

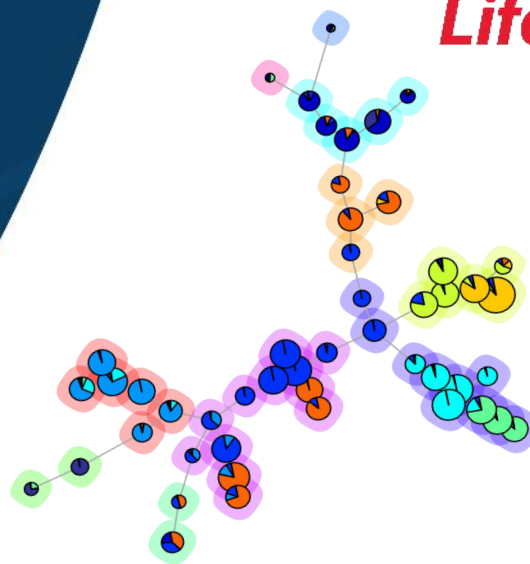
# 高维数据的艺术：用Cytobank 实现降维分析的最佳实践

贝克曼库尔特生命科学



**BECKMAN  
COULTER**

**Life Sciences**

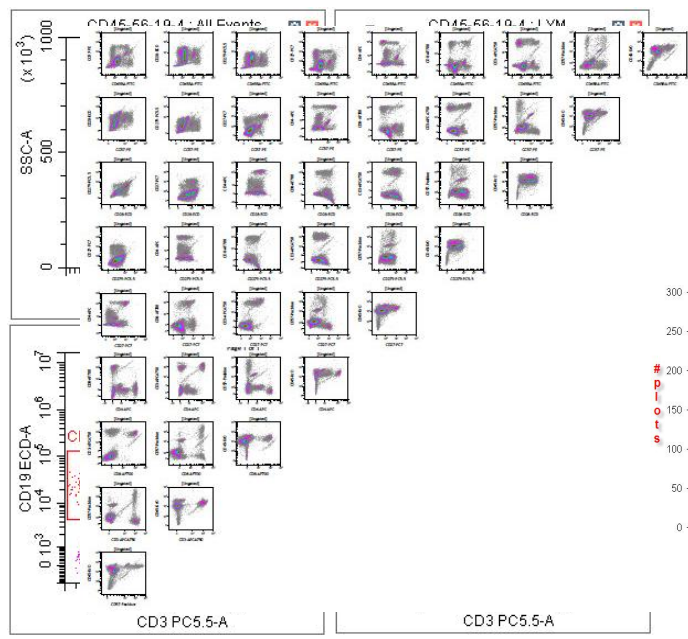


# 流式分析中遇到的问题？

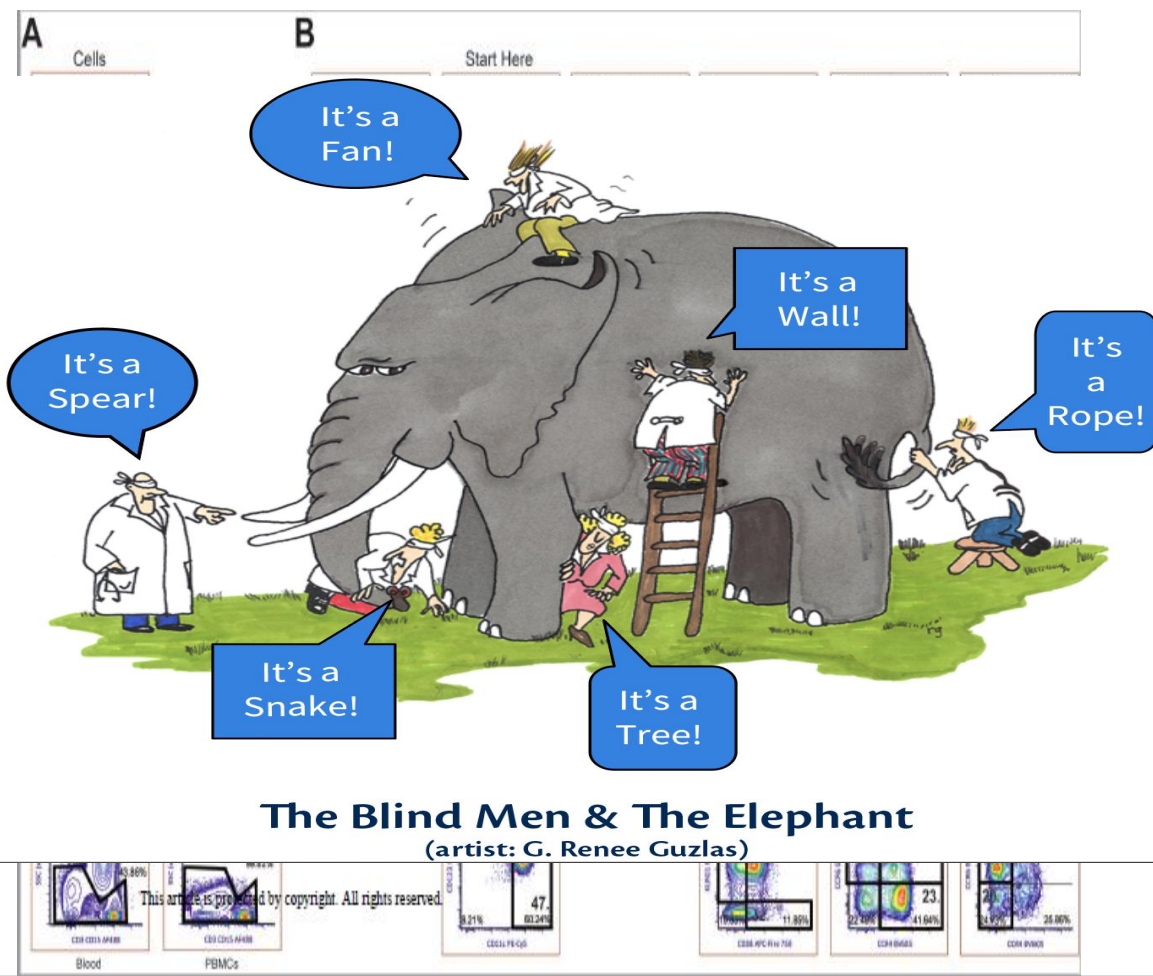
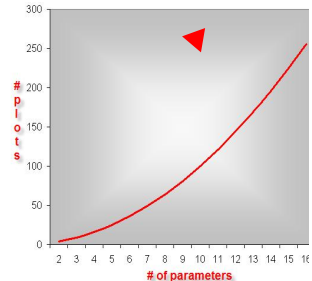
- 多参数下数据分析难度加大
- 按现有免疫学知识，错失可能的群体
- 不同样本分群差异，不能按原有SOP圈门
- 人为圈门差异或逻辑差异导致重复性差

25色人外周血免疫监测

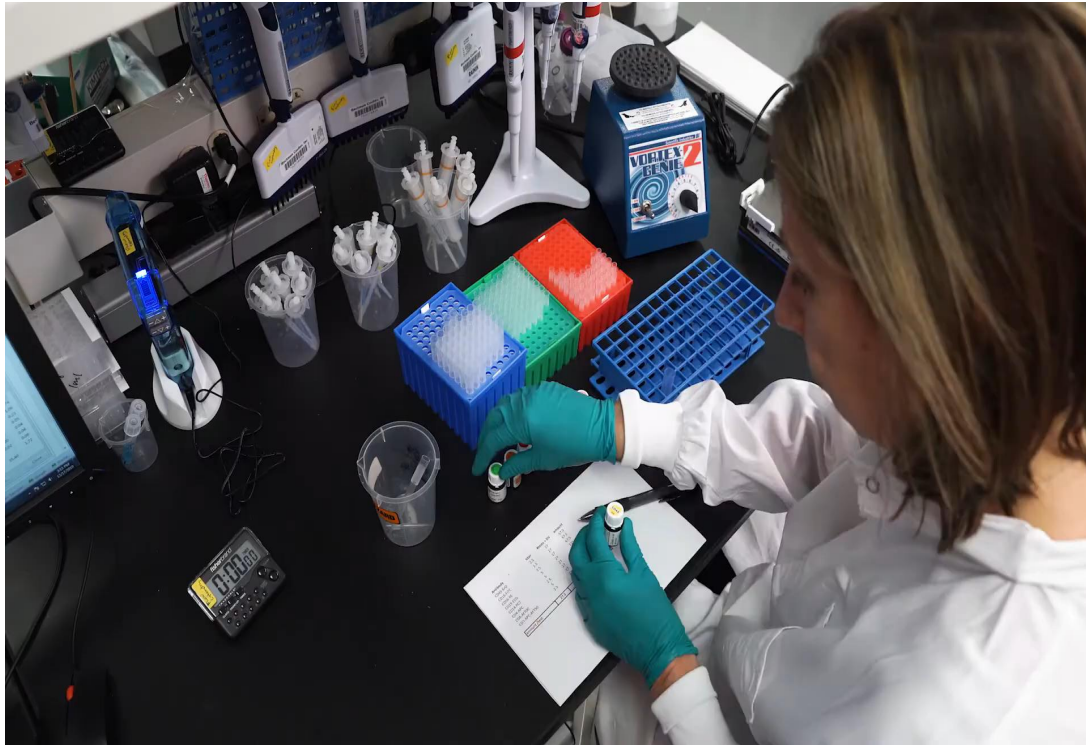
10<sup>4</sup> CD45.4.8.3 抗体管 combinations



更多参数下分析

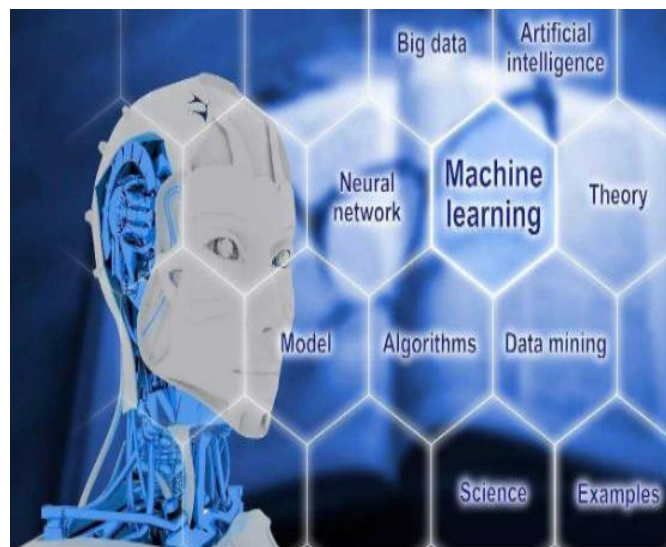
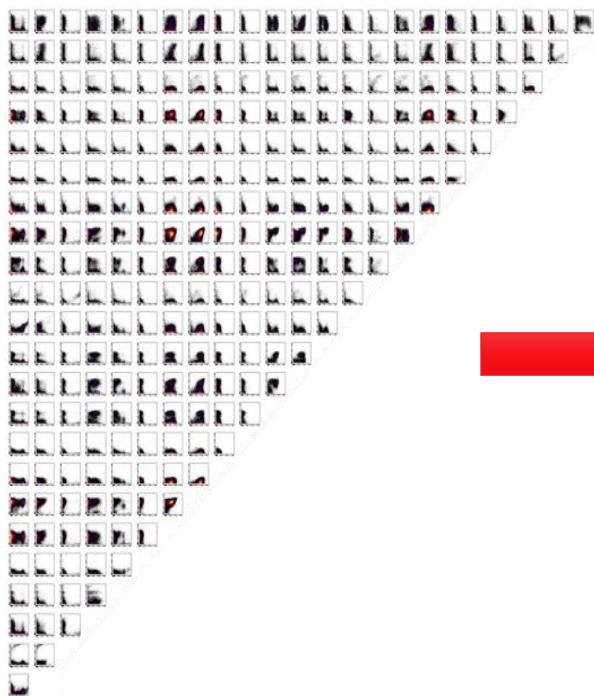


# 如何提高效率的同时减少误差？

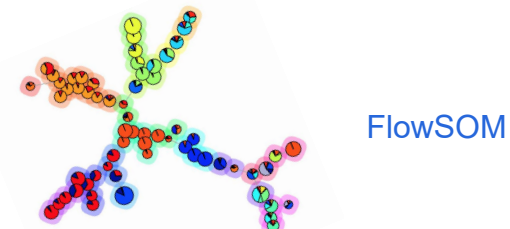


# 机器学习助力流式数据分析

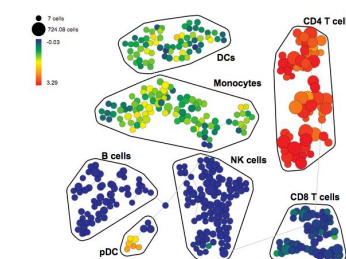
传统的流式数据分析



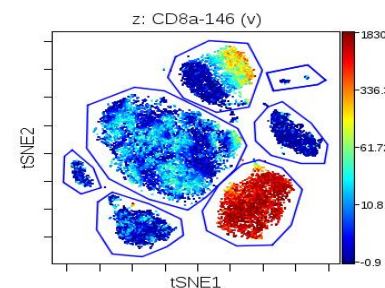
聚类&降维分析



FlowSOM



SPADE



viSNE

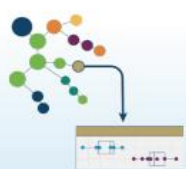
# 更新脚步从未停止...

