

flowDensity

Automated alternative to the current manual gating practice

Jafar Taghiyar, Mehrnoush Malek

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1 Licensing

Under the Artistic License, you are free to use and redistribute this software.

2 Introduction

Expert humans use flowJo software to manually gate FCS data files either individually or by setting a static gate to apply on all the files. The former is very tedious specially when there is a large number of files and the cost for the latter is to ignore characteristics of individual samples.

flowDensity is a supervised clustering algorithm based on density estimation techniques designed specifically to overcome these problems. It automates the current practice of manual 2D gating and adjusts the gates for each FCS data file individually.

Although automated flow cytometry methods developed to date have focused on fully automated analysis which is especially suited for discovery, they seldom match manual results where this is desirable (e.g., for diagnosis). In contrast, flowDensity aims to gate predefined cell populations of interest where the gating strategy, *i.e.*, sequence of gates, is

known. This helps it take advantage of expert knowledge and as a result it often matches manual results very well. In addition, since `flowDensity` uses only two dimensions at a time, it is very fast and requires much less computational power.

3 How to use `flowDensity`?

In order to use `flowDensity`, the gating strategy is required. A gating strategy here means the sequence of 2D gates needed to apply one at a time on a FCS file to eventually extract the cell subset of interest.

A 2D gate consists of two channels (dimensions) or equivalently a phenotype with two markers. In addition, the corresponding expression level for each channel is given. For example, phenotype “CD19+CD20-” has markers CD19 and CD20 with expression values “positive” and “negative”, respectively.

To use `flowDensity`, this 2D gate is input to the function `flowDensity(.)`. The channels in the gate are used for the `channels` argument and the expression values are used for the `position` argument of the function.

Let assume for example that CD19 is on channel “PerCP-Cy5-5-A” and CD20 is on channel “APC-H7-A”. Therefore, the corresponding input arguments are: `channels=c(PerCP-Cy5-5-A, APC-H7-A)` and `position=c(TRUE,FALSE)`.

In general, `channels` argument can be set using either names of the channels or their corresponding indices (column numbers in the FCS file) and `position` argument could be one the four logical pairs `(TRUE,FALSE)`, `(FALSE,TRUE)`, `(FALSE,FALSE)` and `(TRUE,TRUE)`. If the user needs to set the thresholds for only one of the channels, then position for the other channel must be set to `NA`.

The expression value “high” can also be identified by `flowDensity` but some specific (optional) arguments must be set accordingly. More on this later.

In addition to the above arguments, either `cell.population` or `flow.frame` argument is required where the former is an object of class “CellPopulation” loaded from `flowDensity` namespace and the latter is a “flowFrame” object loaded from `flowCore` namespace.

4 Examples

In this section we present several examples to elaborate how to use the `flowDensity(.)` function.

4.1 Extracting lymphocytes/Singlets/Bcell

This example shows how to use `flowDensity` to extract B cells by using the gating strategy lymphocytes/viability-CD3-/CD19+CD20+ or equivalently lymphocytes/singlets/Bcell. The Figure 1 shows this gating.

```
> library(flowCore)
> library(flowDensity)
```

```
> library(GEOmap)
> data_dir <- system.file("extdata", package = "flowDensity")
> load(list.files(pattern = 'sampleFCS_1', data_dir, full = TRUE))
> f
```

```
flowFrame object ''
with 23000 cells and 13 observables:
```

	name	desc	range	minRange	maxRange
\$P1	FSC-A	<NA>	262144	-111.00000000	262143.0
\$P2	FSC-H	<NA>	262144	0.00000000	262143.0
\$P3	SSC-A	<NA>	262144	-111.00000000	262143.0
\$P4	SSC-H	<NA>	262144	0.00000000	262143.0
\$P5	APC-A	CD38	262144	-0.04496801	4.5
\$P6	APC-H7-A	CD20	262144	0.57425502	4.5
\$P7	FITC-A	<NA>	262144	0.17100441	4.5
\$P8	PerCP-Cy5-5-A	CD19	262144	-0.06225046	4.5
\$P9	V450-A	CD3	262144	0.15907409	4.5
\$P10	V500-A	IgD	262144	0.22768370	4.5
\$P11	PE-A	CD24	262144	-0.05101856	4.5
\$P12	PE-Cy7-A	CD27	262144	-0.23198773	4.5
\$P13	Time	<NA>	262144	0.00000000	262143.0

211 keywords are stored in the 'description' slot

```
> lymph <- flowDensity(obj=f, channels=c('FSC-A', 'SSC-A'),
+                       position=c(TRUE, FALSE), upper= c(NA, TRUE), debris.gate=c(TRUE, FALSE))
> sgl1 <- flowDensity(obj=lymph, singlet.gate=TRUE)
> bcell <- flowDensity(obj=sgl1, channels=c(9, 3),
+                       position=c(FALSE, NA))

> plot(getflowFrame(sgl1), bcell)
```

