

1.- Presentación del proyecto

Nombre del proyecto: **Recaída 0: Matemáticas contra la leucemia infantil**

Hospital: Hospital de Jerez, Universidad de Cádiz

Investigador/a Principal: Prof. María Rosa Durán

Coordinador/a: Dra. Cristina Blázquez Goñi

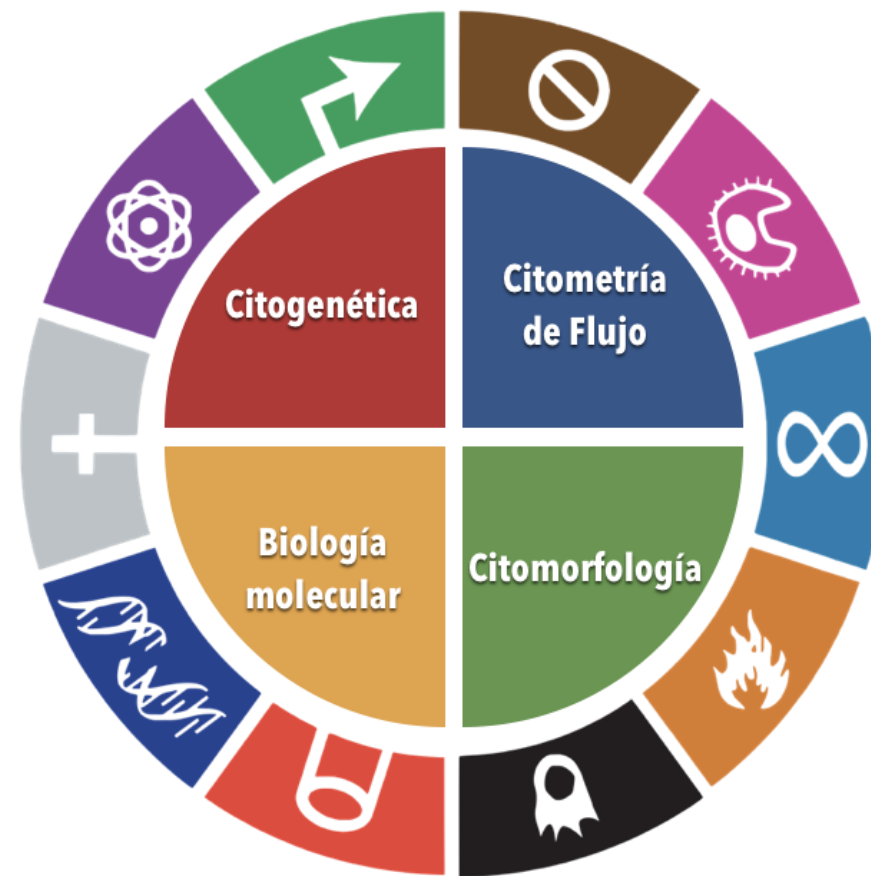
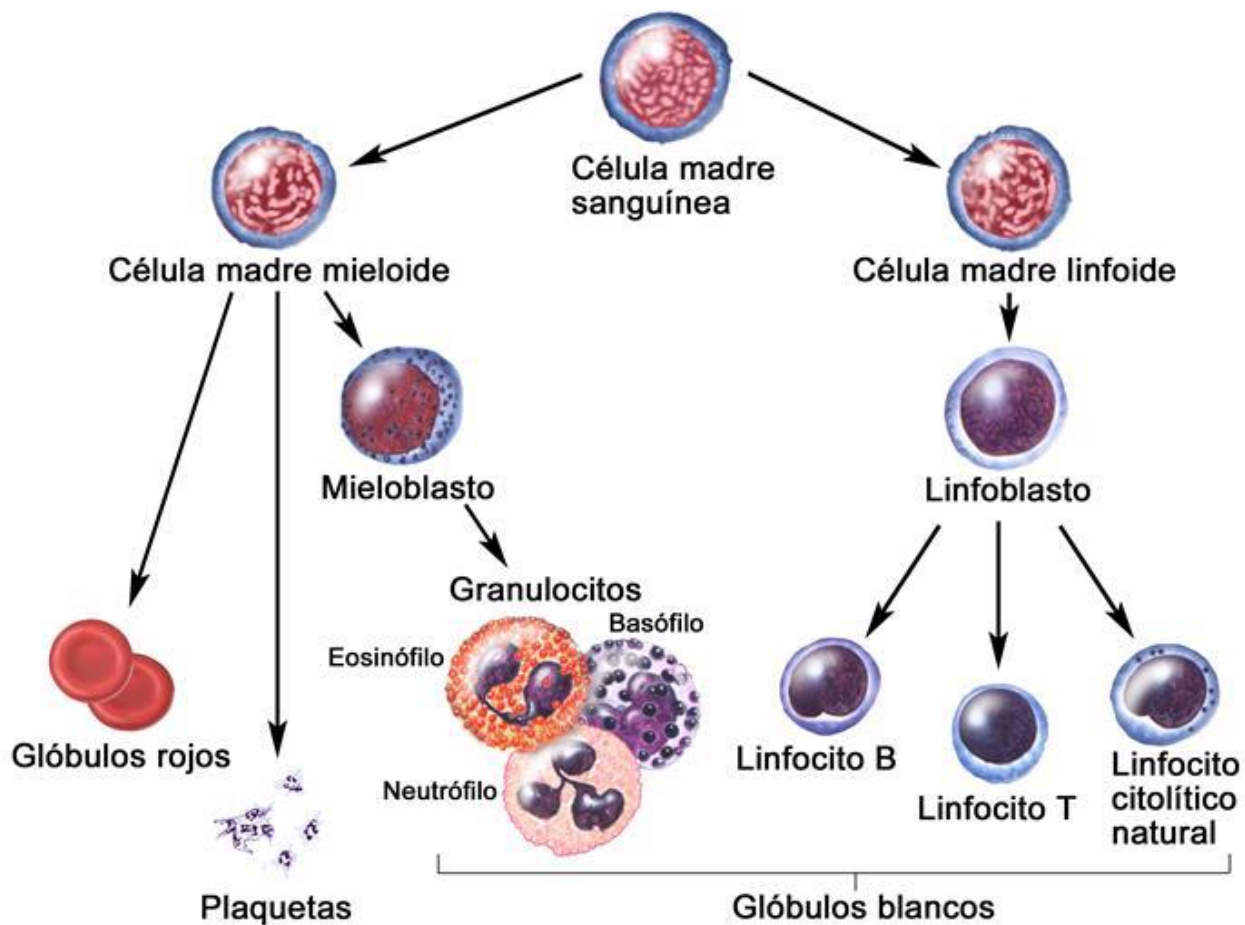
Personal adscrito: Salvador Chulián García

