**Übung 7**

**Genexpressionsanalyse**

**Aufgabe 7.1**

**Ein Bild, das Text enthält.

Automatisch generierte BeschreibungAufgabe 7.2**

Ein Bild, das Text enthält.

Automatisch generierte Beschreibung

**Aufgabe 7.3**

100 Gene getestet: Man kann den kleinsten Effekt als signifikanter Effekt erkennen, d.h. der p-Wert sagt nicht notwendigerweise etwas über die Effektgröße aus. Daher verwendet man die multiple-testing Korrektur – um das Signifikanzniveau anzupassen.

Berechnung der Bonferroni-Korrektur -> α\* = α/100 = 0.05/100 = 5\*

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Gene | HER2 | RAS | BRCA1 | BRCA2 | p53 | TFAM | COX1 |
| p−Wert |  |  |  |  |  |  | 0.04 |
| Signifikant nach der Korrektur? | ja | ja | ja | ja | nicht mehr | nicht mehr | nicht mehr |

Die getestenen Gene sind Onkogene, daher stammt das eine Gewebe aus einem krebserkrankten und das andere aus einem gesunden Patienten.

**Aufgabe 7.4**

> chooseCRANmirror()

Secure CRAN mirrors

1: 0-Cloud [https]

2: Australia (Canberra) [https]

3: Australia (Melbourne 1) [https]

4: Australia (Melbourne 2) [https]

5: Australia (Perth) [https]

6: Austria [https]

7: Belgium (Brussels) [https]

8: Brazil (PR) [https]

9: Brazil (RJ) [https]

10: Brazil (SP 1) [https]

11: Brazil (SP 2) [https]

12: Bulgaria [https]

13: Canada (MB) [https]

14: Canada (ON 3) [https]

15: Chile (Santiago) [https]

16: China (Beijing 2) [https]

17: China (Beijing 3) [https]

18: China (Hefei) [https]

19: China (Hong Kong) [https]

20: China (Guangzhou) [https]

21: China (Lanzhou) [https]

22: China (Nanjing) [https]

23: China (Shanghai 2) [https]

24: China (Shenzhen) [https]

25: Colombia (Cali) [https]

26: Costa Rica [https]

27: Cyprus [https]

28: Czech Republic [https]

29: Denmark [https]

30: East Asia [https]

31: Ecuador (Cuenca) [https]

32: Ecuador (Quito) [https]

33: Estonia [https]

34: France (Lyon 1) [https]

35: France (Lyon 2) [https]

36: France (Marseille) [https]

37: France (Paris 1) [https]

38: Germany (Erlangen) [https]

39: Germany (Leipzig) [https]

40: Germany (Göttingen) [https]

41: Germany (Münster) [https]

42: Germany (Regensburg) [https]

43: Greece [https]

44: Hungary [https]

45: Iceland [https]

46: India [https]

47: Indonesia (Jakarta) [https]

48: Iran (Mashhad) [https]

49: Italy (Milano) [https]

50: Italy (Padua) [https]

51: Japan (Tokyo) [https]

52: Korea (Gyeongsan-si) [https]

53: Korea (Seoul 1) [https]

54: Korea (Ulsan) [https]

55: Malaysia [https]

56: Mexico (Mexico City) [https]

57: Morocco [https]

58: Netherlands [https]

59: New Zealand [https]

60: Norway [https]

61: South Africa (Johannesburg) [https]

62: Spain (A Coruña) [https]

63: Spain (Madrid) [https]

64: Sweden (Borås) [https]

65: Sweden (Umeå) [https]

66: Switzerland [https]

67: Taiwan (Taipei) [https]

68: Turkey (Denizli) [https]

69: Turkey (Istanbul) [https]

70: Turkey (Mersin) [https]

71: UK (Bristol) [https]

72: UK (London 1) [https]

73: USA (IA) [https]

74: USA (KS) [https]

75: USA (MI) [https]

76: USA (OH) [https]

77: USA (OR) [https]

78: USA (TN) [https]

79: USA (TX 1) [https]

