

# Package ‘miRada’

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**Title** MicroRNA Microarray Data Analysis

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**Depends** R (>= 2.10.0), stats

**Description** This package collects algorithms/functions developed for microRNA profiling data analyses. Analytical platforms include traditional hybridization microarray, CGH, beads-based microarray, and qRT-PCR array.

**License** GPL (>= 2)

**Repository** CRAN

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birth *Birth data*

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### Description

Birth data for singleton live births with gestational age at least 38 weeks.

### Usage

`data(birth)`

### Format

A data frame with 28435 observations on 12 variables.

Year	numeric	2006 – 2009
Sex	character	'male' or 'female'
Live.Still	factor	'liveborn' or 'stillborn'
Plurality	numeric	'singleton' or others
Gestation	numeric	Gestational age (in weeks).
Weight	numeric	birth weight.
Length	numeric	height.
Head	numeric	head size.
Chest	numeric	chest size.
Mother.s.age	numeric	chest size.
type	factor	'r' = rural or 'u' = urban.
region	factor	region of the birth.

### References

Wang, B. and Wertelecki, W. (2012) "Density Estimation for Data With Rounding Errors", Computational Statistics and Data Analysis, (in press). doi: 10.1016/j.csda.2012.02.016. link

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CXCR

*Clinical relevance of CXCL12/CXCR4 and Hedgehog*

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### Description

Determine the clinical relevance of CXCL12/CXCR4 and Hedgehog interaction in pancreatic cancer.

### Usage

`data(CXCR)`

**Format**

Three small data set: *cxcr4*, *cxcr7*, and *shh*.

**References**

Sanjeev K. Srivastava , Arun Bhardwaj , Seema Singh , Sumit Arora , Bin Wang , William E. Grizzle and Ajay P. Singh (2011) "MicroRNA-150 directly targets MUC4 and suppresses growth and malignant behavior of pancreatic cancer cells", *Carcinogenesis*, doi:10.1093/carcin/bgr223. (PMID 21983127).

Arora S., Bhardwaj A., Srivastava S.K., Singh S., McClellan S., Wang B., Singh A.P. (2011) "Honokiol arrests cell cycle, induces apoptosis and potentiates the cytotoxic effects of gemcitabine in human pancreatic cancer cells", *PLoS One*, 6 (6), e21573.

**Examples**

```
data(CXCR)
shh
```

---

 illuRNA

*A sample data of two-color microarray*

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**Description**

CGH microarray.

**Usage**

```
data(illuRNA)
```

**Format**

A data frame with 44495 rows and 19 columns (variables).

Class type: *illRNA*, data name is *rna4*.

**References**

Wang, B., Zhang, S-G., Wang, X-F., Tan, M. and Xi, Y. (2012) "Testing for differentially-expressed microRNAs with errors-in-variables nonparametric regression", *PLoS ONE* 7(5): e37537. doi:10.1371/journal.pone.0037537

Wang, B., Wang, X-F. and Xi, Y. (2011) "Normalizing bead-based microRNA expression data: a measurement error model-based approach", *Bioinformatics*, 27(11), 1506-1512.

Wang, B., Howell, P., Bruheim, S. Ju, J, Owen, L.B., Fodstad, O. and Xi, Y. (2011). "Systematic Evaluation of Three microRNA Profiling Platforms: Microarray, Beads Array, and Quantitative Real-Time PCR Array", *PLoS ONE* 6(2): e17167.

Wang, B. and Wertelecki, W. (2012) "Density Estimation for Data With Rounding Errors", *Computational Statistics and Data Analysis*, (in press). doi: 10.1016/j.csda.2012.02.016. link

Wang, B., Wang, X-F. and Xi, Y. (2011) "Normalizing bead-based microRNA expression data: a measurement error model-based approach", *Bioinformatics*, 27(11), 1506-1512.

