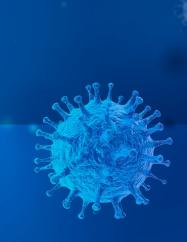
Differential Gene **Expression Analysis of** Ulcerative Colitis and Crohn's Disease Samples and Predictive Modeling for Disease Diagnosis

Patricia Mason December 2020





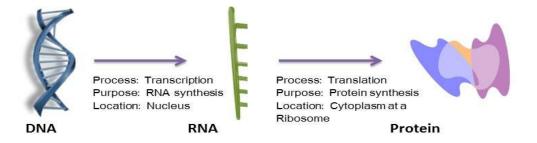
Ulcerative Colitis and Crohn's Disease are inflammatory bowels diseases that cause gastrointestinal inflammation and tissue damage. Both are caused by a combination of inappropriate immune response to normal gut flora and environmental factors. Diagnosis is often made with biopsies from colonoscopies, which are invasive and pose an element of risk, as do all surgeries. Blood samples, in contrast, are easy to obtain, less expensive, and minimally invasive.



- Is there a standard set of genes that distinguish the Peripheral Blood Monocyte Cells (PBMCs) between Ulcerative Colitis, Crohn's Disease, and Normal patients.
- Based on the differentially expressed genes, Is it possible to create a model to predict the origin of the PBMCs.
- Is it possible to replicate the analysis performed by Bioconductor/limma library: a package that has been an open-sourced project for 20 years.



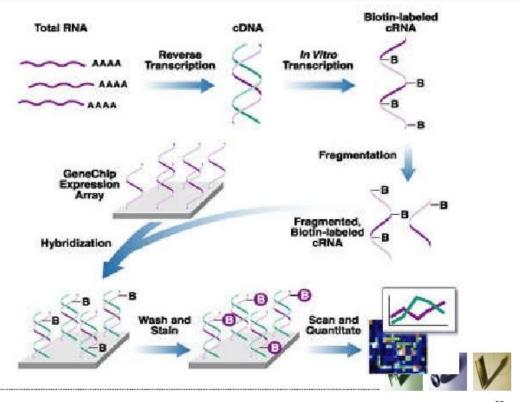
The Central Dogma



DNA contains the original codes for making the proteins that living cells need. mRNA is a copy of a gene located on the DNA molecule. mRNA will leave the nucleus of the cell and the ribosome will read its coding sequences and put the appropriate amino acids together.



Affymetrix GeneChip experiment





Comparison of Packages

Bioconductor (limma library)

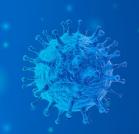
Linear Regression

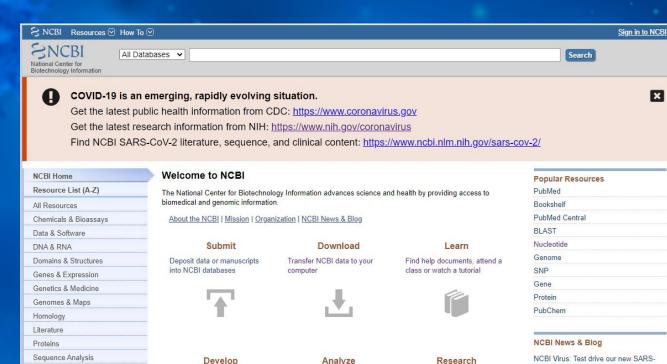
Empirical Bayes

UMAP

<u>Genomatix</u>

PCA





Identify an NCBI tool for your

data analysis task

Explore NCBI research and

collaborative projects

Use NCBI APIs and code

libraries to build applications

Taxonomy

Variation

Training & Tutorials

NCBI Virus: Test drive our new SARS-CoV-2 interactive data dashboard 03 Dec 2020

Are you looking for SARS-CoV-2

semience data? I nok no further! The December 9 Webinar: Using BLAST+ in

Docker and on the cloud

×

Join us on December 9, 2020 to learn about containerized RI AST+ in Docker

Read assembly and Annotation Pipeline Tool (RAPT) is available for use and

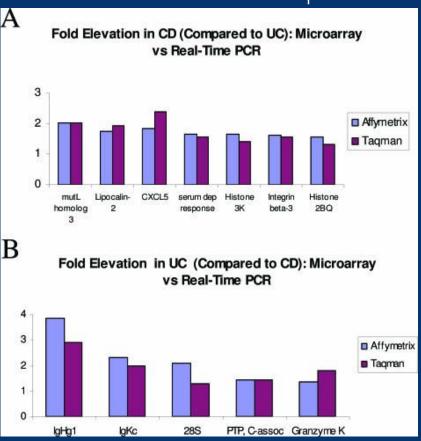
24 Nov 2020

We are excited to launch a heta version.