## Cytobank | Timeline of Releases

2.4 SPADE



5.4 CITRUS

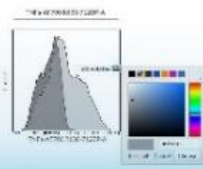


Cytobank joins Beckman Coulter Life Sciences

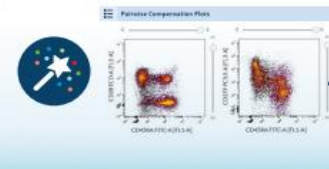


Security Improvements

8.1 TOP20



9.4 Autocomp



21 CFR Part 11

2012

2014

2016

2018

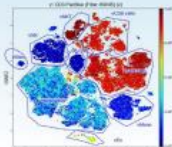
2019

2020

2021

2022

2023



viSNE 4.0



FlowSOM 7.0



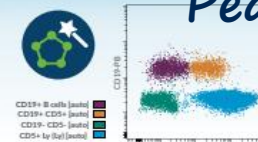
Illustration Editor 8.0



DRS 9.0



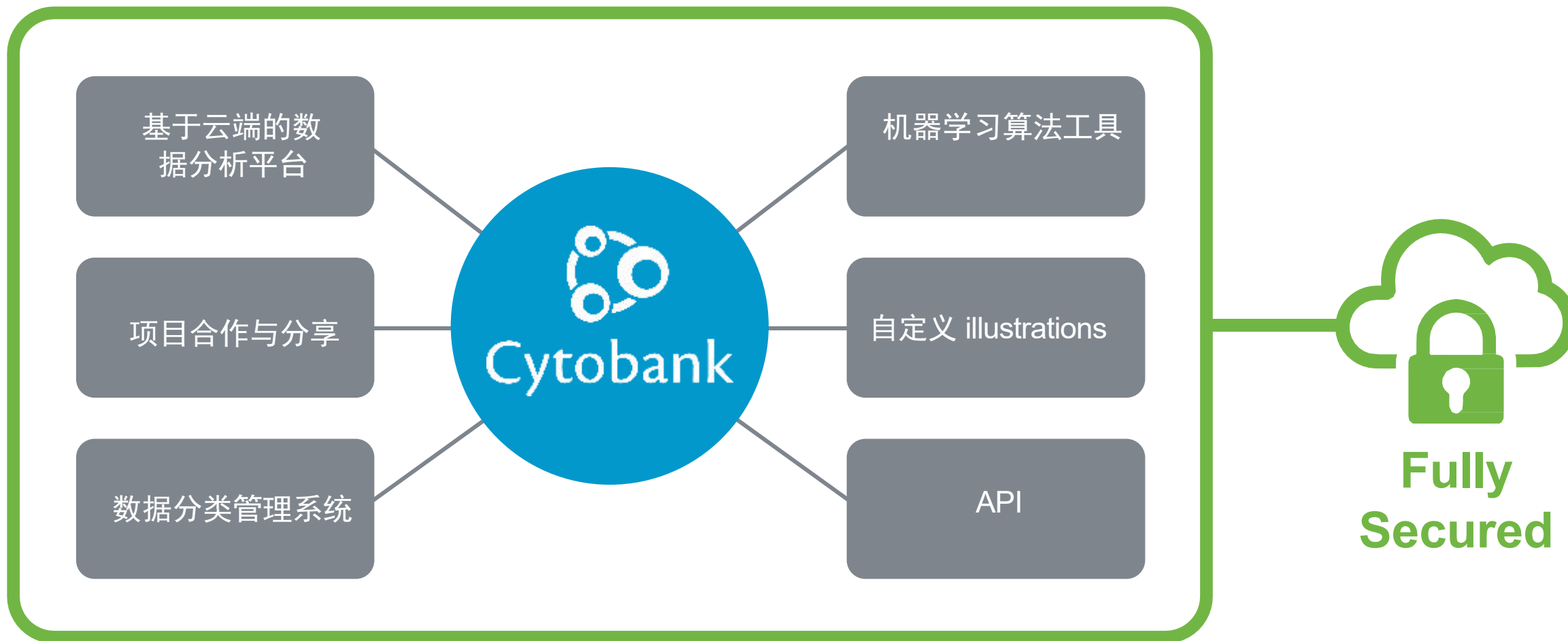
9.1 Statistical Inference



10.0 Autogating

PeacoQC

# 何为Cytobank platform?

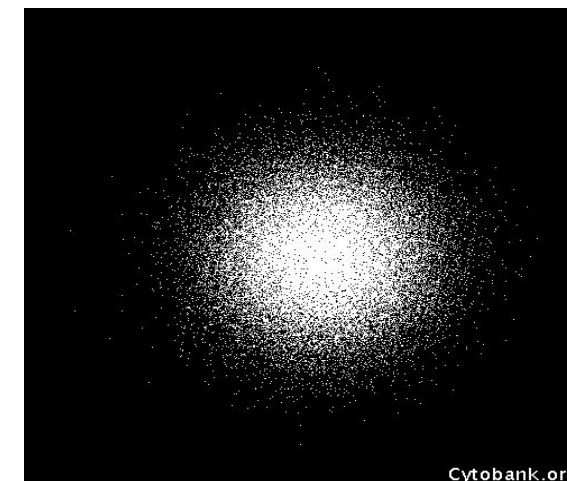


# t-SNE (viSNE): t-分布随机邻接嵌入算法

## t-Distributed Stochastic Neighbor Embedding

一种探索高维数据的降维算法，常用于可视化数据的整体结构。

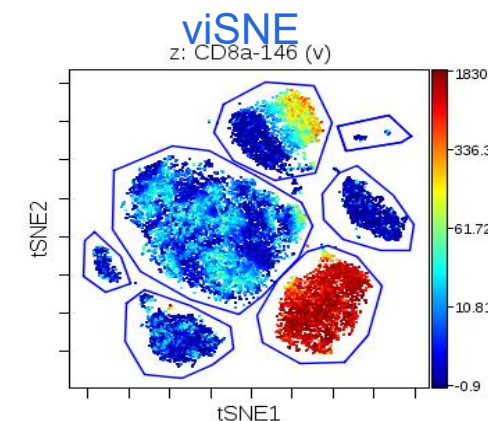
- 多维数据通过迭代过程简化为二维“地图”
- 每个点表示一个细胞/事件
- 在viSNE“图上相邻的细胞彼此更相似，每个“小岛”为相似的细胞群
- 可通过细胞颜色判断Marker表达强弱



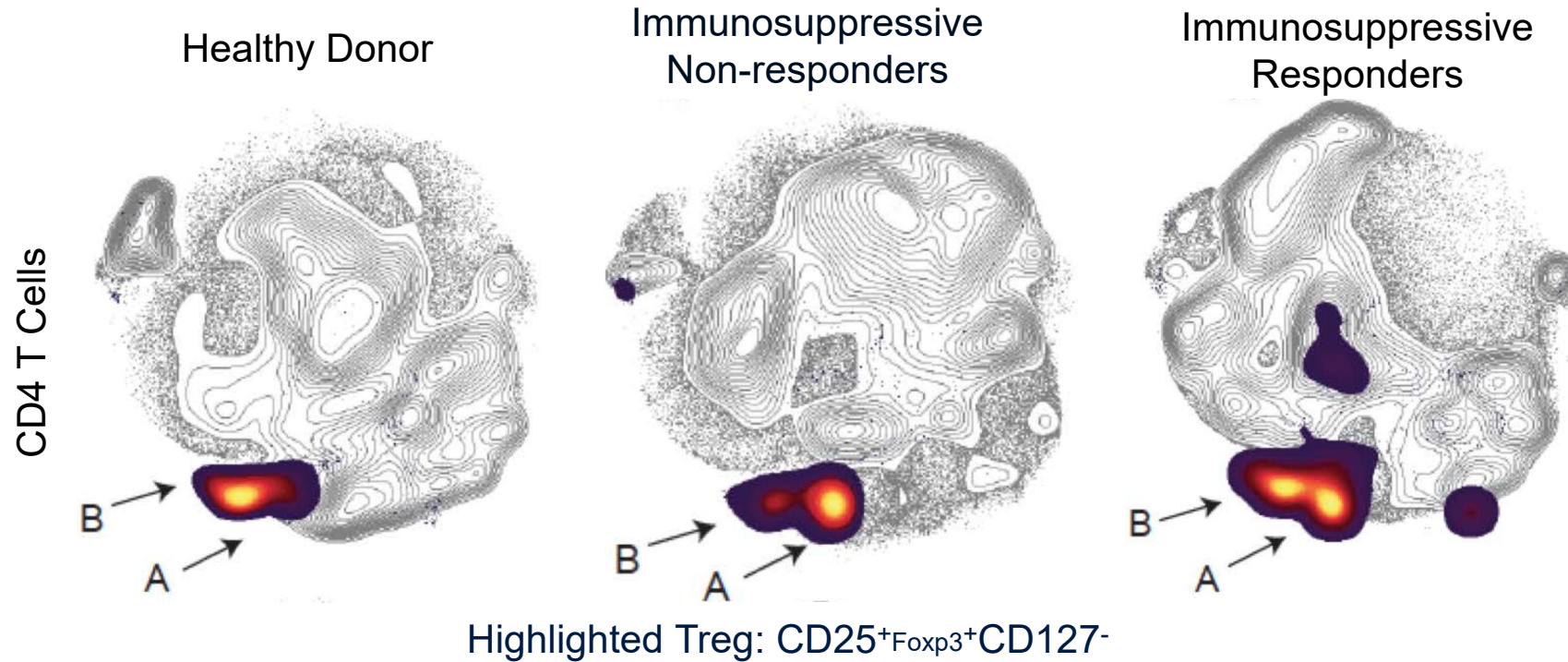
viSNE enables visualization of high dimensional single-cell data and reveals phenotypic heterogeneity of leukemia

El-ad David Amir<sup>1</sup>, Kara L Davis<sup>2,3</sup>, Michelle D Tadmor<sup>1,2</sup>, Erin F Simonds<sup>2,3</sup>, Jacob H Levine<sup>1,3</sup>, Sean C Bendall<sup>2,3</sup>, Daniel K Shenfeld<sup>1,3</sup>, Smita Krishnaswamy<sup>1</sup>, Garry P Nolan<sup>2,4</sup> & Dana Pe'er<sup>1,4</sup>

NATURE BIOTECHNOLOGY VOLUME 31 NUMBER 6 JUNE 2013



# 客观地观察所有细胞有助于新发现



- viSNE density plots revealed two Treg subpopulations
- Non-responders have more A subpopulation than responders/healthy
- B subpopulation has more memory/activation phenotype