Personal adscrito: Juan Francisco Rodríguez

Personal adscrito: Álvaro Martínez

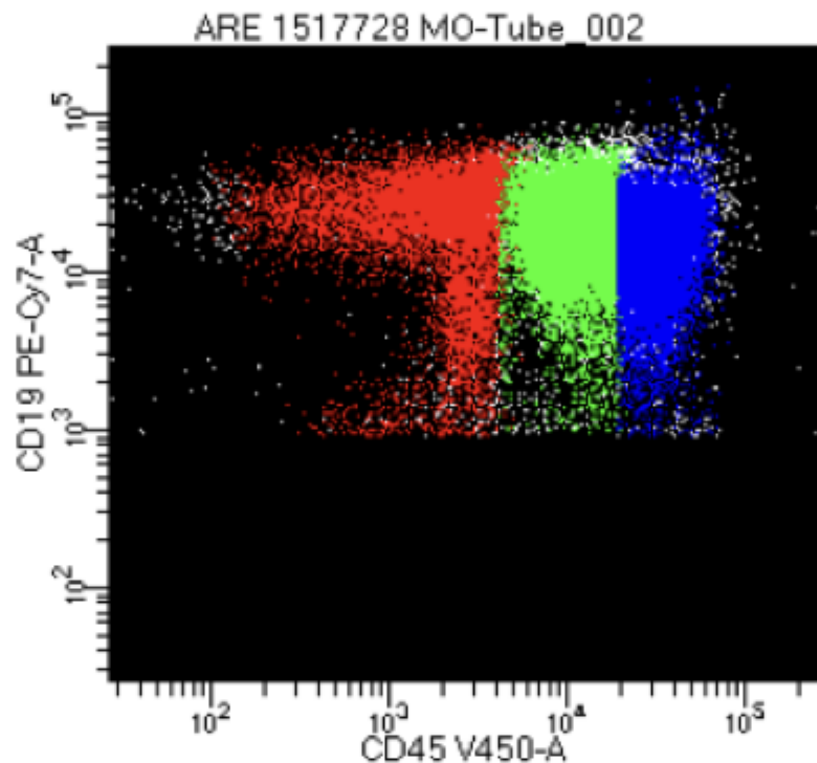


2.- Necesidades previas del proyecto

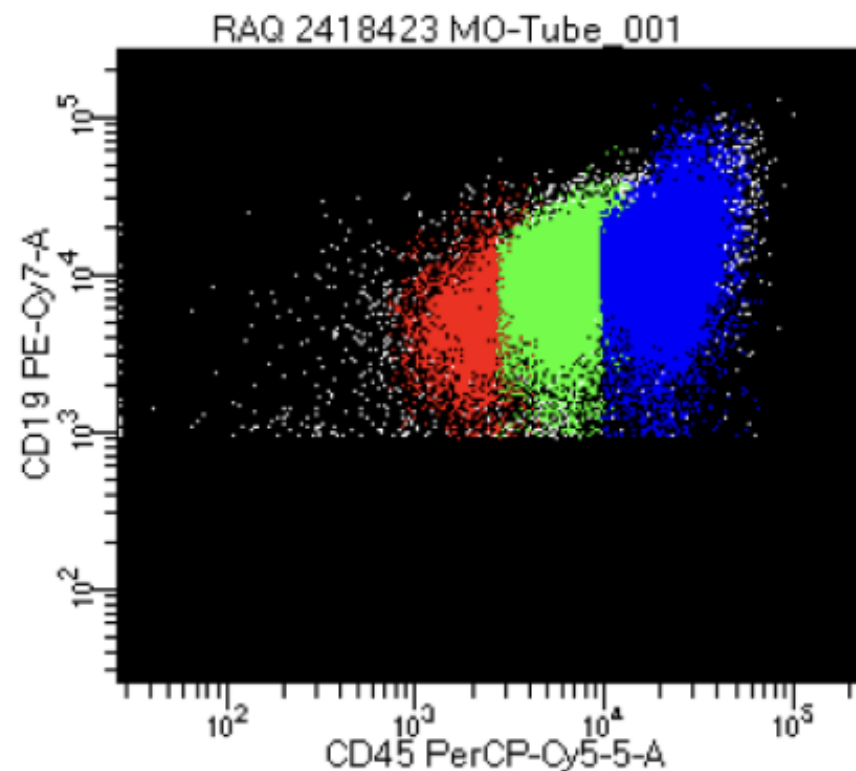


2.- Necesidades previas del proyecto

Pathologic BM



Normal BM



3.- ¿En qué os ayuda APU?