Wang, X-F. and Wang, B. (2011) "Deconvolution Estimation in Measurement Error Models: The R Package *decon*", *Journal of Statistical Software*, 39(10), 1-24.

### Examples

```
data(illuRNA)
```

---

miRada

*Algorithms for MicroRNA Microarray Data Analyses*

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### Description

This package collects measurement error model-based algorithms for microRNA/RNA microarray data analyses.

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ofc

*occipitofrontal head circumference data*

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### Description

OFC data for singleton live births with gestational age at least 38 weeks.

### Usage

```
data(ofc)
```

### Format

A data frame with 2019 observations on 4 variables.

Year	numeric	2006 – 2009
Sex	character	'male' or 'female'
Gestation	numeric	Gestational age (in weeks).
Head	numeric	head size.

### References

Wang, B. and Wertelecki, W. (2012) "Density Estimation for Data With Rounding Errors", *Computational Statistics and Data Analysis*, (in press). doi: 10.1016/j.csda.2012.02.016. link

OX40Exiqon

*A sample data of Exiqon microRNA microarray***Description**

A sample microRNA expression profiling data using miRCURY LNA microRNA Array based on miRbase 9.2 (Exiqon Inc., Denmark) for 40 human osteosarcoma xenograft specimens, including 10 samples for each chemotherapeutic treatment (Cisplatin, Doxorubicin, and Ifosfamide) plus 10 non-treated samples.

**Usage**

```
data(OX40Exiqon)
```

**Format**

A data frame with 168192 rows and 7 columns (variables).

Gene	character	MicroRNA names.
Flag	numeric	an indicator showing the probe signal quality.
Repeat	numeric	an indicator showing the technical replicates.
Treat	numeric	treatment type: coded.
Sample	numeric	sample id.
Signal	numeric	fluorescence intensity measures
Background	numeric	measures of background noises

**References**

- Wang, B., Zhang, S-G., Wang, X-F., Tan, M. and Xi, Y. (2012) "Testing for differentially-expressed microRNAs with errors-in-variables nonparametric regression", PLoS ONE 7(5): e37537. doi:10.1371/journal.pone.0037537
- Wang, B., Wang, X-F. and Xi, Y. (2011) "Normalizing bead-based microRNA expression data: a measurement error model-based approach", Bioinformatics, 27(11), 1506-1512.
- Wang, B., Howell, P., Bruheim, S. Ju, J, Owen, L.B., Fodstad, O. and Xi, Y. (2011). "Systematic Evaluation of Three microRNA Profiling Platforms: Microarray, Beads Array, and Quantitative Real-Time PCR Array", PLoS ONE 6(2): e17167.
- Wang, B. and Wertenlecker, W. (2012) "Density Estimation for Data With Rounding Errors", Computational Statistics and Data Analysis, (in press). doi: 10.1016/j.csda.2012.02.016. link
- Wang, B., Wang, X-F. and Xi, Y. (2011) "Normalizing bead-based microRNA expression data: a measurement error model-based approach", Bioinformatics, 27(11), 1506-1512.
- Wang, X-F. and Wang, B. (2011) "Deconvolution Estimation in Measurement Error Models: The R Package decon", Journal of Statistical Software, 39(10), 1-24.

**Examples**

```
data(OX40Exiqon)
ex = structure(list(x = ox40ex92), class='exiqon')
print(ex)
```

---

OX40Luminex

*A sample data of beads based microRNA microarray*


---

## Description

A sample data of Luminex beads based microRNA microarray.

## Usage

```
data(OX40Luminex)
```

## Format

A data frame with 3640 rows and 8 columns (variables).

Gene	character	MicroRNA names.
Treat0	numeric	measures under treatment with code '0'
Treat1	numeric	measures under treatment with code '1'
Treat2	numeric	measures under treatment with code '2'
Treat3	numeric	measures under treatment with code '3'
Background	numeric	measures of background noises
Sample	numeric	sample id.
Pool	numeric	Pool id.

An object `lum` of class `luminx`.

