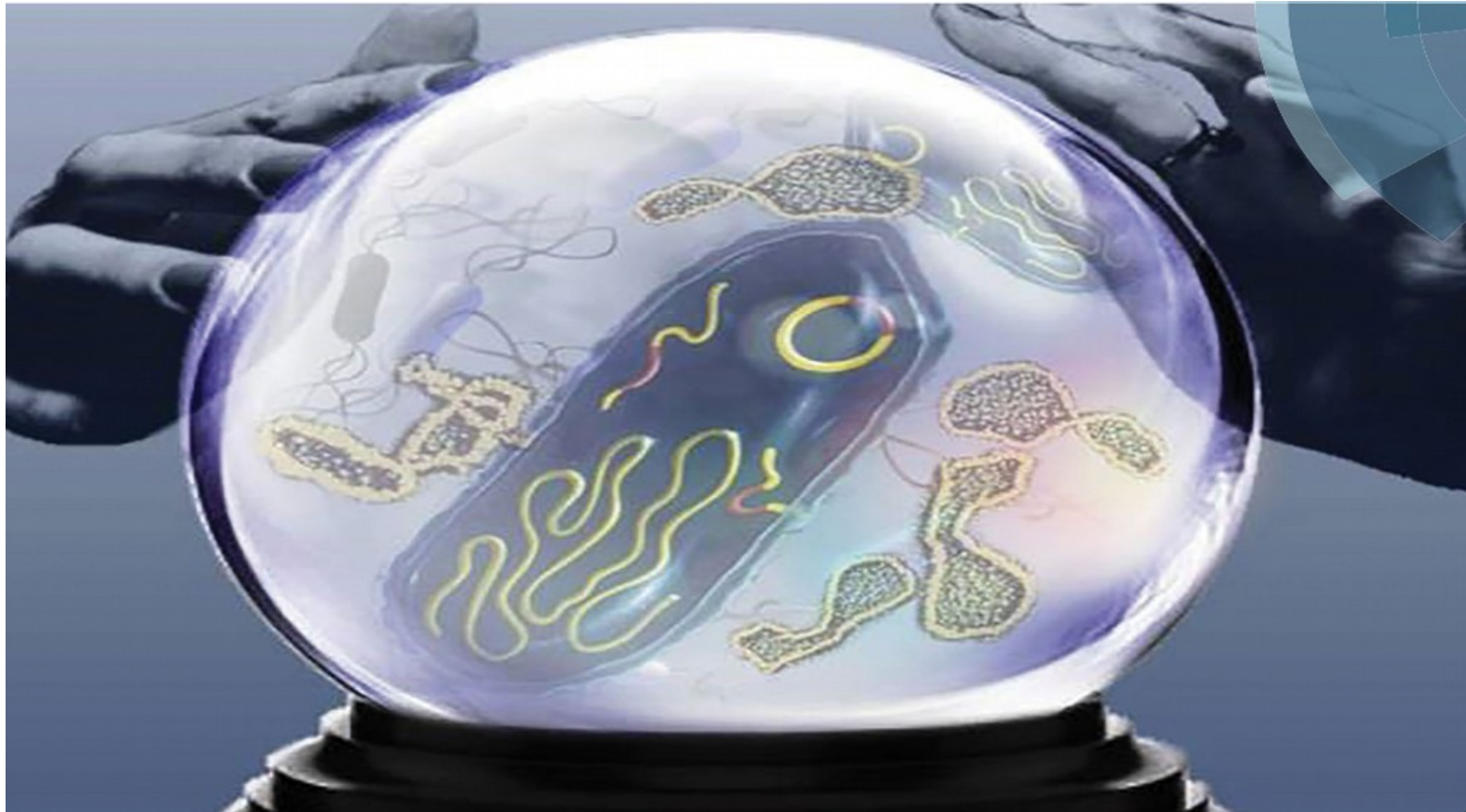


Machine Learning View of OMICs Integration

OMICs Integration and Systems Biology course

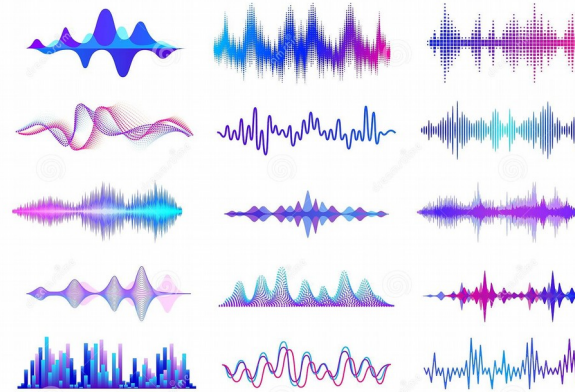
Nikolay Oskolkov, NBIS SciLifeLab

Lund, 6.09.2021



Tabular

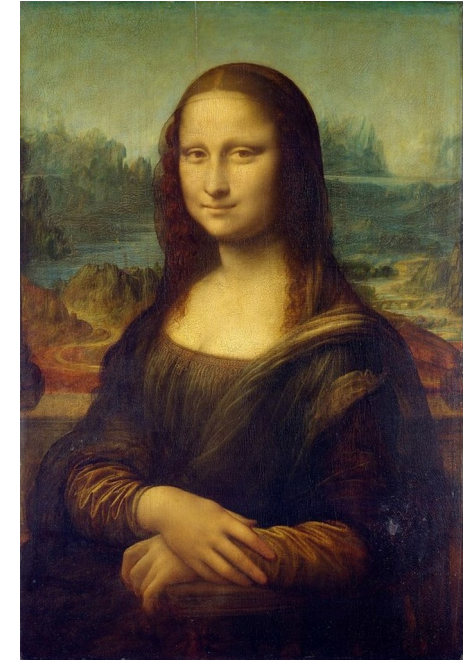
Sound



dreamstime.com

ID 142115245 © Spicytruffel

Image



Text

Editing Wikipedia articles on Medicine

Editing Wikipedia can be daunting for novices, 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.