4.2 Gating rare cell populations

To emulate the practice of expert humans for identification of high, flowDensity provides two parameters that help fine tune the algorithm for identification of small cell populations. These parameters are set by providing following arguments in the *flowDensity(.)* function:

- *upper*: This argument is used to identify small cell subsets present at the tail or head of the density distribution curve where they are typically camouflaged due to the presence of adjacent large cell populations. If it is set to “TRUE” (“FALSE”), flowDensity checks the tail (head) of the density distribution. If it is required to use *upper* for one channel and not the other, the “NA” value should be used; for example *upper=c(FALSE,NA)*.

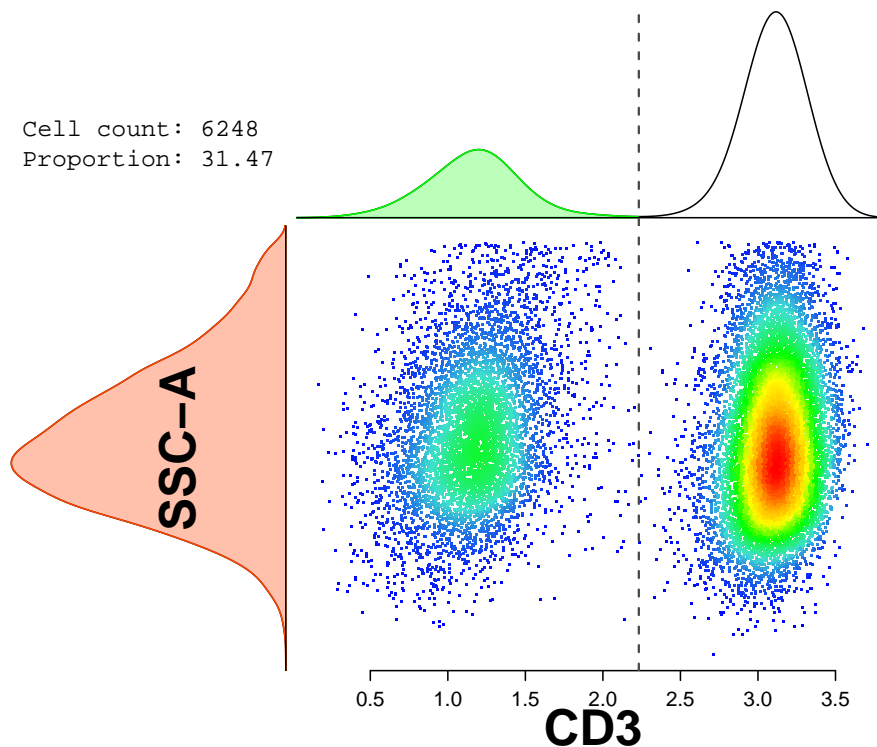


Figure 1: B cells from gating strategy lymphocytes/singlets/CD3-

- *percentile*: This argument gets a value of $[0,1)$ and provides the ability to set a threshold based on the percentile of the density distribution. To force using this threshold, argument *use.percentile* should be set to “TRUE”, otherwise the percentile threshold will be automatically used when appropriate.

For example, we can use `flowDensity` to extract “plasmablasts” cell population as follows:

```
> CD19pCD20n <- flowDensity(obj=bcell, channels=c(8, 6),
+                           position=c(T,F))
> plasmablasts <- flowDensity(obj=CD19pCD20n, channels=c(5, 12),
+                             position=c(T, T))
> plotDens(getflowFrame(CD19pCD20n), plasmablasts@channels, pch=19)
> points(plasmablasts@filter, type='l', col=2, lwd=2)
```

To overcome this problem, `flowDensity` tracks the slope of the curve of the density distribution by comparing the slope of a window of points on the curve with specific

