

# immunoClust - Automated Pipeline for Population Detection in Flow Cytometry

*Till Sörensen*<sup>1</sup>

November 25, 2024

## Contents

1	Licensing . . . . .	2
2	Overview. . . . .	2
3	Getting started . . . . .	2
4	Example Illustrating the immunoClust Pipeline . . . . .	2
4.1	Cell Event Clustering . . . . .	3
4.2	Meta Clustering . . . . .	6
4.3	Meta Annotation . . . . .	7
5	Session Info . . . . .	10

---

<sup>1</sup>till-antoni.soerensen@charite.de

## 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: 12
Cluster      Proportion  Observations
    1         0.091847         890
    2         0.005918          57
    3         0.040373         391
    4         0.034168         333
    5         0.015829         154
    6         0.008026          79
    7         0.084084         827
    8         0.033522         312
    9         0.637715        6166
   10         0.012627         122
   11         0.007322          70
   12         0.028569         281

    Min.         0.005918          57
    Max.         0.637715        6166

** Information Criteria **
Log likelihood: -254005 -254201.8 -173041.3
BIC: -254005
ICL: -254201.8

```

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: 15

Cluster	Proportion	Observations
1	0.240825	2148
2	0.397232	4013
3	0.027603	280
4	0.012644	122
5	0.006011	58
6	0.007310	70
7	0.084019	824
8	0.033561	315
9	0.019420	189
10	0.020952	202
11	0.035175	343
12	0.015464	149
13	0.007818	79
14	0.037265	367
15	0.054700	523
Min.	0.006011	58
Max.	0.397232	4013

**\*\* Information Criteria \*\***

Log likelihood: -253561 -255002.3 -173347.2

BIC: -253561

ICL: -255002.3

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.

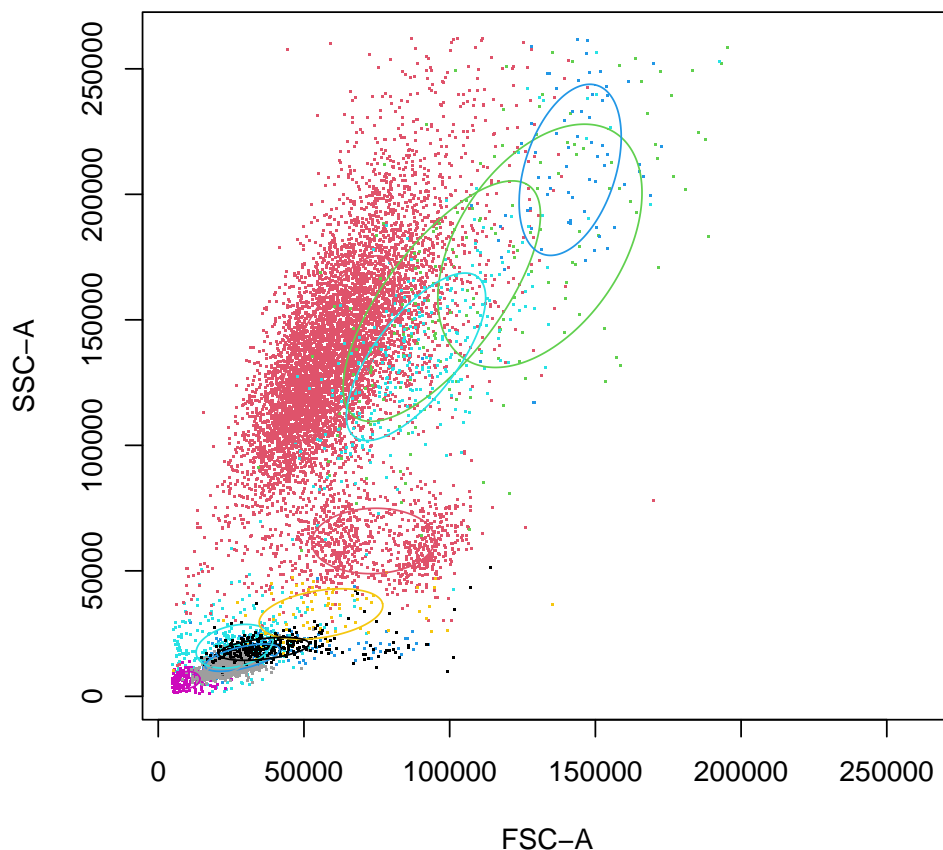
```
> dat.transformed <- trans.ApplyToData(res.fcs, dat.fcs)
```

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

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

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

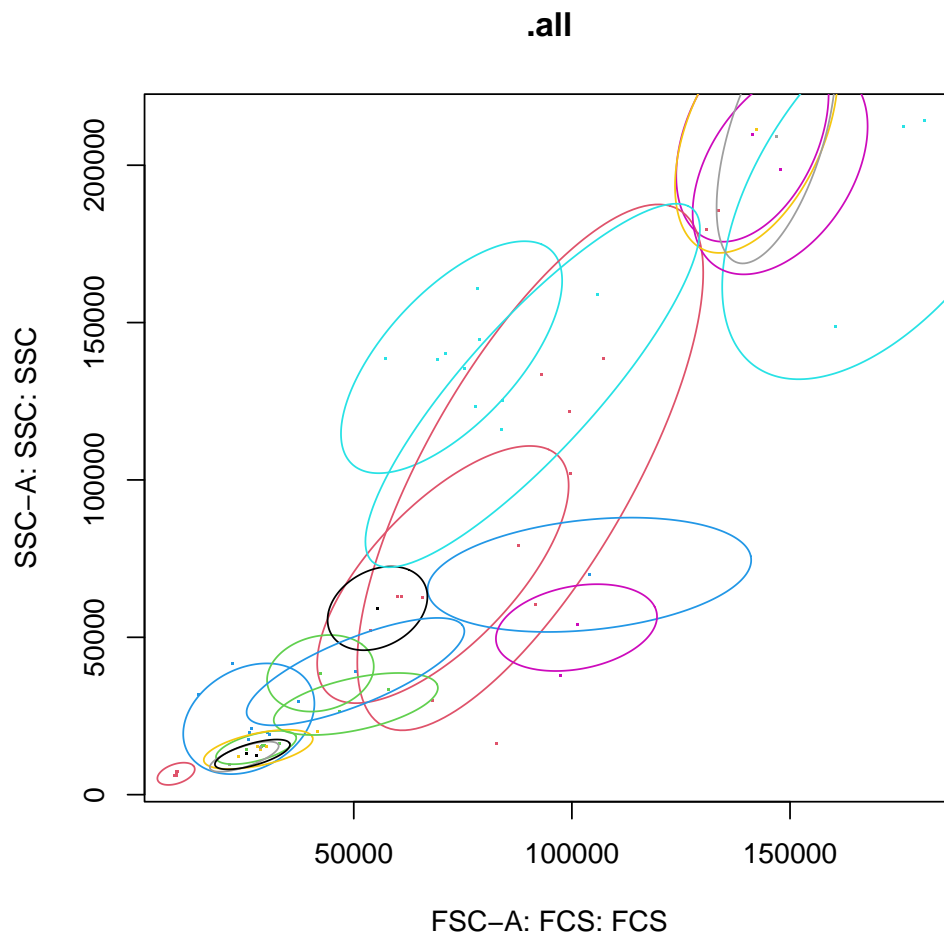
For meta-clustering the cell-clustering results of all FC samples obtained by the `cell.process` function are collected in a vector of *immunoClust*-objects and processed by the `meta.process` function.