+



=



INVESTIGAC
IÓN

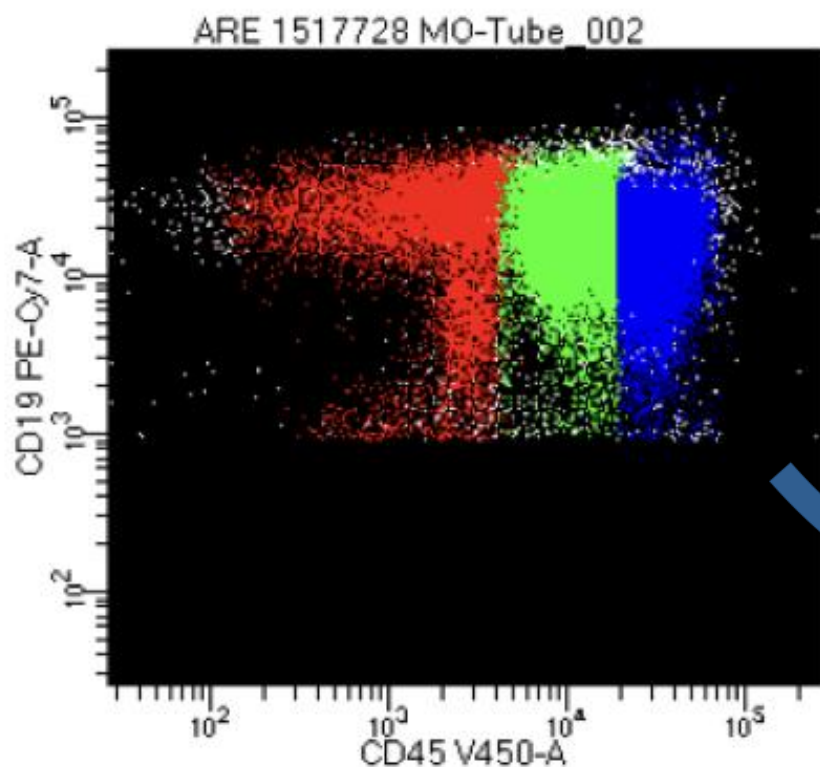


+



4.- Logros

Pathologic BM



Matriz de Datos

Parameter	1	2	3	4	5	6	7	8	9
Name	FSC-A	FSC-H	SSC-A	FLTC-A	PE-A	PerCP-Cy5-5-A	PE-Cy7-A	APC-A	APC-H7-A
String				CD20	CD10	CD45	CD19	CD34	
Range	262144	262144	262144	262144	262144	262144	262144	262144	262144
Bits	32	32	32	32	32	32	32	32	32
1	73289,81	66616,00	15845,38	110,96	59,86	39487,16	2772,54	2202,48	645,12
2	52434,44	46499,00	6588,98	93,44	16,06	84,68	-5,84	-64,26	79,38
3	54941,26	47385,00	7900,06	4325,98	2957,96	7238,68	13202,78	713,16	1207,08
4	105408,35	82997,00	42796,98	191,26	125,56	35009,34	3168,20	3468,78	718,20
5	159172,13	124336,00	71897,70	110,96	14,60	10510,54	962,14	706,86	-80,64
6	52566,57	47163,00	7526,30	35,04	56,94	125,56	83,22	22,68	-183,96
7	144442,19	118302,00	99112,10	86,14	1766,60	6111,56	973,82	700,56	273,42
8	55758,13	49806,00	7135,02	-17,52	49,64	89,06	48,18	-51,66	-107,10
9	94992,71	79271,00	17664,54	52,56	0,00	49891,12	4855,96	2406,60	740,88
10	146782,56	122120,00	80428,48	115,34	544,58	5637,06	623,42	573,30	98,28
11	157746,44	127660,00	95647,52	219,00	608,82	5799,12	351,86	813,96	406,98
12	94037,88	77662,00	15728,58	78,84	4,38	97,82	-18,98	209,16	-163,80
