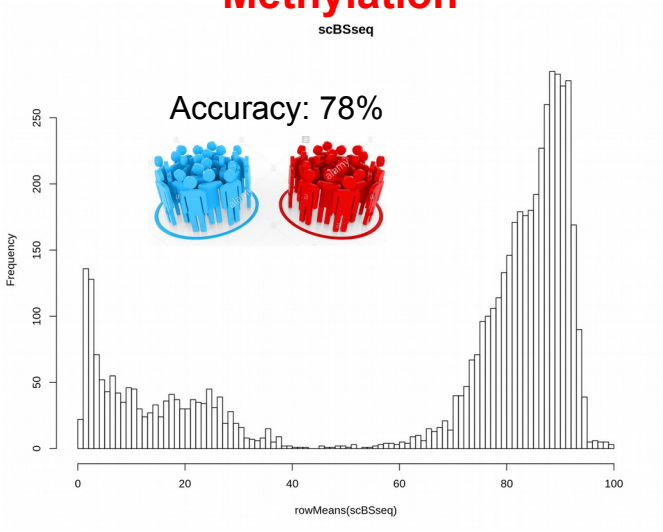


Consequence

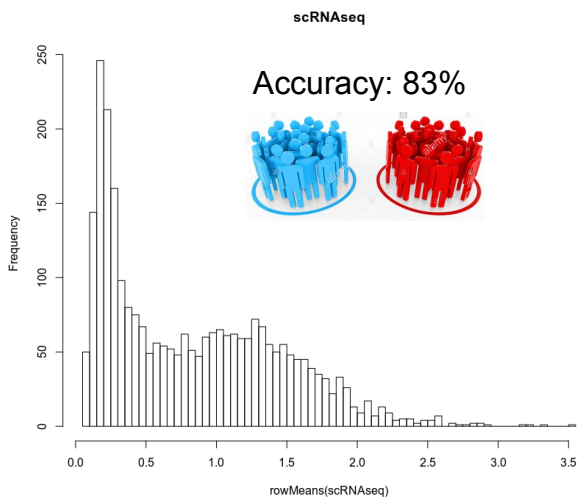


How I Evaluate Omics Integration

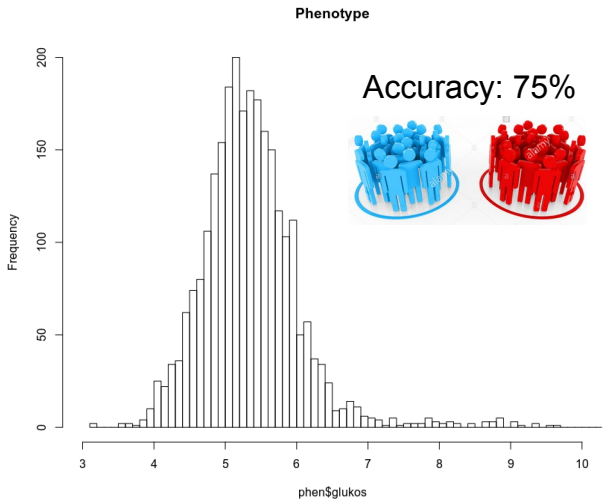
Methylation



Gene Expression



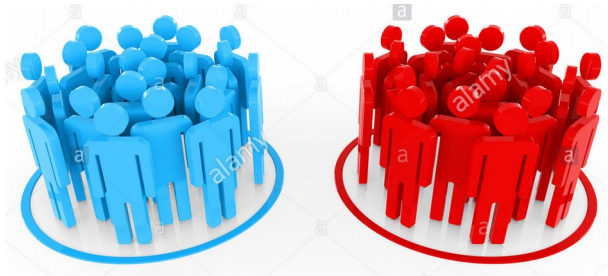
Clinical variable



1) Convert to common space:
Neural Networks, SNF, UMAP

2) Explicitly model distributions:
MOFA, Bayesian Networks

3) Extract common variation:
PLS, CCA, Factor Analysis

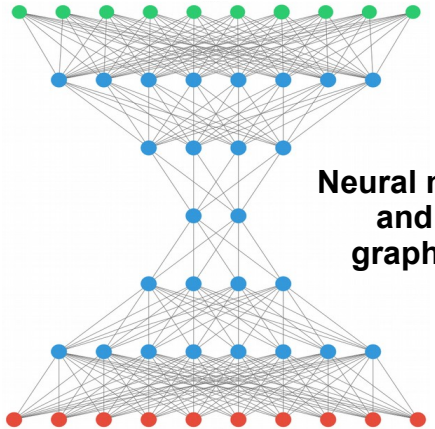


HEALTHY SICK

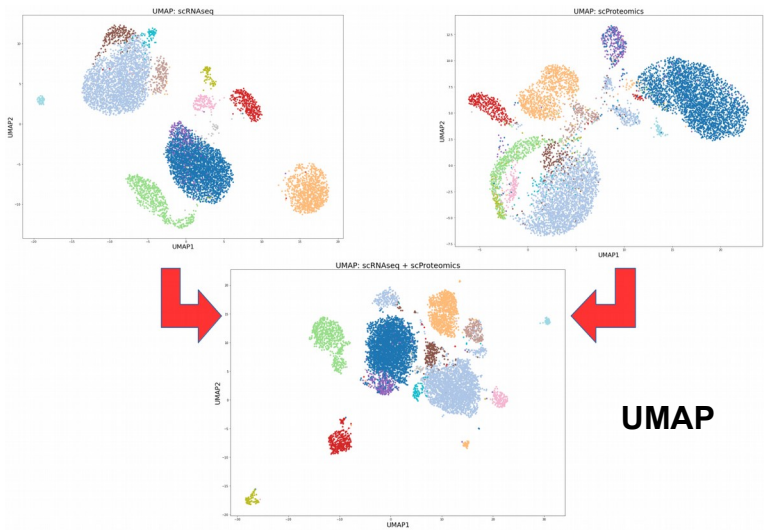