# 降维算法在传统流式中多色分析流程

检测试剂: DuraClone

数据采集: CytoFLEX

数据分析: 手动和降维



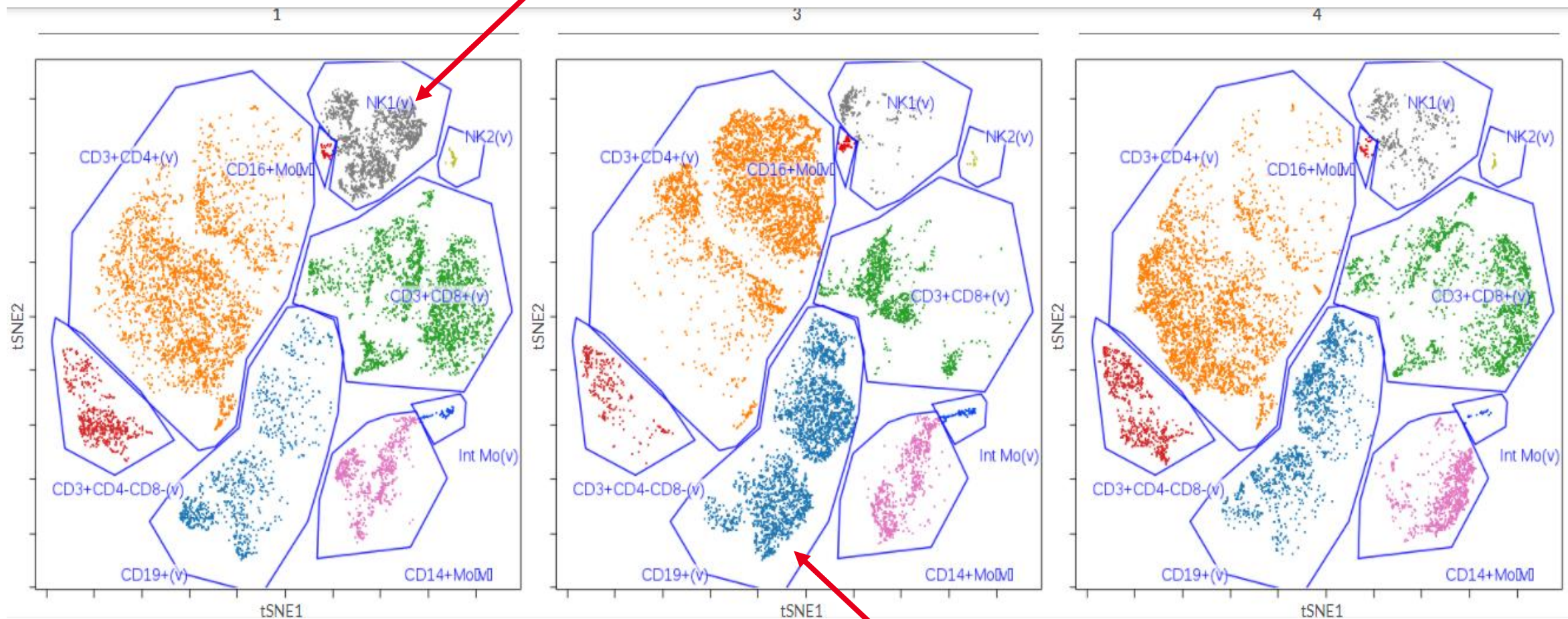
Product	405 nm			488 nm				633 nm				Quality Standard
	FB	Kr10	FITC	PE	ECD	PC55	PC7	APC	APC-A700	APC-A750	APC-A750	
IM Phenotyping Basic Tube 853309 (25 tests RUO)	-	CD45	CD16	CD56	CD19	-	CD14	CD4	-	CD8	-	CD3
IM B Cell Tube 853318 (25 tests RUO)	IgM	CD45	IgD	CD21	CD19	-	CD27	CD24	-	-	-	CD38
IM T Cell Subsets Tube 853328 (25 tests RUO)	CD57	CD45	CD45RA	CCR7	CD28	PD1	CD27	CD4	-	CD8	-	CD3
IM Dendritic Cells Tube 853331 (25 tests RUO)	HLA-DR	CD45	CD16	Lineage*	-	CD1c	CD11c	CD135A	-	-	CD123	-
IM TCRs Tube 853340 (25 tests RUO)	TCRV2	CD45	TCRγδ	TCRαβ	HLA-DR	-	TCRV1	CD4	-	CD8	-	CD3
IM Treg Tube 853346 (25 tests RUO)	Helios	CD45	CD45RA	CD25	-	CD39	CD4	-	FoxP3	-	-	CD3
IM Granulocytes Tube 888651 (25 tests RUO)	CD15	CD45	CD204	-	CD16	CD33	CD11b	PD-L1	-	-	Lineage**	CD62L
IM Count Tube 00162 (25 tests RUO)	-	-	CD45	Counting Beads	-	7-AAD	-	-	-	-	-	-

\*: CD5 / CD19 / CD20 / CD14 / CD56  
 \*\*: CD5 / CD14 / CD19 / CD56



FITC	PE	ECD	PC7	APC	APC-A700	APC-A750	BV421	KO
CD16	CD56	CD19	CD14	CD4	CD8	CD3	HLA-DR	CD45

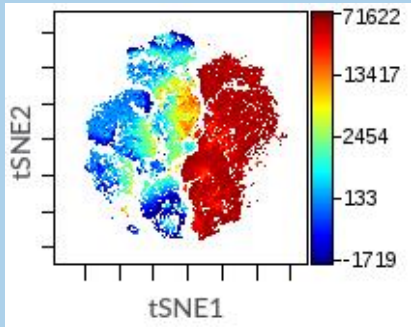
# 降维图中识别所有细胞群的变化



# Cytobank 的多种降维算法

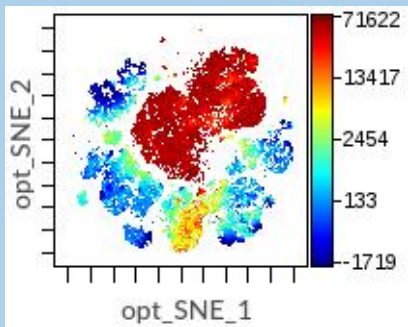
➤ 相比viSNE/ tSNE，更新更快功能更强大的降维工具，助力降维中的参数自动优化以及缩短分析时间

## viSNE/ tSNE



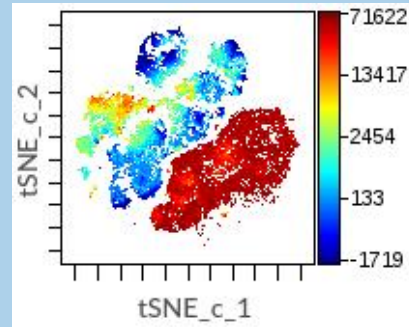
t-分布随机近邻嵌入 (t-Distributed Stochastic Neighbor Embedding, t-SNE) 是一种非线性降维算法, 在亚群细节展示方面会有优势, 能够更好的展示亚群之间的细微差异最高可 2M events

## opt-SNE



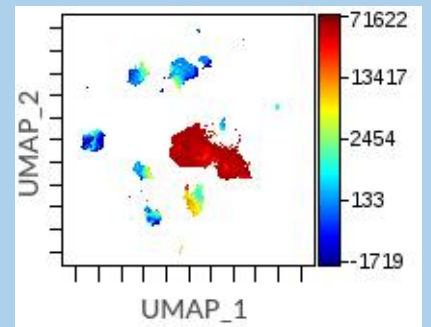
在t-SNE的基础上, 针对所选数据集自动优化参数设置, 从而得到更好的数据分辨率以及降低数据分析时间, 最高可3M events

## tSNE-CUDA



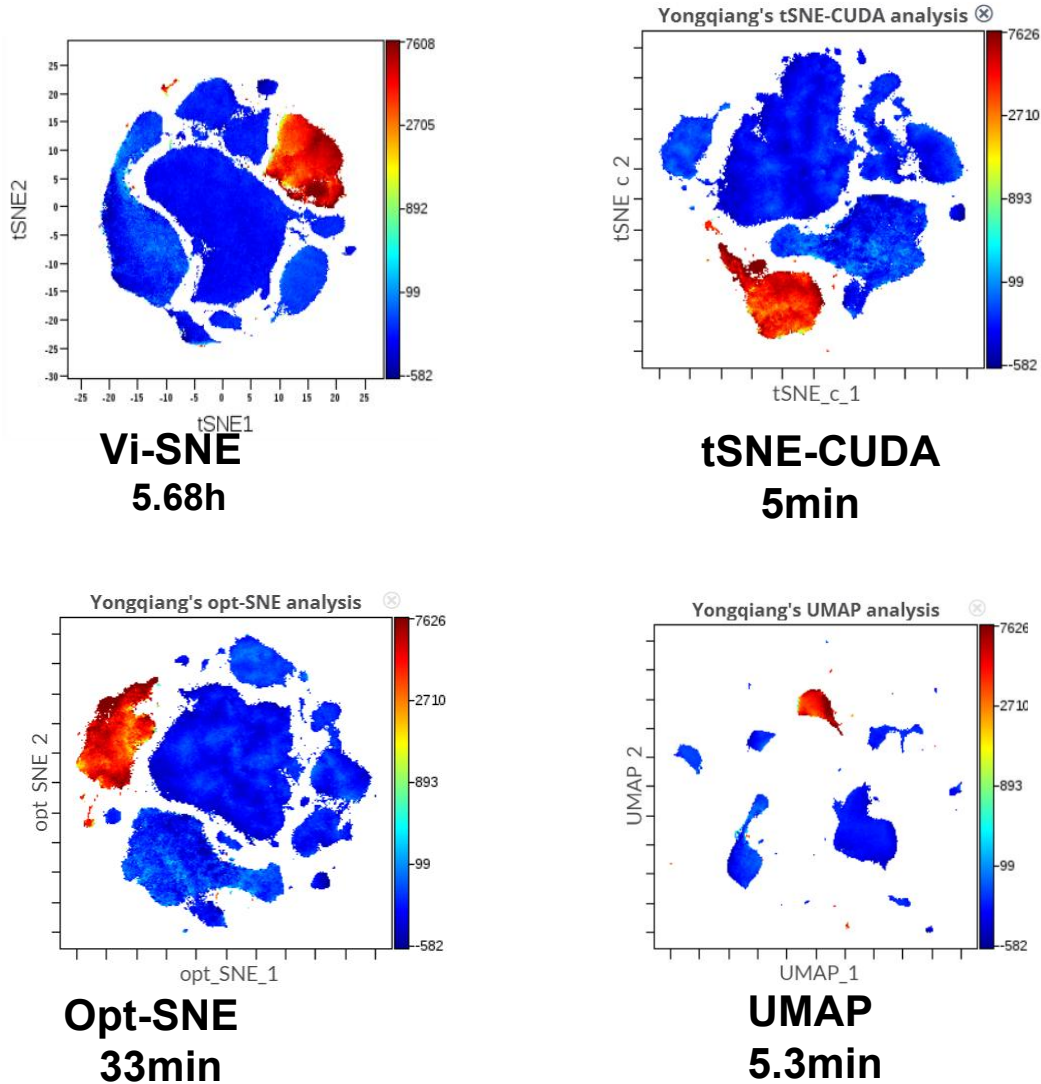
在t-SNE的基础上, 基于GPU加速, 运算速度更快, 节约时间, 最高可 10M events

## UMAP

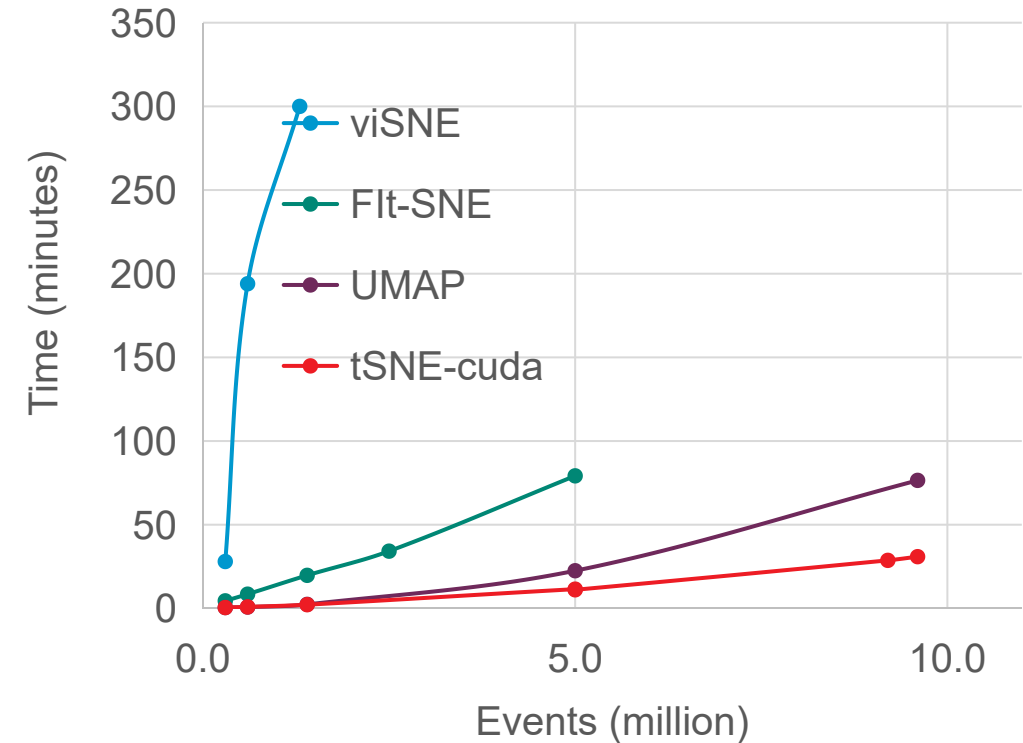


与t-SNE不同, 它使用拓扑框架对数据集的底层模式进行建模, 相比其他算法, 更为保存全局的整体结构, 同时基于GPU加速, 运算速度更快, 节约时间, 最高可10M events

# 新算法更好解决降维分析中的难点



Speed as events increase  
(preliminary data)



