# Novel Differential Flow Cytometry Data Analyses Method Using Data Nuggets Compression and Projection Pursuit Algorithms

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# **Our Team**

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# 14 Stones of Ryoan-ji



- A 15<sup>th</sup> century Japanese temple of Ryoan-ji featuring a meditation stone garden
- Veranda that wraps around the garden opens to a view of 14 large stones

# 15 (!) Stones of Ryoan-ji



- A 15<sup>th</sup> century Japanese temple of Ryoan-ji featuring a meditation stone garden
- Veranda that wraps around the garden opens to a view of 14 large stones
- Moving from one sitting spot to another, a careful observer will soon realize that the number of the stones is, in fact 15
- But at no point will all 15 stones be revealed to the observer at ones!

# Study Design

- Blood samples from 44 infants: 24 Unexposed (UE) and 20 Exposed to HIV (HEU), i.e., mothers diagnosed with HIV
- Samples either untreated (Unstimulated) or treated with one of six compounds. We examined Untreated and LPS (lipopolysaccharide) treated samples only.
- Each sample analyzed on a flow cytometer. Data published as .FSC files on a public repository.
- Combined data had >42M rows (cells or particles). Out of these, ~14M identified as lymphocytes.
- Delta[*i*, *j*,*k*] = LPS[*i*, *j*,*k*] mean(Unstimulated)[\*, *j*,*k*] for *j*th subject and *k*-th marker (protein)
- Remaining ~6.9M lymphocytes (=LPS group)



# **Flow Panel Design**

100

80

60 -

40 -

103

CR-65134 CD4 (OKT4)

0

104

105

Fluorophore	Marker	Description
FSC-A	Size	
SSC-A	Granularity	
FITC	IFNa	Pro-inflammatory cytokine (Th cell response)
PerCP-Cy5-5	MHCII	Expressed by APCs (B cells, Mono/Macs, DCs),
		upregulated upon infection and presentation of
		antigen
АРС-Су7-А	IL6	Pro-inflammatory cytokine (Th cell response)
Pac Blue	IL12	Pro-inflammatory cytokine (Th cell response)
Alexa Fluor 700	TNFa	Pro-inflammatory cytokine (Th cell response)
PE	CD123	Dendritic cells
PE-Cy7	CD14	Monocytes/Macrophages
APC-A	CD11c	Dendritic cells





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#### **Flow Panel Design**



## Automated Gating for Data Preprocessing

0e+00

0e+00

- In each sample, estimate density in FSC vs SSC plot
- Identify landmarks ("hill tops")
- Lymphocytes are the bottom right cluster
- Identify boundary of the cluster by pixels above a threshold
- Delete stand-alone points on the periphery of the cluster (pixel with most neighboring pixels being below the threshold)
- Convex hull ("rubber band model") to smooth the boundaries
- Map pixels in density plot back to cells; delete all but lymphocytes



1e+05

FSC-A

2e+05

#### 0010.FCS

# **Principal Components Analysis**



- PC1 explained 52.2% of variability; PC2 21.5%
- MHCII, IL6 and TNFa drove the differences in PC1 direction; IL12 and INFa in PC2 direction
- Majority of points from UE and HEU overlap. However, we are interested in profiles of cells that are different between UE and HEU
- Therefore, a different approach is needed instead of looking for max variability (PCA), we want to look for max difference (PP)

#### Rotated Principal Components and Differentially Populated Regions



## Data Compression with Data Nuggets



Data Nuggets: A Method for Reducing Big Data While Preserving Data Structure. Beavers et al, arXiv 2024



## Data Nuggets Biplot by %HEU in Each Nugget vs. in Total (40.5%)



RED=%HEU<Overall BLUE=%HEU>Overall YELLOW=No Difference(+/-20% of Overall)

# Key Technology

- PP searches multivariate *p*-dimensional data for lower *d*-dimensional projections, revealing the main structure of the data, i.e., clusters, outliers, and any other low-dimensional nonlinear structure (see Friedman and Tukey 1974).
- PP indices (e.g., Natural Hermite index) are functions to numerically measure features of lowdimensional projections
- Higher values of PP index = more interesting structures
- For PP index optimization, used Grand Tour Simulated Annealing (GTSA) algorithm

