

Intro to the *HumanAffyData* experimental data package

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1 Introduction

HumanAffyData is a re-analysis of human gene expression data generated on the Affymetrix HG_U133PlusV2 (EH176) and Affymetrix HG_U133A (EH177) platforms, provide as *ExpressionSet* objects. The original data were normalized using robust multiarray averaging (RMA) to obtain an integrated gene expression atlas across diverse biological sample types and conditions. The entire compendia comprise 9395 arrays for EH176 and 5372 arrays for EH177. It is intended to be used as a starting point for gene co-expression analysis, or as a resource to quickly examine where a gene is expressed from within the R environment.

EH176: the original data were gathered by [1] and normalized using robust multiarray averaging (RMA). The `phenoData` of the *ExpressionSet* object contains the title and description of the source entries on GEO.

EH177: the original data were gathered by [2] and normalized using robust multiarray averaging (RMA). [2] manually curated the dataset to establish uniform phenotypic information for each sample, which is available in the `phenoData` of the *ExpressionSet* object. This data is accesible on ArrayExpress under accession [E-MTAB-62](#). The RMA-normalized expression values were then adjusted to reduce the influence of technical bias (i.e. variation in hybridization conditions or starting material) using the R package *bias 0.0.3* [3]. Finally, probesets were mapped to Entrez gene identifiers using the *Bioconductor* annotation package [hgu133a.db](#), and values for probesets mapping to the same gene were averaged to produce a single expression measurement for each gene.

2 Dataset overview

First, access the HumanAffyData from ExperimentHub:

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```
> library(ExperimentHub)
> hub <- ExperimentHub()
> x <- query(hub, "HumanAffyData")
> x

ExperimentHub with 2 records
# snapshotDate(): 2026-04-23
# $dataproducer: GEO, ArrayExpress
# $species: Homo sapiens
# $rdaclass: ExpressionSet
# additional mcols(): taxonomyid, genome, description,
#   coordinate_1_based, maintainer, rdatadateadded, preparerclass, tags,
#   rdatapath, sourceurl, sourcetype
# retrieve records with, e.g., 'object[["EH176"]]'

      title
EH176 | GEO accession data GSE64985 as an ExpressionSet
EH177 | ArrayExpress accession data E-MTAB-62 as an ExpressionSet
```

Data can then be extracted using:

```
> E.MTAB.62 <- x[["EH177"]]
```

This downloads the EH177 dataset, which contains an *ExpressionSet* object containing expression data from ArrayExpress accession E-MTAB-62:

```
> E.MTAB.62

ExpressionSet (storageMode: lockedEnvironment)
assayData: 12496 features, 5372 samples
  element names: exprs
protocolData: none
phenoData
  sampleNames: GSM23227.CEL 1229968152.CEL ... 676426699.CEL (5372
    total)
  varLabels: OperatorVariation DataSource ... ArrayDataFile (16 total)
  varMetadata: labelDescription
featureData: none
experimentData: use 'experimentData(object)'
Annotation: hgu133a
```

The experiment data can be extracted using the `exprs` function:

```
> data <- exprs(E.MTAB.62)
> dim(data)

[1] 12496 5372

> data[1:5,1:5]

      GSM23227.CEL 1229968152.CEL GSM133626.CEL GSM47465.CEL GSM124909.CEL
5982      8.055513      7.431500      8.222138      7.757324      7.660949
3310      6.444028      6.639300      6.652987      6.716288      6.509133
7849      6.403596      6.447042      7.294512      6.506119      6.309392
```

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2978	5.460372	5.363735	5.454068	5.496320	5.272762
7318	6.293562	7.422237	7.540636	7.433086	6.893468

This results in a matrix of expression data with the column names indicating the Array Data File name of each sample, and the rownames providing the human Entrez IDs of each gene.

Similarly, the phenotype data can be extracted using the `pData` function:

```
> pDat <- pData(E.MTAB.62)
> print(summary(pDat))
```

OperatorVariation	DataSource	Groups_4
Justin,,Lamb : 324	GSE5258 : 324	cell line:1259
Milton,W,Taylor : 308	GSE7123 : 308	disease : 765
Roel,,Verhaak : 284	GSE1159 : 284	neoplasm :2315
Benjamin,,Haibe-Kains: 273	GSE4475 : 213	normal :1033
Michael,,Hummel : 213	E-AFMX-6: 195	
Angela,,Hodges : 195	GSE2990 : 167	
(Other) :3775	(Other) :3881	

Groups_15
solid tissue neoplasm cell line: 831
breast cancer : 672
leukemia : 567
normal solid tissue : 566
normal blood : 467
blood non neoplastic disease : 388
(Other) :1881

Groups_369	BloodNonBloodmetagroups
breast cancer : 672	blood :1922
mononuclear cell infection : 314	non blood:3450
acute myeloid leukemia : 295	
B-cell lymphoma : 213	
MCF7 breast epithelial adenocarcinoma: 213	
mononuclear cell : 143	
(Other) :3522	

Organism	OrganismPart
Homo sapiens:5369	blood :1089
Mus musculus: 3	mammary gland:1033
	bone marrow : 733
	: 287
	lung : 286
	brain : 166
	(Other) :1778

CellType	CellLine
:3333	:4112
peripheral blood mononuclear cell: 452	mcf7 : 213
blast cell, mononuclear cell : 284	cultured: 88
CD138+ plasma cell : 142	pc3 : 64
Leukocyte : 107	k562 : 48
lymphocyte : 88	a549 : 30
(Other) : 966	(Other) : 817

DiseaseState	DevelopmentalStage
--------------	--------------------

```

                                :1274          :4816
breast cancer                   : 686  adult : 404
acute myeloid leukemia          : 322  embryo: 110
hepatitis c                     : 192  fetus : 42
diffuse large B-cell lymphoma: 160
breast tumor                    : 154
(Other)                         :2584

      DiseaseStage              Sex              Age
      :4236                    :3037              :4681
primary      : 500  female      :1016  10 days to 12 days: 23
aggressive   : 141  hermaphrodite: 4  69              : 18
grade 2      : 74  male          :1272  62              : 17
lymph node metastasis: 59  mixed sex : 9  65              : 17
grade 1      : 39  unknown sex : 34  61              : 15
(Other)      : 323              (Other)      : 601

      ArrayDataFile
1102960533.CEL: 1
1102960569.CEL: 1
1102960602.CEL: 1
1102960632.CEL: 1
1102960664.CEL: 1
1102960695.CEL: 1
(Other)      :5366

```

The pheontypic data contains several "meta groups", labeled as "Groups_4", "Groups_15", and "Groups_369". These are curated labels that group samples from a particular tissue, cell line, disease status, etc. The meta groups are explained further in [2]. [2] also discuss a "96 meta group" category, which is simply any members of the "369 meta groups" that contain at least 10 samples. The "96 meta groups" category can be re-created from the phenotypic data as follows:

```

> Groups_96 <- as.character(pDat$Groups_369)
> Groups_96[Groups_96 %in% names(which(table(pDat$Groups_96) < 10))] <- ''
> pDat$Groups_96 <- as.factor(Groups_96)

```

3 Citation

```
> citation("HumanAffyData")
```

Please cite Engreitz, et al. (2010) for the EH176 dataset and Lukk, et al. (2010) for the EH177 dataset:

Engreitz JM, Daigle BJ Jr, Marshall JJ, Altman RB. Independent component analysis: mining microarray data for fundamental human gene expression modules. *J Biomed Inform* 2010, 43(6):932-44.

Lukk M, Kapushesky M, Nikkila J, Parkinson H, Goncalves A, Huber W, Ukkonen E, Brazma A. A global map of human gene expression. *Nat Biotechnol* 2010, 28(4):322-324.

```
Brad Nelms (2016). _HumanAffyData experimental data package_. R  
package version 1.39.0,  
<https://www.bioconductor.org/packages/release/data/experiment/html/HumanAffyData.html>.
```

```
To see these entries in BibTeX format, use 'print(<citation>,  
bibtex=TRUE)', 'toBibtex(.)', or set  
'options(citation.bibtex.max=999)'.
```

References

- [1] Jesse M. Engreitz, Bernie J. Daigle, Jonathan J. Marshall, and Russ B. Altman. Independent component analysis: Mining microarray data for fundamental human gene expression modules. *Journal of Biomedical Informatics*, 43(6):932–944, dec 2010. URL: <http://dx.doi.org/10.1016/j.jbi.2010.07.001>, doi:10.1016/j.jbi.2010.07.001.
- [2] Margus Lukk, Misha Kapushesky, Janne Nikkilä, Helen Parkinson, Angela Goncalves, Wolfgang Huber, Esko Ukkonen, and Alvis Brazma. A global map of human gene expression. *Nature Biotechnology*, 28(4):322–324, 2010. URL: <http://dx.doi.org/10.1038/nbt0410-322>, doi:10.1038/nbt0410-322.
- [3] Aron C Eklund and Zoltan Szallasi. Correction of technical bias in clinical microarray data improves concordance with known biological information. *Genome Biology*, 9(2):R26, 2008. URL: <http://dx.doi.org/10.1186/gb-2008-9-2-r26>, doi:10.1186/gb-2008-9-2-r26.