

yeastCC

March 19, 2011

breeden

Breeden et al. yeast cell cycle experiment

Description

ExpressionSet instance; 50 samples from a 25-sample dye-swap of alpha-synchronized yeast cultures

Usage

```
data(breeden)
```

Format

The format is:

Formal class 'ExpressionSet' [package "Biobase"] with 7 slots

..@ assayData :<environment: 0x10221ebc8>

..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots

.. ..@ varMetadata :'data.frame': 37 obs. of 1 variable:

..\$ labelDescription: chr [1:37] NA NA NA NA ...

.. ..@ data :'data.frame': 50 obs. of 37 variables:

..\$ title : Factor w/ 50 levels "Yeast cell cycle-time point 0 min 2001-08-17_0000.rfm Yeast W303 cells",...: 1 29 3 15 17 19 21 23 25 27 ...

..\$ geo_accession : Factor w/ 50 levels "GSM112133","GSM112134",...: 1 2 3 4 5 6 7 8 9 10

...

..\$ status : Factor w/ 1 level "Public on Aug 05 2006": 1 1 1 1 1 1 1 1 1 1 ...

..\$ submission_date : Factor w/ 1 level "Jun 01 2006": 1 1 1 1 1 1 1 1 1 1 ...

..\$ last_update_date : Factor w/ 1 level "Jun 23 2006": 1 1 1 1 1 1 1 1 1 1 ...

..\$ type : Factor w/ 1 level "RNA": 1 1 1 1 1 1 1 1 1 1 ...

..\$ channel_count : Factor w/ 1 level "2": 1 1 1 1 1 1 1 1 1 1 ...

..\$ source_name_ch1 : Factor w/ 25 levels "Yeast cell cycle-time point 0 min",...: 1 15 2 8 9 10 11 12 13 14 ...

..\$ organism_ch1 : Factor w/ 1 level "Saccharomyces cerevisiae": 1 1 1 1 1 1 1 1 1 1 ...

..\$ characteristics_ch1 : Factor w/ 25 levels "Yeast cell cycle-time point 0 min",...: 1 15 2 8 9 10 11 12 13 14 ...