13	145449,58	118816,00	112695,95	197,10	604,44	4197,50	217,54	824,04	139,86
14	172240,58	129169,00	142755,89	220,46	1262,90	5577,20	638,02	647,64	161,28
15	245353,00	165012,00	87821,92	175,20	39,42	4863,26	572,32	646,38	216,72
16	177277,58	125988,00	262143,00	1249,76	819,06	20199,10	2260,08	2012,22	350,28

1.000.000 células **por paciente**

4.- Logros

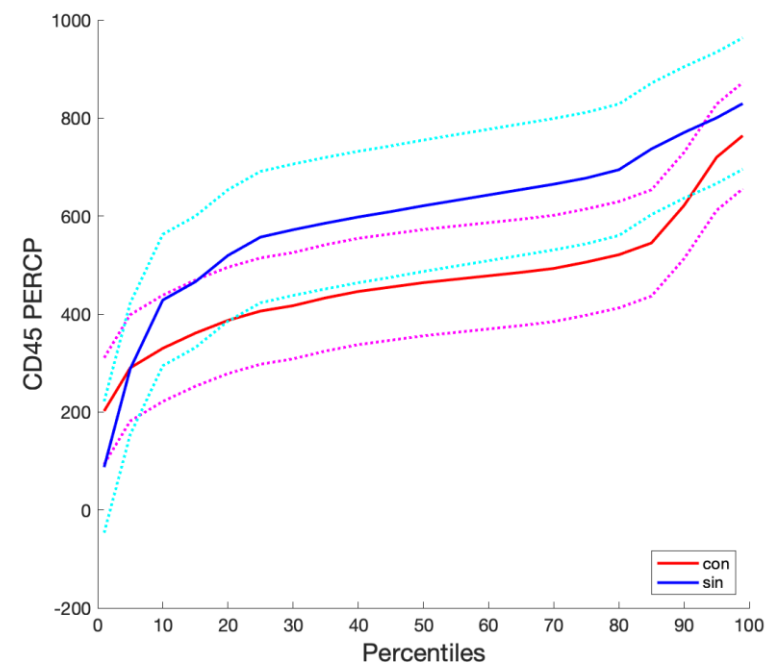
	MeanCon	MedianCon	StdCon	IQRCon	CON_SIN	MeanSin	MedianSin	StdSin	IQRSin
CD10	504.23	584	234.32	478.25		788.68	464	1476.7	614.99
CD19	447.47	498	132.81	128.5		1546.9	517	4275.2	153
CD19 PERCP	504.7	557	116.67	118.88		513.48	498	199.32	153
CD20	241.8	242	46.17	201.25		229	193.5	99.747	173
CD34	487.16	406	170.65	321.12		535.71	552	272.81	345.75
CD34 APC	345.14	394	88.793	192.12		231.73	253	112.78	194.5
CD38	279.6	272	136.73	125.75		981.22	480	1536.7	181.25
CD45	556.62	643.5	191.54	92.125		812.8	565	920.1	264.5
CD45 PERCP	426.7	464	141.9	108.5		584.32	621	164.56	134.12
FL1-A	12.163	0	57.066	1		2.5789	0	5.6725	1
FL2-A	146.86	0	150.61	15.75		163.83	0	328.84	22.875
FL4-H	35.875	16.5	35.609	83.75		37.932	10.5	48.591	85.625
FSC-H	365.22	321.5	197.9	181.5		5837.7	302	18442	188.62
SSC-H	132.95	72.5	127.17	47.625		66.629	61	16.91	52.625
TDT	358	354.5	97.13	112.25		295.36	288.5	117.24	171.12