 The Natural Hermite index measures the distance between the *d*-dimensional distribution *f*(*y*) and the *d*dimensional normal distribution φ(*y*):

$$I^N = \int_{\mathbb{R}^d} [f(y) - \phi(y)]^2 \phi(y) dy$$

- Grand Tour algorithm assigns a sequence of projections onto (usually) 2-dimensional planes to any given dimension of Euclidean space.
- Flipping through the sequence of projection creates "data movie"

# **Differential Projection Pursuit**

Let's define **Differential Natural Hermite** dissimilarity for *k d*-dimensional distributions:

- Let  $f_1(x), \ldots, f_k(x)$  be a set of k density functions
- Let  $f(x) = \frac{w_1 f_1(x) + \dots + w_k f_k(x)}{w_1 + \dots + w_k}$  be the weighted average
- For every pair of densities f<sub>i</sub>(x), f<sub>j</sub>(x) the differential Natural Hermite dissimilarity with respect to f(y) is defined by:

$$d_{f}(f_{i}, f_{j}) = \left| \int_{\mathbb{R}^{d}} [f_{i}(x) - f_{j}(x)]^{2} f(x) dx \right|^{\frac{1}{2}}$$

Apply projection matrix OR stop if improvement is small Calculate density Calculate the index estimators  $\hat{f}_1(y)$  and  $d_{H,\hat{f}}(\hat{f}_1,\hat{f}_2)$  for  $\hat{f}_2(y)$  with Kernel projection P density estimator  $\hat{f}_B(\mathbf{y}) = \sum_{i=1}^{m} \frac{W_i}{\sum_{i=1}^{m} W_i} |\mathbf{S}_i|^{-1/2} \phi\left(\mathbf{S}_i^{-1/2} (\mathbf{y} - \mathbf{y}_i)\right)$ 

where  $\mathbf{S}_{i} = \max{\{\mathbf{s}_{i}^{2}, \delta^{2}\}} \mathbf{I}_{d}$  with a pre-determined minimal scale level  $\delta$ .

Density estimator for big data sets based on data nuggets. Duan et al 2024 :

#### dPP Projection 1

Data Nuggets PP Projection 1 RED=%HEU<Overall BLUE=%HEU>Overall YELLOW=No Difference(+/-10% of Overall)



#### dPP Projection 2

Data Nuggets PP Projection 2 RED=%HEU<Overall BLUE=%HEU>Overall YELLOW=No Difference(+/-10% of Overall)



#### dPP Projection 3

Data Nuggets PP Projection 3 RED=%HEU<Overall BLUE=%HEU>Overall YELLOW=No Difference(+/-10% of Overall)



#### LPS vs Untreated Projections



- 3 projections of LPS vs. Untreated, optimized for dPP
- In the 3<sup>rd</sup> columnBLUE = LPS>Untreated; RED = LPS<Untreated difference between the two densities</li>



#### **Profiling Cells in Differentially Populated Regions**



Novel machine learning approach to differential flow cytometry analysis base on projection pursuit. Dastgiri et al, 2024 (submitted)

# Conclusion

- Manual or automated gating of flow cytometry data might not be able to capture the structure of multidimensional data
- Differential Projection Pursuit creates 2D views complex multidimensional structures, optimized for maximal separation between the experimental groups
- The scientists and the statisticians must work as a team to correctly design, analyze and interpret the results of the experiments

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# **References and Publications**

- A New Projection Pursuit Index for Big Data. Yajie Duan, Javier Cabrera, arXiv 2021 (under revision for JCGS)
- Novel Machine Learning Approach to Differential Flow Cytometry Analysis base on differential Projection Pursuit. Mahan Dastgiri, Yajie Duan, Davit Sargsyan, Abraham Adkwei, Rebecca Mary Peters, PoChung Chou, Ge Cheng, Chun-Pang Lin, Jocelyn Sendecki, Helena Geys, Kanaka Tatikola, Ah-Ng Kong and Javier Cabrera (under revision for JBS)

Data Nuggets: A Method for Reducing Big Data While Preserving Data Structure. Traymon E. Beavers, Ge Cheng, Yajie Duan, Javier Cabrera, Mariusz Lubomirski, Dhammika Amaratunga and Jeffrey E. Teigler. arXiv 2024

# Thank you!

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