..\$ treatment_protocol_ch1 : Factor w/ 1 level "Cells were arrested with alpha factor, and released into YEPD to get a synchronized population. Cells were sampled every 5 min a"l __truncated__": 1 1 1 1 1 1 1 1 1 1 ...

```

.. .. ..$ molecule_ch1 : Factor w/ 1 level "total RNA": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..$ label_ch1 : Factor w/ 2 levels "Cy3","Cy5": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..$ source_name_ch2 : Factor w/ 1 level "Yeast asynchronous culture": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..$ organism_ch2 : Factor w/ 1 level "Saccharomyces cerevisiae": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..$ characteristics_ch2 : Factor w/ 1 level "Yeast asynchronous culture": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..$ treatment_protocol_ch2 : Factor w/ 1 level "Cells were grown overnight to an OD of 0.6
in YEPD": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..$ molecule_ch2 : Factor w/ 1 level "total RNA": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..$ label_ch2 : Factor w/ 2 levels "Cy3","Cy5": 2 2 2 2 2 2 2 2 2 2 ...
.. .. ..$ description : Factor w/ 1 level "Yeast cell cycle": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..$ data_processing : Factor w/ 1 level "normalized log ratio using Rosetta Resolver": 1 1 1 1
1 1 1 1 1 1 ...
.. .. ..$ platform_id : Factor w/ 1 level "GPL1914": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..$ contact_name : Factor w/ 1 level "Tata,,Pramila": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..$ contact_email : Factor w/ 1 level "tpramila@fhcrc.org": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..$ contact_phone : Factor w/ 1 level "(206)6674483": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..$ contact_laboratory : Factor w/ 1 level "Breeden Lab": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..$ contact_department : Factor w/ 1 level "Basic Sciences": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..$ contact_institute : Factor w/ 1 level "FHCRC": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..$ contact_address : Factor w/ 1 level "1100, Fairview Avenue N": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..$ contact_city : Factor w/ 1 level "Seattle": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..$ contact_state : Factor w/ 1 level "WA": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..$ contact_zip/postal_code: Factor w/ 1 level "98109": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..$ contact_country : Factor w/ 1 level "USA": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..$ supplementary_file : Factor w/ 50 levels "ftp://ftp.ncbi.nih.gov/pub/geo/DATA/supplementary/samples/GSM111
1 2 3 4 5 6 7 8 9 10 ...
.. .. ..$ data_row_count : Factor w/ 1 level "6228": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..$ mins : num [1:50] 0 5 10 15 20 25 30 35 40 45 ...
.. .. ..$ sign : num [1:50] 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..@ dimLabels : chr [1:2] "sampleNames" "sampleColumns"
.. .. ..@ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots
.. .. ..@ featureData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots
.. .. ..@ varMetadata :'data.frame': 10 obs. of 3 variables:
.. .. .. ..$ Column : chr [1:10] "ID" "ORF" "SPOT_ID" "Gene" ...
.. .. .. ..$ Description : Factor w/ 2 levels "", "LINK_PRE:\\"http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?CMD=search&
LINK_SUF:\\"[gene name]\"": 1 2 1 1 1 1 1 1 1 1
.. .. .. ..$ labelDescription: chr [1:10] NA NA NA NA ...
.. .. ..@ data :'data.frame': 6228 obs. of 10 variables:
.. .. .. ..$ ID : Factor w/ 6337 levels "YPR105C","YPR106W",...: 116 6322 119 6327 124 133 6328
6329 6330 6331 ...
.. .. .. ..$ ORF : Factor w/ 6222 levels "YPR105C","YPR106W",...: 6221 6221 6221 6221 6221
6221 6221 6221 6221 6221 ...
.. .. .. ..$ SPOT_ID : chr [1:6228] "<blank>" "blank" "E. coli control" "empty" ...
.. .. .. ..$ Gene : Factor w/ 3347 levels "", "AOS1","APG13",...: 1 1 1 1 1 1 1 1 1 1 ...
.. .. .. ..$ SGDID : Factor w/ 6205 levels "S0006309","S0006310",...: 1001 1001 1001 1001 1001
1001 1001 1001 1001 1001 ...
.. .. .. ..$ CHR : Factor w/ 17 levels "XVI","XV","XIV",...: 13 13 13 13 13 13 13 13 13 13 ...
.. .. .. ..$ ORF.Length: chr [1:6228] "" "" "" "" ...
.. .. .. ..$ Process : Factor w/ 488 levels "DNA repair*",...: 194 194 194 194 194 194 194 194 194
194 ...
.. .. .. ..$ Function : Factor w/ 760 levels "CDP-diacylglycerol-inositol 3-phosphatidyltransferase",...:
215 215 215 215 215 215 215 215 215 ...

```

```

.. .. ..$ Component : Factor w/ 211 levels "19S proteasome regulatory particle",...: 90 90 90 90 90
90 90 90 90 90 ...
.. .. ..@ dimLabels : chr [1:2] "featureNames" "featureColumns"
.. .. ..@ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots
.. .. .. ..@ .Data:List of 1
.. .. .. ..$ : int [1:3] 1 1 0
..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots
.. .. ..@ name : chr [1:2] "Pramila T" "Breedden LL"
.. .. ..@ lab : chr "Fred Hutchinson Cancer Research Center, Seattle, Washington 98109, USA."
.. .. ..@ contact : chr ""
.. .. ..@ title : chr "The Forkhead transcription factor Hcm1 regulates chromosome segregation
genes and fills the S-phase gap in the transcriptional "|__truncated__
.. .. ..@ abstract : chr "Transcription patterns shift dramatically as cells transit from one phase of
the cell cycle to another. To better define this t"|__truncated__
.. .. ..@ url : chr "http://labs.fhcrc.org/breedden/cellcycle/index.html"
.. .. ..@ pubMedIds : chr "16912276"
.. .. ..@ samples : list()
.. .. ..@ hybridizations : list()
.. .. ..@ normControls : list()
.. .. ..@ preprocessing : list()
.. .. ..@ other : list()
.. .. ..@ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots
.. .. .. ..@ .Data:List of 1
.. .. .. ..$ : int [1:3] 1 0 0
..@ annotation : chr(0)
..@ protocolData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots
.. .. ..@ varMetadata :'data.frame': 0 obs. of 1 variable:
.. .. .. ..$ labelDescription: chr(0)
.. .. ..@ data :'data.frame': 50 obs. of 0 variables
.. .. ..@ dimLabels : chr [1:2] "sampleNames" "sampleColumns"
.. .. ..@ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots
.. .. .. ..@ .Data:List of 1
.. .. .. ..$ : int [1:3] 1 1 0
..@ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots
.. .. ..@ .Data:List of 4
.. .. .. ..$ : int [1:3] 2 10 0
.. .. .. ..$ : int [1:3] 2 5 5
.. .. .. ..$ : int [1:3] 1 3 0
.. .. .. ..$ : int [1:3] 1 0 0

```

Details

Retrieved from GEO using getGEO in package GEOquery, August 27 2009. Variables mins and sign added to pData manually.

