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**High-Dimensional Data Analysis**

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**Course** Progress Dates Discussion Data Analysis for Life Sciences Series FAQ

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## Quiz

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## Assignment Setup

The `bladderbatch` dataset from Bioconductor is a collection of gene expression data on bladder cancers from 5 different batches.

```r
if (!requireNamespace("BiocManager", quietly = TRUE))
    install.packages("BiocManager")

BiocManager::install("bladderbatch")

library(bladderbatch)
data(bladderdata)

# Get the expression data
edata = exprs(bladderEset)
# Get the pheno data
pheno = pData(bladderEset)
```

Create a reduced dataset containing only batches 1-3. Save the subsetted expression data as `expr` and save the subsetted sample data as `pdata`:

```r
ind = which(pheno$batch %in% 1:3)

# subset expression data
expr = edata[ ,ind]

# subset pheno data and redefine factor levels
```

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