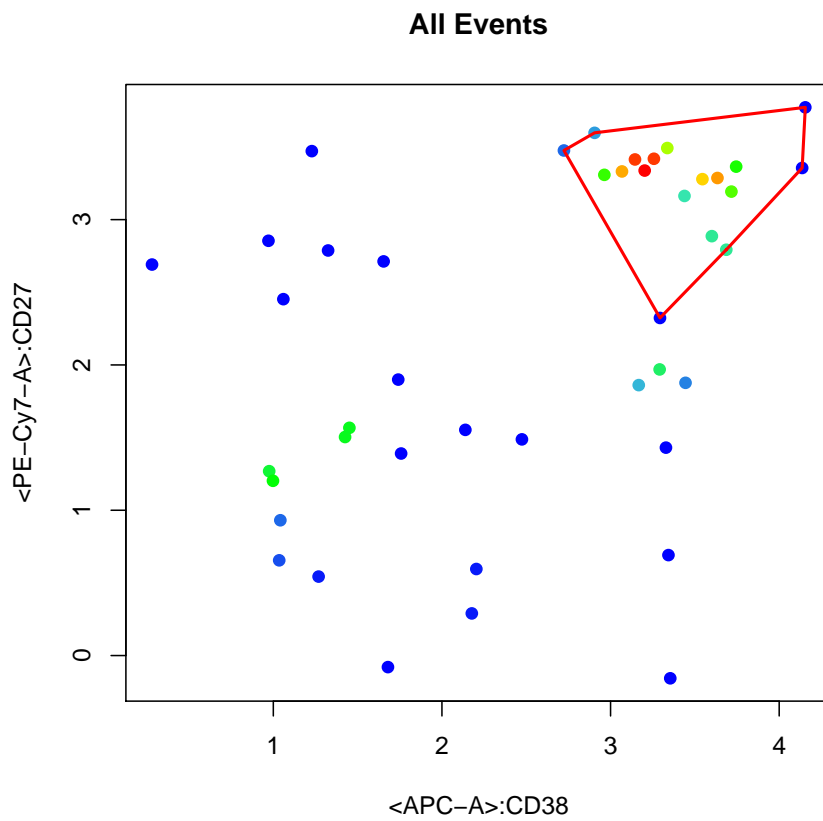


Figure 2: plasmablasts cell population, a small subset of B cells

length to examine if it drops below a threshold relative to the adjacent windows. This way, once the large cell subset ends and the rare one starts the dramatic change in the slope can be detected by `flowDensity` and the threshold is set. We call this technique as *slopeTrack*

In seldom cases the slope varies slowly and smoothly so that no relatively huge change is sensed by this technique. If such, the 90th percentile is used as a gate. A rule of thumb is that if the spread of the density distribution is mostly around the mean, *i.e.*, the standard deviation is small relative to the mean, then most likely the `trackSlope` returns better results than 90th. If neither of these techniques are bale to set a proper threshold, the peak value plus a multiplier of the standard deviation is chosen as the threshold.

`flowDensity` is able to decide on which of these methods to use. However, the user can also modify this decision by setting certain parameters specifically for tricky cell populations.

In Figure 2, `flowDensity` has been used to gate “Plasma blasts” cell population which is a rare cell subset of CD3+CD19+CD20- cell population. On the *x*-axis for the marker CD38 the `slopeTrack` technique is used whereas on the *y*-axis for the markerCD27 HLA-DR the peak plus 1.5×standard deviation gives a proper gate. ¹

To plot the gating results, there is custom `plot(.)` method where its arguments are a `flowFrame` object and an object of class `CellPopulation`. For example:

where `getflowFrame(.)` function is an accessor to get the `flowFrame` of a `CellPopulation` object.

4.3 Multiple calls for a single cell population identification

```
> f <- nmRemove(f, c("FSC-A", "SSC-A"))
> #plotDens(f, c("FSC-A", "SSC-A"), devn=F)
> #plot(f, lymph)
```

`flowDensity` can be used recursively to gate a cell population of interest.

In Figure 3, `flowDensity` has been used to gate “lymphocytes” from CD45 vs SSC. In order to gate lymphocytes more accurate and tighter, `flowDensity` can be called several times. First time it finds the thresholds for both channels, then returns SSC-CD45+ as an input for the second call. In the last call thresholds of CD45 from the first call and thresholds of SSC from the second call is given to `flowDensity` to draw ellipse around the lymphocyte population. Figure 4 illustrates the last step. In some cases CD45 has only one peak so the percentile of 0.25 is given to `flowDensity` to detect the right population. For SSC 0.85 would give the optimum threshold.

```
> load(list.files(pattern = 'sampleFCS_2', data_dir, full = TRUE))
> f2
```

¹The multiplier 1.5 is the default value of the algorithm. However, it can be both set by user or set via analyzing the density distribution by `flowDensity`

```

flowFrame object ''
with 7000 cells and 14 observables:
      name desc range minRange maxRange
$P1   FSC-A <NA> 262144 0.00000000 262143.0
$P2   FSC-H <NA> 262144 0.00000000 262143.0
$P3   FSC-W <NA> 262144 0.00000000 262143.0
$P4   SSC-A <NA> 262144 0.00000000 262143.0
$P5   SSC-H <NA> 262144 0.00000000 262143.0
$P6   SSC-W <NA> 262144 0.00000000 262143.0
$P7   FITC-A Lambda 262144 0.16328094 4.5
$P8   PE-A Kappa 262144 0.11965745 4.5
$P9   PerCP-Cy5-5-A CD5 262144 0.52215808 4.5
$P10  PE-Cy7-A CD10 262144 0.83157577 4.5
$P11  APC-A CD19 262144 0.49399988 4.5
$P12  APC-H7-A CD20 262144 0.69680349 4.5
$P13  V450-A CD38 262144 0.37618959 4.5
$P14  V500-A CD45 262144 -0.02725884 4.5
204 keywords are stored in the 'description' slot