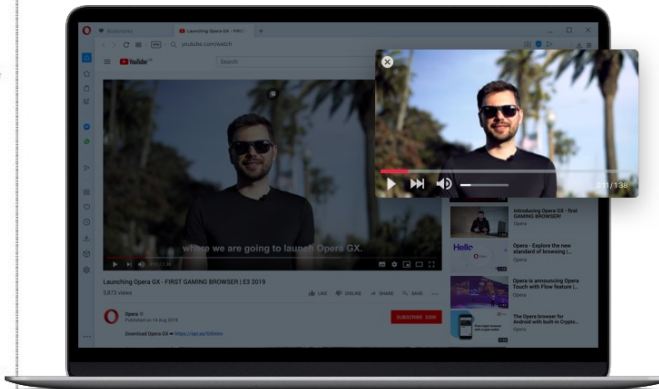
Scared? Don't be!

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!



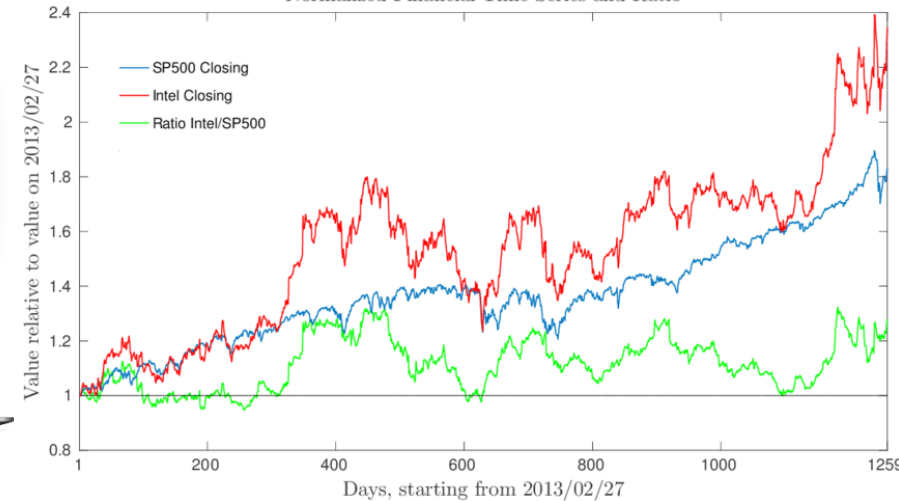
DATA

Video



Time Series

Normalized Financial Time Series and Ratio



The Curse of Dimensionality complicates OMICs Integration

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

Biomedicine

Bayesianism



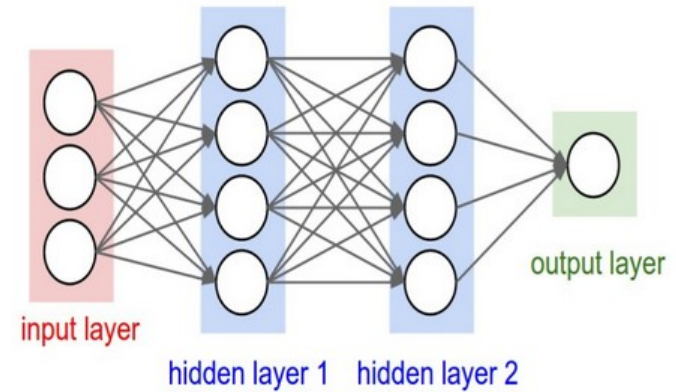
$P \gg N$

Frequentism



$P \sim N$

Deep Learning



$P \ll N$



Amount of Data



Ex.1

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

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

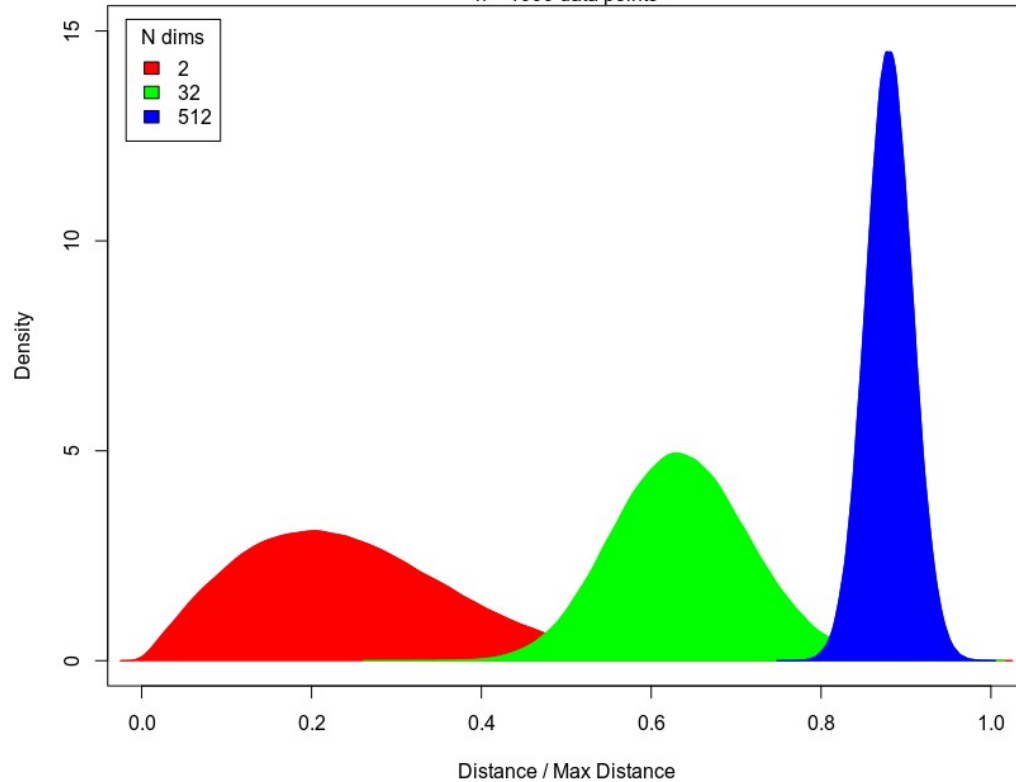
$$(X^T X)^{-1} \sim \frac{1}{\det(X^T X)} \dots \rightarrow \infty, \quad n \ll p$$

