

immunoClust - Automated Pipeline for Population Detection in Flow Cytometry

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1 Licensing

Under the Artistic License, you are free to use and redistribute this software. However, we ask you to cite the following paper if you use this software for publication.

Sörensen, T., Baumgart, S., Durek, P., Grützkau, A. and Häupl, T.

immunoClust - an automated analysis pipeline for the identification of immunophenotypic signatures in high-dimensional cytometric datasets.

Cytometry A (accepted).

2 Overview

immunoClust presents an automated analysis pipeline for uncompensated fluorescence and mass cytometry data and consists of two parts. First, cell events of each sample are grouped into individual clusters (cell-clustering). Subsequently, a classification algorithm assorts these cell event clusters into populations comparable between different samples (meta-clustering). The clustering of cell events is designed for datasets with large event counts in high dimensions as a global unsupervised method, sensitive to identify rare cell types even when next to large populations. Both parts use model-based clustering with an iterative Expectation Maximization (EM) algorithm and the Integrated Classification Likelihood (ICL) to obtain the clusters.

The cell-clustering process fits a mixture model with *t*-distributions. Within the clustering process a optimisation of the *asinh*-transformation for the fluorescence parameters is included.

The meta-clustering fits a Gaussian mixture model for the meta-clusters, where adjusted Bhattacharyya-Coefficients give the probability measures between cell- and meta-clusters.

Several plotting routines are available visualising the results of the cell- and meta-clustering process. Additional helper-routines to extract population features are provided.

3 Getting started

The installation on *immunoClust* is normally done within the Bioconductor.

The core functions of *immunoClust* are implemented in C/C++ for optimal utilization of system resources and depend on the GNU Scientific Library (GSL) and Basic Linear Subprogram (BLAS). When installing *immunoClust* from source using Rtools be aware to adjust the GSL library and include pathes in `src/Makevars.in` or `src/Makevars.win` (on Windows systems) repectively to the correct installation directory of the GSL-library on the system.

immunoClust relies on the *flowFrame* structure imported from the *flowCore*-package for accessing the measured cell events from a flow cytometer device.

4 Example Illustrating the immunoClust Pipeline

The functionality of the immunoClust pipeline is demonstrated on a dataset of blood cell samples of defined composition that were depleted of particular cell subsets by magnetic cell sorting. Whole blood leukocytes taken from three healthy individuals, which were experimen-

tally modified by the depletion of one particular cell type per sample, including granulocytes (using CD15-MACS-beads), monocytes (using CD14-MACS-beads), T lymphocytes (CD3-MACS-beads), T helper lymphocytes (using CD4-MACS-beads) and B lymphocytes (using CD19-MACS-beads).

The example datasets contain reduced (10.000 cell-events) of the first Flow Cytometry (FC) sample in `dat.fcs` and the *immunoClust* cell-clustering results of all 5 reduced FC samples for the first donor in `dat.exp`. The full sized dataset is published and available under <http://flowrepository.org/id/FR-FCM-ZZWB>.

4.1 Cell Event Clustering

```
> library(immunoClust)
```

The cell-clustering is performed by the `cell.process` function for each FC sample separately. Its major input are the measured cell-events in a *flowFrame*-object imported from the *flowCore*-package.

```
> data(dat.fcs)
> dat.fcs

flowFrame object '2d36b4cf-da0f-4b8d-9a4c-fc7e4f5fccc8'
with 10000 cells and 7 observables:
      name desc range minRange maxRange
$P2      FSC-A  NA  262144      0.00  262143
$P5      SSC-A  NA  262144     -111.00  262143
$P8      FITC-A CD14  262144     -111.00  262143
$P9       PE-A CD19  262144     -111.00  262143
$P12     APC-A CD15  262144     -111.00  262143
$P13  APC-Cy7-A CD4   262144     -111.00  262143
$P14 Pacific Blue-A CD3  262144     -98.94  262143
171 keywords are stored in the 'description' slot
```

In the `parameters` argument the parameters (named as observables in the *flowFrame*) used for cell-clustering are specified. When omitted all determined parameters are used.

```
> pars=c("FSC-A", "SSC-A", "FITC-A", "PE-A", "APC-A", "APC-Cy7-A", "Pacific Blue-A")
> res.fcs <- cell.process(dat.fcs, parameters=pars)
```