Data Integration
Accuracy: 96%

Overview of Integrative Methods

Convert to common space

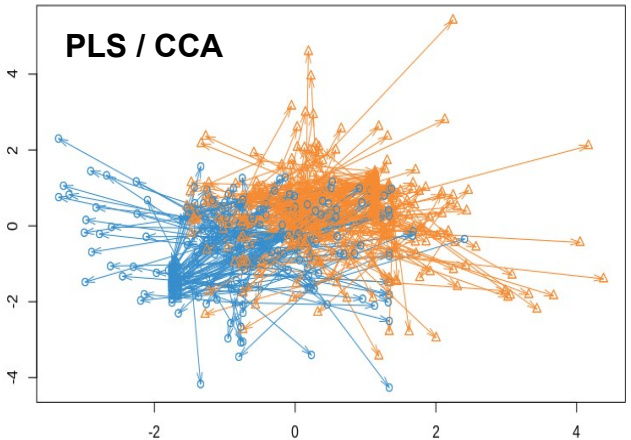


Neural nets and graphs

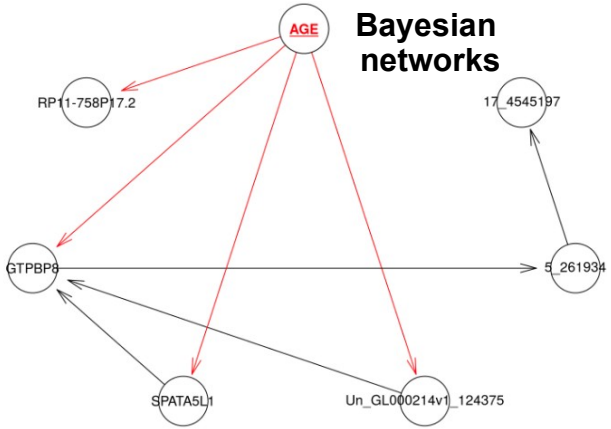


UMAP

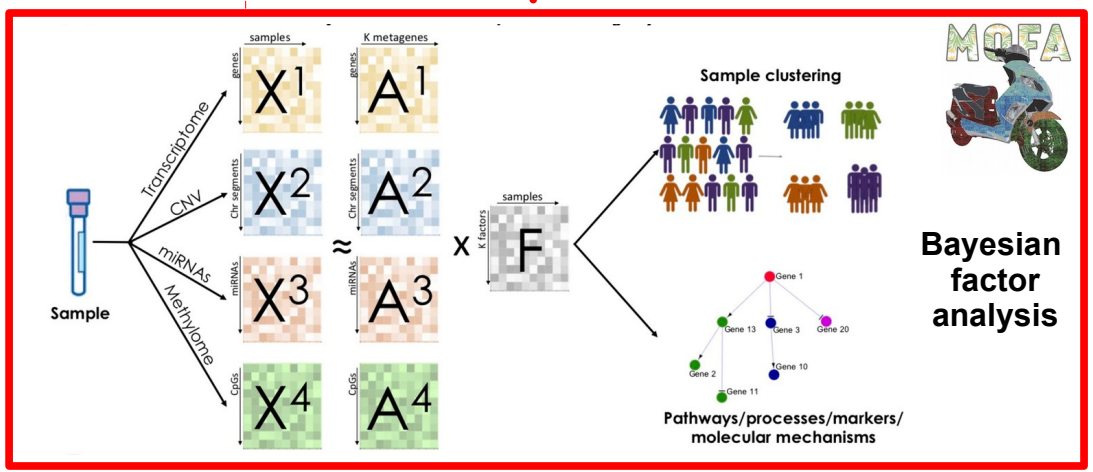
Extract common variation



Combine via Bayes rule



Bayesian networks



Bayesian factor analysis

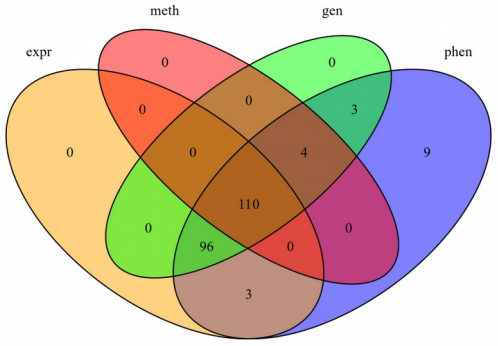
What Method of Integration to Select?

	Linear	Non-Linear
Supervised	PLS / OPLS / mixOmics, LASSO / Ridge / Elastic Net	Neural Networks, Random Forest, Bayesian Networks