Source

PMID 16912276; see url slot of experimentData slot.

Examples

```
data(breedden)
```

```
#
# show how to use the dye-swap 'sign' variable
#
plot(exprs(breeden) ["YBL002W", ] ~ breeden$mins)
plot(I(exprs(breeden) ["YBL002W", ] * breeden$sign) ~ breeden$mins)
```

orf800

Cell cycle regulated genes from Spellman et al. (1998)

Description

Vector of ORF names for the 800 cell cycle regulated genes identified by the analysis of Spellman et al. (1998). The expression measures and sample descriptions are stored in the `ExpressionSet` instance `yeastCC`.

Usage

```
data(orf800)
```

Format

The format is: chr [1:800] "YAL022C" "YAL040C" "YAL053W" "YAL067C" "YAR003W" "YAR007C"
...

Source

The 800 ORF names were obtained from the file "CellCycle98.xls" on the Yeast Cell Cycle Analysis Project website (<http://genome-www.stanford.edu/cellcycle/>). The raw data (images, TIFF) and processed data "combine.txt" used to create the `ExpressionSet` instance `yeastCC` are also available on the website. Gene annotation information is available from the Saccharomyces Genome Database (SGD, http://genome-www.stanford.edu/Saccharomyces/gene_list.shtml). The script "createYeastCC.R" for generating the `yeastCC` package is available in `../doc`.

References

Spellman et al. (1998). Comprehensive Identification of Cell Cycle-regulated Genes of the Yeast *Saccharomyces cerevisiae* by Microarray Hybridization. *Molecular Biology of the Cell*, 9: 3273-3297 (`../doc`).

Examples

```
data(orf800)
```

 spYCCmeta

metadata on yeast cell cycle microarray experiment

Description

data.frame instance with metadata on 800 genes

Usage

```
data(spYCCmeta)
```

Format

A data frame with 800 observations on the following 75 variables.

Process a factor with levels 4-nitroquinoline-N-oxide resistanceATP synthesis
 ...
 Function a factor with levels (1->6)-beta-glucan synthase subunit (putative)
 Glc7p regulatory subunit ...
 X a logical vector
 Peak a factor with levels G1 G2/MM/G1 S S/G2
 Phase.Order a numeric vector
 Cluster.Order a numeric vector
 ORF a factor with levels YAL022C YAL040C YAL053W YAL067C YAR003W YAR007C ...
 YPD a factor with levels AAD10 ACE2 ADA2 ADK2 AFR1 AGA1 AGA2 AGP1 ...
 SGD a factor with levels AAD10 ACE2 ADA2 ADK2 AFR1 AGA1 AGA2 ...
 YPD.1 a factor with levels YPD
 SGD.1 a factor with levels SGD
 MIPS a factor with levels MIPS
 n1 a numeric vector
 n2 a numeric vector
 Geomean a numeric vector
 Absolute a numeric vector
 g1 a numeric vector
 g2 a numeric vector
 Geomean.1 a numeric vector
 Absolute.1 a numeric vector
 Deletion a factor with levels irrelevant lethal undocumented viable
 Known. a factor with levels Known New New
 Description a factor with levels Inhibitor of Cdc28p/Cln1p and Cdc28p/Cln2p
 complexes involved in cell cycle arrest for mating1,3-beta-D-glucan
 synthase3\'-Phosphoadenylylsulfate reductase; part of the sulfate
 assimilation pathway ...
 Aggregate.Score a numeric vector

Phase a numeric vector

No. .Elements a numeric vector

Most.Relevant.Promoter.Elements a factor with levels AATAGATGACCCGATTTGGAAAAAGGTAAACAACA
 ATTTGATTGCCGAAAGAGGCCAAAAC GTAAATAGGTTGTC 156 TCTGCCAGCCAA C 253
 AAAGCCAGCCAT C 256 TATGCCAGCCAA C 276 AAGGCCAGCCTC C 293 TTGACCAGCTAA
 ...

