Linnaeus: Interpretable Deep Learning Classification of Single Cell Transcript Data

Eric Prince[1,2], Todd C. Hankinson[1,2]

[1] *University of Colorado Anschutz Medical Campus, Department of Neurosurgery, Division of Pediatrics, Aurora, USA*
[2] *The Morgan Adams Foundation Pediatric Brain Tumor Research Program, Aurora, USA*

ABSTRACT

High throughput data is commonplace in biomedical research as seen with technologies such as single-cell RNA sequencing (scRNA-seq) and other Next Generation Sequencing. As these techniques continue to be increasingly utilized it is critical to have analysis tools that can identify meaningful complex relationships between variables (i.e., in the case of scRNA-seq: genes) in a way such that human bias is absent. Moreover, it is equally paramount that both linear and non-linear (i.e., one-to-many) variable relationships. Linnaeus is a deep learning-based framework that generates an optimal interpretable classifier a given high-throughput dataset using a simple genetic algorithm as well as an autoencoder to classifier transfer learning approach. Using four unique publicly available scRNA-seq datasets with published ground truth, we demonstrate the robustness of Linnaeus and the ability to identify ontologically accurate gene lists for a given data subset. Linnaeus serves as a bioinformatic tool to allow novice and advanced analysts to gain complex insight into their respective datasets enabling novel hypotheses development.

KEYWORDS

Deep Learning, Genetic Algorithm Parameter Optimization, Interpretable Deep Learning, scRNA-sequencing, High-throughput Data

MAIN

High throughput data has become increasingly ubiquitous in biomedical research, with advances in computer science facilitating the ability of biomedical scientists to complete analyses. Vast clinical datasets are routinely generated in fields such as radiology, and basic science datasets like those yielded by Next Generation Sequencing (NGS) technologies (i.e., single-cell RNA-sequencing [scRNA-seq]) have become relevant in clinical care. In the case of NGS data, current analysis methodologies suffer from a lack of standardization. While some genetic signatures are easy to interpret due to their linear nature, a far greater proportion of genetic interactions are non-linear and therefore not reliably interpretable using manual techniques. Further, novel bioinformatic findings increasingly require the concatenation of multiple high-level mathematical techniques in order to filter out a manageable subset of features of interest. Current methods suffer from both human bias and sampling error present within the dataset. These human biases can arise from an analyst not being blind to the dataset and therefore preferential to a desired outcome, or potentially applying mathematically incorrect/sub-optimal models to the target dataset.

Deep Learning (DL) is a subset of machine learning that is capable of concurrently modeling simple and complex mathematical relationships present within a given dataset. DL – and machine learning in general – is being applied across myriad scientific disciplines with success levels often superior to those of human experts. The DL landscape is vast, although certain architectures are becoming established for given problem sets (e.g., Convolutional Neural Networks [CNN] for image classification and object detection, Long Short-Term Memory [LSTM] networks for sequence-based analysis, and autoencoder networks for anomaly detection). Though methodology and architecture standards of practice are emerging, the successful implementation of these DL models can be elusive.

Among the challenges in developing a reliable DL system is optimization of the various meta-parameters. These parameters include, but are not limited to, learning rate scale and behavior, dropout and regularization, optimizers, and activation functions. Selection of the optimal settings of such parameters is made more complex by the fact the parameters are usually continuous, and their relationships are often non-linear. In order to address this challenge, meta-optimization solutions that can intelligently explore the parameter optimization space have been developed. A promising approach is modeled after the simple Genetic Algorithm (GA)[1]. By treating each possible parameter set as an “individual” and assigning a “fitness” value (i.e. accuracy in a classification task), one can test a population of individuals, rank them by their fitness, and then create a new population using the parameters found in the fittest individuals. As the process iterates for several generations, the most important parameter selections become homogenous and less important parameters become more heterogenous. This approach is significantly less resource intensive than a comparable brute-force approach, which examines all possible parameter value combinations.

We present a computational method, termed Linnaeus, that leverages DL architectures and GA meta-optimization to create optimized novel classifiers and generate feature importance information for high-throughput (HT) datasets. Linnaeus provides an easy-to-use framework for scientists to interrogate differences in HT data (e.g., bulk RNA-seq transcript differences between disease subtypes, identifying interesting genes in unknown scRNA-seq cell clusters with non-canonical signatures, etc.). Further, Linnaeus helps to remove the potential human bias that can be present in advanced analytical pipelines. Finally, by combining Linnaeus results with established techniques, users can identify potential dynamic relationships within a dataset, thereby improving the value of their analysis.

RESULTS

Binary scRNA-seq Dataset Performance

To evaluate the robustness of Linnaeus in a binary classification scenario, we investigated an integrated dataset containing two different sets of control versus IFN-β stimulated immune cells (CD14+ Monocytes and CD4+ Naïve T cells [Figure 1a]). The gene expression signatures of these two populations are not easily differentiable, even when transformed using the non-linear dimension reduction technique UMAP (Figure 1b). The maximum mean performance (AUPR) of Linnaeus, when analyzed using 5-fold cross-validation, was 0.587 and 0.881 for CD4+ T cells and CD14 Monocytes, respectively. To estimate the ontology differences between control and stimulated populations of CD4+ T cells, the top-20 most important (i.e., highest SHAP values; Figure 1c) genes were submitted for Metascape analysis. The resultant list of significant ontologies suggests that the Naïve CD4+ T cell (T_{h0}) population is being activated to the T_{h2} phenotype via IL-4 (Figure 1c; CD4+ Memory T Cells, yellow highlight). Similarly, we collected the top-20 most important genes that distinguish control from IFN-β stimulated CD14 Monocytes and submitted these for Metascape analysis (Figure 1c). Significant ontologies suggest the population contains Monocytes that are being activated (Figure 1c; CD14 Monocytes, yellow highlight). By utilizing SHAP values, we are also able to investigate variable interactions that help differentiate the populations of interest. For example, in CD4+ T cells we can see that increase in TNFSF10 combined with a decrease in RSAD2 expression suggests the cell is stimulated, while the absence of TNFSF10 indicates that the cell belongs to the control group (Figure 1d). However, these interactions can still be difficult to interpret such as the relationship between CCL2 and DHRS9 in CD14 Monocytes (Figure 1e). While it is known that DHRS9 and CCL2 play a role in CD14 Monocyte activation[2], the interaction between expression levels in these genes is convoluted.