The `summary` method for an *immunoClust*-object gives an overview of the clustering results.

```
> summary(res.fcs)

** Experiment Information **
Experiment name: 12443.fcs
Data Filename:   fcs/12443.fcs
Parameters:      FSC-A SSC-A FITC-A PE-A APC-A APC-Cy7-A Pacific Blue-A
Description:     NA NA CD14 CD19 CD15 CD4 CD3

** Data Information **
Number of observations: 10000
Number of parameters:   7
Removed from above:     318 (3.18%)
```

```

Removed from below:    0 (0%)

** Transformation Information **
htrans-A:  0.000000 0.000000 0.010000 0.010000 0.010000 0.010000 0.010000
htrans-B:  0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000
htrans-decade:  -1

** Clustering Summary **
ICL bias: 0.30
Number of clusters: 15
Cluster      Proportion  Observations
    1         0.311100         2914
    2         0.326862         3247
    3         0.027652          279
    4         0.012643          122
    5         0.007364           70
    6         0.034390          337
    7         0.015977          156
    8         0.006937           68
    9         0.035961          352
   10         0.053952          518
   11         0.004091           40
   12         0.005141           50
   13         0.083407          822
   14         0.034150          316
   15         0.040374          391

    Min.         0.004091          40
    Max.         0.326862         3247

** Information Criteria **
Log likelihood: -253610.1 -255125.9 -173470.8
BIC: -253610.1
ICL: -255125.9

```

With the `bias` argument of the `cell.process` function the number of clusters in the final model is controlled.

```

> res2 <- cell.process(dat.fcs, bias=0.25)
> summary(res2)

** Experiment Information **
Experiment name: 12443.fcs
Data Filename:  fcs/12443.fcs
Parameters:  FSC-A SSC-A FITC-A PE-A APC-A APC-Cy7-A Pacific Blue-A
Description:  NA NA CD14 CD19 CD15 CD4 CD3

** Data Information **
Number of observations: 10000
Number of parameters:  7
Removed from above:    318 (3.18%)
Removed from below:    0 (0%)

```

```

** Transformation Information **
htrans-A:  0.000000 0.000000 0.010000 0.010000 0.010000 0.010000 0.010000
htrans-B:  0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000
htrans-decade:  -1

** Clustering Summary **
ICL bias: 0.25
Number of clusters: 19
Cluster      Proportion  Observations
    1         0.018757          178
    2         0.009460           88
    3         0.012078          124
    4         0.032009          317
    5         0.009609           85
    6         0.015577          153
    7         0.074545          731
    8         0.040044          380
    9         0.035796          363
   10         0.030765          282
   11         0.026199          254
   12         0.005998           58
   13         0.637532         6166
   14         0.009892           96
   15         0.002179           21
   16         0.001059           10
   17         0.002631           25
   18         0.028536          281
   19         0.007331           70

    Min.         0.001059           10
    Max.         0.637532         6166

** Information Criteria **
Log likelihood: -254491.9 -254905.1 -172591.1
BIC: -254491.9
ICL: -254905.1