X.1 a factor with levels ATATAGCGACCGAATCAGGAAAAG GTCAACAACGAAGC 102 CGAGCCAGCATT
 C 252 AAGACCAGCATGC 301 AGTGCCAGCAAA C 496 GAAGCCAGCACAC 550 GCGGCCAGCAAC
 c 106 attACGCGaaaat c 112 aaaACGCGagaaa c 121 ggaACGCGacgc ...

X.2 a factor with levels C 125 GCAACCAGCTCTC 146 CAAGCCAGCCAT C 195 CGCACCAGCAAC
 C 212 TATACCAGCGTTC 245 TAAACCAGCGCAC 402 TATGCCAGCAAA c 112 ttaACGCGatcga
 c 115 agtACGCGaaagg c 123 acaACGCGaacac c 127 gtgACGCGaaaaa ...

X.3 a factor with levels C 307 AAGACCAGCATT c 163 ctgACGCGcgaaa c 190 aatACGCGagaaa
 c 220 tagACGCGcctta c 241 cgaACGCGgaaact c 275 aaaACGCGaccgt c 282
 aagACGCGatttt c 289 attACGCGcatta c 290 aggACGCGgaaact ...

X.4 a factor with levels C 200 CAAACCAGCATC c 117 gtcACGCGaaaaa c 314 cctACGCGaaagt
 c 338 caaACGCGaaaaa c 359 acgACGCGccttc c 382 gttACGCGaagt c 384
 tcaACGCGaattt c 397 aaaACGCGgaaa c 440 gtgACGCGcggtt ...

X.5 a factor with levels C 306 GGAGCCAGCGCG c 467 accACGCGaaaag c 588 gaaACGCGcctaa
 w 266 ATAACCAGCAAA w 383 cagACGCGgagaac w 478 GGAGCCAGCGCG w401 tatCGCGAAAatt

X.6 a factor with levels C 337 AGAGCCAGCAAGC 417 TCGGCCAGCAAT c 501 acaACGCGaaaaa
 w 370 gcgACGCGaaaaa w 447 AGAGCCAGCAAG

X.7 a factor with levels C 388 GGAACCAGCAGA w 396 GGAACCAGCAGA

Number a numeric vector

SCB a factor with levels c 103 gacCACGAAAttt c 105 atgCACGAAAaag c 106 ctaCACGAAAcac
 c 108 tacCACGAAAgta c 110 ccaCACGAAAaga c 123 agaCACGAAAatgt c 127
 acaCACGAAAacg c 181 cagCACGAAAatgg ...

SCB.1 a factor with levels c178 tgaCACGAAAaac c232 gaaCACGAAAatgc c539 gtaCACGAAAttc
 w269 agcCACGAAAatgc w347 tgaCACGAAAatgt w541 agtCACGAAAacgc w601 tgtCACGAAAagt

SCB.2 a factor with levels c330 aacCACGAAAaaa c582 agtCACGAAAacgc w467 attCACGAAAata

SCB.3 a factor with levels w435 atcCACGAAAatc

X.8 a factor with levels w252 aacCACGAAAagt

Number.1 a numeric vector

SCB_d a factor with levels c 156 gatCGCGAAAttt c 184 cgaCGCGAAAatgc 218 cagCGCGAAAagt
 c 222 tatCGCGAAAaaa c 229 tgaCGCGAAAacgc c 237 tatCGCGAAAacga c 238
 atcCGCGAAAagga c 283 aagCGCGAAAaaa ...

SCB_d.1 a factor with levels c 126 tttCGCGAAAactg c 415 tttCGCGAAAatct c 566
 ttcCGCGAAAaaa c 592 aggCGCGAAAatc c 633 aaaCGCGAAAatgt c242 gaaCGCGAAAactt
 c297 ctcCGCGAAAaat c306 tcgCGCGAAAaga ...

SCB_d.2 a factor with levels c468 ccaCGCGAAAaga c508 tttCGCGAAAatct

SCB_d.3 a factor with levels c502 caaCGCGAAAaat

Number.2 a numeric vector

MCB a factor with levels w 126 gcaACGCGTcgw 187 caaACGCGTaca w 207 ctcACGCGTcgg
 w 209 attACGCGTttaw 226 cagACGCGTtgcw 228 acaACGCGTcttw 23 acaACGCGTgct
 w 267 cccACGCGTagg ...