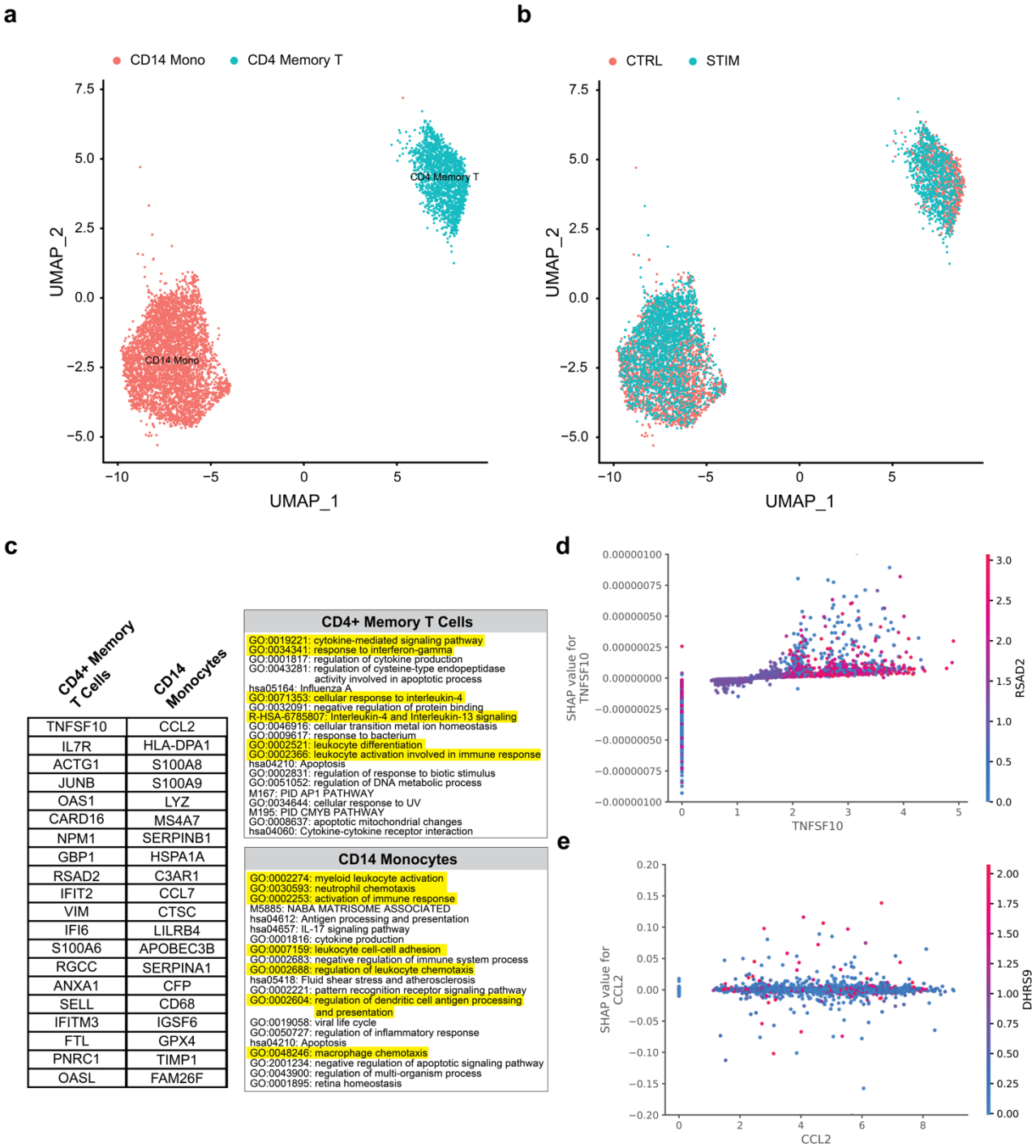
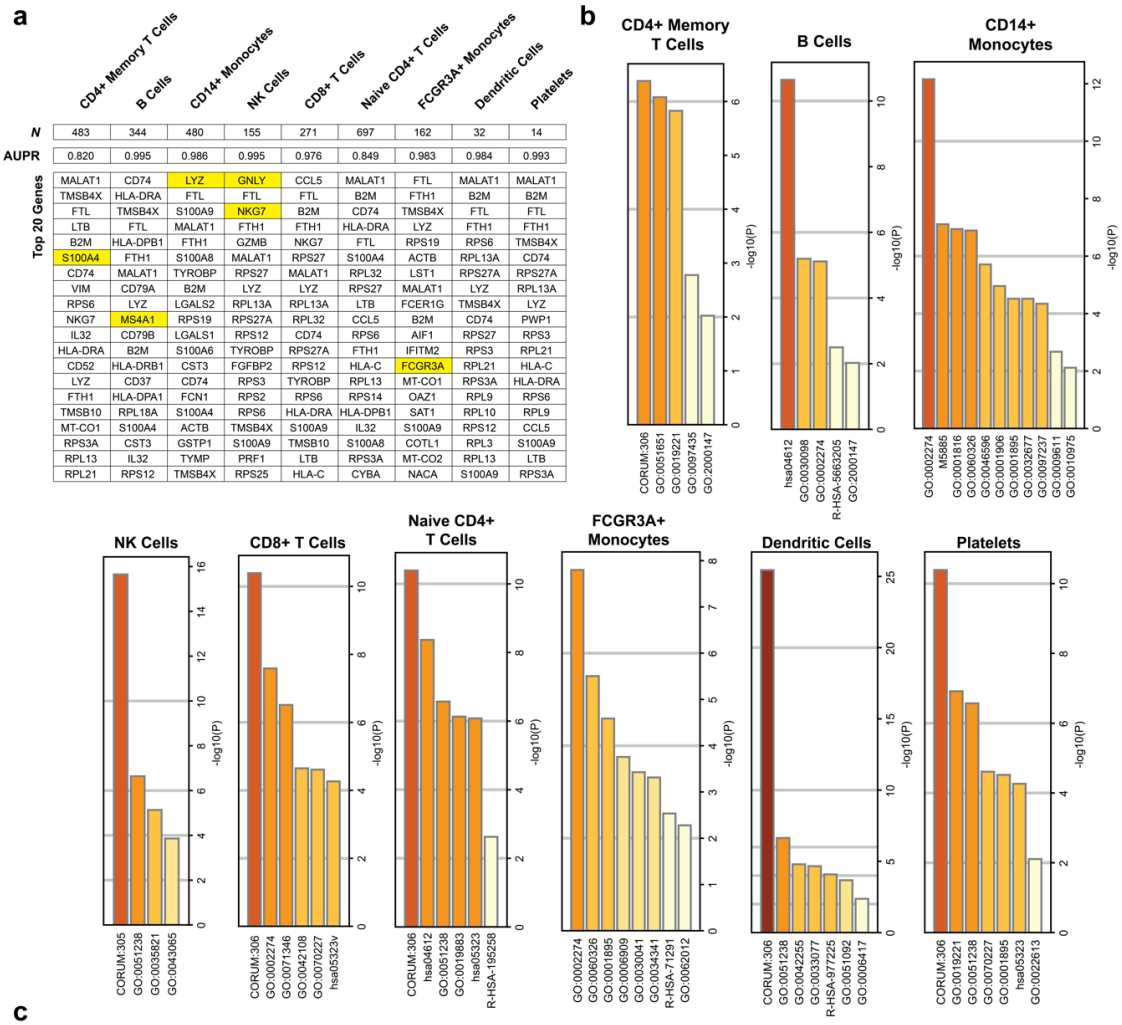


