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Quizzes due Nov 19, 2023 00:37 CST

## Assignment Setup

The `leukemiasEset` contains 60 sets of bone marrow gene expression data from patients with one of the 4 main types of leukemia (ALL, AML, CLL, CML) as well as control patients without leukemia (NoL).

Install and load the `leukemiasEset` data from the **leukemiasEset** Bioconductor package:

```
# BiocManager::install("leukemiasEset")    # install if
library(leukemiasEset)<

## Loading required package: Biobase

## Loading required package: BiocGenerics

## Loading required package: parallel

##

## Attaching package: 'BiocGenerics'

## The following objects are masked from 'package:parallel':
##
##   clusterApply, clusterApplyLB, clusterCall, clusterExport, clusterMap, parApply, parCapply, parLapply, parLapplyLB, parRapply, parSapply, parSapplyLB

## The following objects are masked from 'package:dplyr':
##
##   combine, intersect, setdiff, union

## The following objects are masked from 'package:stats':
##
##   IQR, mad, sd, var, xtabs

## The following objects are masked from 'package:base':
##
##   anyDuplicated, append, as.data.frame, basename, cbind, colnames, dirname, do.call, duplicated, eval, evalq, Filter, find, get, grep, grepl, intersect, is.unsorted, lapply, Map, mapply, max,
##   min, morder, paste, pmax, pmax.int, pmin, pmin.int, Position, rbind, Reduce, rownames, sapply, setdiff, sort, str, sub, tapply, union, unique, unsplit, which, which.max, which.min

## Welcome to Bioconductor
##
##   Vignettes contain introductory material; view with
##   'browseVignettes()'. To cite Bioconductor, see
##   'citation("Biobase")', and for packages 'citation("pkgname")'

data(leukemiasEset)
```

These data are stored in a container called an *ExpressionSet*. In future courses, we will learn how to work with *ExpressionSets* directly, but for now we can extract gene expression data as a

directly, but for now we can extract gene expression data as a matrix `dat` (features are rows, columns are samples):

```
dat = exprs(leukemiasEset)
```

We can also create a vector noting which type of leukemia is present in each sample:

```
leuk = leukemiasEset$LeukemiaType
```

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