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Last login: Sun Sep 22 15:44:40 on ttys000
(base) Vasu's MacBook Pro:~ vasugoel$ r

R version 3.6.1 (2019-07-05) -- "Action of the Toes"
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Platform: x86_64-apple-darwin15.6.0 (64-bit)

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  Natural language support but running in an English locale

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Type 'q()' to quit R.

> library(dslabs)
> data("tissue_gene_expression")
> class(tissue_gene_expression)
[1] "list"
> names(tissue_gene_expression)
[1] "x" "y"
> class(tissue_gene_expression$x)
[1] "matrix"
> class(tissue_gene_expression$y)
[1] "factor"
> dim(tissue_gene_expression$x)
[1] 189 500
> dim(as.matrix(tissue_gene_expression$y))
[1] 189   1
> tissue_gene_expression$x[1:14, 1:14]
                 MAML1     LHPP   SEPT10   B3GNT4  ZNF280D    SOX12 C21orf62
cerebellum_1  9.825680 8.327163 5.499382 8.692371 5.642305 6.254751 5.840938
cerebellum_2  9.631247 8.542827 5.644292 8.833679 5.685083 6.289460 6.065646
cerebellum_3  9.690548 8.476486 5.717187 8.498623 5.958232 6.215924 5.771117
cerebellum_4  9.991592 8.506430 5.789430 8.421143 5.736563 6.512055 5.851617
cerebellum_5  9.578130 8.371783 5.779698 8.818455 5.630886 6.201556 5.965732
cerebellum_6  9.860121 8.278559 5.718611 8.728139 5.708949 6.367384 5.769961
cerebellum_7  9.773119 8.429068 5.833339 8.641901 6.316711 6.251236 5.904653
cerebellum_8  9.683163 8.544539 5.635356 8.810830 5.867560 6.368056 5.925835
cerebellum_9  9.989940 9.350519 6.873389 8.846305 5.749636 6.326722 5.828319
cerebellum_10 10.375016 8.893877 5.920607 8.707563 5.525131 6.616960 5.733619
cerebellum_11  9.933177 8.446754 5.861144 8.645942 5.797602 6.249561 5.929906
cerebellum_12 10.168858 8.344781 5.892142 8.561938 5.898702 6.378242 5.802645
cerebellum_13  9.627088 8.464176 5.694087 8.797170 5.616163 6.297914 6.037832
cerebellum_14  9.871508 9.391781 6.905480 8.600135 6.113970 6.557725 5.845348
                  PER3   HOXA10    HOXC5    BLVRB     ZIM2    HEMK1      FAP
cerebellum_1  8.330565 5.520803 7.660495 7.669237 8.355588 7.336959 6.255661
cerebellum_2  8.263576 5.528077 7.569041 7.779377 8.647475 7.282120 6.382161
cerebellum_3  9.102294 5.599405 7.418460 7.552049 8.853757 7.235601 6.124687
cerebellum_4  9.210058 5.561197 7.332254 7.839703 8.202195 7.206341 6.275629
cerebellum_5  8.502172 5.601099 7.535668 7.598154 8.583114 7.530148 6.344579
cerebellum_6  8.766777 5.681404 7.535398 7.720602 8.917125 7.380461 6.163775
cerebellum_7  9.347572 5.554998 7.377026 7.808214 8.873113 7.302264 6.074489
cerebellum_8  8.303106 5.702986 7.468757 7.914037 8.245058 7.493227 6.226500
cerebellum_9  8.735844 5.532744 7.337115 7.797350 8.147067 7.382768 5.961671
cerebellum_10 7.236387 5.958967 7.314246 8.049486 8.528420 7.653198 6.017743
cerebellum_11 8.740302 5.571117 7.300918 7.833630 8.929024 7.438914 6.054079
cerebellum_12 8.759783 5.675978 7.354098 7.883878 8.521498 7.154629 6.203950
cerebellum_13 8.526193 5.947825 7.359543 7.495558 8.791565 7.490911 6.212345
```

```
cerebellum_14 8.593477 5.632233 7.210026 7.986107 8.506319 7.570622 6.053410
> tissue_gene_expression$y[14]
[1] cerebellum
Levels: cerebellum colon endometrium hippocampus kidney liver placenta
> table(tissue_gene_expression$y)

 cerebellum       colon endometrium hippocampus      kidney       liver
         38          34          15          31          39          26
   placenta
          6
>
>
> d <- dist(tissue_gene_expression$x)
> class(d)
[1] "dist"
> dim(as.matrix(d))
[1] 189 189
> as.matrix(d)[1:5, 1:5]
             cerebellum_1 cerebellum_2 cerebellum_3 cerebellum_4 cerebellum_5
cerebellum_1     0.000000     7.005922     6.635272     7.331041     5.191081
cerebellum_2     7.005922     0.000000     7.034252     6.673085     6.375472
cerebellum_3     6.635272     7.034252     0.000000     5.317608     5.949134
cerebellum_4     7.331041     6.673085     5.317608     0.000000     6.739160
cerebellum_5     5.191081     6.375472     5.949134     6.739160     0.000000
>
>
> ind <- c(1, 2, 39, 40, 73, 74)
> as.matrix(d)[ind,ind]
             cerebellum_1 cerebellum_2   colon_1   colon_2 endometrium_1
cerebellum_1      0.000000     7.005922 22.694801 22.699755      21.12763
cerebellum_2      7.005922     0.000000 22.384821 22.069557      20.87910
colon_1          22.694801    22.384821  0.000000  8.191935      14.99672
colon_2          22.699755    22.069557  8.191935  0.000000      14.80355
endometrium_1    21.127629    20.879099 14.996715 14.803545       0.00000
endometrium_2    21.780792    20.674802 18.089213 17.004456      14.29405
             endometrium_2
cerebellum_1       21.78079
cerebellum_2       20.67480
colon_1            18.08921
colon_2            17.00446
endometrium_1      14.29405
endometrium_2       0.00000
>
>
> image(as.matrix(d))
>
```