# FlowSOM: 一种快速准确的聚类算法



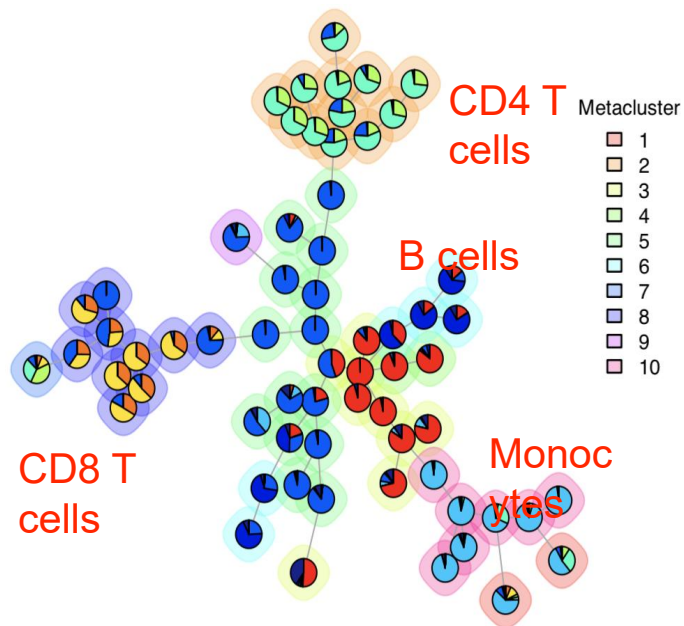
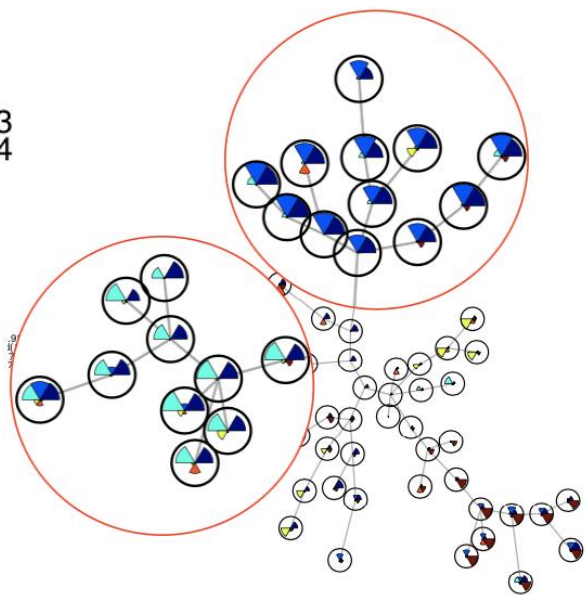
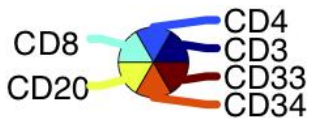
## FlowSOM: Using Self-Organizing Maps for Visualization and Interpretation of Cytometry Data

Sofie Van Gassen,<sup>1,2,3\*</sup> Britt Callebaut,<sup>1</sup> Mary J. Van Helden,<sup>2,3</sup> Bart N. Lambrecht,<sup>2,3</sup> Piet Demeester,<sup>1</sup> Tom Dhaene,<sup>1</sup> Yvan Saeys<sup>2,3</sup>

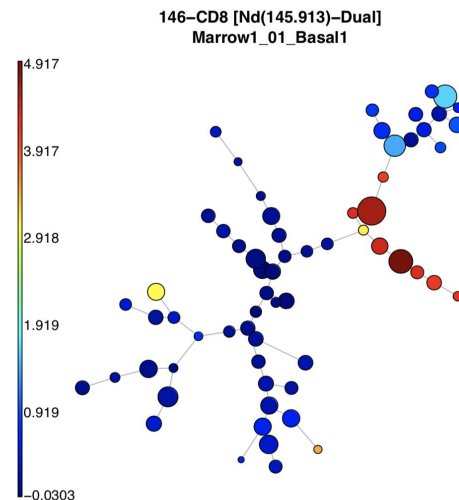
- 使用自组织映射(SOM)来聚类显示所有细胞上的所有标记
- SOM被映射到最小生成树上，并且有星图便于数据可视化分析
- 使用饼图来检测难以定义的子集
- 速度快，可同时运行多个FLOWSOM分析
- 集群自动圈门

# 可视化展示：饼图与星图

- Ungated
- CD123+ DCs
- CD19+CD20+ B cells
- CD3+ T cells
- CD33+ mono
- CD4+CD45RA- memory T cells
- CD4+CD45RA+ T cells
- CD8+CD45RA- memory T cells
- CD8+CD45RA+ naive T cells
- Live cells

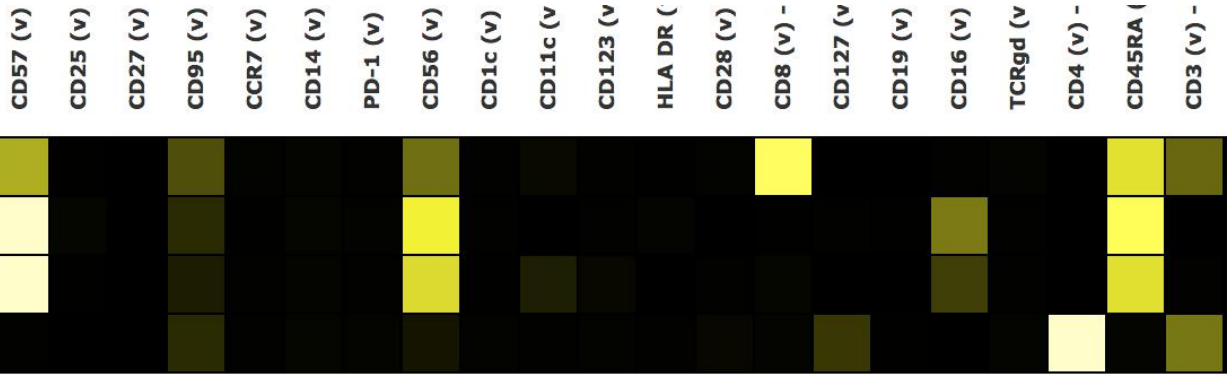
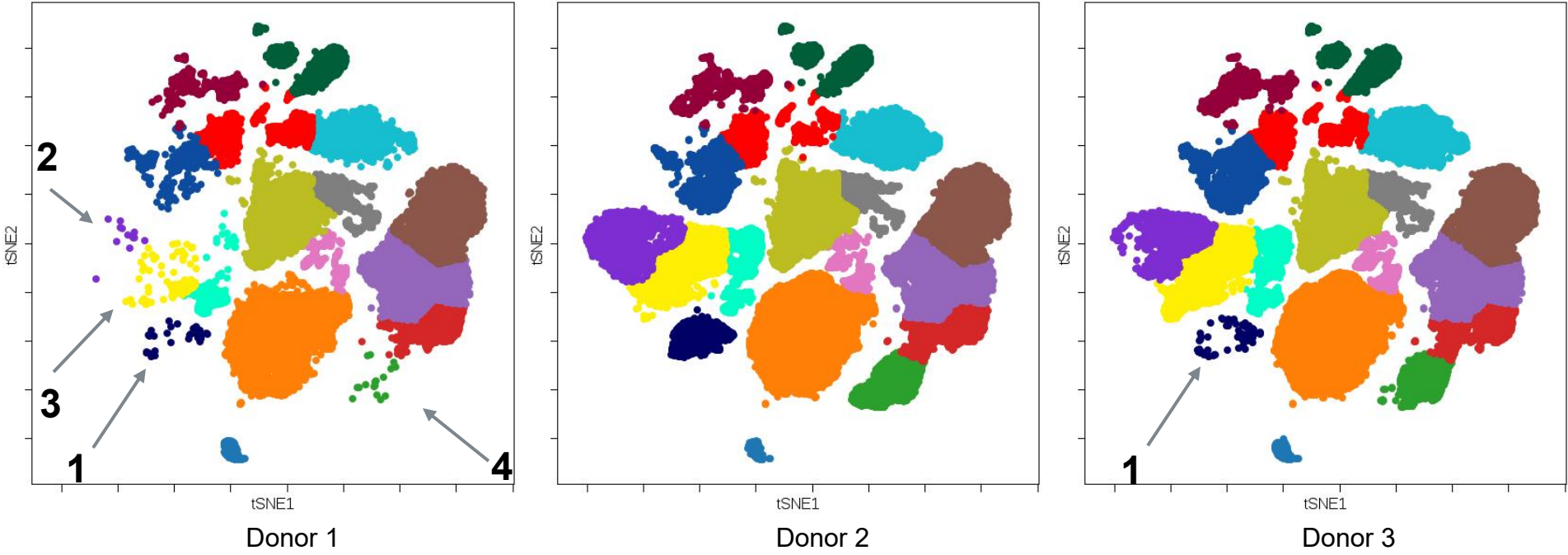


星图



细胞簇抗原表达情况

# Automatic Clustering with FlowSOM on viSNE



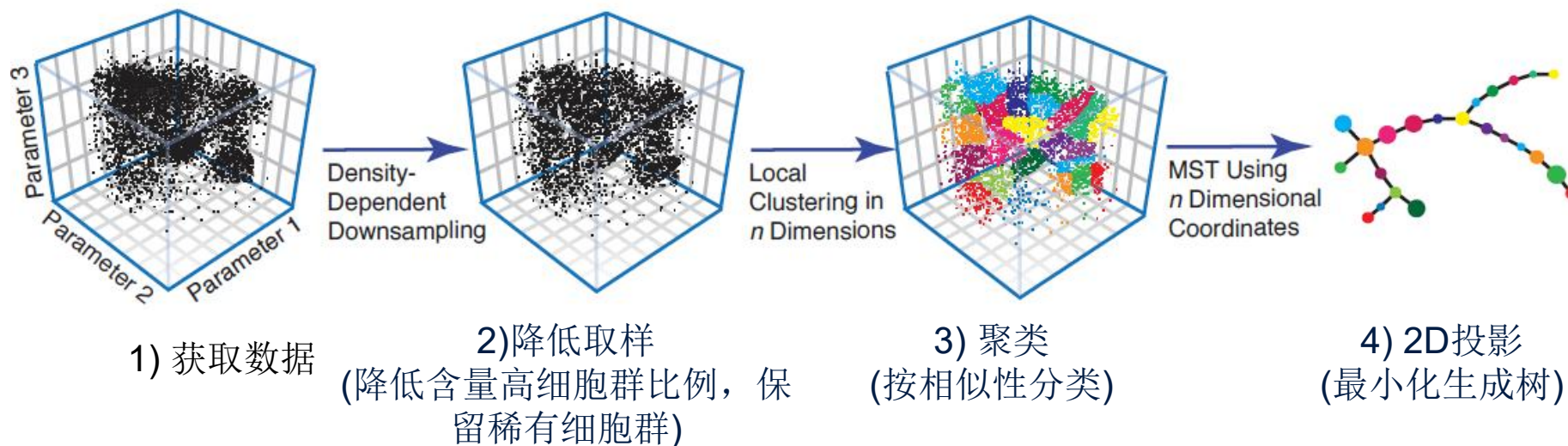
# SPADE:密度标准化事件的生成树连续分析

Extracting a cellular hierarchy from high-dimensional cytometry data with SPADE

Peng Qiu<sup>1,2</sup>, Erin F Simonds<sup>3</sup>, Sean C Bendall<sup>3</sup>, Kenneth D Gibbs Jr<sup>3</sup>, Robert V Bruggner<sup>3</sup>, Michael D Linderman<sup>4</sup>, Karen Sachs<sup>3</sup>, Garry P Nolan<sup>3</sup> & Sylvia K Plevritis<sup>1</sup>