Figure 1. Classification and Feature Importance of IFN-β Treated PBMCs. **a.** UMAP of CD4+ memory T cells (blue) and CD14 monocytes (red). **b.** UMAP of non-treated (CTRL; red) and IFN-β treated (STIM; blue) CD4+ memory T cells and CD14 monocytes. **c.** Top-20 most important (largest SHAP value) genes as determined by Linnaeus for CD4+ memory T and CD14 Monocytes, and respective ontology enrichments as determined by Metascape. **d.** Interaction plot for CD4+ Memory T Cell data regarding TNFSF10 and RSAD2. SHAP values > 0 indicate that the interaction is related to the STIM genetic profile, SHAP values < 0 indicate the inverse. **e.** Interaction plot for CD14 Monocyte data regarding CCL2 and DHRS9. SHAP values > 0 indicate that the interaction is related to the STIM genetic profile, SHAP values < 0 indicate the inverse. TNFSF10 and CCL2 maintain top-ranked SHAP values for CD4+ Memory T and CD14 Monocyte cells, respectively. RSAD2 and DHRS9 were estimated to have the greatest SHAP interaction values with TNFSF10 and CCL2, respectively.

Multiclass Performance on scRNA-seq Dataset

Using the raw feature counts from the 10X 2700 Peripheral Blood Mononuclear Cell (PBMC) scRNA-seq dataset as labeled in the Seurat Vignette (Figure S1), Linnaeus generated a multiclass classifier for the nine different cell types. For each cell type, the top twenty most significant genes utilized in the classification process was determined (Figure 2a). For each top twenty gene list, a Metascape analysis was performed (Figure 2b-c). Linnaeus independently identified genes that were referenced as cell type markers in the Seurat Vignette. Specifically, it identified S100A4 in CD4+ memory T cells, MS4A1 in B cells, LYZ in CD14+ Monocytes, GNLY and NKG7 in Natural Killer (NK) cells, and FCGR3A in FCGR3A+ Monocytes. Moreover, Metascape analysis indicated expected phenotypic qualities. For example, *cytokine-mediated signaling* pathway enrichment in CD4+ memory T cells, *Antigen processing and presentation* in B cells, *positive regulation of apoptotic process* in NK cells, *lymphocyte apoptotic process* in CD8+ T cells, and *phagocytosis* and *response to interferon-gamma* in FCGR3A+ Monocytes. Classes that were highly imbalanced (dendritic cells [n=32] and platelets [n=14], due to the relatively low frequency that they occur in the dataset) were not correctly classified using raw feature counts as input values. The top-20 genes in these scenarios were similar to the most variant genes as identified by PCA (Figure S2). Interestingly, in the multiclass scenario Linnaeus identified many of the same genes identified as important in Principle Component 1 (i.e., the variables with the largest eigenvalues in the first dimension of Principle Component Analysis [PCA]; Figure S2). This reflects model precision, as autoencoders that optimally learn a data manifold

(i.e.,landscape) decompose data similarly to PCA[3].