testing



Verification of Results with TaqMan PCR







Burczynski, Michael E et al. "Molecular classification of Crohn's disease and ulcerative colitis patients using transcriptional profiles in peripheral blood mononuclear cells." *The Journal of molecular diagnostics : JMD* vol. 8,1 (2006): 51-61.

doi:10.2353/jmoldx.2006.050079

Dataset contains microarray signals of
22,283 human genes
assayed against the Peripheral Blood Monocyte Cells (PBMCs) in
127 samples:
26 Ulcerative Colitis
59 Crohn's Disease

96 Normal

Data Cleaning and Processing



Data downloaded in SOFT format (Simple Omnibus Format in Text)



Separate meta-data (clinical and demographic) from raw data into two different csv files



Create lists of accession numbers that correlated with sample types



Calculate log2 of the fluorescence values



Transpose the dataframe such that the genes are the features (columns and the samples are the rows



Scale with StandardScaler for PCA Analysis



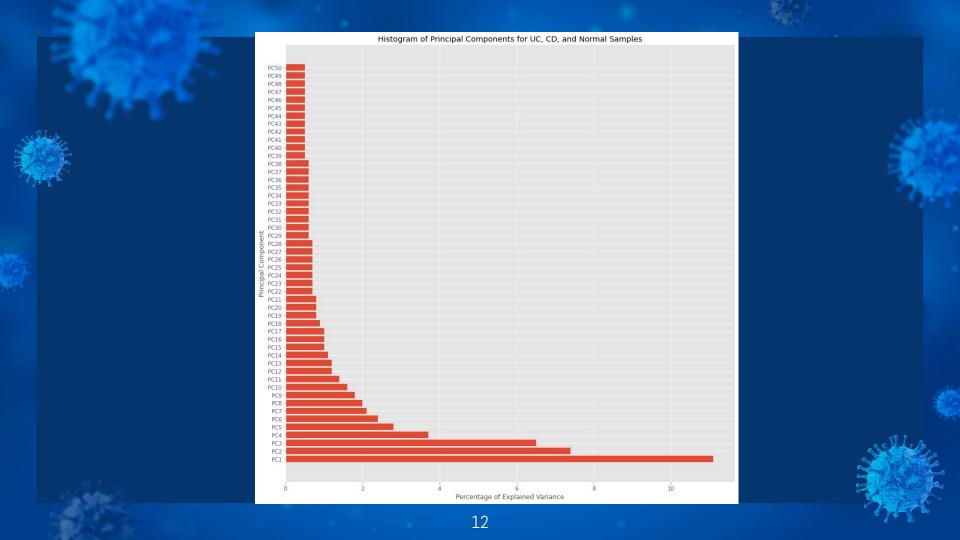
Add category column with UC, CD, NM for modeling



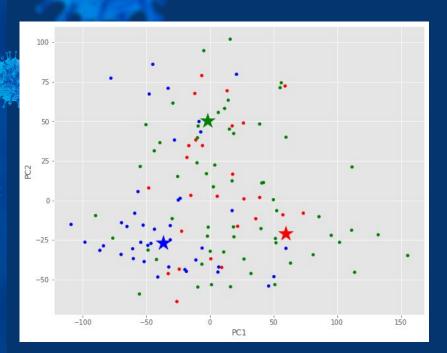
Cumulative Explained Variance - 50 Components (Genes) 0.70

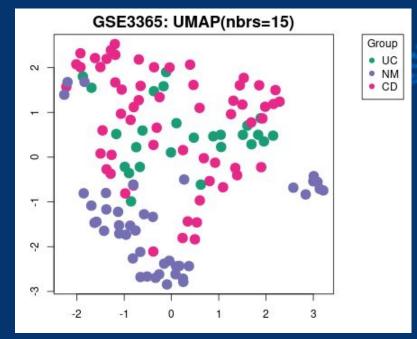
Cumulative Explained Variance - 100 Components (Genes) 0.91