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

Biased ML variance estimator in HD-space

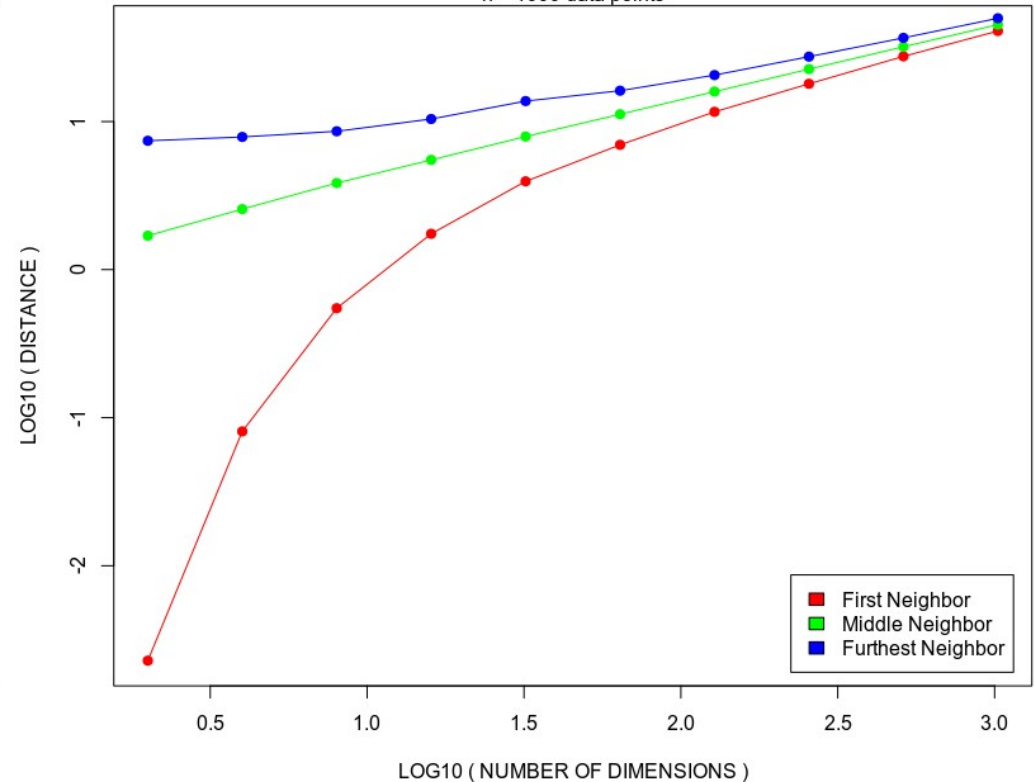
Distances in High Dimensions

n = 1000 data points



Distances in High Dimensions

n = 1000 data points



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

The differences between closest and furthest data point neighbours disappears in high-dimensional spaces – can't cluster

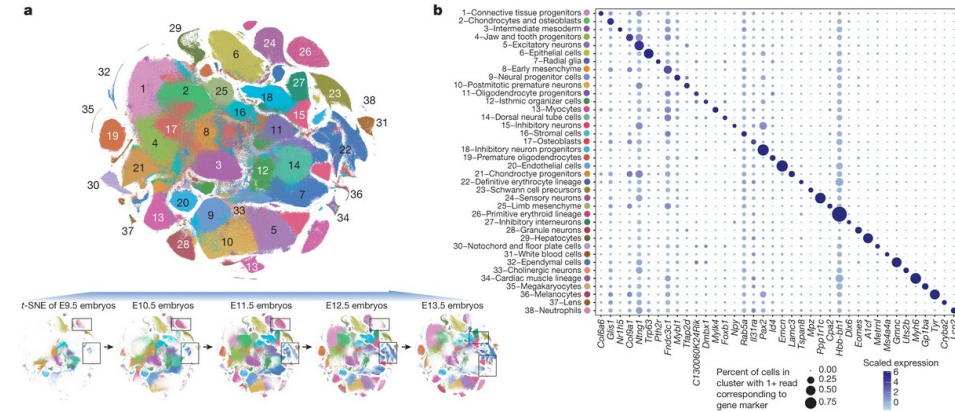
In high-dimensional space we can not separate cases and controls any more

10x GENOMICS SOLUTIONS & PRODUCTS RESEARCH & APPLICATIONS EDUCATION & RESOURCES

nature MENU

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

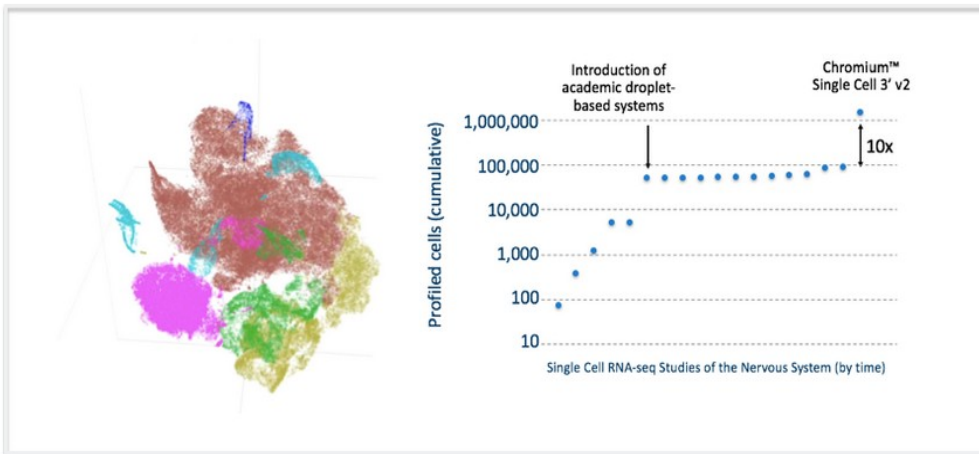
From: The single-cell transcriptional landscape of mammalian organogenesis



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

« Back to Blog

< Newer Article Older Article >



Our 1.3 million single cell dataset is ready to download



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](#).

