Please run :

if (!requireNamespace("BiocManager", quietly = TRUE))

install.packages("BiocManager")

BiocManager::install("FlowSOM")

To install the FlowSOM package as there may be issues installing Franken if this isn’t done separately first.

Next please download sample cytof data from figshare repo and save it in a folder of your choosing (the path to your data folder will henceforth be referred to as *yourdatafolder*):

<https://figshare.com/articles/Levine_32dim_fcs/11295719>

Full citation from raw data:

**Single-Cell Mass Cytometry of Differential Immune and Drug Responses Across a Human Hematopoietic Continuum**

By Sean C. Bendall, Erin F. Simonds, Peng Qiu, El-ad D. Amir, Peter O. Krutzik, Rachel Finck, Robert V. Bruggner, Rachel Melamed, Angelica Trejo, Olga I. Ornatsky, Robert S. Balderas, Sylvia K. Plevritis, Karen Sachs, Dana Pe’er, Scott D. Tanner, Garry P. Nolan

*Science*06 May 2011 : 687-696

This data has been pre-processed according to :

Weber, L.M. and Robinson, M.D. (2016), Comparison of clustering methods for high‐dimensional single‐cell flow and mass cytometry data. Cytometry, 89: 1084-1096. doi:[10.1002/cyto.a.23030](https://doi.org/10.1002/cyto.a.23030)

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