Algoritmo de separación

$$FR_j = \frac{(\mu_{j1} - \mu_{j2})^2}{\sigma_{j1}^2 + \sigma_{j2}^2}$$


Sin recaída


Con recaída



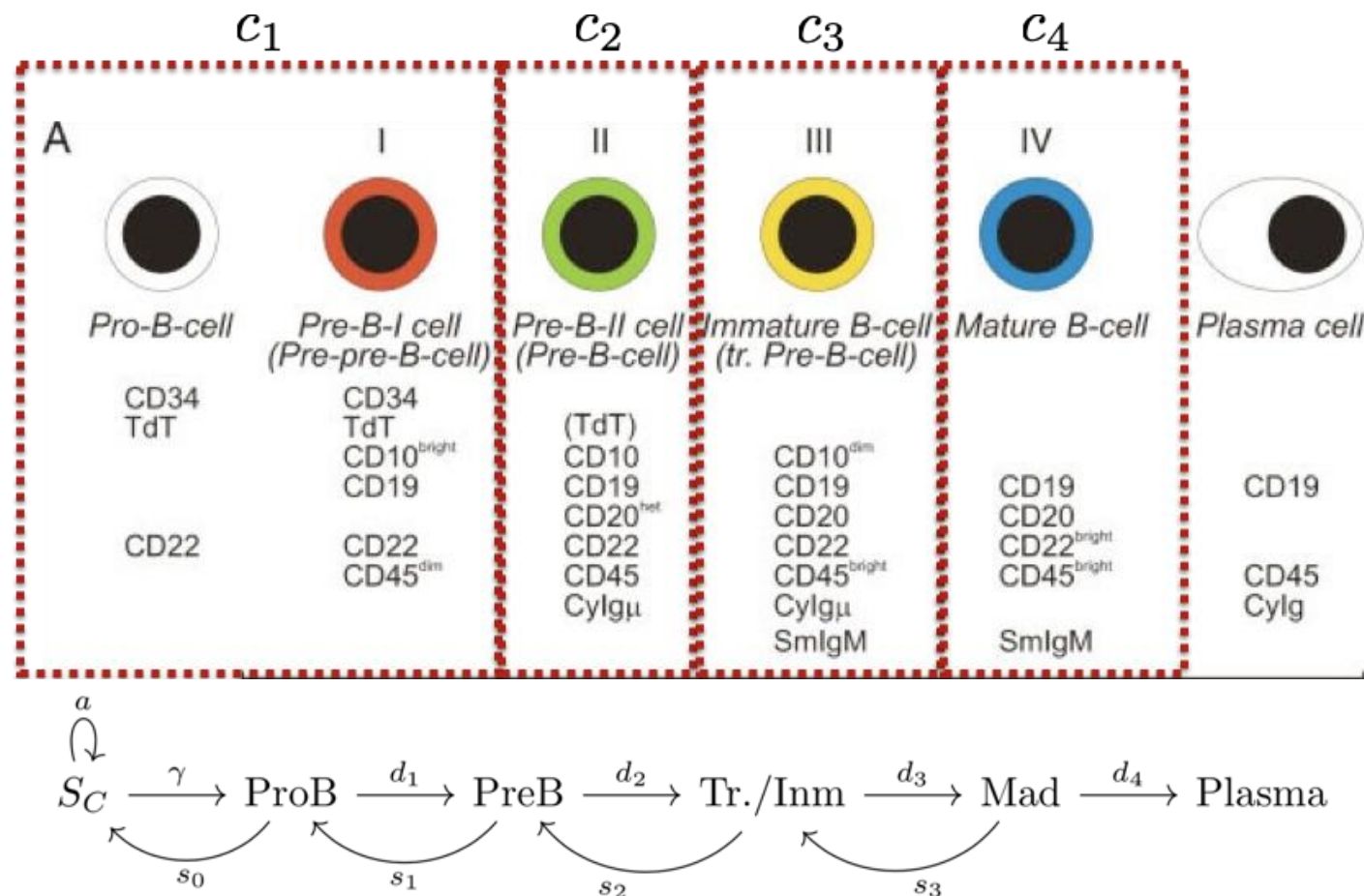
5.- Visión de futuro

Objetivo 1: Modelos Matemáticos

$$\frac{dS_C}{dt} = \frac{S_C}{\tau} \left(1 - \frac{S_C + C_4}{K} \right) - \gamma S_C,$$