```

```

> channels <- c("V500-A", "SSC-A")
> # First call to flowDensity
> tmp.cp1 <- flowDensity(obj=f2, channels=channels,
+                       position=c(TRUE, FALSE), percentile=c(0.25, NA))
> # Second call to flowDensity
> tmp.cp2 <- flowDensity(obj=tmp.cp1, channels=channels,
+                       position=c(TRUE, FALSE), gates=c(FALSE, NA), percentile=c(NA, 0.25))
> # Final call to flowDensity
> lymph <- flowDensity(obj=f2, channels=channels,
+                    position=c(TRUE, FALSE), gates=c(tmp.cp1@gates[1], tmp.cp2@gates[2]),
+                    ellip.gate=TRUE, scale=.99)

> plot(f2, tmp.cp1)

> plot(f2, tmp.cp2)

> plotDens(flow.frame=f2, channels=channels, devn=F)
> points(lymph@filter, type="l", col=2, lwd=2)

```

4.4 Gating cells using a control sample

To utilize matched control samples (*e.g.* FMO controls), the *flowDensity(.)* function has parameters that allow control data to be included. When this option is used, the gating threshold is calculated in the control data and applied to the stimulated data. Control samples are added using two parameters:

- *use.control*: When set to “TRUE”, `flowDensity` uses matched control data to calculate gating thresholds. This argument can be set for both channels. For example: `use.control=c(TRUE, FALSE)`.
- *control*: This argument accepts `flowFrame` or `CellPopulation` objects containing control data matched to the specified stimulated data (passed in the *obj* argument). Control samples can be included for one or both of the channels. If no control is to be used, the argument should be passed an “NA” value (default). For example, if the first channel should be gated using a control but the second channel should be gated normally (using the stimulated data), the user would specify `control=c(fmo.data, NA)`.

When control data is used, the other gating arguments (*upper*, *percentile*, *n.sd*, etc.) are applied to finding the threshold in the control sample instead of the stimulated sample.

For example, an FMO control (*i.e.* negative control) for the ‘BV421-A’ channel can be used for gating as follows:

```
> load(list.files(pattern = 'sampleFCS_3.Rdata', data_dir, full = TRUE))
> f3
```

```
flowFrame object ''
```

```
with 8000 cells and 20 observables:
```

	name	desc	range	minRange	maxRange
\$P1	FSC-A	<NA>	262144	0.000000000	262143.0
\$P2	FSC-W	<NA>	262144	0.000000000	262143.0
\$P3	SSC-A	<NA>	262144	0.000000000	262143.0
\$P4	SSC-W	<NA>	262144	0.000000000	262143.0
\$P5	APC-A	<NA>	262144	1.424618765	4.5
\$P6	Alexa Fluor 700-A	<NA>	262144	1.693370490	4.5
\$P7	APC-Cy7-A	<NA>	262144	-0.006329766	4.5
\$P8	Alexa Fluor 488-A	<NA>	262144	-0.058480480	4.5
\$P9	PerCP-Cy5-5-A	<NA>	262144	1.653328450	4.5
\$P10	BV421-A	<NA>	262144	0.603735357	4.5
\$P11	BV500-A	<NA>	262144	0.054259242	4.5
\$P12	BV570-A	<NA>	262144	1.136510670	4.5
\$P13	BV605-A	<NA>	262144	0.647546933	4.5
\$P14	BV650-A	<NA>	262144	0.788049917	4.5
\$P15	BV700-A	<NA>	262144	0.914095648	4.5
\$P16	BV785-A	<NA>	262144	1.240968280	4.5
\$P17	PE-A	<NA>	262144	0.156357679	4.5
\$P18	PE-Cy5-A	<NA>	262144	0.736939054	4.5
\$P19	PE-Cy7-A	<NA>	262144	0.512480878	4.5
\$P20	Time	<NA>	262144	0.000000000	262143.0

```
269 keywords are stored in the 'description' slot
```



```
> load(list.files(pattern = 'sampleFCS_3_FMO', data_dir, full = TRUE))
> f3.fmo
```

```
flowFrame object ''
```

```
with 8000 cells and 20 observables:
```