**Watch out Underfitting!
Paradise for Deep Learning!**

BioTuring™ Solutions Resources

Explore **4,000,000 CELLS** at ease with **BIOTURING BROWSER**

EXPLORER NOW

A next-generation platform to re-analyze published single-cell sequencing data

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](#).

Search

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

How to define and evaluate OMICs Integration?



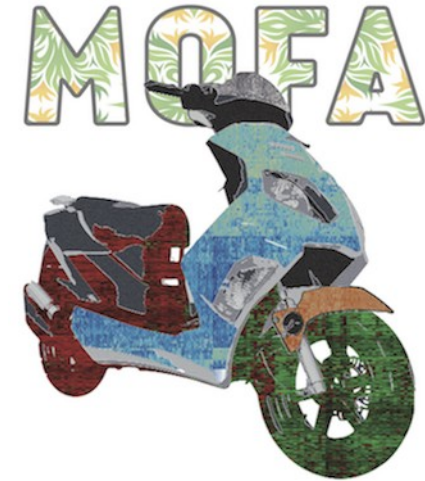
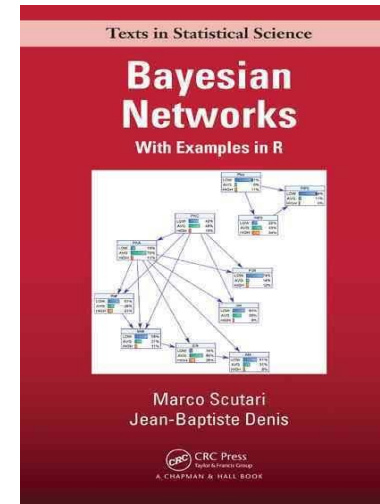
Exploration and
Integration of
Omics datasets

OnPLS

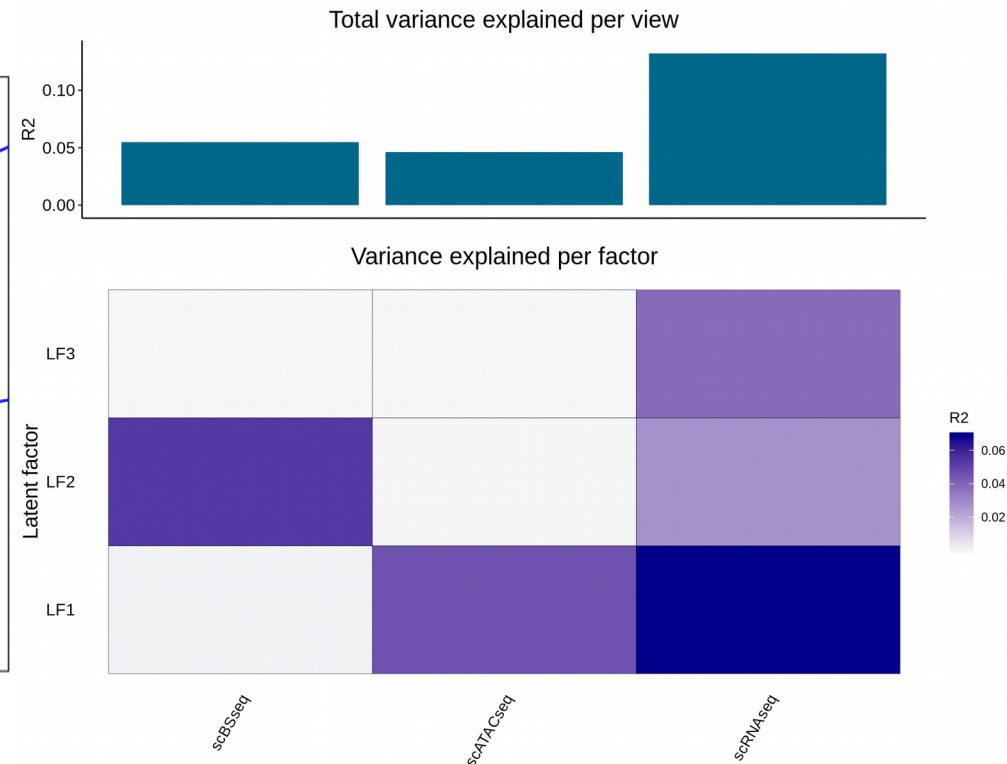
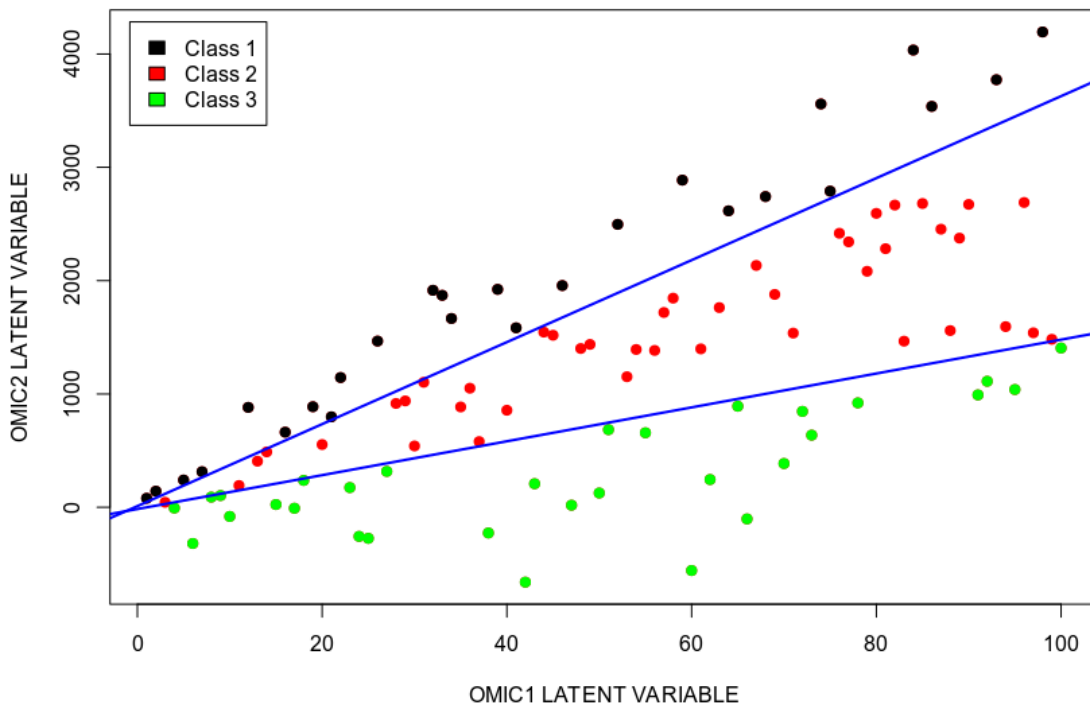
JIVE