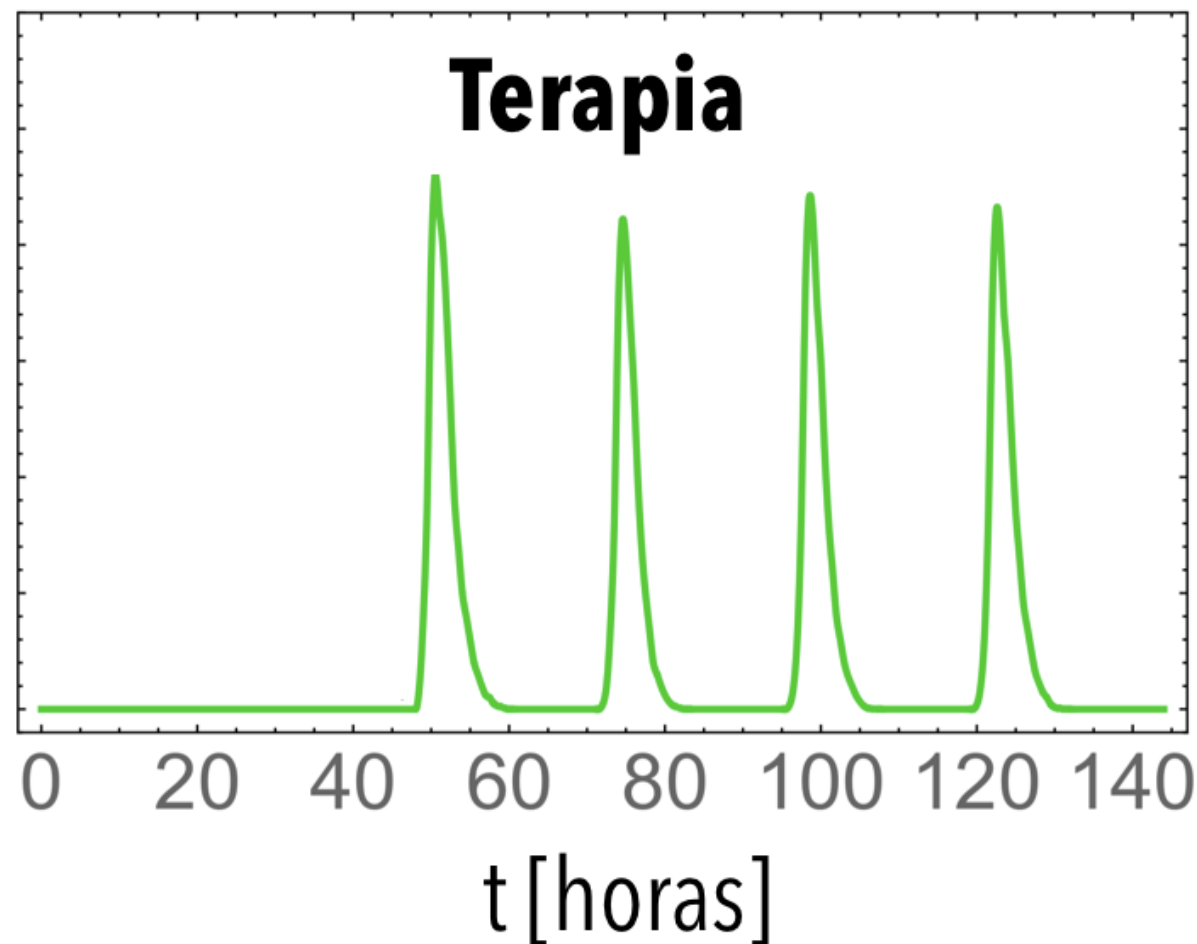
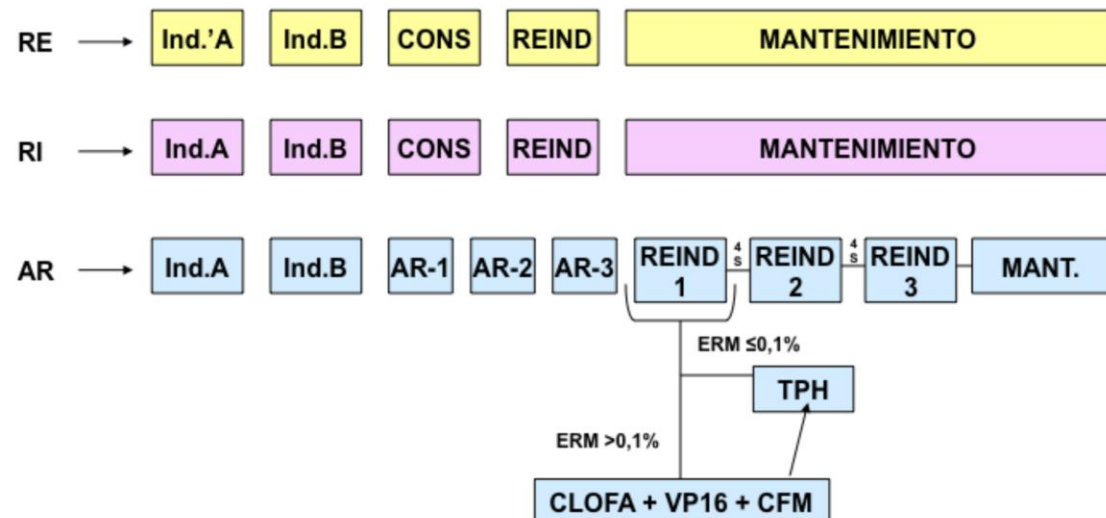
$$\frac{dC_1}{dt} = \gamma S_C - d_1 C_1,$$