	name	desc	range	minRange	maxRange
\$P1	FSC-A	<NA>	262144	0.000000000	262143.0
\$P2	FSC-W	<NA>	262144	0.000000000	262143.0
\$P3	SSC-A	<NA>	262144	0.000000000	262143.0
\$P4	SSC-W	<NA>	262144	0.000000000	262143.0
\$P5	APC-A	<NA>	262144	1.424618765	4.5
\$P6	Alexa Fluor 700-A	<NA>	262144	1.693370490	4.5
\$P7	APC-Cy7-A	<NA>	262144	-0.006329766	4.5
\$P8	Alexa Fluor 488-A	<NA>	262144	-0.058480480	4.5
\$P9	PerCP-Cy5-5-A	<NA>	262144	1.653328450	4.5
\$P10	BV421-A	<NA>	262144	0.606985391	4.5
\$P11	BV500-A	<NA>	262144	0.054259242	4.5
\$P12	BV570-A	<NA>	262144	1.136510670	4.5
\$P13	BV605-A	<NA>	262144	0.647546933	4.5
\$P14	BV650-A	<NA>	262144	0.788049917	4.5
\$P15	BV700-A	<NA>	262144	0.914095648	4.5
\$P16	BV785-A	<NA>	262144	1.240968280	4.5
\$P17	PE-A	<NA>	262144	0.156357679	4.5
\$P18	PE-Cy5-A	<NA>	262144	0.736939054	4.5
\$P19	PE-Cy7-A	<NA>	262144	0.512480878	4.5
\$P20	Time	<NA>	262144	0.000000000	262143.0

```
269 keywords are stored in the 'description' slot
```

```
> f3.gated <- flowDensity(obj=f3, channels=c('BV421-A', 'FSC-A'),
+                               position = c(TRUE, NA),
+                               use.control = c(TRUE, F), control = c(f3.fmo, NA))
> f3.fmo.gated <- flowDensity(obj=f3.fmo, channels=c('BV421-A', 'FSC-A'),
+                               position=c(TRUE, NA),
+                               gates=c(f3.gated@gates[1], NA))

> plot(f3.fmo, f3.fmo.gated)

> plot(f3, f3.gated)
```

Figure 5 shows the gating of 'BV421-A' on both stimulated and control samples.

For finer control, additional gating arguments can be passed that will be applied to the control sample. For example, the below example will gate using the 98th percentile in control data:

```
> f3.gated.98p <- flowDensity(obj=f3, channels=c('BV421-A', 'FSC-A'),
+                               position = c(TRUE, NA),
```

```

+                               use.percentile = c(TRUE, NA), percentile = 0.98,
+                               use.control = c(TRUE, FALSE), control = c(f3.fmo, NA))
> f3.fmo.gated.98p <- flowDensity(obj=f3.fmo, channels=c('BV421-A', 'FSC-A'),
+                               position = c(TRUE, NA),
+                               gates=c(f3.gated.98p@gates[1], NA))

> plot(f3.fmo, f3.fmo.gated.98p)

> plot(f3, f3.gated.98p)

```

Figure 6 Shows the gating based on 98th percentile gate in FMO data.

Note: When using controls, setting *position=TRUE* will treat the data as a negative control and extract the population above the threshold. Setting *position=FALSE* will treat it as a positive control.