VOLUME 29 NUMBER 10 OCTOBER 2011 NATURE BIOTECHNOLOGY

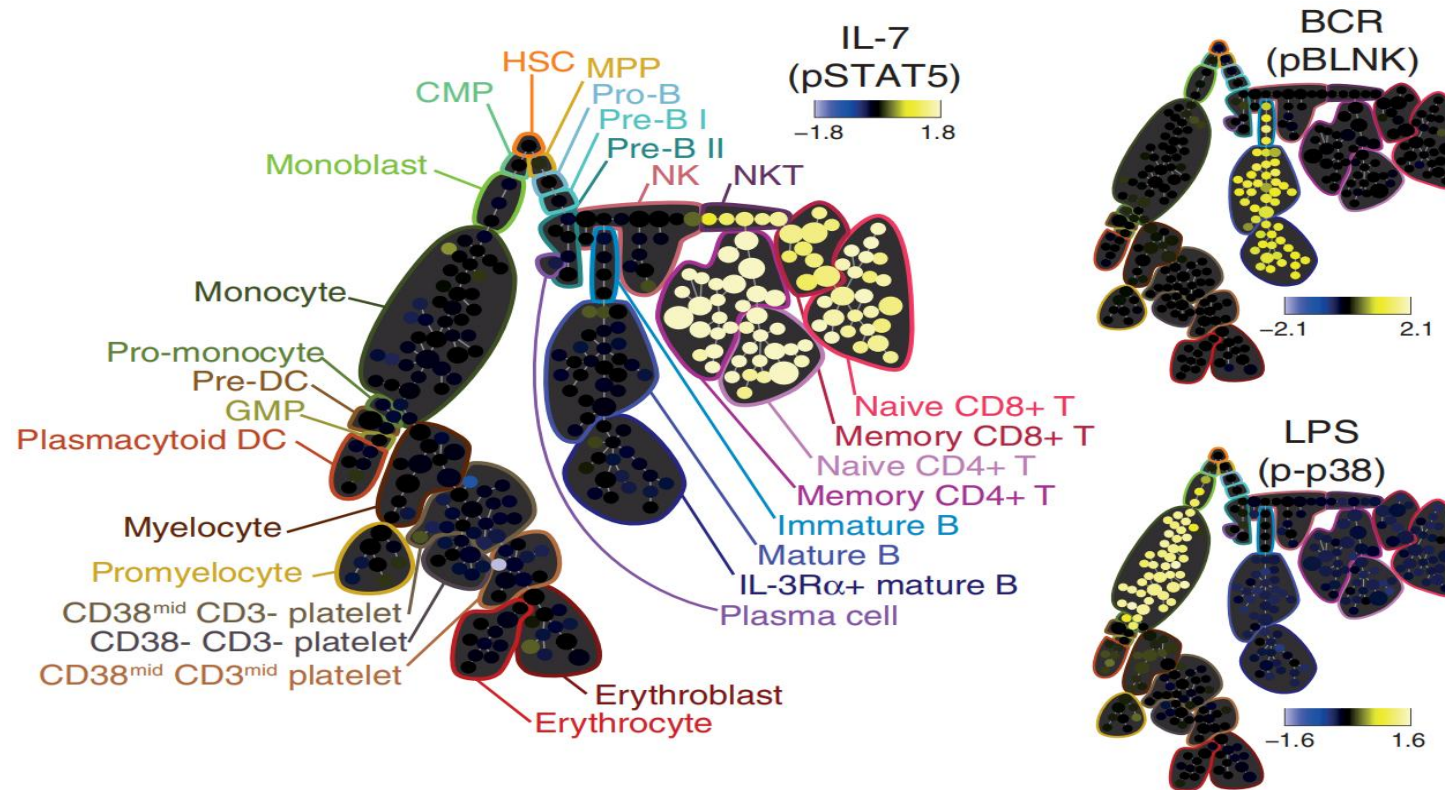
## SPADE method:





# 免疫系统中单细胞信号分子表达

- 骨髓细胞采用IL-7, BCR和LPS 刺激, 检测pSTAT5
- IL-7, BCR和LPS刺激后pSTAT5 水平变化分别发生在T cells, B cells, 和 monocytes



Bendall et al. Science. (2011)

# 降维分析操作流程

# Cytobank 账号登录

网址: <https://www.cytobank.cn>



Cytobank 平台 ▾ 服务 培训 技术博客 联系我们 客户支持

登录 ▾

免费试用

高级版  
企业版

## 单细胞 全局图

分析和显示细胞仪数据集

了解更多



从数据快速得到结果。Cytobank 是基于云的平台，可同时分析和显示多个单细胞数据，提高研究效率。使您能够同时分析和可视化多个单细胞数据

## Cytobank 平台

- 可在任何地方任何连接网络的设备上工作
- 快速沟通和呈现结果
- 安全地与跨学科和地域的同事进行联系和协作

了解更多»

## 通过 科学服务 (科学服务) 让我们的专家团队支持您的团队

- 无需增加人手更快获得更好的结果
- 在设置、分析、成像或整个工作流程中利用我们经验丰富的科学家的专业知识
- 联系我们:  
[Cytobank\\_ScientificServices@beckman.com](mailto:Cytobank_ScientificServices@beckman.com)  
了解更多信息并开始使用

## 试用 Cytobank

Cytobank 将高维度质谱和流式细胞数据转化为深度结果。借助 Cytobank 平台集成的高级可视化工具进行深入研究。

30 天免费试用 (Cytobank 高级版) »

## Register Now for Premium China Cytobank

Free and full-featured for 30 days - No credit card required!

Username  Invalid characters in username

First name

Last name

Contact email

Confirm email

Use the address you want to receive Cytobank email (e.g. jane@companyx.com or john@institution.org)

Privacy  Do not display my email address to other users

Password:

Confirm password:

Passwords should be 8 to 40 characters, with at least one letter and one number.

Company or Organization

Country or Region

Optional Information

Phone number

Please keep me informed about Beckman Coulter webinars, products, goods and services, including products, goods and services from our related companies.

Do you consent to be contacted

By phone:  I consent  I do not consent

By email:  I consent  I do not consent

By submitting this form I confirm that I have reviewed and agree with the [Privacy Policy](#) and the [Cytobank Terms of Use](#). I also understand my privacy choices as they pertain to my personal data as provided in the [Privacy Policy](#) under "Your Privacy Choices".



Username or Email

Password

Login

Forgot password  
Use OpenID

Create an account

## User Resources

- Learn more about Cytobank: [Cytobank Support](#)
- Get started on Cytobank: [Cytobank Bootcamp](#)
- See Cytobank in action: [Cytobank Learning Center](#)

Cytobank is CyTOF® compatible.

# 便捷的数据分类管理--软件主界面

- 所有数据基于标签分类和关键词查找
- 单个实验以总表形式呈现，一键溯源分析
- 数据分析，即刻自动保存，避免丢失信息

Annotations in the screenshot:

- Create New Experiment
- Search bar to filter experiments
- Summary values for each experiment
- Different pre-set filters to organize visible experiments
- Labels for experiments

Sections shown in the screenshot:

- Linked experiments
- Illustrations
- Dimensionality reduction analyses
- Attachments
- Protocols
- FCS files

Name	Settings	Size	Author	Status	Created
lym-1	Settings	3.06 MB	Gravatar Image Yongqiang Wu	Completed	Jul 2021
LYM2	Settings	3.06 MB	Gravatar Image Yongqiang Wu	Completed	Jul 2021
LYM	Settings	3.37 MB	Gravatar Image Yongqiang Wu	Completed	Jul 2021

File Name	Sample Name	Sample Tags	Panel	Events
T cell AE-56.fcs		Plate 1	Panel 1	500,688
T cell AE-60.fcs		Plate 1	Panel 1	216,177
Total:				716,865

# 数据上传--Cytobank

Cytobank Premium China Experiments Projects

Create new experiment **Create via ACS file**

\* Experiment Name: PBMC Experiment (Fluorescence)-test20220505

Project: BCCE test

\* Primary Researcher: min gao

\* Principal Investigator: min gao

Invite a new user  
Allow Principal Investigator to have full access to experiment

Source(s): Nothing selected

\* Purpose: 1. Stimulate PBMC with IL6, IL10, and LPS. 2. Measure phosphorylation of Stat3 and P38 after 15 minutes of stimulation. 3. Stain for CD4+ T cells, CD4- T cells, monocytes, and B cells.

Comments: Stain CD33-PE, CD4-PB, CD3-PC7, CD20-PerCPCy5.5, pStat3-AX488, pP38-AX647

**Create experiment**

PBMC Experiment (Fluorescence)-test20220505

Actions Sample tags Gates Advanced analyses Illustrations

Uploading files Status: Upload 26% complete...

Name	Size	Type	
pbmc_lrs005_unstim2.fcs	22.3 MB	FCS	
pbmc_lrs005_il10.fcs	22.3 MB	FCS	18%
pbmc_lrs005_lps.fcs	22.3 MB	FCS	
pbmc_lrs005_unstim1.fcs	22.4 MB	FCS	
pbmc_lrs005_il6.fcs	22.4 MB	FCS	71%
comp_percp_cy55.fcs	433 KB	FCS	
comp_pe.fcs	455 KB	FCS	
comp_alex647.fcs	472 KB	FCS	
comp_alex488.fcs	494 KB	FCS	
comp_paclu.fcs	498 KB	FCS	
comp_pe_cy7.fcs	508 KB	FCS	
114.66 MB		11 files	

# 创建实验

Cytobank Premium China Experiments Projects

test

Actions Sample tags Data QC Gates Advanced analyses Illustrations

Set up new experiment

Success! You uploaded 6 files to this experiment. Here are the next steps:

1. Adjust your **scales**
2. Set the experiment **compensation**
3. Perform **Data QC**
4. Annotate your files with **sample tags**
5. Review or adjust your **panel assignments** or channel names
6. Done with setup and ready to view your **data**

Learn more about Data QC

Articles on data QC: PeacoQC

- Introduction to PeacoQC, the automated data QC tool in the Cytobank platform
- How to set up a PeacoQC process
- How to navigate to the PeacoQC result page
- How to analyze the PeacoQC results
- Benchmark for PeacoQC run capacity

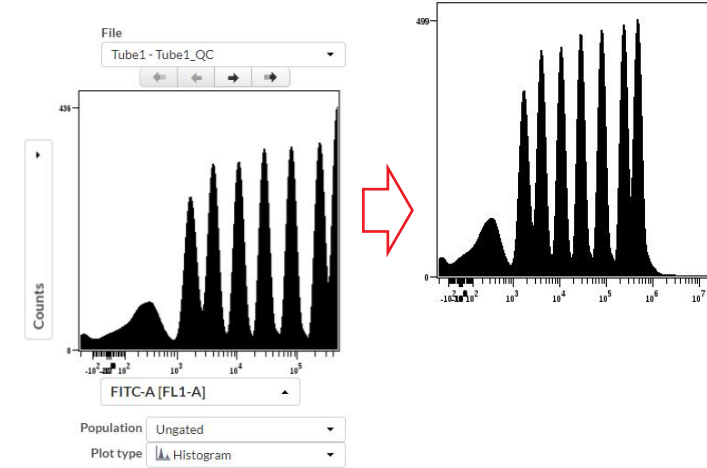
Peak Extraction And Cleaning Oriented Quality Control (PeacoQC) is a data QC tool developed by Emmaneel et al. from the VIB Center for Inflammation Research, Ghent, Belgium. It is implemented in the Cytobank platform to enable automated cleaning of cytometry data. The algorithm will determine density peaks per channel on which it will remove low-quality events based on their position in the isolation tree (IT) and on their mean absolute deviation distance (MAD) to these density peaks. PeacoQC works with all types of data, mass, flow, and spectral cytometry data. It needs to work with a preprocessed (transformed and, if appropriate, compensated or unmixing) FCS file.

Introducing PeacoQC for Data QC

# 1.调整坐标轴--Adjust your scales

## Cytobank支持便捷的坐标轴调整

- 支持荧光通道坐标轴显示方式切换，以及动态范围自定义展示
- 批量修改坐标轴
- 相似方案坐标轴设置参数一键导入



Click to edit scale settings for a channel

Channel	Type	Arg.	Minimum	Maximum
FSC-H	Linear	1	1.0	1677720.0
FSC-A	Linear	1	1.0	1677720.0
SSC-H	Linear	1	1.0	1077720.0
SSC-A	Linear	1	1.0	1277700.0
CD16 FITC-H [FL1-H]	Arcsinh	150	-200.0	16777200.0
CD16 [FL1-A]	Arcsinh	20000	-20000.0	16777200.0
CD56 PE-H [FL2-H]	Arcsinh	150	-600.0	16777200.0
CD56 [FL2-A]	Arcsinh	20000	-20000.0	16777200.0
CD19 ECD-H [FL3-H]	Arcsinh	150	-200.0	16777200.0
CD19 [FL3-A]	Arcsinh	20000	-20000.0	16777200.0
CD14 PC7-H [FL5-H]	Arcsinh	150	-200.0	16777200.0
CD14 [FL5-A]	Arcsinh	20000	-20000.0	16777200.0

File/sample name: 1

Population: lymphocytes  
Compensation: File-Internal Compensation  
Plot type: Density Dot

Bulk edit scales for all selected and unfiltered channels

Scale Type	Argument	Minimum	Maximum
Arcsinh	5000	-5000	16777200.0

Import scales from another experiment

Select an experiment

Channel	Type	Arg.	Minimum	Maximum
CD16 [FL1-A]	Arcsinh	20000	-20000.0	16777200.0
CD56 PE-H [FL2-H]	Arcsinh	150	-600.0	16777200.0

Channel	Type	Arg.	Minimum	Maximum
CD16 [FL1-A]	Arcsinh	20000	-20000.0	16777200.0
CD56 [FL2-A]	Arcsinh	20000	-20000.0	16777200.0
CD19 [FL3-A]	Arcsinh	20000	-20000.0	16777200.0
CD14 [FL5-A]	Arcsinh	20000	-20000.0	16777200.0
CD4 [FL6-A]	Arcsinh	30000	-20000.0	16777200.0
CD8 [FL7-A]	Arcsinh	20000	-20000.0	16777200.0
CD3 [FL8-A]	Arcsinh	20000	-20000.0	16777200.0
HLA-DR [FL9-A]	Arcsinh	2000	-2000.0	16777200.0
CD45 [FL10-A]	Arcsinh	2000	-20000.0	16777200.0