K-Means Clustering and UMAP of Ulcerative Colitis, Crohn's Disease, and Normal Samples



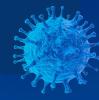


Silhouette scores

UC = 0.41

CD = 0.39

NM = 0.52

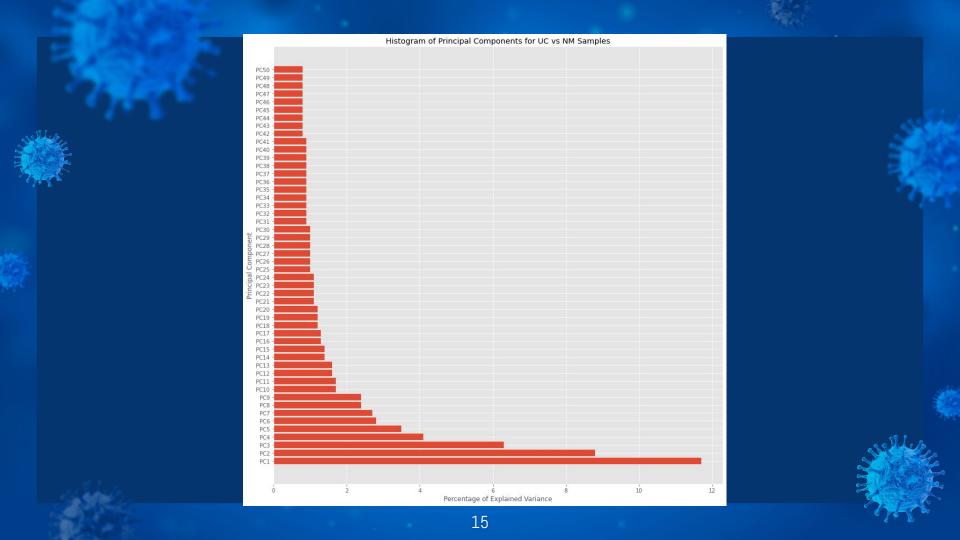




Bioconductor Differential/UC, CD, NM	PCA Differential/UC, CD, NM
histone cluster 1, H2ac	solute carrier family 4 member 3
histone cluster 1, H2bk	stearoyl-CoA desaturase
brain abundant membrane attached signal protein 1	alkaline phosphatase, intestinal
progesterone receptor membrane component 1	HAUS augmin like complex subunit 7///three pri
histone cluster 2, H2be	ATPase H+ transporting V0 subunit a1
folate receptor 1	bone morphogenetic protein 1
serpin family B member 2	Kruppel like factor 1
monocyte to macrophage differentiation associated	TBC1 domain family member 10B
amyloid beta precursor protein	homeobox B5
transmembrane protein 158 (gene/pseudogene)	crystallin beta B3





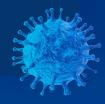




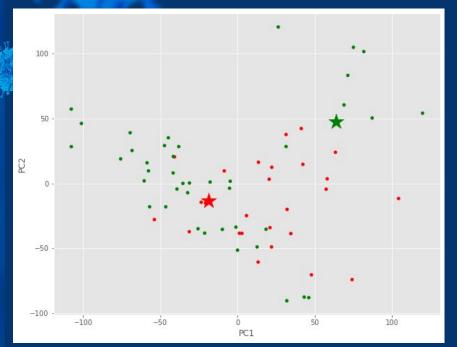
PCA Differential/UC vs NM	Bioconductor Differential/UC vs NM
ubiquitin conjugating enzyme E2 L3	folate receptor 1
NMD3 ribosome export adaptor	brain abundant membrane attached signal protein 1
proteasome subunit alpha 3	Affy Gene
cold shock domain containing E1	high mobility group box 1
small ubiquitin-like modifier 1	S100 calcium binding protein A11
basic leucine zipper and W2 domains 1	microRNA 8071-2///microRNA 8071-1///immunoglob
poly(A) polymerase alpha	ARP5 actin-related protein 5 homolog
KRR1, small subunit processome component homolog	lysine demethylase 2A
transcription elongation factor B subunit 1	solute carrier family 22 member 4
heat shock protein family A (Hsp70) member 13	immunoglobulin kappa locus///immunoglobulin ka