```
> 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(), plot.subset=c(1,2))
```



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 and first sort the meta-clusters according to the scatter parameter into five major areas

```
> cls <- clusters(meta,c())
> inc <- mu(meta,cls,1) > 20000 & mu(meta,cls,1) < 150000
> addLevel(meta,c(1),"leucocytes") <- cls[inc]
> cls <- clusters(meta,c(1))
> sort(mu(meta,cls,2))
```

cls-7	cls-8	cls-6	cls-2	cls-3	cls-18	cls-10	cls-19
12073.50	12781.05	14379.67	14987.31	24119.51	28807.31	38562.50	39089.67
cls-21	cls-16	cls-11	cls-1	cls-9	cls-20	cls-4	cls-13

## immunoClust

```

53084.06 59202.13 69861.55 69936.06 103994.99 130008.05 138993.45 198539.11
  cls-15   cls-5   cls-14
209082.92 209737.65 211263.42

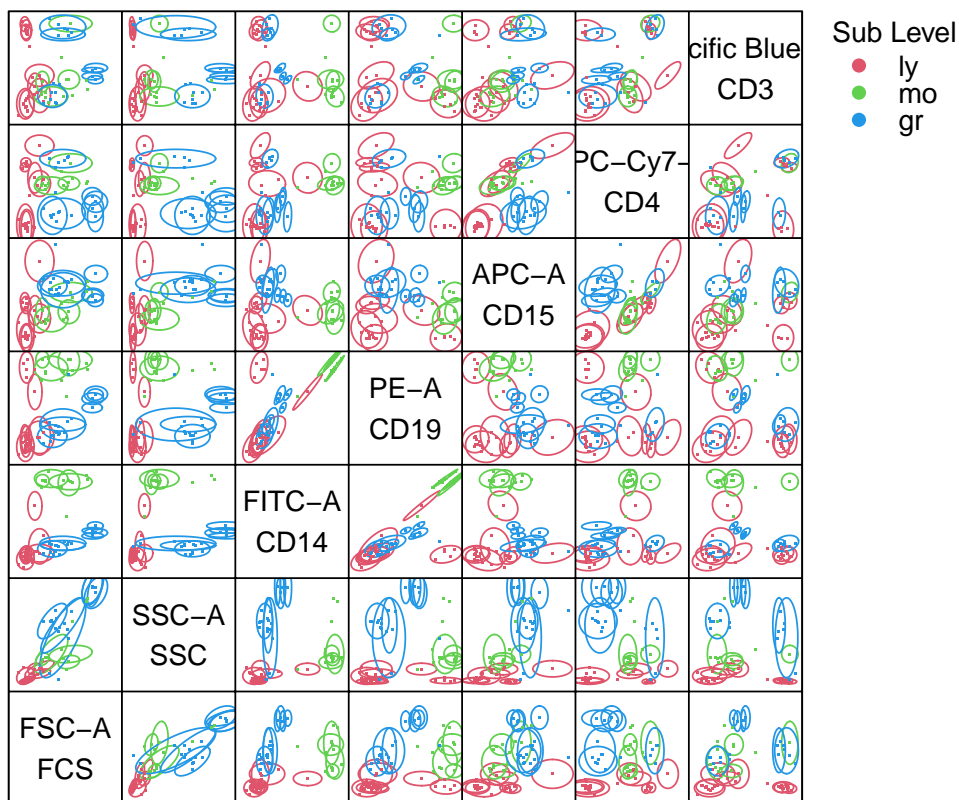
> inc <- (mu(meta,cls,2)) < 40000
> addLevel(meta,c(1,1), "ly") <- cls[inc]
> addLevel(meta,c(1,2), "mo") <- c()
> inc <- (mu(meta,cls,2)) > 100000
> addLevel(meta,c(1,3), "gr") <- cls[inc]
> move(meta,c(1,2)) <- unclassified(meta,c(1))

```

In the plot of this level the three major scatter 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(1,1))
> sort(mu(meta,cls,7)) ## CD3 expression