Bulk edit scales for all 9 selected and unfiltered channels

Scale Type: Arcsinh, Argument: 5000, Minimum: -5000, Maximum: 16777200.0, Apply

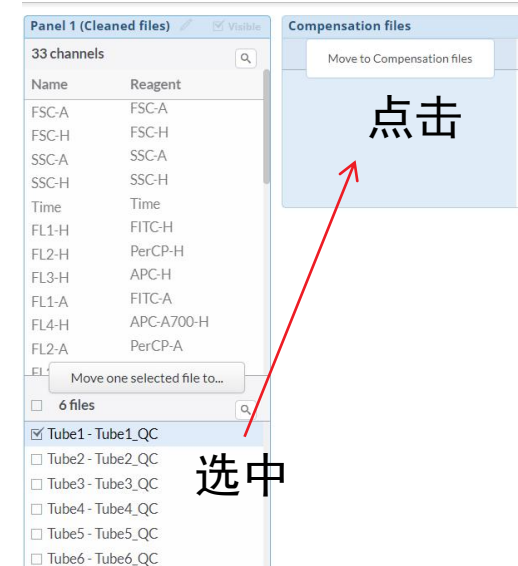
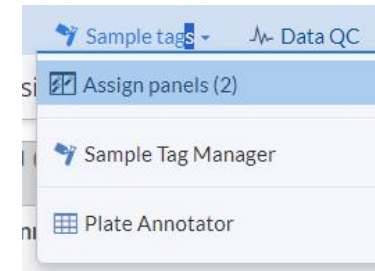
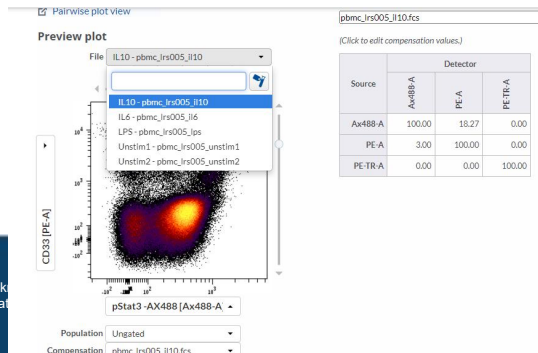
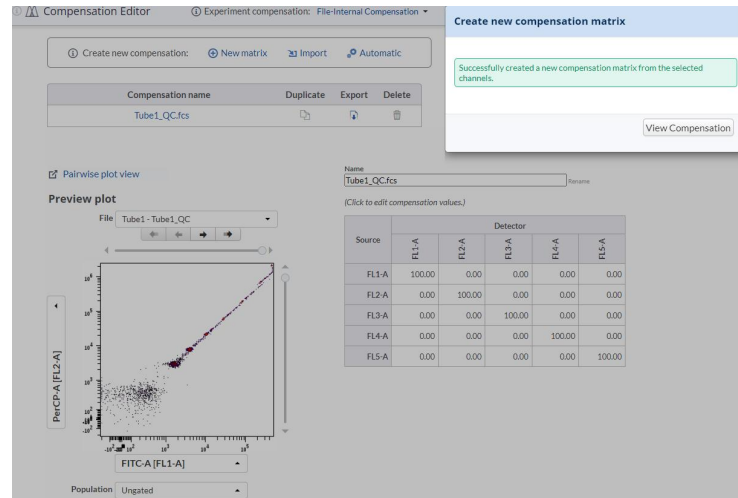
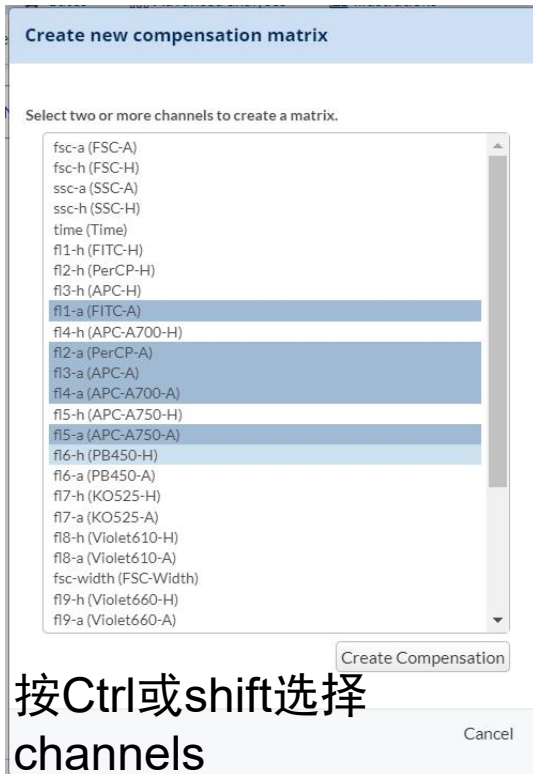
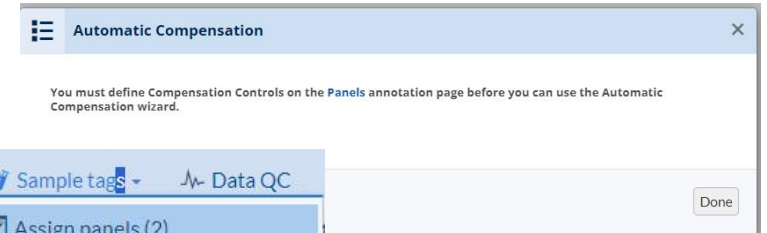
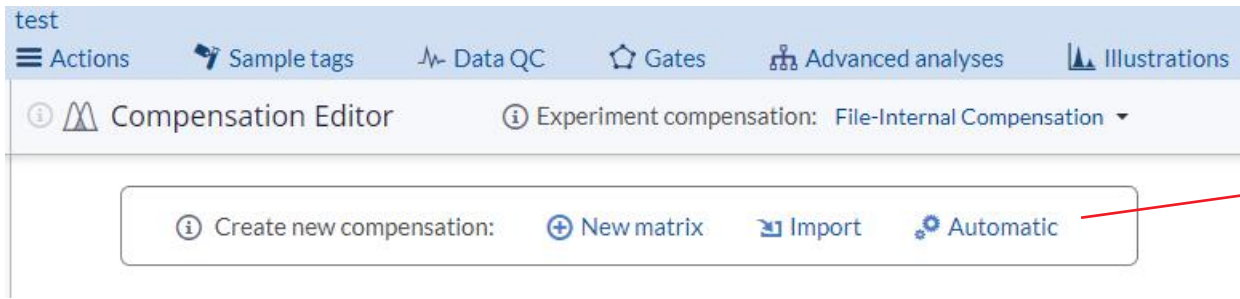
Import scales from another experiment

Select an experiment

# 2. 设置补偿-- Set the experiment compensation

Tips:

1. 需把补偿管设置到compensation files (界面Sample tags→Assign panels) 中
2. 手动补偿时选择不了 设置在compensation files中的文件 (管)



选中



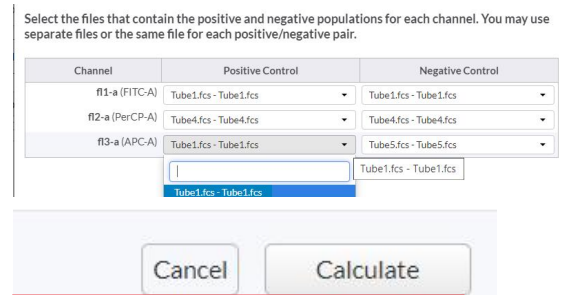
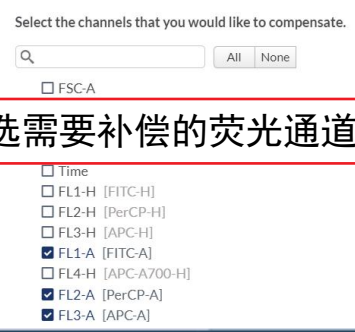
# 2. 设置补偿 -- Set the experiment compensation



1. 选细胞群体的坐标轴，比如 FSC/SSC

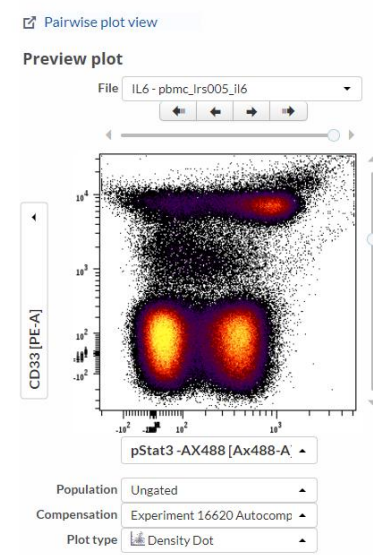


2. 选需要补偿的荧光通道



3. 选需要补偿通道的单染（补偿）管

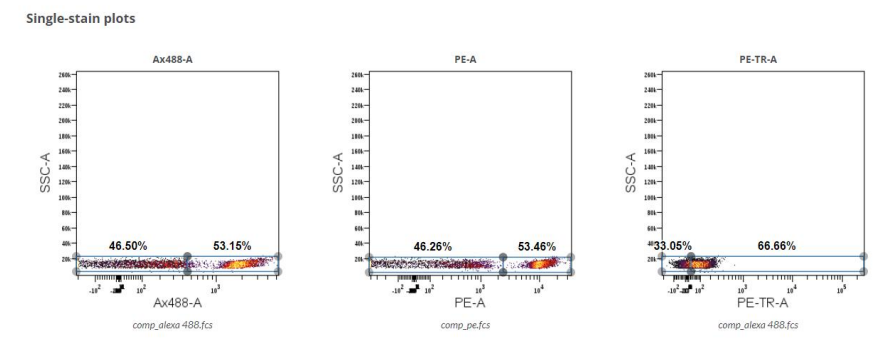
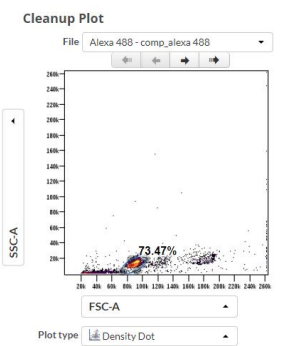
4. 用全染管验证补偿，如需，可再微调



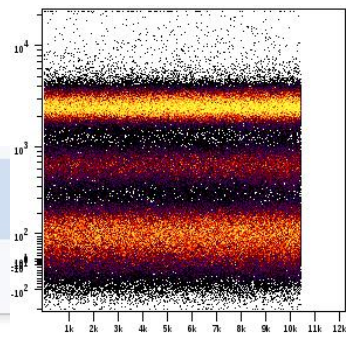
Name: Experiment 16620 Autocomp

(Click to edit compensation values.)

Source	Detector					
	Ax488-A	PE-A	PerCP-Cy55-A	PE-Cy7-A	Ax647-A	PacBlu-A
Ax488-A	100.00	29.67	1.59	0.24	9.89	0.59
PE-A	2.72	100.00	7.21	0.55	1.84	0.16
PerCP-C...	0.00	0.23	100.00	12.66	9.16	1.30
PE-Cy7-A	0.23	7.01	1.46	100.00	5.82	0.45
Ax647-A	0.01	0.06	0.39	0.04	100.00	0.25
PacBlu-A	0.24	0.24	0.30	0.03	4.90	100.00