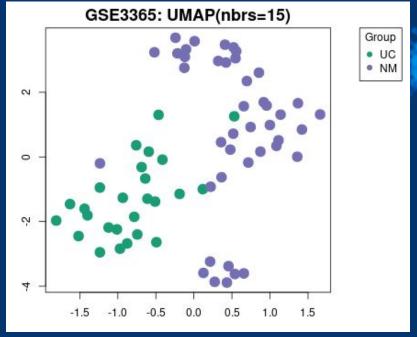


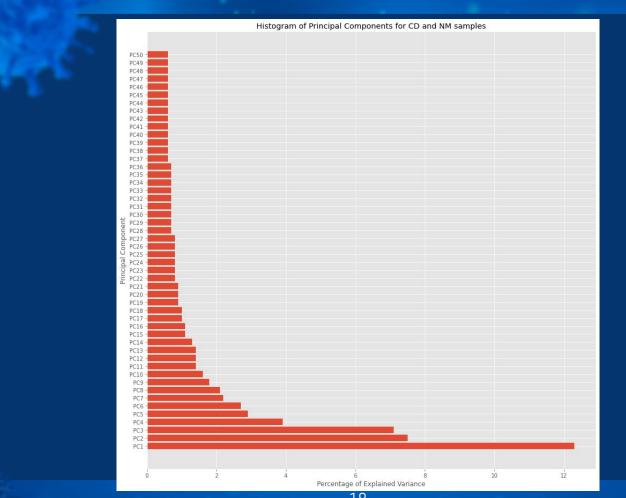


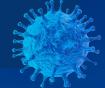


K-Means Clustering and UMAP(Bioconductor) of Ulcerative Colitis vs. Normal Samples





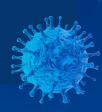




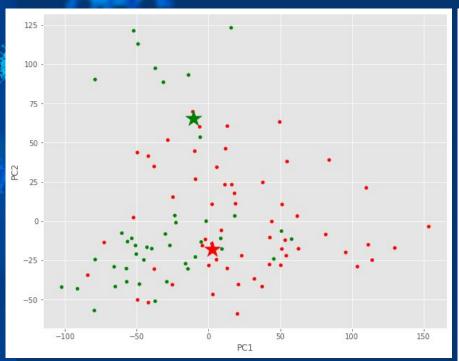


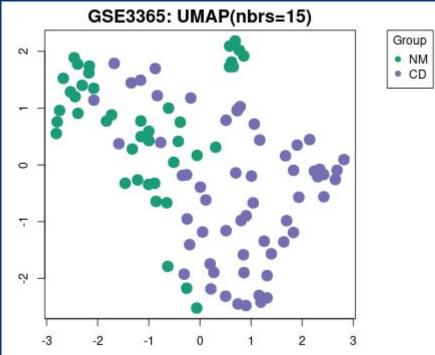
PCA Differential/CD vs NM	Bioconductor Differential/CD vs NM
solute carrier family 4 member 3	histone cluster 1, H2ac
stearoyl-CoA desaturase	histone cluster 1, H2bk
bone morphogenetic protein 1	progesterone receptor membrane component 1
alkaline phosphatase, intestinal	serpin family B member 2
crystallin beta B3	histone cluster 2, H2be
3B, cell surface associated///mucin 3A,	monocyte to macrophage differentiation associated
ugmin like complex subunit 7///three pri	brain abundant membrane attached signal protein 1
NEDD4 binding protein 1	transmembrane protein 158 (gene/pseudogene)
collagen type XI alpha 2 chain	histone cluster 1, H2bd
homeobox B5	amyloid beta precursor protein