	CD4+ Memory T Cells	B Cells	CD14+ Monocytes	NK Cells	CD8+ T Cells	Naive CD4+ T Cells	FCGR3A+ Monocytes	Dendritic Cells	Platelets
N	483	344	480	155	271	697	162	32	14
AUPR	0.820	0.995	0.986	0.995	0.976	0.849	0.983	0.984	0.993
Top 20 Genes	MALAT1	CD74	LYZ	GNLY	CCL5	MALAT1	FTL	MALAT1	MALAT1
	TMSB4X	HLA-DRA	FTL	FTL	FTL	B2M	FTH1	B2M	B2M
	FTL	TMSB4X	S100A9	NKG7	B2M	CD74	TMSB4X	FTL	FTL
	LTB	FTL	MALAT1	FTH1	FTH1	HLA-DRA	LYZ	FTH1	FTH1
	B2M	HLA-DPB1	FTH1	GZMB	NKG7	FTL	RPS19	RPS6	TMSB4X
	S100A4	FTH1	S100A8	MALAT1	RPS27	S100A4	ACTB	RPL13A	CD74
	CD74	MALAT1	TYROBP	RPS27	MALAT1	RPL32	LST1	RPS27A	RPS27A
	VIM	CD79A	B2M	LYZ	LYZ	RPS27	MALAT1	LYZ	RPL13A
	RPS6	LYZ	LGALS2	RPL13A	RPL13A	LTB	FCER1G	TMSB4X	LYZ
	NKG7	MS4A1	RPS19	RPS27A	RPL32	CCL5	B2M	CD74	PWP1
	IL32	CD79B	LGALS1	RPS12	CD74	RPS6	AIF1	RPS27	RPS3
	HLA-DRA	B2M	S100A6	TYROBP	RPS27A	FTH1	IFITM2	RPS3	RPL21
	CD52	HLA-DRB1	CST3	FGFBP2	RPS12	HLA-C	FCGR3A	RPL21	HLA-C
	LYZ	CD37	CD74	RPS3	TYROBP	RPL13	MT-CO1	RPS3A	HLA-DRA
	FTH1	HLA-DPA1	FCN1	RPS2	RPS6	RPS14	OAZ1	RPL9	RPS6
	TMSB10	RPL18A	S100A4	RPS6	HLA-DRA	HLA-DPB1	SAT1	RPL10	RPL9
	MT-CO1	S100A4	ACTB	TMSB4X	S100A9	IL32	S100A9	RPS12	CCL5
	RPS3A	CST3	GSTP1	S100A9	TMSB10	S100A8	COTL1	RPL3	S100A9
	RPL13	IL32	TYMP	PRF1	LTB	RPS3A	MT-CO2	RPL13	LTB
	RPL21	RPS12	TMSB4X	RPS25	HLA-C	CYBA	NACA	S100A9	RPS3A

c

CD4+ Memory T Cells
CORUM:306: Ribosome, cytoplasmic
GO:0051651: maintenance of location in cell
GO:0019221: cytokine-mediated signaling pathway
GO:0097435: supramolecular fiber organization
GO:2000147: positive regulation of cell motility

B Cells
hsa04612: Antigen processing and presentation
GO:0030098: lymphocyte differentiation
GO:0002274: myeloid leukocyte activation
R-HSA-5663205: Infectious disease
GO:2000147: positive regulation of cell motility

CD14 Monocytes
GO:0002274: myeloid leukocyte activation
M5885: NABA MATRISOME ASSOCIATED
GO:0001816: cytokine production
GO:0060326: cell chemotaxis
GO:0046596: regulation of viral entry into host cell
GO:0001906: cell killing
GO:0001895: retina homeostasis
GO:0032677: regulation of interleukin-8 production
GO:0097237: cellular response to toxic substance
GO:0009611: response to wounding
GO:0010975: regulation of neuron projection development

NK Cells
CORUM:305: 40S ribosomal subunit, cytoplasmic
GO:0051238: sequestering of metal ion
GO:0035821: modification of morphology or physiology of other organism
GO:0043065: positive regulation of apoptotic process

CD8+ T Cells
CORUM:306: Ribosome, cytoplasmic
GO:0002274: myeloid leukocyte activation
GO:0071346: cellular response to interferon-gamma
GO:0042108: positive regulation of cytokine biosynthetic process
GO:0070227: lymphocyte apoptotic process
hsa05323: Rheumatoid arthritis

Naive CD4+ T Cells
CORUM:306: Ribosome, cytoplasmic
hsa04612: Antigen processing and presentation
GO:0051238: sequestering of metal ion
GO:0019883: antigen processing and presentation of endogenous antigen
hsa05323: Rheumatoid arthritis
R-HSA-195258: RHO GTPase Effectors

FCGR3A+ Monocytes
GO:0002274: myeloid leukocyte activation
GO:0060326: cell chemotaxis
GO:0001895: retina homeostasis
GO:0006909: phagocytosis
GO:0030041: actin filament polymerization
GO:0034341: response to interferon-gamma
R-HSA-71291: Metabolism of amino acids and derivatives
GO:0062012: regulation of small molecule metabolic process

Dendritic Cells
CORUM:306: Ribosome, cytoplasmic
GO:0051238: sequestering of metal ion
GO:0042255: ribosome assembly
GO:0033077: T cell differentiation in thymus
R-HSA-977225: Amyloid fiber formation
GO:0051092: positive regulation of NF-kappaB transcription factor activity
GO:0006417: regulation of translation

Platelets
CORUM:306: Ribosome, cytoplasmic
GO:0019221: cytokine-mediated signaling pathway
GO:0051238: sequestering of metal ion
GO:0070227: lymphocyte apoptotic process
GO:0001895: retina homeostasis
hsa05323: Rheumatoid arthritis
GO:0022613: ribonucleoprotein complex biogenesis

Figure 2. Linnaeus Analysis of 10X 2700 PBMC Dataset Raw Feature Counts. **a.** Top-20 most important (largest SHAP values) transcripts for each class as determined in a one-versus-all approach for each class (i.e., cell type). **b.** Metascape-determined significant ontologies based on Linnaeus-identified gene lists. **c.** Long-form names of GO, KEGG, and Reactome pathways returned in Metascape analysis. Values that are highlighted yellow correspond with genes and ontologies discussed in the Results section.