Unsupervised	Factor Analysis / MOFA	Autoencoder, SNF, UMAP, Clustering of Clusters

For Example:

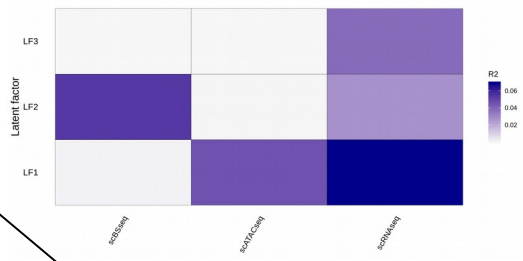
1) With ~100 samples it is a good idea to do **linear** Omics integration
2) T2D is a phenotype of interest, therefore **supervised** integration

Typical Workflow for Omics Integration



Data Set (4 Omics)
110 overlapping individuals

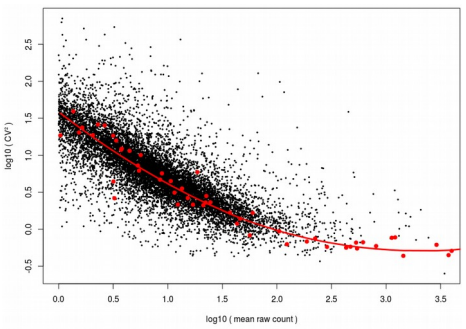
Check covariance



Train Set (n = 80)

Test Set (n = 30)