```

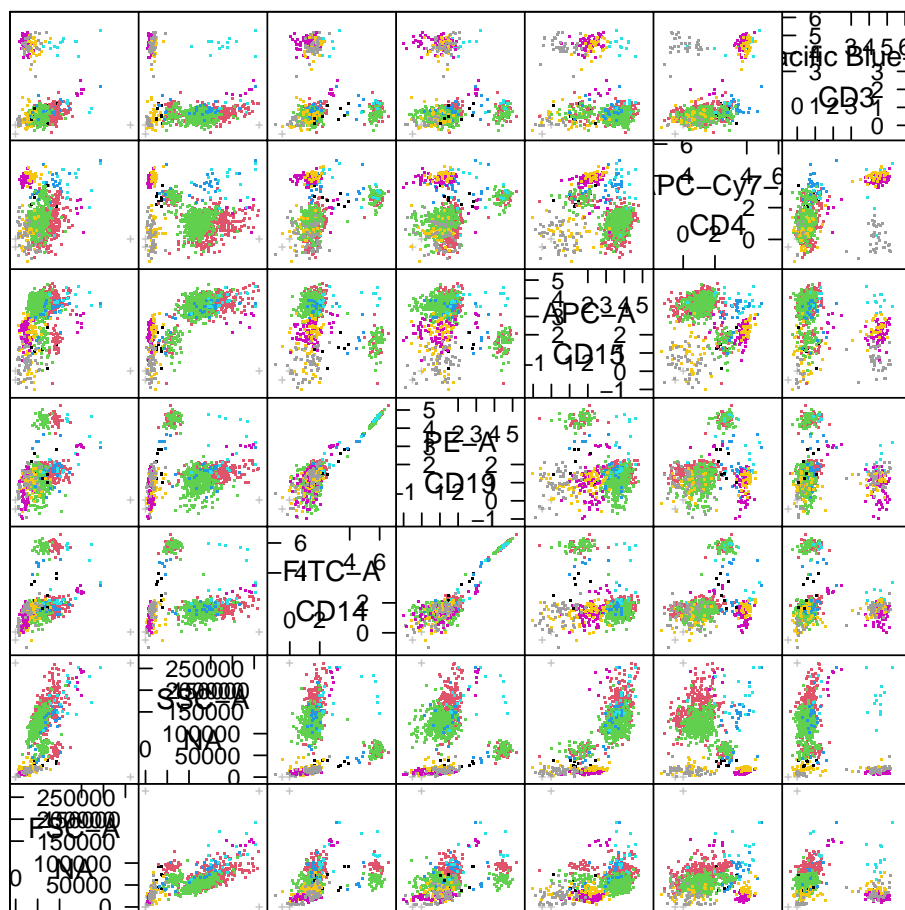
An ICL-bias of 0.3 is reasonable for fluorescence cytometry data based on our experiences, whereas the number of clusters increase dramatically when a `bias` below 0.2 is applied. A principal strategy for the ICL-bias in the whole pipeline is the use of a moderately small `bias` (0.2 - 0.3) for cell-clustering and to optimise the `bias` on meta-clustering level to retrieve the common populations across all samples.

For plotting the clustering results on cell event level, the optimised *asinh*-transformation has to be applied to the raw FC data first.

```
> dat.transformed <- trans.ApplyToData(res.fcs, dat.fcs)
```

A scatter plot matrix of all used parameters for clustering is obtained by the `splom` method.

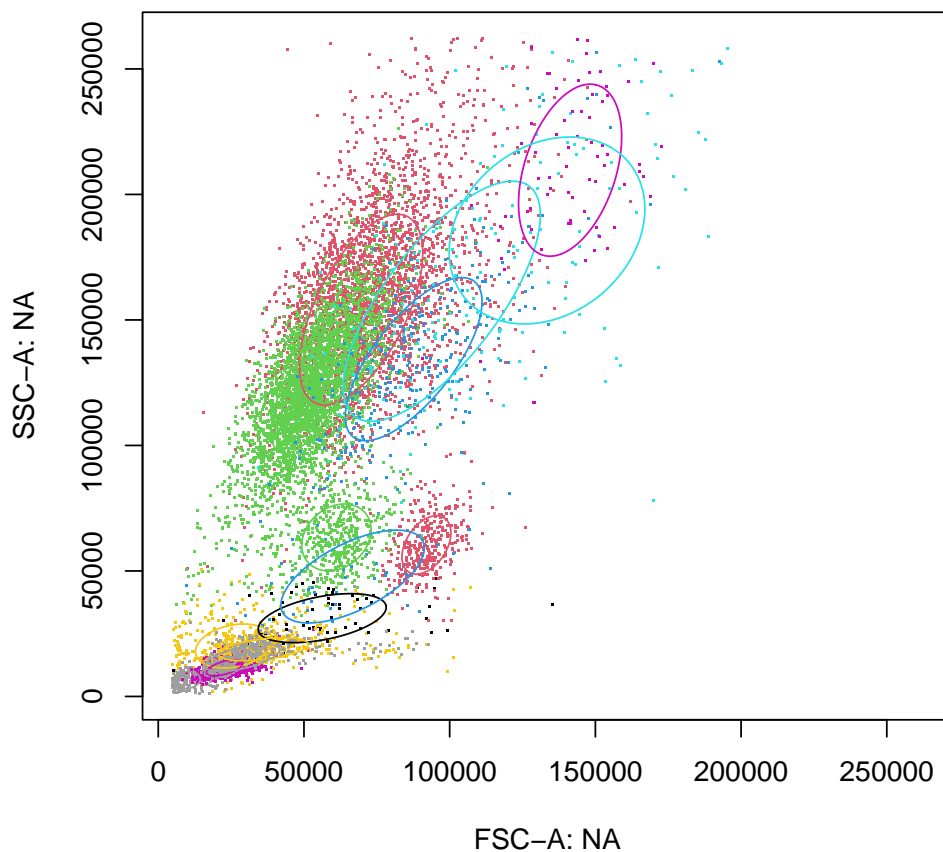
```
> splom(res.fcs, dat.transformed, N=1000)
```