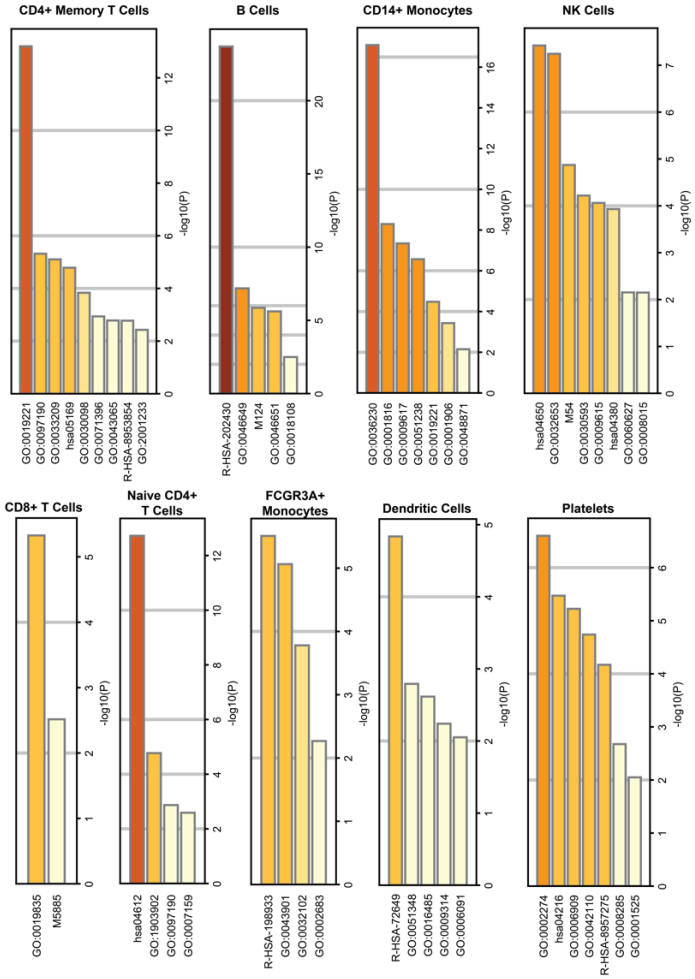
Comparison of Single Cell Feature Counts and Single Cell Scaled Expression Values

The 10X 2700 PBMC dataset was normalized and submitted for Linnaeus analysis. The 20 most significant genes for each cell type (Figure 3a) and the significantly enriched ontologies (Figure 3b-c) were identified. While raw feature counts generated 62 significant ontologies across the nine cell types, only 39 (63%) were unique. With normalized expression values, the sequence of Linnaeus followed by Metascape analysis returned 50 significant ontologies, of which 48 (96%) were unique. This suggests that the quality of information is enhanced when submitting normalized data to Linnaeus. Evidence for quality of information improvement is also observed in the ontologies and top 20 genes for each cell type. For example, using raw feature counts the CD4+ memory T cell phenotype is suggested through enrichment of cytokine-mediated signaling (*GO:0019221*). Using normalized expression values, the same pathway is enriched, but other pathways that have known associations with CD4+ memory T cells are also identified. These include *Tumor Necrosis Factor-mediated signaling pathway*[4], *Epstein-Bar virus infection*[5], and *lymphocyte differentiation*[6]. This improved quality of information can also be seen in B cells[7], in CD14 Monocytes, in NK cells[8], in CD8+ T cells, in CD4+ naïve T cells[9], and in FCGR3A+ Monocytes. While Linnaeus failed to yield accurate estimates for dendritic cells and platelets when using raw feature counts, it returned more phenotypically consistent genes lists when using scaled expression values. For example, Dendritic cells have known interactions with translation initiation complex formation[10] and are activated in response radiation[11], both of which were identified. Additionally, CCDC94 (YJU2) also has relatively high expression in dendritic cells according to BioGPS[12]. Finally, platelets are known to be activated via reactive oxygen species and ferroptosis[13] and play a role in angiogenesis[14].

a

	CD4+ Memory T Cells	B Cells	CD14+ Monocytes	NK Cells	CD8+ T Cells	Naive CD4+ T Cells	FCGR3A+ Monocytes	Dendritic Cells	Platelets
N	483	344	480	155	271	697	162	32	14
AUPR	0.970	0.990	0.993	0.972	0.909	0.961	0.994	0.986	0.993
Top 20 Genes	TNFRSF4	CD79A	S100A8	GNLY	GZMK	S100A4	FCGR3A	CCDC94	MAN2C1
	IL32	MS4A1	S100A9	XCL2	CCL5	MALAT1	CDKN1C	RPS23	SAT1
	CRIP1	CD79B	LGALS2	XCL1	NKG7	CD74	HES4	S100A4	TYROBP
	TRADD	HLA-DQB1	MS4A6A	GZMB	GZMA	CLIC1	RHOC	PCYOX1	FTH1
	VIM	HLA-DRA	CD14	IL2RB	CD8A	ANXA2	LILRA3	ATP5S	PLD4
	KLF6	HLA-DRB1	LYZ	HOXB-AS1	KLRG1	LEPROTL1	MS4A7	HLA-B	CST3
	ANXA1	CD74	FCN1	TYROBP	CST7	HLA-DRA	IFITM2	EMP3	CD3D
	PLP2	HLA-DQA1	CEBPD	FCER1G	GZMH	DLA-DQB1	ADA	RPS17	FTL
	LTB	HLA-DPB1	FPR1	TIGIT	CTSW	PSME2	ABI3	SH3BGRL3	FCER1G
	HNRNPF	HLA-DRB5	TYROBP	IFITM3	LYAR	HLA-DRB1	LST1	NKG7	LGALS1
	ABARAPL2	HLA-DPA1	MALAT1	SPON2	TMSB10	SELL	RPL-290F20.3	PPIP5K2	AIF1
	ISG20	LINC00926	GSTP1	CPEB4	CLN3.1	PPIB	IFITM3	EIF4A2	NEAT1
	SRSF2	TCL1A	CCL3	FCGR3A	LPXN	HLA-DPB1	RPS19	CYBA	WARS
	RAN	BLK	GPX1	MAP2K6	GZMM	CRIP1	WARS	CEP85L	PRELID1
	FOSB	KIAA0125	CTSD	FGFBP2	C6orf48	KLF6	MS4A4A	NPM1	TYMP
	ARL6IP5	BANK1	B2M	PRF1	APOBEC3G	ARL6IP5	CKB	SPRTN	ARPC2
	CTSW	FCRLA	CDA	C1orf21	TUBA4A	CD37	PILRA	BIRC3	NPC2
	CD27	CD3D	FTL	NR1H3	LTB	PDIA3	STXBP2	SRGN	TIMP1
	YWHAZ	HLA-DQA2	LTB	ATP2A2	KMT2E	PRR13	CARD16	YWHAG	ABHD13
	PRDX2	GNG7	C20orf24	SELM	PIM1	CD7	SIGLEC10	CST7	LST1