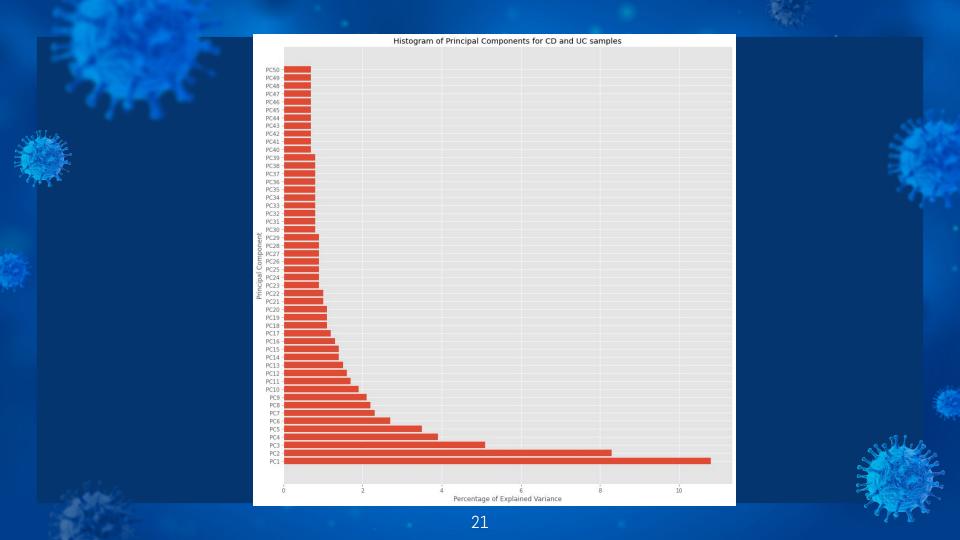




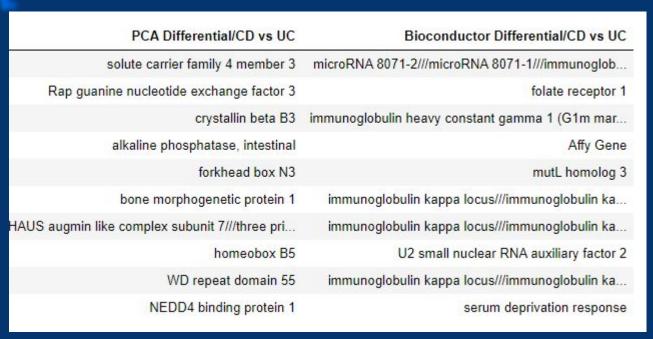
K-Means Clustering and UMAP(Bioconductor) of Crohn's Disease vs. Normal Samples







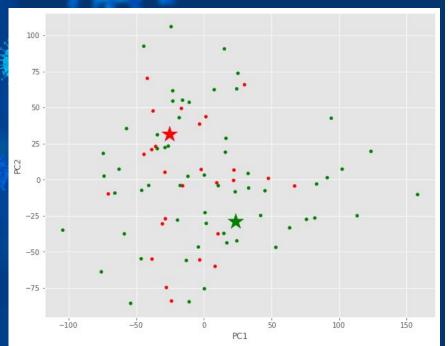


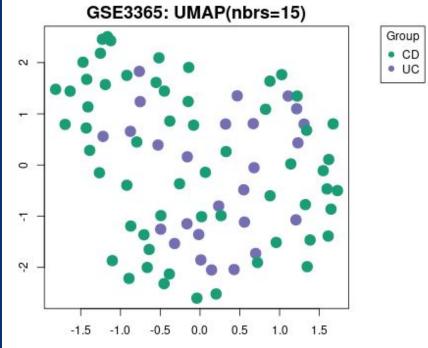






K-Means Clustering and UMAP (Bioconductor - Crohn's Disease vs Ulcerative Colitis Samples





UC, CD, & NM Sample Classification Models

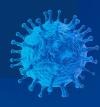
Model	Train	Test	Best Parameters
kNN with PCA	1.0	0.72	Metric:Euclidean n-neighbors: 1
kNN all genes	0.75	0.59	Metric: Manhattan n-neighbors: 21
Random Forest with PCA	1.0	0.65	Max-Depth: None n-estimators: 150
Random Forest All genes	1.0	0.70	Max-Depth: None n-estimators: 150

PCA = 100 Components

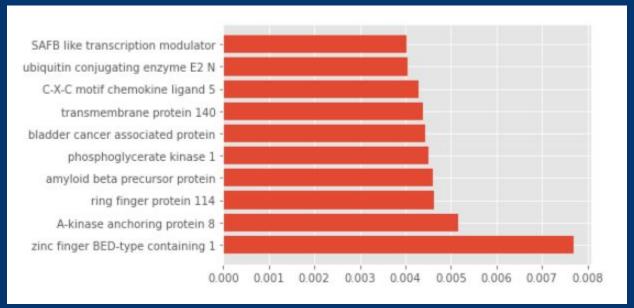
Binary Classification

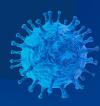
Logistic Regression (default)	Baseline	Train	Test
UC vs NM with PCA	0.62	1.0	1.0
UC vs NM All Genes	0.62	1.0	1.0
CD vs NM with PCA	0.58	1.0	0.88
CD vs NM All Genes	0.58	1.0	0.92