# 3. 数据质控--Perform Data QC



Premium China

test

Actions Sample tags Data QC Gates Advanced analyses Illustrations

PeacoQC setup Copy settings Status: New Run PeacoQC process

**FCS files** Choose

Tube1

Tube2

Tube3

Tube4

Tube5

Tube6

6 of 6 selected

**Channels** Choose

Time

**Unselected channels:**

FSC-H

FSC-A

SSC-H

SSC-A

FITC-H

FITC-A

PerCP-H

PerCP-A

APC-H

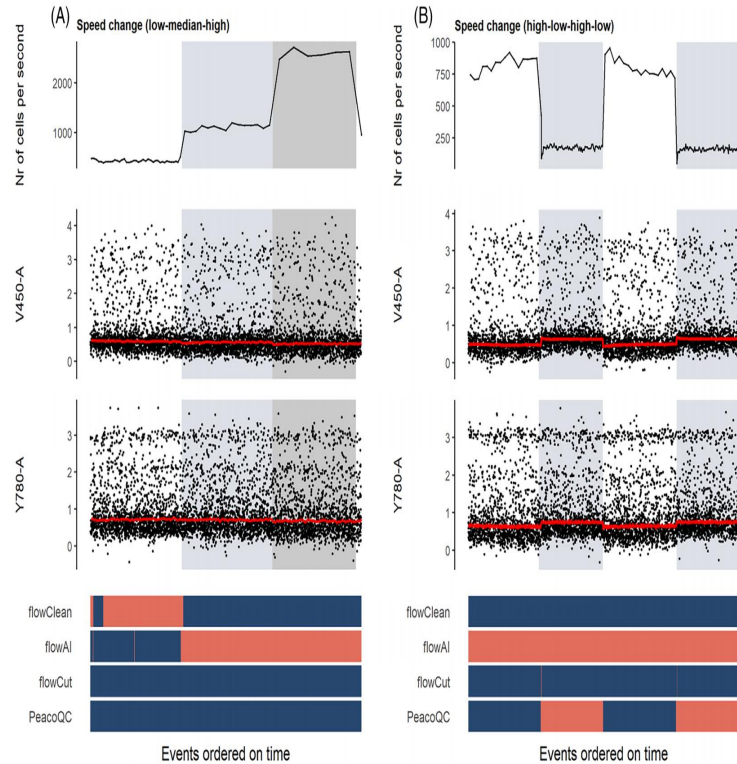
APC-A

APC-A700-H

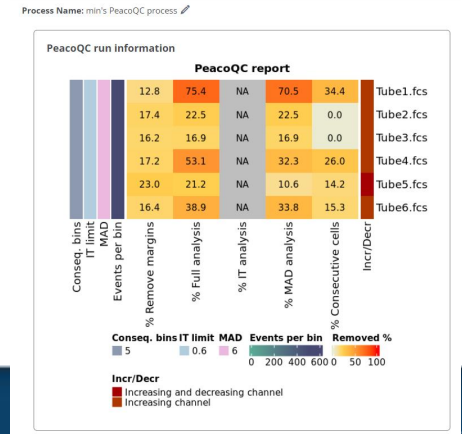
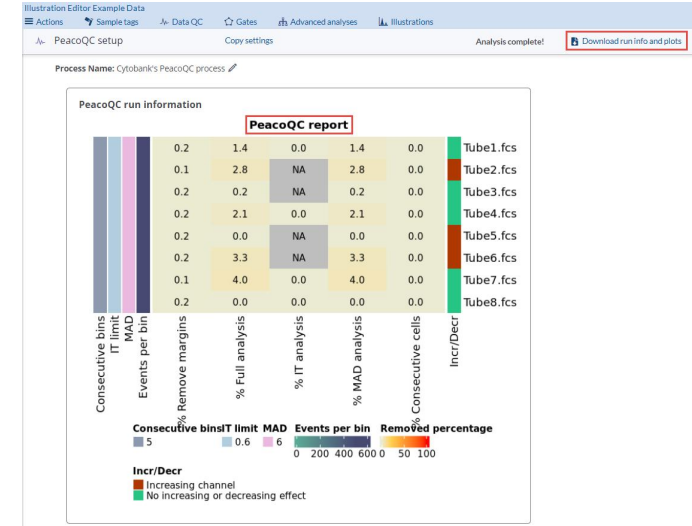
APC-A700-A

APC-A750-H

1 of 32 selected



  Perturbation 1
   Removed by algorithm
   Perturbation 2
   Kept by algorithm



# 4. Gating Editor

Create new compensation: New matrix Import Automatic

Compensation name	Duplicate	Export	Delete
Experiment 16620 Autocomp			
Experiment 16620 Autocomp (2)			
pbmc_lrs005_il10.fcs			

点击此处可跳转到调补偿界面可更改选择应用补偿值

Compensation: Experiment 16620 Autoc...

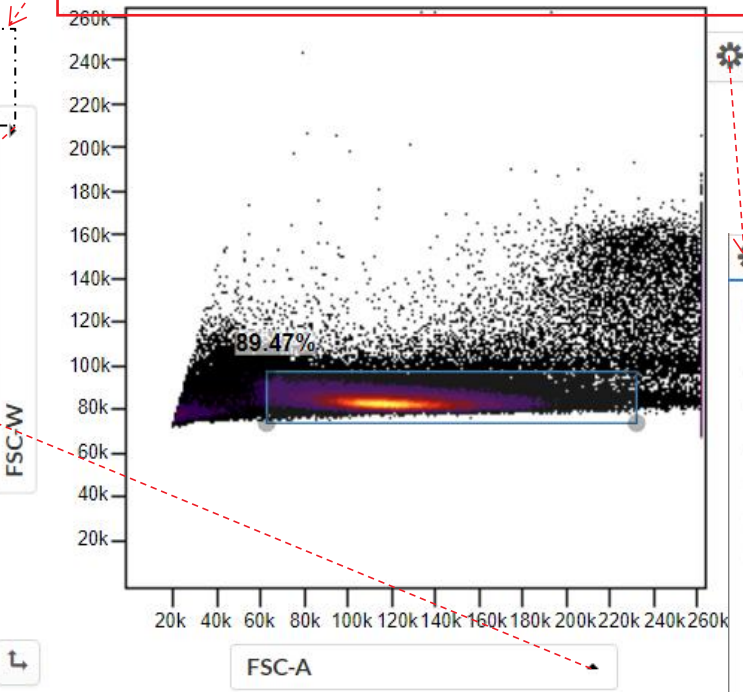
- Gates
- Advanced analyse
- Gating Editor**
- Gating strategy
- Upload gates from Gating-ML
- Download Gating-ML

图设置区

画门工具



Population: Ungated  
 File: IL10 - pbmc\_lrs005\_il10



- Plot type
- Contour - Uncolored
  - Dot - Color By Density
  - Dot - Color By Z axis Channel
  - Dot - Black
  - Contour - Uncolored**
  - Contour - Color By Density
  - Histogram

- Gate label
- Percent
  - Event Count
  - Mean **横坐标mean/median**
  - Median
  - Percent**
  - Gate Name

- Plot colors
- En Fuego
  - En Fuego**
  - Pale Fire
  - Phoenix
  - Chill Out
  - A la Glace
  - Rainbow
  - Spectrum
  - Shadow & Flame
  - Grayscale

**Plot settings**

Plot type: Dot - Color By Density

Gate label: Percent

Plot colors: En Fuego

More

Kernel smoothing: 0

Percent per contour: 10

Outliers start at: 10

选择查看群体或文件

- 此处输入关键词，方便查找
- FSC-A**
  - FSC-W
  - SSC-A
  - pStat3 - AX488 [Ax488-A]
  - CD33 [PE-A]
  - PE-TR [PE-TR-A]
  - CD20-PerCPCy5.5 [PerCP-Cy55]
  - CD3-PC7 [PE-Cy7-A]
  - pP38-AX647 [Ax647-A]
  - Ax700-A
  - Ax750-A
  - CD4 [PerCP-Cy55-A]

# 5. 降维ViSNE分析

The image shows a software interface with a sidebar on the left and a main dialog box on the right. The sidebar has a 'Dimensionality reduction' section highlighted with a red box and a red arrow pointing to the right. Below this section are 'Clustering', 'CITRUS', and 'Automatic gating' sections, each with a 'New analysis' button. The main dialog box is titled 'New dimensionality reduction analysis' and contains the following elements:

- Algorithm:** A list of radio buttons for selecting an algorithm: tSNE-CUDA, UMAP, opt-SNE, and viSNE.
- Analysis name:** A text input field with the placeholder text 'Enter an analysis name'.
- Buttons:** 'Cancel' and 'Create' buttons at the bottom.

tSNE-CUDA analysis setup Status: New Run tSNE-CUDA analysis

Analysis name: min's tSNE-CUDA analysis-241014

Algorithm: tSNE-CUDA

Population	FCS files	Channels																												
Ungated Unselected population: B cell CD3+ PBMC pStat3+ (B cell) pStat3+ (CD3+) Single cell 7 present	<table border="1"> <thead> <tr> <th>Selected files</th> <th>Total events</th> <th>Ungated</th> <th>To sample</th> </tr> </thead> <tbody> <tr><td><input checked="" type="checkbox"/> IL10</td><td>325,374</td><td>325,374</td><td>50,000</td></tr> <tr><td><input checked="" type="checkbox"/> Unstim2</td><td>324,639</td><td>324,639</td><td>50,000</td></tr> <tr><td><input checked="" type="checkbox"/> Unstim1</td><td>326,623</td><td>326,623</td><td>50,000</td></tr> <tr><td><input checked="" type="checkbox"/> LPS</td><td>325,430</td><td>325,430</td><td>50,000</td></tr> <tr><td><input checked="" type="checkbox"/> IL6</td><td>326,838</td><td>326,838</td><td>50,000</td></tr> <tr><td><b>Total:</b></td><td><b>1,628,904</b></td><td><b>1,628,904</b></td><td><b>250,000</b></td></tr> </tbody> </table> 5 of 5 files selected — Sampling 250,000 total events	Selected files	Total events	Ungated	To sample	<input checked="" type="checkbox"/> IL10	325,374	325,374	50,000	<input checked="" type="checkbox"/> Unstim2	324,639	324,639	50,000	<input checked="" type="checkbox"/> Unstim1	326,623	326,623	50,000	<input checked="" type="checkbox"/> LPS	325,430	325,430	50,000	<input checked="" type="checkbox"/> IL6	326,838	326,838	50,000	<b>Total:</b>	<b>1,628,904</b>	<b>1,628,904</b>	<b>250,000</b>	Unselected channels: CD20-PerCPCy5.5 CD3-PC7 CD33 CD4 PE-TR pP38-AX647 pStat3-AX488 Ax700-A Ax750-A FSC-A FSC-W PacOrange-A Qdot525-A Qdot605-A 0 of 18 selected
Selected files	Total events	Ungated	To sample																											
<input checked="" type="checkbox"/> IL10	325,374	325,374	50,000																											
<input checked="" type="checkbox"/> Unstim2	324,639	324,639	50,000																											
<input checked="" type="checkbox"/> Unstim1	326,623	326,623	50,000																											
<input checked="" type="checkbox"/> LPS	325,430	325,430	50,000																											
<input checked="" type="checkbox"/> IL6	326,838	326,838	50,000																											
<b>Total:</b>	<b>1,628,904</b>	<b>1,628,904</b>	<b>250,000</b>																											

**Event sampling**

Equal  
 Proportional  
 Use all events

Desired events per file: 50000 × 5 files = 250,000 desired events  
 Actual events to sample: 50,000 × 5 files = 250,000

**Advanced settings**

Iterations: 750  
 Automatic  
 Perplexity: 30  
 Learning rate: 20833  
 Automatic  
 Early exaggeration: 12

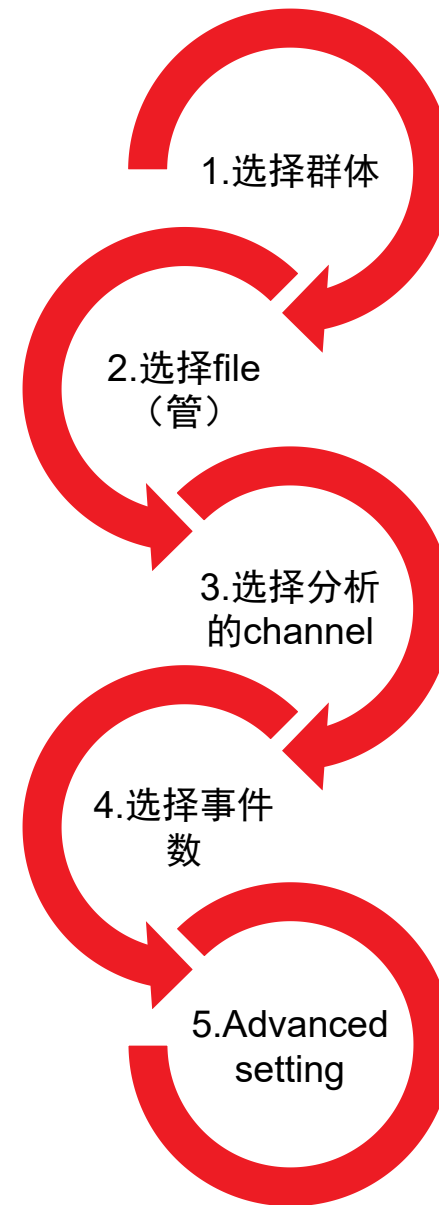
**Transformations**

Data scaling  
 Data will be scaled according to the scale settings of the experiment. Edit scales

Normalize scales

Compensation  
 The experiment compensation will be used: Experiment 16620 Autocomp Edit

# • tSNE-CUDA analysis setup



Equal (均等)  
 Proportional (按比例)  
 Use all events (所有)

Iterations  
 Perplexity  
 Learning rate  
 Early exaggeration

# 6. 分析结束

## 1. 邮件提醒

[Premium China Cytobank] Your tSNE-CUDA analysis is complete



If there are problems with how this message is displayed, click here to view it in a web browser. Some of the content in this message couldn't be downloaded because you're working offline or aren't connected to a network.

Hi min,

The tSNE-CUDA analysis '[min's tSNE-CUDA analysis-241014 \(copy\)](#)' for experiment [PBMC Experiment \(Fluorescence\)-test20220505 \(Clone\)](#) is now complete.