80: Uruguay [https]

81: (other mirrors)

Selection: install.packages("BiocManager")

Enter an item from the menu, or 0 to exit

Selection: 0

> source("~/Universität/12. Semester/Bioinformatik/R/Assignment7/DESEQ2\_example.R")

Loading required package: S4Vectors

Loading required package: stats4

Loading required package: BiocGenerics

Attaching package: ‘BiocGenerics’

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, match, mget, order, paste, pmax, pmax.int, pmin, pmin.int,

Position, rank, rbind, Reduce, rownames, sapply, setdiff, sort, table, tapply, union,

unique, unsplit, which.max, which.min

Attaching package: ‘S4Vectors’

The following objects are masked from ‘package:base’:

expand.grid, I, unname

Loading required package: IRanges

Attaching package: ‘IRanges’

The following object is masked from ‘package:grDevices’:

windows

Loading required package: GenomicRanges

Loading required package: GenomeInfoDb

Loading required package: SummarizedExperiment

Loading required package: MatrixGenerics

Loading required package: matrixStats

Attaching package: ‘MatrixGenerics’

The following objects are masked from ‘package:matrixStats’:

colAlls, colAnyNAs, colAnys, colAvgsPerRowSet, colCollapse, colCounts, colCummaxs,

colCummins, colCumprods, colCumsums, colDiffs, colIQRDiffs, colIQRs, colLogSumExps,

colMadDiffs, colMads, colMaxs, colMeans2, colMedians, colMins, colOrderStats, colProds,

colQuantiles, colRanges, colRanks, colSdDiffs, colSds, colSums2, colTabulates,

colVarDiffs, colVars, colWeightedMads, colWeightedMeans, colWeightedMedians,

colWeightedSds, colWeightedVars, rowAlls, rowAnyNAs, rowAnys, rowAvgsPerColSet,

rowCollapse, rowCounts, rowCummaxs, rowCummins, rowCumprods, rowCumsums, rowDiffs,

rowIQRDiffs, rowIQRs, rowLogSumExps, rowMadDiffs, rowMads, rowMaxs, rowMeans2,

rowMedians, rowMins, rowOrderStats, rowProds, rowQuantiles, rowRanges, rowRanks,

rowSdDiffs, rowSds, rowSums2, rowTabulates, rowVarDiffs, rowVars, rowWeightedMads,

rowWeightedMeans, rowWeightedMedians, rowWeightedSds, rowWeightedVars

Loading required package: Biobase

Welcome to Bioconductor

Vignettes contain introductory material; view with 'browseVignettes()'. To cite

Bioconductor, see 'citation("Biobase")', and for packages 'citation("pkgname")'.

Attaching package: ‘Biobase’

The following object is masked from ‘package:MatrixGenerics’:

rowMedians

The following objects are masked from ‘package:matrixStats’:

anyMissing, rowMedians

Error in h(simpleError(msg, call)) :

error in evaluating the argument 'x' in selecting a method for function 'as.matrix': cannot open the connection

In addition: Warning message:

In file(file, "rt") :

cannot open file './data/df\_sc.csv': No such file or directory

> read.csv("C:\\Users\\raliz\\Documents\\Universität\\12. Semester\\Bioinformatik\\R\\Assignment7\\df\_sc.csv")