DISCO

Clustering of Clusters



Idea Behind OMICs Integration: See Patterns Hidden in Individual OMICS



TEXT (78%)

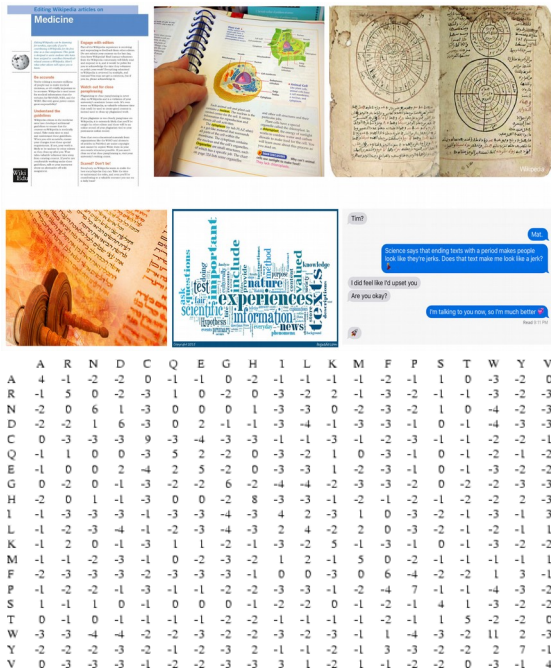
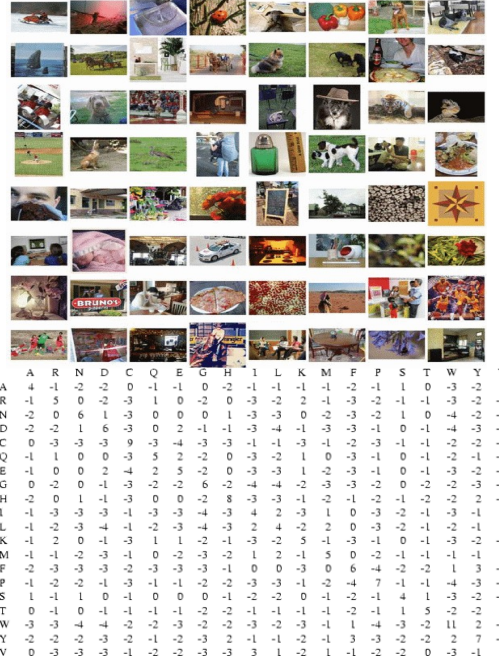
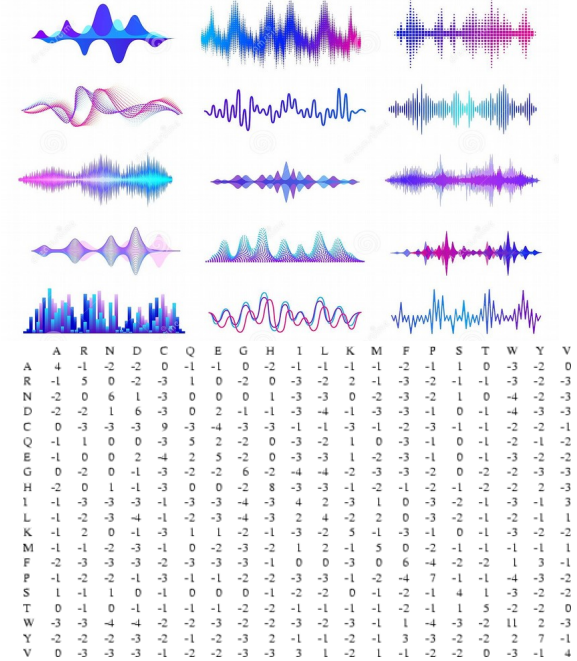