b



c

CD4+ Memory T Cells

GO:0019221: cytokine-mediated signaling pathway
GO:0097190: apoptotic signaling pathway
GO:0033209: tumor necrosis factor-mediated signaling pathway
hsa05169: Epstein-Barr virus infection
GO:0030098: lymphocyte differentiation
GO:0071396: cellular response to lipid
GO:0043065: positive regulation of apoptotic process
R-HSA-8953854: Metabolism of RNA
GO:2001233: regulation of apoptotic signaling pathway

B Cells

R-HSA-202430: Translocation of ZAP-70 to Immunological synapse
GO:0046649: lymphocyte activation
M124: PID CXCR4 PATHWAY
GO:0046651: lymphocyte proliferation
GO:0018108: peptidyl-tyrosine phosphorylation

CD14 Monocytes

GO:0036230: granulocyte activation
GO:0001816: cytokine production
GO:0009617: response to bacterium
GO:0051238: sequestering of metal ion
GO:0019221: cytokine-mediated signaling pathway
GO:0001906: cell killing
GO:0048871: multicellular organismal homeostasis

NK Cells

hsa04650: Natural killer cell mediated cytotoxicity
GO:0032653: regulation of interleukin-10 production
M54: PID IL12 2PATHWAY
GO:0030593: neutrophil chemotaxis
GO:0009615: response to virus
hsa04380: Osteoclast differentiation
GO:0060627: regulation of vesicle-mediated transport
GO:0008015: blood circulation

CD8+ T Cells

GO:0019835: cytolysis
M5885: NABA MATRISOME ASSOCIATED

Naive CD4+ T Cells

hsa04612: Antigen processing and presentation
GO:1903902: positive regulation of viral life cycle
GO:0097190: apoptotic signaling pathway
GO:0007159: leukocyte cell-cell adhesion

FCGR3A+ Monocytes

R-HSA-198933: Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell
GO:0043901: negative regulation of multi-organism process
GO:0032102: negative regulation of response to external stimulus
GO:0002683: negative regulation of immune system process

Dendritic Cells

R-HSA-72649: Translation initiation complex formation
GO:0051348: negative regulation of transferase activity
GO:0016485: protein processing
GO:0009314: response to radiation
GO:0006091: generation of precursor metabolites and energy

Platelets

GO:0002274: myeloid leukocyte activation
hsa04216: Ferroptosis
GO:0006909: phagocytosis
GO:0042110: T cell activation
R-HSA-8957275: Post-translational protein phosphorylation
GO:0008285: negative regulation of cell proliferation
GO:0001525: angiogenesis

Figure 3. Linnaeus Analysis of 10X 2700 PBMC Dataset Normalized Expression Values. **a.** Top-20 most important (largest SHAP values) transcripts for each class as determined in a one-versus-all approach for each class (i.e., cell type). **b.** Metascape-determined significant ontologies based on Linnaeus-identified gene lists. **c.** Long-form names of GO, KEGG, and Reactome pathways returned in Metascape analysis. Values that are highlighted yellow correspond with genes and ontologies discussed in the Results section.

Discussion

This manuscript preliminarily assesses a deep learning approach for analyzing complex linear and non-linear relationships in high-dimensional data, such as scRNA-seq, in a manner that is free of human bias. The impetus was to create a method, downstream of clustering, to distinguish cell populations that lack canonical gene signatures, and may be difficult to separate. Using two scRNA-seq datasets, we demonstrated that Linnaeus inferred meaningful gene importance rankings, which estimated the given scenarios well. In the context of feature counts versus scaled data, both scenarios yielded genes and enriched ontologies that accurately infer at least some of the cell types. Scaled data resulted in improved classification performance, enhanced quality of information, and was more robust in the classes with low sample sizes (dendritic cells and platelets).

In addition to statistically describing unknown cell populations (data classes), there are other applications for this approach. Linnaeus lowers the barrier for interpretation of complex data by enabling researchers who lack sophisticated computational experience to analyze their own dataset without the need for a bioinformatician. Linnaeus is also well suited as an adjunct for advanced bioinformaticians. For example, it can be used to generate statistical insight regarding data relationships, to validate analytical findings, or to generate new potential research directions. Additionally, Linneaus can serve as an optimized classifier that can compare and contrasting multiple datasets. For example, a previously analyzed dataset can be directly compared to a new, non-analyzed, dataset of the same type and variable structure, in order to determine how the datasets are related.

