This vignette demonstrates the processing steps of cytometry data using the workflow in `CytoAnalyze` package.

```
In [3]:  library(CytoAnalyze)
```

Arcsin transformation

First, we start with the arcsin transformation of the data, using `arcsin_trans()` function.

```
In [4]:  arcsin_trans(input_folder = input_folder <- "~/Data/clean_fcs",
                      cofactor = 5,
                      #value that controls the extent of the linear region of the scale.
                      output_folder = "~/Data/CytoAnalyze_results",
                      channel.plot = TRUE
                      #If True, export histograms for visual inspection of the transformation.
                      )
```

```
Transforming..../Users/ramygadalla/Data/clean_fcs/Donor_1_ControlBatch1.fcs

Transforming..../Users/ramygadalla/Data/clean_fcs/Donor_10.fcs

Transforming..../Users/ramygadalla/Data/clean_fcs/Donor_11.fcs

Transforming..../Users/ramygadalla/Data/clean_fcs/Donor_2_ControlBatch2.fcs

Transforming..../Users/ramygadalla/Data/clean_fcs/Donor_3.fcs

Transforming..../Users/ramygadalla/Data/clean_fcs/Donor_5.fcs

Transforming..../Users/ramygadalla/Data/clean_fcs/Donor_8.fcs

Transforming..../Users/ramygadalla/Data/clean_fcs/Donor_9.fcs

Done transformation
.
.

Plotting histograms

/Users/ramygadalla/Data/clean_fcs/Donor_3.fcs was chosen randomly for plotting
.
.

Plotting....X138Ba

Plotting....X209Bi

Plotting....X140Ce_EQ

Plotting....X133Cs

Plotting....X161Dy

Plotting....X162Dy_CD28

Plotting....X163Dy

Plotting....X164Dy_CD34

Plotting....X166Er
```

```
Plotting....X167Er_CD95

Plotting....X168Er_CXCR5

Plotting....X170Er

Plotting....X151Eu_EQ_._CD39

Plotting....X153Eu_EQ_._CD3

Plotting....X155Gd_CD45RO

Plotting....X156Gd_CD14

Plotting....X158Gd_CD27

Plotting....X160Gd_CD25

Plotting....X165Ho_EQ

Plotting....X127I

Plotting....X113In

Plotting....X115In

Plotting....X139La

Plotting....X175Lu_EQ_._PD.L1

Plotting....X142Nd_HLA.DR

Plotting....X143Nd_CD57

Plotting....X144Nd_CD33

Plotting....X145Nd_CXCR3

Plotting....X146Nd_CD8a

Plotting....X148Nd

Plotting....X150Nd_CD103

Plotting....X208Pb

Plotting....X102Pd

Plotting....X104Pd

Plotting....X105Pd

Plotting....X106Pd

Plotting....X108Pd

Plotting....X110Pd

Plotting....X141Pr_CD45RA

Plotting....X195Pt_Cisplatin

Plotting....X147Sm_CD4

Plotting....X149Sm_PERFORIN
```

```
Plotting....X152Sm_CD11C

Plotting....X154Sm_IgM

Plotting....X159Tb_CD19

Plotting....X169Tm_TCRgd

Plotting....X89Y_CD45

Plotting....X171Yb_GrzB

Plotting....X172Yb_CD127

Plotting....X173Yb_CD56

Plotting....X174Yb_TIGIT

Plotting....X176Yb_CD16
```

Out[1]:
```
.
├── RDS
│   ├── corrected_SE.rds
│   └── pheno_umap_SE.rds
├── Tables
│   ├── clusters_proportions_per_group.csv
│   ├── clusters_proportions_per_sample.csv
│   ├── heatmap_markers_median.csv
│   ├── samples correlation matrix pvals.csv
│   ├── samples correlation matrix.csv
│   ├── treated correlation matrix pvals.csv
│   └── treated correlation matrix.csv
├── UMAPs
│   ├── Markers intensity per group
│   ├── Overall markers intensity
│   ├── groups_umap.pdf
│   └── universal_umap.pdf
├── cluster abundaces correlation in group treated.pdf
├── cluster abundaces correlation in samples.pdf
├── clusters_heatmap.pdf
├── pie chart.pdf
├── sample_cluster_col_plot.pdf
├── stacked column plot.pdf
├── stats
│   ├── Cluster abundance
│   └── Differential expression
└── violins
    ├── Markers intensity per group
    └── Overall markers intensity
```

Out[10]: 15

In [ ]:
```