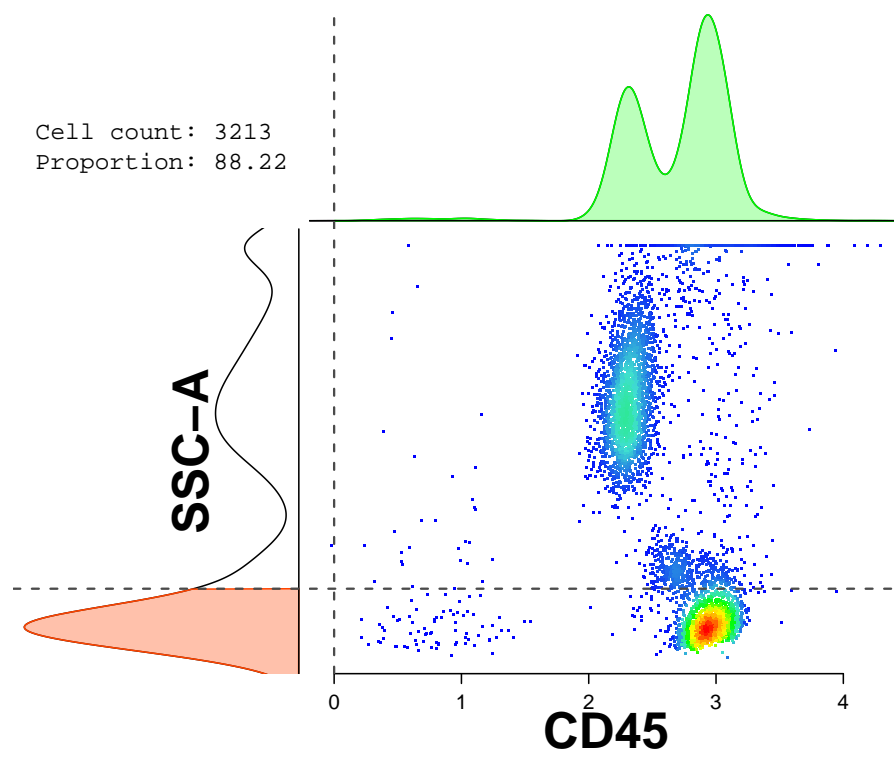
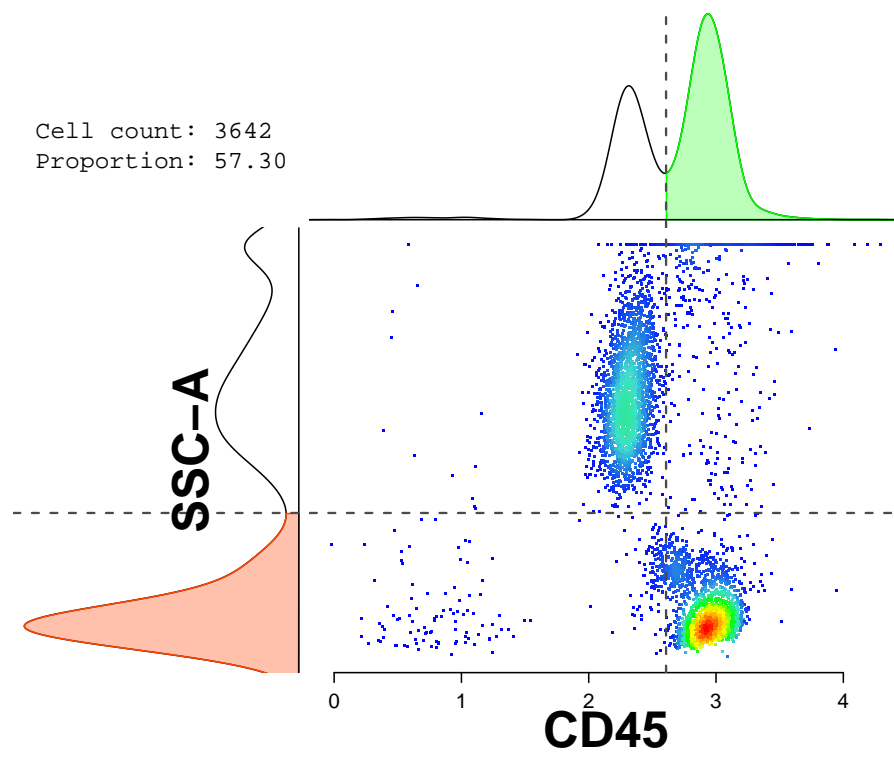