Scatter Plot Matrix

For a scatter plot of 2 particular parameters the `plot` method can be used, where parameters of interest are specified in the `subset` argument.

```
> plot(res.fcs, data=dat.transformed, subset=c(1,2))
```



4.2 Meta Clustering

For meta-clustering the cell-clustering results of all FC samples obtained by the `cell.process` function are collected in a `vector` of `immunoClust`-objects and processed by the `meta.process` function.

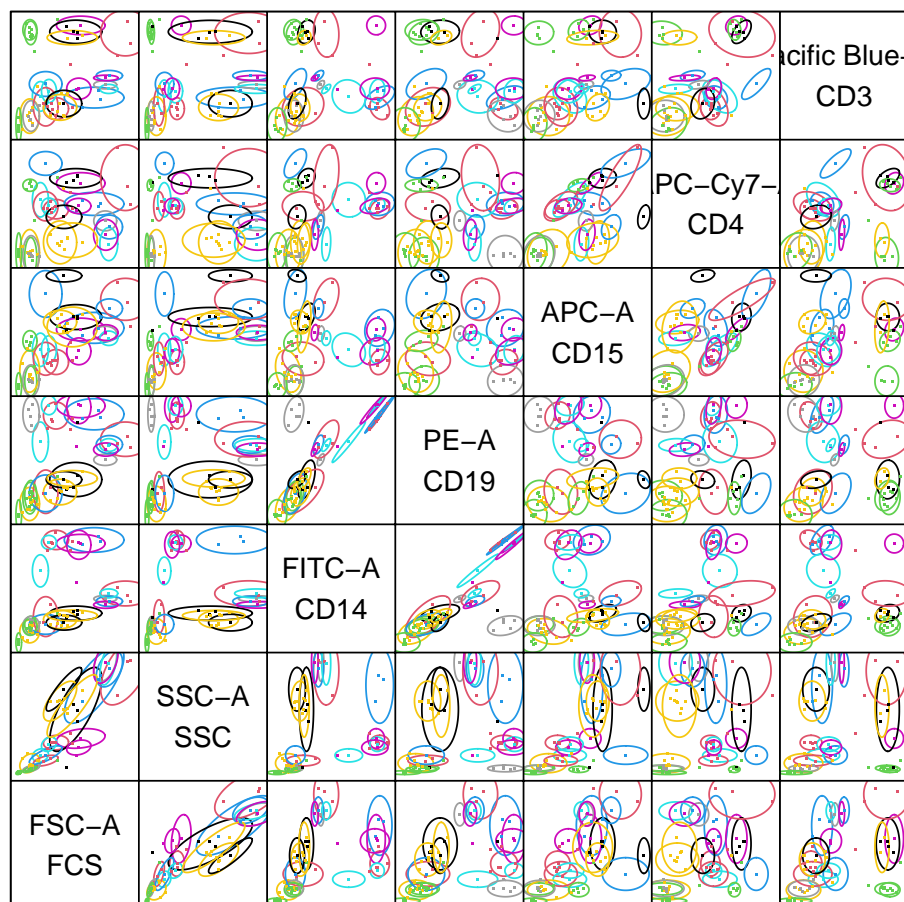
```
> data(dat.exp)
> meta<-meta.process(dat.exp, meta.bias=0.3)
```

The obtained `immunoMeta`-object contains the meta-clustering result in `$res.clusters`, and the used cell-clusters information in `$dat.clusters`. Additionally, the clusters can be structures manually in a hierarchical mannner using methods of the `immunoMeta`-object.