MCB.1 a factor with levels w111 gaaACGCGTtct w124 ttgACGCGTttc w128 gtgACGCGTtat
w130 agaACGCGTtct w131 gcgACGCGTaac w138 aagACGCGTgaa w139 attACGCGTtta
w153 ctaACGCGTttt ...

MCB.2 a factor with levels w374 taaACGCGTcat

MCB.3 a factor with levels w309 aggACGCGTaaa

Number.3 a numeric vector

MCB_d a factor with levels c 106 attACGCGaaaat c 109 acaACGCGactggc 112 aaaACGCGagaaa
c 115 agtACGCGaaaggc 117 gtcACGCGaaaaa c 121 ggaACGCGacgc c 127
gtgACGCGaaaaa c 129 acaACGCGccccga ...

MCB_d.1 a factor with levels c 123 acaACGCGaacac c 136 aatACGCGattgg c 147
gcaACGCGagaga c 158 tctACGCGcgaag c 163 ctgACGCGcgaac 176 gcgACGCGgttgt
c 187 agtACGCGatttg c 189 gaaACGCGggcac ...

MCB_d.2 a factor with levels c 112 ttaACGCGatcga c 220 tagACGCGcctta c 294
ttcACGCGcttaac 382 gttACGCGaagt c 477 gcaACGCGcctggc 501 acaACGCGaaaa
c 549 attACGCGcacg c 557 tgtACGCGcgaac ...

MCB_d.3 a factor with levels c 617 gaaACGCGcagta w 50 gtaACGCGctttt

X.9 a factor with levels c 359 acgACGCGccttc

Number.4 a numeric vector

SFF a factor with levels AATAGATGACCCGATTTGGAAAAAGGTAAACAACAATG ATTTGATTGCCGAAAGAGGCCAAAA
GTAAATAGGTTGT CAAAACAAACCCAATAAAGAAAATCCAAAATATAGAAC GACTTTAACCTGTTTAGGAAAAA
GTAACAATAACA TCGAACAATTCTAAAAAGGTAAAT AAAAAACAATGGTA ...

Number.5 a factor with levels 1 2 3 4 ATATAGCGACCGAATCAGGAAAAGGTCAACAACGAAG

Swi5 a factor with levels C 102 CGAGCCAGCATT C 156 TCTGCCAGCCAA C 200 CAAACCAGCATC
C 252 AAGACCAGCATG C 253 AAAGCCAGCCAT C 256 TATGCCAGCCAA C 276 AAGCCAGCCTC
C 293 TTGACCAGCTAA ...

Swi5.1 a factor with levels C 125 GCAACCAGCTCT C 146 CAAGCCAGCCAT C 195 CGCACCAGCAAC
C 245 TAAACCAGCGCA C 301 AGTGCCAGCAAA C 306 GGAGCCAGCGCG C 307 AAGACCAGCATT
C 402 TATGCCAGCAAA ...

Swi5.2 a factor with levels C 212 TATACCAGCGTT C 337 AGAGCCAGCAAG c 19 AGAACCAGCTGA
c 320 ACCACCAGCTTA c 545 ACCACCAGCGTA c 569 TTCACCAGCGGC c 642 GAGACCAGCGGA
c 651 ATCACCAGCAAA ...

Swi5.3 a factor with levels C 388 GGAACCAGCAGAC 417 TCGGCCAGCAAT c 336 TTTACCAGCTCA
c 363 TGCACCAGCATT c 494 CTGGCCAGCAAG w 396 GGAACCAGCAGA

Number.6 a numeric vector

Swi5e a factor with levels c 102 CGAGCCAGCATT c 137 TAGGCCAGCAAA c 155 ACAACCAGCAGT
c 156 CTAACCAGCAAG c 16 AGAGCCAGCAGA c 174 TAAACCAGCATT c 184 ATGGCCAGCATA
c 200 CAAACCAGCATC ...