$$\frac{dC_i}{dt} = d_{i-1} C_{i-1} - d_i C_i, \quad i = 2, \dots, 4$$



5.- Visión de futuro

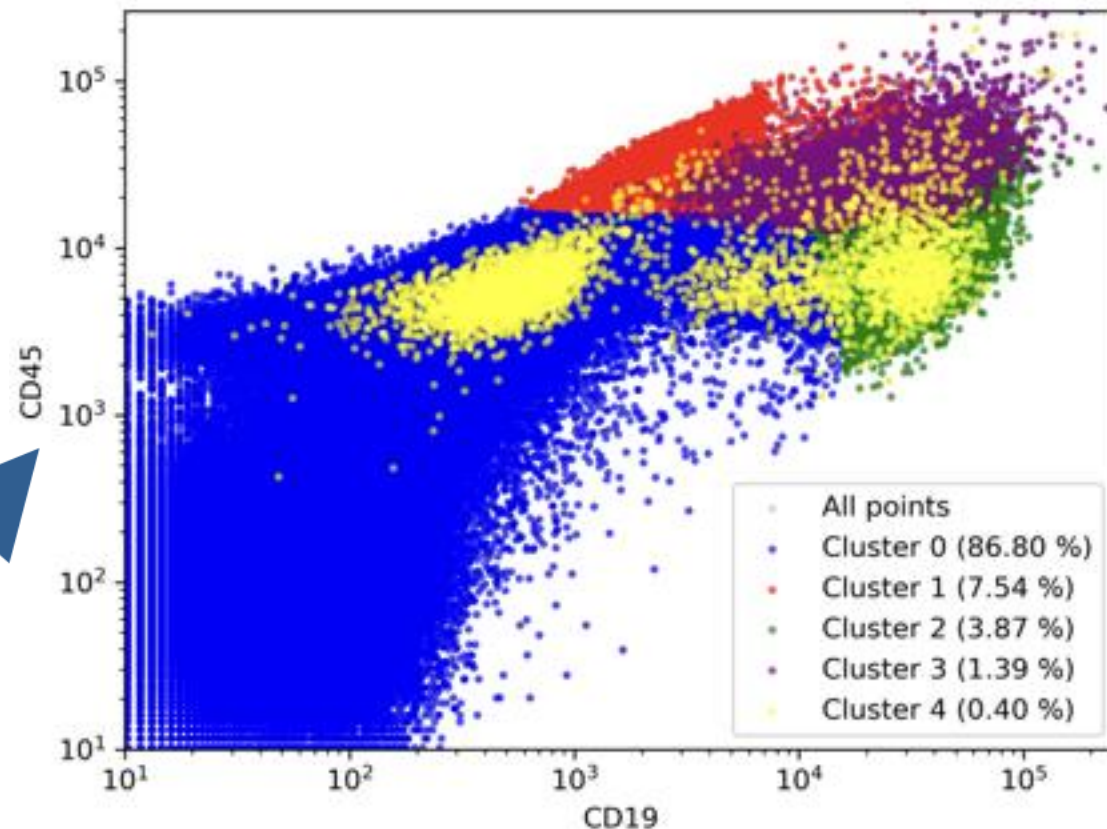
Objetivo 2: Optimización de tratamiento



5.- Visión de futuro

Objetivo 3: Detección de biomarcadores

1	13233,81	15671,00	15743,78	1116,95	58,84	33487,78	2772,54	2202,48	645,12
2	12134,47	46491,00	6138,50	937,41	16,00	94,58	-5,84	-64,26	79,38
3	54941,26	47385,00	7900,06	4325,98	2957,96	7238,68	13202,78	713,16	1207,08
4	105408,35	82997,00	42796,98	191,26	125,56	35009,34	3168,20	3468,78	718,20
5	159172,13	124336,00	71897,70	110,96	14,60	10510,54	962,14	706,86	-80,64
6	52566,57	47163,00	7526,30	35,04	56,94	125,56	83,22	22,68	-183,96
7	144442,19	118302,00	99112,10	86,14	1766,60	6111,56	973,82	700,56	273,42
8	55758,13	49806,00	7135,02	-17,52	49,64	89,06	48,18	-51,66	-10,00
9	94992,71	79271,00	17664,54	52,56	0,00	49891,12	4855,96	2406,60	740,88
10	146782,56	122120,00	80428,48	115,34	544,58	5637,06	623,42	573,30	98,28
11	157746,44	127660,00	95647,52	219,00	608,82	5799,12	351,86	813,96	406,98
12	94037,88	77662,00	15728,58	78,84	4,38	97,82	-18,98	209,16	-163,80
13	145449,58	118816,00	112695,95	197,10	604,44	4197,50	217,54	824,04	139,86
14	172240,58	129169,00	142755,89	220,46	1262,90	5577,20	638,02	647,64	161,28
15	245353,00	165012,00	87821,92	175,20	39,42	4863,26	572,32	646,38	216,72
16	177277,58	125988,00	262143,00	1249,76	819,06	20199,10	2260,08	2012,22	350,28