gene ctr1 ctr2 ctr3 trt1 trt2 trt3 length

1 Sobic.001G000200 338 324 246 291 202 168 1982

2 Sobic.001G000400 49 21 53 16 16 11 4769

3 Sobic.001G000700 39 49 30 46 52 25 1096

4 Sobic.001G000800 530 530 499 499 386 264 3868

5 Sobic.001G001000 12 3 4 3 10 7 702

6 Sobic.001G001132 4 2 2 3 4 1 291

7 Sobic.001G001200 2 3 4 3 1 1 2263

8 Sobic.001G001300 24 34 38 24 21 13 1592

9 Sobic.001G001400 826 968 712 918 669 472 4498

10 Sobic.001G001900 163 137 137 121 81 75 3173

11 Sobic.001G002000 248 242 243 214 161 112 4274

12 Sobic.001G002200 100 39 78 35 30 18 4960

13 Sobic.001G002700 2 4 3 7 3 1 1856

14 Sobic.001G002800 62 144 57 102 91 47 2846

15 Sobic.001G003000 16 15 30 27 38 6 3046

16 Sobic.001G003100 1389 1400 1408 1274 1258 750 2397

17 Sobic.001G003200 137 237 172 172 95 82 1668

18 Sobic.001G003300 47 20 37 4 24 14 2990

19 Sobic.001G003500 66 41 68 67 64 33 2635

20 Sobic.001G003900 24 12 23 10 7 6 2052

21 Sobic.001G004000 6 34 11 32 18 16 2306

22 Sobic.001G004100 61 57 63 56 37 27 2046

23 Sobic.001G004200 120 72 96 83 81 42 1563

24 Sobic.001G004400 993 583 1001 688 553 360 4241

25 Sobic.001G004700 20 17 26 12 15 21 2550

26 Sobic.001G004800 13 15 16 25 25 33 1063

27 Sobic.001G005000 10 6 10 9 13 5 1599

28 Sobic.001G005200 298 307 319 141 166 123 2163

29 Sobic.001G005500 86 158 125 50 92 62 1229

30 Sobic.001G005600 220 193 231 248 195 100 2542

31 Sobic.001G005800 128 59 114 66 65 51 2538

32 Sobic.001G005900 62 60 65 60 70 20 796

33 Sobic.001G006000 29 43 35 28 42 36 2566

34 Sobic.001G006400 86 137 129 135 127 79 2087

35 Sobic.001G006500 6 6 4 1 10 3 1977

36 Sobic.001G006600 3 7 6 4 1 6 5575

37 Sobic.001G006700 438 349 390 713 336 228 3415

38 Sobic.001G006900 11 23 6 10 18 8 855

39 Sobic.001G007000 77 101 85 84 74 38 1647

40 Sobic.001G007100 6 2 1 2 3 1 3093

41 Sobic.001G007200 156 175 219 207 168 108 3586

42 Sobic.001G007300 48 74 54 51 45 34 552

43 Sobic.001G007400 50 34 41 45 43 20 1837

44 Sobic.001G007500 88 69 98 71 62 34 1900

45 Sobic.001G007600 152 189 164 181 175 108 1904

46 Sobic.001G007800 194 126 193 115 116 69 1891

47 Sobic.001G008000 26 12 21 20 20 5 1797

48 Sobic.001G008100 169 114 171 143 165 86 1275

49 Sobic.001G008200 67 47 68 65 56 28 3519

50 Sobic.001G008300 38 22 27 27 32 22 2169

51 Sobic.001G008400 7 3 7 1 8 2 1801

52 Sobic.001G008500 56 43 57 42 52 29 2428

53 Sobic.001G008600 16 37 16 73 44 18 2597

54 Sobic.001G008800 5 10 5 5 7 1 895

55 Sobic.001G009200 15 5 25 16 7 6 1906

56 Sobic.001G009300 308 379 336 359 311 214 1392

57 Sobic.001G009500 38 91 64 32 38 7 1976

58 Sobic.001G009600 294 312 284 282 176 94 2872

59 Sobic.001G009700 1081 192 897 280 535 317 7022

60 Sobic.001G009800 333 488 341 676 490 254 1662

61 Sobic.001G009900 10 10 7 5 10 6 1008

62 Sobic.001G010100 834 981 996 403 595 430 1448

63 Sobic.001G010200 55 137 69 112 90 51 1949

64 Sobic.001G010400 109 110 108 126 116 72 944