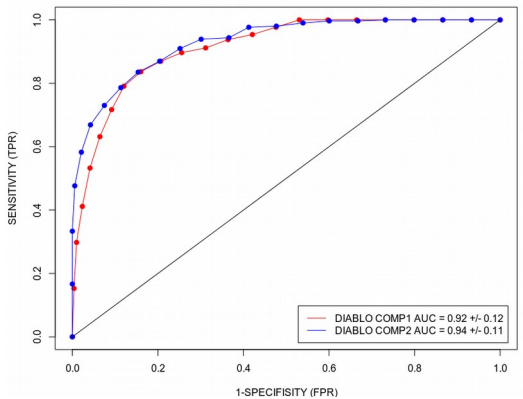
Unsupervised:
remove low-variance



Supervised:
LASSO

Feature Selection

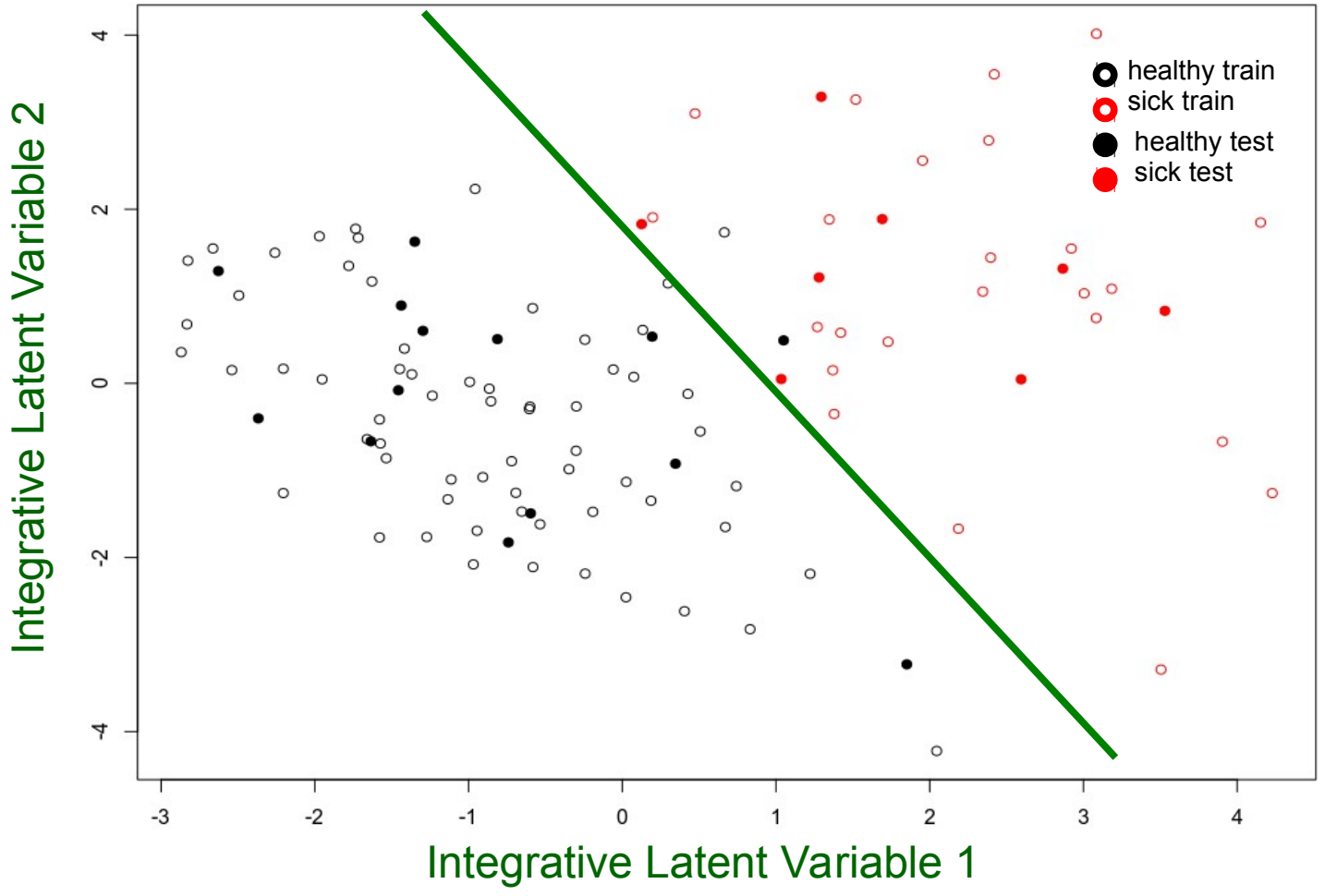
Evaluation



Omics Integration

Trained Model

Linear Separation: Decision Boundary



Take Home Messages

1) Biological data are high-dimensional and are notoriously difficult to analyze

2) Integration across Omics is very sensitive to the Curse of Dimensionality

3) Integrating across Omics we expect to discover novel patterns in the data

4) Increased prediction accuracy is an indication of successful data integration

5) Single cell Omics have enough statistical power for integrative analysis

National Bioinformatics Infrastructure Sweden (NBIS)

Knut och Alice Wallenbergs Stiftelse

Vetenskapsrådet

LUNDS UNIVERSITET