```



```

      cls-3   cls-6   cls-18   cls-10   cls-19   cls-8   cls-2   cls-7
1.017751 1.023148 1.501441 2.043337 2.686877 5.248953 5.339878 5.693991
> sort(mu(meta,cls,6)) ## CD4 expression
      cls-2   cls-6   cls-3   cls-18   cls-10   cls-7   cls-8   cls-19
0.3526607 0.4631971 0.5680941 3.0448631 3.3933842 4.0296976 4.3310119 5.3378243
> inc <- mu(meta,cls,7) > 5 & mu(meta,cls,6) > 4
> addLevel(meta,c(1,1,1), "CD3+CD4+") <- cls[inc]
> inc <- mu(meta,cls,7) > 5 & mu(meta,cls,6) < 4
> addLevel(meta,c(1,1,2), "CD3+CD4-") <- cls[inc]
> cls <- unclassified(meta,c(1,1))
> inc <- (mu(meta,cls,4)) > 3
> addLevel(meta,c(1,1,3), "CD19+") <- cls[inc]
> cls <- clusters(meta,c(1,2))
> inc <- mu(meta,cls,3) > 5 & mu(meta,cls,7) < 5
> addLevel(meta,c(1,2,1), "CD14+") <- cls[inc]
> cls <- clusters(meta,c(1,3))
> inc <- mu(meta,cls,5) > 3 & mu(meta,cls,7) < 5
> addLevel(meta,c(1,3,1), "CD15+") <- 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.unclassified=FALSE)
> tbl[,1:5]

```

	12543	12546	12549	12552	12555
measured	10000	10000	10000	10000	10000
.all	9682	9842	9736	9736	9510
1.all_leucocytes	9531	9244	9479	9489	9232
1.1.all_leucocytes_ly	1911	6570	3391	1291	771
1.1.1.all_leucocytes_ly_CD3+CD4+	1107	3332	1585	0	0
1.1.2.all_leucocytes_ly_CD3+CD4-	389	1079	574	433	46
1.1.3.all_leucocytes_ly_CD19+	0	926	452	331	325
1.2.all_leucocytes_mo	948	2472	0	823	1044
1.2.1.all_leucocytes_mo_CD14+	948	2370	0	823	1044
1.3.all_leucocytes_gr	6672	202	6088	7375	7417
1.3.1.all_leucocytes_gr_CD15+	6459	101	5717	7280	7417

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. 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.

```
> plot(meta, c(1,2,1), plot.subset=c(1,2,3,4))
```

### 1.2.1.all\_leucocytes\_mo\_CD14+



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 Under development (unstable) (2024-11-20 r87352), x86\_64-apple-darwin20
- Locale: C/en\_US.UTF-8/en\_US.UTF-8/C/en\_US.UTF-8/en\_US.UTF-8
- Time zone: America/New\_York

- TZcode source: internal
- Running under: macOS Monterey 12.7.6
- Matrix products: default
- BLAS:  
/Library/Frameworks/R.framework/Versions/4.5-x86\_64/Resources/lib/libRblas.0.dylib
- LAPACK:  
/Library/Frameworks/R.framework/Versions/4.5-x86\_64/Resources/lib/libRlapack.dylib  
; LAPACK version3.12.0
- Base packages: base, datasets, grDevices, graphics, methods, stats, utils
- Other packages: flowCore 2.19.0, immunoClust 1.39.3
- Loaded via a namespace (and not attached): Biobase 2.67.0, BiocGenerics 0.53.3, BiocManager 1.30.25, BiocStyle 2.35.0, RProtoBufLib 2.19.0, S4Vectors 0.45.2, cli 3.6.3, compiler 4.5.0, cytolib 2.19.0, digest 0.6.37, evaluate 1.0.1, fastmap 1.2.0, generics 0.1.3, grid 4.5.0, htmltools 0.5.8.1, knitr 1.49, lattice 0.22-6, matrixStats 1.4.1, rlang 1.1.4, rmarkdown 2.29, stats4 4.5.0, tools 4.5.0, xfun 0.49, yaml 2.3.10