Figure 3: Two steps of gating lymphocytes

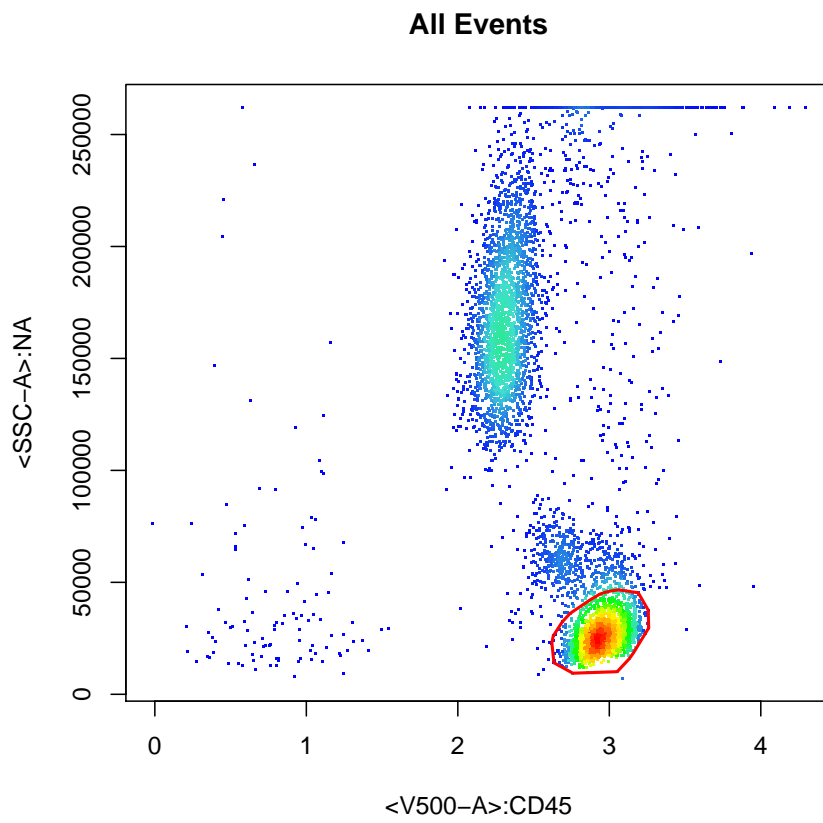


Figure 4: lymphocyte cels

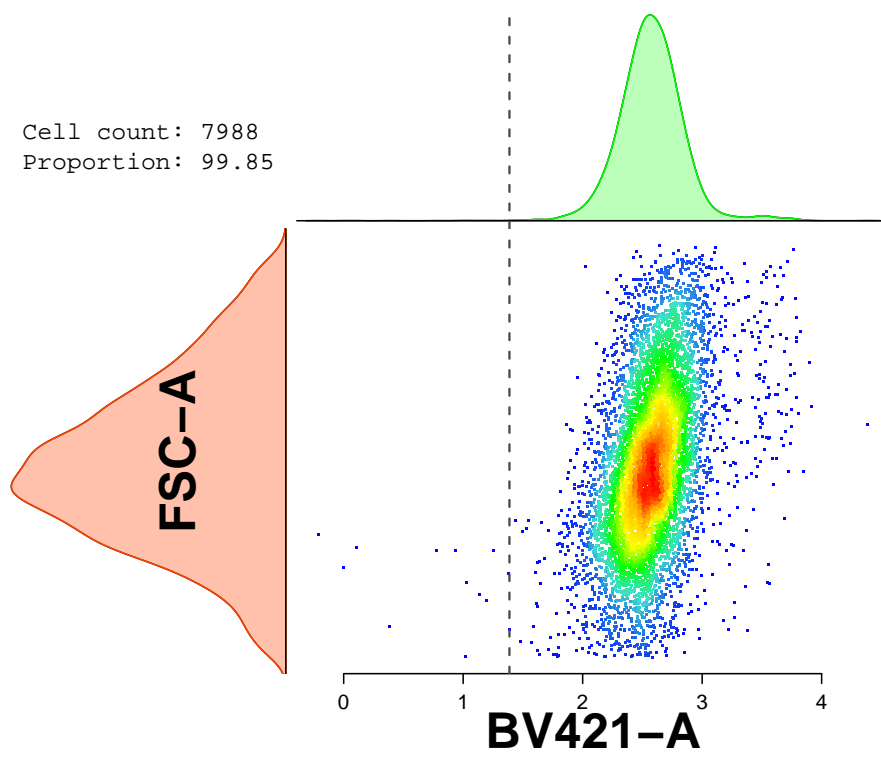
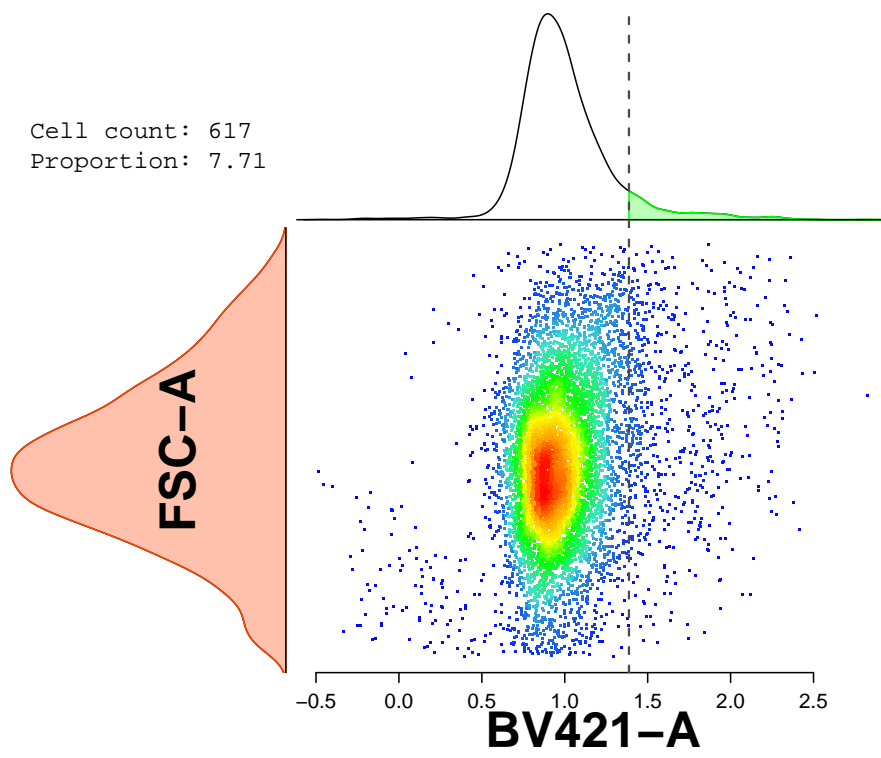