An obvious limitation of Linnaeus is the computational demand. The algorithm was developed using high performance computing (HPC)-caliber hardware, with multiple accessible GPUs. Real-time turnaround is reduced by asynchronously evaluating models within each Genetic Algorithm iteration. A potential method to decrease this computational requirement would be to implement an early stopping method to the GA. In this case, the GA would only proceed if model fitness was improving, thus eliminating potentially unnecessary training. Another limitation in our approach is that we have characterized immune cell types that are more easily differentiated than cell types in many other biological contexts. For example, subtyping within a cell or tumor type may prove to be a greater challenge than the proof of principle we present here. Future work to address this would be to stress test the Linnaeus algorithm across more complex scRNA-seq datasets, as well as exploring other types of high-throughput biomedical data (i.e., ATAC-seq, high-dimension flow cytometry, multi-color histology, etc.).

METHODS

Summary

Linnaeus is a three-step machine learning process that seeks to optimize a classifier for a given dataset and then determine which variables are most important in the decision-making process (Figure M1). All models were constructed using the TensorFlow 2.0 (TF2) python framework and are cross-compatible with CPU, GPU, and/or TPU-based systems. First, using a simple Genetic Algorithm (GA) as a meta-optimization framework, an autoencoder is optimized to a custom fitness function (details below) in order to compress data information for classification. Second, weights from the encoder component of the optimized autoencoder are transferred to a classifier network, which is subsequently optimized via GA. Third, using the python Shapley Additive Explanations (SHAP) module, dataset feature importance is evaluated as Shapley values[15].

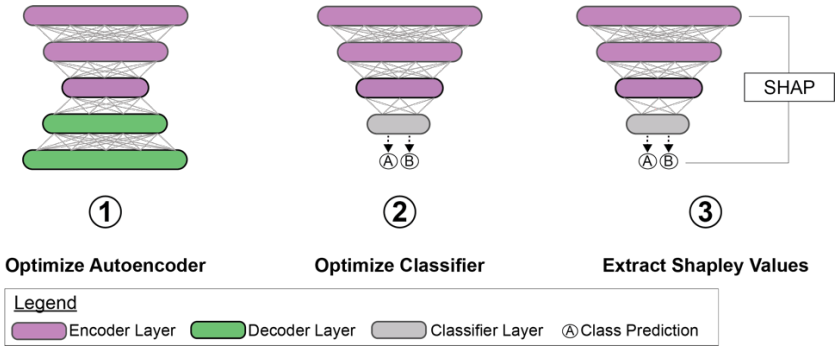


Figure M1. High-Level Overview of Linnaeus Framework. Weights from optimized encoder layers are used to initialize classifiers which are then optimized. Feature importance is determined using Shapley values via the python SHAP module.

Data Acquisition

Validation of Linnaeus efficacy was achieved utilizing two datasets published with the R-based Seurat single-cell analysis framework[16,17]. The first dataset (control versus IFN-β-stimulated PBMCs) was generated by integrating two single cell RNAseq datasets[18] as described in the Seurat vignette[19] using the SeuratData R package. The second dataset was sourced from 10X genomics and it is known as the 2,700 Peripheral Blood Mononuclear Cells (PBMCs) dataset. The Seurat object for this dataset contains feature counts and scaled data (scaled via the Seurat `LogNormalize` function) with designated cell type labels, and is publicly available[20]. For each dataset, values were extracted and transposed such that columns are genes and rows are Unique Molecular Identifiers (UMIs; i.e., cells). The right-most column is set to contain the class label (i.e., cell type) as given in the published datasets. Finally, datasets were exported as comma-delimited tables.

Genetic Algorithm Meta-optimizer

The GA was adapted from a publicly available repository[21,22]. The general algorithm is as follows:

Algorithm I

Genetic Algorithm: $Compute\ N_{trained}$

Input:

$list,$ search space parameters ($Params$)

$integer,$ number of solutions in population (n_{pop})

$integer,$ number of generations to evolve (n_{gen})

Output:

$list,$ trained Network class objects with test accuracy of size n_{pop} ($N_{trained,pop}$)

```
for each gen ∈ n_gen do
    for each pop ∈ n_pop do
        params_pop ← Random select for each param ∈ Params
        N_trained,pop ← train and evaluate N(params_pop)
        N_trained,pop ← descending rank N_trained,pop
        while gen < n_gen do
            N_trained,pop ← select top 40% N ∈ N_trained,pop
            while length N_trained,pop,fit < n_pop do
                N_mother ← Random select N_trained,pop
                N_father ← Random select N_trained,pop
                assert N_mother ≠ N_father
                N_child ← Random select for each param
                            ∈ {N_mother, N_father}_Params
                Params_mutated ← Random select 20% param ∈ Params
                for each param ∈ Params_mutated do
                    param_new ← Random select param ∈ Params
                    {N_child}_Params ← update param_new
                    N_trained,pop ← append N_child
                end for
            end do
        end do
    end for
end for
                        return N_trained,pop
```

Defining the GA Optimization Search Space

By default, the GA utilizes a pool of variables that include architectural and learning algorithm features. This parameter pool is slightly different for the autoencoder (Table 1) and the classifier networks. Specifically, classifier networks are given two additional parameters that are a selection of the top 5 optimized autoencoders and the ability to continue to train the encoder layer in the classifier or just extract the feature embeddings (i.e., trainable or not, respectively). The distinction between *inner* activation and *final* activation is that final activation is the activation of the final layer, and inner is the activation of all other previous layers. Additionally, all models were trained for 1,000

epochs but with early stopping, which was triggered either when values were incomputable (*NaN*) or when 5 epochs occurred without model performance improvement. This allowed us to ignore the training duration variable during model optimization.