A scatter plot matrix of the meta-clustering is obtained by the `plot` method.

```
> plot(meta, c())
```

.all



In these scatter plots each cell-cluster is marked by a point of its centre. With the default `plot.ellipse=TRUE` argument the meta-clusters are outlined by ellipses of the 90% quantile.

4.3 Meta Annotation

We take a look on the event numbers of all meta-clusters in each sample

```
> cls <- clusters(meta, c())
> events(meta, cls)
```

	cls-1	cls-2	cls-3	cls-4	cls-5	cls-6	cls-7	cls-8	cls-9	cls-10	cls-11
exp-1	898	389	50	0	0	344	0	143	71	1107	0
exp-2	0	1079	0	173	102	695	926	8	145	3425	220
exp-3	0	574	0	0	0	780	452	199	0	1585	0
exp-4	761	433	62	0	0	527	331	0	0	0	0
exp-5	950	46	94	0	0	400	325	0	0	0	0
	cls-12	cls-13	cls-14	cls-15	cls-16	cls-17	cls-18	cls-19	cls-20	cls-21	

immunoClust

exp-1	0	0	6459	70	0	0	151	0	0	0
exp-2	1447	923	0	0	24	103	495	77	0	0
exp-3	0	0	5717	0	0	10	247	0	0	132
exp-4	0	0	7280	0	0	0	247	0	95	0
exp-5	0	0	7417	0	0	0	278	0	0	0
cls-22										
exp-1	0									
exp-2	0									
exp-3	40									
exp-4	0									
exp-5	0									

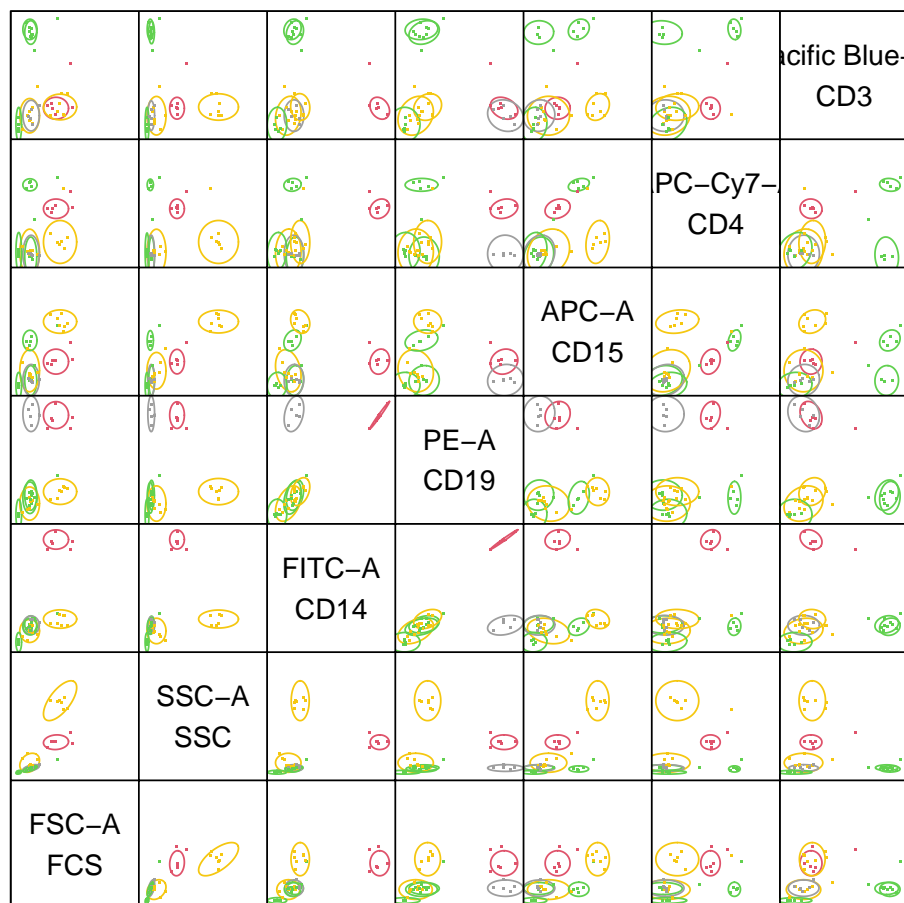
and pick the meta-clusters of the five commonly found population, with respect to the technical depletion to collect them in a first annotation level

```
> addLevel(meta, c(1), "leucocytes") <- c(1, 2, 6, 7, 10, 14, 18)
```