Figure 5: Default gate in FMO data applied to itself (top) and stimulated data (bottom)

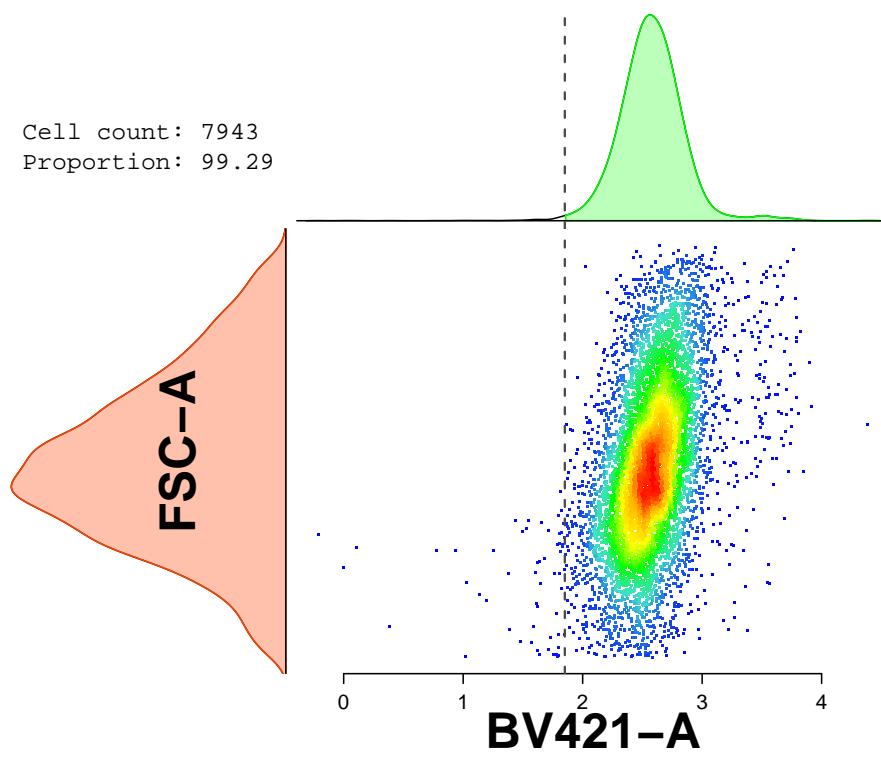
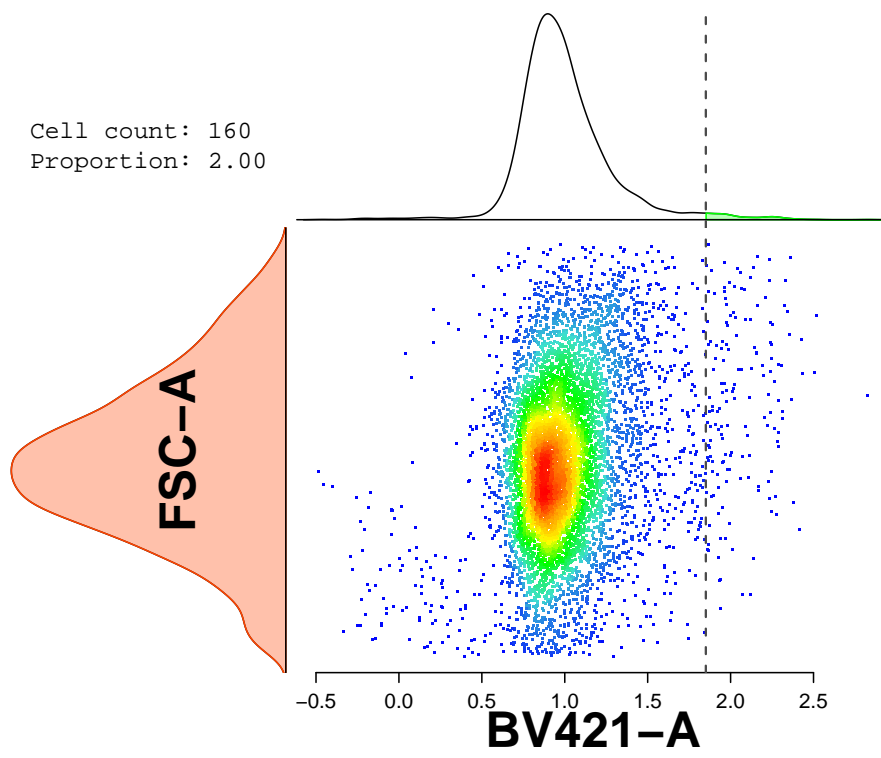


Figure 6: 98th percentile gate in FMO data applied to itself (top) and stimulated data (bottom)