Table 1. Parameter Pool for GA Optimization

Batch Size	Learning Rate	Dropout Rate	Inner Activation	Final Activation	Optimizer	L1/L2-Kernel/Bias/Activity Weight
128	0.1	0.0	Sigmoid	Sigmoid	RMSProp	0.0
256	0.01	0.2	Softplus	Softplus	AdaGrad	0.1
512	0.001	0.5	Softsign	Softsign	Adam	0.01
1024	0.0001		Softmax	Softmax	AdaDelta	0.001
			EIU	EIU	AdaMax	0.0001
			Hard Sigmoid	Hard Sigmoid	SGD	0.00001
			Linear	Linear		
			SeLU	SeLU		
			Tanh	Tanh		

The decision to include the types of parameters utilized in Linnaeus was driven by a desire to reinforce the model in small dataset scenarios (specifically dropout and regularization). Moreover, model fitness was determined using 5-fold cross-validation for the classifier. Linnaeus, by default, monitors several metrics, including categorical accuracy, AUROC, AUPR, precision, recall, and top-*k* categorical accuracy (in multi-class scenarios). It utilizes AUPR as the fitness metric. This is because AUPR is robust in situations that are highly class imbalanced, but it is also inherently connected to AUROC and therefore is also effective in class balanced situations.

By default, the GA is set to perform 10 generations of populations containing 100 solutions. This means the GA will assess 1,000 solutions, which equates to 7.38×10^{-6}% of the possible parameter combinations in the autoencoder optimization (N = 13,548,902,400) and 7.38×10^{-8}% of the possible parameter combinations in the classifier optimization (N = 1,354,890,240,000). While omitting the majority of solutions, the selection of 100 solutions per population enables a minimum parameter frequency of 12.5 per population, meaning the population contains more than 10% of each parameter. The intuition is that parameter selections with more profound impact on model performance will become homogenous in later generations, and less important parameters will remain heterogeneous in top solutions. Linnaeus computational time is decreased by performing iterative training/evaluation cycles in an asynchronous fashion using the python ray and asyncio modules. This is important due to TF2 not releasing memory when iterations are not handled in unique process IDs (PIDs), which will cause an out-of-memory error if not accounted for.

Defining the Autoencoder Fitness Function

Autoencoders are utilized to compress the data information to a lower dimensionality, which enables the utilization of a smaller classifier. This is because more compressed data will require fewer, but more relevant, DL network nodes to learn the dataset objective function, when compared to a dataset with a high degree of sparsity. In Linnaeus, autoencoders are utilized in an unsupervised manner, which means that the network is modeling the dataset in its entirety, and *not* considering class labels in the process. The loss function utilized is the Mean Squared Error (MSE) between input and output values, and there is no accuracy metric implemented. To employ the GA, we required a static value to rank-order, as the fitness function and the final loss is inadequate for this purpose. In the fitness function, we sought to derive a function that would reflect the qualitative characteristics of an ideal loss curve: a quick training duration (i.e., rapid convergence of the objective function), and a low final loss. Intuitively, these characteristics reflect a model that has learned the data distribution in a stable manner. As such, the following fitness function was derived.

$$Fitness = \frac{\int_1^N \big(g(x) - L(x)\big)dx}{L(x_N)}$$

Where x is the number of epochs (x: $\{1,2,\ldots,N\}$), $L(x)$ is the loss function of the model over the training duration, $L(x_N)$ is the final loss value of training, and $g(x)$ is a first-order polynomial (linear) regression mapped from $L(x_1)$ to $L(x_N)$. Importantly, if the slope of $g(x)$ > 0, a penalty term (-1x10^9) is multiplied with the fitness function to downrank such loss curves that are increasing. This function therefore transforms a series of metrics into a static method that will increase when a loss function has greater concavity (i.e., the fitness function has a larger numerator) and finishes with a lower final loss (i.e., smaller denominator).

Optimizing Autoencoder

It is well known that autoencoders with three or more layers are difficult to successfully train. To overcome this, layers can be individually pretrained in the form of a Restricted Boltzmann Machine (RBM), which is an energy-based Markov Random Field model. In Linnaeus, a new model is first created by pretraining each layer as an RBM using the contrastive-divergence method for 50 epochs. This number is arbitrary, though this is simply a layer weight initialization step and does not appear to require any tuning. Once model weights are initialized, the GA process is completed for the autoencoder, using the previously defined custom fitness function. Upon completion of GA optimization, the top 5 most-fit autoencoders are exported as saved models for downstream consideration.

Optimizing Classifier

Classification networks were constructed using the encoder layers from the autoencoder as a foundation. Batch normalization, 2D convolution, 2D max pool, and a

final softmax fully-connected layer were then appended to the encoder to create the final classifier architecture. Batch normalization was performed to improve model performance in small dataset or class-imbalanced scenarios. Convolution and max pool layers were utilized to extract more complex latent data relationships. Classifier optimization was then performed using the GA, as described above.

Feature Importance Evaluation Using Shapley Values

The purpose of this effort was to develop an unbiased analytical method for high-throughput (i.e., high-dimensional) data capable of separating data into predetermined groups and subsequently returning the most important features (i.e., genes) the classifier used to separate the groups. To do so we utilize the python SHAP module to calculate Shapley additive values. This approach was selected due to the direct compatibility with TF2 models, as well as the ability to generate feature importance rankings and force plots to glean a linear insight into *how* features were utilized in the decision-making process.

Metascape Analysis of Shapley Values

To determine enriched ontologies of genes filtered by importance, we utilized the Metascape online analysis tool[23]. Gene lists were submitted and analyzed as Homo sapiens in 'Express Analysis' mode.

Computational Hardware

Linnaeus was developed on an HPC server running a 10-core Intel Skylake Processor and 6 GPUs (4 NVIDIA Tesla K80 and 2 NVIDIA Tesla T4 GPU cards). On top of a CentOS 7 environment, we developed Linnaeus using the publicly available TF2 docker image (https://hub.docker.com/r/tensorflow/tensorflow/).

Code Availability

Linnaeus is provided as-is without warranty on GitHub to encourage improvement and adaptation by the broader scientific community.

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