## References

- Wang, B., Zhang, S-G., Wang, X-F., Tan, M. and Xi, Y. (2012) "Testing for differentially-expressed microRNAs with errors-in-variables nonparametric regression", *PLoS ONE* 7(5): e37537. doi:10.1371/journal.pone.0037537
- Wang, B., Wang, X-F. and Xi, Y. (2011) "Normalizing bead-based microRNA expression data: a measurement error model-based approach", *Bioinformatics*, 27(11), 1506-1512.
- Wang, B., Howell, P., Bruheim, S. Ju, J, Owen, L.B., Fodstad, O. and Xi, Y. (2011). "Systematic Evaluation of Three microRNA Profiling Platforms: Microarray, Beads Array, and Quantitative Real-Time PCR Array", *PLoS ONE* 6(2): e17167.
- Wang, B. and Wertelecki, W. (2012) "Density Estimation for Data With Rounding Errors", *Computational Statistics and Data Analysis*, (in press). doi: 10.1016/j.csda.2012.02.016. link
- Wang, B., Wang, X-F. and Xi, Y. (2011) "Normalizing bead-based microRNA expression data: a measurement error model-based approach", *Bioinformatics*, 27(11), 1506-1512.

Wang, X-F. and Wang, B. (2011) "Deconvolution Estimation in Measurement Error Models: The R Package decon", Journal of Statistical Software, 39(10), 1-24.

### Examples

```
data(OX40Luminex)
```

---

OX40Qpcr

*qRT-PCR results*

---

### Description

The qRT-PCR microRNA microarray profiles for 10 samples under four different treatments.

### Usage

```
data(OX40Qpcr)
```

### Format

A data frame with 27000 rows and 6 columns (variables).

Sample	numeric	sample id.
Treat	numeric	codes of treatments: 0,1,2,3.
Gene	character	MicroRNA names.
dCT	numeric	delta Ct values.
ddCt	numeric	delta delta Ct values.
RQ	numeric	$RQ = 2^{(-ddCt)}$ .

An object qpcr of class qrtpcr.

### References

Wang, B., Wang, X-F. and Xi, Y. (2011) "Normalizing bead-based microRNA expression data: a measurement error model-based approach", Bioinformatics, 27(11), 1506-1512.

Wang, B., Howell, P., Bruheim, S. Ju, J, Owen, L.B., Fodstad, O. and Xi, Y. (2011). Systematic Evaluation of Three microRNA Profiling Platforms: Microarray, Beads Array, and Quantitative Real-Time PCR Array, PLoS ONE 6(2): e17167.

### Examples

```
data(OX40Qpcr)
```

---

robot

*Robot surgery.*

---

### **Description**

Robot surgery results.

### **Usage**

```
data(robot)
```

### **Format**

A data frame with 388 rows and 111 columns (variables).

### **References**

de Leval, M. R., Francois, K., Bull, C., Brawn, W., Spiegelhalter, D., Mar 1994. Analysis of a cluster of surgical failures. Application to a series of neonatal arterial switch operations. *J. Thorac. Cardiovasc. Surg.* 107, 914–923.

Page, E. S., 1954. Continuous inspection schemes. *Biometrika* 41 (1/2), pp. 100–115. URL <http://www.jstor.org/stable/2333009>

Parsonnet, V., Dean, D., Bernstein, A. D., Jun 1989. A method of uniform stratification of risk for evaluating the results of surgery in acquired adult heart disease. *Circulation* 79, 3–12.

Steiner, S. H., Cook, R. J., Farewell, V. T., Jan 1999. Monitoring paired binary surgical outcomes using cumulative sum charts. *Stat Med* 18, 69–86.

Steiner, S. H., Cook, R. J., Farewell, V. T., Treasure, T., Dec 2000. Monitoring surgical performance using risk-adjusted cumulative sum charts. *Biostatistics* 1, 441–452.

### **Examples**

```
data(robot)  
dim(robot)
```



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