PCA = 50 Components



Top 10 Genes Differentially Expressed Between Ulcerative Colitis, Crohn's Disease and Normal Samples Random Forest



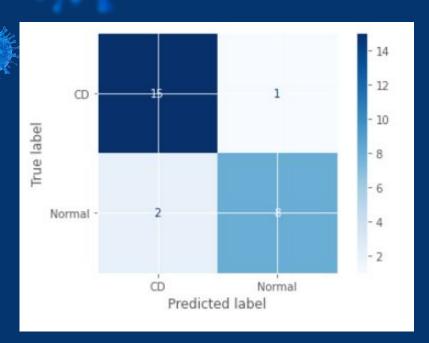


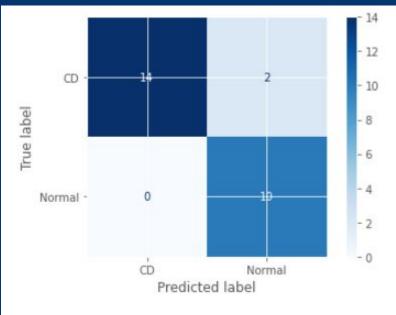
Top Ten Differentially Expressed Genes - Ulcerative Colitis, Crohn's Disease, Normal Samples for Random Forest and Bioconductor

RF Differential/UC,CD,NM	Bioconductor Differential/UC,CD,NM
zinc finger BED-type containing 1	histone cluster 1, H2ac
A-kinase anchoring protein 8	histone cluster 1, H2bk
ring finger protein 114	brain abundant membrane attached signal protein 1
amyloid beta precursor protein	progesterone receptor membrane component 1
phosphoglycerate kinase 1	histone cluster 2, H2be
bladder cancer associated protein	folate receptor 1
transmembrane protein 140	serpin family B member 2
C-X-C motif chemokine ligand 5	monocyte to macrophage differentiation associated
ubiquitin conjugating enzyme E2 N	amyloid beta precursor protein
SAFB like transcription modulator	transmembrane protein 158 (gene/pseudogene)



Ulcerative Colitis vs Normal Samples

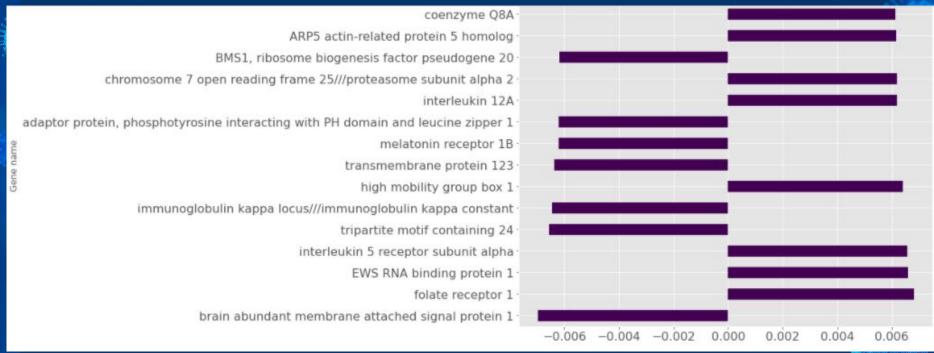




PCA (50) and Linear Regression

Linear Regression

Top 15 Genes Differentially Expressed Between Ulcerative Colitis and Normal Samples Logistic Regression



Top Ten Differentially Expressed Genes - Ulcerative Colitis vs Normal Samples for Linear Regression and Bioconductor