[View results](#)

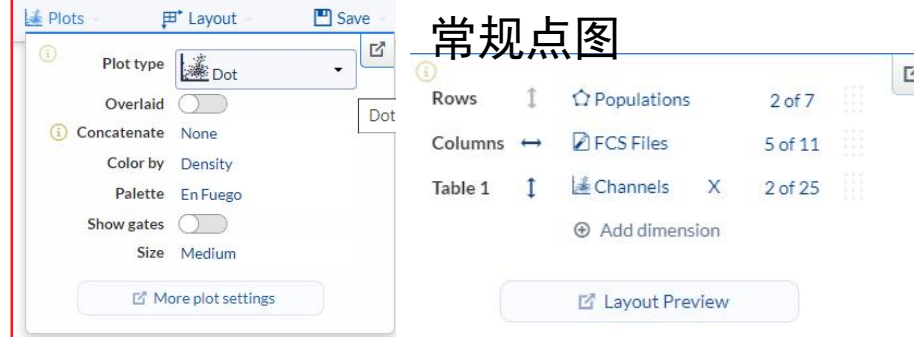
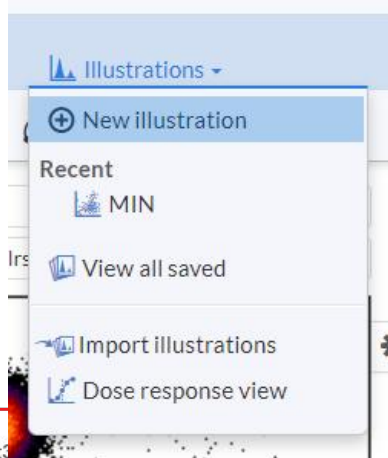
- The Cytobank Team

## 2. 软件界面会出结果

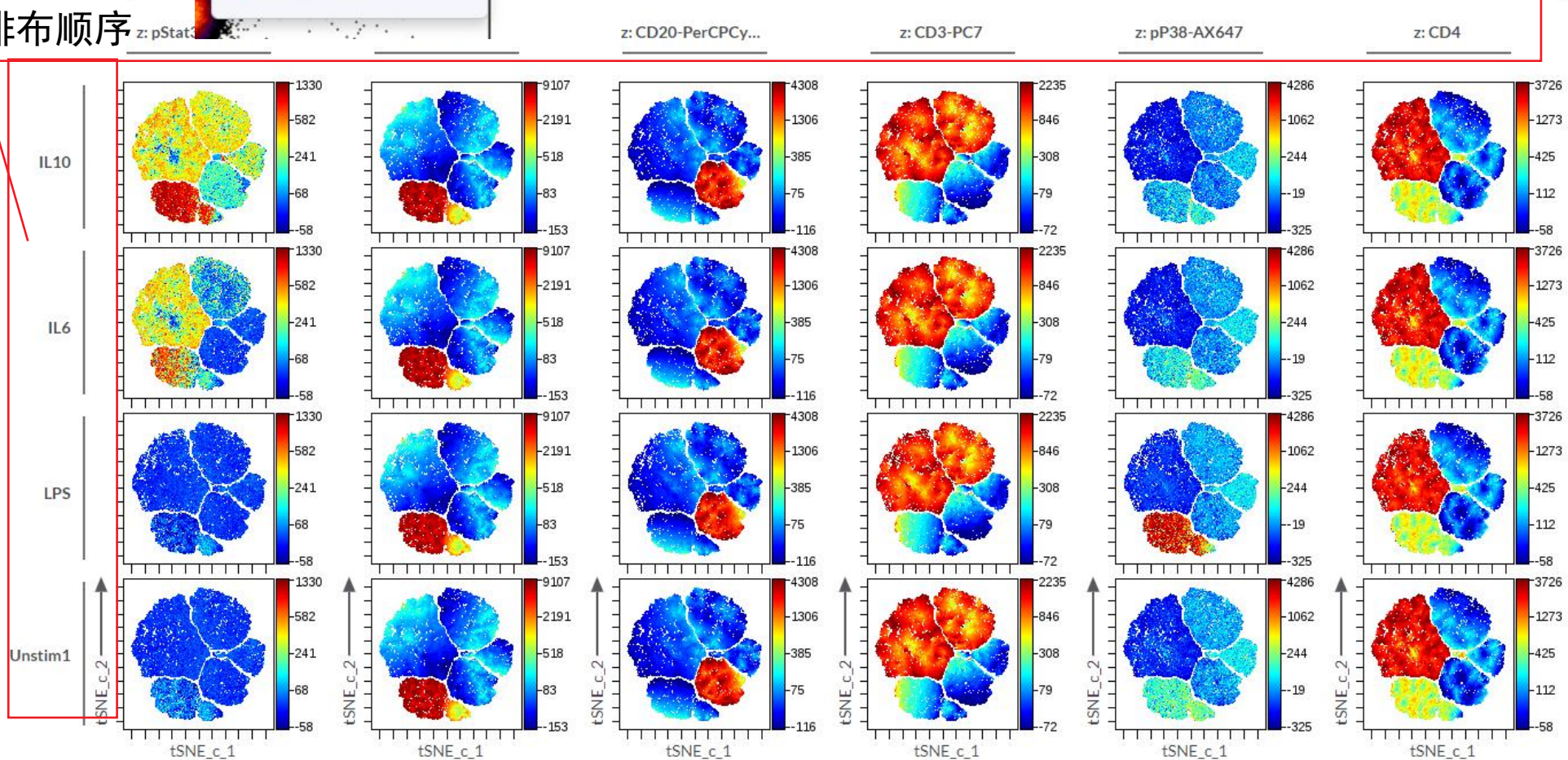
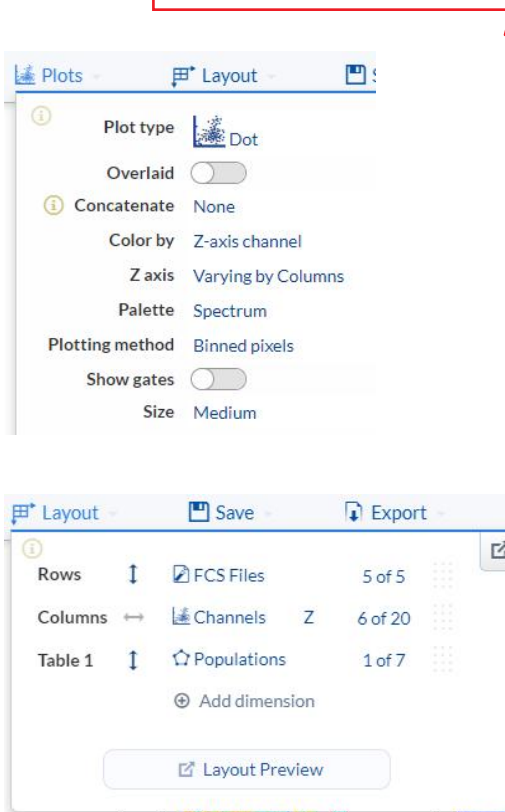
查看

The screenshot shows the software interface for PBMC Experiment (Fluorescence)-test20220505 (Clone). The main panel displays the 'min's tSNE-CUDA analysis' results, including a tSNE plot and analysis run info (Runtime: 2.4 minutes total). A 'Compare dimensionality reduction analysis results' panel is open on the right, showing a list of analyses to compare. A 'View results' button is visible in the top right corner of the main panel.

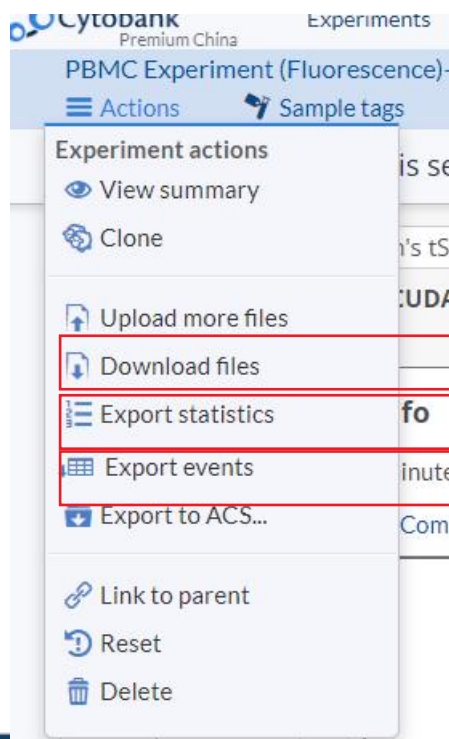
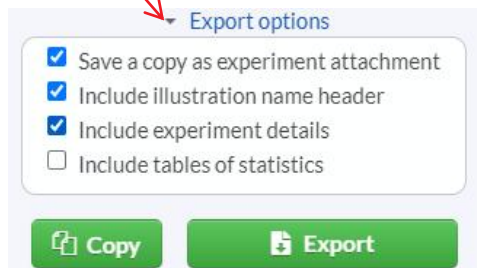
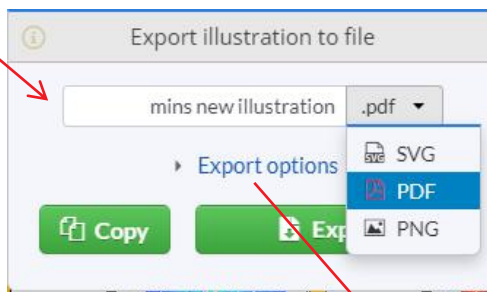
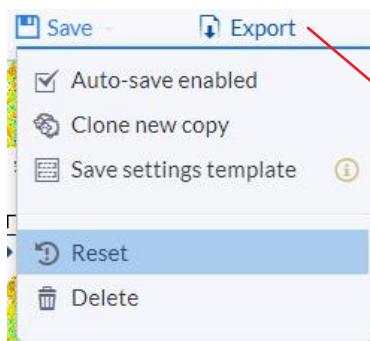
# 7. 结果展示



拖动此处可以改排布顺序



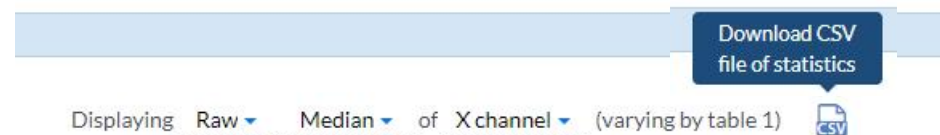
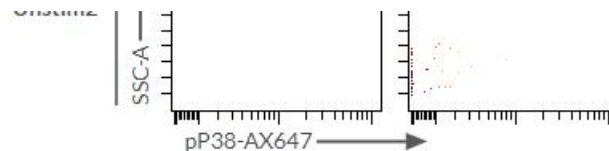
# 8. 数据保存及导出



可下载.FCS文件

可导出每个事件（event）的信息（光强度）

可导出门控的信息（百分比、MFI, keyword等）



**pStat3 -AX488**

	pStat3+ (B cell)	pStat3+ (CD3+)
IL10	449.735	423.774
IL6	441.028	423.207
LPS	476.51	313.274
Unstim1	485.396	213.673
Unstim2	2665.882	224.553

**pP38-AX647**

	pStat3+ (B cell)	pStat3+ (CD3+)
IL10	-35.681	-116.637
IL6	-20.708	-127.047
LPS	224.919	-83.813
Unstim1	1114.999	63.116
Unstim2	8061.213	-53.486



# 哪里使用Cytobank?

哪里使用  
Cytobank?

是否有教程?

能否中文教学?

还有问题怎么  
办?



Cytobank Premium China

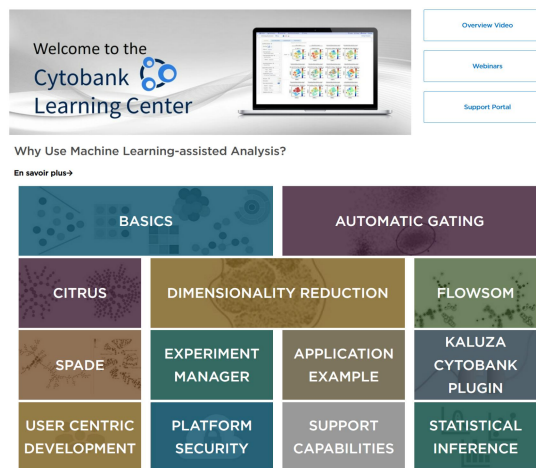
Username or Email

Password

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Forgot password  
Use OpenID

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Why Use Machine Learning-assisted Analysis?

En savoir plus →

BASICS	AUTOMATIC GATING		
CITRUS	DIMENSIONALITY REDUCTION	FLOWSOM	
SPADE	EXPERIMENT MANAGER	APPLICATION EXAMPLE	KALUZA CYTObANK PLUGIN
USER CENTRIC DEVELOPMENT	PLATFORM SECURITY	SUPPORT CAPABILITIES	STATISTICAL INFERENCE



2022年1月17日

Cytobank软件操作-基础篇更新+1  
本期给大家介绍下Cytobank软件9.1的更新, 即染色指数曲线, 以及统计图和统计分析的操作视频

2022年1月4日

Cytobank软件操作-降维算法工具合集  
Cytobank中的降维算法, 包括tsne-CUDA, UMAP, opt-SNE 以及VISNE四种算法, 本文介绍四种算法的操作

2021年12月27日

Cytobank软件操作-基础篇  
Cytobank软件的基础操作部分, 视频演示



Submit Support Request

网址: <https://www.cytobank.cn/>

网址: <https://www.beckman.fr/flow-cytometry/software/cytobank-premium/learning-center>

微信公众号: CR7的流式技术分享

# 谢谢

  
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