Swi5e.1 a factor with levels c 222 TTGACCAGCGCC c 256 TAAACCAGCAAA c 306 GGAGCCAGCGCG
c 307 AAGACCAGCATT c 637 GGAGCCAGCGAT w 265 TAAACCAGCAAT w 266 ATAACCAGCAAA
w 467 TGAGCCAGCAAT w 478 GGAGCCAGCGCG w 536 GAAACCAGCAAC w 554 ATGGCCAGCACC

Swi5e.2 a factor with levels c 337 AGAGCCAGCAAG c 417 TCGGCCAGCAAT c 642 GAGACCAGCGGA
w 447 AGAGCCAGCAAG

Swi5e.3 a factor with levels c 388 GGAACCAGCAGA w 396 GGAACCAGCAGA

Number.7 a numeric vector

```
ECB a factor with levels c 185 TTACCCATTTAGGAAA c 221 TTACCCAATTAGGAAA c 251
TTTCCCTTTAAGGAAA c 258 TTTCCCAAAAAGGAAA c 387 TTTCCCTTTTAGGAAA c
394 TTACCCACTTAGGAAA w 154 TTTCCCTTTTAGGAAA w 177 TTACCCACTTAGGAAA
w 229 TTACCCAGAAAGGAAA w 378 TTTCCCTAATAGGAAA w 453 TTTCCCGTTTAGGAAA
w 595 TTTCCCACTAAGGAAA
```

Number.8 a numeric vector

```
STE12 a factor with levels c 243 CCTTTTTTCAGTTTTCTATTTTTTAACACTGAAACT w 112 CCCTATTTGGTTGCAA
w 119 CCCAATGTAGAAAAGTACATCATATGAAACA w 218 CCTAATTGGGTAAGTACATGATGAAACA
w 224 CCAAAAAGGAAATTTACATGTTAAATGAAACC ...
```

```
MIG1.sites a factor with levels c 114 AATAGACTGGGG c 137 TCTATCCTGGGG c 147
TGAATGCTGGGG c 165 AATAAAGTGGGG c 215 TATAATGCGGGG c 304 AAATCGCCGGGG
c 332 AAATATCTGGGG c 368 AATTGCGCGGGG ...
```

```
X.10 a factor with levels c 161 AGTTTGGTGGGG c 262 AAGATGGTGGGG c 498 AAAAAACCGGGG
c 499 AAAAATGCGGGG w 296 TATTCGCGGGG w 578 CTTTTGCCGGGG
```

X.11 a logical vector

Details

taken from the Spellman support web site.

Source

cellcycle-www.stanford.edu

References

PMID 9843569

Examples

```
data(spYCCmeta)
spYCCmeta[1:5,1:6]
```

yeastCC

Data from the Spellman et al. (1998) yeast cell cycle microarray experiment

Description

This data package contains an [ExpressionSet](#) instance for the yeast cell cycle microarray experiment. The dataset contains gene expression measures (log-ratios, with Cy3-labeled common reference) for 6,178 yeast genes in 77 conditions.

Usage

```
data(yeastCC)
```


Details

There are four main timecourses: alpha (alpha factor arrest), cdc15, cdc28, and elu (elutriation), corresponding to different synchronization methods. For details on experimental procedures and analysis, refer to Spellman et al. (1998) (in `../doc`) and the Yeast Cell Cycle Analysis Project website (<http://genome-www.stanford.edu/cellcycle/>). The `ExpressionSet` instance `yeastCC` was derived from the file "combined.txt" on the website. The ORF names for the 800 cell cycle regulated genes are stored in `orf800`.

Source

The raw data (images, TIFF) and processed data "combine.txt" used to create the `ExpressionSet` instance `yeastCC` are available from the Yeast Cell Cycle Analysis Project website (<http://genome-www.stanford.edu/cellcycle/>). Gene annotation information is available from the Saccharomyces Genome Database (SGD, http://genome-www.stanford.edu/Saccharomyces/gene_list.shtml). The script "createYeastCC.R" for generating the `yeastCC` package is available in `../doc`.

Note that `spYCCES` is an `ExpressionSet` instance with the same data and slightly different phenodata annotation.

References

Spellman et al. (1998). Comprehensive Identification of Cell Cycle-regulated Genes of the Yeast *Saccharomyces cerevisiae* by Microarray Hybridization. *Molecular Biology of the Cell*, 9: 3273-3297.

Examples

```
data(yeastCC)
yeastCC
varLabels(yeastCC)
pData(yeastCC)
description(yeastCC)
abstract(yeastCC)
featureNames(yeastCC)[1:10]
dim(exprs(yeastCC))
```

Index

*Topic **datasets**

- breeden, [1](#)
- orf800, [4](#)
- spYCCmeta, [5](#)
- yeastCC, [8](#)

breeden, [1](#)

ExpressionSet, [4](#), [8](#), [9](#)

orf800, [4](#), [9](#)

spYCCES (*yeastCC*), [8](#)

spYCCmeta, [5](#)

yeastCC, [4](#), [8](#)