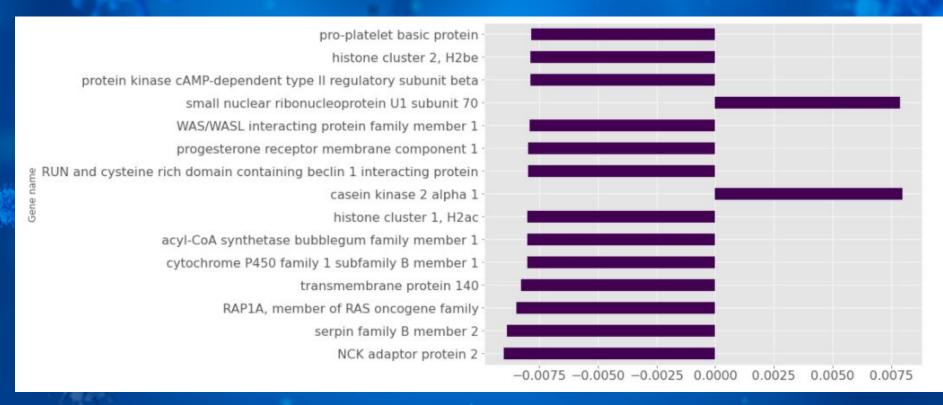


LR Differential/UC vs NM	Bioconductor Differential/UC vs NM
brain abundant membrane attached signal protein 1	folate receptor 1
folate receptor 1	brain abundant membrane attached signal protein 1
EWS RNA binding protein 1	Affy Gene
interleukin 5 receptor subunit alpha	high mobility group box 1
tripartite motif containing 24	S100 calcium binding protein A11
immunoglobulin kappa locus///immunoglobulin ka	microRNA 8071-2///microRNA 8071-1///immunoglob
high mobility group box 1	ARP5 actin-related protein 5 homolog
transmembrane protein 123	lysine demethylase 2A
melatonin receptor 1B	solute carrier family 22 member 4
adaptor protein, phosphotyrosine interacting w	immunoglobulin kappa locus///immunoglobulin ka





Top 15 Genes Differentially Expressed Between CD and NM Logistic Regression





LR Differential/CD vs NM	Bioconductor Differential/CD vs NM
NCK adaptor protein 2	histone cluster 1, H2ac
serpin family B member 2	histone cluster 1, H2bk
RAP1A, member of RAS oncogene family	progesterone receptor membrane component 1
transmembrane protein 140	serpin family B member 2
cytochrome P450 family 1 subfamily B member 1	histone cluster 2, H2be
acyl-CoA synthetase bubblegum family member 1	monocyte to macrophage differentiation associated
histone cluster 1, H2ac	brain abundant membrane attached signal protein 1
casein kinase 2 alpha 1	transmembrane protein 158 (gene/pseudogene)
RUN and cysteine rich domain containing beclin	histone cluster 1, H2bd
progesterone receptor membrane component 1	amyloid beta precursor protein





Conclusions:

- PCA does not produce any of the same genes as Bioconductor in any of the four comparisons that were
 performed-that is not to say the genes that PCA chooses as principal components are not important in the
 disease model
- PCA did not produce clear distinction of clusters in the K-means model, in spite of the fact that the number
 of clusters were known in advance. At the the same time, UMAP was not able to cluster the samples well
 either.
- Both kNN and Random Forest performed better on train and test sets with all genes as opposed to models based on PCA components
- Logistic Regression classification with and without PCA produced perfect scores for classifying ulcerative
 colitis samples. The model that used all the genes had 4 genes in common with the Bioconductor analysis.
- Logistic Regression classification with and without PCA produced perfect scores for train sets and 0.88 and 0.92,respectively, for each analysis of Crohn's disease samples in the test set. The model that used all the genes had 3 genes in common with the Bioconductor analysis.
- Differential gene expression analysis can be a multi-pronged approach using several methods, including PCA, PCA + logistic regression, logistic regression solo on top of the Bioconductor analysis



Further Study:

- Increase Sample Size: Blood draws are often easily obtained from voluntary blood from donation
- TaqMan PCR verification of differentially expressed genes identified by various models in this study
- Use other microarray data to compare/contrast the different models used in this study
- Compare the ulcerative colitis and Crohn's disease samples through additional modeling

Thank you!

Global Instructors: Dan, Noelle, and Riley

<u>Local Instructors</u>: Caroline, Kai, and Heather

<u>Outcomes</u>: Rachel

Support: Naida

Guest Speakers

Fellow Students in the East Coast Cohort