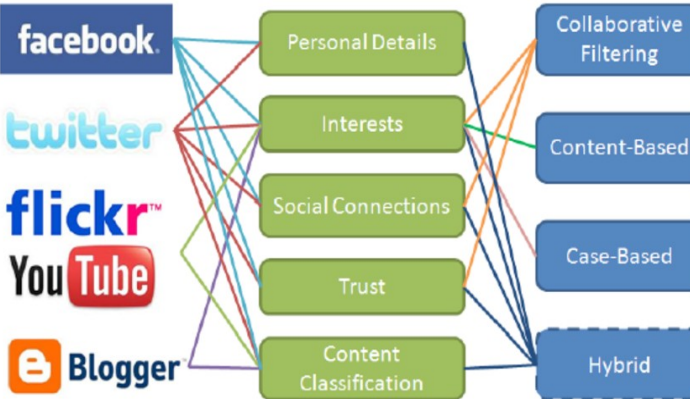
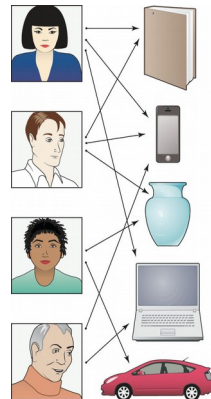
IMAGE (83%)



SOUND (75%)



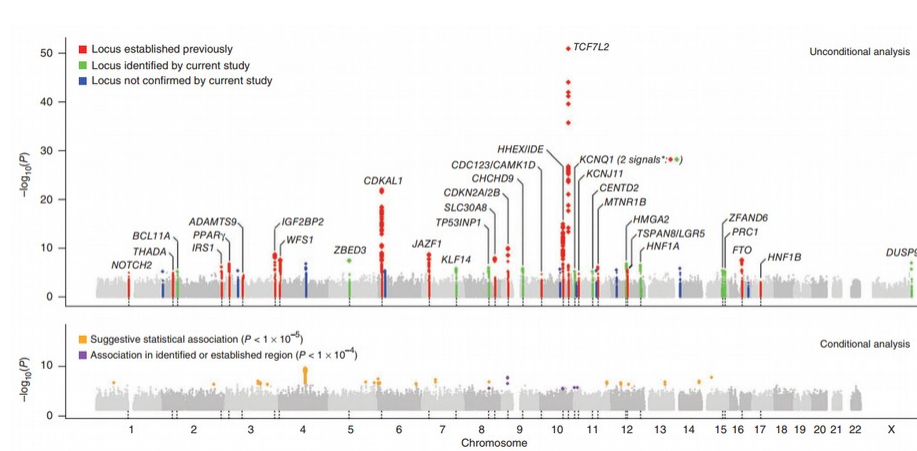
Predict Facebook user interests



Data Integration Accuracy: 96%

Statistics searches for candidates

Machine Learning optimizes prediction



Consequence



nature > letters > article

nature
International journal of science

Letter | Published: 31 July 2019

A clinically applicable approach to continuous prediction of future acute kidney injury

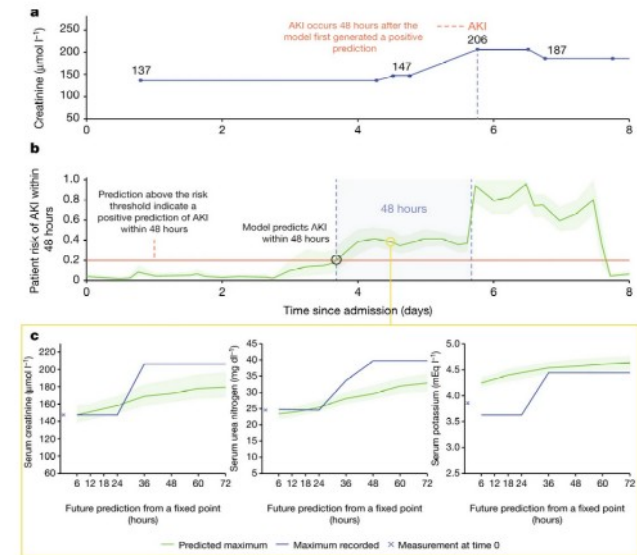
Nenad Tomasev, Xavier Giorot, [...] Shakir Mohamed

Nature 572, 116–119 (2019) | Download Citation

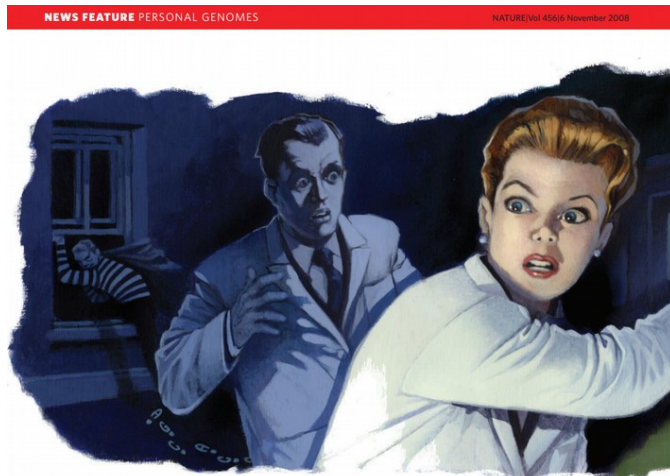
Abstract

The early prediction of deterioration could have an important role in supporting healthcare professionals, as an estimated 11% of deaths in hospital follow a failure to promptly recognize and treat deteriorating patients¹. To achieve this goal requires predictions of patient risk that are continuously updated and accurate, and delivered at an individual level with sufficient context and enough time to act. Here we develop a deep learning approach for the continuous risk prediction of future deterioration in patients, building on recent work that models adverse events from electronic health records^{2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17} and using acute kidney injury—a common and potentially life-threatening condition¹⁸—as an exemplar. Our model was developed on a large, longitudinal dataset of electronic health records that cover diverse

From: A clinically applicable approach to continuous prediction of future acute kidney injury