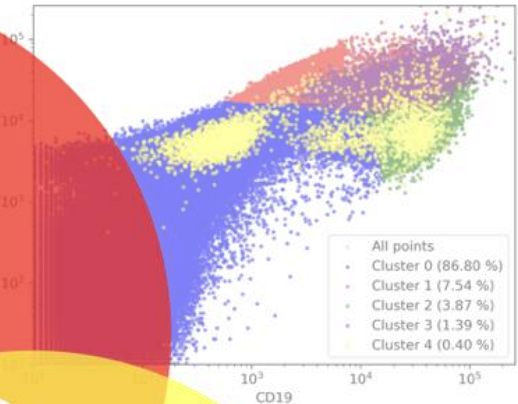
6.- Conclusiones

Técnicas de Clustering

LLA

Programación matemática

Modelos matemáticos



$$\frac{d}{dt}c_1(t) = (2\hat{a}_c s(t) - 1) p_c c_1(t)$$

$$\frac{d}{dt}c_2(t) = 2(1 - \hat{a}_{cs}(t))$$

$$\frac{d}{dt}l_1^1(t) = (2\hat{a}_1^1s(t) - 1)p_1^1l_1^1(t)$$

$$\frac{d}{dt}l_2^1(t) = 2(1 - \hat{a}_l^1 s(t))p_l^1 l_1^1(t)$$

• • •

$$\frac{d}{dt}l_1^n(t) = (2\hat{a}_l^n s(t) - 1) p_l^n l_1^n(t)$$

$$\frac{d}{dt} l_2^n(t) = 2(1 - \hat{a}_l^n s(t)) p_l^n l_1^n(t)$$

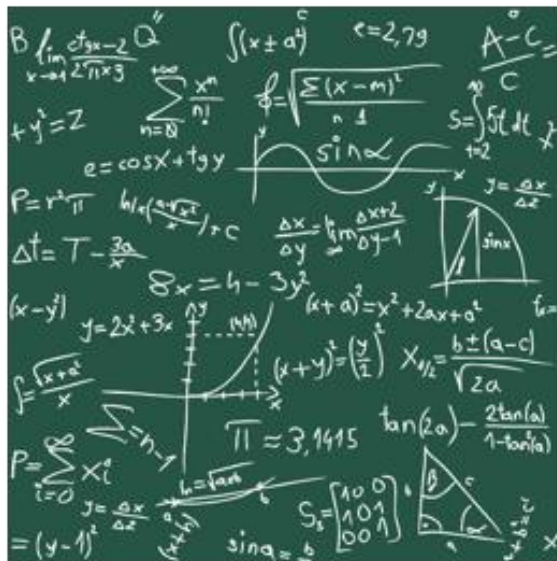
$$s(t) = \frac{1}{1 + kc_2(t) + k \sum_{i=1}^n l_2^i}$$

```
Python Shell 4.3.1  
In [0]: conda activate base (default, Jan 16 2018, 12:04:33)  
Copyright (c) 2017 Anaconda, Inc. (default, Jan 16 2018, 12:04:33)  
Python 6.2.1 -- An enhanced Interactive Python. Type '?' for help.  
  
In [1]: import FlowCytometryTools #Fluorite de analisis  
import numpy as np  
import matplotlib.pyplot as plt  
from FlowCytometryTools import load_data_dir, test_data_file  
datadir = '/Users/Salvi/Flow'  
datafile = '/Users/Salvi/Flow/F1.fcs'  
sample = 'sample.png'  
parameter_with_kmeans = 'parameter_with_kmeans.png'  
measurement = 'measurement'  
# lecture de Datos  
sample = FCMMeasurement('Test Sample', datafile=datafile)  
# Datos de la muestra  
data=sample.data  
# Archivo de información del citómetro  
archive-sample.meta.items() # 'sample.meta.keys()' da los  
rombres y 'sample.meta.values()' los valores de archive
```

6.- Conclusiones



Medicina



Matemáticas



RECAÍDA Ø
MATEMÁTICAS CONTRA LA LEUCEMIA INFANTIL