In the plot of this level the five major population are seen easily

```
> plot(meta, c(1))
```

1.all_leucocytes



and we identify the clusters for the particular populations successively by their expression levels.

```
> cls <- clusters(meta,c(1))
> sort(mu(meta,cls,7))      ## CD3 expression

   cls-18   cls-6   cls-7   cls-1   cls-14   cls-2   cls-10
0.5563285 1.0177510 1.0231479 1.4074683 1.4710931 5.3398778 5.5034995

> inc <- mu(meta,cls,7) > 5   ## CD3+ clusters
> cls[inc]

[1] 2 10

> mu(meta,cls[inc],6)      ## CD4 expression

   cls-2   cls-10
0.3526607 4.1704618

> addLevel(meta,c(1,1), "CD3+CD4+") <- 10
> addLevel(meta,c(1,2), "CD3+CD4-") <- 2
> cls <- unclassified(meta,c(1))
> sort(mu(meta,cls,5))      ## CD15 expression
```

```

      cls-18      cls-7      cls-6      cls-1      cls-14
0.1607839 0.4098828 0.8552890 1.2885715 3.1912791

> inc <- mu(meta,cls,5) > 3
> addLevel(meta,c(1,3), "CD15+") <- cls[inc]
> cls <- unclassified(meta,c(1))
> sort(mu(meta,cls,3))      ## CD14 expression

      cls-18      cls-6      cls-7      cls-1
0.2970245 0.8748380 1.1685025 5.5770927

> inc <- mu(meta,cls,3) > 5
> addLevel(meta,c(1,4), "CD14+") <- cls[inc]
> cls <- unclassified(meta,c(1))
> sort(mu(meta,cls,4))      ## CD19 expression

      cls-18      cls-6      cls-7
0.2053237 0.6140560 3.9759928

> inc <- mu(meta,cls,4) > 3
> addLevel(meta,c(1,5), "CD19+") <- cls[inc]

```

The whole analysis is performed on uncompensated FC data, thus the high CD19 values on the CD14-population is explained by spillover of FITC into PE.

The event numbers of each meta-cluster and each sample are extracted in a numeric matrix by the `meta.numEvents` function.

```

> tbl <- meta.numEvents(meta, out.all=FALSE)
> tbl[,1:5]