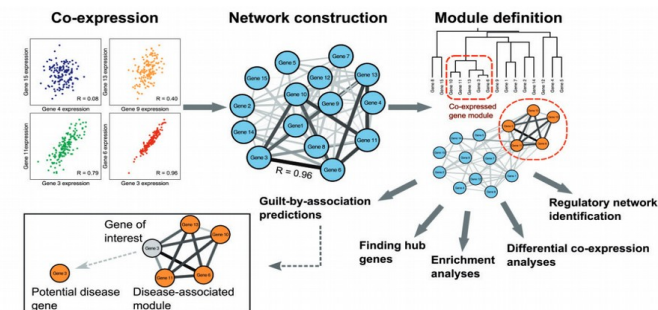


Consequence

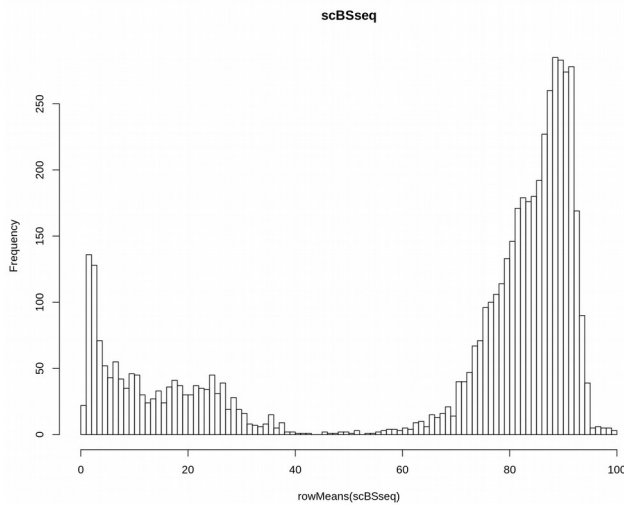


The case of the missing heritability

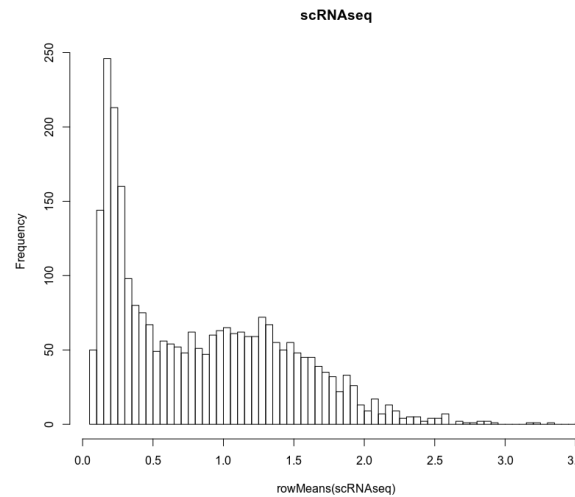
B. Maher, Nature 456, 18–21 (2008)



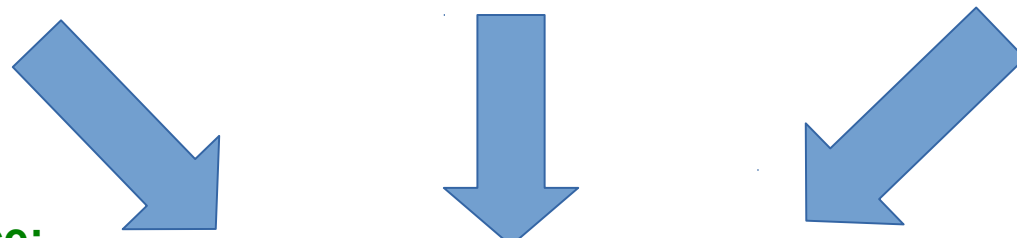
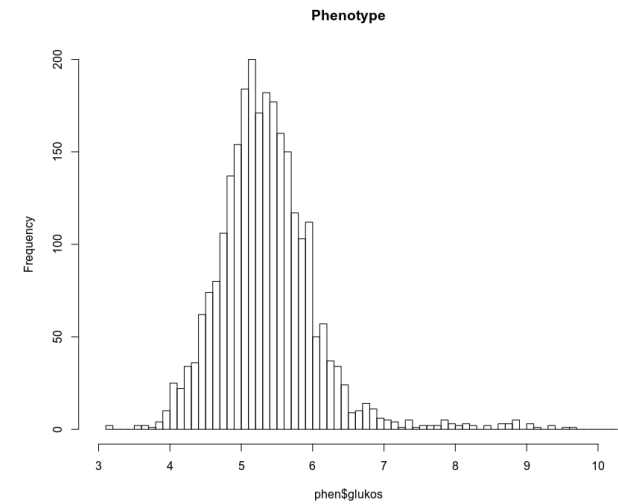
Methylation (78%)



Gene Expression (83%)



Phenotype (75%)



1) Convert to common space:

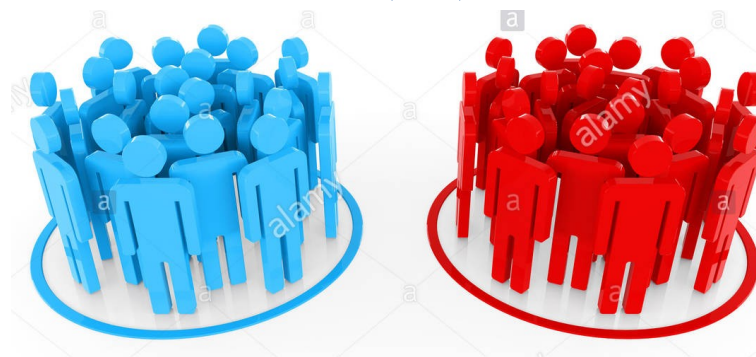
Neural Networks, SNF, UMAP

2) Explicitly model distributions:

MOFA, Bayesian Networks

3) Extract common variation:

PLS, CCA, Factor Analysis



HEALTHY

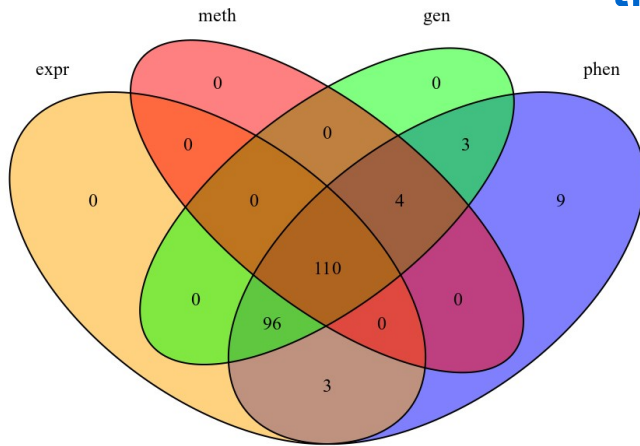
SICK

**Data Integration
Accuracy: 96%**

	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 ~110 samples it is a good idea to do **linear** OMICs integration
- 2) T2D is a phenotype of interest, therefore **supervised** integration



29% of Diabetics

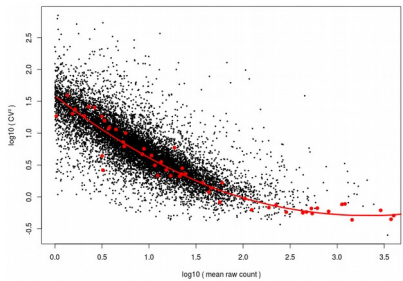
Data Set (4 OMICs)

~~WGS (~30 mln dims)
BSseq (~30 mln dims)~~

Train Set (n = 88)

Test Set (n = 22)

unsupervised



supervised

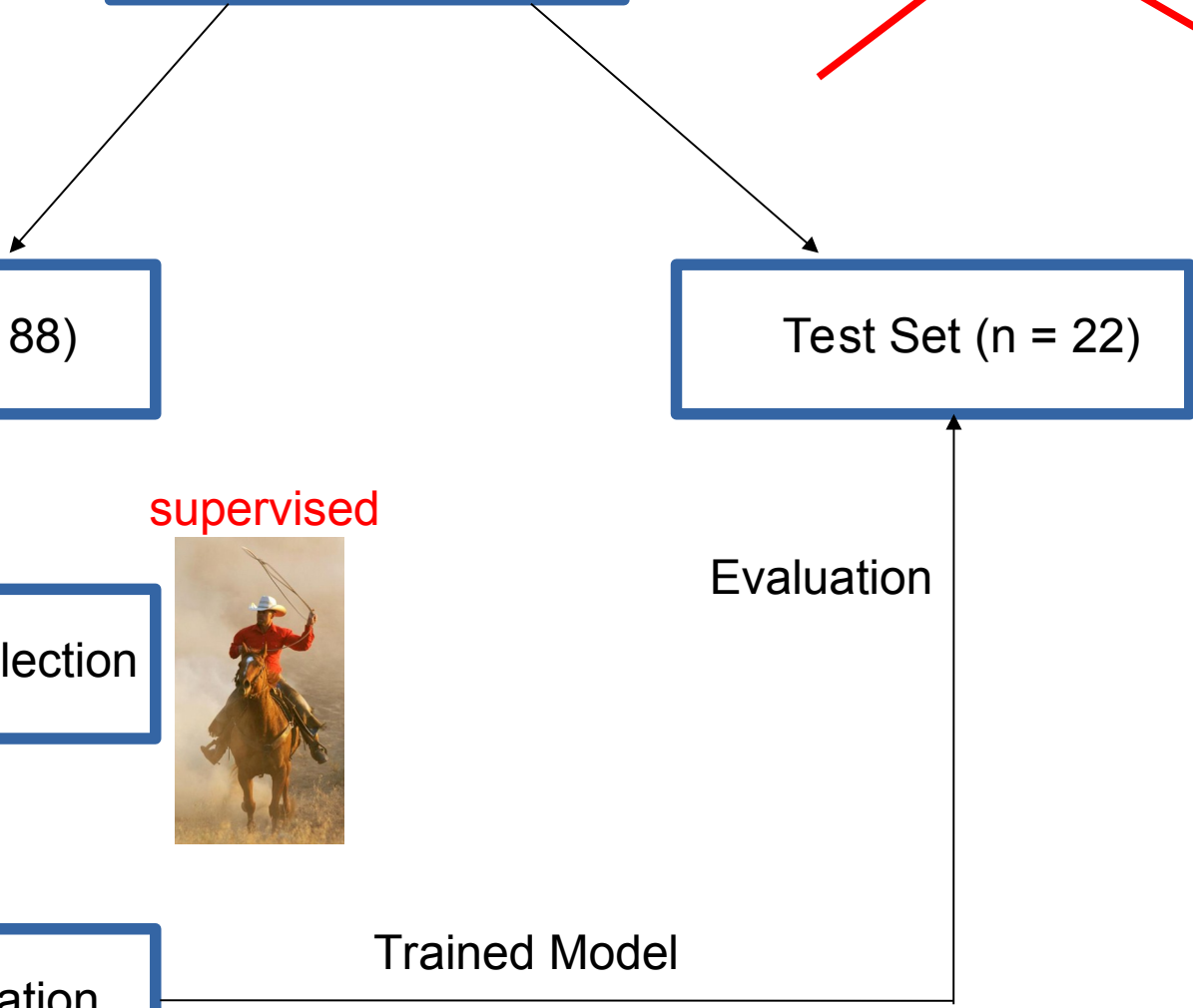


Feature Pre-Selection

OMICs Integration

Evaluation

Trained Model



- 1) Check that there is a relation between the OMICs (MOFA)
- 2) Choose integrative model based on amount of data and goal (linear, supervised)
- 3) Do feature pre-selection (supervised or unsupervised) on train data set
- 4) Integrate the OMICs using your favorite model chosen in 2) on train data set
- 5) Compare prediction of integrative model with predictions from individual OMICs



*Knut och Alice
Wallenbergs
Stiftelse*



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