65 Sobic.001G010500 5 4 13 2 5 2 2555

66 Sobic.001G010600 295 176 279 220 188 113 1404

67 Sobic.001G010700 451 351 422 385 361 208 1825

68 Sobic.001G010800 35 60 55 43 73 34 1090

69 Sobic.001G010900 29 50 42 33 35 11 2970

70 Sobic.001G011000 350 217 357 351 361 224 1827

71 Sobic.001G011200 191 163 236 205 239 108 1041

72 Sobic.001G011400 23 111 47 16 29 13 1379

73 Sobic.001G011600 16 29 17 5 4 2 1976

74 Sobic.001G011700 85 109 146 124 159 81 2170

75 Sobic.001G011800 16 11 17 8 12 6 762

76 Sobic.001G012000 7 56 18 3 21 12 2442

77 Sobic.001G012100 22 26 20 26 21 10 1168

78 Sobic.001G012200 5 40 6 1 1 1 1864

79 Sobic.001G012700 8 12 8 7 5 7 2363

80 Sobic.001G012800 29 97 53 61 38 37 1917

81 Sobic.001G012900 333 346 333 312 322 158 6526

82 Sobic.001G013000 45 22 31 14 14 3 1210

83 Sobic.001G013100 93 67 81 77 97 39 1514

84 Sobic.001G013200 112 90 129 94 108 68 1002

85 Sobic.001G013300 106 75 117 84 62 37 3009

86 Sobic.001G013500 42 20 35 40 38 27 832

87 Sobic.001G013600 3 1 4 3 1 4 1416

88 Sobic.001G013800 12 7 7 8 25 11 2085

89 Sobic.001G013900 12 13 10 7 4 11 2738

90 Sobic.001G014000 5 17 3 3 8 6 1260

91 Sobic.001G014100 126 146 121 157 90 53 3363

92 Sobic.001G014200 196 176 192 259 186 111 2176

93 Sobic.001G014500 80 64 105 58 59 36 1228

94 Sobic.001G014800 367 412 398 415 303 234 1378

95 Sobic.001G014900 118 68 97 61 68 63 2828

96 Sobic.001G015100 5 8 12 16 9 3 1374

97 Sobic.001G015200 62 67 79 35 37 29 2464

98 Sobic.001G015400 513 377 410 361 277 178 4868

99 Sobic.001G015500 93 76 118 75 82 51 2156

100 Sobic.001G015700 156 22 126 41 83 84 1456

101 Sobic.001G015800 32 36 33 48 39 15 2460

102 Sobic.001G016000 32 31 30 39 32 10 1997

103 Sobic.001G016201 2 1 5 1 1 1 1408

104 Sobic.001G016600 81 58 74 51 46 37 3924

105 Sobic.001G016700 101 125 118 127 95 57 3376

106 Sobic.001G016800 17 4 11 9 1 11 1620

107 Sobic.001G016900 993 693 1010 614 381 246 2428

108 Sobic.001G017000 4 10 5 2 4 1 983

109 Sobic.001G017100 623 615 674 517 721 426 1656

110 Sobic.001G017200 312 277 291 256 240 118 1620

111 Sobic.001G017300 13 8 10 4 1 7 2070

112 Sobic.001G017600 16 17 27 30 13 22 1801

113 Sobic.001G017700 83 43 64 51 39 23 2314

114 Sobic.001G017800 24 18 20 12 13 6 2314

115 Sobic.001G017900 30 10 26 19 9 16 1622

116 Sobic.001G018000 38 48 35 22 24 10 2695

117 Sobic.001G018100 121 115 113 103 78 49 1884

118 Sobic.001G018200 49 48 54 62 74 39 2919

119 Sobic.001G018500 66 62 72 68 71 48 793

120 Sobic.001G018800 23 10 11 11 16 10 318

121 Sobic.001G018900 687 464 751 544 615 377 1160

122 Sobic.001G019200 32 28 34 15 19 21 1685

123 Sobic.001G019300 37 67 52 27 49 38 3080

124 Sobic.001G019400 47 23 26 30 20 23 4016

125 Sobic.001G019700 1 6 6 6 7 6 4232

[ reached 'max' / getOption("max.print") -- omitted 15827 rows ]

> genes <- read.csv(file ="C:\\Users\\raliz\\Documents\\Universität\\12. Semester\\Bioinformatik\\R\\Assignment7\\df\_sc.csv")