```

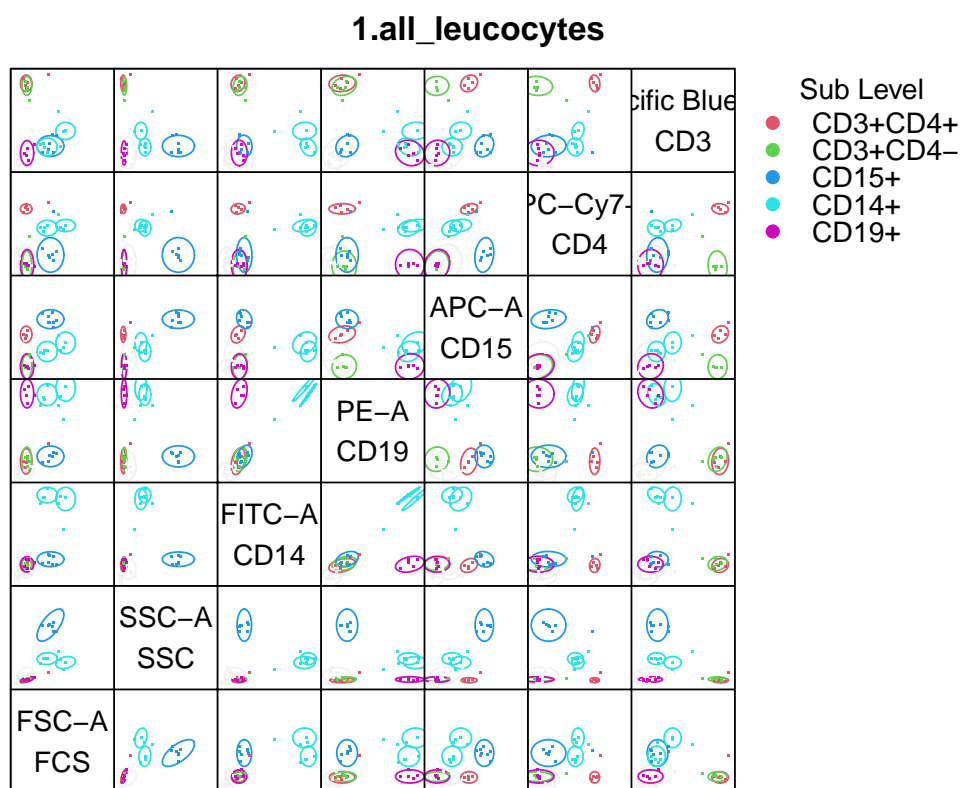
	12543	12546	12549	12552	12555
1.1.all_leucocytes_CD3+CD4+.10.green3	1107	3425	1585	0	0
1.2.all_leucocytes_CD3+CD4-.2.green3	389	1079	574	433	46
1.3.all_leucocytes_CD15+.14.yellow	6459	0	5717	7280	7417
1.4.all_leucocytes_CD14+.1.red	898	0	0	761	950
1.5.all_leucocytes_CD19+.7.gray	0	926	452	331	325
1.all_leucocytes.6.yellow	344	695	780	527	400
1.all_leucocytes.18.green3	151	495	247	247	278
.all.3.blue	50	0	0	62	94
.all.4.cyan	0	173	0	0	0
.all.5.magenta	0	102	0	0	0
.all.8.black	143	8	199	0	0
.all.9.red	71	145	0	0	0
.all.11.blue	0	220	0	0	0
.all.12.cyan	0	1447	0	0	0
.all.13.magenta	0	923	0	0	0
.all.15.gray	70	0	0	0	0
.all.16.black	0	24	0	0	0
.all.17.red	0	103	10	0	0
.all.19.blue	0	77	0	0	0
.all.20.cyan	0	0	0	95	0
.all.21.magenta	0	0	132	0	0
.all.22.yellow	0	0	40	0	0

Each row denotes an annotated hierarchical level or/and meta-cluster and each column a data sample used in meta-clustering. The row names give the annotated population name, the meta-cluster index and the default color used in the plot routines for each meta-cluster. In the last columns additionally the meta-cluster centre values in each parameter are given, which helps to identify the meta-clusters. Further export functions retrieve relative cell event frequencies and sample meta-cluster centre values in a particular parameter.

We see here, that for sample 12546 where the CD15-cells are depleted, the CD14-population is missing. Anyway, this missing cluster could be in the so far unclassified clusters.

```
> move(meta, c(1,4)) <- 13
```

```
> plot(meta, c(1))
```



We see the CD14 population of sample 12546 shifted in FSC and CD3 expression levels, probably due to technical variation in the measurement of the CD15-depleted sample, where the granulocytes are missing which constitute about 60% - 70% of the events in the other samples.

5 Session Info

The documentation and example output was compiled and obtained on the system:

```
> toLatex(sessionInfo())
```

- R version 4.2.1 Patched (2022-07-09 r82577), x86_64-apple-darwin17.0
- Locale: C/en_US.UTF-8/en_US.UTF-8/C/en_GB/en_US.UTF-8
- Running under: macOS Big Sur ... 10.16
- Matrix products: default
- BLAS:
/Library/Frameworks/R.framework/Versions/4.2/Resources/lib/libRblas.0.dylib
- LAPACK:
/Library/Frameworks/R.framework/Versions/4.2/Resources/lib/libRlapack.dylib
- Base packages: base, datasets, grDevices, graphics, methods, stats, utils
- Other packages: flowCore 2.10.0, immunoClust 1.30.0
- Loaded via a namespace (and not attached): Biobase 2.58.0, BiocGenerics 0.44.0, BiocManager 1.30.19, BiocStyle 2.26.0, RProtoBufLib 2.10.0, Rcpp 1.0.9, S4Vectors 0.36.0, cli 3.4.1, compiler 4.2.1, cytolib 2.10.0, digest 0.6.30, evaluate 0.17, fastmap 1.1.0, grid 4.2.1, htmltools 0.5.3, knitr 1.40, lattice 0.20-45, matrixStats 0.62.0, rlang 1.0.6, rmarkdown 2.17, stats4 4.2.1, tools 4.2.1, xfun 0.34, yaml 2.3.6