IO17 | Large Scale Bioinformatics for Immuno-Oncology

Deconvolution: exercise 5

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Analyze the PBMC expression data with another algorithm, **DeconRNASeq**, using the LM22 signature matrix.

DeconRNASeq R package:
https://www.bioconductor.org/packages/release/bioc/html/DeconRNASeq.html

```
library("DeconRNASeq")
results <- DeconRNASeq(mixture, signature)
cellfractions <- results$out.all
```

Assess the performance using the PBMC flow cytometry data.

Run again the analysis and the performance assessment after removing from the signature matrix the naïve B cells. What happens to the fraction of memory B cell cells?